

Pacific Symposium on Biocomputing 2019

January 3-7, 2019

Big Island of Hawaii

Program Book



PACIFIC SYMPOSIUM ON BIOCOMPUTING 2019

Big Island of Hawaii, January 3-7, 2019

Welcome to PSB 2019!

We have prepared this program book to give you quick access to information you need for PSB 2019.

Enclosed you will find:

- Logistics information
- Menus for PSB hosted meals
- Full conference schedule
- Call for Session and Workshop Proposals for PSB 2020
- Poster/abstract titles and authors
- Participant List

Conference materials are also available online at <http://psb.stanford.edu/conference-materials/>.

PSB 2019 gratefully acknowledges the support of the Cleveland Institute for Computational Biology, Second Genome, Icahn Institute for Data Science and Genomic Technology, CIPHEROME, and DNANexus; the National Institutes of Health (NIH); and the International Society for Computational Biology (ISCB). If you or your institution are interested in sponsoring, PSB, please contact Tiffany Murray at psb.hawaii@gmail.com

If you have any questions, the PSB registration staff (Tiffany Murray, Kasey Miller, BJ Morrison-McKay, and Cindy Paulazzo) are happy to help you.

Aloha!

Russ Altman
Keith Dunker
Larry Hunter
Teri Klein
Maryln Ritchie

The PSB 2019 Organizers

PACIFIC SYMPOSIUM ON BIOCOMPUTING 2019

Big Island of Hawaii, January 3-7, 2019

SPEAKER INFORMATION

Oral presentations of accepted proceedings papers will take place in Salon 2 & 3. ***Speakers are allotted 10 minutes for presentation and 5 minutes for questions for a total of 15 minutes. Instructions for uploading talks were sent to authors with oral presentations.*** If you need assistance with this, please see Tiffany Murray or another PSB staff member.

POSTER INFORMATION

Please set up your poster upon arrival. Please use the easel marked with the same number that your poster abstract has been assigned in abstract book (e.g., if your abstract is on page 50 of the book, use the easel marked #50). Once your poster is displayed, please make sure that the number is still visible. ***Please remove your poster by 7:30pm, Sunday, January 6.***

The poster session is on Saturday, January 5 12:00-2:30.

12:30-1:30: Posters on ODD numbered boards presented.

1:30-2:30: Posters on EVEN numbered boards presented.

The poster session is centered around lunch. Please eat, talk, and network.

INTERNET CONNECTIVITY

Please help keep the PSB wireless network stable: Do not download large data files due to limited bandwidth.

PSB is connected to the Internet via a secure wireless network for the conference. For transferring your data/presentations or technical difficulties with the network, please see PSB IT/AV staff members Al Conde, Ryan Whaley, or Paul Murray.

To connect to the PSB wireless network, you will need to explicitly join the “PSB” SSID, and use the passphrase “orcpsb123” with WPA2-Personal security type and AES encryption.

PSB’s wireless Internet access (802.11b/g/n) is available in the Salons 1, 2, 3, the Plaza Ballroom, and the Ballroom Courtyard of the Fairmont Orchid.

PACIFIC SYMPOSIUM ON BIOCOMPUTING 2019

Big Island of Hawaii, January 3-7, 2019

PSB 2019 HOSTED RECEPTIONS & MEALS

Thursday, January 3

7:00-8:00pm 24th Anniversary Reception, Kilohana Room (near Concierge)
Sponsored by the Cleveland Institute for Computational Biology

Friday, January 4

7:30-8:45am Continental Breakfast, Ballroom Courtyard
12:00-1:00pm PSB Hosted Lunch, Ballroom Courtyard

Saturday, January 5

7:30-8:45am Continental Breakfast, Ballroom Courtyard
12:00-2:30pm Poster Session with Lunch, Salon 1 and Ballroom Courtyard

Sunday, January 6

7:30-8:45am Continental Breakfast, Ballroom Courtyard
5:30-7:15pm Dinner Banquet, Coconut Grove

Monday, January 7

7:30-8:30am Continental Breakfast, Ballroom Courtyard

If you would like to buy meal or dinner tickets for your guest/s, please see the PSB registration staff.

Meal tickets for Non-Participants/Guests

- All Meals: \$550 adults; \$275 children 6-12 years
- Banquet Ticket Only: \$150 adults; \$75 children 6-12 years
- Welcome Reception & Banquet Only: \$180 adults; \$85 children 6-12 years

Please remember to wear your PSB nametag & lanyard at all PSB functions.

Enjoy the conference!

Pacific Symposium on Biocomputing 2019
Hosted Meals Menus

Thursday, January 3, 2019

Welcome Reception (7:00-8:00pm)

Desserts, Beer & Wine, Coffee & Tea Service

Friday, January 4, 2019

Breakfast (7:30-8:45am)

Fresh Orange Juice, Guava Juice, Pineapple Juice
Selection of Sliced Seasonal Fruits
Island Fruit Breads, Freshly Baked Croissants, Danishes, Muffins
Assorted Sliced Bread, Bagels, Cream Cheese
Tropical Fruit Preserves, Butter
Selection of Dry Cereals, Muesli, Raisins, Brown Sugar, Skim Milk, 2% Milk, Soy Milk
Yogurt Bar with Assorted Fruit Yogurts, Mango, Strawberries, Bananas, Macadamia Nut Granola
Scrambled Eggs
Waimea Vegetarian Egg Scramble
Cherrywood Smoked Bacon
Portuguese Sausage
Artichoke & Red Bliss Potato
Regular, Decaffeinated Coffee & Fairmont Signature Teas

Lunch (12-1pm)

Freshly Tossed Kekela Farms Baby Greens with Garden Vegetables, Spiced Mac Nuts,
Caramelized Hilo Papaya & Ka'u Orange Vinaigrette
Garlic Soy Glazed Edamame
Li Hing Mui Pineapple Fruit Salad
Warm Soba Noodles, Charred Brussel Sprouts, Pickled Hamakua Mushrooms, Crispy Tofu
Furikake Seared Mahi Mahi, Lemongrass Emulsion
Korean Fried Chicken
Kim Chee & Vegetable Fried Rice
Chocolate Chip Macadamia Nut Pie
Mango Ginger Crisp with Raw Sugar Streusel
Freshly Brewed Iced Tea & Lemonade
Beer & Wine

Saturday, January 5, 2019

Breakfast (7:30-8:45am)

Orange Juice, Guava Juice & Pineapple Juice
Selection of Sliced Seasonal Fruits
Freshly Baked Croissant, Macadamia Nut Sticky Buns, Banana Nut Bread
Sweet Cream Butter & Tropical Fruit Preserves
Selection of Dry Cereals, Muesli, with Fat Free Milk, Soy Milk & Almond Milk, Raisins, Brown Sugar
Kohala Biscuit: Sausage, Egg, American Cheese (vegetarian option available)
Coffee, Decaffeinated Coffee & Fairmont Signature Teas

Poster Lunch (12-2:30pm)

Freshly Tossed Kekela Farms Baby Greens with Garden Vegetables, Spiced Mac Nuts, Caramelized Hilo Papaya & Ka'u Orange Vinaigrette

**Pacific Symposium on Biocomputing 2019
Hosted Meals Menus**

Mac 'n Cheese
Fresh Fruit
Taro & Maui Potato Chips
Toy Dogs: Wagyu Mini Dogs {& Vegetarian Option} Pretzel Buns, Pickle Relish, Hot Peppers, Onions,
Mustard, Ketchup, Salsa, Shredded Cheese, Paniolo Cowboy Chili
Ice Cream Bars
Freshly Brewed Iced Tea & Lemonade
Beer & Wine

Sunday, January 6, 2019

Breakfast (7:30-8:45am)

Orange, guava and pineapple juice
Sliced seasonal fresh island fruit
Malasadas: Plain and Cinnamon Sugar
Dry cereal and muesli, raisins, brown sugar, regular, 2% and skim milk
Paniolo Breakfast Wrap: Diced Portuguese Sausage, Scrambled Eggs & Monterey Jack Cheese
[vegetarian option available]
Royal Kona Blend Coffee, Royal Kona Blend Decaffeinated Coffee and Fairmont Specialty Teas

Dinner Banquet (5:30-7:15pm)

Fresh Baby Greens, Tomato Wedges, Cucumbers, Shaved Onions, Sliced Mushrooms, White
Balsamic Vinaigrette & Ranch Dressing
Waimea Tomato & Marinated Artichoke Salad
Big Island Style Ahi Poke with Crushed Kukui Nuts, Onions, Ogo, Shoyu, Sesame Oil & Sambal
Dim Sum Station - Char Siu Bao, Island Style Pot Stickers, Pork & Shrimp Siu Mai, Shrimp Har Gau, Soy-
Mustard Ponzu Sauce & Sweet Chili Sauce
Micro Steam Buns & Hoisin Kalua Pork
Furikake Seared Mahi Mahi, Lemongrass Emulsion
Imu-Style Cooked Kalua Pork
Roast Turkey with cranberry relish
Crispy Curry Tofu, Japanese Eggplant, Asparagus, Shiitake Mushrooms, Spinach with Thai Curry Sauce
Chef's Seasonal Vegetable
Crispy Fried Rice Cake, Hamakua Mushrooms & Kimchee
Dessert
Royal Kona Blend Regular & Decaffeinated Coffee & Fairmont Signature Teas
Complete open bar including cocktails, blended drinks, wine, beer, non-alcoholic drinks

Monday, January 7, 2019

Breakfast (7:30am-8:30am)

Orange Juice, Guava Juice & Pineapple Juice
Selection of Sliced Seasonal Fruits
Island Fruit Breads, Freshly Baked Croissants, Danishes, Muffins
Sweet Cream Butter & Tropical Fruit Preserves
Selection of Dry Cereals, Muesli, with Fat Free Milk, Soy Milk & Almond Milk, Raisins, Brown Sugar
Holualoa Croissant: Scrambled Eggs, Black Forest Ham, Swiss Cheese, Chives (vegetarian option
available)
Coffee, Decaffeinated Coffee & Fairmont Signature Teas

Pacific Symposium on Biocomputing (PSB) 2019 Schedule

January 3-7, 2019, Big Island of Hawaii

Thursday, January 3, 2019

Registration

7:30-9:30	Registration	Ballroom Prefunction
12:00-2:00	Registration	Ballroom Prefunction
7:00-8:00	Registration	Kilohana

Workshop

9:00-12:00	Merging Heterogeneous Data to Enable Knowledge Discovery Organizers: Tina Hernandez-Boussard, Michael Kahn	Salon 2&3
------------	--	-----------

Break

12:00-1:30	Lunch on own	
------------	--------------	--

Workshop

1:30-4:30	Translational informatics of population health: How large biomolecular and clinical datasets Organizers: Yves Lussier, Atul Butte, Jason Moore, Rong Chen, Haiquan Li	Salon 2&3
-----------	---	-----------

Break

4:30-7:00	Dinner on own	
-----------	---------------	--

Reception

7:00-8:00	24 th Anniversary Reception Sponsored by the Cleveland Institute for Computational Biology	Kilohana
-----------	--	----------

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

December 12, 2018

Pacific Symposium on Biocomputing (PSB) 2019 Schedule

January 3-7, 2019, Big Island of Hawaii

Friday, January 4, 2019

Registration

7:30-9:00	Registration	Ballroom Prefunction
10:30-11:30	Registration	Ballroom Prefunction
12:00-1:00	Registration	Ballroom Prefunction

Breakfast

7:30-8:45	PSB Breakfast	Ballroom Courtyard
-----------	---------------	--------------------

Welcome

8:30-8:40	Welcome	Salon 2&3
-----------	---------	-----------

Session 1

Salon 2&3

Pattern recognition in biomedical data: challenges in putting big data to work

Co-chairs: Shefali Setia Verma, Anurag Verma, Dokyoon Kim, Christian Darabos

8:40-8:50	Introduction
8:50-9:10	Invited Talk: Barbara Engelhardt
9:10-9:25	<i>The Effectiveness of Multitask Learning for Phenotyping with Electronic Health Records Data</i> <u>Daisy Yi Ding</u> , Chloe Simpson, Stephen Pfohl, Dave Kale, Kenneth Jung, Nigam Shah
9:25-9:40	<i>ODAL: A one-shot distributed algorithm to perform logistic regressions on electronic health records data from multiple clinical sites</i> Rui Duan, Mary Regina Boland, Jason Moore, <u>Yong Chen</u>
9:40-9:55	<i>PVC Detection Using a Convolutional Autoencoder and Random Forest Classifier</i> <u>Max Gordon</u> , Cranos Williams
9:55-10:10	<i>Removing Confounding Factors Associated Weights in Deep Neural Networks Improves the Prediction Accuracy for Healthcare Applications</i> <u>Haohan Wang</u> , Zhenglin Wu, Eric Xing
10:10-10:25	<i>DeepDom: Predicting protein domain boundary from sequence alone using stacked bidirectional LSTM</i> <u>Yuexu Jiang</u> , Duolin Wang, Dong Xu
10:25-10:40	<i>Res2s2aM: Deep residual network-based model for identifying functional noncoding SNPs in trait-associated regions</i> <u>Zheng Liu</u> , Yao Yao, Qi Wei, Benjamin Weeder, Stephen Ramsey

Break

10:40-10:50

Keynote

10:50-12:00	Informatics to understand and predict drug action Russ Altman with introduction by Steven Brenner	Salon 2&3
-------------	---	-----------

Lunch

12:00-1:00	PSB Hosted Lunch	Ballroom Courtyard
------------	------------------	--------------------

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

December 12, 2018

Pacific Symposium on Biocomputing (PSB) 2019 Schedule

January 3-7, 2019, Big Island of Hawaii

Friday, January 4, 2019 (continued)

Session 1 (continued)

Salon 2&3

- Pattern recognition in biomedical data: challenges in putting big data to work**
Co-chairs: Shefali Setia Verma, Anurag Verma, Dokyoon Kim, Christian Darabos
- 1:00-1:10 Introduction to second half of session
- 1:10-1:25 *Bi-directional Recurrent Neural Network Models for Geographic Location Extraction in Biomedical Literature*
Arjun Magge, Davy Weissenbacher, Abeed Sarker, Matthew Scotch, Graciela Gonzalez-Hernandez
- 1:25-2:40 *PLATYPUS: A Multiple-View Learning Predictive Framework for Cancer Drug Sensitivity Prediction*
Kiley Graim, Verena Friedl, Kathleen E. Houlahan, Joshua Stuart
- 2:40-2:55 *Computational KIR copy number discovery reveals interaction between inhibitory receptor burden and survival*
Rachel Pyke, Raphael Genolet, Alexandre Harari, George Coukos, David Gfeller, Hannah Carter
- 2:55-3:10 *Implementing and Evaluating A Gaussian Mixture Framework for Identifying Gene Function from TnSeq Data*
Kevin Li, Rachel Chen, William Lindsey, Aaron Best, Matthew DeJongh, Christopher Henry, Nathan Tintle
- 3:10-3:25 *Extracting allelic read counts from 250,000 human sequencing runs in Sequence Read Archive*
Brian Tsui, Michelle Dow, Dylan Skola, Hannah Carter
- 3:25-3:40 *Semantic workflows for benchmark challenges: Enhancing comparability, reusability and reproducibility*
Arunima Srivastava, Ravali Adusumilli, Hunter Boyce, Daniel Garijo, Varun Ratnakar, Rajiv Mayani, Thomas Yu, Raghu Machiraju, Yolanda Gil, Parag Mallick
-

Discussion Session

Salon 2&3

- 3:40-4:40 **Pattern recognition in biomedical data: challenges in putting big data to work**
-

Working Group Meeting (all invited)

Salon 2&3

- 4:45-6:00 **Writing bio-computational manuscripts with Manubot**
Organizer: Daniel Himmelstein
Manubot is an open source tool for writing manuscripts on GitHub in markdown format. Attendees are encouraged to bring a laptop if they would like assistance setting up a manuscript during the last 40 minutes of the workshop.
-

Break

- 6:00- Dinner & Evening on own
-

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

December 12, 2018

Pacific Symposium on Biocomputing (PSB) 2019 Schedule

January 3-7, 2019, Big Island of Hawaii

Saturday, January 5, 2019

Registration		Ballroom Prefunction
7:30-8:30	Registration	
Breakfast		Ballroom Courtyard
7:30-8:45	PSB Breakfast	
Announcements		Salon 2&3
8:30-8:40	Morning Announcements	
TERI Talks		Salon 2&3
8:40-9:10	Dennis Wall, Stanford University	
9:10-9:40	Marylyn Ritchie, University of Pennsylvania	
Session 2		Salon 2&3
	When biology gets personal: hidden challenges of privacy and ethics in biological big data	
	Co-chairs: Gamze Gürsoy, Arif Harmanci, Haixu Tang, Erman Ayday, Steven Brenner	
9:45-9:55	Introduction	
9:55-10:15	Invited Talk: Greg Hampikian	
10:15-10:30	<i>Leveraging summary statistics to make inferences about complex phenotypes in large biobanks</i>	
	Angela Gasdaska, Derek Friend, Rachel Chen, Jason Westra, Matthew Zawistowski, William Lindsey, <u>Nathan Tintle</u>	
10:30-10:45	<i>Protecting Genomic Data Privacy with Probabilistic Modeling</i>	
	<u>Sean Simmons</u> , Bonnie Berger, Cenk Sahinalp	
10:45-11:00	<i>Evaluation of patient re-identification using laboratory test orders and mitigation via latent space variables</i>	
	Kipp Johnson, <u>Jessica De Freitas</u> , Benjamin Glicksberg, Jason Bobe, Joel Dudley	
Discussion Session		Salon 2&3
11:00-12:00	When biology gets personal: hidden challenges of privacy and ethics in biological big data	
Poster Session Lunch		Salon 1 and Ballroom Courtyard
12:00-2:30	Poster Session with Lunch (Posters on ODD numbered boards presented from 12:30-1:30) (Posters on EVEN numbered boards presented from 1:30-2:30)	
Workshop		Salon 2&3
2:30-5:30	Text Mining and Machine Learning for Precision Medicine Organizers: Graciela Gonzalez, Hongfang Liu, Zhiyong Lu, Robert Leaman	
Meeting		Salon 2&3
5:30-6:00	ISCB Meeting	
Break		
6:00-	Dinner & Evening on own	

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

December 12, 2018

Pacific Symposium on Biocomputing (PSB) 2019 Schedule

January 3-7, 2019, Big Island of Hawaii

Sunday, January 6, 2019

Breakfast Ballroom Courtyard

7:30-8:45 PSB Breakfast

Announcements Salon 2&3

8:30-8:40 Morning Announcements

Session 3 Salon 2&3

Precision medicine: improving health through high-resolution analysis of personal data

Co-chairs: Steven Brenner, Martha Bulyk, Dana Crawford, Jill Mesirov, Alexander Morgan, Predrag Radivojac

8:40-8:50 Introduction

8:50-9:10 Invited Talk: John Witte

9:10-9:25 *CrowdVariant: a crowdsourcing approach to classify copy number variants*
Peyton Greenside, Justin Zook, Marc Salit, Madeleine Cule, Ryan Poplin, Mark DePristo

9:25-9:40 *A repository of microbial marker genes related to human health and diseases for host phenotype prediction using microbiome data*
Wontack Han, Yuzhen Ye

9:40-9:55 *AICM: A Genuine Framework for Correcting Inconsistency Between Large Pharmacogenomics Datasets*

Zhiyue Tom Hu, Yuting Ye, Patrick A. Newbury, Haiyan Huang, Bin Chen
9:55-10:10 *Outgroup Machine Learning Approach Identifies Single Nucleotide Variants in Noncoding DNA Associated with Autism Spectrum Disorder*
Maya Varma, Kelley Marie Paskov, Jae-Yoon Jung, Brianna Sierra
Chrisman, Nate Tyler Stockham, Peter Yigitcan Washington, Dennis Paul Wall

10:10-10:25 *Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network*

Xinyuan Zhang, Yogasudha Veturi, Shefali Verma, William Bone, Anurag Verma, Anastasia Lucas, Scott Hebring, Joshua C. Denny, Ian Stanaway, Gail Jarvik, David Crosslin, Eric Larson, Laura Rasmussen-Torvik, Sarah A. Pendergrass, Jordan W. Smoller, Hakon Hakonarson, Patrick Sleiman, Chunhua Weng, David Fasel, Wei-Qi Wei, Iftikhar Kullo, Daniel Schaid, Wendy Chung, Marylyn Ritchie

10:25-10:40 *Integrating RNA expression and visual features for immune infiltrate prediction*

Derek Reiman, Lingdao Sha, Irvin Ho, Timothy Tan, Denise Lau, Aly Khan

10:40-10:55 *Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms*
Francesca Vitali, Joanne Berghout, Jungwei Fan, Jianrong Li, Qike Li, Haiquan Li, Yves Lussier

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

December 12, 2018

Pacific Symposium on Biocomputing (PSB) 2019 Schedule

January 3-7, 2019, Big Island of Hawaii

Sunday, January 6, 2019 (continued)

Session 3 (continued)		Salon 2&3
10:55-11:10	<i>An Optimal Policy for Patient Laboratory Tests in Intensive Care Units</i> Li-Fang Cheng, Niranjani Prasad, Barbara Engelhardt	
Discussion Session		Salon 2&3
11:10-12:10	Precision medicine: improving health through high-resolution analysis of personal data	
Break		
12:10-1:30	Lunch on Own	
Workshop		Salon 2&3
1:30-4:30	Reading between the genes: interpreting non-coding DNA in high-throughput Organizers: Joanne Berghout, Yves Lussier, Francesca Vitali, Martha Bulyk, Maricel Kann, Jason Moore	
Special Topics		
4:30-5:00	Parasite & Symbiont Awards	Salon 2&3
Break		
5:00-5:30	Break	
Dinner		Coconut Grove
5:30-7:15	PSB Dinner Banquet	
Keynote		Salon 2&3
7:30-8:30	Sex, Race, Nature, Genomics & AI: A values-laden hour in Hawaii Lawrence Hunter with introduction by Russ Altman	

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

December 12, 2018

Pacific Symposium on Biocomputing (PSB) 2019 Schedule

January 3-7, 2019, Big Island of Hawaii

Monday, January 7, 2019

Breakfast		Ballroom Courtyard
7:30-8:30	Breakfast	
Closing		Salon 2&3
8:30-8:40	Closing Announcements	
TERI Talks		Salon 2&3
8:40-9:10	Graciela Gonzalez, University of Pennsylvania	
9:10-9:40	Keith Dunker, University of Indiana	
Session 4		Salon 2&3
	Single cell analysis, what is in the future?	
	Co-chairs: Lana X. Garmire, Guo-Cheng Yuan, Rong Fan, Gene Yeo, John Quackenbush	
9:45-9:55	Introduction	
9:55-10:15	Invited Talk: Zemin Zhang	
10:15-10:30	<i>LISA: Accurate reconstruction of cell trajectory and pseudo-time for massive single cell RNA-seq data</i> Yang Chen, Yuping Zhang, <u>Zhengqing Ouyang</u>	
10:30-10:45	<i>Topological Methods for Visualization and Analysis of High Dimensional Single-Cell RNA Sequencing Data</i> <u>Tongxin Wang</u> , Travis Johnson, Jie Zhang, Kun Huang	
10:45-11:00	<i>Parameter tuning is a key part of dimensionality reduction via deep variational autoencoders for single cell RNA transcriptomics</i> <u>Qiwen Hu</u> , Casey Greene	
Discussion Session		Salon 2&3
11:00-12:00	Single cell analysis, what is in the future?	

PSB over--see you next year!

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

December 12, 2018

Call for Session Proposals Pacific Symposium on Biocomputing

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

This is an invitation to submit proposals for sessions in the 25th Pacific Symposium on Biocomputing (PSB), to be held January 3-7, 2020 on the Kohala Coast, the Big Island of Hawaii. PSB will bring together top researchers from the US, the Asian Pacific nations and around the world to exchange research for the presentation of work in databases, algorithms, interfaces, natural language processing, modeling and other computational methods, as applied to biological problems, with emphasis on applications in data-rich areas of molecular biology.

PSB has been designed to be responsive to the need for critical mass in sub-disciplines within biocomputing. For that reason, it is the only meeting whose sessions are defined dynamically each year in response to specific proposals. PSB sessions are organized by leaders in the emerging areas and targeted to provide a forum for publication and discussion of research in biocomputing's "hot topics." In this way, PSB provides an early forum for serious examination of emerging methods and approaches in this rapidly changing field.

Proposals for such sessions are hereby solicited. A proposal should identify a coherent topic that can be addressed by 3 to 12 papers. For example, a session might bring together papers on alternative approaches to a particular biological question or it might examine the applications of a particular technology in a variety of biological areas. A sample of more than 20 different decisions at previous PSB meetings have included:

- Applications of Genetics, Genomics and Bioinformatics in Drug Discovery
- Challenges of Pattern Recognition in Biomedical Data
- Democratizing Health Data for Translational Research
- Imaging Genomics
- Precision Medicine: from diplotypes to disparities towards improved health and therapies
- Reading Between the Genes: Computational Models to Discover Function and/or Clinical Utility from Noncoding DNA
- Text Mining and Visualization for Precision Medicine

A major goal of PSB is to create productive interaction among the rather different research cultures of computer science and biology. Recognizing that many in the computational community believe the value of a meeting depends on the quality of its review process, every full manuscript submitted to PSB is reviewed by at least two anonymous reviewers, as well as the session organizers and meeting chairs. Accepted papers are distributed in a proceedings volume at the meeting and are indexed in Medline and other bibliographic databases. However, we also recognize that many potential participants, particularly from the biological community, do not choose to submit full papers to conferences, even with assurance of availability and broad indexing. Therefore, PSB also includes a separate open submission abstract book and open poster presentations in which any registrant can present research.

Responsibilities of a session chair

As a proposer of an accepted session, you will become the session chair. The chair's primary responsibility is to solicit high quality papers for the session, oversee the review, and write a tutorial introduction to your session. You are to solicit manuscripts, have them refereed, collaborate with the conference chairs in determining which manuscripts are to be accepted and structure presentation time in your session. Please contact us at the address below if you have any questions about the obligations entailed in becoming a session organizer.

**Call for Session Proposals
Pacific Symposium on Biocomputing**

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

Procedure for submitting proposals

Session proposals can be as short as a single page and should in no case be more than 6 pages. The proposal should:

- Define a specific technical area to be covered.
- Justify why the proposed area is appropriate for PSB. Discuss why the topic is timely and important, and how the topic has been addressed in other conferences or recent publications.
- Argue that there is likely to be sufficient high quality, unpublished material to fill the session, e.g., a list of researchers you intend to solicit for papers. If there are unlikely to be adequate paper submissions, consider applying for a PSB workshop instead.
- Provide a short autobiographical sketch and an explicit statement that your organization endorses your involvement.
- Proposals must be submitted online at <http://psb.wufoo.com/forms/psb-session-proposal-submission-form/>.

Important Dates

February 8, 2019	Proposals Due
March 8, 2019	Notification Regarding the Proposals

Each proposal will be evaluated by the organizing committee. We look forward to your submissions.

Questions? Please send email to

Lawrence Hunter, Ph.D.

Director, Center for Computational Pharmacology & Computational Bioscience Program
Professor of Pharmacology (Denver) & Computer Science (Boulder)
E-mail: larry.hunter@ucdenver.edu

Call for Workshop Proposals Pacific Symposium on Biocomputing

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

This is an invitation to submit proposals for workshops at the 25th Pacific Symposium on Biocomputing (PSB), to be held January 3-7, 2020 on the Kohala Coast, the Big Island of Hawaii. PSB will bring together top researchers from the US, the Asian Pacific nations and around the world to exchange research for the presentation of work in databases, algorithms, interfaces, natural language processing, modeling and other computational methods, as applied to biological problems, with emphasis on applications in data-rich areas of molecular biology.

We are soliciting proposals for three-hour workshops appropriate to the diverse PSB conference community. Workshops can include: panels of experts on emerging areas of computational biology that are not likely to attract the number of paper submissions required for a session; open discussions of topics important to the computational biology community; or other topics and formats. Workshops at previous PSB meetings have included:

- The Future of Genome-Based Medicine
- Modeling Cell Heterogeneity: from Single-Cell Variations to Mixed Cells Populations
- Training the Next Generation of Quantitative Biologists
- Uncovering the Etiology of Autism Spectrum Disorders: Genomics, Bioinformatics, Environment, Data Collection and Exploration, and Future Possibilities
- Diversity and Disparity in Biomedical Informatics
- Integrating Community-level Data Resources for Precision Medicine Research
- Machine Learning and Deep Analytics for Biocomputing: Call for Better Explainability
- Methods for Examining Data Quality in Healthcare Integrated Data Repositories

Responsibilities of a workshop chair

As a proposer of an accepted workshop, you will become the workshop chair. The chair's primary responsibility is to organize and preside over the presentations related to your workshop.

Procedure for submitting proposals

Proposals can be as short as a single page and should in no case be more than 6 pages. The proposal should:

- Define a specific technical area to be covered, and a format for the workshop.
- Justify why the proposed area is appropriate for PSB. Discuss why the topic is timely and important, and how the topic has been addressed in other conferences or recent publications. Describe why the proposed format is appropriate for the workshop.
- If the workshop proposes invited experts, provide evidence that the experts will attend the workshop. Participants are required to register for the conference, and, unlike sessions, no financial support from the conference is offered to workshop organizers. Emails from potential participants are sufficient.
- Provide a short autobiographical sketch and an explicit statement that your organization endorses your involvement.
- Proposals must be submitted online at <https://psb.wufoo.com/forms/psb-workshop-proposal-submission-form/>.

**Call for Workshop Proposals
Pacific Symposium on Biocomputing**

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

Important Dates

February 8, 2019 Proposals Due
March 8, 2019 Notification Regarding the Proposals

Each proposal will be evaluated by the organizing committee. We look forward to your submissions.

Questions? Please send email to

Lawrence Hunter, Ph.D.

Director, Center for Computational Pharmacology & Computational Bioscience Program
Professor of Pharmacology (Denver) & Computer Science (Boulder)
E-mail: larry.hunter@ucdenver.edu

**Abstract Book Table of Contents
and Author Index Only**

PACIFIC SYMPOSIUM ON BIOCOMPUTING 2019

ABSTRACT BOOK

Poster Presenters: Poster space is assigned by abstract page number. Please find the page that your abstract is on and put your poster on the poster board with the corresponding number (e.g., if your abstract is on page 50, put your poster on board #50).

Proceedings papers with oral presentations #2-29 are not assigned poster space.

Abstracts are organized first by session, then the last name of the first author. Presenting authors' names are in **bold** text.

TABLE OF CONTENTS

PROCEEDINGS PAPERS WITH ORAL PRESENTATION

PATTERN RECOGNITION IN BIOMEDICAL DATA: CHALLENGES IN PUTTING BIG DATA TO WORK

THE EFFECTIVENESS OF MULTITASK LEARNING FOR PHENOTYPING WITH ELECTRONIC HEALTH RECORDS DATA	2
<i>Daisy Yi Ding, Chloe Simpson, Stephen Pfohl, Dave C. Kale, Kenneth Jung, Nigam H. Shah</i>	
ODAL: A ONE-SHOT DISTRIBUTED ALGORITHM TO PERFORM LOGISTIC REGRESSIONS ON ELECTRONIC HEALTH RECORDS DATA FROM MULTIPLE CLINICAL SITES.....	3
<i>Rui Duan, Mary Regina Boland, Jason H. Moore, Yong Chen</i>	
PVC DETECTION USING A CONVOLUTIONAL AUTOENCODER AND RANDOM FOREST CLASSIFIER.....	4
<i>Max Gordon, Cranos Williams</i>	
PLATYPUS: A MULTIPLE-VIEW LEARNING PREDICTIVE FRAMEWORK FOR CANCER DRUG SENSITIVITY PREDICTION	5
<i>Kiley Graim, Verena Friedl, Kathleen E. Houlahan, Joshua M. Stuart</i>	
DEEPPDOM: PREDICTING PROTEIN DOMAIN BOUNDARY FROM SEQUENCE ALONE USING STACKED BIDIRECTIONAL LSTM	6
<i>Yuexu Jiang, Duolin Wang, Dong Xu</i>	
IMPLEMENTING AND EVALUATING A GAUSSIAN MIXTURE FRAMEWORK FOR IDENTIFYING GENE FUNCTION FROM TNSEQ DATA.....	7
<i>Kevin Li, Rachel Chen, William Lindsey, Aaron Best, Matthew DeJongh, Christopher Henry, Nathan Tintle</i>	
RES2S2AM: DEEP RESIDUAL NETWORK-BASED MODEL FOR IDENTIFYING FUNCTIONAL NONCODING SNPS IN TRAIT-ASSOCIATED REGIONS.....	8
<i>Zheng Liu, Yao Yao, Qi Wei, Benjamin Weeder, Stephen A. Ramsey</i>	
BI-DIRECTIONAL RECURRENT NEURAL NETWORK MODELS FOR GEOGRAPHIC LOCATION EXTRACTION IN BIOMEDICAL LITERATURE	9
<i>Arjun Magge, Davy Weissenbacher, Abeed Sarker, Matthew Scotch, Graciela Gonzalez-Hernandez</i>	
COMPUTATIONAL KIR COPY NUMBER DISCOVERY REVEALS INTERACTION BETWEEN INHIBITORY RECEPTOR BURDEN AND SURVIVAL.....	10
<i>Rachel M. Pyke, Raphael Genolet, Alexandre Harari, George Coukos, David Gfeller, Hannah Carter</i>	
SEMANTIC WORKFLOWS FOR BENCHMARK CHALLENGES: ENHANCING COMPARABILITY, REUSABILITY AND REPRODUCIBILITY.....	11
<i>Arunima Srivastava, Raval Adusumilli, Hunter Boyce, Daniel Garijo, Varun Ratnakar, Rajiv Mayani, Thomas Yu, Raghu Machiraju, Yolanda Gil, Parag Mallick</i>	
REMOVING CONFOUNDING FACTORS ASSOCIATED WEIGHTS IN DEEP NEURAL NETWORKS IMPROVES THE PREDICTION ACCURACY FOR HEALTHCARE APPLICATIONS	12
<i>Haohan Wang, Zhenglin Wu, Eric P. Xing</i>	

PRECISION MEDICINE: IMPROVING HEALTH THROUGH HIGH-RESOLUTION ANALYSIS OF PERSONAL DATA

AN OPTIMAL POLICY FOR PATIENT LABORATORY TESTS IN INTENSIVE CARE UNITS..... 14
*Li-Fang Cheng, **Niranjani Prasad**, Barbara E. Engelhardt*

CROWDVARIANT: A CROWDSOURCING APPROACH TO CLASSIFY COPY NUMBER VARIANTS 15
***Peyton Greenside**, Justin Zook, Marc Salit, Ryan Poplin, Madeleine Cule, Mark DePristo*

A REPOSITORY OF MICROBIAL MARKER GENES RELATED TO HUMAN HEALTH AND DISEASES FOR HOST PHENOTYPE PREDICTION USING MICROBIOME DATA..... 16
***Wontack Han**, Yuzhen Ye*

AICM: A GENUINE FRAMEWORK FOR CORRECTING INCONSISTENCY BETWEEN LARGE PHARMACOGENOMICS DATASETS 17
***Zhiyue Tom Hu**, Yuting Ye, Patrick A. Newbury, Haiyan Huang, Bin Chen*

INTEGRATING RNA EXPRESSION AND VISUAL FEATURES FOR IMMUNE INFILTRATE PREDICTION 18
*Derek Reiman, Lingdao Sha, Irvin Ho, Timothy Tan, Denise Lau, **Aly A. Khan***

OUTGROUP MACHINE LEARNING APPROACH IDENTIFIES SINGLE NUCLEOTIDE VARIANTS IN NONCODING DNA ASSOCIATED WITH AUTISM SPECTRUM DISORDER 19
***Maya Varma**, Kelley Marie Paskov, Jae-Yoon Jung, Brianna Sierra Chrisman, Nate Tyler Stockham, Peter Yigitcan Washington, Dennis Paul Wall*

PRECISION DRUG REPURPOSING VIA CONVERGENT eQTL-BASED MOLECULES AND PATHWAY TARGETING INDEPENDENT DISEASE-ASSOCIATED POLYMORPHISMS 20
***Francesca Vitali**, Joanne Berghout, Jungwei Fan, Jianrong Li, Qike Li, Haiquan Li, Yves A. Lussier*

DETECTING POTENTIAL PLEIOTROPY ACROSS CARDIOVASCULAR AND NEUROLOGICAL DISEASES USING UNIVARIATE, BIVARIATE, AND MULTIVARIATE METHODS ON 43,870 INDIVIDUALS FROM THE eMERGE NETWORK..... 21
***Xinyuan Zhang**, Yogasudha Veturi, Shefali S. Verma, William Bone, Anurag Verma, Anastasia M. Lucas, Scott Hebring, Joshua C. Denny, Ian Stanaway, Gail P. Jarvik, David Crosslin, Eric B. Larson, Laura Rasmussen-Torvik, Sarah A. Pendergrass, Jordan W. Smoller, Hakon Hakonarson, Patrick Sleiman, Chunhua Weng, David Fasel, Wei-Qi Wei, Iftikhar Kullo, Daniel Schaid, Wendy K. Chung, Marylyn D. Ritchie*

SINGLE CELL ANALYSIS – WHAT IS THE FUTURE?

LISA: ACCURATE RECONSTRUCTION OF CELL TRAJECTORY AND PSEUDO-TIME FOR MASSIVE SINGLE CELL RNA-SEQ DATA..... 23
*Yang Chen, Yuping Zhang, **Zhengqing Ouyang***

PARAMETER TUNING IS A KEY PART OF DIMENSIONALITY REDUCTION VIA DEEP VARIATIONAL AUTOENCODERS FOR SINGLE CELL RNA TRANSCRIPTOMICS..... 24
***Qiwen Hu**, Casey S. Greene*

TOPOLOGICAL METHODS FOR VISUALIZATION AND ANALYSIS OF HIGH DIMENSIONAL SINGLE-CELL RNA SEQUENCING DATA 25
***Tongxin Wang**, Travis Johnson, Jie Zhang, Kun Huang*

WHEN BIOLOGY GETS PERSONAL: HIDDEN CHALLENGES OF PRIVACY AND ETHICS IN BIOLOGICAL BIG DATA

LEVERAGING SUMMARY STATISTICS TO MAKE INFERENCES ABOUT COMPLEX PHENOTYPES IN LARGE BIOBANKS	27
<i>Angela Gaskaska, Derek Friend, Rachel Chen, Jason Westra, Matthew Zawistowski, William Lindsey, Nathan Tintle</i>	
EVALUATION OF PATIENT RE-IDENTIFICATION USING LABORATORY TEST ORDERS AND MITIGATION VIA LATENT SPACE VARIABLES.....	28
<i>Kipp W. Johnson, Jessica K. De Freitas, Benjamin S. Glicksberg, Jason R. Bobe, Joel T. Dudley</i>	
PROTECTING GENOMIC DATA PRIVACY WITH PROBABILISTIC MODELING.....	29
<i>Sean Simmons, Bonnie Berger, Cenk Sahinalp</i>	

PROCEEDINGS PAPERS WITH POSTER PRESENTATIONS

PATTERN RECOGNITION IN BIOMEDICAL DATA: CHALLENGES IN PUTTING BIG DATA TO WORK

SNPs2CHIP: LATENT FACTORS OF CHIP-SEQ TO INFER FUNCTIONS OF NON-CODING SNPs.....	31
<i>Shankara Anand, Laurynas Kalesinskas, Craig Smail, Yosuke Tanigawa</i>	
DNA STEGANALYSIS USING DEEP RECURRENT NEURAL NETWORKS.....	32
<i>Ho Bae, Byunghan Lee, Sunyoung Kwon, Sungroh Yoon</i>	
LEARNING CONTEXTUAL HIERARCHICAL STRUCTURE OF MEDICAL CONCEPTS WITH POINCAIRÉ EMBEDDINGS TO CLARIFY PHENOTYPES	33
<i>Brett K. Beaulieu-Jones, Isaac S. Kohane, Andrew L. Beam</i>	
EXPLORING MICRORNA REGULATION OF CANCER WITH CONTEXT-AWARE DEEP CANCER CLASSIFIER.....	34
<i>Blake Pyman, Alireza Sedghi, Shekoofeh Azizi, Kathrin Tyryshkin, Neil Renwick, Parvin Mousavi</i>	
ESTIMATING CLASSIFICATION ACCURACY IN POSITIVE-UNLABELED LEARNING: CHARACTERIZATION AND CORRECTION STRATEGIES	35
<i>Rashika Ramola, Shantanu Jain, Predrag Radivojac</i>	
EXTRACTING ALLELIC READ COUNTS FROM 250,000 HUMAN SEQUENCING RUNS IN SEQUENCE READ ARCHIVE.....	36
<i>Brian Tsui, Michelle Dow, Dylan Skola, Hannah Carter</i>	
AUTOMATIC HUMAN-LIKE MINING AND CONSTRUCTING RELIABLE GENETIC ASSOCIATION DATABASE WITH DEEP REINFORCEMENT LEARNING.....	37
<i>Haohan Wang, Xiang Liu, Yifeng Tao, Wenting Ye, Qiao Jin, William W. Cohen, Eric P. Xing</i>	

PRECISION MEDICINE: IMPROVING HEALTH THROUGH HIGH-RESOLUTION ANALYSIS OF PERSONAL DATA

INFLUENCE OF TISSUE CONTEXT ON GENE PRIORITIZATION FOR PREDICTED TRANSCRIPTOME-WIDE ASSOCIATION STUDIES	39
<i>Binglan Li, Yogasudha Veturi, Yuki Bradford, Shefali S. Verma, Anurag Verma, Anastasia M. Lucas, David W. Haas, Marylyn D. Ritchie</i>	

SINGLE CELL ANALYSIS – WHAT IS THE FUTURE?

SHALLOW SPARSELY-CONNECTED AUTOENCODERS FOR GENE SET PROJECTION	41
<i>Maxwell P. Gold, Alexander LeNail, Ernest Fraenkel</i>	

WHEN BIOLOGY GETS PERSONAL: HIDDEN CHALLENGES OF PRIVACY AND ETHICS IN BIOLOGICAL BIG DATA

IMPLEMENTING A UNIVERSAL INFORMED CONSENT PROCESS FOR THE ALL OF US RESEARCH PROGRAM	43
<i>Megan Doerr, Shira Grayson, Sarah Moore, Christine Suver, John Wilbanks, Jennifer Wagner</i>	

POSTER PRESENTATIONS

GENERAL

A CONVOLUTIONAL NEURAL NET PREDICTS BINDING PROPERTIES OF AN ANTIBODY LIBRARY	45
<i>Rishi Bedi, Rachel Hovde, Jacob Glanville</i>	
CNVAR: A SOFTWARE TOOL FOR GENOTYPING CYP2D6 USING SHORT READ NEXT GENERATION SEQUENCING TECHNOLOGY	46
<i>John Logan Black III MD, Hugues Sicotte PhD, Sandra E. Peterson, Kimberley J. Harris, Liewei Wang MD PhD, Steven Scherer PhD, Eric Boerwinkle PhD, Richard A. Gibbs PhD, Suzette J. Bielinski PhD, Richard Weinshilboum MD</i>	
NETWORK ANALYSIS OF DISTINCT COHORTS ALLOWS FOR THE COMPARISON OF KEY BIOLOGICAL FUNCTIONS RELATED TO TB PATHOGENESIS	47
<i>Carly Bobak, Meghan E. Muse, Alexander J. Titus, Brock C. Christensen, A. James O'Malley, Jane E. Hill</i>	
VARIATION IN OPIOID PRESCRIBING PATTERNS IN SURGICAL POPULATIONS.....	48
<i>Soline M. Boussard, Marylyn D. Ritchie, Michelle Whirl-Carrillo, Tina Hernandez-Boussard, Teri E. Klein</i>	
REGIONAL HETEROGENEITY IN GENE EXPRESSION, REGULATION AND COHERENCE IN HIPPOCAMPUS AND DORSOLATERAL PREFRONTAL CORTEX ACROSS DEVELOPMENT AND SCHIZOPHRENIA	49
<i>Leonardo Collado-Torres, Emily E. Burke, Amy Peterson, Joo Heon Shin, Richard E. Straub, Anandita Rajpurohit, Stephen A. Semick, William S. Ulrich, BrainSeq Consortium, Cristian Valencia, Ran Tao, Amy Deep-Soboslay, Thomas M. Hyde, Joel E. Kleinman, Daniel R Weinberger, Andrew E. Jaffe¹</i>	
FULL-LENGTH SEQUENCE ASSEMBLY AND CHARACTERIZATION OF HIGHLY PURIFIED CIRC RNA ISOFORMS.....	50
<i>Supriyo De, Amaresh C. Panda, Myriam Gorospe</i>	

A COMPREHENSIVE REVIEW AND ASSESSMENT OF EXISTING PATHWAY ANALYSIS APPROACHES	51
<i>Tuan-Minh Nguyen, Adib Shafi, Tin Nguyen, Sorin Draghici</i>	
A NEW PHYLOGENETIC SAMPLING METHOD USING GENERALIZED-ENSEMBLE ALGORITHM.....	52
<i>Tetsu Furukawa, Hiroyuki Toh</i>	
CONVERGENT MECHANISMS PERTURBED BY SCATTERED SNPs SUSCEPTIBLE TO ALZHEIMER'S DISEASE	53
<i>Jiali Han, Edwin Baldwin, Jin Zhou, Fei Yin, Haiquan Li</i>	
IDENTIFICATION AND EVALUATION OF CO-EXPRESSION GENE NETWORKS FOR PACLITAXEL-INDUCED PERIPHERAL NEUROPATHY IN BREAST CANCER SURVIVORS	54
<i>Kord M. Kober, Jon D. Levine, Judy Mastick, Bruce Cooper, Steven Paul, Christine Miaskowski¹</i>	
VARIFI - WEB-BASED AUTOMATIC VARIANT IDENTIFICATION, FILTERING AND ANNOTATION OF AMPLICON SEQUENCING DATA	55
<i>Milica Kronic, Peter Venhuizen, Leonhard Müllauer, Bettina Kaserer, Arndt von Haeseler</i>	
STATISTICAL INFERENCE RELIEF (STIR) FEATURE SELECTION	56
<i>Trang T. Le, Ryan J. Urbanowicz, Jason H. Moore, Brett A. McKinney</i>	
DEEP LEARNING-BASED LONGITUDINAL HETEROGENEOUS DATA INTEGRATION FRAMEWORK FOR AD-RELEVANT FEATURE EXTRACTION	57
<i>Garam Lee, Kwangsik Nho, Byungkon Kang, Kyung-Ah Sohn, Dokyoon Kim</i>	
MICROBIOME ANALYSIS OF UNEXPLAINED CASES OF PNEUMONIA IN SOUTH KOREA.....	58
<i>Sooyeon Lim, Jae Kyung Lee, Ji Yun Noh, Woo Joo Kim</i>	
POTRA: PATHWAY ANALYSIS OF CANCER GENOMICS DATA IN THE CLOUD	59
<i>Margaret Linan, Junwen Wang, Valentin Dinu</i>	
EVALUATING CELL LINES AS MODELS FOR METASTATIC CANCER THROUGH INTEGRATIVE ANALYSIS OF OPEN GENOMIC DATA	60
<i>Ke Liu, Patrick A. Newbury, Benjamin S. Glicksberg, William Zeng, Eran R. Andrechek, Bin Chen</i>	
PATHWAY ANALYSIS OF EHR AND NON-EHR-BASED GWAS CONNECTS LIPID METABOLISM TO THE IMMUNE RESPONSE	61
<i>Jason E. Miller, Thomas J. Hoffmann, Elizabeth Theusch, Carlos Iribarren, Marisa W. Medina, Neil Risch, Ronald M. Krauss, Marylyn D. Ritchie</i>	
META-ANALYSIS OF HETEROGENEITY AND BATCH EFFECTS IN THE A549 CELL LINE	62
<i>Abigail Moore, John Castorino</i>	
HYPERPARAMETER TUNING FOR CHIP-SEQ PEAK CALLING SOFTWARE TOOLS USING PARALLELIZED BAYESIAN OPTIMIZATION.....	63
<i>Dongpin Oh, Jinhee Lee, Seonghyeon Kim, Dohyeon Lee, Dongwon Choo, Giltae Song</i>	

CROSS-STUDY META-ANALYSIS IDENTIFIES ALTERED BACTERIAL STRAINS SEPARATING RESPONDER AND NON-RESPONDER POPULATIONS ACROSS MULTIPLE CHECKPOINT-INHIBITOR THERAPY DATASETS.....	64
<i>Jayamary Divya Ravichandar, Erica Rutherford, Yonggan Wu, Thomas Weinmaier, Cheryl-Emiliane Chow, Shoko Iwai, Helena Kiefel, Kareem Graham, Karim Dabbagh, Todd DeSantis</i>	
A HYPOTHESIS OF THE STABILIZING ROLE OF ALU EXPANSION VIA HOMOLOGY DIRECTED REPAIR OF SPONTANEOUS DNA DOUBLE STRANDED BREAKS	65
<i>Tanmoy Roychowdhury, Alexej Abyzov</i>	
STATISTICAL LEARNING WITH HIGH-DIMENSIONAL MASS CYTOMETRY DATA.....	66
<i>Pratyaydipta Rudra, Elena Hsieh, Debashis Ghosh</i>	
HARDWARE ACCELERATION OF APPROXIMATE STRING MATCHING FOR BOTH SHORT AND LONG READ MAPPING	67
<i>Damla Senol Cali, Lavanya Subramanian, Zülal Bingöl, Jeremie S. Kim, Rachata Ausavarungnirun, Anant V. Nori, Gurpreet S. Kalsi, Sreenivas Subramoney, Saugata Ghose, Can Alkan, Onur Mutlu</i>	
TRANSITION OF REGULATORY FORCE TOWARD THE GENE EXPRESSIONS DURING OSTEOBLAST CELL DIFFERENTIATION.....	68
<i>Yoichi Takenaka</i>	
METHYLATION PROFILES OF MELANOMA TO PREDICT TILS	69
<i>Yihuan Tsai, Nana Nikolaishvili Feinberg, Kathleen Conway, Sharon N. Edmiston, Nancy E. Thomas, Joel S. Parker</i>	
HIGH-THROUGHPUT GENE TO KNOWLEDGE MAPPING THROUGH MASSIVE INTEGRATION OF PUBLIC SEQUENCING DATA.....	70
<i>Brian Tsui, Hannah Carter</i>	
MANTA-RAE, PREDICTING THE IMPACT OF GENOME VARIANTS ON THE TRANSCRIPTION FACTOR BINDING POTENTIAL OF REGULATORY ELEMENTS	71
<i>Robin van der Lee, Phillip A. Richmond, Oriol Fornes, Wyeth W. Wasserman</i>	
USING QUANTITATIVE PHOSPHOPROTEOMICS TO UNDERSTAND FUNCTIONAL SELECTIVITY OF RECEPTOR TYROSINE KINASES	72
<i>J. Watson, C. Francavilla, J.M. Schwartz</i>	
ANERIS APPLIED: SPARK-ENABLED ANALYTICS FOR FULL-SCALE AND REPRODUCIBLE ANNOTATION-BASED GENOMIC STUDIES.....	73
<i>Nicholas Wheeler, Jeremy Fondran, Penny Benckek, Jonathan Haines, William S. Bush</i>	
PUTTING RELICANTHUS IN ITS PLACE: IMPACT OF MIXTURE MODEL CHOICE ON PHYLOGENETIC RECONSTRUCTION	74
<i>Madelyne Xiao, Mercer R. Brugler, Estefania Rodriguez</i>	
RATIONAL DESIGN OF NOVEL SKP2 INHIBITORS USING DEEP NEURAL NETWORKS.....	75
<i>Shuxing Zhang, Beibei Huang, Lon W. Fong</i>	

PATTERN RECOGNITION IN BIOMEDICAL DATA: CHALLENGES IN PUTTING BIG DATA TO WORK

ODAL: A ONE-SHOT DISTRIBUTED ALGORITHM TO PERFORM LOGISTIC REGRESSIONS ON ELECTRONIC HEALTH RECORDS DATA FROM MULTIPLE CLINICAL SITES..... 77
*Rui Duan, Mary Regina Boland, Jason H. Moore, **Yong Chen***

PLATYPUS: A MULTIPLE-VIEW LEARNING PREDICTIVE FRAMEWORK FOR CANCER DRUG SENSITIVITY PREDICTION..... 78
*Kiley Graim, **Verena Friedl**, Kathleen E. Houlahan, Joshua M. Stuart*

A SOFTWARE PIPELINE FOR DETERMINING FINE-SCALE TEMPORAL GENOME VARIATION PATTERNS IN EVOLVING POPULATIONS USING A NON-PARAMETRIC STATISTICAL TEST 79
*Minjung Kwak, Seokwoo Kang, Dongwon Choo, Dohyeon Lee, Jinhee Lee, Seonghyeon Kim, **Giltae Song***

A DEEP LEARNING APPROACH TO IDENTIFYING THE CELLULAR COMPOSITION OF SOLID TISSUE WITH DNA METHYLATION DATA 80
***Meghan E. Muse**, Curtis L. Petersen, Carmen J. Marsit, Diane Gilbert-Diamond, Brock C. Christensen*

DIRECTLY MEASURING THE RATE AND DYNAMICS HUMAN MUTATION BY SEQUENCING LARGE, MULTI-GENERATIONAL PEDIGREES 81
*Thomas A. Sasani, Brent S. Pedersen, Mark Leppert, Ray White, Lisa Baird, **Aaron R. Quinlan**, Lynn B. Jorde*

AVAILABLE PROTEIN 3D STRUCTURES DO NOT REFLECT HUMAN GENETIC AND FUNCTIONAL DIVERSITY..... 82
*Gregory Sliwoski, Neel Patel, R. Michael Sivley, Charles R. Sanders, Jens Meiler, **William S. Bush**, John A. Capra*

SEMANTIC WORKFLOWS FOR BENCHMARK CHALLENGES: ENHANCING COMPARABILITY, REUSABILITY AND REPRODUCIBILITY..... 83
***Arunima Srivastava**, Raval Adusumilli, Hunter Boyce, Daniel Garijo, Varun Ratnakar, Rajiv Mayani, Thomas Yu, Raghu Machiraju, Yolanda Gil, Parag Mallick*

PRECISION MEDICINE: IMPROVING HEALTH THROUGH HIGH-RESOLUTION ANALYSIS OF PERSONAL DATA

CLASS PRIOR ESTIMATION AND QUANTIFICATION OF THE LOSS AND GAIN OF RESIDUE FUNCTION UPON MUTATION..... 85
***Shantanu Jain**, Jose Lugo-Martinez, Martha White, Michael W. Trosset, Predrag Radivojac*

PREDICTION OF TIME TO INSULIN USING CLINICAL AND GENETIC BIOMARKERS IN TYPE 2 DIABETES PATIENTS..... 86
***Rikke Linnemann Nielsen**, Louise Donnelly, Agnes Martine Nielsen, Konstantinos Tsirigos, Kaixin Zhou, Bjarne Ersboell, Line Clemmensen, Ewan Pearson, Ramneek Gupta*

PATHOGENICITY AND FUNCTIONAL IMPACT OF INSERTION/DELETION AND STOP GAIN VARIATION IN THE HUMAN GENOME 87
*Kymerleigh A. Pagel, Danny Antaki, Matthew Mort, David N. Cooper, Jonathan Sebat, Lilia M. Iakoucheva, Sean D. Mooney, **Predrag Radivojac***

DETECTING POTENTIAL PLEIOTROPY ACROSS CARDIOVASCULAR AND NEUROLOGICAL DISEASES USING UNIVARIATE, BIVARIATE, AND MULTIVARIATE METHODS ON 43,870 INDIVIDUALS FROM THE EMERGE NETWORK	88
<i>Xinyuan Zhang, Yogasudha Veturi, Shefali S. Verma, William Bone, Anurag Verma, Anastasia M. Lucas, Scott Hebring, Joshua C. Denny, Ian Stanaway, Gail P. Jarvik, David Crosslin, Eric B. Larson, Laura Rasmussen-Torvik, Sarah A. Pendergrass, Jordan W. Smoller, Hakon Hakonarson, Patrick Sleiman, Chunhua Weng, David Fasel, Wei-Qi Wei, Iftikhar Kullo, Daniel Schaid, Wendy K. Chung, Marylyn D. Ritchie</i>	
PHARMGKB: THE API AND INFOBUTTONS	89
<i>Michelle Whirl-Carrillo, Ryan M. Whaley, Mark Woon, Russ B. Altman, Teri E. Klein</i>	
SINGLE CELL ANALYSIS – WHAT IS IN THE FUTURE?	
INTRA TUMOR HETEROGENEITY (ITH) METRIC OF CIRCULATING TUMOR CELL (CTC)-DERIVED XENOGRAFT MODELS IN SMALL CELL LUNG CANCER	91
<i>Yuanxin Xi, C. Allison Stewart, Carl M. Gay, Hai Tran, Bonnie Glisson, John V. Heymach, Paul Robson, Lauren A. Byers, Jing Wang</i>	
WHEN BIOLOGY GETS PERSONAL: HIDDEN CHALLENGES OF PRIVACY AND ETHICS IN BIOLOGICAL BIG DATA	
QUANTIFYING THE IDENTIFIABILITY OF INDIVIDUALS USING A SPARSE SET OF SNPs	93
<i>Prashant S. Emani, Gamze GURSOY, Mark B. Gerstein</i>	
TRANSCRIPTOMIC SUMMARY SPLICING DATA MAY LEAK PERSONAL PRIVATE INFORMATION BY COMPUTATIONAL LINKAGE TO THE GENOMIC VARIANTS	94
<i>Zhiqiang Hu, Mark B. Gerstein, Steven E. Brenner</i>	
WORKSHOPS	
MERGING HETEROGENEOUS DATA TO ENABLE KNOWLEDGE DISCOVERY	
TO SEARCH A HETNET... HOW ARE TWO NODES CONNECTED?.....	96
<i>Daniel Himmelstein, Michael Zietz, Kyle Kloster, Michael Nagle, Blair Sullivan, Casey S. Greene</i>	
TEXT MINING AND MACHINE LEARNING FOR PRECISION MEDICINE	
LITVAR: MINING GENOMIC VARIANTS FROM BIOMEDICAL LITERATURE FOR DATABASE CURATION AND PRECISION MEDICINE	98
<i>Alexis Allot, Yifan Peng, Chih-Hsuan Wei, Kyubum Lee, Lon Phan, Zhiyong Lu</i>	
AUTHOR INDEX.....	99

AUTHOR INDEX

A

Abyzov, Alexej · 65
Adusumilli, Ravali · 11, 83
Alkan, Can · 67
Allot, Alexis · 98
Altman, Russ B. · 89
Anand, Shankara · 31
Andrechek, Eran R. · 60
Antaki, Danny · 87
Ausavarungnirun, Rachata · 67
Azizi, Shekoofeh · 34

B

Bae, Ho · 32
Baird, Lisa · 81
Baldwin, Edwin · 53
Beam, Andrew L. · 33
Beaulieu-Jones, Brett K. · 33
Bedi, Rishi · 45
Benckek, Penny · 73
Berger, Bonnie · 29
Berghout, Joanne · 20
Best, Aaron · 7
Bielinski, Suzette J. · 46
Bingöl, Zülal · 67
Black III, John Logan · 46
Bobak, Carly · 47
Bobe, Jason R. · 28
Boerwinkle, Eric · 46
Boland, Mary Regina · 3, 77
Bone, William · 21, 88
Boussard, Soline M. · 48
Boyce, Hunter · 11, 83
Bradford, Yuki · 39
BrainSeq Consortium · 49
Brenner, Steven E. · 94
Brugler, Mercer R. · 74
Burke, Emily E. · 49
Bush, William S. · 73, 82
Byers, Lauren A. · 91

C

Capra, John A. · 82
Carter, Hannah · 10, 36, 70
Castorino, John · 62
Chen, Bin · 17, 60
Chen, Rachel · 7, 27
Chen, Yang · 23
Chen, Yong · 3, 77
Cheng, Li-Fang · 14
Choo, Dongwon · 63, 79
Chow, Cheryl-Emiliane · 64
Chrisman, Brianna Sierra · 19
Christensen, Brock C. · 47, 80
Chung, Wendy K. · 21, 88
Clemmensen, Line · 86
Cohen, William W. · 37
Collado-Torres, Leonardo · 49
Conway, Kathleen · 69
Cooper, Bruce · 54
Cooper, David N. · 87
Coukos, George · 10
Crosslin, David · 21, 88
Cule, Madeleine · 15

D

Dabbagh, Karim · 64
De Freitas, Jessica K. · 28
De, Supriyo · 50
Deep-Soboslay, Amy · 49
DeJongh, Matthew · 7
Denny, Joshua C. · 21, 88
DePristo, Mark · 15
DeSantis, Todd · 64
Ding, Daisy Yi · 2
Dinu, Valentin · 59
Doerr, Megan · 43
Donnelly, Louise · 86
Dow, Michelle · 36
Draghici, Sorin · 51
Duan, Rui · 3, 77
Dudley, Joel T. · 28

E

Edmiston, Sharon N. · 69
Emani, Prashant S. · 93
Engelhardt, Barbara E. · 14
Ersboell, Bjarne · 86

F

Fan, Jungwei · 20
Fasel, David · 21, 88
Feinberg, Nana Nikolaishvili · 69
Fondran, Jeremy · 73
Fong, Lon W. · 75
Fornes, Oriol · 71
Fraenkel, Ernest · 41
Francavilla, C. · 72
Friedl, Verena · 5, 78
Friend, Derek · 27
Furukawa, Tetsu · 52

G

Garijo, Daniel · 11, 83
Gasdaska, Angela · 27
Gay, Carl M. · 91
Genolet, Raphael · 10
Gerstein, Mark B. · 93, 94
Gfeller, David · 10
Ghose, Saugata · 67
Ghosh, Debashis · 66
Gibbs, Richard A. · 46
Gil, Yolanda · 11, 83
Gilbert-Diamond, Diane · 80
Glanville, Jacob · 45
Glicksberg, Benjamin S. · 28, 60
Glisson, Bonnie · 91
Gold, Maxwell P. · 41
Gonzalez-Hernandez, Graciela · 9
Gordon, Max · 4
Gorospe, Myriam · 50
Graham, Kareem · 64
Grim, Kiley · 5, 78
Grayson, Shira · 43
Greene, Casey S. · 24, 96
Greenside, Peyton · 15
Gupta, Ramneek · 86
Gursoy, Gamze · 93

H

Haas, David W. · 39
Haines, Jonathan · 73
Hakonarson, Hakon · 21, 88
Han, Jiali · 53
Han, Wontack · 16
Harari, Alexandre · 10
Harris, Kimberley J. · 46
Hebbring, Scott · 21, 88
Henry, Christopher · 7
Hernandez-Boussard, Tina · 48
Heymach, John V. · 91
Hill, Jane E. · 47
Himmelstein, Daniel · 96
Ho, Irvin · 18
Hoffmann, Thomas J. · 61
Houlahan, Kathleen E. · 5, 78
Hovde, Rachel · 45
Hsieh, Elena · 66
Hu, Qiwen · 24
Hu, Zhiqiang · 94
Hu, Zhiyue Tom · 17
Huang, Beibei · 75
Huang, Haiyan · 17
Huang, Kun · 25
Hyde, Thomas M. · 49

I

Iakoucheva, Lilia M. · 87
Iribarren, Carlos · 61
Iwai, Shoko · 64

J

Jaffe, Andrew E. · 49
Jain, Shantanu · 35, 85
Jarvik, Gail P. · 21, 88
Jiang, Yuexu · 6
Jin, Qiao · 37
Johnson, Kipp W. · 28
Johnson, Travis · 25
Jorde, Lynn B. · 81
Jung, Jae-Yoon · 19
Jung, Kenneth · 2

K

Kale, Dave C. · 2
Kalesinskis, Laurynas · 31
Kalsi, Gurpreet S. · 67
Kang, Byungkon · 57
Kang, Seokwoo · 79
Kaserer, Bettina · 55
Khan, Aly A. · 18
Kiefel, Helena · 64
Kim, Dokyoon · 57
Kim, Jeremie S. · 67
Kim, Seonghyeon · 63, 79
Kim, Woo Joo · 58
Klein, Teri E. · 48, 89
Kleinman, Joel E. · 49
Kloster, Kyle · 96
Kober, Kord M. · 54
Kohane, Isaac S. · 33
Krauss, Ronald M. · 61
Kronic, Milica · 55
Kullo, Iftikhar · 21, 88
Kwak, Minjung · 79
Kwon, Sunyoung · 32

L

Larson, Eric B. · 21, 88
Lau, Denise · 18
Le, Trang T. · 56
Lee, Byunghan · 32
Lee, Dohyeon · 63, 79
Lee, Garam · 57
Lee, Jae Kyung · 58
Lee, Jinhee · 63, 79
Lee, Kyubum · 98
LeNail, Alexander · 41
Leppert, Mark · 81
Levine, Jon D. · 54
Li, Binglan · 39
Li, Haiquan · 20, 53
Li, Jianrong · 20
Li, Kevin · 7
Li, Qike · 20
Lim, Sooyeon · 58
Linan, Margaret · 59
Lindsey, William · 7, 27
Liu, Zheng · 8
Liu, Ke · 60

L continued

Liu, Xiang · 37
Lu, Zhiyong · 98
Lucas, Anastasia M. · 21, 39, 88
Lugo-Martinez, Jose · 85
Lussier, Yves A. · 20

M

Machiraju, Raghu · 11, 83
Magge, Arjun · 9
Mallick, Parag · 11, 83
Marsit, Carmen J. · 80
Mastick, Judy · 54
Mayani, Rajiv · 11, 83
McKinney, Brett A. · 56
Medina, Marisa W. · 61
Meiler, Jens · 82
Miaskowski, Christine · 54
Miller, Jason E. · 61
Mooney, Sean D. · 87
Moore, Abigail · 62
Moore, Jason H. · 3, 56, 77
Moore, Sarah · 43
Mort, Matthew · 87
Mousavi, Parvin · 34
Müllauer, Leonhard · 55
Muse, Meghan E. · 47, 80
Mutlu, Onur · 67

N

Nagle, Michael · 96
Newbury, Patrick A. · 17, 60
Nguyen, Tin · 51
Nguyen, Tuan-Minh · 51
Nho, Kwangsik · 57
Nielsen, Agnes Martine · 86
Nielsen, Rikke Linnemann · 86
Noh, Ji Yun · 58
Nori, Anant V. · 67

O

O'Malley, A. James · 47
Oh, Dongpin · 63
Ouyang, Zhengqing · 23

P

Pagel, Kimberleigh A. · 87
Panda, Amaresh C. · 50
Parker, Joel S. · 69
Paskov, Kelley Marie · 19
Patel, Neel · 82
Paul, Steven · 54
Pearson, Ewan · 86
Pedersen, Brent S. · 81
Pendergrass, Sarah A. · 21, 88
Peng, Yifan · 98
Petersen, Curtis L. · 80
Peterson, Amy · 49
Peterson, Sandra E. · 46
Pfohl, Stephen · 2
Phan, Lon · 98
Poplin, Ryan · 15
Prasad, Niranjani · 14
Pyke, Rachel M. · 10
Pyman, Blake · 34

Q

Quinlan, Aaron R. · 81

R

Radivojac, Predrag · 35, 85, 87
Rajpurohit, Anandita · 49
Ramola, Rashika · 35
Ramsey, Stephen A. · 8
Rasmussen-Torvik, Laura · 21, 88
Ratnakar, Varun · 11, 83
Ravichandar, Jayamary Divya · 64
Reiman, Derek · 18
Renwick, Neil · 34
Richmond, Phillip A. · 71
Risch, Neil · 61
Ritchie, Marylyn D. · 21, 39, 48, 61, 88
Robson, Paul · 91
Rodriguez, Estefania · 74
Roychowdhury, Tanmoy · 65
Rudra, Pratyaydipta · 66
Rutherford, Erica · 64

S

Sahinalp, Cenk · 29
Salit, Marc · 15
Sanders, Charles R. · 82
Sarker, Abeed · 9
Sasani, Thomas A. · 81
Schaid, Daniel · 21, 88
Scherer, Steven · 46
Schwartz, J.M. · 72
Scotch, Matthew · 9
Sebat, Jonathan · 87
Sedghi, Alireza · 34
Semick, Stephen A. · 49
Senol Cali, Damla · 67
Sha, Lingdao · 18
Shafi, Adib · 51
Shah, Nigam H. · 2
Shin, Joo Heon · 49
Sicotte, Hugues · 46
Simmons, Sean · 29
Simpson, Chloe · 2
Sivley, R. Michael · 82
Skola, Dylan · 36
Sleiman, Patrick · 21, 88
Sliwoski, Gregory · 82
Smail, Craig · 31
Smoller, Jordan W. · 21, 88
Sohn, Kyung-Ah · 57
Song, Giltae · 63, 79
Srivastava, Arunima · 11, 83
Stanaway, Ian · 21, 88
Stewart, C. Allison · 91
Stockham, Nate Tyler · 19
Straub, Richard E. · 49
Stuart, Joshua M. · 5, 78
Subramanian, Lavanya · 67
Subramoney, Sreenivas · 67
Sullivan, Blair · 96
Suver, Christine · 43

T

Takenaka, Yoichi · 68
Tan, Timothy · 18
Tanigawa, Yosuke · 31
Tao, Ran · 49
Tao, Yifeng · 37

T continued

Theusch, Elizabeth · 61
Thomas, Nancy E. · 69
Tintle, Nathan · 7, 27
Titus, Alexander J. · 47
Toh, Hiroyuki · 52
Tran, Hai · 91
Trosset, Michael W. · 85
Tsai, Yihsuan · 69
Tsirigos, Konstantinos · 86
Tsui, Brian · 36, 70
Tyryshkin, Kathrin · 34

U

Ulrich, William S. · 49
Urbanowicz, Ryan J. · 56

V

Valencia, Cristian · 49
van der Lee, Robin · 71
Varma, Maya · 19
Venhuizen, Peter · 55
Verma, Anurag · 21, 39, 88
Verma, Shefali S. · 21, 39, 88
Veturi, Yogasudha · 21, 39, 88
Vitali, Francesca · 20
von Haeseler, Arndt · 55

W

Wagner, Jennifer · 43
Wall, Dennis Paul · 19
Wang, Duolin · 6
Wang, Haohan · 12, 37
Wang, Jing · 91
Wang, Junwen · 59
Wang, Liewei · 46
Wang, Tongxin · 25
Washington, Peter Yigitcan · 19
Wasserman, Wyeth W. · 71
Watson, J. · 72
Weeder, Benjamin · 8
Wei, Chih-Hsuan · 98
Wei, Qi · 8
Wei, Wei-Qi · 21, 88

W continued

Weinberger, Daniel R · 49
Weinmaier, Thomas · 64
Weinshilboum, Richard · 46
Weissenbacher, Davy · 9
Weng, Chunhua · 21, 88
Westra, Jason · 27
Whaley, Ryan M. · 89
Wheeler, Nicholas · 73
Whirl-Carrillo, Michelle · 48, 89
White, Martha · 85
White, Ray · 81
Wilbanks, John · 43
Williams, Cranos · 4
Woon, Mark · 89
Wu, Yonggan · 64
Wu, Zhenglin · 12

X

Xi, Yuanxin · 91
Xiao, Madelyne · 74
Xing, Eric P. · 12, 37
Xu, Dong · 6

Y

Yao, Yao · 8
Ye, Wenting · 37
Ye, Yuting · 17
Ye, Yuzhen · 16
Yin, Fei · 53
Yoon, Sungroh · 32
Yu, Thomas · 11, 83

Z

Zawistowski, Matthew · 27
Zeng, William · 60
Zhang, Jie · 25
Zhang, Shuxing · 75
Zhang, Xinyuan · 21, 88
Zhang, Yuping · 23
Zhou, Jin · 53
Zhou, Kaixin · 86
Zietz, Michael · 96
Zook, Justin · 15

Pacific Symposium on Biocomputing 2019

Participant List

as of December 6, 2018

Max Alekseyev
George Washington University

Russ Altman
Stanford University

Kiyoshi Asai
University of Tokyo

Folkert Asselbergs
University Medical Center Utrecht

Ho Bae
Seoul National University

Brett Beaulieu-Jones
Harvard Medical School

George Bebis
University of Nevada

Joanne Berghout
University of Arizona

John Black
Mayo Clinic

Carly Bobak
Darmouth College

Mary Boland
University of Pennsylvania

Philip Bourne
UVA Data Science Institute

Soline Boussard
Castilleja High School

Steven Brenner
University of California, Berkeley

Soren Brunak
Novo Nordisk Foundation Center for Protein
Research

Martha Bulyk
Brigham and Women's Hospital and
Harvard Medical School

William Bush
Case Western Reserve University

Bin Chen
Michigan State University

Rachel Chen
North Carolina State University

Yong Chen
University of Pennsylvania

Jane Chiang
Cipherome, Inc.

Jongmun Choi
Green Cross Genome

DongWon Choo
Pusan National University

Christopher Chute
Johns Hopkins University

Leonardo Collado Torres
Lieber Institute for Brain Development

Christian Darabos
Dartmouth College

Supriyo De
NIH

Pacific Symposium on Biocomputing 2019

Participant List

as of December 6, 2018

Jessica De Freitas
Icahn School of Medicine at Mount Sinai

Kimberley Ferguson
Roche

Scott Delp
Stanford University

James Foster
University of Idaho

Emek Demir
OHSU

Verena Friedl
University of California, Santa Cruz

Daisy Yi Ding
Stanford University

Weixuan Fu
University of Pennsylvania

Valentin Dinu
Arizona State University

Tetsu Furukawa
Kwansei Gakuin University

Megan Doerr
Sage Bionetworks

Lana Garmire
Univeristy of Michigan

Ernst Dow
Eli Lilly and Company

Maxwell Gold
Massachusetts Institute of Technology

Sorin Draghici
Wayne State University

Graciela Gonzalez Hernandez
University of Pennsylvania

A Keith Dunker
Indiana University

Raluca Gordan
Duke University

Claire Duvallat
Massachusetts Institute of Technology

Max Gordon
North Carolina State University

Prashant Emani
Yale University

Kiley Graim
Flatiron Institute

Peter Embi
Regenstrief Institute

Casey Greene
University of Pennsylvania

Barbara Engelhardt
Princeton University

Peyton Greenside
Stanford University

Yayin Fang
Howard University

Gamze Gursoy
Yale University

Pacific Symposium on Biocomputing 2019

Participant List

as of December 6, 2018

Jonathan Haines
Case Western Reserve University

Shantanu Jain
Northeastern University

Greg Hampikian
Boise State University

Yuxu Jiang
University of Missouri

Jiali Han
The University of Arizona

Kipp Johnson
Icahn School of Medicine at Mount Sinai

Wontack Han
Indiana University

Kory Johnson
NINDS/NIH

David Haussler
Howard Hughes Medical Institute/UC Santa Cruz

Indika Kahanda
Montana State University

Tina Hernandez-Boussard
Stanford University

Laurynas Kalesinskas
Stanford Biomedical Informatics

Daniel Himmelstein
University of Pennsylvania

Michael Keiser
UCSF

Michael Hoffman
Princess Margaret Cancer Centre/University of Toronto

Andreas Keller
Saarland University

John Holmes
University of Pennsylvania Perelman School of Medicine

Colleen Kenost
The University of Arizona

Rachel Hovde
Distributed Bio

Dokyoon Kim
Geisinger

Qiwen Hu
University of Pennsylvania

Jeremie Kim
Carnegie Mellon University

Zhiyue Hu
University of California, Berkeley

Teri Klein
Stanford University

Lawrence Hunter
University of Colorado

Kord Kober
University of California San Francisco

Pacific Symposium on Biocomputing 2019

Participant List

as of December 6, 2018

Milica Kronic
University of Vienna

Hongfang Liu
Mayo Clinic

Adam Kurkiewicz
University of Glasgow

Zheng Liu
Oregon State University

Nicholas Larson
Mayo Clinic

Xueqing Lu
University of Pennsylvania

Janet Layne
Boise State University

Zhiyong Lu
National Library of Medicine

Trang Le
University of Pennsylvania

Yves Lussier
University of Arizona

Jinhee Lee
Pusan National University

Arjun Magge
ASU

Nicholas Lee
Wellcome Sanger Institute

Lara Mangravite
Sage Bionetworks

DoHyeon Lee
Pusan National University

Serghei Mangul
UCLA

Binglan Li
University of Pennsylvania

Gabor Marth
University of Utah

Haiquan Li
University of Arizona

Rachel Marty
University of California, San Diego

Hua Li
Stowers Institute for Medical Research

Wouter Meuleman
Altius Institute

Jianrong Li
The University of Arizona

Jason Miller
University of Pennsylvania

Kevin Li
Columbia University

Stephen Montgomery
Stanford University

Sooyeon Lim
Korea University

Abigail Moore
Hampshire College

Pacific Symposium on Biocomputing 2019

Participant List

as of December 6, 2018

Jason Moore
University of Pennsylvania

Blake Pyman
Queen's University

Alexander Morgan
Khosla Ventures

Tielin Qin
Immune Tolerance Network

Sorana Morrissy
University of Calgary

Aaron Quinlan
University of Utah

Meghan Muse
Dartmouth College

Predrag Radivojac
Northeastern University

Rikke Nielsen
Technical University of Denmark

Rashika Ramola
Northeastern University

William Noble
University of Washington

Jayamary Divya Ravichandar
Second Genome

Soichi Ogishima
Tohoku University

Derek Reiman
University of Illinois at Chicago

Lawrence Oloff
St Mary's Medical Center

Haluk Resat
NIH/NIGMS

Zhengqing Ouyang
The Jackson Laboratory for Genomic
Medicine

Marylyn Ritchie
University of Pennsylvania

Philip Payne
Washington University School of Medicine

David Rocke
University of California, Davis

Matteo Pellegrini
UCLA

Pratyaydipta Rudra
Oklahoma State University

Luca Pinello
Massachusetts General Hospital/ Harvard
Medical School

Indra Sarkar
Brown University

Niranjani Prasad
Princeton University

Sebastian Schaaf
Fraunhofer Institute for Algorithms and
Scientific Computing (SCAI)

Ralph Schlapbach
Functional Genomics Center Zurich

Pacific Symposium on Biocomputing 2019

Participant List

as of December 6, 2018

Christine Scholberg
Stanford University

Lin Tang
Celgene Corp

Ashwini Sehgal
Case Western Reserve University

Yosuke Tanigawa
Stanford University

Martin Seneviratne
Stanford University

Cui Tao
University of Texas

Matthew Settles
University of California, Davis

Jaclyn Taroni
Alex's Lemonade Stand Foundation

James Sikela
University of Colorado Denver

Gunjan Thakur
Merck Exploratory Science Center

Sean Simmons
Broad Institute

Robert Thurman
Seattle Genetics

Marina Sirota
UCSF

Nathan Tintle
Dordt College

Giltae Song
Pusan National University

Yihuan Tsai
University of North Carolina

Paul Spellman
Oregon Health and Science University

Brian Yik Tak Tsui
University of California, San Diego

Arunima Srivastava
The Ohio State University

Anders Ulrik Eliassen
Technical University of Denmark

Josh Stuart
UC Santa Cruz

Paul Utz
Stanford University

Yoichi Takenaka
Kansai University

Robin van der Lee
The University of British Columbia

Eric Talevich
DNAnexus

Maya Varma
Stanford University

Haixu Tang
Indiana University, Bloomington

Anurag Verma
University of Pennsylvania

**Pacific Symposium on Biocomputing 2019
Participant List
as of December 6, 2018**

Shefali Verma
University of Pennsylvania

John Witte
UC San Francisco

Yogasudha Veturi
University of Pennsylvania

Yuanxin Xi
MD Anderson Cancer Center

Francesca Vitali
University of Arizona

Madelyne Xiao
American Museum of Natural History

Dennis Wall
Stanford University

Yuzhen Ye
Indiana University, Bloomington

Duolin Wang
University of Missouri

Shuxing Zhang
MD Anderson Cancer Center

Haohan Wang
Carnegie Mellon University

Xinyuan Zhang
The University of Pennsylvania

Jing Wang
UT MD Anderson Cancer Center

Yuping Zhang
University of Connecticut

Tongxin Wang
Indiana University

Zemin Zhang
Peking University

Yong Wang
Academy of Mathematics and Systems
Science, Chinese Academy of Sciences

Joanne Watson
University of Manchester

Ryan Whaley
Stanford University

Nicholas Wheeler
Case Western Reserve University

Michelle Whirl-Carrillo
Stanford University

Scott Williams
Case Western Reserve University