Welcome to PSB 2020!

We have prepared this program book to give you quick access to information you need for PSB 2020.

Enclosed you will find:

- Logistics information
- Medical services information
- Full conference schedule (see website for the latest version)
- Agendas for workshops and JBrowse demo
- Call for Session and Workshop Proposals for PSB 2021
- Poster/abstract titles and author index
- Participant list

The latest conference materials are available online at http://psb.stanford.edu/conference-materials/.

PSB 2020 gratefully acknowledges the support of the Cleveland Institute for Computational Biology; UPenn Institute for Biomedical Informatics; Variant Bio; Penn Center for Precision Medicine, Penn Medicine; Cipherome; Translational Bioinformatics Conference (TBC); 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 2020 Organizers
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 and remove it by Monday, January 6 at 5:30pm.

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.

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

**The poster session is on Sunday, January 5 12:45-2:30.**
12:45-2:00: Food available; drinks served until 2:30.
1:00-1:45: Posters on ODD numbered boards presented.
1:45-2:30: Posters on EVEN numbered boards presented.

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.
PSB 2020 HOSTED RECEIPTIONS & MEALS

**Friday, January 3**
5:00-6:00pm  25th Anniversary Reception, Croquet Lawn  
  *Sponsored by the Cleveland Institute for Computational Biology*

**Saturday, January 4**
7:30-8:45am  Continental Breakfast, Ballroom Courtyard  
12:00-1:15pm  PSB Hosted Lunch, Ballroom Courtyard

**Sunday, January 5**
7:30-8:45am  Continental Breakfast, Ballroom Courtyard  
12:00-2:00pm  Poster Session with Lunch, Salon 1 and Ballroom Courtyard

**Monday, January 6**
7:30-8:45am  Continental Breakfast, Ballroom Courtyard  
5:30-7:00pm  Dinner Banquet, Coconut Grove  
7:00-7:30pm  25th Anniversary Celebration Dessert, Ballroom Courtyard

**Tuesday, 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!
The safety and well-being of our guests and colleagues is our primary concern. We have listed below local organizations that we partner with to ensure that everyone is well taken care of during their time here at the Fairmont Orchid.

**Fairmont Orchid**  
One North Kaniku Drive, Kohala Coast, Hawaii 96743  
Telephone Number: (808) 885-2000

**Medical Service and Facilities:**

Waimea Urgent Care (30 minutes)  
65-1230 Mamalahoa Highway, Suite A10, Kamuela, Hawaii 96743  
Hours: Mon - Fri 8:30am - 7:00 pm / Sat 8:00am - 4:00pm  
Capable of handling non-emergency care up to and including sutures

Closest Hospital: North Hawaii Community Hospital (30 minutes)  
Mamalahoa Highway, Route 190, Kamuela, Hawaii 96743  
Level III Trauma Center  
(808) 881-4730 (ER)  (808) 885-4444 (General)

Closest Pharmacy: Waikoloa Village Market Pharmacy  
68-3916 Paniolo Ave  
Waikoloa Village, Hawaii 96738  
Direct: (808) 883-8434  Fax: (808) 883-8540  
Hours: 9am - 6pm Monday - Friday, 9:30am – 1:30pm Saturday, closed Sunday

The **Fairmont Orchid Security Staff** consists of a minimum of three Security Officers on each shift, providing 24-hour coverage for the resort property. The Security Staff is trained and certified in First Aid, CPR and A.E.D. Security patrols are conducted on a continuous basis throughout the resort. All patrols are radio dispatched.

The resort has in place an emergency team of A.E.D. (Automatic External Defibrillator) certified users in the event of sudden cardiac arrest. The team is trained in its use in conjunction with cardio pulmonary resuscitation. We have 6 A.E.D.s throughout the property so full coverage of the property is more easily maintained.

**Security**
- Electronic locks for guestrooms
- Secondary locking device for entry, balcony and connecting guestroom doors
- Entry door viewer
- Self closing guestroom entry door
- 24 hour Security, extension 7600 (non-emergencies)
- 24 hour Emergency Hotline, extension “66” from any house phone
- Security cameras are provided in public areas
Pacific Symposium on Biocomputing (PSB) 2020 Schedule
January 3-7, 2020, Big Island of Hawaii

**Friday, January 3, 2020**

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:30-9:30</td>
<td>Registration</td>
<td>Ballroom Prefunction</td>
</tr>
<tr>
<td>12:00-2:00</td>
<td>Registration</td>
<td>Ballroom Prefunction</td>
</tr>
<tr>
<td>5:00-5:30</td>
<td>Registration</td>
<td>Croquet Lawn</td>
</tr>
</tbody>
</table>

**Workshops 1 & 2**

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>9:00-12:00</td>
<td>AI Ethics and Values in Biomedicine – Technical Challenges and Solutions</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td></td>
<td>Organizers: Dragutin Petkovic, Lester Kobzik, Reza Ghanadan</td>
<td></td>
</tr>
<tr>
<td>9:00-12:00</td>
<td>Packaging Biocomputing Software to Maximize Distribution and Reuse</td>
<td>Plaza</td>
</tr>
<tr>
<td></td>
<td>Organizers: William S. Bush, Nicholas Wheeler, Brett Beaulieu-Jones,</td>
<td>Plaza</td>
</tr>
<tr>
<td></td>
<td>Christian Darabos</td>
<td></td>
</tr>
</tbody>
</table>

**Break**

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
</tr>
</thead>
<tbody>
<tr>
<td>12:00-1:30</td>
<td>Lunch on own</td>
</tr>
</tbody>
</table>

**Workshop 3**

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>1:30-4:30</td>
<td>Navigating Ethical Quandaries with the Privacy Dilemma of Biomedical</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td></td>
<td>Datasets</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Organizers: Gamze Gursoy, Megan Doerr, Steven E. Brenner, Haixu Tang,</td>
<td></td>
</tr>
<tr>
<td></td>
<td>John Wilbanks, Jennifer K. Wagner</td>
<td></td>
</tr>
</tbody>
</table>

**Break**

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
</tr>
</thead>
<tbody>
<tr>
<td>4:30-5:00</td>
<td>Break</td>
</tr>
</tbody>
</table>

**Reception**

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>5:00-6:00</td>
<td>25th Anniversary Reception including PSB group photo</td>
<td>Croquet Lawn</td>
</tr>
<tr>
<td></td>
<td>Sponsored by the Cleveland Institute for Computational Biology</td>
<td></td>
</tr>
</tbody>
</table>

**Break**

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
</tr>
</thead>
<tbody>
<tr>
<td>6:00-</td>
<td>Dinner &amp; Evening on own</td>
</tr>
</tbody>
</table>

*Please wear your PSB name tag and lanyard for admission to all events and hosted meals.*
## Pacific Symposium on Biocomputing (PSB) 2020 Schedule

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

### Saturday, January 4, 2020

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:30-9:00</td>
<td>Registration</td>
<td>Ballroom Prefunction</td>
</tr>
<tr>
<td>10:30-11:30</td>
<td>Registration</td>
<td>Ballroom Prefunction</td>
</tr>
<tr>
<td>12:00-1:00</td>
<td>Registration</td>
<td>Ballroom Prefunction</td>
</tr>
<tr>
<td>7:30-8:45</td>
<td>PSB Breakfast</td>
<td>Ballroom Courtyard</td>
</tr>
<tr>
<td>8:30-8:40</td>
<td>Welcome</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>8:40-8:50</td>
<td>Introduction</td>
<td></td>
</tr>
<tr>
<td>8:50-9:05</td>
<td><em>Robustly Extracting Medical Knowledge from EHRs: A Case Study of Learning a Health Knowledge Graph</em>&lt;br&gt;Irene Y. Chen, Monica Agrawal, Steven Horng, David Sontag</td>
<td></td>
</tr>
<tr>
<td>9:05-9:20</td>
<td><em>Predicting Longitudinal Outcomes of Alzheimer’s Disease via a Tensor-Based Joint Classification and Regression Model</em>&lt;br&gt;Lodewijk Brand, Kai Nichols, Hua Wang, Heng Huang, Li Shen, for the ADNI</td>
<td></td>
</tr>
<tr>
<td>9:20-9:35</td>
<td><em>Monitoring ICU Mortality Risk with a Long Short-Term Memory Recurrent Neural Network</em>&lt;br&gt;Ke Yu, Mingda Zhang, Tianyi Cui, Milos Hauskrecht</td>
<td></td>
</tr>
<tr>
<td>9:35-9:50</td>
<td><em>Addressing the Credit Assignment Problem in Treatment Outcome Prediction Using Temporal Difference Learning</em>&lt;br&gt;Sahar Harati, Andrea Crowell, Helen Mayberg, Shamim Nemati</td>
<td></td>
</tr>
<tr>
<td>9:50-10:05</td>
<td><em>From Genome to Phenome: Predicting Multiple Cancer Phenotypes Based on Somatic Genomic Alterations via the Genomic Impact Transformer</em>&lt;br&gt;Yifeng Tao, Chunhui Cai, William W. Cohen, Xinghua Lu</td>
<td></td>
</tr>
<tr>
<td>10:05-10:20</td>
<td><em>Automated Phenotyping of Patients with Non-Alcoholic Fatty Liver Disease Reveals Clinically Relevant Disease Subtypes</em>&lt;br&gt;Maxence Vandromme, Tomi Jun, Ponni Perumalswami, Joel T. Dudley, Andrea Branch, Li Li</td>
<td></td>
</tr>
</tbody>
</table>

### Break

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:35-10:50</td>
<td>Break</td>
</tr>
</tbody>
</table>
Pacific Symposium on Biocomputing (PSB) 2020 Schedule
January 3-7, 2020, Big Island of Hawaii

**Saturday, January 4, 2020 continued**

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:50-12:00</td>
<td><strong>Building the FAIR Research Commons for Life Sciences: the pain, the glory</strong>&lt;br&gt;Carole Goble with introduction by Larry Hunter</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>12:00-1:15</td>
<td>Lunch</td>
<td>Ballroom Courtyard</td>
</tr>
<tr>
<td>1:30-4:30</td>
<td><strong>Translational Bioinformatics Workshop: Biobanks in the Precision Medicine Era</strong>&lt;br&gt;Co-chairs: Marylyn Ritchie, Jason Moore, Ju Han Kim</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>4:30-</td>
<td>Dinner &amp; Evening on own</td>
<td></td>
</tr>
</tbody>
</table>

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

*December 19, 2019*
Pacific Symposium on Biocomputing (PSB) 2020 Schedule
January 3-7, 2020, Big Island of Hawaii

Sunday, January 5, 2020

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:30-8:30</td>
<td>Registration</td>
<td>Ballroom Prefunction</td>
</tr>
<tr>
<td>7:30-8:45</td>
<td>Breakfast</td>
<td>Ballroom Courtyard</td>
</tr>
<tr>
<td>8:30-8:40</td>
<td>Morning Announcements</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>8:40-9:10</td>
<td>Steven Brenner, University of California, Berkeley</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>9:10-9:40</td>
<td>Greg Hampikian, Boise State University</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td></td>
<td>Session 2</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>9:45-9:55</td>
<td>Introduction</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>9:55-10:15</td>
<td>Invited Talk: Kristin Lauter</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>10:15-10:30</td>
<td>Integrated Cancer Subtyping using Heterogeneous Genome-Scale Molecular Datasets</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>10:30-10:45</td>
<td>Assessment of coverage for endogenous metabolites and exogenous chemical compounds using an untargeted metabolomics platform</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>10:45-11:00</td>
<td>Coverage profile correction of shallow-depth circulating cell-free DNA sequencing via multi-distance learning</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>11:00-11:15</td>
<td>PGxMine: Text mining for curation of PharmGKB</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>11:15-11:30</td>
<td>Break</td>
<td></td>
</tr>
<tr>
<td>11:30-11:45</td>
<td>The power of dynamic social networks to predict individuals’ mental health</td>
<td></td>
</tr>
<tr>
<td>11:45-12:00</td>
<td>Implementing a Cloud Based Method for Protected Clinical Trial Data Sharing</td>
<td></td>
</tr>
<tr>
<td>12:00-12:15</td>
<td>Pathway and network embedding methods for prioritizing psychiatric drugs</td>
<td></td>
</tr>
</tbody>
</table>

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

December 19, 2019
## Sunday, January 5, 2020 continued

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>12:15-12:30</td>
<td><strong>Robust-ODAL: Learning from heterogeneous health systems without sharing patient-level data</strong>&lt;br&gt;   Jiayi Tong, Rui Duan, Ruowang Li, Martijn J. Scheuemie, Jason H. Moore, Yong Chen</td>
</tr>
<tr>
<td>12:30-12:45</td>
<td><strong>Computationally efficient, exact, covariate-adjusted genetic principal component analysis by leveraging individual marker summary statistics from large biobanks</strong>&lt;br&gt;   Jack Wolf, Martha Barnard, Xueting Xia, Nathan Ryder, Jason Westra, Nathan Tintle</td>
</tr>
</tbody>
</table>

### Poster Session Lunch

**Poster Session with Lunch** (food available 12:45-2:00; drinks until 2:30)<br>   (Posters on ODD numbered boards presented from 1:00-1:45)<br>   (Posters on EVEN numbered boards presented from 1:45-2:30)

### Discussion Session

**Joint Discussion Session: Artificial Intelligence for Enhancing Clinical Medicine and Precision medicine: addressing the challenges of sharing, analysis, and privacy at scale**

### Parasite & Symbiont Awards

**Parasite & Symbiont Awards**

### Break

5:00- 

**Dinner and evening on own**

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

*December 19, 2019*
Monday, January 6, 2020

Breakfast
7:30-8:45  PSB Breakfast

Announcements
8:30-8:40  Morning Announcements

Session 3  Salon 2&3

Pattern Recognition in Biomedical Data: Challenges in Putting Big Data to Work
Co-chairs: Brett Beaulieu-Jones, Christian Darabos, Dokyoon Kim, Shilpa Kobren, Anurag Verma

8:40-8:50  Introduction
8:50-9:10  Invited Talk: Gabriel Brat
9:10-9:25  Clinical Concept Embeddings Learned from Massive Sources of Multimodal Medical Data

Jie Hao, Sai Chandra Kosaraju, Nelson Zange Tsaku, Dae Hyun Song, Mingon Kang

9:40-9:55  Microvascular Dynamics from 4D Microscopy Using Temporal Segmentation
Shir Gur, Lior Wolf, Lior Golgher, Pablo Blinder

9:55-10:10  Assessment of Imputation Methods for Missing Gene Expression Data in Meta-Analysis of Distinct Cohorts of Tuberculosis Patients
Carly A. Bobak, Lauren McDonnell, Matthew D. Nemesure, Justin Lin, Jane E. Hill

10:10-10:25  Using Transcriptional Signatures to Find Cancer Drivers with LURE
David Haan, Ruikang Tao, Verena Friedl, Ioannis N Anastopoulos, Christopher K Wong, Alana S Weinstein, Joshua M Stuart

10:25-10:40  Two-stage ML Classifier for Identifying Host Protein Targets of the Dengue Protease
Jacob T. Stanley, Alison R. Gilchrist, Alex C. Stabell, Mary A. Allen, Sara L. Sawyer, Robin D. Dowell

10:40-11:00  Break

11:00-11:15  Machine learning algorithms for simultaneous supervised detection of peaks in multiple samples and cell types
Toby Dylan Hocking, Guillaume Bourque

11:15-11:30  Graph-based information diffusion method for prioritizing functionally related genes in protein-protein interaction networks
Minh Pham, Olivier Lichtarge

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.
**Monday, January 6, 2020 continued**

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
</table>
| 11:30-11:45 | A Literature-Based Knowledge Graph Embedding Method for Identifying Drug Repurposing Opportunities in Rare Diseases  
Daniel N. Sosa, Alexander Derry, Margaret Guo, Eric Wei, Connor Brinton, Russ B. Altman |
| 11:45-12:00 | Enhancing Model Interpretability and Accuracy for Disease Progression Prediction via Phenotype-Based Patient Similarity Learning  
Yue Wang, Tong Wu, Yunlong Wang, Gao Wang |
| 12:00-12:15 | Towards identifying drug side effects from social media using active learning and crowd sourcing  
Sophie Burkhardt, Julia Siekiera, Josua Glodde, Miguel A. Andrade-Navarro, Stefan Kramer |

**Break**

<table>
<thead>
<tr>
<th>Time</th>
<th>Lunch on Own</th>
</tr>
</thead>
<tbody>
<tr>
<td>12:15-2:00</td>
<td></td>
</tr>
</tbody>
</table>

**Discussion Session**  
Plaza

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>2:00-3:00</td>
<td>Pattern Recognition in Biomedical Data: Challenges in Putting Big Data to Work</td>
</tr>
</tbody>
</table>

**Session 4**  
Salon 2&3

**Mutational Signatures: Etiology, Properties and Role in Cancer**  
Co-chairs: Max Leiserson, Teresa Przytycka, Roded Sharan

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>3:00-3:10</td>
<td>Introduction</td>
</tr>
<tr>
<td>3:10-3:30</td>
<td>Invited Talk: Ludmil Alexandrov</td>
</tr>
</tbody>
</table>
| 3:30-3:45 | DNA Repair Footprint Uncovers Contribution of DNA Repair Mechanism to Mutational Signatures  
Damian Wojtowicz, Mark D.M. Leiserson, Roded Sharan, Teresa M. Przytycka |
| 3:45-4:00 | TrackSigFreq: Subclonal Reconstructions Based on Mutation Signatures and Allele Frequencies  
Caitlin F Harrigan, Yulia Rubanova, Quaid Morris, Alina Selega |
| 4:00-4:15 | PhySigs: Phylogenetic Inference of Mutational Signature Dynamics  
Sarah Christensen, Mark D.M. Leiserson, Mohammed El-Kebir |

**Discussion Session**  
Salon 2&3

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>4:15-5:15</td>
<td>Mutational Signatures</td>
</tr>
</tbody>
</table>

**Dinner**  
Coconut Grove

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>5:30-7:00</td>
<td>PSB Dinner Banquet</td>
</tr>
</tbody>
</table>

**Dessert**  
Ballroom Courtyard

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:00-7:30</td>
<td>25th Anniversary Celebration Dessert</td>
</tr>
</tbody>
</table>

**Keynote**  
Salon 2&3

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
</table>
| 7:30-8:30 | Valid or Invalid?: Genetic Data as part of Workplace Wellness Programs  
Ifeoma Ajunwa with introduction by Marylyn Ritchie |

*Please wear your PSB name tag and lanyard for admission to all events and hosted meals.*
Pacific Symposium on Biocomputing (PSB) 2020 Schedule
January 3-7, 2020, Big Island of Hawaii

**Tuesday, January 7, 2020**

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:30-8:30</td>
<td>Breakfast</td>
<td>Ballroom Courtyard</td>
</tr>
<tr>
<td>8:30-8:40</td>
<td>Closing</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>8:40-9:10</td>
<td>TERI Talks</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>9:10-9:40</td>
<td>Session 5</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>9:45-9:55</td>
<td>Introduction</td>
<td></td>
</tr>
<tr>
<td>9:55-10:15</td>
<td>Invited Talk: Lukasz Kurgan</td>
<td></td>
</tr>
<tr>
<td>10:15-10:30</td>
<td>Disordered Function Conjunction: On the in-silico function annotation of intrinsically disordered regions</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>10:30-10:45</td>
<td>De novo ensemble modeling suggests that AP2-binding to disordered regions can increase steric volume of Epsin but not Eps15</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>10:45-11:00</td>
<td>Modulation of p53 transactivation domain conformations by ligand binding and cancer-associated mutations</td>
<td>Salon 2&amp;3</td>
</tr>
<tr>
<td>11:00-11:15</td>
<td>Exploring relationships between the density of charged tracts within disordered regions and phase separation</td>
<td>Salon 2&amp;3</td>
</tr>
</tbody>
</table>

**Discussion Session**

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>11:15-12:15</td>
<td>Intrinsically Disordered Proteins (IDPs) and Their Functions</td>
<td>Salon 2&amp;3</td>
</tr>
</tbody>
</table>

*PSB over--see you next year!*

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

*December 19, 2019*
Workshop: AI Ethics and Values in Biomedicine–Technical Challenges and Solutions

Updated: 12/30/19

Organizers: Dragutin Petkovic, Lester Kobzik, Reza Ghanadan

Friday 01/03/2020  
9:00-12:00

Salon 2&3

9:00 - 9:20 Welcome and Introduction – D. Petkovic

9:20 – 9:45 Social Biases: Propagation and Creation through Predictive Models, Claudia Perlich, Senior Data Scientist, Two Sigma; Stern NYU

9:45 – 10:10 Stories from the Sewer: A Call to Improve How We Shape Training Sets  
Chris Re, Computer Science, Stanford University

10:10 - 10:35 Detecting Bugs in Machine Learning Models Using Data Perturbations  
Sameer Singh, Information and Computer Science, UC Irvine

10:35 - 10:50 BREAK

10:50 – 11:15 I’m not biased, I’m a computer. Trust me (at your own peril)  
Jessica Tenenbaum, Biostatistics and Bioinformatics, Duke University

11:15 – 11:55 Moderated Panel discussion with speakers as panelists  
Moderators: L. Kobzik and D. Petkovic

11:55 - 12:00 Discussion summary by workshop moderators
# PACKAGING BIOCOMPUTING SOFTWARE TO MAXIMIZE DISTRIBUTION AND REUSE

PSB Tutorial Workshop  
January 3rd, 2020 9:00-12:00 in Plaza Ballroom

## Agenda

<table>
<thead>
<tr>
<th>Time</th>
<th>Activity</th>
<th>Presenter</th>
</tr>
</thead>
<tbody>
<tr>
<td>9:00 – 9:10</td>
<td>Install Software and Group Introductions</td>
<td>Will Bush</td>
</tr>
<tr>
<td></td>
<td>Intro and Overview of Software Packaging, Distribution, and Its Importance</td>
<td>Will Bush</td>
</tr>
<tr>
<td>9:10 – 9:20</td>
<td></td>
<td></td>
</tr>
<tr>
<td>9:20 – 10:05</td>
<td>Intro to Jupyter Notebooks</td>
<td>Christian Darabos</td>
</tr>
<tr>
<td>10:05 – 10:50</td>
<td>R Packages and CRAN Submission</td>
<td>Nicholas Wheeler</td>
</tr>
<tr>
<td>10:50 – 11:35</td>
<td>Creating a Reproducible Computing Environment</td>
<td>Brett Beulieu-Jones</td>
</tr>
<tr>
<td>11:35 – 12:00</td>
<td>Distribution and Version Control</td>
<td>Everyone</td>
</tr>
</tbody>
</table>
Navigating Ethical Quandaries with the Privacy Dilemma of Biomedical Datasets

January 3, 2020 1:30-4:30pm in Salon 2&3

1:30 – 1:50 Introduction (Meg Doerr and Gamze Gursoy)

1:50 – 2:10 John Wilbanks: Translational bioethics in a monopoly network era

2:10 – 2:30 Jennifer Wagner: Legal Angles and the ‘Illusion’ of Certainty: Regulation of Diverse Data Sets

2:30 – 2:50 Heidi Sofia: Advancing data sharing with security and privacy at NIH

2:50 – 3:10 Lucila Ohno-Machado: Responsible data sharing: Patient preferences, institutional policies, and privacy technology

3:10– 3:25 Corey Hudson: From buffer overflowing genomics tools to securing genomic pipelines

3:25 – 3:40 Charlotte Brannon: Applications of blockchain technology to genomics

3:40 – 3:45 Lightning Talk, Xiaoqian Jiang: Secure Cohort Identification for Clinical Trial using Heterogeneous Healthcare Data

3:45 – 4:30 Panel Discussion facilitated by Meg Doerr and Steven Brenner
Introduction to the JBrowse genome browser
January 3, 2020 1:30-3:00pm
Plaza Ballroom

Schedule

<table>
<thead>
<tr>
<th>Time</th>
<th>Presenter</th>
<th>Topic</th>
</tr>
</thead>
<tbody>
<tr>
<td>1:30-1:40</td>
<td>Ian Holmes</td>
<td>Welcome, JBrowse and JBrowse 2 overview</td>
</tr>
<tr>
<td>1:40-2:40</td>
<td>Colin Diesh and Garrett Stevens</td>
<td>JBrowse 2 architecture, SV inspector, and detailed overview of JBrowse 2</td>
</tr>
<tr>
<td>2:40-3:00</td>
<td>Ian Holmes</td>
<td>Coverage of the JBrowse ecosystem, including plugins, JBrowse Connect, Apollo, and the future.</td>
</tr>
</tbody>
</table>
# Workshop Agenda

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker &amp; Affiliation</th>
<th>Topic</th>
</tr>
</thead>
<tbody>
<tr>
<td>1:30-2:00</td>
<td><strong>Marilyn Ritchie</strong>, University of Pennsylvania</td>
<td><em>Why use biobanks for precision medicine</em></td>
</tr>
<tr>
<td>2:00-2:30</td>
<td><strong>Matt Nelson</strong>, Deerfield</td>
<td><em>How pharma uses biobanks for precision medicine</em></td>
</tr>
<tr>
<td>2:30-3:00</td>
<td><strong>Joanna Mountain</strong>, 23andMe</td>
<td><em>23andMe's Customer-Powered Research</em></td>
</tr>
<tr>
<td>3:00-3:30</td>
<td><strong>Ju Han Kim</strong>, Seoul National Univ. College of Medicine</td>
<td><em>Towards precision pharmacotherapy from rare and common variants in your personal genome</em></td>
</tr>
<tr>
<td>3:30-4:00</td>
<td><strong>Jason Moore</strong>, University of Pennsylvania</td>
<td><em>Harnessing AI and Machine Learning in biobanks - the future and the now</em></td>
</tr>
<tr>
<td>4:00-4:30</td>
<td></td>
<td><strong>Discussion</strong></td>
</tr>
</tbody>
</table>
Call for Session Proposals
Pacific Symposium on Biocomputing

The Big Island of Hawaii, January 3-7, 2021

This is an invitation to submit proposals for sessions in the 26th Pacific Symposium on Biocomputing (PSB), to be held January 3-7, 2021 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:

- Artificial Intelligence for Enhancing Clinical Medicine
- Pattern Recognition in Biomedical Data: Challenges in Putting Big Data to Work
- Democratizing Health Data for Translational Research
- Imaging Genomics
- Precision medicine: addressing the challenges of sharing, analysis, and privacy at scale
- 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.

http://psb.stanford.edu/callfor/sessionproposals/
Call for Session Proposals
Pacific Symposium on Biocomputing

The Big Island of Hawaii, January 3-7, 2021

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 7, 2020    Proposals Due
March 6, 2020      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

http://psb.stanford.edu/callfor/sessionproposals/
Call for Workshop Proposals
Pacific Symposium on Biocomputing

The Big Island of Hawaii, January 3-7, 2021

This is an invitation to submit proposals for workshops at the 26th Pacific Symposium on Biocomputing (PSB), to be held January 3-7, 2021 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:

- AI Ethics and Values in Biomedicine – Technical Challenges and Solutions
- Navigating ethical quandaries with the privacy dilemma of biomedical datasets
- Training the Next Generation of Quantitative Biologists
- Packaging Biocomputing Software to Maximize Distribution and Reuse
- Diversity and Disparity in Biomedical Informatics
- Integrating Community-level Data Resources for Precision Medicine Research
- Translational Bioinformatics Workshop: Biobanks in the Precision Medicine Era
- 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/.

http://psb.stanford.edu/callfor/workshopproposals/
Call for Workshop Proposals
Pacific Symposium on Biocomputing

The Big Island of Hawaii, January 3-7, 2021

Important Dates

February 7, 2020         Proposals Due
March 6, 2020           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

http://psb.stanford.edu/callfor/workshopproposals/
Abstract titles and author index only.

**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 #2-39 are not assigned poster space.

Abstracts are organized first by session, then the last name of the first author. Presenting authors’ names are **underlined** in the Table of Contents and in **bold** text on the abstracts.
PROCEEDINGS PAPERS WITH ORAL PRESENTATIONS

ATRIFICIAL INTELLIGENCE FOR ENHANCING CLINICAL MEDICINE ..................................................... 1
PREDICTING LONGITUDINAL OUTCOMES OF ALZHEIMER’S DISEASE VIA A TENSOR-BASED JOINT
CLASSIFICATION AND REGRESSION MODEL .............................................................................................. 2
Lodewijk Brand, Kai Nichols, Hua Wang, Heng Huang, Li Shen, for the ADNI
ROBUSTLY EXTRACTING MEDICAL KNOWLEDGE FROM EHRs: A CASE STUDY OF LEARNING A HEALTH
KNOWLEDGE GRAPH .......................................................................................................................................... 3
Irene Y. Chen, Monica Agrawal, Steven Horng, David Sontag
INCREASING CLINICAL TRIAL ACCRUAL VIA AUTOMATED MATCHING OF BIOMARKER CRITERIA ................. 4
ADDRESSING THE CREDIT ASSIGNMENT PROBLEM IN TREATMENT OUTCOME PREDICTION USING TEMPORAL
DIFFERENCE LEARNING ............................................................................................................................... 5
Sahar Harati, Andrea Crowell, Helen Mayberg, Shamim Nemati
FROM GENOME TO PHENOME: PREDICTING MULTIPLE CANCER PHENOTYPES BASED ON SOMATIC GENOMIC
ALTERATIONS VIA THE GENOMIC IMPACT TRANSFORMER ........................................................................ 6
Yifeng Tao, Chunhui Cai, William W. Cohen, Xinghua Lu
AUTOMATED PHENOTYPING OF PATIENTS WITH NON-ALCOHOLIC FATTY LIVER DISEASE REVEALS CLINICALLY
RELEVANT DISEASE SUBTYPES .................................................................................................................. 7
Maxence Vandromme, Tomi Jun, Ponn Peramalswami, Joel T. Dudley, Andrea Branch, Li Li
MONITORING ICU MORTALITY RISK WITH A LONG SHORT-TERM MEMORY RECURRENT NEURAL NETWORK... 8
Ke Yu, Mingda Zhang, Tianyi Cui, Milos Hauskrecht

INTRINSICALLY DISORDERED PROTEINS (IDPS) AND THEIR FUNCTIONS .............................................. 9
DISORDERED FUNCTION CONJUNCTION: ON THE IN-SILICO FUNCTION ANNOTATION OF INTRINSICALLY
DISORDERED REGIONS ................................................................................................................................. 10
Sina Ghadermarzi, Akila Katiwawala, Christopher J. Oldfield, Amita Barik, Lukasz Kurgan
DE NOVO ENSEMBLE MODELING SUGGESTS THAT AP2-BINDING TO DISORDERED REGIONS CAN INCREASE STERIC
VOLUME OF EPSIN BUT NOT EPS15 ............................................................................................................... 11
N. Suhas Jagannathan, Christopher W. V. Hogue, Lisa Tucker-Kellogg
MODULATION OF p53 TRANSACTIONAL DOMAIN CONFORMATIONS BY LIGAND BINDING AND CANCER-
ASSOCIATED MUTATIONS ............................................................................................................................ 12
Xiaorong Liu, Jianhan Chen
EXPLORING RELATIONSHIPS BETWEEN THE DENSITY OF CHARGED TRACTS WITHIN DISORDERED REGIONS AND
PHASE SEPARATION ...................................................................................................................................... 13
Ramiz Somjee, Diana M. Mitrea, Richard W. Kriwacki

MUTATIONAL SIGNATURES ......................................................................................................................... 14
PHYSIGS: PHYLOGENETIC INFERENCE OF MUTATIONAL SIGNATURE DYNAMICS .................................. 15
Sarah Christensen, Mark D.M. Leiserson, Mohammed El-Kebir
TRACKSIGFREQ: SUBCLONAL RECONSTRUCTIONS BASED ON MUTATION SIGNATURES AND ALLELE FREQUENCIES.. 16
Caitlin F. Harrigan, Yulia Rubanova, Quaid Morris, Alina Selega
DNA REPAIR FOOTPRINT UNCOVERS CONTRIBUTION OF DNA REPAIR MECHANISM TO MUTATIONAL
SIGNATURES .................................................................................................................................................. 17
Damian Wojtowicz, Mark D.M. Leiserson, Roded Sharan, Teresa M. Przytycka

PATTERN RECOGNITION IN BIOMEDICAL DATA: CHALLENGES IN PUTTING BIG DATA TO
WORK .............................................................................................................................................................. 18
CLINICAL CONCEPT EMBEDDINGS LEARNED FROM MASSIVE SOURCES OF MULTIMODAL MEDICAL DATA ........ 19
ASSESSMENT OF IMPUTATION METHODS FOR MISSING GENE EXPRESSION DATA IN META-ANALYSIS OF DISTINCT COHORTS OF TUBERCULOSIS PATIENTS .................................................................................................................. 20
   Carly A. Bobak, Lauren McDonnell, Matthew D. Nemesure, Justin Lin, Jane E. Hill
TOWARDS IDENTIFYING DRUG SIDE EFFECTS FROM SOCIAL MEDIA USING ACTIVE LEARNING AND CROWD SOURCING ........................................................................................................................................... 21
   Sophie Burkhardt, Julia Siekiera, Josua Glodde, Miguel A. Andrade-Navarro, Stefan Kramer
MICROVASCULAR DYNAMICS FROM 4D MICROSCOPY USING TEMPORAL SEGMENTATION ................................................................................................................................. 22
   Shir Gur, Lior Wolf, Lior Golgher, Pablo Blinder
USING TRANSCRIPTIONAL SIGNATURES TO FIND CANCER DRIVERS WITH LURE ................................................................................................................................. 23
   David Haan, Ruikang Tao, Verena Friedl, Ioannis N. Anastopoulos, Christopher K. Wong, Alana S. Weinstein, Joshua M. Stuart
PAGE-NET: INTERPRETABLE AND INTEGRATIVE DEEP LEARNING FOR SURVIVAL ANALYSIS USING HISTOPATHOLOGICAL IMAGES AND GENOMIC DATA ................................................................................................................................. 24
   Jie Hao, Sai Chandra Kosaraju, Nelson Zange Tsaku, Dae Hyun Song, Mingon Kang
MACHINE LEARNING ALGORITHMS FOR SIMULTANEOUS SUPERVISED DETECTION OF PEAKS IN MULTIPLE SAMPLES AND CELL TYPES ................................................................................................................................. 25
   Toby Dylan Hocking, Guillaume Bourque
GRAPH-BASED INFORMATION DIFFUSION METHOD FOR PRIORITIZING FUNCTIONALLY RELATED GENES IN PROTEIN-PROTEIN INTERACTION NETWORKS ................................................................................................................................. 26
   Minh Pham, Olivier Lichtarge
A LITERATURE-BASED KNOWLEDGE GRAPH EMBEDDING METHOD FOR IDENTIFYING DRUG REPURPOSING OPPORTUNITIES IN RARE DISEASES ................................................................................................................................. 27
   Daniel N. Sosa, Alexander Derry, Margaret Guo, Eric Wei, Connor Brinton, Russ B. Altman
TWO-STAGE ML CLASSIFIER FOR IDENTIFYING HOST PROTEIN TARGETS OF THE DENGUE PROTEASE ................................................................................................................................. 28
   Jacob T. Stanley, Alison R. Gilchrist, Alex C. Stabell, Mary A. Allen, Sara L. Sawyer, Robin D. Dowell
ENHANCING MODEL INTERPRETABILITY AND ACCURACY FOR DISEASE PROGRESSION PREDICTION VIA PHENOTYPE-BASED PATIENT SIMILARITY LEARNING ................................................................................................................................. 29
   Yue Wang, Tong Wu, Yunlong Wang, Gao Wang

PRECISION MEDICINE: ADDRESSING THE CHALLENGES OF SHARING, ANALYSIS, AND PRIVACY AT SCALE ........................................................................................................................................... 30
INTEGRATED CANCER SUBTYPING USING HETEROGENEOUS GENOME-SCALE MOLECULAR DATASETS ................................................................................................................................. 31
   Suzan Arslanturk, Sorin Draghici, Tin Nguyen
ASSESSMENT OF COVERAGE FOR ENDOGENOUS METABOLITES AND EXOGENOUS CHEMICAL COMPOUNDS USING AN UNTARGETED METABOLICOMIC PLATFORM ................................................................................................................................. 32
   Sek Won Kong, Carles Hernandez-Ferrer
COVERAGE PROFILE CORRECTION OF SHALLOW-DEPTH CIRCULATING CELL-FREE DNA SEQUENCING VIA MULTI-DISTANCE LEARNING ................................................................................................................................. 33
   Nicholas B. Larson, Melissa C. Larson, Jie Na, Carlos P. Sosa, Chen Wang, Jean-Pierre Kocher, Ross Rowsey
PGXMINE: TEXT MINING FOR CURATION OF PHARMGKB ................................................................................................................................. 34
   Jake Lever, Julia M. Barbarino, Li Gong, Rachel Huddart, Katrin Sangkuhl, Ryan Whaley, Michelle Whirl-Carrillo, Mark Woon, Teri E. Klein, Russ B. Altman
THE POWER OF DYNAMIC SOCIAL NETWORKS TO PREDICT INDIVIDUALS’ MENTAL HEALTH ................................................................................................................................. 35
   Shikang Liu, David Hachen, Omar Lizardo, Christian Poellabauer, Aaron Striegel, Tijana Milenkovic
IMPLEMENTING A CLOUD-BASED METHOD FOR PROTECTED CLINICAL TRIAL DATA SHARING ................................................................................................................................. 36
   Gaurav Luthria, Qingbo Wang
PATHWAY AND NETWORK EMBEDDING METHODS FOR PRIORITIZING PSYCHIATRIC DRUGS ................................................................................................................................. 37
   Yash Pershad, Margaret Guo, Russ B. Altman
ROBUST-ODAL: LEARNING FROM HETEROGENEOUS HEALTH SYSTEMS WITHOUT SHARING PATIENT-LEVEL DATA ................................................................................................................................. 38
   Jiayi Tong, Rui Duan, Ruowang Li, Martijn J. Scheuemi, Jason H. Moore, Yong Chen
PROCEEDINGS PAPERS WITH POSTER PRESENTATIONS

ARTIFICIAL INTELLIGENCE FOR ENHANCING CLINICAL MEDICINE..............................................40
   MULTICLASS DISEASE CLASSIFICATION FROM MICROBIAL WHOLE-COMMUNITY METAGENOMES..................41
      Saad Khan, Libusha Kelly
   LITGEN: GENETIC LITERATURE RECOMMENDATION GUIDED BY HUMAN EXPLANATIONS..........................42
      Allen Nie, Arturo L. Pineda, Matt W. Wright, Hannah Wand, Bryan Wulf, Helio A. Costa, Ronak Y. Patel,
      Carlos D. Bustamante, James Zou
   MULTILEVEL SELF-ATTENTION MODEL AND ITS USE ON MEDICAL RISK PREDICTION..........................43
      Xianlong Zeng, Yunyi Feng, Soheil Moosavinasab, Deborah Lin, Simon Lin, Chang Liu
   IDENTIFYING TRANSITIONAL HIGH COST USERS FROM UNSTRUCTURED PATIENT PROFILES WRITTEN BY
   PRIMARY CARE PHYSICIANS............................................................................................................44
      Haoran Zhang, Elisa Candido, Andrew S. Wilton, Raquel Duchen, Liisa Jaakkimainen, Walter Wodchis,
      Quaid Morris
   OBTAINING DUAL-ENERGY COMPUTED TOMOGRAPHY (CT) INFORMATION FROM A SINGLE-ENERGY CT IMAGE
   FOR QUANTITATIVE IMAGING ANALYSIS OF LIVING SUBJECTS BY USING DEEP LEARNING..................45
      Wei Zhao, Tianling Lv, Rena Lee, Yang Chen, Lei Xing
   INTRINSICALLY DISORDERED PROTEINS (IDPS) AND THEIR FUNCTIONS.............................................46
   MANY-TO-ONE BINDING BY INTRINSICALLY DISORDERED PROTEIN REGIONS........................................47
      Wei-Lun Alterovitz, Eshel Faraghi, Christopher J. Oldfield, Jingwei Meng, Bin Xue, Fei Huang, Pedro Romero,
      Andrzej Kloczkowski, Vladimir N. Uversky, A. Keith Dunker
   MUTATIONAL SIGNATURES................................................................................................................48
   IMPACT OF MUTATIONAL SIGNATURES ON MICRORNA AND THEIR RESPONSE ELEMENTS..................49
      Eirini Stamoulakatou, Pietro Pinoli, Stefano Ceri, Rosario Piro
   GENOME GERRYMANDERING: OPTIMAL DIVISION OF THE GENOME INTO REGIONS WITH CANCER TYPE SPECIFIC
   DIFFERENCES IN MUTATION RATES.................................................................................................50
      Adamo Young, Jacob Chmura, Yoonsik Park, Quaid Morris, Gurnit Atwal
   PATTERN RECOGNITION IN BIOMEDICAL DATA: CHALLENGES IN PUTTING BIG DATA TO
   WORK ...............................................................................................................................................51
   LEARNING A LATENT SPACE OF HIGHLY MULTIDIMENSIONAL CANCER DATA.......................................52
      Benjamin Kompa, Beau Coker
   SCALING STRUCTURAL LEARNING WITH NO-BEARS TO INFERN CAUSAL TRANSCRIPTOME NETWORKS........53
      Hao-Chih Lee, Matteo Danileietto, Riccardo Miotto, Sarah T. Cherng, Joel T. Dudley
   PATHFLOWAI: A HIGH-THROUGHPUT WORKFLOW FOR PREPROCESSING, DEEP LEARNING AND
   INTERPRETATION IN DIGITAL PATHOLOGY.........................................................................................54
      Joshua J. Levy, Lucas A. Salas, Brock C. Christensen, Aravindhan Sriharan, Louis J. Vaikus
   IMPROVING SURVIVAL PREDICTION USING A NOVEL FEATURE SELECTION AND FEATURE REDUCTION
   FRAMEWORK BASED ON THE INTEGRATION OF CLINICAL AND MOLECULAR DATA*..............................55
      Lisa Neumy, Richard Meier, Devin C. Koestler, Jeffrey A. Thompson
   BAYESIAN SEMI-NONNEGATIVE MATRIX TRI-FACTORIZATION TO IDENTIFY PATHWAYS ASSOCIATED WITH
   CANCER PHENOTYPES.....................................................................................................................56
      Sunho Park, Nabhoil Kar, Jae-Ho Cheong, Tae Hyun Hwang
   TREE-WEIGHTING FOR MULTI-STUDY ENSEMBLE LEARNERS................................................................57
      Maya Ramchandran, Prasad Patil, Giovanni Parmigiani
   PTR EXPLORER: AN APPROACH TO IDENTIFY AND EXPLORE POST TRANSCRIPTIONAL REGULATORY
   MECHANISMS USING PROTEOGENOMICS.........................................................................................58
      Arunima Srivastava, Michael Sharpmack, Kun Huang, Parag Mallick, Raghu Machiraju
Network Representation of Large-Scale Heterogeneous RNA Sequences with Integration of Diverse Multi-omics, Interactions, and Annotations Data ................................................................. 59

Nhat Tran, Jean Gao

Hadoop and PySpark for Reproducibility and Scalability of Genomic Sequencing Studies .......... 60
Nicholas R. Wheeler, Penelope Benchek, Brian W. Kunkle, Kara L. Hamilton-Nelson, Mike Warfe, Jeremy R. Fodran, Jonathan L. Haines, William S. Bush

CERENKOV3: Clustering and Molecular Network-Derived Features Improve Computational Prediction of Functional Noncoding SNPs ............................................................................. 61
Yao Yao, Stephen A. Ramsey

Precision Medicine: Addressing the Challenges of Sharing, Analysis, and Privacy at Scale .......................................................................................................................... 62

AnomIGAN: Generative Adversarial Networks for Anonymizing Private Medical Data ............ 63
Ho Bae, Dahuin Jung, Hyun-Soo Choi, Sangroh Yoon

Frequency of ClinVar Pathogenic Variants in Chronic Kidney Disease Patients Surveyed for Return of Research Results at a Cleveland Public Hospital ............................................. 64
Dana C. Crawford, John Lin, Jessica N. Cooke Bailey, Tyler Kinzy, John R. Sedor, John F. O’Toole, Williams S. Bush

Network-Based Matching of Patients and Targeted Therapies for Precision Oncology ........... 65
Qingzhi Liu, Min Jin Ha, Rupam Bhattacharyya, Lana Garmire, Veerabhadran Baladandayuthapani

Phenome-Wide Association Studies on Cardiovascular Health and Fatty Acids Considering Phenotype Quality Control Practices for Epidemiological Data ........................................... 66
Kristin Passero, Xi He, Jiayan Zhou, Bertram Mueller-Myhsok, Marcus E. Kleber, Winfried Maerz, Molly A. Hall

ATEMPO: Pathway-Specific Temporal Anomalies for Precision Therapeutics ............................. 67
Christopher Michael Pietras, Liam Power, Donna K. Slonim

Feature Selection and Dimension Reduction of Social Autism Data ........................................... 68
Peter Washington, Kelley Marie Paskov, Haik Kalantarian, Nathaniel Stockham, Catalin Voss, Aaron Kline, Ritik Patnaik, Brianna Chrisman, Maya Varma, Qandeel Tariq, Kaitlyn Dunlap, Jesse Schwartz, Nick Haber, Dennis P. Wall

Poster Presentations

Artificial Intelligence for Enhancing Clinical Medicine ................................................................ 69

Prioritizing Copy Number Variants Using Phenotype and Gene Functional Similarity .......... 70
Azza Althagafi, Jun Chen, Robert Hoehndorf

Inferring the Reward Functions that Guide Cancer Progression .................................................. 71
John Kalantari, Heidi Nelson, Nicholas Chia

Predicting Disease-Associated Mutation of Metal-Binding Sites in Proteins Using a Deep Learning Approach ........................................................................................................ 72
Mohamad Koohi-Moghadam, Haibo Wang, Yuchuan Wang, Ximning Yang, Hongyan Li, Junwen Wang, Hongze Sun

General ........................................................................................................................................ 73

Ranking Ras Pathway Mutations Using Evolutionary History of MEK1 .......................................... 74
Katia Andrianova, Igor Jouline

Integrative Analysis of COPD and Lung Cancer Metadata Reveals Shared Alterations in Immune Response, PTEN and PI3K-AKT Pathways} ........................................................................... 75
Donnielle Skander, Arda Durmaz, Mohammed Orloff, Gurkan Bebek

Investigating Sources of Irreproducibility in Analysis of Gene Expression Data .......................... 76
Carly A. Bobak, Jane E. Hill

Ethereum and MultiChain Blockchains as Secure Tools for Individualized Medicine .................. 77
Charlotte Brannon, Gamze Gursoy, Sarah Wagner, Mark Gerstein
GENOMIC PREDICTORS OF L-ASPARAGINASE-INDUCED PANCREATITIS IN PEDIATRIC CANCER PATIENTS .......... 78
Britt Drogemoller, Galen E. B. Wright, Shahrad Raskek, Shinya Ito, Bruce Carleton, Colin Ross, The
Canadian Pharmacogenomics Network for Drug Safety Consortium

NITECAP: A NOVEL METHOD AND INTERFACE FOR THE IDENTIFICATION OF CIRCADIAN BEHAVIOR IN HIGHLY
PARALLEL TIME-COURSE DATA .............................................................................................................. 79
Thomas G. Brooks, Cris W. Lawrence, Nicholas F. Lahens, Soumyashant Nayak, Dimitra Sarantopoulou,
Garret A. FitzGerald, Gregory R. Grant

THE INTERPLAY OF OBESITY AND RACE/ETHNICITY ON MAJOR PERINATAL COMPLICATIONS ............. 80
Yaadira Brown, MPH; Olubode A. Olufajo, MD, MPH; Edward E. Cornwell III, MD; William Southerland, PhD

A COMPARISON OF PHARMACOGENOMIC INFORMATION IN FDA-APPROVED DRUG LABELS AND CPIC
GUIDELINES .................................................................................................................................................. 81
Katherine I. Carrillo, Teri E. Klein

XTEA: A TRANSPOSABLE ELEMENT INSERTION ANALYZER FOR GENOME SEQUENCING DATA FROM MULTIPLE
TECHNOLOGIES ............................................................................................................................................. 82
Chong Chu, Rebeca Monroy, Soohyun Lee, E. Alice Lee, Peter J. Park

GO GET DATA (GGD): SIMPLE, REPRODUCIBLE ACCESS TO SCIENTIFIC DATA ........................................ 83
Michael Cormier, Jon Belyeu, Brent Pedersen, Joe Brown, Johannes Koster, Aaron R. Quinlan

GLOBAL EPIGENOMIC REGULATION OF GENE EXPRESSION AND CELLULAR PROLIFERATION IN T-CELL LEUKEMIA .. 84
Sinisa Dovat, Yali Ding, Bo Zhang, Jonathan L. Payne, Feng Yue

A PHARMACOGENOMIC INVESTIGATION OF THE CARDIAC SAFETY PROFILE OF ONDANSETRON IN CHILDREN AND
IN PREGNANT WOMEN .......................................................................................................................... 85
Galen E. B. Wright, Britt I. Drogemoller, Jessica Trueman, Kaitlyn Shaw, Michelle Staub, Shahnaz Chaudhry,
Sholeh Ghasyoori, Fudan Miao, Michelle Higsinson, Gabriella S.S. Groeneweg, James Brown, Laura A Magee,
Simon D. Whyte, Nicholas West, Sonia Brodie, Geert ‘t Jong, Howard Berger, Shinya Ito, Shahrad R. Rassekh,
Shubhayan Sanatani, Colin J.D. Ross, Bruce C. Carleton

TREND: A PLATFORM FOR EXPLORING PROTEIN FUNCTION IN PROKARYOTES USING PHYLOGENETICS, DOMAIN
ARCHITECTURES, AND GENE NEIGHBORHOODS INFORMATION .................................................................. 86
Vadim M. Gumerev, Igor B. Zhulin

TRACKSigFREQ: SUBCLONAL RECONSTRUCTIONS BASED ON MUTATION SIGNATURES AND ALLELE FREQUENCIES .. 87
Caitlin F. Harrigan, Yulia Rubanova, Quaid Morris, Alina Selega

A FLEXIBLE PIPELINE FOR THE PREDICTION OF BIOMARKERS RELEVANT TO DRUG SENSITIVITY ................ 88
V. Keith Hughitt, Sayeh Gorjifard, Aleksandra M. Michalowski, John K. Simmons, Ryan Dale, Eric C. Polley,
Jonathan J. Keats, Beverly A. Mock

CREATING A METABOLIC SYNDROME RESEARCH RESOURCE (MetSRR) ......................................................... 89
Willysha Jenkins, Christian Richardson, ClarLynda Williams-DeVane PhD

UTILIZING CORTHOM INFORMATION TO FIND CAUSATIVE VARIANTS ....................................................... 90
Senay Kafkas, Robert Hoehndorf

INTEGRATED ANALYSIS OF JAK-STAT PATHWAY IN HOMEOSTASIS, SIMULATED INFLAMMATION AND TUMOUR... 91
Milica Krunic, Anzhelika Karjalainen, Mojaysola Joanna Ola, Stephen Shoebridge, Sabine Macho-Masclier,
Caroline Lassnig, Andrea Poezol, Matthias Farlik, Nikolaus Fortelny, Christoph Bock, Birgit Strobl, Mathias Mueller

BEERS 2: THE NEXT GENERATION OF RNA-SEQ SIMULATOR ..................................................................... 92
Nicholas F. Lahens, Thomas G. Brooks, Dimitra Sarantopoulou, Soumyashant Nayak, Cris Lawrence, Anand
Srinivasan, Jonathan Schug, Garret A. FitzGerald, John B. Hogenesch, Yoseph Barash, Gregory R. Grant

EFFECT MODIFICATION BY AGE ON A DIAGNOSTIC THREE-GENE-SIGNATURE IN PATIENTS WITH ACTIVE
TUBERCULOSIS ................................................................................................................................................... 93
Lauren McDonnell, Carly Bobak, Matthew Nemesure, Justin Lin, Jane Hill

CLASSIFICATION AND MUTATION PREDICTION FROM GASTROINTESTINAL CANCER HISTOPATHOLOGY IMAGES
USING DEEP LEARNING .................................................................................................................................. 94
Sung Hak Lee, Hyun-Jong Jang
PATTERN RECOGNITION IN BIOMEDICAL DATA: CHALLENGES IN PUTTING BIG DATA TO WORK

112

STRATIFICATION OF KIDNEY TRANSPLANT RECIPIENTS BASED ON TEMPORAL DISEASE TRAJECTORIES

Isabella Friis Jørgensen PhD, Søren Schwartz Sørensen PhD, Søren Brunak PhD

MODELING GENE EXPRESSION LEVELS FROM EPIGENETIC MARKERS USING A DYNAMICAL SYSTEMS APPROACH

James Brunner, Jacob Kim, Kord M. Kober

TRANSLATING BIG DATA NEUROIMAGING FINDINGS INTO MEASUREMENTS OF INDIVIDUAL VULNERABILITY

Peter Kochunov, Paul Thompson, Neda Jahanshad, Elliot Hong

AUTOMATING NEW-USER COHORT CONSTRUCTION WITH INDICATION EMBEDDINGS

Rachel D. Melamed

REPRODUCIBILITY-OPTIMIZED STATISTICAL TESTING FOR OMICS STUDIES

Tomi Suomi, Laura Elo

DATA INTEGRATION EXPECTATION MAPS: TOWARDS MORE INFORMED 'OMIC DATA INTEGRATION

Tia Tate, Christain Richardson, ClarLynda Williams-DeVane

PRECISION MEDICINE: ADDRESSING THE CHALLENGES OF SHARING, ANALYSIS, AND PRIVACY AT SCALE

119

INTEGRATED OMICS DATA MINING OF SYNERGISTIC GENE PAIRS FOR CANCER PRECISION MEDICINE

Euna Leong, Choo Park, Sukjoon Yoon

THE POWER OF DYNAMIC SOCIAL NETWORKS TO PREDICT INDIVIDUALS’ MENTAL HEALTH

Shikang Liu, David Hachen, Omar Lizardo, Christian Poellabauer, Aaron Striegel, Tijana Milenkovic

ROBUST-ODAL: LEARNING FROM HETEROGENEOUS HEALTH SYSTEMS WITHOUT SHARING PATIENT-LEVEL DATA

Jiayi Tong, Rui Duan, Ruowang Li, Martijn J. Scheuemie, Jason H. Moore, Yong Chen

PHARMGKB: AUTOMATED LITERATURE ANNOTATIONS

Michelle Whirl-Carrillo, Li Gong, Rachel Huddart, Katrin Sangkuhl, Ryan Whaley, Mark Woon, Julia Barbarino, Jake Lever, Russ B. Altman, Teri E. Klein

WORKSHOPS WITH POSTER PRESENTATIONS

PACKAGING BIOCOMPUTING SOFTWARE TO MAXIMIZE DISTRIBUTION AND REUSE

124

APOLLO PROVIDES COLLABORATIVE GENOME ANNOTATION EDITING WITH THE POWER OF JBrowse

Nathan Dunn, Colin Diesh, Robert Buels, Helena Rasche, Anthony Bretaudeau, Nomi Harris, Ian Holmes

G:Profiler - ONE FUNCTIONAL ENRICHMENT ANALYSIS TOOL, MANY INTERFACES SERVING LIFE SCIENCE COMMUNITIES

Liis Kolberg, Uku Raudvere, Ivan Kuzmin, Jaak Vilo, Hedi Peterson

INCREASING USABILITY AND DISSEMINATION OF THE PATHFX ALGORITHM USING WEB APPLICATIONS AND DOCKER SYSTEMS

Jennifer Wilson, Nicholas Stepanov, Ajinkya Chalke, Mike Wong, Dragutin Petkovic, Russ B. Altman

TRANSLATIONAL BIOINFORMATICS WORKSHOP: BIOBANKS IN THE PRECISION MEDICINE ERA

128

IDENTIFICATION OF BIOMARKERS RELATED TO AUTISM SPECTRUM DISORDER USING GENOMIC INFORMATION

Leena Sait, Martha Gizaw, and Iosif Vaisman

A PAN-CANCER 3-GENE SIGNATURE TO PREDICT DORMANCY

Ivy Tran, Anchal Sharma, Subhajyoti De

AUTHOR INDEX

131
# AUTHOR INDEX

<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>'tJong, Geert</td>
<td>85</td>
</tr>
<tr>
<td>Abyzov, Alexej</td>
<td>111</td>
</tr>
<tr>
<td>Adkins, Joshua</td>
<td>96</td>
</tr>
<tr>
<td>Agrawal, Monica</td>
<td>3</td>
</tr>
<tr>
<td>Alavi, Ali</td>
<td>99</td>
</tr>
<tr>
<td>Allen, Mary A.</td>
<td>28</td>
</tr>
<tr>
<td>Alterovitz, Wei-Lun</td>
<td>47</td>
</tr>
<tr>
<td>Altagafi, Azza</td>
<td>70</td>
</tr>
<tr>
<td>Altman, Russ B.</td>
<td>27, 34, 37, 123, 127</td>
</tr>
<tr>
<td>Anastopoulos, Ioannis N.</td>
<td>23</td>
</tr>
<tr>
<td>Andrade-Navarro, Miguel A.</td>
<td>21</td>
</tr>
<tr>
<td>Andrianova, Katerina</td>
<td>74</td>
</tr>
<tr>
<td>Arslanturk, Suzan</td>
<td>31</td>
</tr>
<tr>
<td>Atwal, Gurnit</td>
<td>50</td>
</tr>
<tr>
<td>Bae, Ho</td>
<td>63</td>
</tr>
<tr>
<td>Bae, Taejeong</td>
<td>111</td>
</tr>
<tr>
<td>Baladandayuthapani, Veerabhadran</td>
<td>65</td>
</tr>
<tr>
<td>Baltrus, David</td>
<td>96</td>
</tr>
<tr>
<td>Barash, Joseph</td>
<td>92</td>
</tr>
<tr>
<td>Barbarino, Julia M.</td>
<td>34, 123</td>
</tr>
<tr>
<td>Barik, Amita</td>
<td>10, 108</td>
</tr>
<tr>
<td>Barlaskar, Sabiha</td>
<td>99</td>
</tr>
<tr>
<td>Barnard, Martha</td>
<td>39</td>
</tr>
<tr>
<td>Beam, Andrew L.</td>
<td>19</td>
</tr>
<tr>
<td>Bebek, Gurkan</td>
<td>75</td>
</tr>
<tr>
<td>Belyeu, Jon</td>
<td>83</td>
</tr>
<tr>
<td>Benchek, Penelope</td>
<td>60</td>
</tr>
<tr>
<td>Berger, Howard</td>
<td>85</td>
</tr>
<tr>
<td>Bhattacharyya, Rupam</td>
<td>65</td>
</tr>
<tr>
<td>Blinder, Pablo</td>
<td>22</td>
</tr>
<tr>
<td>Bobak, Carly A.</td>
<td>20, 76, 93</td>
</tr>
<tr>
<td>Bock, Christoph</td>
<td>91</td>
</tr>
<tr>
<td>Bourque, Guillaume</td>
<td>25</td>
</tr>
<tr>
<td>Branch, Andrea</td>
<td>7</td>
</tr>
<tr>
<td>Brand, Lodewijk</td>
<td>2</td>
</tr>
<tr>
<td>Brannon, Charlotte</td>
<td>77</td>
</tr>
<tr>
<td>Bretaudeau, Anthony</td>
<td>125</td>
</tr>
<tr>
<td>Brinton, Connor</td>
<td>27</td>
</tr>
<tr>
<td>Brodie, Sonia</td>
<td>85</td>
</tr>
<tr>
<td>Brooks, Thomas G.</td>
<td>79, 92</td>
</tr>
<tr>
<td>Brown, James</td>
<td>85</td>
</tr>
<tr>
<td>Brown, Joe</td>
<td>83</td>
</tr>
<tr>
<td>Brown, Yaadira</td>
<td>80</td>
</tr>
<tr>
<td>Brunak, Søren</td>
<td>113</td>
</tr>
<tr>
<td>Brunner, James</td>
<td>114</td>
</tr>
<tr>
<td>Buels, Robert</td>
<td>125</td>
</tr>
<tr>
<td>Bui, Nam</td>
<td>4</td>
</tr>
<tr>
<td>Bull, Shelley B.</td>
<td>105</td>
</tr>
<tr>
<td>Burkhardt, Sophie</td>
<td>21</td>
</tr>
<tr>
<td>Bush, William S.</td>
<td>60, 64</td>
</tr>
<tr>
<td>Bustamante, Carlos D.</td>
<td>42</td>
</tr>
<tr>
<td>Cai, Chunhui</td>
<td>6</td>
</tr>
<tr>
<td>Cai, DanDan</td>
<td>99</td>
</tr>
<tr>
<td>Cai, Tianxi</td>
<td>19</td>
</tr>
<tr>
<td>Calvanese, Vincenzo</td>
<td>95</td>
</tr>
<tr>
<td>Candido, Elisa</td>
<td>44</td>
</tr>
<tr>
<td>Capellera-Garcia, Sandra</td>
<td>95</td>
</tr>
<tr>
<td>Carleton, Bruce C.</td>
<td>78, 85</td>
</tr>
<tr>
<td>Carrillo, Katherine I.</td>
<td>81</td>
</tr>
<tr>
<td>Ceri, Stefano</td>
<td>49</td>
</tr>
<tr>
<td>Chalke, Ajinkyia</td>
<td>127</td>
</tr>
<tr>
<td>Chaudhry, Shahnaz</td>
<td>85</td>
</tr>
<tr>
<td>Chen, Irene Y.</td>
<td>3</td>
</tr>
<tr>
<td>Chen, Jessica W.</td>
<td>4</td>
</tr>
<tr>
<td>Chen, Jianhan</td>
<td>12</td>
</tr>
<tr>
<td>Chen, Jun</td>
<td>70</td>
</tr>
<tr>
<td>Chen, Yang</td>
<td>45</td>
</tr>
<tr>
<td>Chen, Yong</td>
<td>38, 122</td>
</tr>
<tr>
<td>Cheong, Hee Jin</td>
<td>102</td>
</tr>
<tr>
<td>Cheong, Jae-Ho</td>
<td>56</td>
</tr>
<tr>
<td>Chiesa, Sarah T.</td>
<td>53</td>
</tr>
<tr>
<td>Chia, Nicholas</td>
<td>71</td>
</tr>
<tr>
<td>Chmura, Jacob</td>
<td>50</td>
</tr>
<tr>
<td>Choi, Hyun-Soo</td>
<td>63</td>
</tr>
<tr>
<td>Chrisman, Brianna</td>
<td>68, 103</td>
</tr>
<tr>
<td>Christensen, Brock C.</td>
<td>54</td>
</tr>
<tr>
<td>Christensen, Sarah</td>
<td>15</td>
</tr>
<tr>
<td>Chu, Chong</td>
<td>82</td>
</tr>
<tr>
<td>Cohen, William W.</td>
<td>6</td>
</tr>
<tr>
<td>Coker, Beau</td>
<td>52</td>
</tr>
<tr>
<td>Cooke Bailey, Jessica N.</td>
<td>64</td>
</tr>
<tr>
<td>Cormier, Michael</td>
<td>83</td>
</tr>
<tr>
<td>Cornwall III, Edward E.</td>
<td>80</td>
</tr>
<tr>
<td>Costa, Helio A.</td>
<td>4, 42</td>
</tr>
<tr>
<td>Crawford, Dana C.</td>
<td>64</td>
</tr>
<tr>
<td>Crowell, Andrea</td>
<td>5</td>
</tr>
<tr>
<td>Cui, Tianyi</td>
<td>8</td>
</tr>
<tr>
<td>Dale, Ryan</td>
<td>88</td>
</tr>
<tr>
<td>Danieletto, Matteo</td>
<td>53</td>
</tr>
<tr>
<td>De, Subhajyoti</td>
<td>130</td>
</tr>
<tr>
<td>Derry, Alexander</td>
<td>27</td>
</tr>
<tr>
<td>Diesh, Colin</td>
<td>125</td>
</tr>
<tr>
<td>Ding, Yali</td>
<td>84</td>
</tr>
</tbody>
</table>
Dovat, Sinisa · 84
Dowell, Robin D. · 28
Draghici, Sorin · 31
Drögemöller, Britt i · 78, 85
Duan, Rui · 38, 122
Duchen, Raquel · 44
Dudley, Joel T. · 7, 53
Dunker, A. Keith · 47
Dunlap, Kaiti · 103
Dunlap, Kaitlyn · 68
Dunn, Nathan · 125
Durmaz, Arda · 75

E
Ekstrand, Sophia · 95
El-Kebir, Mohammed · 15
Elo, Laura · 117

F
Faraggi, Eshel · 47
Farlik, Matthias · 91
Feng, Song · 96
Feng, Yunyi · 43
FitzGerald, Garret A. · 79, 92
Fondran, Jeremy R. · 60
Fortelny, Matthias · 91
Fried, Inbar · 19
Friedl, Verena · 23

G
Gao, Jean · 59
Garmire, Lana · 65
Gerstein, Mark · 77
Ghadermarzi, Sina · 10, 108
Ghayoori, Sholeh · 85
Ghosh, Sayan · 96
Gilchrist, Alison R. · 28
Gizaw, Martha · 129
Glodde, Josua · 21
Golgher, Lior · 22
Gong, Li · 34, 123
Gorjifard, Sayeh · 88
Grant, Gregory R. · 79, 92
Groeneweg, Gabriella S.S. · 85
Gumerov, Vadim M. · 86
Guo, Margaret · 27, 37
Guo, Yicheng · 106
Gur, Shir · 22
Gursoy, Gamze · 77

H
Ha, Min Jin · 65
Haan, David · 23
Haber, Nick · 68, 103
Hachen, David · 35, 121
Haines, Jonathan L. · 60
Halappanavar, Mahantesh · 96
Hall, Molly A. · 66
Hamilton-Nelson, Kara L. · 60
Hao, Jie · 24
Harati, Sahar · 5
Harrigan, Caitlin F. · 16, 87
Harris, Nomi · 125
Hauskrecht, Milos · 8
He, Xi · 66
Hernandez-Ferrer, Carles · 32
Higginson, Michelle · 85
Hill, Jane E. · 20, 76, 93
Hocking, Toby Dylan · 25
Hoehndorf, Robert · 70, 90
Hogenesch, John B. · 92
Hogue, Christopher W. V. · 11
Holmes, Ian · 125
Hong, Elliot · 115
Horng, Steven · 3
Huang, Fei · 47
Huang, Heng · 2
Huang, Kun · 58
Huddart, Rachel · 34, 123
Hughitt, V. Keith · 88
Husic, Arman · 103
Hwang, Tae Hyun · 56

I
Ito, Shinya · 78, 85

J
Jaakkimainen, Liisa · 44
Jagannathan, N. Suhas · 11
Jahanshad, Neda · 115
Jang, Hyun-Jong · 94
Jenkins, Willysha · 89
Jeong, Euna · 120
Jørgensen, Isabella Friis · 113
Jouline, Igor · 74
Jun, Tomi · 7
Jung, Dahun · 63
Jung, Jae-Yoon · 103
K

Kafkas, Senay · 90
Kalanteri, John · 71
Kalantarian, Haik · 68
Kalyva, Maria · 111
Kang, Mingon · 24
Kar, Nabholz · 56
Karjalainen, Anzhelika · 91
Katuwawala, Akila · 10, 108
Keats, Jonathan J. · 88
Kelly, Libusha · 41
Kent, Jack · 103
Kim, Soo Joo · 102
Kim, Tyler · 64
Kleber, Marcus E. · 66
Klein, Tari E. · 34, 81, 123
Kline, Aaron · 103
Kloczkowski, Andrzej · 47
Kober, Kord M. · 114
Koch, Jean-Pierre · 33
Kochunov, Peter · 115
Koestler, Devin C. · 55
Kohane, Isaac S. · 19
Kolberg, Liis · 126
Kompa, Benjamin · 19, 52
Kong, Sek Won · 32
Kooi, Mohagham, Mohamad · 72
Kosaraju, Sai Chandra · 24
Koster, Johannes · 83
Kramer, Stefan · 21
Kriwacki, Richard W. · 13
Krumic, Milica · 91
Kunder, Christian A. · 4
Kunkle, Brian W. · 60
Kurgan, Lukasz · 10, 108
Kuzmin, Ivan · 126

L

Lahens, Nicholas F. · 79, 92
Larson, Melissa C. · 33
Larson, Nicholas B. · 33
Lassnig, Caroline · 91
Lawrence, Cris W. · 79, 92
LeBlanc, Emilie · 103
Lee, E. Alice · 82
Lee, Han Sol · 102
Lee, Hao-Chih · 53
Lee, Joon-Yong · 96
Lee, Rena · 45
Lee, Soohyun · 82
Lee, Sung Hak · 94
Leiserson, Mark D.M. · 15, 17
Lever, Jake · 34, 123
Levy, Joshua J. · 54
Li, Hongyan · 72
Li, Li · 7
Li, Ruowang · 38, 122
Lichtarge, Olivier · 26
Lim, Sooyeon · 102
Lin, Deborah · 43
Lin, John · 64
Lin, Justin · 20, 93
Lin, Simon · 43
Liu, Chang · 43
Liu, Qingzhi · 65
Liu, Shikang · 35, 121
Liu, Xiaorong · 12
Liu, Zhandong · 100
Lizardo, Omar · 35, 121
Lowry, William E. · 100
Lv, Tianling · 45

M

Ma, Feiyang · 95
Machiraju, Raghv · 98
Macho-Maschler, Sabine · 91
Maerz, Winfried · 66
Magee, Laura A. · 85
Mallick, Parag · 58
Manlove, Logan · 111
Mandri, Arjun K. · 101
Mariani, Jessica · 111
Mayberg, Helen · 5
McDermott, Jason · 96
McDonnell, Lauren · 20, 93
Meier, Richard · 55
Melamed, Rachel D. · 116
Melas-Kyriazi, Luke · 101
Meng, Jingwei · 47
Miao, Pudan · 85
Michalowski, Aleksandra M. · 88
Mikkola, Hanna K. A. · 95
Milem, Tijana · 35, 121
Miotto, Riccardo · 53
Mitrea, Diana M. · 13
Mock, Beverly A. · 88
Monroy, Rebeca · 82
Moore, Jason H. · 38, 122
Moosavinasab, Soheil · 43
Morris, Quaid · 16, 44, 50, 87
Mueller, Mathias · 91
Mueller, Myhsok, Bertram · 66

N

Na, Jie · 33
Nakatoochi, Masahiro · 97
Nayak, Soumyashant · 79, 92
Nelson, Heidi · 71
Sosa, Daniel N. · 27
Southerland, William · 80
Sriharan, Aravindhan · 54
Sriniwasan, Anand · 92
Srivastava, Arunima · 58
Stabell, Alex C. · 28
Stamoulakatou, Eirini · 49
Stanley, Jacob T. · 28
Staub, Michelle · 85
Stehr, Henning · 4
Stepanov, Nicholas · 127
Stockham, Nathaniel · 68, 103
Striegel, Aaron · 35, 121
Strobl, Birgit · 91
Stuart, Joshua M. · 23
Sun, Hongzhe · 72
Sun, Min Woo · 103
Suomi, Tomi · 117

T

Tao, Ruikang · 23
Tao, Yifeng · 6
Tariq, Qandeel · 68
Tate, Tia · 118
Thompson, Jeffrey A. · 55
Thompson, Paul · 115
Tintle, Nathan · 39
Tomasi, Livia · 111
Tong, Jiayi · 38, 122
Tran, Ivy · 130
Tran, Nhat · 59
Trueman, Jessica · 85
Tsak, Nelson Zange · 24
Tucker-Kellogg, Lisa · 11

U

Urban, Alexander E. · 111
Uversky, Vladimir N. · 47

V

Vaccarino, Flora M. · 111
Vaickus, Louis J. · 54
Vaisman, Iosif · 129
Vandromme, Maxence · 7
Varma, Maya · 68, 103
Vito, Jaak · 126
Voss, Catalin · 68, 103

W

Wagner, Sarah · 77
Wall, Dennis P. · 68, 103
Wan, Ying-Wooi · 100
Wand, Hannah · 42
Wang, Chen · 33
Wang, Gao · 29
Wang, Halbo · 72
Wang, Hua · 2
Wang, Junwen · 72
Wang, Qingbo · 36
Wang, Yuchuan · 72
Wang, Yue · 29
Wang, Yunlong · 29
Warfa, Mike · 60
Washington, Peter · 68, 103
Weber, Griffin · 19
Wei, Eric · 27
Weinstein, Alana S. · 23
West, Nicholas · 85
Westra, Jason · 39
Whaley, Ryan · 34, 123
Wheeler, Nicholas R. · 60
Whirl-Carrillo, Michelle · 34, 123
Whyte, Simon D. · 85
Williams-DeVane, ClarLynda · 89, 118
Wilson, Jennifer · 127
Wilton, Andrew S. · 44
Wodchis, Walter · 44
Wojtowicz, Damian · 17
Wolf, Jack · 39
Wolf, Lior · 22
Wong, Christopher K. · 23
Wong, Mike · 127
Woon, Mark · 34, 123
Wright, Galen E. B. · 78, 85
Wright, Matt W. · 42
Wu, Tong · 29
Wulf, Bryan · 42

X

Xia, Xueting · 39
Xing, Lei · 45
Xue, Bin · 47

Y

Yalamanchili, Hari Krishna · 100
Yang, Hee Chul · 104
Yang, Jizhou · 99
Yang, Xinming · 72
Yao, Yao · 61
Yavartanu, Fatemeh · 105
Yoo, Yun Joo · 105
Yoon, Sukjoon · 120
Yoon, Sungroh · 63
Young, Adamo · 50
Yu, Ke · 8
Yue, Feng · 84
<table>
<thead>
<tr>
<th>Name</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Zehnder, James L.</td>
<td>4</td>
</tr>
<tr>
<td>Zeng, Xianlong</td>
<td>43</td>
</tr>
<tr>
<td>Zhang, Bo</td>
<td>84</td>
</tr>
<tr>
<td>Zhang, Haoran</td>
<td>44</td>
</tr>
<tr>
<td>Zhang, Lin</td>
<td>106</td>
</tr>
<tr>
<td>Zhang, Mingda</td>
<td>8</td>
</tr>
<tr>
<td>Zhao, Wei</td>
<td>45</td>
</tr>
<tr>
<td>Zhou, Bo</td>
<td>111</td>
</tr>
<tr>
<td>Zhou, Jiayan</td>
<td>66</td>
</tr>
<tr>
<td>Zhulin, Igor B.</td>
<td>86</td>
</tr>
<tr>
<td>Zoghbi, Huda Y.</td>
<td>100</td>
</tr>
<tr>
<td>Zou, James</td>
<td>42</td>
</tr>
<tr>
<td>Name</td>
<td>Institution</td>
</tr>
<tr>
<td>---------------------------</td>
<td>--------------------------------------------------</td>
</tr>
<tr>
<td>Alexej Abyzov</td>
<td>Mayo Clinic</td>
</tr>
<tr>
<td>Olga Afanasiev</td>
<td>Dermatology</td>
</tr>
<tr>
<td>Nima Aghaeepour</td>
<td>Stanford University</td>
</tr>
<tr>
<td>Ifeoma Ajunwa</td>
<td>Cornell University</td>
</tr>
<tr>
<td>Ludmil Alexandrov</td>
<td>University of California San Diego</td>
</tr>
<tr>
<td>Azza Althagafi</td>
<td>KAUST</td>
</tr>
<tr>
<td>Russ Altman</td>
<td>Stanford University</td>
</tr>
<tr>
<td>Ekaterina Andrianova</td>
<td>The Ohio State University</td>
</tr>
<tr>
<td>Gurnit Atwal</td>
<td>University Of Toronto</td>
</tr>
<tr>
<td>Ho Bae</td>
<td>Seoul National University</td>
</tr>
<tr>
<td>Hyoeun Bang</td>
<td>Korea Advanced Institute of Science and Technology (KAIST)</td>
</tr>
<tr>
<td>Brett Beaulieu-Jones</td>
<td>Harvard Medical School</td>
</tr>
<tr>
<td>Gurkan Bebek</td>
<td>Case Western Reserve University</td>
</tr>
<tr>
<td>Carly Bobak</td>
<td>Dartmouth College</td>
</tr>
<tr>
<td>Mary Boland</td>
<td>University of Pennsylvania, School of Medicine</td>
</tr>
<tr>
<td>Philip Bourne</td>
<td>UVA Data Science Institute</td>
</tr>
<tr>
<td>Charlotte Brannon</td>
<td>Yale University</td>
</tr>
<tr>
<td>Gabriel Brat</td>
<td>Beth Israel Deaconess Medical Center</td>
</tr>
<tr>
<td>Steven Brenner</td>
<td>University of California, Berkeley</td>
</tr>
<tr>
<td>Fiona Brinkman</td>
<td>Simon Fraser University</td>
</tr>
<tr>
<td>Thomas Brooks</td>
<td>University of Pennsylvania</td>
</tr>
<tr>
<td>Yaadira Brown</td>
<td>Howard University</td>
</tr>
<tr>
<td>Søren Brunak</td>
<td>Novo Nordisk Foundation Center for Protein Research</td>
</tr>
<tr>
<td>Martha Bulyk</td>
<td>BWH &amp; HMS</td>
</tr>
<tr>
<td>Sophie Burkhardt</td>
<td>JGU Mainz</td>
</tr>
<tr>
<td>William Bush</td>
<td>Case Western Reserve University</td>
</tr>
<tr>
<td>J. Brian Byrd</td>
<td>University of Michigan / Michigan Medicine</td>
</tr>
<tr>
<td>Katherine Carrillo</td>
<td>Gunn High School</td>
</tr>
<tr>
<td>Benoit Chabot</td>
<td>Université de Sherbrooke</td>
</tr>
<tr>
<td>Mark Chance</td>
<td>Case Western Reserve University</td>
</tr>
<tr>
<td>Irene Chen</td>
<td></td>
</tr>
<tr>
<td>Jessica Chen</td>
<td>Stanford University</td>
</tr>
<tr>
<td>Jianhan Chen</td>
<td>University of Massachusetts Amherst</td>
</tr>
<tr>
<td>Jonathan Chen</td>
<td>Stanford Department of Medicine</td>
</tr>
<tr>
<td>Chao Cheng</td>
<td>Baylor College of Medicine</td>
</tr>
<tr>
<td>Jane Chiang</td>
<td>Cipherome, Inc.</td>
</tr>
</tbody>
</table>
Pacific Symposium on Biocomputing 2020
Participant List
as of December 5, 2019

Tony Chiang
Allen Institute for Immunology

Geetha Chittoor
Geisinger

Sarah Christensen
University of Illinois at Urbana-Champaign

Dana Crawford
Case Western Reserve University

Tianyi Cui
University of Pittsburgh

Roxana Daneshjou
Stanford University

Christian Darabos
Dartmouth College

Alexander Derry
Stanford University

Colin Diesh

Megan Doerr
Sage Bionetworks

Sinisa Dovat
Penn State University College of Medicine

Sorin Draghici
Wayne State University

Britt Drogemoller
University of British Columbia

A Keith Dunker
Indiana University

Nathan Dunn
Lawrence Berkeley National Lab

Mohammed El-Kebir
University of Illinois Urbana-Champaign

Laura Elo
University Of Turku

Anne-Katrin Emde
Variant Bio

Yayin Fang
Howard University College of Medicine

James Foster
University of Idaho

Andre Franke
Institute of Clinical Molecular Biology, Kiel University

Verena Friedl
University of California, Santa Cruz

Isabella Friis Jørgensen
NNF Center for Protein Research

Jean Gao
University of Texas Arlington

Sina Ghadermarzi
Virginia Commonwealth University

Carole Goble
University of Manchester

Graciela Gonzalez Hernandez
University of Pennsylvania

Derek Gordon
Rutgers University

Casey Greene
University of Pennsylvania

Dorothy Griffen

Vadim Gumerov
The Ohio State University

Margaret Guo
Stanford University

Gamze Gursoy
Yale University

David Haan
UCSC

Jonathan Haines
Case Western Reserve University

Greg Hampikian
Boise State University
Hyun Wook Han
CHA University

Jie Hao
University of Pennsylvania

Sahar Harati
Stanford University

Cait Harrigan
University of Toronto

Steven Hart
Mayo Clinic

David Haussler
Howard Hughes Medical Institute/UC Santa Cruz Genomics Institute

Georg Hemmrich-Stanisak
IKMB, Kiel University

Jane Hill
Dartmouth College/Thayer School of Eng.

Toby Hocking
Northern Arizona University

Ian Holmes
UC Berkeley

John Holmes
University of Pennsylvania Perelman School of Medicine

Mark Holmstrom
Roche Sequencing Solutions

Corey Hudson
Sandia National Laboratories

V. Keith Hughitt
NIH/NCI

Larry Hunter
University of Colorado

Torgeir Hvidsten
Norwegian University of Life Sciences

S M Ashiqul Islam
University of California San Diego

Willysha Jenkins
Fisk University

Euna Jeong
Sookmyung Women's University

Tomi Jun
Mount Sinai

Senay Kafkas
KAUST

John Kalantari
Mayo Clinic

Mingon Kang
University of Nevada, Las Vegas

Akila Katuwawala
Virginia Commonwealth University

Michael Keiser
UCSF

Mohammed Khalfan
New York University

Saad Khan
Albert Einstein College of Medicine

Dokyoon Kim
University of Pennsylvania

Juhan Kim
Seoung National University College of Medicine

Min Kim
Cipherome

Teri Klein
Stanford University

Kord Kober
University of California San Francisco

Shilpa Kobren

Lester Kobzik
Collecta, Inc

Peter Kochunov
University of Maryland
Participant List
as of December 5, 2019

Liis Kolberg
University of Tartu
Joshua Levy
Dartmouth College Geisel School of Medicine

Benjamin Kompa
Harvard University
Ruijiang Li
Stanford University

Sek Won Kong
Boston Children's Hospital
Olivier Lichtarge
Baylor College of Medicine

Milica Krunic
University of Veterinary Medicine Vienna
Sooyeon Lim
Korea University

Lukasz Kurgan
Virginia Commonwealth University
Qingzhi Liu
University of Michigan, Ann Arbor

William La Cava
University of Pennsylvania
Shikang Liu
University of Notre Dame

Nicholas Lahens
Perelman School of Medicine at the University of Pennsylvania
Tommy Liu
Sirona Genomics

Nicholas Larson
Mayo Clinic
Gaurav Luthria
Harvard University

Kristin Lauter
Microsoft Research
Feiyang Ma
UCLA

Janet Layne
Boise State University
Serghei Mangul
University of Southern California

Hao-Chih Lee
Icahn school of medicine
Andre Marette
Laval University

Soo Young Lee
Ewha Womans University
Gabor Marth
University of Utah

Su-In Lee
Paul G. Allen School of Computer Science & Engineering, University of Washington
Jason McDermott
Pacific Northwest National Laboratory

Sung Hak Lee
Seoul St. Mary's Hospital
Lauren McDonnell
Dartmouth College

E. Alice Lee
Boston Children's Hospital
Rachel Melamed
University of Chicago

Max Leiserson
University of Maryland
Robert Modlin
David Geffen School of Medicine at UCLA

Jake Lever
Stanford University
Jason Moore
University of Pennsylvania

Quaid Morris
University of Toronto
Pacific Symposium on Biocomputing 2020
Participant List
as of December 5, 2019

Marco Morselli
UCLA

Minh Pham
Baylor College of Medicine

Joanna Mountain
23andme

Christopher Pietras
Tufts University

Masahiro Nakatochi
Nagoya University

Teresa Przytycka
NIH

Jin-Wu Nam
Hanyang University

Aaron Quinlan
University of Utah

Matthew Nelson
Deerfield

Predrag Radivojac
Northeastern University

Lisa Neums
University of Kansas Medical Center

Ayush Raman
Broad Institute of MIT and Harvard

Allen Nie
Stanford University

Maya Ramchandran
Harvard T.H. Chan School of Public Health

Christopher Oldfield
Virginia Commonwealth University

Chris Ré
Stanford University

Annie Ostojic
Purdue University

Juri Reimand
Ontario Institute for Cancer Research / University of Toronto

Choa Park
Sookmyung Women's University

Stefano Rensi
Stanford University

Jung Min Park
Hanyang University

Marylyn Ritchie
University of Pennsylvania

Sunho Park
Cleveland Clinic

David Rocke
University of California, Davis

Bogdan Pasaniuc
UCLA

Luke Sagers
Boston Children's Hospital Computational Health Informatics Program

Kristin Passero
The Pennsylvania State University

Leena Sait
George Mason University

Matteo Pellegrini
UCLA

Nilanjana Samanta
University of Pennsylvania

Yash Pershad
Stanford University

Katrin Sangkuhl
Stanford University

Hedi Peterson
University of Tartu

Neil Sarkar
Brown University

Dragutin Petkovic
San Francisco State University
Ken Saville  
Albion College

Roland Schwarz  
Max-Delbrück-Centrum für Molekulare Medizin  
Berlin

Ash Sehgal  
Case Western Reserve University

Alina Selega  
University of Toronto

Roded Sharan  
Tel Aviv University

Hyunchul Shin  
Hanyang University

James Sikela  
University of Colorado Denver

Sameer Singh  
University of California, Irvine

Randy Soares  
Stanford University

Ramiz Somjee  
St. Jude Children’s Research Hospital

Daniel Sosa  
Stanford University

William Southerland  
Howard University

Arunima Srivastava  
The Ohio State University

Eirini Stamoulakatou  
Politecnico di Milano Universita

Jacob Stanley  
BioFrontiers Institute, University of Colorado Boulder

Garrett Stevens  
University of California Berkeley

S. Joshua Swamidass  
Washington University in St. Louis

Ken Saville  
Albion College

Roland Schwarz  
Max-Delbrück-Centrum für Molekulare Medizin  
Berlin

Ash Sehgal  
Case Western Reserve University

Alina Selega  
University of Toronto

Roded Sharan  
Tel Aviv University

Hyunchul Shin  
Hanyang University

James Sikela  
University of Colorado Denver

Sameer Singh  
University of California, Irvine

Randy Soares  
Stanford University

Ramiz Somjee  
St. Jude Children’s Research Hospital

Daniel Sosa  
Stanford University

William Southerland  
Howard University

Arunima Srivastava  
The Ohio State University

Eirini Stamoulakatou  
Politecnico di Milano Universita

Jacob Stanley  
BioFrontiers Institute, University of Colorado Boulder

Garrett Stevens  
University of California Berkeley

S. Joshua Swamidass  
Washington University in St. Louis

Ken Saville  
Albion College

Roland Schwarz  
Max-Delbrück-Centrum für Molekulare Medizin  
Berlin

Ash Sehgal  
Case Western Reserve University

Alina Selega  
University of Toronto

Roded Sharan  
Tel Aviv University

Hyunchul Shin  
Hanyang University

James Sikela  
University of Colorado Denver

Sameer Singh  
University of California, Irvine

Randy Soares  
Stanford University

Ramiz Somjee  
St. Jude Children’s Research Hospital

Daniel Sosa  
Stanford University

William Southerland  
Howard University

Arunima Srivastava  
The Ohio State University

Eirini Stamoulakatou  
Politecnico di Milano Universita

Jacob Stanley  
BioFrontiers Institute, University of Colorado Boulder

Garrett Stevens  
University of California Berkeley

S. Joshua Swamidass  
Washington University in St. Louis

Ken Saville  
Albion College

Roland Schwarz  
Max-Delbrück-Centrum für Molekulare Medizin  
Berlin

Ash Sehgal  
Case Western Reserve University

Alina Selega  
University of Toronto

Roded Sharan  
Tel Aviv University

Hyunchul Shin  
Hanyang University

James Sikela  
University of Colorado Denver

Sameer Singh  
University of California, Irvine

Randy Soares  
Stanford University

Ramiz Somjee  
St. Jude Children’s Research Hospital

Daniel Sosa  
Stanford University

William Southerland  
Howard University

Arunima Srivastava  
The Ohio State University

Eirini Stamoulakatou  
Politecnico di Milano Universita

Jacob Stanley  
BioFrontiers Institute, University of Colorado Boulder

Garrett Stevens  
University of California Berkeley

S. Joshua Swamidass  
Washington University in St. Louis
Michelle Whirl-Carrillo  
Stanford University  

Haoran Zhang  
University of Toronto  

John Wilbanks  
Sage Bionetworks  

Yanfei Zhang  
Geisinger  

Scott Williams  
Case Western Reserve University  

Changsheng Zhao  
Northwestern University  

ClarLynda Williams-DeVane  
Fisk University  

Xi Zhao  
AbbVie  

Damian Wojtowicz  
NIH/NCBI  

Chengyi Zheng  
Kaiser Permanente  

Lior Wolf  
Facebook AI Research and Tel Aviv University  

Mike Wong  
San Francisco State University  

Mark Woon  
Stanford University  

Lei Xing  
Stanford University  

Galen Wright  
University of British Columbia  

Daniel Yang  
Gordon and Betty Moore Foundation  

Hee Chul Yang  
National Cancer Center, Korea  

Yao Yao  
Oregon State University  

Yun Joo Yoo  
Seoul National University  

Sukjoon Yoon  
Sookmyung Women's University  

Adamo Young  
University of Toronto  

Ke Yu  
University of Pittsburgh  

Xianlong Zeng  
Nationwide Childrens