ISMB 2016

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY
OFFICIAL CONFERENCE

Beyond the Limits of Standard Computation

ORLANDO
FLORIDA • USA
JULY 8 to 12, 2016

Discover ➤ Innovate ➤ Engage

CONFERENCE PROGRAM

ISMB
2016
ORLANDO
FLORIDA•USA

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Welcome to Orlando!

On behalf of the organizing committee of ISMB 2016, and the Board of Directors of the International Society for Computational Biology (ISCB), we wish you a very warm welcome. ISMB takes place in the United State this year and promises to be the key meeting for Computational Biology in 2016, and the largest annual computational biology and bioinformatics event worldwide. Attendees will have the opportunity to participate in a multi-track program presenting cutting-edge research in a wide-ranging set of topics and to network with other members of our community.

The steering and scientific organizing committees have prepared a program including a variety of scientific offerings for the meeting and we hope the diversity of options and depth of presented research affords you a stimulating and productive time in Orlando. Following the practice introduced at ISMB 2015 in Dublin last year, all presentations have been organized into one of five Themes: Data, Disease, Proteins, Genes, and Systems. This helps both to logically organize the presentations as well as help you to decide which sessions to attend.

The program includes:

- 3 renowned Keynote speakers.
- 3 Keynote addresses from the 2016 ISCB Award Winners.
- 111 Theme Talks consisting of:
  - 42 Proceedings presentations based on peer-reviewed, original research papers;
  - 36 Highlights Track presentations on recently published work of high impact; and,
  - 33 Late Breaking Research Track papers.
- 4 Special Sessions on current and emerging hot topics.
- 1 ISMB 2016 Industry Session
- 38 Oral Poster presentations.
- 30 Technology Track demonstrations and presentations.
- 3 Workshops, including a full day Junior Principal Investigator program.
- 11 Special Interest Group (SIG) and 2 Satellite Meetings in one- and two-day formats.
- 1 pre-conference Student Council Symposium organized by and for students.
- 3 pre-conference Applied Knowledge Exchange Sessions (AKES)

In addition there are more than 500 posters on display throughout the conference and presented by their authors in two sessions.

We wish to acknowledge all the members of the Scientific Organizing Committee, the Theme Chairs, the Area Chairs, the Applied Knowledge Exchange Sessions Chairs, the Poster Chairs, the Special Interest Groups Chairs, the Special Sessions Chair, the Technology Track Chair, the Travel Fellowship Chairs, the Art and Science Chair, and the Student Council Symposium Chairs. Their dedication and leadership in working with their committees have been invaluable. Over the course of the conference please take a moment to thank them for their efforts and dedication to the success of ISMB 2016.

As Conference Chairs we also appreciate the support of the very many volunteers that have helped guide the development of the conference and of course all the Reviewers who have played an essential role towards forging the scientific program of the conference. A special thanks to our colleagues from the Steering Committee: Janet Kelso, Diane Kovats, Steven Leard, Christine Orengo, and Alfonso Valencia and also to the staff and volunteer leadership of the ISCB organization.

As many of you know, without Steven Leard, the ISMB Conferences Director, there would be no ISMB! We are immensely grateful to Steven and his team for the dedication and effort that they put into organizing all the logistics of this very parallel and complex meeting.

We thank our conference sponsors and exhibitors for their ongoing support. This year's exhibition features commercial and non-profit providers of bioinformatics tools, technologies and publications. We hope you take advantage of everything the conference has to offer, especially the endless opportunity to meet, network, and connect with your fellow researchers.

Finally, we thank the city of Orlando for its welcoming hospitality.

We wish you all a great conference!

Yours sincerely,

Teresa Przytycka,
Conference Co-Chair

Pierre Baldi,
Conference Co-Chair

ISMB 2016 ORGANIZATION

CONFERENCE CHAIRS

Pierre Baldi, *Conference Co-chair, University of California, Irvine, United States*
Teresa Przytycka, *Conference Co-chair, NCBI/NLM/NIH, Bethesda, United States*

STEERING COMMITTEE

Pierre Baldi, *Conference Co-chair, University of California, Irvine, United States*
Teresa Przytycka, *Conference Co-chair, NCBI /NLM/ NIH, Bethesda, United States*
Janet Kelso, *Conferences Committee Co-chair, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany*
Diane E. Kovats, *ISCB Executive Director, Bethesda, United States*
Steven Leard, *ISMB Conference Director, Edmonton, Canada*
Christine Orengo, *ISCB Conferences Committee Co-chair, University College London, United Kingdom*
Alfonso Valencia, *Spanish National Cancer Research Centre (CNIO), Madrid, Spain*

SCIENTIFIC ORGANIZING COMMITTEE

Applied Knowledge Exchange Sessions (AKES) Chair: Michelle D. Brazas, *Ontario Institute for Cancer Research, Toronto, Canada*
Posters Chair: Iddo Friedberg, *Iowa State University, United States*
Scheduling Chair: Dietlind Gerloff, *Foundation for Applied Molecular Evolution (FfAME), Gainesville, United States*
Special Interest Groups Chair: Christine Orengo, *University College London, United Kingdom*
Special Sessions Chair: Michal Linial, *The Hebrew University of Jerusalem, Israel*
Technology Track Chair: Rodrigo Lopez, *European Bioinformatics Institute, EMBL-EBI, Cambridge, United Kingdom*
Travel Fellowships: Guilherme Oliveira, *Vale Technology Institute, Brazil*
Art & Science Chair: Milana Frenkel-Morgenstern, *Bar-Ilan University, Safed, Israel*

APPLIED KNOWLEDGE EXCHANGE SESSIONS (AKES)

Chair: Michelle D. Brazas, *Ontario Institute for Cancer Research, Toronto, Canada*
Co-chair: Fran Lewitter, *Whitehead Institute for Biomedical Research, Cambridge, United States*
Co-chair: Patricia M. Palagi, *SIB Swiss Institute of Bioinformatics, Switzerland*

POSTERS COMMITTEE

Chair: Iddo Friedberg, *Iowa State University, United States*
Co-chair: Casey Greene, *University of Pennsylvania, United States*
Frederic B. Bastian, *University of Lausanne, Swiss Institute of Bioinformatics, Switzerland*
Yana Bromberg, *Rutgers, The State University of New Jersey, United States*
Jacqueline Campbell, *Iowa State University, United States*
Hannah Carter, *University of California San Diego, United States*
Jeroen De Ridder, *Delft University of Technology, Netherlands*
Mikhail Dozmorov, *Virginia Commonwealth University, United States*
Tatyana Goldberg, *Technical University Munich, Germany*
John Hsieh, *Iowa State University, United States*
Yuxiang Jiang, *Indiana University Bloomington, United States*
John Karro, *Miami University (Ohio), United States*
Edda Kloppmann, *Technische Universität München, Germany*
Arjun Krishnan, *Princeton University, United States*
Hande Kucuk, *University of Miami, United States*
Asaf Levy, *DOE Joint Genome Institute, United States*
Yannick Mahlich, *Technische Universität München, Germany*
Jason McDermott, *Pacific Northwest National Laboratory (US Dept of Energy), United States*
Magali Michaut, *Netherlands Cancer Institute*
James Morton, *University of California, San Diego, United States*
Leighton Pritchard, *The James Hutton Institute, United Kingdom*
Jonas Reeb, *Technical University of Munich, Germany*
Surya Saha, *Boyce Thompson Institute, United States*
Venkata Pardhasaradhi Satagopam, *University of Luxembourg*
Avner Schlessinger, *Mount Sinai School of Medicine, United States*
Eric Talevich, *University of California, San Francisco, United States*
Jie Tan, *Dartmouth College, United States*
Peter Ung, *Icahn School of Medicine at Mount Sinai, United States*
Aaron Wong, *Princeton University, United States*
Victoria Yao, *Princeton University, United States*
Yan Zhang, *Yale University, United States*
Jian Zhou, *Princeton University, United States*
Chengsheng Zhu, *Rutgers University, United States*

SPECIAL INTEREST GROUPS COMMITTEE

Chair: Christine Orengo, *University College London, United Kingdom*
Jill Mesirov, *UC San Diego, United States*
Guilherme Oliveira, *Vale Technology Institute, Brazil*

SPECIAL SESSIONS

Chair: Michal Linial, *The Hebrew University of Jerusalem, Israel*

TECHNOLOGY TRACK

Chair: Rodrigo Lopez, *European Bioinformatics Institute, Cambridge, United Kingdom*
Christophe Blanchet, *CNRS-UMS, France*
Yana Bromberg, *Rutgers, The State University of New Jersey, United States*
Dominic Clark, *European Bioinformatics Institute, Cambridge, United Kingdom*
Desmond Higgins, *Conway Institute, Dublin, Ireland*
Claire O'Donovan, *European Bioinformatics Institute, Cambridge, United Kingdom*
Sandra Orchard, *European Bioinformatics Institute, Cambridge, United Kingdom*
William Pearson, *University of Virginia School of Medicine, United States*

TRAVEL FELLOWSHIP COMMITTEE

Chair: Guilherme Oliveira, *Vale Technology Institute, Brazil*
Co-chair: Lucia Peixoto, *Washington State University, Spokane, United States*
Ronnie Alves, *The Computational Biology Institute (IBC), LIRMM, France*
Joel Arrais, *University of Coimbra, Portugal*
Marcelo Brandao, *UNICAMP, Brazil*
Alan Christoffels, *University of Western Cape, South Africa*
Rohit Ghai, *Universidad Miguel Hernandez, San Juan de Alicante, Spain*
Magali Michaut, *The Netherlands Cancer Institute, Amsterdam, The Netherlands*
Mark Pauley, *University of Nebraska, United States*
Olena Piontkivska, *Kent State University, United States*
Brent Petersen, *Center for Biological Sequence Analysis, Lyngby, Denmark*
Neil Sarkar, *Brown University, Providence, United States*
Venkata Pardhasaradhi Satagopam, *University of Luxembourg*
Clare Sansom, *Birkbeck College London, United Kingdom*
Andreas Schuller, *Pontificia Universidad Catolica de Chile, Santiago*
Guenter Tusch, *Grand Valley State University, Allendale, United States*

ART & SCIENCE COMMITTEE

Chair: Milana Frenkel-Morgenstern, *Bar-Ilan University, Safed, Israel*
Venkata Satagopam, *Luxembourg Centre For Systems Biomedicine (LCSB), University of Luxembourg*
Ricardo de Matos Simoes, *Dana-Farber Cancer Institute, Boston, United States*

STUDENT COUNCIL SYMPOSIUM COMMITTEE

Chair: Bart Cuypers, *Biomedical Informatics Research Center Antwerp (Biomina), University of Antwerp, Antwerp University Hospital, Belgium*
Co-Chair: Ben Siranosian, *Broad Institute of MIT and Harvard, Brown University, United States*
Venkata Satagopam, *Luxembourg Centre For Systems Biomedicine (LCSB), University of Luxembourg*
Finance Chair: Ashley Mae Conard, *Brown University, DePauw University, United States*
Web Chair: Mehedi Hassan, *University of South Wales, United Kingdom*
Outreach Chair: Nazeefa Fatima, *University of Huddersfield, United Kingdom*
Outreach Committee: Pankhuri Wanjari, *The University of Texas at El Paso, United States*
Travel Fellowships Chair: Melissa Woghiren, *University of Windsor, Canada*
Student Council Executive Team Representative: Anupama Jigisha, *University of Geneva, Switzerland*

ISMB 2016 Keynote Presentations

Northern Hemisphere BCD, Dolphin Hotel

Sunday, July 10

9:00 AM – 10:00 AM

ISCB FELLOWS KEYNOTE

KN01: RUTH NUSSINOV

Leidos Biomedical Research, Inc., National Cancer Institute, Frederick, United States;
Sackler School of Medicine, Tel Aviv University Israel

Ras signaling: A challenge to the biological sciences

4:40 PM – 5:40 PM

ISCB 2016 OVERTON AWARD KEYNOTE

KN02: DEBORA MARKS

Department of Systems Biology, Harvard Medical School Boston, United States

Molecular structure and organism fitness from genomic sequences

Monday, July 11

9:00 AM – 10:00 AM

KN03: SANDRINE DUDOIT

Division of Biostatistics and Department of Statistics, University of California, Berkeley, United States

Identification of novel cell types in the brain using single-cell transcriptome sequencing

4:40 PM – 5:40 PM

KN04: SARAH TEICHMANN

EMBL-EBI and Head of Cellular Genetics at Wellcome Trust Sanger Institute Hinxton, United Kingdom

Understanding cellular heterogeneity

Tuesday, July 12

9:00 AM – 10:00 AM

ISCB 2016 INNOVATOR AWARD KEYNOTE

KN05: SERAFIM BATZOGLOU

Department of Computer Science, Stanford University, United States

Computational challenges in personalized genomics

4:40 PM – 5:40 PM

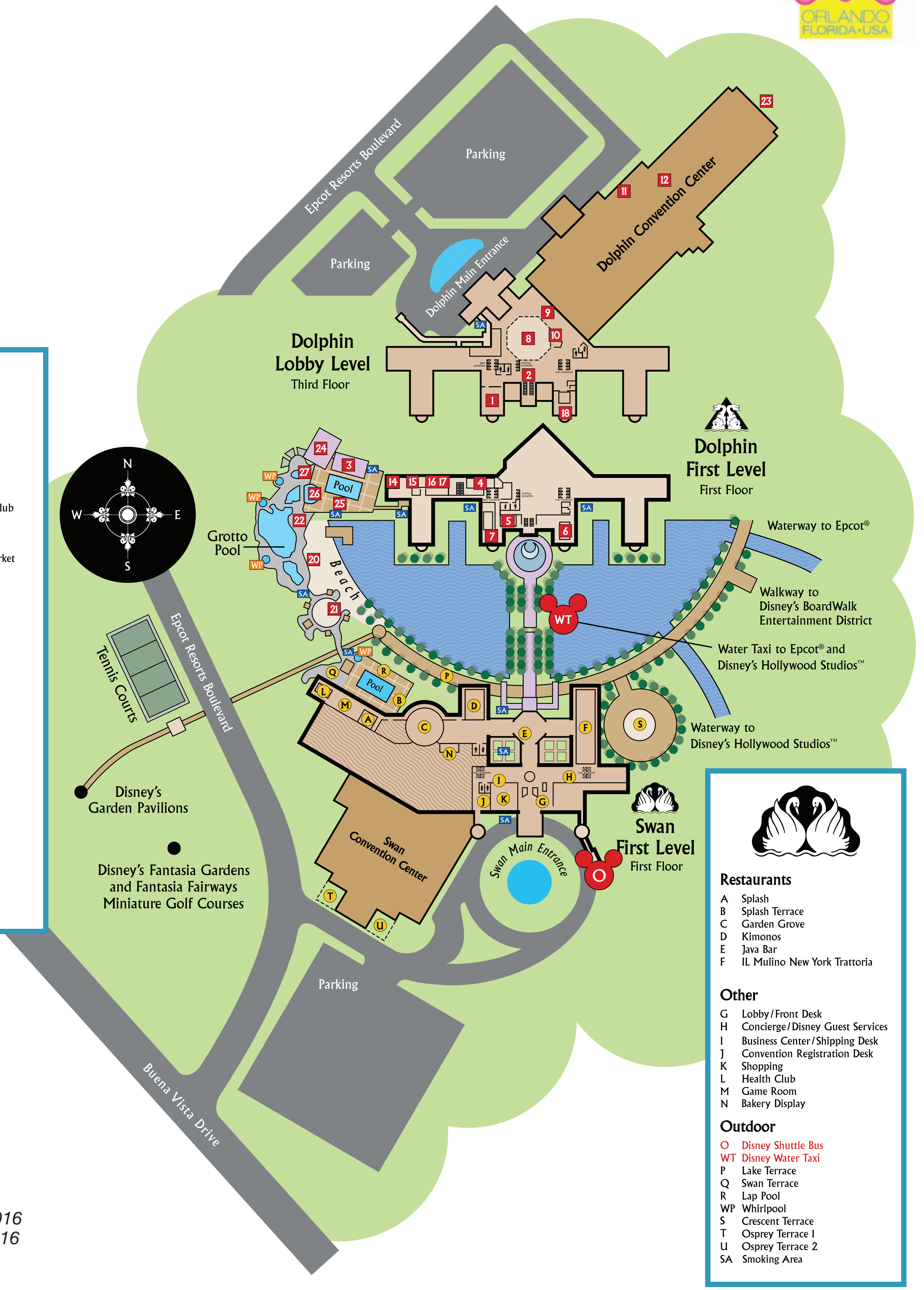
ISCB 2016 ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD KEYNOTE

KN06: SØREN BRUNAK

Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, Denmark

Creating disease trajectories of time-ordered comorbidities from big biomedical data covering millions of patients

Walt Disney World Swan and Dolphin Resort



Restaurants

1	Shula's Steak House
2	Lobby Lounge
3	Cabana Bar and Beach Club
4	Picabu
5	The Fountain
6	Todd English's bluezoo
7	Fresh Mediterranean Market

Other

8	Lobby/Front Desk
9	Concierge
10	Disney Guest Services
11	Business Center
12	Shipping Desk
14	Health Club
15	Camp Dolphin
16	Guest Laundry
17	Game Room
18	Mandara Spa

Outdoor

WT	Disney Water Taxi
20	Grotto Pool and Beach
WP	Whirlpools
21	Children's Playground
22	Cabana Beach Hut
23	Pacific Terrace
24	Cabana Deck
25	Lap Pool
26	Spring Pool
27	Kiddie Pool
SA	Smoking Area

Restaurants

A	Splash
B	Splash Terrace
C	Garden Grove
D	Kimonos
E	Java Bar
F	IL Mulino New York Trattoria

Other

G	Lobby/Front Desk
H	Concierge/Disney Guest Services
I	Business Center/Shipping Desk
J	Convention Registration Desk
K	Shopping
L	Health Club
M	Game Room
N	Bakery Display

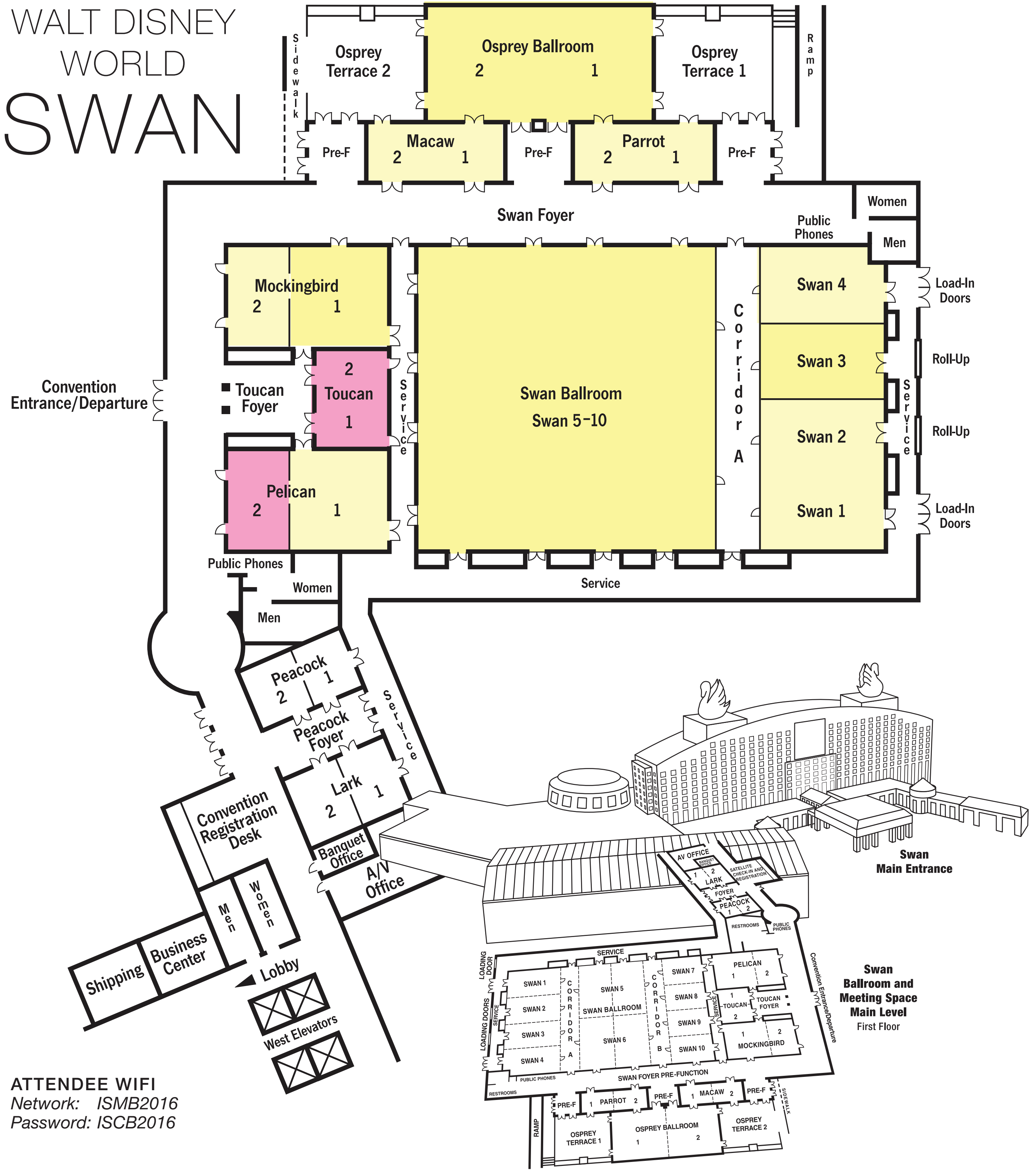
Outdoor

O	Disney Shuttle Bus
WT	Disney Water Taxi
P	Lake Terrace
Q	Swan Terrace
R	Lap Pool
WP	Whirlpool
S	Crescent Terrace
T	Osprey Terrace I
U	Osprey Terrace 2
SA	Smoking Area

ATTENDEE WIFI
Network: ISMB2016
Password: ISCB2016

SIGs, Satellites, SCS12 and AKES Schedule

Swan Hotel Conference Centre



ATTENDEE WIFI

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Password: ISCB2016

SIGs, Satellites, SCS12 and AKES Schedule

Swan Hotel Conference Centre

Thursday, July 7

3:00 PM – 6:00 PM	**REGISTRATION** • *Dolphin Hotel Convention Foyer (near Dolphin Hotel guest desk)*

Friday, July 8

ROOMS	**OSPREY 1/2**	**MACAW 1/2**	**SWAN 3**	**MOCKING-BIRD 1**	**SWAN 1/2**	**PELICAN 2**	**MOCKING-BIRD 2**	**SWAN 4**	**PELICAN 1**	**PARROT 1/2**
8:30 AM - 10:15 AM	**3Dsig (Two Day)**	**CAMDA (Two Day)** *Starts at 4:00 pm*	**BOSC (Two Day)**	**Bio-Ontologies (Two Day)**	**HitSeq: High Throughput Sequencing Algorithms & Applications (Two Day)**	**BioVis: Biological Data Visualization (One Day)**	**Integrative RNA Biology (One Day)**	**Network Biology SIG (One Day)**	**TransMed SIG (One Day)**	**Student Council Symposium 12 (One Day)**
10:15 AM - 10:45 AM	**COFFEE BREAK** • *Swan Foyer*									
10:45 AM - 12:30 PM										
12:30 PM - 1:30 PM	**LUNCH (WITH POSTERS)** • *Swan 5–10*									
1:30 PM - 3:30 PM	**3Dsig** *Continued*		**BOSC** *Continued*	**Bio-Ontologies** *Continued*	**HitSeq: High Throughput Sequencing Algorithms & Applications** *Continued*	**BioVis: Biological Data Visualization** *Continued*	**Integrative RNA Biology** *Continued*	**Network Biology SIG** *Continued*	**TransMed SIG** *Continued*	**Student Council Symposium 12** *Continued*
3:30 PM - 4:00 PM	**COFFEE BREAK** • *Swan Foyer*									
4:00PM - 6:00 PM		**CAMDA (Two Day)** *Starts at 4:00 pm*								
6:00 PM - 8:00 PM	**POSTERS • VARIOUS SIGs (FINISH TIMES MAY VARY)** • *Swan 5–10*									

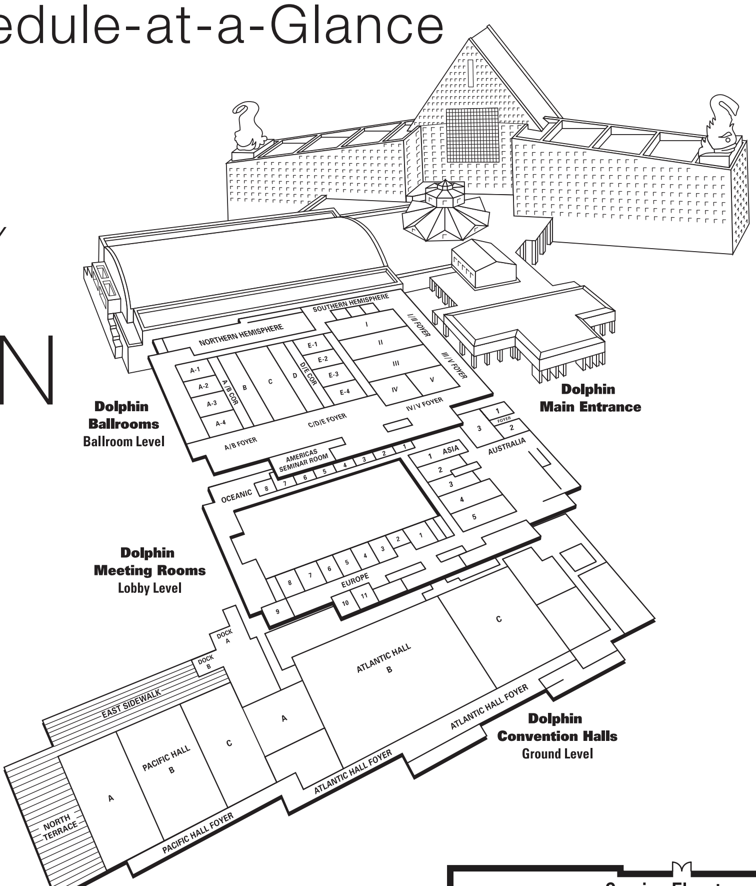
Saturday, July 9

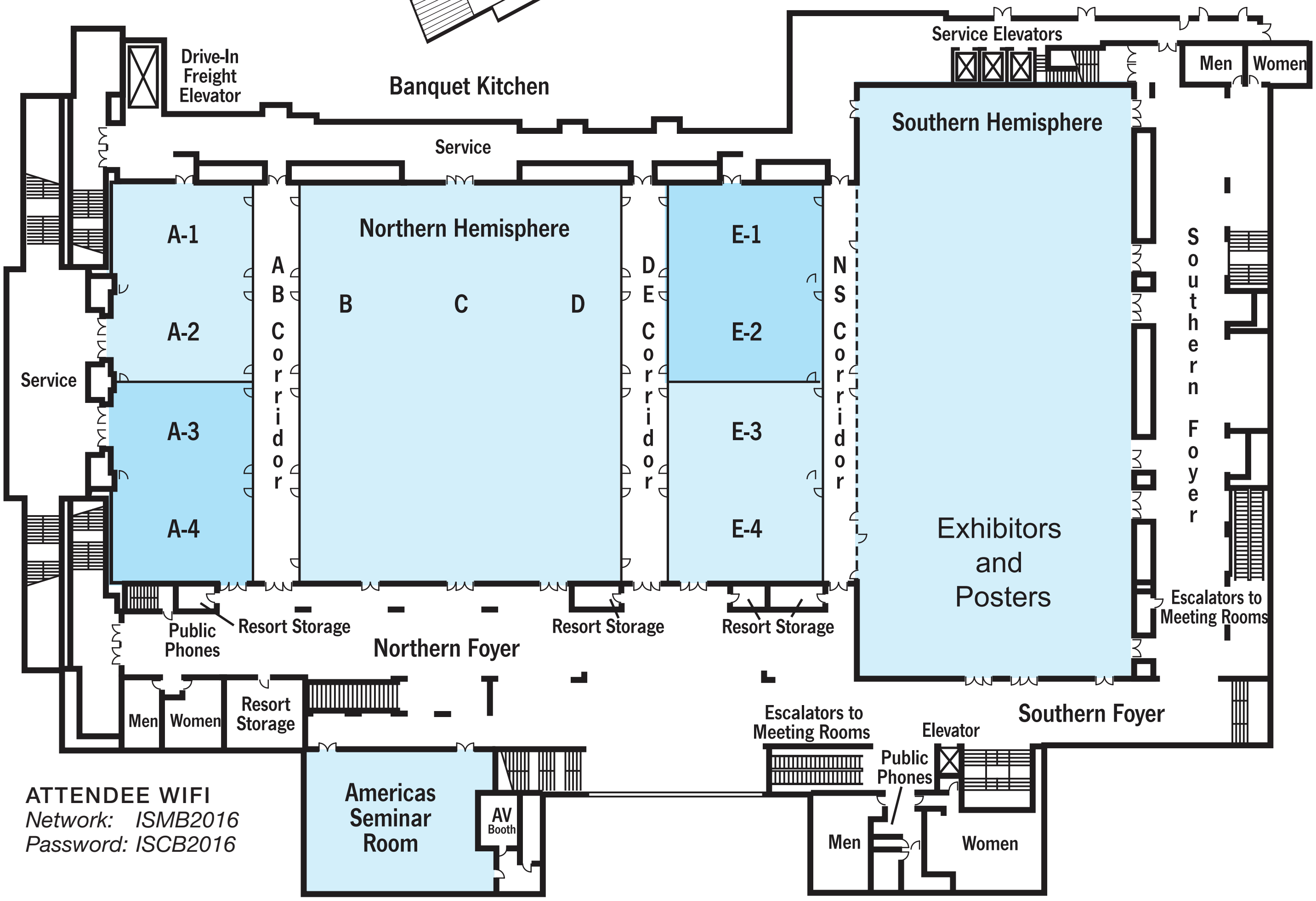
ROOMS	**OSPREY 1/2**	**MACAW 1/2**	**SWAN 3**	**MOCKING-BIRD 1**	**SWAN 1/2**	**PARROT 1/2**	**SWAN 4**	**PELICAN 1**	**MOCKING-BIRD 2**	**PELICAN 2**	**TOUCAN 1/2**
8:30 AM - 10:15 AM	**3Dsig (Two Day)**	**CAMDA (Two Day)** *Starts 9:00 am*	**BOSC (Two Day)**	**Bio-Ontologies (Two Day)**	**HitSeq: High Throughput Sequencing Algorithms & Applications (Two Day)**	**Function SIG (One Day)**	**Regulatory Genomics SIG — RegGenSIG (One Day)**	**SysMod SIG (One Day)**	**VarI-SIG (One Day)**	**AKES01: Clouds, Clusters, and Containers**	**AKES02: Community Efforts to Enable Data Analyses**
10:15 AM - 10:45 AM	**COFFEE BREAK** • *Swan Foyer*										
10:45 AM - 12:30 PM											
12:30 PM - 1:30 PM	**LUNCH (WITH POSTERS)** • *Swan 5–10*										
1:30 PM - 3:30 PM	**3Dsig** *Cont'd*	**CAMDA** *Cont'd*	**BOSC** *Cont'd*	**Bio-Ontologies** *Cont'd*	**HitSeq: High Throughput Sequencing Algorithms & Applications** *Cont'd*	**Function SIG** *Cont'd*	**Regulatory Genomics SIG — RegGenSIG** *Cont'd*	**SysMod SIG** *Cont'd*	**VarI-SIG** *Cont'd*	**AKES01** *Cont'd*	**AKES04: Living on the Edge (of Translational Informatics)**
3:30 PM - 4:00 PM	**COFFEE BREAK** • *Swan Foyer*										
4:00PM - 6:00 PM											
5:30 PM - 7:30 PM	**OPENING RECEPTION WITH EXHIBITORS** • *Southern Hemisphere — Dolphin Hotel*										

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

WALT DISNEY
WORLD
DOLPHIN





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ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

🧬 Genes 💊 Disease 🌀 Protein 🕸 Systems 💾 Data

H Highlights Track **L** Late Breaking Research **P** Proceedings Track

Saturday, July 9

5:30 PM - 7:30 PM	**OPENING RECEPTION WITH EXHIBITORS** • *Southern Hemisphere — Dolphin Hotel*

Sunday, July 10

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
8:45 AM - 9:00 AM	**Opening Welcome** *Room: Northern Hemisphere BCD*					
9:00 AM - 10:00 AM	**ISCB FELLOWS KEYNOTE** **KN01: Ras signaling: a challenge to the biological sciences** **Ruth Nussinov,** *National Cancer Institute, United States and Tel Aviv University, Israel*					
10:00 AM - 10:10 AM	**MOVEMENT TO SESSIONS**					
10:10 AM - 10:30 AM	**COSI: Common NetBio/SysMod.** *Chairs: Nicolas Le Novere and Alex Pico. Presenters: Lars Juhl Jensen, Nathan Price*	**TP001: Robust Detection of Alternative Splicing in a Population of Single Cells.** *Joshua Welch* **H** 🧬	**TP002: DFLpred: High throughput prediction of disordered flexible linker regions in protein sequences.** *Fanchi Meng* **P** 🌀	**TP003: Functionally profiling metagenomes and metatranscriptomes at species-level resolution.** *Eric Franzosa* **H** 🧬 🕸	**Oral Presentations** **OP01: Leslie D. Seitz** **OP03: Joseph Crawford** **OP04: Alon Diament** **OP05: Nicolle Witte** **OP06: Nguyen Vo** **OP07: Deepthi Rajagopalan** **OP08: Wen-Chang Lin** **OP09: Hosna Jabbari** **OP10: Hans-Ulrich Klein**	**WK01: JPI (Junior Principal Investigator)** *Organizers: Manuel Corpas, Lucia Peixoto, Washington State; Geoff Macintyre* **Part A: Welcome and icebreaker.** *Lucia Peixoto* **Part B: How to outline an individualized career development plan to become a successful PI.** *Sandrine Dudoit*
10:30 AM - 10:50 AM		**TP004: Scalable latent-factor models applied to single-cell RNA-seq data separate biological drivers from confounding effects.** *Florian Buettner* **L** 🧬	**TP005: Unexpected Features of the Dark Proteome.** *Nelson Perdigão* **H** 🌀	**TP006: Integrating very large multi'omics data by hierarchical all-against-all association testing.** *Gholamali Rahnavard* **L** 🧬 🕸		
10:50 AM - 11:10 AM		**TP007: Lightweight transcriptomics.** *Surojit Biswas* **L** 🧬	**TP008: Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing.** *Yu Xia* **H** 🌀	**TP009: Single molecule-level characterization of bacterial epigenomes, heterogeneity and gene regulation.** *Gang Fang* **H** 🧬		
11:10 AM - 11:40 AM	**COFFEE BREAK WITH EXHIBITORS** • *Southern Hemisphere Ballroom*					
11:40 AM - 12:00 PM	**COSI: Common NetBio/SysMod** *Continued* **Joint Community Discussion with** *Natasa Przulj and Jonathan Karr* **Closing Comments by Co-chairs**	**TP010: Analysis of aggregated cell-cell statistical distances within pathways unveils therapeutic-resistance mechanisms in circulating tumor cells.** *Alfred Schissler* **P** 💊 🕸	**TP011: Large-scale Text Mining Web Services for Bioinformatics Research.** *Zhiyong Lu* **H** 💾	**TP012: Genetic Architectures of Quantitative Variation in RNA Editing Pathways.** *Tongjun Gu* **H** 🧬	**OP11: Francislon Silva de Oliveira** **OP12: Loukia Lili** **OP13: Sophia Banton** **OP14: Lilah Toker** **OP15: Seungyeul Yoo** **OP16: Hui Liu** **OP17: Urszula Czerwinska** **OP18: Taejeong Bae** **OP19: Chia-Jung Chang** **OP20: Manuel Zahariev**	**WK01: JPI** *Continued* **Climbing the grant ladder: The importance of establishing a record of funding early in your career** **Part A: Outline of funding opportunities for early career scientists by stage.** *Lucia Peixoto* **Part B: Climbing the tenure ladder: strategic decisions for promotion.** *Yana Bromberg* **Structured Discussion**
12:00 PM - 12:20 PM		**TP013: Development of a Bayesian tensor factorization model to predict drug response curves in cancer cell lines.** *Nathan Lazar* **L** 💊 💾	**TP014: Text as Data: Using text-based features for proteins representation and for computational prediction of their characteristics.** *Hagit Shatkay* **H** 🌀 💾	**TP015: A novel algorithm for calling mRNA m6A peaks by modeling biological variances in MeRIP-seq data.** *Yufei Huang* **P** 🧬		
12:20 PM - 12:40 PM		**TP016: DrugE-Rank: Improving Drug-Target Interaction Prediction of New Candidate Drugs or Targets by Ensemble Learning to Rank.** *Shanfeng Zhu* **P** 💊 💾	**TP017: Good news: we are getting better at predicting protein function.** *Iddo Friedberg* **L** 🌀 💾	**TP018: RNAiFold2T: Constraint Programming design of thermo-IRES switches.** *Juan Antonio Garcia-Martin* **P** 🧬		

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

BoF: Birds of a Feather
OP: Oral Poster
SST: Special Sessions Track
TP: Themed Presentations
TT: Technology Track
WK: Workshop

Sunday, July 10

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
12:40 PM - 2:00 PM	**LUNCH AVAILABLE FOR PURCHASE** • *Hotel and Exhibition Hall*					
12:45 PM - 1:45 PM	*"Birds-of-a-feather" (BoFs) are open meetings for participants to meet and talk about topics of mutual interest.*	**BoF01: Exploring and Refining Core Competencies for Bioinformatics (ISCB Curriculum Task Force)** *Leader: Lonnie Welch*	**BoF02: Commons Credits Pilot — Exploring New Ways to Pay for Biomedical Computing** *Leader: David M. Tanenbaum*	**BoF03: Cytoscape Q&A for Users and Developers** *Leaders: Alex Pico, Scooter Morris*	**BoF04: Equal Opportunity in Science — Overcoming Challenges, Increasing Diversity: Gender Balance** *Leader: Bonnie Berger*	**BoF05: Student Council Career Central** *Leader: Student Council*
2:00 PM - 2:20 PM	**SST01: Lost in ribosome profiling,** *Organizer: Tamir Tuller* **Part A: Lost in ribosome-profiling.** *Tamir Tuller* **Part B: The hidden code behind the genetic code.** *Antonio J. Giraldez*	**TP019: Temporal dynamics of collaborative networks in large scientific consortia.** *Daifeng Wang* **H**	**TP020: Integrative computational modeling across tumors reveals context specific impact of mutations.** *Hatice Osmanbeyoglu* **L**	**TP021: Boosting alignment accuracy through adaptive local realignment.** *Dan Deblasio* **L**	**Oral Posters** **OP21: Amir Karger** **OP22: Francesca Rizzato** **OP23: Zebulun Arendsee** **OP24: Fan Zheng** **OP25: Varsha D. Badal** **OP26: Zhouxi Wang** **OP27: Maria Anna Rapsomaniki** **OP28: Jing Wang** **OP29: Ying Jin** **OP30: Qingyu Chen**	**WK01** *Continued* **Strategies to generate data: wet-lab, collaborations and consortia.** *Chair: Logan Everett. Presenter: Trey Ideker* **Structured Discussion** **Roundtable Discussion:** *Sandrine Dudoit, Trey Ideker, Curtis Huttenhower* **Part C: Questions & Wrap up**
2:20 PM - 2:40 PM		**TP022: Positive and negative forms of replicability in gene network analysis.** *Jesse Gillis* **H**	**TP023: COSMOS: accurate detection of somatic structural variations through asymmetric comparison between tumor and normal samples.** *Jun Sese* **H**	**TP024: The Post-Genomic Era of Biological Network Alignment: Latest Insights.** *Vipin Vijayan* **L**		
2:40 PM - 3:00 PM		**TP025: Efficient Data-Driven Model Learning for Dynamical Systems.** *Ermao Cai* **L**	**TP026: intSKAT, an integrated Sequence Kernel Association Test, to identify novel clinically impactful somatic mutations in melanomas.** *Y. Ann Chen* **L**	**TP027: Covariation Is a Poor Measure of Molecular Coevolution.** *David Talavera* **H**		
3:00 PM - 3:30 PM	**COFFEE BREAK WITH EXHIBITORS** • *Southern Hemisphere Ballroom*					
3:30 PM - 3:50 PM	**SST01** *Continued* **Part C: Uncovering tumor-specific amino acid vulnerabilities by differential ribosome codon reading.** *Reuven Agami* **Part D: Statistical Methods for the Analysis of Ribosome Profiling Data.** *Adam Olshen* **Part E: Understanding Biases in Ribosome Profiling Experiments Reveals Signatures of Translation Dynamics in Yeast.** *Jeff Hussmann*	**TP028: Quantitative analysis of microRNA mediated regulation on competing endogenous RNAs.** *Xiaowo Wang* **H**	**TP029: A Weighted Exact Test for Significance of Mutually Exclusive Mutations in Cancer.** *Mark Leiserson* **L**	**TP030: CMsearch: simultaneous exploration of protein sequence space and structure space improves not only protein homology detection but also protein structure prediction.** *Xin Gao* **P**	**OP31: Catherine Snow** **OP32: Stefano Ceri** **OP33: Marcel Grunert** **OP34: Yin Tang** **OP35: Hao Sun** **OP36: Lina Zheng** **OP37: Megan Crow** **OP38: Amrita Roy Choudhury** **OP39: Alastair M. Kilpatrick**	**WK01** *Continued* *Chair: Curtis Huttenhower* **Part A: How to get involved in the ISCB as a JPI.** *Diane Kovats* **Part B: Roundtable Discussion:** *Sandrine Dudoit, Trey Ideker, Curtis Huttenhower*
3:50 PM - 4:10 PM		**TP031: Reconstructing the temporal progression of HIV-1 immune response pathways.** *Siddhartha Jain* **P**	**TP032: Clonal evolution inference and metastatic colorectal cancer.** *Ha X. Dang* **L**	**TP033: Ensemble-Based Evaluation for Protein Structure Models.** *Daisuke Kihara* **P**		
4:10 PM - 4:30 PM		**TP034: Identification of essential molecular and cellular processes controlling the response time and intensity of inflammation.** *Alexander Mitrophanov* **H**	**TP035: Robust discrimination of cell types from tissue expression profiles.** *Aaron M. Newman* **H**	**TP036: Investigating molecular determinants of ebolavirus pathogenicity.** *Mark Wass* **L**		

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

Genes Disease Protein Systems Data

H Highlights Track **L** Late Breaking Research **P** Proceedings Track

Sunday, July 10

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
4:30 PM - 4:40 PM	**MOVEMENT TO KEYNOTE**					
4:40 PM - 5:40 PM	**ISCB OVERTON AWARD KEYNOTE** *Room: Northern Hemisphere BCD* **KN02: 3D Structure and Fitness of Proteins and RNA from Evolutionary Sequences** **Deborah Marks,** *Harvard Medical School, United States*					
5:40 PM - 7:30 PM	**Poster Session (odd numbered posters)** **SOUTHERN HEMISPHERE BALLROOM**					
6:00 PM - 7:00 PM	*Room: American Seminar* **TT01: Transparent toxicology via enhanced peer review platform,** *Stephanie Boue, Philip Morris International R&D*					

Monday, July 11

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
8:45 AM - 9:00 AM	**Morning Welcome — ECCB 2016 Presentation/PhRMA Award Presentations** *Room: Northern Hemisphere BCD*					
9:00 AM - 10:00 AM	**KEYNOTE PRESENTATION** **KN03: Identification of Novel Cell Types in the Brain Using Single-Cell Transcriptome Sequencing** **Sandrine Dudoit,** *University of California, Berkeley, United States*					
10:00 AM - 10:10 AM	**MOVEMENT TO SESSIONS**					
10:10 AM - 10:30 AM	**SST02: DATA: Compressive Omics: Making Big Data Manageable through Data Compression,** *Organizer(s): Peter Rose, Olgica Milenkovic* **Part A: Computational Biology in the 21st Century: Scaling with Compressive Algorithms.** *Bonnie Berger* **Part B: Trends and Methods in Genomic Data Compression.** *Idoia Ochoa* **Part C: Meaningful Data Compression and Reduction of High-Throughput Sequencing Data.** *Alexander Schliep*	**TP037: LINEs between species: Evolutionary dynamics of LINE-1 retrotransposons across the eukaryotic tree of life.** *David Adelson* **L**	**TP038: Convolutional neural network architectures for predicting DNA-protein binding.** *Haoyang Zeng* **P**	**TP039: What Time is It? Deep Learning Approaches for Circadian Rhythms.** *Forest Agostinelli* **P**	**TT02: Chemical Exposure Response Markers Identification in Blood and Genomic-based Diagnostics - Lessons Learned from the sbv IMPROVER Systems Toxicology Computational Challenge,** *Carine Poussin, Philip Morris International R&D*	**WK02: Workshop on Education in Bioinformatics (WEB): Exploiting Cloud and Virtual Resources for Training.** *Organizers: Mainá Bitar, Michelle D. Brazas, Fran Lewitter, Patricia M. Palagi* **Part A: Getting the Best Training in Computational Biology in an Era of Cloud Computing and Big Data.** *Phil Bourne* **Part B: How to Scale Science and People Using the Cloud.** *Nirav Merchant*
10:30 AM - 10:50 AM		**TP040: phRAIDER: Pattern-Hunter Based Rapid Ab Initio Detection of Elementary Repeats.** *John Karro* **P**	**TP041: RCK: accurate and efficient inference of sequenceand structure-based protein-RNA binding models from RNAcompete data.** *Yaron Orenstein* **P**	**TP042: Core Regulatory Circuitry of the Plant Circadian System.** *Pan-Jun Kim* **H**		
10:50 AM - 11:10 AM		**TP043: DNA editing of LTR retrotransposons reveals the impact of APOBECs on vertebrate genomes.** *Binyamin Knisbacher* **H**	**TP044: Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning.** *Hannes Bretschneider* **H**	**TP045: A Framework for Integrating Co-expression Networks with GWAS to Prioritize Candidate Genes in Maize.** *Chad Myers* **H**		
11:10 AM - 11:40 AM	**COFFEE BREAK WITH EXHIBITORS •** *Southern Hemisphere Ballroom*					

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Network: ISMB2016
Password: ISCB2016

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

OP: Oral Poster
SST: Special Sessions Track
TP: Themed Presentations
TT: Technology Track
WK: Workshop

Monday, July 11

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
11:40 AM - 12:00 PM	**SST02:** *Continued* **Part D: Compressive Structural Bioinformatics: High Efficiency 3D Structure Compression.** *Peter Rose*	**TP046: Read-Based Phasing of Related Individuals.** *Shilpa Garg* **P**	**TP047: Revisiting the computational analysis of DNase sequencing.** *Ivan G. Costa* **H**	**TP048: Novel Applications of Multi-task Learning and Multiple Output Regression to Multiple Genetic Trait Prediction.** *Dan He* **P**	**TT02:** *Continued*	**WK02: WEB** *Continued* **Part C: Packaging computational biology tools for broad distribution and ease-of-reuse.** *Matthew Vaughn* **Part D Panel: Experience Exchange: Ideas for Exploiting the Cloud in Bioinformatics Training.** *Moderator: Michelle Brazas* *Panelists: Phil Bourne, Nirav Merchant, Annette McGrath, Matthew Vaughn*
12:00 PM - 12:20 PM	**Part E: Theoretical Foundations and Software Infrastructure for Biological Network Databases.** *Mehmet Koyuturk* **Part F: Task-Specific Compression for Biomedical Big Data.** *Ali Bilgin*	**TP049: An Algorithm for Computing the Gene Tree Probability under the Multispecies Coalescent and its Application in the Inference of Population Tree.** *Yufeng Wu* **P**	**TP050: The Role of Genome Accessibility in Transcription Factor Binding in Bacteria.** *Antonio Gomes* **L**	**TP051: A Network-driven Approach for Genome-wide Association Mapping.** *Seunghak Lee* **P**		
12:20 PM - 12:40 PM		**TP052: Deciphering evolutionary strata on plant sex chromosomes and fungal mating-type chromosomes through compositional segmentation.** *Rajeev Azad* **H**	**TP053: Predicting effects of noncoding variants with deep learning-based sequence model.** *Jian Zhou* **H**	**TP054: Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions.** *Haiquan Li* **H**		
12:40 PM - 2:00 PM	**LUNCH AVAILABLE FOR PURCHASE •** *Hotel and Exhibition Hall*				**ISCB Town Hall 12:45 – 1:50 PM**	
2:00 PM - 2:20 PM	**TP055: DeepMeSH: Deep Semantic Representation for Improving Large-scale MeSH Indexing.** *Shanfeng Zhu* **P**	**TP056: Alignment-free scaffolding of large genome drafts using long sequences and jumping library MPET reads.** *Rene Warren* **H**	**TP057: A Cross-Species Bi-Clustering Approach to Identifying Conserved Co-regulated Genes.** *Jiangwen Sun* **P**	**TP058: Candidate gene prioritization with Endeavour.** *Amin Ardeshirdavani* **L**	**TT03: Repeatable Science at Scale: Using Common Workflow Language and Docker for science on AWS,** *Angel Pizarro, Amazon Web Services*	**WK03: Bioinfo-Core Workshop** *Organizers: Charlie Whittaker, Jian-Liang (Jason) Li, Madelaine Gogol* **Part A: Big Data.** *Presenters: Yury Bukhman, Alberto Riva* **Big Data Panel** *Moderator: Madelaine Gogol* *Panelists: Yury Bukhman, Alberto Riva, Hua Li, Jyothi Thimmapuram*
2:20 PM - 2:40 PM	**TP059: Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems.** *Michael Ku Yu* **H**	**TP060: Genome assembly from synthetic long read clouds.** *Volodymyr Kuleshov* **P**	**TP061: Most of the tight positional conservation of transcription factor binding sites near the transcription start site is due to their co-localization within regulatory modules.** *John Spouge* **L**	**TP062: Furthering understanding of human diseases through integrative cross-species analysis.** *Victoria Yao* **L**		
2:40 PM - 3:00 PM	**TP063: Jumping across biomedical contexts using compressive data fusion.** *Marinka Zitnik* **P**	**TP064: Multi-Genome Scaffold Co-Assembly Based on the Analysis of Gene Orders and Genomic Repeats.** *Sergey Aganezov* **L**	**TP065: Structure-Based Prediction of Transcription Factor Binding Specificity using an Integrative Energy Function.** *Alvin Farrel* **P**	**TP066: SynLethDB: synthetic lethality database toward discovery of selective and sensitive anticancer drug targets.** *Jie Zheng* **H**		
3:00 PM - 3:30 PM	**COFFEE BREAK WITH EXHIBITORS**					**SOUTHERN HEMISPHERE BALLROOM**

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

Genes Disease Protein Systems Data

H Highlights Track **L** Late Breaking Research **P** Proceedings Track

Monday, July 11

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
3:30 PM - 3:50 PM	**TP067: CellCODE: a robust latent variable approach to differential expression analysis for heterogeneous cell populations.** *Maria Chikina* H	**TP068: deBWT: parallel construction of Burrows-Wheeler Transform for large collection of ge-nomes with de Bruijn-branch encoding.** *Bo Liu* P	**TP069: Finding correct protein-protein docking models using ProQDock.** *Sankar Basu* P	**TP070: Gene essentiality and synthetic lethality in haploid human cells.** *Jacques Colinge* H	**TT04: Biological interpretation of 'omics data: The power of causal analysis,** *Andreas Kraemer, QIAGEN Bioinformatics*	**WK03: Bioinfo-Core Workshop** *Continued* **Part B: Big Compute.** *Presenters: Sergi Sayols Puig, Jingzhi Zhu* **Big Compute Panel.** *Moderator: Brent Richter* *Panelists: Sergi Sayols Puig, Jingzhi Zhu, Sara Grimm*
3:50 PM - 4:10 PM	**TP071: Solving the influence maximization problem on biological networks; a case study involving the cell cycle regulatory network in Saccharomyces cerevisiae.** *David Gibbs* L	**TP072: Compacting de Bruijn graphs from sequencing data quickly and in low memory.** *Rayan Chikhi* P	**TP073: Human Protein Complex Map: integration of 10K mass spectrometry experiments.** *Kevin Drew* L	**TP074: Influence maximization in time bounded network identifies transcription factors regulating perturbed pathways.** *Kyuri Jo* H		
4:10 PM - 4:30 PM	**TP075: Scalable Tools for Quantitative Analysis of Chemical-Genetic Interactions from Sequencing-Based Chemical-Genetic Interaction Screens.** *Scott Simpkins* L	**TP076: Succinct Colored de Bruijn Graphs.** *Martin Muggli* L	**TP077: An Integer Programming Framework for Inferring Disease Complexes from Network Data.** *Konrad Klockmeier* P	**TP078: Mogrify: a predictive system for cell reprogramming.** *Julian Gough* H		
4:30 PM - 4:40 PM	**MOVEMENT TO KEYNOTE**					
4:40 PM - 5:40 PM	**ISCB 2016 Outstanding Contributions Award Presentation to Burkhard Rost** *Room: Northern Hemisphere BCD* **KEYNOTE PRESENTATION** **KN04: Understanding Cellular Heterogeneity** **Sarah Teichmann,** *Wellcome Trust Sanger Institute, Hinxton, United Kingdom*					
5:40 PM - 7:30 PM	**POSTER SESSION (EVEN NUMBERED POSTERS)** • *Southern Hemisphere Ballroom*					

ROOMS	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	AMERICA'S SEMINAR
6:00 PM - 6:20 PM	**TT05: Bisulfite sequence analysis on CyVerse Discovery Environment,** *Jawon Song, Texas Advanced Computing Center*	**TT06: GenePattern Notebook: An integrated analytical environment for genomic research,** *Michael Reich, UC San Diego*	**TT07: BioSchemas: schema.org development for the Life Sciences,** *Niall Beard, University of Manchester*
6:20 PM - 6:40 PM	**TT08: The bioBakery: a platform for comprehensive analysis of microbial community shotgun sequencing data,** *Eric Franzosa, Harvard T. H. Chan School of Public Health*	**TT09: Introducing N-of-1-pathways transcriptome analytic tools: Enabling precision medicine through single-subject studies,** *Yves Lussier, University of Arizona*	**TT10: FAIRDOM: Publishing FAIR Data and Models in Interdisciplinary Life Sciences,** *Natalie Stanford, University of Manchester*
6:40 PM - 7:00 PM	**TT11: PISKa: a HPC tool for stochastic agent and rule-based modeling of spatially explicit complex biological systems,** *Tomas Perez-Acle, Fundacion Ciencia & Vida*		
7:00 PM - 9:00 PM			**ET01: ISCB Wikipedia and Wikidata Edit-a-thon** *Leader: Wiki Foundation Group*

ATTENDEE WIFI

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Password: ISCB2016

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

OP: Oral Poster
SST: Special Sessions Track
TP: Themed Presentations

TT: Technology Track
WK: Workshop
IS: Industry Session

Tuesday, July 12

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
08:45 AM - 9:00 AM	**Morning Welcome and Announcements: ISMB/ECCB 2017 Presentation** *Room: Northern Hemisphere BCD*					
9:00 AM - 10:00 AM	**ISCB INNOVATOR AWARD KEYNOTE** **KN05: Computational Challenges in Personalized Genomics** **Serafim Batzoglou,** *Stanford University, United States*					
10:00 AM - 10:10 AM	**MOVEMENT TO SESSIONS**					
10:10 AM - 10:30 AM	**SST03: Genomic Big Data Management, Modeling and Computing,** *Organizer(s): Stefano Ceri, Marco Masseroli, Emanuel Weitschek* **Part A: Genomic big data management and the GenoMetric Query Language.** *Stefano Ceri* **Part B: TCGA2BED and CAMUR for cancer NGS data processing.** *Emanuel Weitschek* **Part C: Searching patterns in genomic feature regions.** *Ilaria Bartolini*	**TP079: Compressive Mapping for Next-Generation Sequencing.** *Deniz Yorukoglu* **H**	**TP080: Interactome based drug discovery and disease-disease connections.** *Gaurav Chopra* **L**	**TP081: Classifying Cancer Samples by microRNA Profiles: Read the Fine Print!** *Roni Rasnic* **L**	**TT12: Big data technology for designing high-quality oligonucleotides via exhaustive homology tests.** *Min-Soo Kim, DGIST*	**IS01: Computational Opportunities and Challenges from Leading Companies in Industrial Biotechnology (IB),** *Leader: Jean-Francois Tomb*
10:30 AM - 10:50 AM		**TP082: RapMap: A Rapid, Sensitive and Accurate Tool for Mapping RNA-seq Reads to Transcriptomes.** *Avi Srivastava* **P**	**TP083: A convex optimization approach for identification of human tissue-specific interactomes.** *Shahin Mohammadi* **P**	**TP084: RNA sequencing-based cell proliferation analysis across 19 cancers identifies a subset of proliferation-informative cancers with a common survival signature.** *Brittany Lasseigne* **L**	**TT13: MyGene.info and MyVariant.info: high-performance web services for querying gene and variant annotation.** *Chuniel Wu, The Scripps Research Institute*	**Introduction to Industrial Biotechnology: Effective Strategies for Protein Engineering and Economical Large Scale Protein Production.** *David Estell, DuPont Industrial Biosciences*
10:50 AM - 11:10 AM		**TP085: ADAGE-Based Extraction of Biological Context from Public Gene Expression Data.** *Jie Tan* **H**	**TP086: Precision drug repurposing and multi-target drug design using structural systems pharmacology.** *Thomas Hart* **H**	**TP087: Data-Driven Analysis of Lymphocyte Infiltration in Breast Cancer Development and Progression.** *Ruth Dannenfelser* **L**	**TT14: Exploring Open-Access Genetic Variants & Clinical Associations: The European Variation Archive at EMBL-EBI.** *Cristina Gonzalez Garcia, EMBL-EBI*	**Bioinformatics in the Biotech Industry – Tales from the Trenches.** *Bastien Chevreux, DSM Nutritional Products* **Computational Biology Challenges at an Industrial Biotech.** *Amoolya Singh, Amyris*
11:10 AM - 11:40 AM	**COFFEE BREAK WITH EXHIBITORS •** *Southern Hemisphere Ballroom*					
11:40 AM - 12:00 PM	**SST03** *Continued* **Part D:** *Alfonso Valencia* **Part E: Semi-automated human genome annotation using chromatin data.** *Michael Hoffman*	**TP088: SHARAKU: An algorithm for aligning and clustering read mapping profiles of deep sequencing in non-coding RNA processing.** *Yasubumi Sakakibara* **P**	**TP089: Nucleotide sequence composition adjacent to intronic 5' end improves translation costs in fungi.** *Zohar Zafrir* **L**	**TP090: Phenotype Stratification from the Electronic Health Record using Autoencoders.** *Brett K Beaulieu-Jones* **L**	**TT15: GenomeSpace: An environment for frictionless bioinformatics.** *Sara Garamszegi, The Broad Institute of MIT and Harvard*	**IS01** *Continued* **Beyond Silos: Knowledge Management as the Key to Operational Excellence — the BioXM System, a Universal Framework.** *Sascha Losko, Biomax Informatics AG*
12:00 PM - 12:20 PM		**TP091: Analysis of differential splicing suggests different modes of short-term splicing regulation.** *Hande Topa* **P**	**TP092: Prediction of Ribosome Footprint Profile Shapes from Transcript Sequences.** *Tzu-Yu Liu* **P**	**TP093: Leveraging electronic medical records for systematic drug repositioning.** *Hyojung Paik* **H**	**TT16: Recent Developments in the Pathway Tools Software and BioCyc Databases.** *Peter Karp, SRI International*	**Scaling up of Renewable Chemicals.** *Karl Sanford, DuPont Industrial Biosciences*
12:20 PM - 12:40 PM		**TP094: Fast and accurate computation of differential splicing across multiple conditions.** *Eduardo Eyras* **H**	**TP095: Rapid Translation Initiation Prevents Mitochondrial Localization of mRNA.** *Paul Horton* **L**	**TP096: Comparative Analyses of Population-scale Phenomic Data in Electronic Medical Records Reveal Race-specific Disease Networks.** *Benjamin S. Glicksberg* **P**	**TT17: Open PHACTS now offers patent information and interactions from pathways.** *Chris Evelo, Maastricht University*	
12:40 PM - 2:00 PM	**LUNCH AVAILABLE FOR PURCHASE •** *Hotel and Exhibition Hall*					

ISMB 2016 Schedule-at-a-Glance
Dolphin Hotel

Genes Disease Protein Systems Data
H Highlights Track **L** Late Breaking Research **P** Proceedings Track

Tuesday, July 12

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
12:45 PM - 1:45 PM			**BoF07: Synthetic Biology & SBOL** *Leader: Kevin Clancy*		**BoF06: Navigating the Industry Career Path** *Leader: ISCB Industry Advisory Council*	
2:00 PM - 2:20 PM	**SST04: Molecular Communication and Networking with Applications to Precision Medicine,** *Organizer: Radu Marculescu* **Part A: Biological Basis for Modeling Bacterial Communities.** *Luisa Hiller* **Part B: Molecular Tweeting: Bacteria Network Formation, Dynamics, and Control with Healthcare Applications.** *Radu Marculescu*	**TP097: Using genomic annotations increases statistical power to detect eGenes.** *Dat Duong* **P**	**TP098: Simultaneous prediction of enzyme orthologs from chemical transformation patterns for de novo metabolic pathway reconstruction.** *Masaaki Kotera* **P**	**TP099: Classifying and Segmenting Microscopy Images with Deep Multiple Instance Learning.** *Oren Kraus* **P**	**TT18: Integrating 3D Structure with Protein, Gene, and Validation Information at the RCSB PDB.** *Peter Rose, UC San Diego*	**TT19: Accelerated NGS Interpretation via the GeneCards Suite.** *Marilyn Safran, Weizmann Institute of Science*
2:20 PM - 2:40 PM		**TP100: GeneiASE: Detection of condition dependent and static allele-specific expression from RNA-seq data without haplotype information.** *Daniel Edsgärd* **H**	**TP101: Fast metabolite identification with Input Output Kernel Regression.** *Céline Brouard* **P**	**TP102: PHOCOS: Inferring Multi-Feature Phenotypic Crosstalk Networks.** *Yue Deng* **P**	**TT20: Phyre2: Protein modeling and analysis made easy.** *Mark Wass, University of Kent, United Kingdom*	**TT21: Read-Based Phasing Using WhatsHap.** *Marcel Martin, SciLifeLab*
2:40 PM - 3:00 PM		**TP103: Data-driven mechanistic analysis method to reveal dynamically evolving regulatory networks.** *Jukka Intosalmi* **P**	**TP104: Faster and More Accurate Graphical Model Identification of Tandem Mass Spectra using Trellises.** *Shengjie Wang* **P**	**TP105: CD30 cell graphs of Hodgkin lymphoma are not scale-free—an image analysis approach.** *Tim Schäfer* **H**	**TT22: Using CATH-Gene3D to predict the structure and function of novel protein sequences.** *Christine Orengo, University College London*	**TT23: Large Scale Analyses with Galaxy.** *John Chilton, Galaxy Project*
3:00 PM - 3:30 PM	**COFFEE BREAK WITH EXHIBITORS •** *Southern Hemisphere Ballroom*					
3:30 PM - 3:50 PM	**SST04** *Continued* **Part C: Data-Driven Modeling and In Silico Simulation of Cell Signaling Pathways.** *Diana Marculescu* **Part D: On Scaling Graph Algorithms for Microbiome Applications.** *Ananth Kalyanaraman* **Part E: Panel**	**TP106: A novel method for discovering local spatial clusters of genomic regions with functional relationships from DNA contact maps.** *Kevin Yip* **P**	**TP107: BioASF: A Framework for Automatically Generating Executable Pathway Models Specified in BioPAX.** *Reza Haydarlou* **P**	**TT24: Images for Massively Parallel Drug Discovery.** *Blake Borgeson, Recursion Pharmaceuticals*	**TT25: bio.tools – life science software registry.** *Jon Ison, ELIXIR Denmark*	**TT26: IOBIO: interactive, visually-drive, real-time analysis of genomic big data.** *Alistair Ward, University of Utah*
3:50 PM - 4:10 PM		**TP108: Tracking the Evolution of 3D Gene Organization.** *Alon Diament* **L**	**TP109: PSAMM: A Portable System for the Analysis of Metabolic Models.** *Ying Zhang* **H**		**TT27: Visualizing and analyzing protein data with UniProt.** *Sangya Pundir, EMBL-EBI*	**TT28: BACNET: An interactive platform for analysis and publication of multi-omics study.** *Christophe Bécavin, Institut Pasteur*
4:10 PM - 4:30 PM		**TP110: A low-latency, big database system and browser for storage, querying and visualization of 3D genomic data.** *Alexander Butyaev* **H**	**TP111: Linear effects models of signaling pathways from combinatorial perturbation data.** *Ewa Szczurek* **P**		**TT29: Linking literature and data through text mining in Europe PMC: SciLite — An annotation platform for biocuration.** *Senay Kafkas, EMBL-EBI*	**TT30: GeneWeaver.org A system for cross-species heterogeneous functional genomic data integration.** *Elissa Chesler, The Jackson Laboratory*
4:30 PM - 4:40 PM	**MOVEMENT TO KEYNOTE**					
4:40 PM - 5:40 PM	**ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD KEYNOTE** *Room: Northern Hemisphere BCD* **KN06: Creating Disease Trajectories of Time-Ordered Comorbidities from Big Biomedical Data Covering Millions of Patients** **Søren Brunak,** *University of Copenhagen, Denmark*					
5:40 PM - 6:00 PM	**Conference Awards and Closing**					

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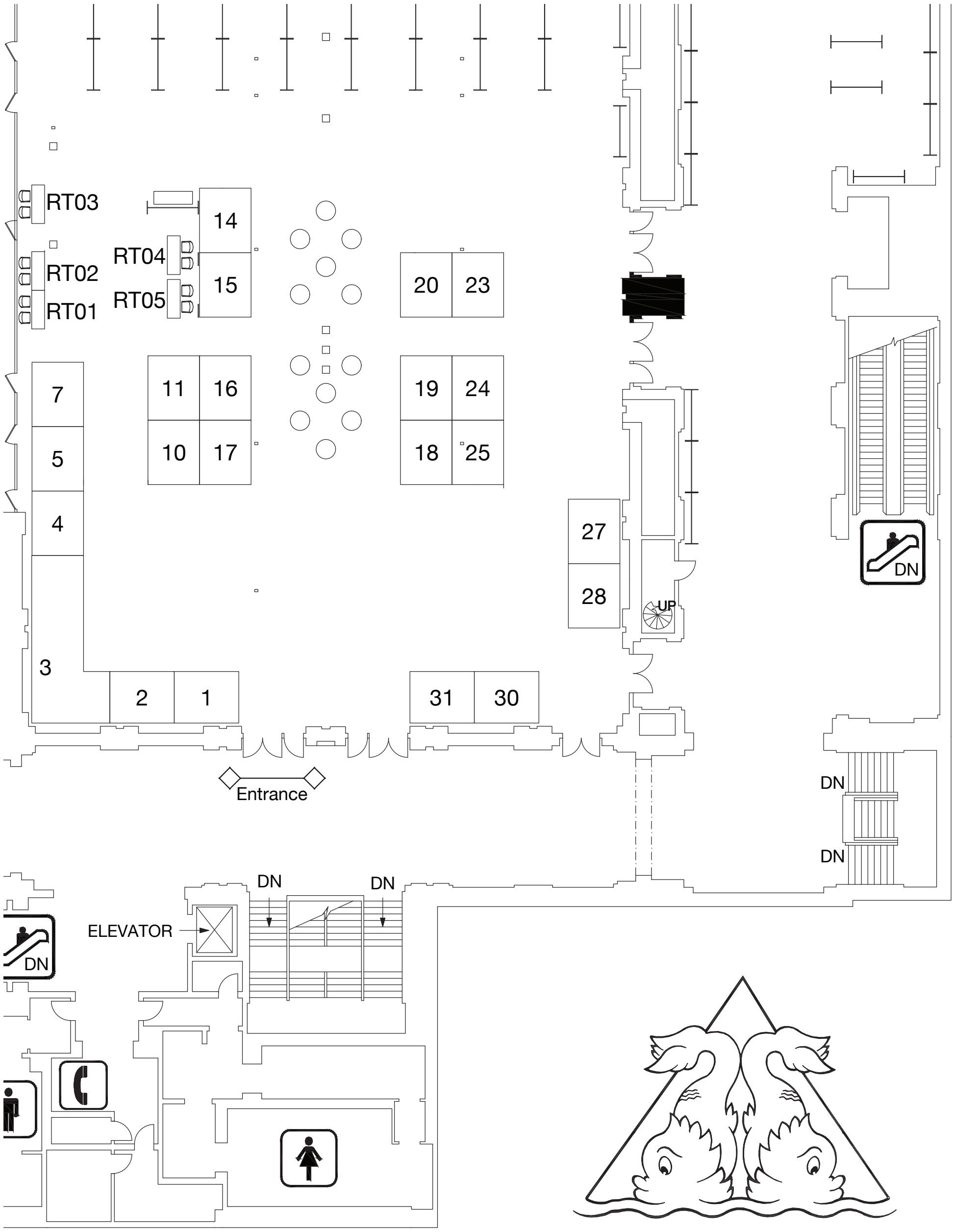
Overleaf

Exhibition Floor Plan

Southern Hemisphere Ballroom



WALT DISNEY WORLD
DOLPHIN

BOOTH	EXHIBITOR
1	ISCB COMMUNITIES OF SPECIAL INTEREST
2	ISCB AFFILIATED GROUPS
3	ISCB STUDENT COUNCIL (ISCB-SC)
3	INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY (ISCB)
4	F1000RESEARCH
5	EMBL AUSTRALIA BIOINFORMATICS RESOURCE
7	AMAZON WEB SERVICES
10	EUROPEAN BIOINFORMATICS INSTITUTE
11	SPRINGER
14	ST. JUDE CHILDREN'S RESEARCH HOSPITAL
15	SBV IMPROVER
16	NDEX PROJECT
17	CAMBRIDGE UNIVERSITY PRESS
18	PLOS
19	GOBLET
20	CRC PRESS
23	ECCB 2016
24	TRAVEL FELLOWSHIP DESK
25	OXFORD UNIVERSITY PRESS
27	ELIXIR DENMARK
28	ELSEVIER
30	RECURSION PHARMACEUTICALS
31	QIAGEN BIOINFORMATICS

RECRUITER TABLES	
RT01	THE JACKSON LABORATORY
RT02	UNIVERSITY OF NEBRASKA AT OMAHA
RT03	DUKE UNIVERSITY
RT04	BIOINFORMATICS AND COMPUTATIONAL BIOLOGY @ ISU
RT05	SYLVESTER COMPREHENSIVE CANCER CENTER AT UNIVERSITY OF MIAMI, MILLER SCHOOL OF MEDICINE

Art and Science Exhibition 2016

The Art & Science Exhibition 2016 presents artworks that have been generated as part of research projects. The prize for Best Art & Science work is 200USD. Winners will be announced online following ISMB 2016.

Vote for your favorite work at www.iscb.org/artsciencevote

Exhibitors

Booth 1

ISCB Communities of Special Interest (COSI)

https://www.iscb.org/iscb-cosis

COSIs are Communities of Special Interest. They have been built around major research themes within computational biology, or important activities such as networks of training, mentoring or support. COSIs hold regular meetings usually as SIGs or workshops in the main ISMB meeting. The ISCB COSI Connect web-portal displays information on COSI themes and activities.

Booth 2

ISCB Affiliated Groups

The booth will showcase the ISCB Affiliates program, which links ISCB and regional non-profit membership groups, centers, institutes and networks within specific geographic regions. Come to learn about the meetings and activities of ISCB's current Affiliates, and to discuss the possibility of affiliating your regional group with ISCB.

Booth 3

ISCB Student Council (ISCB-SC)

www.iscbsc.org

ISCB Student Council (SC) is an international network of young researchers in the broader disciplines of the field of Computational Biology. SC provides opportunities for networking, career enhancement and skills development for the next generation of Computational Biology leaders. The SC Symposium (symposium.iscbsc.org) is organized as a part of the annual ISMB conference with student presentations, keynotes, panel discussions and a poster session. Come visit our friendly SC representatives at the booth for more information.

Booth 3

International Society for Computational Biology

http://www.iscb.org

ISCB The International Society for Computational Biology (ISCB) (www.iscb.org) was the first and continues to be the only society representing computational biology and bioinformatics worldwide. ISCB serves a global community of nearly 3,400 scientists dedicated to advancing the scientific understanding of living systems through computation by:

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

ISCB has three official journals – OUP Bioinformatics, PLOS Computational Biology and F1000Research ISCB Community Journal, and has affiliations in place with several other publications for the benefit of our members.

Booth 4

F1000Research

http://f1000research.com/

F1000Research is an Open Science publishing platform offering immediate publication of posters, slides and articles with no editorial bias. All articles benefit from transparent peer review and the inclusion of all source data. F1000Research publishes the ISCB Community Journal.

Booth 5

EMBL Australia Bioinformatics Resource

http://embl-abr.org.au

The EMBL Australia Bioinformatics Resource (EMBL-ABR) is a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia. It was set up as a collaboration with the European Bioinformatics Institute (EMBL-EBI) to maximise Australia's bioinformatics capability. This close partnership is made possible in the context of Australia's associate membership of EMBL. Its Hub is hosted at VLSCI through a funding agreement between the University of Melbourne and Bioplatforms Australia.

Booth 7

Amazon Web Services

http://aws.amazon.com/health

Amazon Web Services (AWS) provides life sciences and genomics organizations with secure, reliable, low-cost, easy-to-scale, global IT infrastructure "in the cloud." Hundreds of thousands of customers in 190 countries, rely on AWS for their bioinformatics needs, whether it is working with large public data sets or conducting clinical research that combines medical records with genomic information at population scale.

Booth 10

European Bioinformatics Institute

https://www.ebi.ac.uk

At the European Bioinformatics Institute (EMBL-EBI), we help scientists realise the potential of 'big data' in biology, helping them exploit complex information to make discoveries that benefit mankind. We manage the world's public biological data and make it freely available to the scientific community via a range of services and tools, perform basic research and provide professional training in bioinformatics. We are part of the European Molecular Biology Laboratory (EMBL), a non-profit, intergovernmental organisation funded by 21 member states and two associate member states. Our 570 staff represent 57 nationalities, and we welcome a regular stream of visiting scientists throughout the year. We are located on the Wellcome Genome Campus in Hinxton, Cambridge in the United Kingdom.

Booth 11

Springer

http://www.springer.com/

Looking to publish your research? Discover Springer's print and electronic publication services, including Open Access! Get high-quality review, maximum readership and rapid distribution. Visit our booth or springer.com/authors. You can also browse key titles in your field and buy (e)books at discount prices. With Springer you are in good company.

Booth 14

St. Jude Children's Research Hospital

https://www.stjude.org

A non-profit biomedical research institution where mathematics and computer science are applied to the study of genomics, epigenetics, systems biology, biological image analysis, and structural & chemical biology. Our high-performance computing facility allows seamless integration of computational scientists with experimentalists. Visit our booth to discuss postdoctoral fellowship opportunities.

Booth 15

sbv IMPROVER

http://www.sbvimprover.com

The scope of the sbv IMPROVER project, funded by PMI, is the verification of methods and concepts in systems biology research. It already successfully demonstrated that crowdsourcing is a viable strategy to verify scientific methods and concepts in an industrial context. The latest challenge is the Systems Toxicology Computational Challenge and aims to to verify that robust gene signatures predictive of exposure status to chemical mixtures can be extracted from blood gene expression data.

Booth 16

The NDEx Project

http://www.ndexbio.org

NDEx, the Network Data Exchange, is a collaborative software infrastructure for storing, sharing and publishing biological network knowledge. The NDEx Project maintains a free, public website and is developed in close collaboration with the Cytoscape team and the Ideker laboratory at UC San Diego.

Booth 17

Cambridge University Press

http://www.cambridge.org/lifesciences

Cambridge University Press is a not-for-profit organization that advances learning, knowledge and research worldwide. It is an integral part of the University of Cambridge and for centuries has extended its research and teaching activities through a remarkable range of academic and educational books and journals.

Exhibitors

Booth 18

PLOS

http://www.plos.org

PLOS (Public Library of Science) is a nonprofit Open Access publisher, innovator and advocacy organization dedicated to accelerating progress in science and medicine by leading a transformation in research communication. The PLOS suite of influential journals contain rigorously peer-reviewed Open Access research articles from all areas of science and medicine.

Booth 19

GOBLET: Global Organisation for Bioinformatics Learning Education & Training

http://www.mygoblet.org

GOBLET's mission is to provide a global, sustainable support and networking structure for bioinformatics educators/trainers and students/trainees. This includes a training portal for sharing materials, tools and techniques; guidelines and best practice documents; opportunities to train the trainers; and a community of individuals actively engaged in bioinformatics training and learning).

Booth 20

CRC Press

http://www.crcpress.com

CRC Press, part of the Taylor and Francis Group, is the premier publisher of textbooks, reference books, and ebooks on computational biology. Stop by our booth to view our latest titles on computational biology and systems biology and take advantage of our conference discount and be sure to enter our raffle for your chance to win. If you are interested in writing a book please stop by the booth to speak with Sunil Nair about your idea.

Booth 23

European Conference on Computational Biology (ECCB 2016)

http://www.eccb2016.org/ ECCB 2016

European Conference on Computational Biology (The Hague, The Netherlands, 3-7 September 2016) warmly welcomes scientists working in a variety of disciplines, including bioinformatics, (computational/systems) biology, and medicine. Participating in ECCB 2016 will be the perfect opportunity to network and keep abreast of cutting edge research. Early bird registration deadline: July 29.

Exhibitors

Booth 25

Oxford University Press

http://www.oup.com

Oxford University Press publishes some of most respected and prestigious computational biology journals in the world. They include Bioinformatics, an official journal of ISCB, Database: The Journal of Biological Databases and Curation, and Nucleic Acids Research, among many others. Visit our stand to browse books and to pick up sample copies of journals.

Booth 27

ELIXIR Denmark

http://www.elixir-denmark.org

ELIXIR Denmark, which is established in partnership between Danish Universities, leads the community-driven development of the ELIXIR Tools and Data Services Registry. This provides essential scientific and technical information about analytical tools and data services for bioinformatics; It is freely accessible, via the bio.tools portal, and available for registering resources.

Booth 28

Elsevier

http://www.elsevier.com

Elsevier is a world-leading provider of information solutions that enhance the performance of science, health, and technology professionals, empowering them to make better decisions, and deliver better care.

Booth 30

Recursion Pharmaceuticals

http://www.recursionpharma.com

Recursion is a 2-year-old startup with fewer than 20 people, but we generate rich biological data at a pace comparable to some of the biggest institutions doing biology and disease research. We combine high-throughput cellular imaging experiments with intelligent computational methods, rapidly testing thousands of drugs against hundreds of diseases.

Booth 31

QIAGEN Bioinformatics

https://www.qiagenbioinformatics.com

QIAGEN Bioinformatics is powered by CLC bio, Ingenuity, and BIOBASE. We offer bioinformatics software tools for next generation sequencing (NGS) data analysis and interpretation. Our solutions are designed to be universal, so you can mix and match the technologies best suited to your needs.

RT01-RT05

Career/Recruiters Tables

https://www.iscb.org/ismb2016-career

RT01	THE JACKSON LABORATORY
RT02	UNIVERSITY OF NEBRASKA AT OMAHA
RT03	DUKE UNIVERSITY
RT04	BIOINFORMATICS AND COMPUTATIONAL BIOLOGY @ ISU
RT05	SYLVESTER COMPREHENSIVE CANCER CENTER AT UNIVERSITY OF MIAMI, MILLER SCHOOL OF MEDICINE

sbv™ IMPROVER

SYSTEMS BIOLOGY VERIFICATION

sbv IMPROVER Systems Toxicology Computational Challenge Results

The aim of this Challenge was to verify that robust and sparse human-specific or species-independent gene signatures predictive of exposure status can be extracted from whole blood gene expression data.

Technology Track Agenda:

Dr Bob Terbrueggen, DxTerity:
- How signatures could be used in a clinical setting

sbv IMPROVER Scientists & Best Performers:
- Challenge Introduction
- Scoring approach and lessons learned
- Presentation of best performing methods

Monday July 11th 2016
10:10am - 12:40pm
America's Seminar Room, Dolphin Hotel, 5th Floor

www.sbvimprover.com/comp-start

Technology Track Presentations

Sunday, July 10

6:00 PM - 7:00 PM	TT01	**Transparent toxicology via enhanced peer review platform** • *Stephanie Boue, Philip Morris International R&D*	**AMERICA'S SEMINAR**

Monday, July 11

10:10 AM - 12:40 PM	TT02	**Chemical Exposure Response Markers Identification in Blood and Genomic-based Diagnostics — Lessons Learned from the sbv IMPROVER Systems Toxicology Computational Challenge** • *Carine Poussin, Philip Morris International R&D*	**AMERICA'S SEMINAR**
2:00 PM - 3:00 PM	TT03	**Repeatable Science at Scale: Using Common Workflow Language and Docker for science on AWS** • *Angel Pizarro, Amazon Web Services*	**AMERICA'S SEMINAR**
3:30 PM - 4:30 PM	TT04	**Biological interpretation of 'omics data: The power of causal analysis** • *Andreas Kraemer, QIAGEN Bioinformatics*	**AMERICA'S SEMINAR**
6:00 PM - 6:20 PM	TT05	**Bisulfite sequence analysis on CyVerse Discovery Environment** • *Jawon Song, Texas Advanced Computing Center*	**NORTHERN HEMISPHERE A1/A2**
6:00 PM - 6:20 PM	TT06	**GenePattern Notebook: An integrated analytical environment for genomic research** • *Michael Reich, UC San Diego*	**NORTHERN HEMISPHERE A3/A4**
6:00 PM - 6:20 PM	TT07	**BioSchemas: schema.org development for the Life Sciences** • *Niall Beard, University of Manchester*	**AMERICA'S SEMINAR**
6:20 PM - 6:40 PM	TT08	**The bioBakery: a platform for comprehensive analysis of microbial community shotgun sequencing data** • *Eric Franzosa, Harvard T. H. Chan School of Public Health*	**NORTHERN HEMISPHERE A1/A2**
6:20 PM - 6:40 PM	TT09	**Introducing N-of-1-pathways transcriptome analytic tools: Enabling precision medicine through single-subject studies** • *Yves Lussier, University of Arizona*	**NORTHERN HEMISPHERE A3/A4**
6:20 PM - 6:40 PM	TT10	**FAIRDOM: Publishing FAIR Data and Models in Interdisciplinary Life Sciences** • *Natalie Stanford, University of Manchester*	**AMERICA'S SEMINAR**
6:40 PM - 7:00 PM	TT11	**PISKa: a HPC tool for stochastic agent and rule-based modeling of spatially explicit complex biological systems** • *Tomas Perez-Acle, Fundacion Ciencia & Vida*	**NORTHERN HEMISPHERE A1/A2**

Tuesday, July 12

10:10 AM - 10:30 AM	TT12	**Big data technology for designing high-quality oligonucleotides via exhaustive homology tests** • *Min-Soo Kim, DGIST*	**AMERICA'S SEMINAR**
10:30 AM - 10:50 AM	TT13	**MyGene.info and MyVariant.info: high-performance web services for querying gene and variant annotation** • *Chunlei Wu, The Scripps Research Institute*	**AMERICA'S SEMINAR**
10:50 AM - 11:10 AM	TT14	**Exploring Open-Access Genetic Variants & Clinical Associations: The European Variation Archive at EMBL-EBI** • *Cristina Gonzalez Garcia, EMBL-EBI*	**AMERICA'S SEMINAR**
11:40 AM - 12:00 PM	TT15	**GenomeSpace: An environment for frictionless bioinformatics** • *Sara Garamszegi, The Broad Institute of MIT and Harvard*	**AMERICA'S SEMINAR**
12:00 PM - 12:20 PM	TT16	**Recent Developments in the Pathway Tools Software and BioCyc Databases** • *Peter Karp, SRI International*	**AMERICA'S SEMINAR**
12:20 PM - 12:40 PM	TT17	**Open PHACTS now offers patent information and interactions from pathways** • *Chris Evelo, Maastricht University*	**AMERICA'S SEMINAR**
2:00 PM - 2:20 PM	TT18	**Integrating 3D Structure with Protein, Gene, and Validation Information at the RCSB PDB** • *Peter Rose, UC San Diego*	**AMERICA'S SEMINAR**
2:00 PM - 2:20 PM	TT19	**Accelerated NGS Interpretation via the GeneCards Suite** • *Marilyn Safran, Weizmann Institute of Science*	**NORTHERN HEMISPHERE E3/E4**
2:20 PM - 2:40 PM	TT20	**Phyre2: Protein modeling and analysis made easy** • *Mark Wass, University of Kent, United Kingdom*	**AMERICA'S SEMINAR**
2:20 PM - 2:40 PM	TT21	**Read-Based Phasing Using WhatsHap** • *Marcel Martin, SciLifeLab*	**NORTHERN HEMISPHERE E3/E4**
2:40 PM - 3:00 PM	TT22	**Using CATH-Gene3D to predict the structure and function of novel protein sequences** • *Christine Orengo, University College London*	**AMERICA'S SEMINAR**
2:40 PM - 3:00 PM	TT23	**Large Scale Analyses with Galaxy** • *John Chilton, Galaxy Project*	**NORTHERN HEMISPHERE E3/E4**
3:30 PM - 4:30 PM	TT24	**Images for Massively Parallel Drug Discovery** • *Blake Borgeson, Recursion Pharmaceuticals*	**NORTHERN HEMISPHERE E1/E2**
3:30 PM - 3:50 PM	TT25	**bio.tools - life science software registry** • *Jon Ison, ELIXIR Denmark*	**AMERICA'S SEMINAR**
3:30 PM - 3:50 PM	TT26	**IOBIO: interactive, visually-drive, real-time analysis of genomic big data** • *Alistair Ward, University of Utah*	**NORTHERN HEMISPHERE E3/E4**
3:50 PM - 4:10 PM	TT27	**Visualizing and analyzing protein data with UniProt** • *Sangya Pundir, EMBL-EBI*	**AMERICA'S SEMINAR**
3:50 PM - 4:10 PM	TT28	**BACNET: An interactive platform for analysis and publication of multi-omics study** • *Christophe Bécavin, Institut Pasteur*	**NORTHERN HEMISPHERE E3/E4**
4:10 PM - 4:30 PM	TT29	**Linking literature and data through text mining in Europe PMC: SciLite - An annotation platform for biocuration** • *Senay Kafkas, EMBL-EBI*	**AMERICA'S SEMINAR**
4:10 PM - 4:30 PM	TT30	**GeneWeaver.org: A system for cross-species heterogeneous functional genomic data integration** • *Elissa Chesler, The Jackson Laboratory*	**NORTHERN HEMISPHERE E3/E4**

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