

Join us for the BMES Track on Bioinformatics, Computational and Systems Biology. The theme of this year's track is discovery from mathematical modeling of large-scale biomedical data. This multidisciplinary and international track features a record eleven platform sessions and more than a hundred posters by bioengineers, computer scientists, electrical engineers, mathematicians, medical researchers and physicists from sixteen countries.

Track: Bioinformatics, Computational and Systems Biology

Track Chair: Orly Alter

Thursday, September 26, 2013

8:00AM-9:30AM

OP - Thurs - 1 – 11 - Room 615

Genomics, Transcriptomics and Proteomics I

Session Chairs: Orly Alter, Phil Green, Matteo Pellegrini

8:00AM-8:30AM

Discovery of Mechanisms and Prognosis of Cancers from Matrix and Tensor Modeling of Large-Scale Molecular Biological Data (Invited)

O. Alter¹

¹University of Utah, Salt Lake City, UT

8:30AM-9:00AM

How Much of the Human Genome is Functional? (Invited)

P. Green¹

¹University of Washington, Seattle, WA

9:00AM-9:30AM

Transgenerational Inheritance of DNA Methylation (Invited)

M. Pellegrini¹

¹UCLA, Los Angeles, CA

1:30PM-3:00PM

OP - Thurs - 2 – 11 - Room 615

Modeling of Regulatory Networks

Session Chairs: Douglas A. Lauffenburger, Jason A. Papin, Nathan D. Price

1:30PM-2:00PM

Integrative Network Model for Cell Kinase Signaling Pathways with Proteolytic Ligand/Receptor Shedding Feedback: Application to Invasive Cell Migration in Endometriosis (Invited)

D. A. Lauffenburger¹, M. A. Miller¹, A. S. Meyer¹, M. Beste¹, K. Isaacson², and L. G. Griffith¹

¹MIT, Cambridge, MA, ²Newton-Wellesley Hospital, Newton, MA

2:00PM-2:30PM

Synergistic Drug Targets of Human Pathogens Identified with Analysis of Integrated Transcriptional Regulatory and Metabolic Networks (Invited)

J. Papin¹

¹University of Virginia, Charlottesville, VA

2:30PM-3:00PM **Systems Approaches to Multi-Parameter Disease Diagnostics** (Invited)

N. D. Price¹

¹Institute for Systems Biology, Seattle, WA

4:00PM – 5:30PM

OP - Thurs - 3 – 11 - Room 615

Analysis and Control of Cell Signaling I

Session Chairs: Adam P. Arkin, Kevin A. Janes, H. Steven Wiley

4:00PM-4:30PM **Quantitative Understanding of Gene Expression for Systems and Synthetic Biology** (Invited)

A. P. Arkin^{1,2}

¹U.C. Berkeley, Berkeley, CA, ²Lawrence Berkeley National Laboratory, Berkeley, CA

4:30PM-5:00PM **Linking Signal-Transduction and Gene-Expression Networks by Statistical Modeling** (Invited)

Z. Chitforoushzadeh¹, S. I. LaRue¹, M. B. Yaffe², D. A. Lauffenburger², P. K. Sorger³, R. C. Fry⁴, and K. A. Janes¹

¹University of Virginia, Charlottesville, VA, ²Massachusetts Institute of Technology, Cambridge, MA,

³Harvard Medical School, Boston, MA, ⁴University of North Carolina at Chapel Hill, Chapel Hill, NC

5:00PM-5:30PM **Differential EGFR Signaling from Autocrine versus Paracrine Mode of Ligand Presentation** (Invited)

B. E. Linggi¹, W-J. Qian¹, W. Chrisler¹, and H. S. Wiley¹

¹Pacific Northwest National Laboratory, Richland, WA

Friday, September 27, 2013

8:00AM - 9:30AM

OP - Fri - 1 – 11 - Room 615

Modeling in Personalized Medicine

Session Chairs: Andrea H. Bild, Mark R. Chance, Adam A. Margolin

8:00AM-8:30AM **Genomics-Based Discovery of Novel Drug Regimens Effective in RAS-Driven Tumors** (Invited)

A. Bild¹

¹University of Utah, Salt lake city, UT

8:30AM-9:00AM **Network Biology and Personalized Medicine in Multiple Sclerosis** (Invited)

R. Nibbe¹, Y. Liu², M. Koyuturk², and M. Chance^{1,2}

¹NeoProteomics, Inc., Cleveland, OH, ²Case Western Reserve U, Cleveland, OH

9:00AM-9:30AM **Computational Models and Crowd-Sourcing Initiatives for Inferring Genetic Predictors of Cancer Phenotypes.** (Invited)

A. A. Margolin¹

¹Sage Bionetworks, Seattle, WA

1:30PM - 2:30PM

OP - Fri - 2 – 11 - Room 615

Multiscale Spatiotemporal Modeling and Simulation

Session Chairs: Michael R. King, J. Nathan Kutz

1:30PM-2:00PM **Simulation of Platelet, Thrombus and Erythrocyte Hydrodynamic Interactions in a 3D Arteriole with *in vivo* Comparison** (Invited)

W. Wang¹, T. G. Diacovo², J. Chen², J. B. Freund³, and M. R. King¹

¹Cornell University, Ithaca, NY, ²Columbia University, New York, NY, ³University of Illinois at Urbana-Champaign, Urbana, IL

2:00PM-2:30PM **Motifs for Encoding/Decoding of Neuro-Sensory Information** (Invited)
J. Kutz¹
¹University of Washington, Seattle, WA

2:45PM - 3:45PM

OP - Fri - 3 – 11 - Room 615

Image-Based Modeling

Session Chairs: Michael Hawrylycz, Christopher R. Johnson

2:45PM-3:15PM **A High Resolution Spatiotemporal Atlas of Gene Expression of the C57G1/6J Developing Mouse Brain** (Invited)
M. Hawrylycz¹, L. Ng¹, and C. Thompson¹
¹Allen Institute for Brain Science, Seattle, WA

3:15PM-3:45PM **Image-Based Biomedical Modeling, Simulation, and Visualization** (Invited)
C. R. Johnson¹
¹University of Utah, Salt Lake City, UT

Saturday, September 28, 2013

8:00AM-9:30AM

OP - Sat - 1 – 11 - Room 615

Computational Bioengineering I

Session Chairs: Evrim Acar, Michael A. Saunders, Lawrence Sirovich

8:00AM-8:30AM **Structure-Revealing Data Fusion Model with Applications in Metabolomics** (Invited)
E. Acar¹, A. J. Lawaetz¹, M. A. Rasmussen¹, and R. Bro¹
¹University of Copenhagen, Frederiksberg C, Denmark

8:30AM-9:00AM **Numerical Linear Algebra and Optimization Tools for Bioinformatics** (Invited)
M. A. Saunders¹, S. Akle¹, D. Ma¹, Y. Sun¹, R. M. Fleming², and I. Thiele²
¹Stanford University, Stanford, CA, ²University of Luxembourg, Esch-sur-Alzette, Luxembourg

9:00AM-9:30AM **Reduction and Analysis of Large Scale Systems** (Invited)
L. Sirovich¹
¹Rockefeller University, New York, NY

1:30PM-3:00PM

OP - Sat - 2 – 11 - Room 615

Computational Bioengineering II

Session Chairs: Kristen M. Naegle, Matthew A. Oberhardt

1:30PM-1:45PM **Maximization of Rate of Entropy Production Reveals Growth Principles of Respiring Microorganisms**
M. A. Oberhardt¹, R. Zarecki¹, K. Yizhak¹, R. Pugatch², A. Wagner¹, E. Shtifman Segal¹, S. Freilich³, C. S. Henry⁴, U. Gophna¹, and E. Ruppin¹
¹Tel Aviv University, Tel Aviv, Israel, ²Princeton, NJ, Princeton, NJ, ³Agricultural Research Organization, Volcani Center, Newe Ya'ar, Israel, ⁴Argonne National Laboratory, Argonne, IL

1:45PM-2:00PM **A Higher-Order Generalized Singular Value Decomposition for Comparison of Global mRNA Expression from Multiple Organisms**
S. P. Ponnappalli¹, M. A. Saunders², C. F. Van Loan³, and O. Alter⁴
¹Bloomberg LP, New York, NY, ²Stanford University, Stanford, CA, ³Cornell University, Ithaca, NY,
⁴University of Utah, Salt Lake City, UT

2:00PM-2:15PM **Multi-Layer Motion Estimation for Fluoroscopic Imaging**
C. Rottman¹, J. S. Preston¹, A. Cheryauka², L. Anderton², R. Whitaker¹, and S. Joshi¹
¹University of Utah, Salt Lake City, UT, ²GE Healthcare, Salt Lake City, UT

2:15PM-2:30PM **Multiscale modeling of Nanog heterogeneity in pluripotent stem cell populations**
J. Wu¹ and E. S. Tzanakakis^{1,2}
¹Chemical and Biological Engineering, SUNY-Buffalo, Buffalo, NY, ²Biomedical Engineering, SUNY-Buffalo, Buffalo

2:30PM-2:45PM **Quantifying Spatial Patterns of Mouse Embryonic Stem Cell Differentiation within Embryoid Bodies**
D. White¹, T. McDevitt¹, and M. Kemp¹
¹Georgia Institute of Technology, Atlanta, GA

2:45PM-3:00PM **PTMScout: Understanding protein post-translational modifications**
M. Matlock¹, A. Holehouse¹, C. Zhang¹, and K. Naegle¹
¹Washington University in St Louis, St Louis, MO

1:30PM-3:00PM

OP - Sat - 2 – 10 - Room 602

Analysis and Control of Cell Signaling II

Session Chairs: Jeffery J. Saucerman, Alejandro Wolf-Yadlin

1:30PM-1:45PM **Using Phosphoproteomics and Gene Expression Profiling to Reveal Systems-Wide Changes in Response to EGF Receptor Activation**
A. Wolf-Yadlin¹, K. Beck¹, A. Hu¹, A. McKenna¹, and J. Shendure¹
¹University of Washington, Seattle, WA

1:45PM-2:00PM **Oncogenic Phospho-Tyrosine Signaling in the Absence of Mutated or Amplified Tyrosine Kinases**
N. A. Graham¹, J. M. Drake¹, M. Tahmasian¹, K. J. Pienta², O. N. Witte^{1,3}, and T. G. Graeber¹
¹University of California, Los Angeles, Los Angeles, CA, ²University of Michigan, Ann Arbor, MI, ³Howard Hughes Medical Institute, Los Angeles, CA

2:00PM-2:15PM **A Microfluidic Platform for Visualizing Single-Cell Regulatory Dynamics in Mycobacteria**
J. P. Keller¹, W-H. Yu¹, J. E. Galagan¹, and C. M. Klapperich¹
¹Boston University, Boston, MA

2:15PM-2:30PM **Gene Expression from the Gq Transgenic Mouse is Sufficient to Mechanistically Predict Altered Cardiac EC Coupling**
F. Wu¹, J. Wadden¹, J. Lach¹, K. Skadron¹, and J. J. Saucerman¹
¹University of Virginia, Charlottesville, VA

2:30PM-2:45PM **Comparative Metabolic Capacities of Bacterial Pathogens Using Reconciled Genome-Scale Metabolic Reconstructions**
P. Yen¹, J. A. Bartell¹, J. J. Varga², J. B. Goldberg², and J. A. Papin¹
¹University of Virginia, Charlottesville, VA, ²Emory University, Atlanta, GA

2:45PM-3:00PM **Entrainment of a Population of NF- κ B Oscillators Under Periodic Inputs**

S. Tay¹ and R. Kellog¹
¹ETH Zurich, Basel, Switzerland

3:15PM-4:45PM

Genomics, Transcriptomics and Proteomics II

OP - Sat - 3 – 11 - Room 615

Session Chairs: Valerie Daggett, Kimmen Sjölander

3:15PM-3:30PM **The PhyloFacts FAT-CAT Web Server: Functional Annotation and Ortholog Identification for Sequences Across the Tree of Life**

K. Sjölander¹
¹University of California, Berkeley, Berkeley, CA

3:30PM-3:45PM **Inferring Single-Cell Gene Expression Frequencies from Stochastic Transcriptional Profiles**

S. S. Bajikar¹, C. Fuchs², A. Roller², F. J. Theis², and K. A. Janes¹
¹University of Virginia, Charlottesville, VA, ²Helmholtz Center Munich, Munich, Germany

3:45PM-4:00PM **Misfolded Conformations of the Bovine Prion Protein at Acidic pH**

C. Cheng¹ and V. Daggett¹
¹University of Washington, Seattle, WA

4:00PM-4:15PM **Genome-Wide Epigenetic Regulation in Endothelial Cells by Disturbed Flow and its Role in Atherosclerosis**

J. Dunn^{1,2}, S. Kim^{1,2}, C. Qiu^{1,2}, C. Kim^{1,2}, R. Hoffman¹, I. Jang^{1,2}, and H. Jo^{1,2}
¹Wallace H. Coulter Department of Biomedical Engineering, Georgia Institute of Technology and Emory, Atlanta, GA, ²Division of Cardiology, Department of Medicine, Emory University, Atlanta, GA

4:15PM-4:30PM **A Profile of RNA Editing in the Human Brain and Gliomas**

A. T. Magis^{1,2}, C. C. Funk², and N. D. Price²
¹University of Illinois, Urbana-Champaign, Urbana, IL, ²Institute for Systems Biology, Seattle, WA

4:30PM-4:45PM **Family Genomics Reveals Disease Genetics**

A. Stittrich¹, H. Cox¹, H. Li¹, S. Ament¹, P. May^{1,2}, D. Mauldin¹, S. Montsaroff¹, R. Hubley¹, R. Gelinas¹, M. Brunkow¹, L. Rowen¹, A. Smit¹, G. Glusman¹, J. Roach¹, and L. Hood¹
¹Institute for Systems Biology, Seattle, WA, ²Luxembourg Centre for Systems Biomedicine, University Luxembourg, Esch-sur-Alzette, Luxembourg

3:15PM-4:45PM

OP - Sat - 3 – 10 - Room 602

Dynamics of Biological Systems

Session Chairs: Fernando R. Fernandez, Eli Shlizerman

3:15PM-3:30PM **Dynamics of Olfactory Neural Codes**

E. Shlizerman¹, J. Riffell¹, and J. Kutz¹
¹University of Washington, Seattle, WA

3:30PM-3:45PM **Understanding Signal Transduction at the Neuroelectronic Interface**

V. Thakore¹, P. Molnar^{1,2}, A. Behal¹, and J. J. Hickman¹
¹University of Central Florida, Orlando, FL, ²University of West Hungary, Szombathely, Hungary

- 3:45PM-4:00PM **Tensor GSVD for Comparison of Two Column-Matched and Row-Independent Large-Scale Biomedical Datasets**
T. E. Schomay¹, P. Sankaranarayanan¹, and O. Alter¹
¹University of Utah, Salt Lake City, UT
- 4:00PM-4:15PM **Analysis of Cell Cycle Transition in Embryonic Stem Cells During Self-Renewal and Differentiation Through an Integrated Experimental and Computational Approach**
K. Task¹, O. Koubaa¹, and I. Banerjee¹
¹University of Pittsburgh, Pittsburgh, PA
- 4:15PM-4:30PM **What is the Optimal Amount of Somatic Repair?**
D. C. Vural¹ and L. Mahadevan¹
¹Harvard University, Cambridge, MA
- 4:30PM-4:45PM **Supra-threshold Membrane Properties Control Response Magnitude to Noisy Input Fluctuations in Neurons**
F. R. Fernandez¹, P. Malerba¹, and J. A. White¹
¹University of Utah, Salt Lake City, UT