BMES 2013 ANNUAL MEETING September 25–28, 2013 **Seattle** www.bmes.org

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. Alter[1] [1]University of Utah, Salt Lake City, UT
8:30AM-9:00AM	**How Much of the Human Genome is Functional?** (Invited) P. Green[1] [1]University of Washington, Seattle, WA
9:00AM-9:30AM	**Transgenerational Inheritance of DNA Methylation** (Invited) M. Pellegrini[1] [1]UCLA, 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. Lauffenburger[1], M. A. Miller[1], A. S. Meyer[1], M. Beste[1], K. Isaacson[2], and L. G. Griffith[1] [1]MIT, Cambridge, MA, [2]Newton-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. Papin[1] [1]University of Virginia, Charlottesville, VA

2:30PM-3:00PM	**Systems Approaches to Multi-Parameter Disease Diagnostics** (Invited)
	N. D. Price[1]
	[1]Institute 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]
	[1]U.C. Berkeley, Berkeley, CA, [2]Lawrence Berkeley National Laboratory, Berkeley, CA
4:30PM-5:00PM	**Linking Signal-Transduction and Gene-Expression Networks by Statistical Modeling** (Invited)
	Z. Chitforoushzadeh[1], S. I. LaRue[1], M. B. Yaffe[2], D. A. Lauffenburger[2], P. K. Sorger[3], R. C. Fry[4], and K. A. Janes[1]
	[1]University of Virginia, Charlottesville, VA, [2]Massachusetts Institute of Technology, Cambridge, MA, [3]Harvard Medical School, Boston, MA, [4]University 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. Linggi[1], W-J. Qian[1], W. Chrisler[1], and H. S. Wiley[1]
	[1]Pacific 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. Bild[1]
	[1]University of Utah, Salt lake city, UT
8:30AM-9:00AM	**Network Biology and Personalized Medicine in Multiple Sclerosis** (Invited)
	R. Nibbe[1], Y. Liu[2], M. Koyuturk[2], and M. Chance[1,2]
	[1]NeoProteomics, Inc., Cleveland, OH, [2]Case 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. Margolin[1]
	[1]Sage 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. Wang[1], T. G. Diacovo[2], J. Chen[2], J. B. Freund[3], and M. R. King[1]
	[1]Cornell University, Ithaca, NY, [2]Columbia University, New York, NY, [3]University of Illinois at Urbana-Champaign, Urbana, IL
2:00PM-2:30PM	**Motifs for Encoding/Decoding of Neuro-Sensory Information** (Invited)
	J. N. Kutz[1]
	[1]University 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 C57Gl/6J Developing Mouse Brain** (Invited) M. Hawrylycz[1], L. Ng[1], and C. Thompson[1] [1]Allen Institute for Brain Science, Seattle, WA
3:15PM-3:45PM	**Image-Based Biomedical Modeling, Simulation, and Visualization** (Invited) C. R. Johnson[1] [1]University 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. Acar[1], A. J. Lawaetz[1], M. A. Rasmussen[1], and R. Bro[1] [1]University of Copenhagen, Frederiksberg C, Denmark
8:30AM-9:00AM	**Numerical Linear Algebra and Optimization Tools for Bioinformatics** (Invited) M. A. Saunders[1], S. Akle[1], D. Ma[1], Y. Sun[1], R. M. Fleming[2], and I. Thiele[2] [1]Stanford University, Stanford, CA, [2]University of Luxembourg, Esch-sur-Alzette, Luxembourg
9:00AM-9:30AM	**Reduction and Analysis of Large Scale Systems** (Invited) L. Sirovich[1] [1]Rockefeller 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. Oberhardt[1], R. Zarecki[1], K. Yizhak[1], R. Pugatch[2], A. Wagner[1], E. Shtifman Segal[1], S. Freilich[3], C. S. Henry[4], U. Gophna[1], and E. Ruppin[1] [1]Tel Aviv University, Tel Aviv, Israel, [2]Princeton, NJ, Princeton, NJ, [3]Agricultural Research Organization, Volcani Center, Newe Ya'ar, Israel, [4]Argonne 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. Ponnapalli[1], M. A. Saunders[2], C. F. Van Loan[3], and O. Alter[4]
	[1]Bloomberg LP, New York, NY, [2]Stanford University, Stanford, CA, [3]Cornell University, Ithaca, NY, [4]University of Utah, Salt Lake City, UT
2:00PM-2:15PM	**Multi-Layer Motion Estimation for Fluoroscopic Imaging**
	C. Rottman[1], J. S. Preston[1], A. Cheryauka[2], L. Anderton[2], R. Whitaker[1], and S. Joshi[1]
	[1]University of Utah, Salt Lake City, UT, [2]GE Healthcare, Salt Lake City, UT
2:15PM-2:30PM	**Multiscale modeling of Nanog heterogeneity in pluripotent stem cell populations**
	J. Wu[1] and E. S. Tzanakakis[1,2]
	[1]Chemical and Biological Engineering, SUNY-Buffalo, Buffalo, NY, [2]Biomedical Engineering, SUNY-Buffalo, Buffalo
2:30PM-2:45PM	**Quantifying Spatial Patterns of Mouse Embryonic Stem Cell Differentiation within Embryoid Bodies**
	D. White[1], T. McDevitt[1], and M. Kemp[1]
	[1]Georgia Institute of Technology, Atlanta, GA
2:45PM-3:00PM	**PTMScout: Understanding protein post-translational modifications**
	M. Matlock[1], A. Holehouse[1], C. Zhang[1], and K. Naegle[1]
	[1]Washington 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-Yadlin[1], K. Beck[1], A. Hu[1], A. McKenna[1], and J. Shendure[1]
	[1]University of Washington, Seattle, WA
1:45PM-2:00PM	**Oncogenic Phospho-Tyrosine Signaling in the Absence of Mutated or Amplified Tyrosine Kinases**
	N. A. Graham[1], J. M. Drake[1], M. Tahmasian[1], K. J. Pienta[2], O. N. Witte[1,3], and T. G. Graeber[1]
	[1]University of California, Los Angeles, Los Angeles, CA, [2]University of Michigan, Ann Arbor, MI, [3]Howard Hughes Medical Institute, Los Angeles, CA
2:00PM-2:15PM	**A Microfluidic Platform for Visualizing Single-Cell Regulatory Dynamics in Mycobacteria**
	J. P. Keller[1], W-H. Yu[1], J. E. Galagan[1], and C. M. Klapperich[1]
	[1]Boston University, Boston, MA
2:15PM-2:30PM	**Gene Expression from the Gq Transgenic Mouse is Sufficient to Mechanistically Predict Altered Cardiac EC Coupling**
	F. Wu[1], J. Wadden[1], J. Lach[1], K. Skadron[1], and J. J. Saucerman[1]
	[1]University of Virginia, Charlottesville, VA
2:30PM-2:45PM	**Comparative Metabolic Capacities of Bacterial Pathogens Using Reconciled Genome-Scale Metabolic Reconstructions**
	P. Yen[1], J. A. Bartell[1], J. J. Varga[2], J. B. Goldberg[2], and J. A. Papin[1]
	[1]University of Virginia, Charlottesville, VA, [2]Emory University, Atlanta, GA

2:45PM-3:00PM	**Entrainment of a Population of NF-κB Oscillators Under Periodic Inputs**
	S. Tay[1] and R. Kellog[1]
	[1]ETH 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. Sjolander[1]
	[1]University of California, Berkeley, Berkeley, CA
3:30PM-3:45PM	**Inferring Single-Cell Gene Expression Frequencies from Stochastic Transcriptional Profiles**
	S. S. Bajikar[1], C. Fuchs[2], A. Roller[2], F. J. Theis[2], and K. A. Janes[1]
	[1]University of Virginia, Charlottesville, VA, [2]Helmholtz Center Munich, Munich, Germany
3:45PM-4:00PM	**Misfolded Conformations of the Bovine Prion Protein at Acidic pH**
	C. Cheng[1] and V. Daggett[1]
	[1]University 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. Hoffman[1], I. Jang[1,2], and H. Jo[1,2]
	[1]Wallace H. Coulter Department of Biomedical Engineering, Georgia Institute of Technology and Emory, Atlanta, GA, [2]Division 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. Funk[2], and N. D. Price[2]
	[1]University of Illinois, Urbana-Champaign, Urbana, IL, [2]Institute for Systems Biology, Seattle, WA
4:30PM-4:45PM	**Family Genomics Reveals Disease Genetics**
	A. Stittrich[1], H. Cox[1], H. Li[1], S. Ament[1], P. May[1,2], D. Mauldin[1], S. Montsaroff[1], R. Hubley[1], R. Gelinas[1], M. Brunkow[1], L. Rowen[1], A. Smit[1], G. Glusman[1], J. Roach[1], and L. Hood[1]
	[1]Institute for Systems Biology, Seattle, WA, [2]Luxembourg 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. Shlizerman[1], J. Riffell[1], and J. Kutz[1]
	[1]University of Washington, Seattle, WA
3:30PM-3:45PM	**Understanding Signal Transduction at the Neuroelectronic Interface**
	V. Thakore[1], P. Molnar[1,2], A. Behal[1], and J. J. Hickman[1]
	[1]University of Central Florida, Orlando, FL, [2]University 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. Schomay[1], P. Sankaranarayanan[1], and O. Alter[1]
	[1]University 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. Task[1], O. Koubaa[1], and I. Banerjee[1]
	[1]University of Pittsburgh, Pittsburgh, PA
4:15PM-4:30PM	**What is the Optimal Amount of Somatic Repair?**
	D. C. Vural[1] and L. Mahadevan[1]
	[1]Harvard University, Cambridge, MA
4:30PM-4:45PM	**Supra-threshold Membrane Properties Control Response Magnitude to Noisy Input Fluctuations in Neurons**
	F. R. Fernandez[1], P. Malerba[1], and J. A. White[1]
	[1]University of Utah, Salt Lake City, UT