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. Price\(^1\)  
\(^1\)Institute for Systems Biology, Seattle, WA

4:00PM – 5:30PM  
**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  
**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\(^1\)  
\(^1\)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  
**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\(^1\), 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\(^2\)  
\(^2\)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. 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. Pugatch¹, 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
A Higher-Order Generalized Singular Value Decomposition for Comparison of Global mRNA Expression from Multiple Organisms
S. P. Ponnapalli1, 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

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

Multiscale modeling of Nanog heterogeneity in pluripotent stem cell populations
J. Wu1 and E. S. Tzanakakis1,2
1Chemical and Biological Engineering, SUNY-Buffalo, Buffalo, NY, 2Biomedical Engineering, SUNY-Buffalo, Buffalo

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

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

**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. Geline\(^1\), 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  
**Dynamics of Biological Systems**

**Session Chairs:** Fernando R. Fernandez, Eli Shlizerman

3:15PM-3:30PM  
**Dynamics of Olfactory Neural Codes**  
E. Shlizerman\(^1\), J. Riffel\(^1\), and J. Kutz\(^2\)  
\(^1\)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\textsuperscript{1}, P. Sankaranarayanan\textsuperscript{1}, and O. Alter\textsuperscript{1}
\textsuperscript{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\textsuperscript{1}, O. Koubaa\textsuperscript{1}, and I. Banerjee\textsuperscript{1}
\textsuperscript{1}University of Pittsburgh, Pittsburgh, PA

4:15PM-4:30PM  What is the Optimal Amount of Somatic Repair?
D. C. Vural\textsuperscript{1} and L. Mahadevan\textsuperscript{1}
\textsuperscript{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\textsuperscript{1}, P. Malerba\textsuperscript{1}, and J. A. White\textsuperscript{1}
\textsuperscript{1}University of Utah, Salt Lake City, UT