AGENDA: FIFTH ANNUAL WINTER Q-BIO MEETING
February 21-24, 2017

Monday, February 20
6:00-9:00p  Opening registration and reception (Grand Garden)

Tuesday, February 21
6:15-8:00  Registration and Breakfast (Grand Garden)
8:00-8:15  Opening Remarks
8:15-8:55  Rob Knight, University of California, San Diego
Exploiting temporal and spatial patterning in the human microbiome
8:55-9:35  Radhika Nagpal, Harvard University
Collective intelligence: Cells, robots, and more
9:35-10:00  Coffee Break
10:00-10:20  Mary Teruel, Stanford University
A circadian signaling code restricts the rate of cell differentiation
10:20-10:40  Dennis Vitkup, Columbia University
Receptor-based Mechanism of Relative Sensing in Mammalian Signaling Networks
10:40-11:00  Anne-Ruxandra Carvunis, University of Pittsburgh
On the illusion of evolutionary divergence in regulatory networks
11:00-11:20  Ruth Williams, University of California, San Diego
Criticality and Adaptivity in Enzymatic Networks
11:20-12:30  Lunch on own
12:30-1:10  Marian Walhout, University of Massachusetts Medical School
Gene regulatory and metabolic networks
1:10-1:50  Job Dekker, University of Massachusetts Medical School
Liquified chromatin reveals the dynamic nature of chromatin interactions
1:50-2:20  Coffee and Snack Break
2:20-2:40  Naama Geva-Zatorsky, Harvard Medical School
Shining light on Gut-Microbiota-Host Interactions
2:40-3:00  Vincent Noireaux, University of Minnesota
Quantitative biology with a cell-free TXTL toolbox

Wednesday, February 22
6:30-8:00  Breakfast (Grand Garden)
8:00-10:00  Contributed Sessions (see pages 3-4 for details)
10:00-10:30  Coffee Break
10:30-11:10  Sangeeta Bhatia, Massachusetts Institute of Technology
Activity-based nanosensors as synthetic biomarkers of disease
11:10-11:50  Terry Hwa, University of California, San Diego
Spatiotemporal dynamics of the gut microbiota from quantitative in vitro and in silico models
11:50-1:00  Lunch on own
1:00-1:40  Brenda Andrews, University of Toronto
Quantitative yeast phenomics with single cell analysis of subcellular compartment Morphology
1:40-2:25  Steven Reiner, Stony Brook University
How to talk to the news media - A survivor’s guide
<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>2:25-3:00</td>
<td>Coffee and Snack Break</td>
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<tr>
<td>3:00-3:20</td>
<td>Jeremy Purvis, University of North Carolina at Chapel Hill</td>
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<td></td>
<td>Sibling Cell Rivalry: How Stem Cells Balance Self-Renewal and Differentiation</td>
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<td>3:20-3:40</td>
<td>Kristen Freida, California Institute of Technology</td>
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<td>Synthetic recording and in situ readout of lineage information in single cells</td>
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<td>3:40-4:00</td>
<td>Manoshi Datta, Massachusetts Institute of Technology</td>
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<td>Convergent community assembly dynamics on model particle microhabitats</td>
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**Thursday, February 23**

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<tr>
<td>6:30-8:00</td>
<td>Breakfast (Grand Garden)</td>
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<tr>
<td>8:00-9:30</td>
<td>Contributed Sessions (see page 5 for details)</td>
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<tr>
<td>9:30-10:00</td>
<td>Coffee Break</td>
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<tr>
<td>10:00-10:40</td>
<td>Chris Voigt, Massachusetts Institute of Technology</td>
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<td>Programming cells</td>
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<td>10:40-11:20</td>
<td>Naama Barkai, Weizmann Institute of Science</td>
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<td>Chromatin dynamics during DNA replication</td>
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<td>11:20-11:50</td>
<td>Coffee Break</td>
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<tr>
<td>11:50-12:10</td>
<td>Nan Hao, University of California, San Diego</td>
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<td>Multi-generational silencing dynamics control cell aging</td>
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<tr>
<td>12:10-12:30</td>
<td>Matthias Heinemann, University of Groningen</td>
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<td>A CDK-independent metabolic oscillator orchestrates the budding yeast cell cycle</td>
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<td>12:30-12:50</td>
<td>Rachel Greenstein, University of California, San Francisco</td>
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<td>Probing the intrinsic properties of heterochromatin spreading in single cells via an in vivo fluorescent sensor</td>
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<td>12:50-2:00</td>
<td>Lunch on own</td>
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<tr>
<td>2:00-2:40</td>
<td>Sophie Dumont, University of California, San Francisco</td>
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<td>Cell division: Mechanical integrity with dynamic parts</td>
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<td>2:40-3:20</td>
<td>Markus Covert, Stanford University</td>
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<td>Advances in whole-cell modeling</td>
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<td>3:20-5:00</td>
<td>Poster Session (Grand Prom, See pages 8-10 for details)</td>
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<tr>
<td>6:30-10:00</td>
<td>Banquet Dinner (Illima Garden)</td>
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**Friday, February 24**

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<tr>
<td>6:30-8:00</td>
<td>Breakfast (Dondero’s Restaurant)</td>
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<tr>
<td>8:00-8:40</td>
<td>Manu Prakash, Stanford University</td>
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<td>Life in Flatland: Complex morphogenetic and behavioral traits of a simple basal metazoa</td>
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<td>8:40-9:20</td>
<td>Martha Bulyk, Harvard University</td>
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<td>Genetic variation in human transcription factors</td>
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<td>9:20-9:50</td>
<td>Coffee Break</td>
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<tr>
<td>9:50-10:10</td>
<td>Erzsébet Regan, The College of Wooster</td>
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<td>Do heart capillary vessels blink? Noise-driven mosaic heterogeneity of the endothelium</td>
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<td>10:10-10:30</td>
<td>Kana Ishimatsu, Harvard Medical School</td>
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<td>Somite Scaling -wave vs gradient-</td>
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<tr>
<td>10:30-1:15</td>
<td>Contributed Sessions (see pages 6-7 for details)</td>
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<tr>
<td>1:15</td>
<td>Meeting adjourns</td>
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Wednesday Contributed Talks (8:00 - 10:00 am)

**Contributed session 1 (Grand 1)**

8:00-8:15  Yaron Antebi (Caltech) *Combinatorial Signal Perception in the BMP Pathway*
8:15-8:30  Eric Batchelor (National Cancer Institute) *The Impact of p53 Dynamics on Target Gene Expression, Global Transcriptional Regulation, and Cell Fate*
8:30-8:45  Lukasz Bugaj (UC San Francisco) *Ras/Erk misperception by cancer cells can drive hyperproliferation*
8:45-9:00  Maxwell Wilson (Princeton) *Tracking the dynamics of Ras/Erk target gene activation in live cells yields mechanisms for dynamic decoding*
9:00-9:15  Jose Reyes (Harvard Med School) *Small fluctuations with big consequences: how slight variations in p53 signaling allow cells to escape from cell cycle arrest?*
9:15-9:30  Patrick McCarter (UNC Chapel Hill) *Temporal separation of counter-acting feedback loops leads to robust hyper-osmotic stress adaptation in Saccharomyces Cerevisiae*
9:30-9:45  Alejandro Colman-Lerner (U. of Buenos Aires) *Robustness and information processing in a signal transduction pathway*
9:45-10:00 Silvia Santos (MRC- Imperial College London) *Decoding cellular signals: commitment during hES cells differentiation*

**Contributed session 2 (Grand 7)**

8:00-8:15  Yarden Katz (Harvard Med School) *Probabilistic adaptation in changing microbial environments*
8:15-8:30  Tomasz Lipniacki (Institute of Fundamental Technological Research) *Polarization of concave domains by traveling wave pinning*
8:30-8:45  Leah Santat (Caltech) *A synthetic approach to understanding Notch-based patterning*
8:45-9:00  Gabriel Leventhal (MIT) *Community analysis within an experimental bioreactor reveals micro-scale microbial associations*
9:00-9:15  Zachary Kurtz (NYU) *Rising through the ranks: inferring microbial associations via latent variable graphical models*
9:15-9:30  Andrey Morgun (Oregon State U.) *Transkingdom Networks: Revealing key players of Host-Microbiota Interactions*
9:30-9:45  Anupriya Tripathi (UC San Diego) *Atherosclerosis, sleep apnea and obesity: evidence of a microbiome connection*
9:45-10:00 Moran Yassour (The Broad Institute) *Strain-level identification of mother-to-child bacterial transmission during the first few months of life*

**Contributed session 3 (Grand 2)**

8:00-8:15  Marcella Gomez (UC Berkeley) *A tug-of-war mechanism for pattern formation in a genetic network*
8:15-8:30  Alberto Carignano (U. of Washington) *Programmable and predictable multi-cellular circuits in yeast*
8:30-8:45  Alex Hughes (UC San Francisco) *The mechanics of mesenchymal condensation are sufficient to fold tissue interfaces into diverse forms*
<table>
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<tr>
<th>Time</th>
<th>Speaker</th>
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<tbody>
<tr>
<td>8:45-9:00</td>
<td>Nicolas Pelaez (Caltech)</td>
<td>Ratiometric dynamics of ETS transcription factors regulate cell state transitions during retina patterning</td>
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<tr>
<td>9:00-9:15</td>
<td>Mehdi Sadeghpour (U. of Michigan)</td>
<td>Oscillations and bistability in co-repressive synthetic microbial consortia</td>
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<tr>
<td>9:15-9:30</td>
<td>Pulin Li (Caltech)</td>
<td>Morphogen Gradient Dynamics from the Bottom-up</td>
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<td>9:30-9:45</td>
<td>Justin Chew (U. of Chicago)</td>
<td>Building a Clock out of Stochastic Gears: Experimentally Investigating Molecular Noise in the Cyanobacterial Circadian Clock</td>
</tr>
</tbody>
</table>
Thursday Contributed Talks (8:00 am - 9:30 am)

Contributed session 1 (Grand 1)

8:00-8:15  David Younger (U. of Washington) Reengineering Yeast Mating for the High Throughput Characterization of Protein Interactions
8:15-8:30  Gene-Wei Li (MIT) Convergent protein expression stoichiometry in divergent bacteria
8:30-8:45  Marc Hafner (Harvard Med School) Improving preclinical cancer pharmacogenomics by using alternative drug sensitivity metrics
8:45-9:00  Sriram Chandrasekaran (Harvard) Genome-scale Reconstruction of the Dynamic Pluripotent Stem Cell Metabolic Network
9:00-9:15  Mark Grimes (U. of Montana) Unravelling Hairballs: Biological Pathways From Protein Modification Cluster-Filtered Networks
9:15-9:30  Martin Wühr (Princeton) Systems Biochemistry of the Metaphase Spindle

Contributed session 2 (Grand 7)

8:00-8:15  Neil H. Kim (U. of Illinois, Urbana-Champaign) Observation of real-time transposable element activity in individual live cells
8:15-8:30  Elizabeth Stasiowski (UC San Diego) Microfluidic development for the simultaneous culturing of 2,048 unique E. coli and S. cerevisiae strains
8:30-8:45  Ibrahim Cisse (MIT) Super-resolution imaging of transcription in living mammalian cells
8:45-9:00  Seth Shipman (Harvard Med School) Writing kilobytes of images into living cells over time
9:00-9:15  Lee Organick (U. of Washington) A Random Access Method for DNA-based Storage
9:15-9:30  Anna Grosberg (UC Irvine) Automated Detection of Structure Defects in Cell-Lines with LMNA Mutations

Contributed session 3 (Grand 2)

8:00-8:15  Radek Erban (U. of Oxford) Systematic design of reaction systems with desired behaviors: methods for achieving prescribed dynamical properties and noise control
8:15-8:30  Maria Kochugaeva (Rice U.) How conformational dynamics influences the protein search on DNA
8:30-8:45  Costas Maranas (Penn. State U.) Constructing predictive kinetic models of metabolism for guiding strain design
8:45-9:00  Jae Kyoung Kim (Korea Advanced Inst. of Science and Technology) A Period2 Phosphoswitch Keeps the Beat in the Rising Heat
9:00-9:15  Jaeyoung Sung (Chung-Ang U.) A new concept, mathematical model, chemical fluctuation theorem for vibrant reaction networks in living cells
9:15-9:30  Hye-Won Kang (U. of Maryland) A Mathematical Modeling of the Enzyme Clustering in Glucose Metabolism
### Friday Contributed Talks (10:30 am - 1:15 pm)

#### Contributed session 1 (Grand 1)

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<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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<tbody>
<tr>
<td>10:30-10:45</td>
<td>Jean-Michel Fustin (Kyoto U.)</td>
<td>Regulation of key circadian clock transcripts by m6A mRNA methylation</td>
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<tr>
<td>10:45-11:00</td>
<td>Siting Gan (Harvard)</td>
<td>An unstable singularity underlies stochastic phasing of the circadian clock in individual cyanobacterial cells</td>
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<tr>
<td>11:00-11:15</td>
<td>Philip Bittihn (UC San Diego)</td>
<td>Sensing the Environment through a Protective Shield - Phenotypic Entrainment of a Synthetic Gene Oscillator</td>
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<tr>
<td>11:15-11:30</td>
<td>Gen Kurosawa (RIKEN)</td>
<td>Universality of biological clocks and specificity in the regulatory network structures</td>
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<td>11:30-11:45</td>
<td>Julia Kamenz (Stanford)</td>
<td>An additional phospho-switch ensures robust oscillations during early embryonic cell divisions</td>
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<tr>
<td>11:45-12:00</td>
<td>Xin Zhou (Stanford)</td>
<td>Quantitative Control of Cell Signaling by Single-chain Photoswitchable Kinases</td>
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<td>12:00-12:15</td>
<td>Arvind Subramaniam (Fred Hutch Cancer Center)</td>
<td>Ribosome collisions as a robust timer for recognition of stalled ribosomes</td>
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<td>12:15-12:30</td>
<td>Sahand Hormoz (Caltech)</td>
<td>Inference of quantitative cell state transition dynamics in embryonic stem cells</td>
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<tr>
<td>12:30-12:45</td>
<td>Hao Yuan Kueh (U. of Washington)</td>
<td>Control of a mammalian cell fate decision by a slow, locally acting genetic switch</td>
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<tr>
<td>12:45-1:00</td>
<td>Rohan Maddamsetti (Harvard Med School)</td>
<td>Extreme gene amplifications contribute to adaptation of Escherichia coli to a citrate-only resource environment</td>
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#### Contributed session 2 (Grand 7)

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<tr>
<th>Time</th>
<th>Speaker</th>
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<tbody>
<tr>
<td>10:30-10:45</td>
<td>Antonina Hafner (Harvard)</td>
<td>Genome wide and single cell view of how p53 dynamics regulate gene expression</td>
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<td>10:45-11:00</td>
<td>Mirjam Fehling-Kaschek (Freiburg U.)</td>
<td>Mathematical modeling of drug-induced receptor internalization in the HER2-positive SKBR3 breast cancer cell-line</td>
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<tr>
<td>11:00-11:15</td>
<td>Brian Cleary (MIT/Broad Institute)</td>
<td>Composite measurements and molecular compressed sensing for highly efficient transcriptomics</td>
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<tr>
<td>11:15-11:30</td>
<td>Graham Heimberg (UC San Francisco)</td>
<td>Feature-based representations of scRNA-seq data enable comparisons between patient samples</td>
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<td>11:30-11:45</td>
<td>Melinda Varga (The College of Wooster)</td>
<td>Core-periphery structure of brain cortical networks</td>
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<td>11:45-12:00</td>
<td>Sophia Liu (Northwestern U.)</td>
<td>How to generate random coding sequences using the principle of maximum entropy</td>
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<tr>
<td>12:00-12:15</td>
<td>Karolina Kauppi (UC San Diego)</td>
<td>Antipsychotic target genes overlap with schizophrenia disease gene modules through interactome</td>
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<td>12:15-12:30</td>
<td>Philip Kim (U. of Toronto)</td>
<td>Highly parallel intracellular inhibition of protein-protein interactions identifies novel inhibitors with anti-cancer efficacy</td>
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<td>12:30-12:45</td>
<td>Constantine Dovrolis (Georgia Tech)</td>
<td>A New Perspective on the Developmental Hourglass Effect</td>
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<td>12:45-1:00</td>
<td>Takeshi Sugawara (Hiroshima U.)</td>
<td>Stagnant-itinerant chromatin dynamics and genome structures</td>
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<tr>
<td>1:00-1:15</td>
<td>Hosam Yousif (Salk/UC San Diego)</td>
<td>Reining in the rapidly expanding '-ome'-ome</td>
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</tbody>
</table>
Contributed session 3 (Grand 2)

10:30-10:45 Omar Din (UC San Diego) Synchronized lysis as a platform for engineered therapies
10:45-11:00 Jean-Benoit Lalanne (MIT) Alternative mRNA isoforms drives differential protein production in bacteria
11:00-11:15 Leonidas Bleris (U. of Texas, Dallas) Intragenic microRNAs and Host Transcript Regulation
11:15-11:30 Allison Lopatkin (Duke U.) Reversing plasmid-mediated antibiotic resistance
11:30-11:45 Jan Skotheim (Stanford) On the biosynthetic mechanism coupling cell growth to division
11:45-12:00 Christian Schwall (U. of Cambridge) Single Cell Sigma Factor Dynamic in B. subtilis
12:00-12:15 Severin Josef Schink (Technische Universität München) Origin and consequences of the exponential decay of viability of Escherichia coli during starvation
12:15-12:30 Roee Amit (Technion - Israel Inst. of Technology) Short CT-rich motifs can trigger context-specific silencing of gene expression in bacteria
12:30-12:45 Kole Roybal (UC San Francisco) Precision Control of Therapeutic T cell Responses with Synthetic Notch Receptors
12:45-1:00 Lee Bardwell (UC Irvine) Dangerous Concentrations: A Theoretical Framework for Specificity in Protein-Protein Interaction Networks
1:00-1:15 Lanying Zeng (Texas A&M) Interactions among Individual Phages Result in Different Cell-Fate Developments
Thursday Poster Session (Grand Promenade)

1. Kazuhiro Aoki (National Inst. of Natural Sciences, Okazaki Inst. for Integrative Bioscience)  
   Propagating wave of ERK activation orients collective cell migration
2. Ania-Ariadna Baetica (Caltech)  
   A Bayesian approach to inferring chemical signal timing and amplitude in a temporal logic gate using the cell population distributional response
3. Felix Boos (U. of Kaiserslautern)  
   Novel tools to measure protein turnover - from relative to absolute quantification
4. Emily Capra (Caltech)  
   Understanding and manipulating Notch signaling states in cord blood cells
5. Hui Xiao Chao (UNC Chapel Hill)  
   DNA damage checkpoints impose phase-specific stringencies and temporal locations
6. Susan Chen (UC San Francisco)  
   Using Optogenetics to Control Nuclear Translocation Dynamics of Transcription Factors and to Study its Regulatory Role on Transcription in S. cerevisiae
7. Ahreum Choi (Sogang U.)  
   Expression of Membrane Protein influenced by different codons of 8 residues at N-terminal region of microbial rhodopsin
8. Alejandro Colman-Lerner (U. of Buenos Aires)  
   Robustness and information processing in a signal transduction pathway
9. Alejandro Colman-Lerner (U. of Buenos Aires)  
   Cell surface receptors modify their signaling properties when working far from steady-state: a mathematical/computational study
10. Nicholas Csicsery (UC San Diego)  
    Biosensor development through high-throughput microfluidic screening of fluorescent E. coli and S. cerevisiae libraries
11. Nicholas De Veaux (Flatiron Institute, Simons Foundation)  
    Extending Gene Regulatory Network Inference to Model Predictor Interaction Terms in the Inferelator using ATAC-Seq
12. Justin Feng (Harvard Med School)  
    A general strategy to construct small molecule biosensors in eukaryotes
13. Kawng-Il Goh (Korea U.)  
    Interacting Particle System Model Motivated by Microbial Division of Labor
14. Sachin Goyal (UC Merced)  
    Deriving Mechanical Properties of Microtubules from Molecular Simulations
15. Ana Laura Guerrero (Cal Poly Pomona)  
    Transport of Bioactive Proteins into Breast Milk
16. Shaobin Guo (Caltech)  
    Expressing Soluble and Active Membrane Proteins in a Cell-Free Transcription-Translation Platform
17. Ray Haggerty (UNC Chapel Hill)  
    Mechanism Inference from Single Cells
18. Seth Haney (UC San Diego)  
    Exploiting the Tumor Ecosystem in Cancer Invasion
19. Tetsuhiro Harimoto (Columbia)  
    Dynamics of Bacteria in Tumor Spheroids
20. Marie Harton (NIH/National Cancer Inst.)  
    Determining the Impact of p53 Expression Dynamics on Target Gene Activation in Single Cells
21. Tetsuhiro Hatakeyama (U. of Tokyo)  
    Robustness of spatial pattern in buffered reaction-diffusion systems and Its Reciprocity with the Phase Plasticity
22. John Hughes (U. of Colorado Denver)
Estimating Velocity for Processive Motor Proteins with Random Detachment
Joanna Jaruszewicz-Błońska (Inst. of Fund. Technological Research, Polish Academy of Sciences)

Switching of a synthetic toggle in response to change in growth rate of bacteria
Mike Jin (Harvard)

Sensitive Detection of Biomolecules using Programmable Toehold Switches
DeAñalisa Jones (Icahn School of Medicine at Mount Sinai)

Can Noise Propagation in Gene Regulatory Networks Be Used to Identify Network Structure?
Shota Katayama (Hokkaido U.)

A powerful CRISPR/Cas9-based method for targeted transcriptional activation
Ji-Hyun Kim (Chung-Ang U.)

Quantitative Understanding of Probabilistic Behavior of Living Cells Operated by Vibrant Intracellular Networks
Heidi Klumpe (Caltech)

Map of BMP pairwise interactions describes how cells compute responses to BMP mixtures
Yasuaki Kobayashi (Ochanomizu U.)

Modeling of phase-shifted oscillatory signals driven by Hes7 oscillations
Marek Kochanczyk (Inst. of Fund. Technological Research, Polish Academy of Sciences)

Relaxation oscillations and hierarchy of feedbacks in MAPK signaling
Pawel Kocieniewski (Inst. of Fund. Technological Research, Polish Academy of Sciences)

RAF1 phosphoforms coordinate proliferation, motility, and apoptosis

Identification of two alternatively spliced antagonistic Clock kinase isoforms.
Rika Kojima (Kyoto U.)

Synchronization and complex dynamics in strongly coupled oscillators
Katsuyuki Kunida (U. of Tokyo)

Information transmission of insulin signal transduction based on live-cell active sensing and information theoretic approach

Cellular exosome-based delivery of microRNA in Huntington’s disease models.
Soon-Tae Lee (Seoul National U. Hospital)

Polymorphisms in the yeast galactose sensor underlie a natural continuum of nutrient-decision phenotypes
Kayla Lee (Harvard)

How to generate random coding sequences using the principle of maximum entropy.
Sophia Liu (Northwestern U.)

A novel β-lactam mechanism induces collective cell death
Allison Lopatkin (Duke)

Characterizing the Commander Complex, a Novel Macromolecular Machine Involved in Human Birth Defects
Anna Mallam (UT Austin)

Bottom-up reconstitution of BMP morphogenetic pattern formation
Joseph Markson (Caltech/HHMI)

A TXTL system for rapid prototyping of circuits with CRISPR elements
Ryan Marshall (U. of Minnesota)

Dosing Optimization of OSI-027 in Lymphoid Malignancies
Cordelia McGehee (Mayo Clinic)

Dynamics of antisense RNAs from stress responsive loci
Atsuko Miki (U. of Tokyo)

Single cell analysis of stress signaling dynamics in a life-death decision
Haruko Miura (Kyoto U.)

When structure follows function - structured sparse coding for genomics data
Christian Mueller (Simons Center for Data Analysis, Simons Foundation)

Cellular exosome-based delivery of microRNA in Huntington’s disease models.

Dynamics of antisense RNAs from stress responsive loci
Toshinori Namba (Hiroshima U.)
Synchronization of bacterial flagellar motors induced by intracellular signaling dynamics
47. Libere Ndacayisaba (Novartis Inst. for BioMedical Research)
Proteochemometric Machine Learning Models for Predictive Drug Discovery, Target Identification, and Polypharmacology Deconvolution

48. Daniel Nino (U. of Toronto)
A Redundant Labeling Approach to Molecular Counting in Localization Microscopy

49. Arisa Oda (U. of Tokyo)
Reconstruction of single-cell chromosome 3D structure using recurrence plots

50. Jin Park (Caltech)
Molecular time-sharing through dynamic pulsing in single cells

51. Seong Jun Park (Chung-Ang U.)
Quantitative relationship between the environment-coupled transcription dynamics and the transcription level variability

52. Joshua Porter (National Cancer Inst.)
p53 Alters Global Gene Expression via c-Myc in the DNA Double-Strand Break Response

53. Erzsébet Regan (The College of Wooster)
Modeling epigenetic memory at eukaryotic promoters

54. Sang Woo Seo (Seoul National U.)
Genome-scale Transcriptional Regulatory Network of OmpR in Escherichia coli

55. Christopher Short (West Virginia U.)
Can a Non-Spatial Model Recapitulate a Spatial Stochastic Simulation of ErbB2/ErbB3 Receptor Dimerization?

56. Zakary Singer (Columbia)
Inferring cell state transition dynamics from lineage trees and endpoint single-cell measurements

57. Yuyu Song (Harvard Med School)
Effects of Microtubule Drugs in Neurodevelopment and Injury

58. Kaori Sugimura (Ochanomizu U.)
Phase model for polarity ordering in spatially extended dynamical units: Derivation and dynamical properties

59. Sibo Tao (UC San Diego/HHMI)
Dissecting the functions of Aux/IAA proteins in the auxin pathway

60. Michael Tsabar (Harvard Med School)
Analysis of the naïve cell state on the p53 response to treatment

61. Youichi Uda (Kyoto U.)
Development of genetically-encoded optogenetic system for red light-induced control of cell signaling

62. Sam Wolff (UNC Chapel Hill)
Dynamics of OCT4 signaling in human embryonic stem cells

63. Jumpei Yamagishi (U. of Tokyo)
Symbiotic Cell Differentiation and Cooperative Growth in Multicellular Aggregates