Hawai‘i 2022
Winter q-bio
NINTH ANNUAL WINTER Q-BIO MEETING
February 14-18, 2022

Monday, February 14

5:00-9:00pm Opening registration and welcome reception (Lurline Lawn)
Happy Hour Refreshment
Kid's Science Demos - Foldscope Origami (5:30 – 8pm)

Tuesday, February 15

6:15-8:00 Registration and Breakfast (Ko Olina Lawn)
8:00-8:15 Opening Remarks from organizers (Ko Olina Rooms 3-5)
8:15-8:55 Sara Mostafavi, University of Washington
Deep Learning of Immune Cell Differentiation
8:55-9:35 Alex Sigal, Africa Health Research Institute
Milder disease with Omicron: is it the virus, pre-existing immunity, and will infection protect us from other variants?
9:35-10:00 Coffee Break (Ko Olina Lawn)
Kid’s Science Demos - Helicopters (9:35-11:00)
10:00-10:20 Manon Morin, University of California, San Diego
Microbial interactions are deeply reorganized as community complexity increases
10:20-10:40 David Sprinzak, Tel Aviv University
Mechanical forces drive precise patterning in the mammalian inner ear
10:40-11:00 Lindsey Osimiri, University of California, San Francisco
Optogenetic control of RelA underscores the importance of transcription factor dynamics in downstream gene expression
11:00-12:40 Lunch on own
12:40-1:20 Amy Herr, University of California, Berkeley
Single-cell biology: Microfluidic design to advance targeted proteomics
1:20-1:40 Zara Weinberg, University of California, San Francisco
De novo-designed antigen sensors enable multifaceted cellular engineering
1:40-2:10 Coffee Break (Ko Olina Lawn)
2:10-2:30 Kwonmoo Lee, Boston Children's Hospital, Harvard Medical School
Deep Learning-Based Subcellular Phenotyping of Protrusion Dynamics Reveals Fine Differential Drug Responses at Subcellular and Single Cell Levels
2:30-2:50 Natalie Sauerwald, Flatiron Institute
Pre-infection antiviral innate immunity contributes to sex differences in SARS CoV-2 infection
Wednesday, February 16

6:15-8:00  Breakfast (Ko Olina Lawn)
8:00-10:00  Contributed Sessions (Ko Olina Rooms 1&2, see page #4 for details)
10:00-10:30  Coffee Break (Ko Olina Lawn)
   Kid’s Science Demos – Magnetic Slime (10:00-11:50)
10:30-11:10  Uri Alon, Weizmann Institute of Science
   Design principles of physiological circuits
11:10-11:30  Miri Adler, Broad Institute of MIT and Harvard
   Principles of intra- and inter-cellular hyper-motif circuits in developmental programs
11:30-11:50  Joshua Francois, Harvard Medical School
   The interplay between matrix deformation and the coordination of turning events governs directed neutrophil migration in 3-D matrices
11:50-1:20  Lunch on own
1:20-2:00  Marcella Gomez, University of California, Santa Cruz
   Towards Accelerating Wound Healing with Feedback Control: a data-driven approach
2:00-2:20  Martin Wühr, Princeton University
   Proteomics of unperturbed protein turnover in Escherichia coli
2:20-2:50  Coffee Break (Ko Olina Lawn)
2:50-3:10  Zhen Zhou, University of California, San Diego
   A synthetic Sir2-Hap4 oscillator extends yeast lifespan
3:10-3:30  Lukasz Bugaj, University of Pennsylvania
   Optogenetic dissection of how oncogenic protein condensates alter signal perception and promote drug tolerance.
4:00-6:00  Poster Session (Malolo Room, see page #9 for details)
   Happy Hour Refreshment
NINTH ANNUAL WINTER Q-BIO MEETING
February 14-18, 2022

Thursday, February 17

6:15-8:00 Breakfast (Ko Olina Lawn)
8:00-10:00 **Contributed Sessions** (Ko Olina Rooms 1&2, see page #5 for details)
10:00-10:30 **Coffee Break** (Ko Olina Lawn)
10:30-11:10 **Galit Lahav**, Harvard University
*Protein Dynamics and Decision Making in Single Cells*
11:10-11:30 **Seth Shipman**, Gladstone Institutes and University of California, San Francisco
*Hijacking Bacterial Retrons to Produce DNA-on-Demand for Biotechnology*
11:30-1:00 Lunch on own
1:00-1:20 **Yonatan Chemla**, Massachusetts Institute of Technology
*Models and measurement the translation-initiation modes of operonic mRNAs in bacteria*
1:20-1:40 **Shixuan Liu**, Stanford University
*An organism-wide atlas of hormonal signaling based on the mouse lemur single-cell transcriptome*
1:40-2:10 **Coffee Break** (Ko Olina Lawn)
2:10-2:30 **Ting Lu**, University of Illinois, Urbana-Champaign
*Engineering a Cooperative Microbial Consortium for Chemical Production*
2:30-2:50 **Connie Phong**, Stanford University, School of Medicine
*Temperature scaling in developmental regulatory systems: What molecular mechanisms facilitate early embryonic robustness?*
6:00-9:00 **Banquet Dinner** (Ocean Lawn)

Friday, February 18

6:15-8:00 Breakfast (Ko Olina Lawn)
8:00-10:00 **Contributed Sessions** (Ko Olina Rooms 1&2, see page #6 for details)
10:00-10:30 **Coffee Break** (Ko Olina Lawn)
10:30-11:10 **Katie Pollard**, University of California, San Francisco
*Sequence-structure-function modeling for DNA*
11:10-11:50 **David Van Valen**, California Institute of Technology
*Single-cell biology in a software 2.0 world*
12:00 Meeting adjourns
Wednesday Contributed Talks (8:00 – 10:00 am)

**Contributed session 1** (Ko Olina Room 1)

8:10-8:20  **Gregory Poore** (University of California, San Diego)
Pan-cancer analyses reveal cancer type-specific fungal ecologies and bacteriome interactions

8:20-8:30  **Wojciech Szpankowski** (Purdue University)
Guessing Evolution via Life Science Dynamic Networks

8:30-8:40  **Kathleen Chen** (Princeton University)
A sequence-based global map of regulatory activity for deciphering human genetics

8:40-8:50  **Arianna Miano** (University of California, San Diego)
Survival of the weakest in non-transitive asymmetric interactions among strains of E. coli

9:00-9:10  **Ashley Moon** (University of California, San Diego)
A Magnesium Tug-of-war Impedes Bacterial Antibiotic Resistance

9:10-9:20  **Chloe Fishman** (Gladstone Institutes)
Retron termination depends on host RNase H1 and impacts phage defense

9:20-9:30  **Santiago Lopez** (Gladstone Institutes)
Precise genome editing across kingdoms of life using retron-derived DNA

9:30-9:40  **Rogelio Hernandez-Lopez** (University of California, San Francisco)
T cell circuits that sense antigen density with an ultrasensitive threshold

**Contributed session 2** (Ko Olina Room 2)

8:10-8:20  **Meera Gupta** (Princeton University)
Towards Accurate and Precise Quantification of Protein Copy Numbers on a Genome-Wide Scale

8:20-8:30  **Tinyi Chu** (Memorial Sloan Kettering Cancer Center)
Mapping gene expression cartography along mouse intestinal crypt axes using Bayesian integration of single cell RNA-seq and spatial transcriptomics

8:30-8:40  **Emily Laubscher** (California Institute of Technology)
Polaris: accurate spot detection for single-molecule FISH images with deep learning and weak supervision

8:40-8:50  **Morgan Schwartz** (California Institute of Technology)
Accelerating imaging-based reverse genetics with spatial optical barcodes and deep learning
9:00-9:10  **Wei Chen** (University of Washington)
Multiplex genomic recording of enhancer and signal transduction activities in mammalian cells

9:10-9:20  **Candace Liu** (Stanford University)
Robust phenotyping of highly multiplexed tissue imaging data using pixel-level clustering

9:20-9:30  **Jiaxi Zhao** (University of California, Berkeley)
Optogenetic dissection of transcriptional repression in living embryos

9:30-9:40  **Xinming Tu** (University of Washington)
CLUE: Cross-linked unified embedding for comprehensive single-cell multi-omics data integration

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**Thursday Contributed Talks** (8:00 – 10:00 am)

**Contributed session 1** (Ko Olina Room 1)

8:10-8:20  **Anusorn Mudla** (University of California, San Diego)
Cell-cycle-gated feedback control mediates desensitization to interferon stimulation

8:20-8:30  **Johan Elf** (Uppsala University)
The biophysics of genomic search

8:30-8:40  **Ania-Ariadna Baetica** (University of California San Francisco)
Tuning Incoherent Feedforward Circuit Architectures with Feedback to Rapidly Develop a Modular Toolbox

8:40-8:50  **Neda Bagheri** (Northwestern University)
Cellular and structural heterogeneity bring about counterintuitive emergent phenomena in multicellular biological oscillator systems

9:00-9:10  **Ronghui Zhu** (California Institute of Technology)
Synthetic multistability in mammalian cells

9:10-9:20  **Andrew Lezia** (University of California, San Diego)
Design, Mutate, Screen: High-throughput creation of genetic clocks with different period-amplitude characteristics

9:20-9:30  **Lee Bardwell** (University of California, Irvine)
Dangerous Concentrations: Specificity in Protein-Protein Interaction Networks
9:30-9:40  **Santi Bhattarai-Kline** (Gladstone Institute of Data Science and Biotechnology)
Reconstructing transcriptional histories by CRISPR acquisition of retron-based genetic barcodes

**Contributed session 2** (Ko Olina Room 2)

8:10-8:20  **Greg Reeves** (Texas A&M University)
*Dynamics and memory of BMP signaling in the early Drosophila embryo*

8:20-8:30  **Paula Bucko** (Harvard Medical School)
*The role of p53 dynamics in immune cell regulation*

8:30-8:40  **Kwang-Tao Chou** (University of California, San Diego)
*A segmentation clock patterns cellular differentiation in a bacterial biofilm*

8:40-8:50  **Thao Nguyen** (Princeton University)
*Differential nuclear import sets the timing of protein access to the embryonic genome*

9:00-9:10  **Yue Qin** (University of California, San Diego)
*Mapping cell structure across scales by fusing protein images and interactions*

9:10-9:20  **Inna Averbukh** (Stanford University)
*Spatio-temporal coordination at the maternal-fetal interface promotes trophoblast invasion and vascular remodeling in the first half of human pregnancy*

9:20-9:30  **Xiao Wang** (Arizona State University)
*Cell Cycle Dependent Genome Editing Dynamics Revealed by Single Cell Time Lapse Imaging*

9:30-9:40  **Leo Bleris** (The University of Texas at Dallas)
*Genetic Physical Unclonable Functions in Human Cells*

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**Friday Contributed Talks (8:00 – 10:00 am)**

**Contributed session 1** (Ko Olina Room 1)

8:10-8:20  **Max Wilson** (University of California, Santa Barbara)
*Optogenetic control of cellular signaling through dynamic nucleation of liquid droplets*

8:20-8:30  **Ting-Sung Hsieh** (UT Southwestern Medical Center)
*Dynamic remodeling of host membranes by self-organizing bacterial effectors*
8:30-8:40  **Costas Maranas** (Pennsylvania State University)
On the unreasonable effectiveness of flux balance analysis in metabolic networks

8:40-8:50  **Alex Johnson** (Princeton University)
TMTpro Complementary Ion Quantification Increases Plexing and Sensitivity for Accurate Multiplexed Proteomics at the MS2 Level

9:00-9:10  **Saba Nafees**  (Chan Zuckerberg Biohub)
ortho_seqs: A Python tool for sequence analysis and higher order sequence-phenotype mapping

9:10-9:20  **Frank Zhang** (Center for Computational Biology, Flatiron Institute, Simons Foundation)
Automating Deep Learning in Genomics with AMBER

9:20-9:30  **Euan Joly-Smith** (University of Toronto)
Inferring gene regulation from static snapshots of gene expression variability

9:30-9:40  **Tongli Zhang** (University of Cincinnati)
Understanding virtual patients efficiently and rigorously by combining machine learning with dynamical modelling

**Contributed session 2** (Ko Olina Room 2)

8:10-8:20  **Rong Zhang** (Arizona State University)
Emergent Damped Oscillation Induced by Nutrient-Modulating Growth Feedback

8:20-8:30  **Shalni Kumar** (University of California, San Diego)
Burden-minimizing Adaptation of Populations with Duplicate Origin Plasmid Pairs

8:30-8:40  **Matthias Fischer** (Institute for Theoretical Biology, Humboldt Universitaet Berlin and Charite Berlin, Germany)
Mathematical modelling of colon epithelium population dynamics reveals conditions for maintaining tissue homoeostasis

8:40-8:50  **Ting Gong** (University of California, Davis)
Frequency dependent growth of bacteria in living materials

9:00-9:10  **Alina Glaubitz** (Dartmouth College)
A tale of two vaccine efficacies: Simpson's paradox and bifurcations

9:10-9:20  **Xiaojun Tian** (Arizona State University)
Double-edged role of resource competition in gene expression noise and control
9:20-9:30  Jean-Baptiste Lugagne (Boston University)
High-throughput single-cell control using real-time feedback

9:30-9:40  Chelsea Hu (California Institute of Technology)
Layered Feedback Control Overcomes Performance Trade-off in Synthetic Biomolecular Networks
Poster Session (Wednesday 4:00 – 6:00 pm, Malolo Room)

1. Thinh Huynh (The College of Wooster)
   Elucidating the essentiality of the mitochondrial disulfide relay system in baker’s yeast via flux balance analysis

2. Tara Spencer (University of California, San Diego)
   A model within a model: using cheese microbiomes to investigate host-phage interactions within a community

3. Anita Gola (Rockefeller University)
   A Spatially Patterned Stem Cell and Immune Cell Barrier at the Skin Surface

4. Yubin Xie (Memorial Sloan Kettering Cancer Center)
   Dissect the Tumor Progression and Metastasis of Pancreatic Ductal Adenocarcinoma via Rapid Autopsy Program

5. Aelon Ketema Samuel (The College of Wooster)
   A Knock-out experiment on a neuronal Boolean model

6. Shayna Holness (University of California, San Diego)
   mRNA binding proteins produce foci in replicatively aged yeast cells

7. Kate Crawford (University of California, San Francisco)
   Optimization of Retron Reverse Transcriptase System for Production and Transcriptional Control in Eukaryotes

8. Alain Bonny (The Rockefeller University)
   The Spatiotemporal Coordination Between Inflammation and Wound Repair

9. Meelad Amouzgar (Stanford University)
   Supervised dimensionality reduction for exploration of single-cell data by HSS-LDA

10. Emma Davidson (The College of Wooster)
    An investigation of circadian cycle influence upon cell cycle regulation

11. Matthew Kim (University of California, San Francisco)
    Targeted Protein Degradation Platform for Cell Engineering

12. Rachael Kuintzle (California Institute of Technology)
    Combinatorial interactions in the Notch signaling pathway

13. Seesha Takagishi (University of California, San Francisco)
    Characterizing the Regulatory Significance of Dynamic Transcription Factor Inputs

14. Xi Chen (Flatiron Institute)
    MAGICAL: an integrative approach to identify epi-driven genes from single cell epigenetic and transcriptomic data

15. Emily Pierce (University of California, San Diego)
    From iron to antibiotics: Bacterial-fungal interactions revealed by genome-wide mutational analyses

16. Jamshaid Shahir (University of North Carolina at Chapel Hill)
    Elucidating the role of the cell cycle in stem cell fate using multiplexed imaging

17. Yuting Liu (University of California, San Diego)
    Yeast cell fate can be programmed by modulating the expression of Sir2 and HAP
18. Tiffany Zhou (University of California, San Diego)
   An Engineered Long-Range Intercellular Coupling Platform for Synchronizing Colony Behavior
19. Sierra Lear (University of California, San Francisco)
   Engineering mitochondrial gene editing tools
20. Joy Pai (Stanford University)
   Regional and clonal T cell dynamics at single cell resolution in immune checkpoint blockade
21. Nan Hao (University of California, San Diego)
   Divergent trajectories of single-cell aging
22. Austin Doughty (University of California, San Diego)
   Synthetic population capping circuit in microfluidics
23. Alyssa Chiang (University of California, San Diego)
   Adaptive laboratory evolution in the development of biosensors
24. Joanna Zhang (University of California, San Diego)
   Bacterial circuit dynamics in 3D tumor spheroids
25. Hersh K. Bhargava (University of California, San Francisco)
   Human-Computer Synergy for Principled Design of Cell Therapies
26. Sam Kovaka (Johns Hopkins University)
   Visualization and analysis of nanopore RNA and DNA signal alignments for modification detection, polishing, enrichment, and more with Uncalled4
27. Katharine Jenike (Johns Hopkins University)
   HETTREK: Improving assembly accuracy and contiguity of highly heterozygous genomes
28. Zhen Zhou (University of California, San Diego)
   A synthetic Sir2-Hap4 oscillator extends yeast lifespan
29. Manon Morin (University of California, San Diego)
   Microbial interactions are deeply reorganized as community complexity increases
30. Paula Bucko (Harvard Medical School)
   The role of p53 dynamics in immune cell regulation
31. Ania-Ariadna Baetica (University of California, San Francisco)
   Tuning Incoherent Feedforward Circuit Architectures with Feedback to Rapidly Develop a Modular Toolbox
32. Shalni Kumar (University of California, San Diego)
   Burden-minimizing Adaptation of Populations with Duplicate Origin Plasmid Pairs
33. Kwang-Tao Chou (University of California, San Diego)
   A segmentation clock patterns cellular differentiation in a bacterial biofilm
34. Meera Gupta (Princeton University)
   Towards Accurate and Precise Quantification of Protein Copy Numbers on a Genome-Wide Scale
35. Anusorn Mudla (University of California, San Diego)
   Cell-cycle-gated feedback control mediates desensitization to interferon stimulation
36. Ting-Sung Hsieh (University of Texas, Southwestern)
   Dynamic remodeling of host membranes by self-organizing bacterial effectors
37. Thao Nguyen (Princeton University)
   Differential nuclear import sets the timing of protein access to the embryonic genome
38. Tinyi Chu (Memorial Sloan Kettering Cancer Center)
   Mapping gene expression cartography along mouse intestinal crypt axes using Bayesian integration of single cell RNA-seq and spatial transcriptomics
39. Emily Laubscher (California Institute of Technology)
   Polaris: accurate spot detection for single-molecule FISH images with deep learning and weak supervision
40. Shixuan Liu (Stanford University)
   An organism-wide atlas of hormonal signaling based on the mouse lemur single-cell transcriptome
41. Morgan Schwartz (California Institute of Technology)
   Accelerating imaging-based reverse genetics with spatial optical barcodes and deep learning
42. Yue Qin (University of California, San Diego)
   Mapping cell structure across scales by fusing protein images and interactions
43. Narasimhan Balakrishnan (Northwestern University)
   Cellular and structural heterogeneity bring about counterintuitive emergent phenomena in multicellular biological oscillator systems
44. Candace Liu (Stanford University)
   Robust phenotyping of highly multiplexed tissue imaging data using pixel-level clustering
45. Andrea Brown (The College of Wooster)
   The Seven Deadly Pathways: A Boolean Model of Yeast Apoptosis in Response to Reactive Oxygen Species, DNA damage, Starvation, and Salt
46. Costas Maranas (Penn State University)
   On the unreasonable effectiveness of flux balance analysis in metabolic networks
47. Joseph Chan (Memorial Sloan Kettering Cancer Center)
   Reversal of lineage plasticity in RB1/TP53-deleted prostate cancer through FGFR and Janus kinase inhibition
48. Yered Pita-Juarez (Beth Isreal Deaconess Medical Center)
   A single nucleus and spatial transcriptomic atlas of the liver reveals multicellular changes in response to SARS-CoV2 infection
49. Haley Fuller (University of Pittsburgh)
   Magnetic Microrobots that Demonstrate Liquid-Gel Penetration for Biomolecule Delivery
50. Aleksandrina Goeva (Broad Institute of MIT and Harvard)
   Improved marker detection through label refinement in case-control single-cell RNA-seq studies
51. Shah Md Toufiqur Rahman (National Institute of Health)
   Simultaneous live imaging reveals ligand-specific coordination of NF-xB subunits in primary macrophages
52. Abhineet Nitin (University of California)
   *A data-driven approach to predicting Ras/MAPK pathway activation with downstream target genes*

53. Lukasz Bugaj (University of Pennsylvania)
   *Optogenetic dissection of how oncogenic protein condensates alter signal perception and promote drug tolerance.*
Abstracts of Invited Talks

Tuesday, February 15

8:15-8:55  Sara Mostafavi, University of Washington
Deep Learning of Immune Cell Differentiation

The mammalian genome contains several million cis-regulatory elements, whose differential activity marked by open chromatin determines cellular differentiation. While the growing availability of functional genomics assays allows us to systematically identify cis-regulatory elements across varied cell types, how the DNA sequence of cis-regulatory elements is decoded and orchestrated on the genome scale to determine cellular differentiation is beyond our grasp. In this talk, I'll present recent work using machine learning as a tool to derive an understanding of the relationship between regulatory sequence and cellular function in the context of immune cell differentiation. In particular, I'll present our deep learning approach (AI-TAC) to combining a large and granular compendium of epigenomic data and will describe approaches to robustly interpreting complex, black-box models in order to uncover mechanistic insights into immune gene regulation. Our work shows that a deep learning approach to genome-wide chromatin accessibility can uncover patterns of immune transcriptional regulators that are directly coded in the DNA sequence, and thus providing a powerful in-silico framework (an in-silico assay of sorts) to mechanistically probe the relationship between regulatory sequence and its function.

8:55-9:35  Alex Sigal, Africa Health Research Institute
Milder disease with Omicron: is it the virus, pre-existing immunity, and will infection protect us from other variants?

While the B.1.1.529 Omicron has rapidly spread worldwide, the disease it causes is reported to be milder than other variants. The mechanism for this may be a buildup of immunity from previous infections and vaccination, evolution of attenuated pathogenicity by the virus, or both. I will present evidence for each mechanism from our studies and those of others, discuss a possible evolutionary pathway, and present our latest data on the extent to which Omicron infection elicited immunity protects against the Delta variant, and in whom.

12:40-1:20  Amy Herr, University of California, Berkeley
Single-cell biology: Microfluidic design to advance targeted proteomics

Oncoprotein isoforms and fragments are implicated in cancer drug resistance mechanisms. HER2 and Estrogen Receptor (ER) proteoforms are two important examples in breast cancer.
While proteoforms are of substantial interest, the immunoassay reigns as the de facto standard for direct measurement of protein targets in single cells (i.e., flow cytometry, mass cytometry/CyTOF, immunofluorescence). Yet, immunoassays typically lack the selectivity needed to distinguish proteoforms. To bridge this gap, we have introduced a suite of ‘electrophoretic cytometry’ tools – built on microfluidic principles – designed to increase target selectivity beyond simple immunoassays using immunoblot assay designs. Enhanced selectivity is essential for targets that lack high quality immunoreagents – as is the case for the vast majority of proteoforms. Immunoblots concatenate an upstream electrophoretic separation (equilibrium or non-equilibrium) to a downstream immunoassay to report two physicochemical properties for the targets of interest. In fundamental engineering and design, we will discuss how the physics and chemistry accessible in microsystems allows both the “scale-down” of immunoblotting to single cells and the “scale-up” to concurrent analyses of large numbers of cells. Precision control of fluids and materials transport (primarily diffusion-driven) integrates sophisticated sample preparation – the unsung hero of measurement science. We use the refined single-cell preparation to profile protein targets in specific sub-cellular compartments and eliminate complex post hoc image segmentation algorithms. Lastly, we update on how assay and device developments enhance oncoprotein profiling of HER2 and ER-alpha, including in understanding the role of protein signaling and truncated isoforms in development of breast cancer drug resistance. Taken together, we view microfluidic design strategies as key to advancing protein measurement performance needed to address unmet gaps in quantitative biology and precision medicine.

Wednesday, February 16

10:30-11:10   **Uri Alon**, Weizmann Institute of Science

*Design principles of physiological circuits*

In the past 5 years my lab has focused on principles of human organs and disease. I'm going to ask you at the meeting what you'd like to hear about (feel free to email me with requests at urialonw@gmail.com)

- mathematical essence of aging
- principles of hormone circuits and autoimmunity
- principles of inflammation and fibrosis

Whatever the topic, there will be guitar songs:) 

Online resource: my systems medicine course

https://www.weizmann.ac.il/mcb/UriAlon/courses/systems-medicine-course-2020
**Marcella Gomez, University of California, Santa Cruz**  
*Towards Accelerating Wound Healing with Feedback Control: a data-driven approach*

Controlling biological systems presents challenges not typically dealt with in traditional control theoretic approaches but also gives way to leniencies not traditionally tolerated. We present a holistic view to this new research area and current developments integrating various data-driven approaches towards developing a framework for modeling and control of wound healing.

**Thursday, February 17**

10:30-11:10  
**Galit Lahav, Harvard University**  
*Protein Dynamics and Decision Making in Single Cells*

**Friday, February 18**

10:30-11:10  
**Katie Pollard, University of California, San Francisco**  
*Sequence-structure-function modeling for DNA*

The human genome sequence folds in three dimensions (3D) into a rich variety of locus-specific contact patterns. Despite growing appreciation for the importance of 3D genome folding in evolution and disease, we lack models for relating mutations in genome sequences to changes in genome structure and function. Towards that goal, we developed a deep convolutional neural network model, called Akita, that accurately predicts genome folding from DNA sequence alone. Representations learned by Akita underscore the importance of the structural protein CTCF but also reveal a complex grammar beyond CTCF binding sites that underlies genome folding. Akita enabled rapid in silico predictions for effects of sequence mutagenesis on the 3D genome, including differences in genome folding across species and in disease cohorts, which we are validating with CRISPR-edited genomes. This prediction-first strategy exemplifies my vision for a more proactive, rather than reactive, role for data science in biomedical research.

11:10-11:50  
**David Van Valen, California Institute of Technology**  
*Single-cell biology in a software 2.0 world*

Biological systems are difficult to study because they consist of tens of thousands of parts, vary in space and time, and their fundamental unit—the cell—displays remarkable variation in its behavior. These challenges have spurred the development of genomics and imaging technologies over the past 30 years that have revolutionized our ability to capture information about biological systems in the form of images. Excitingly, these advances are
poised to place the microscope back at the center of the modern biologist’s toolkit. Because we can now access temporal, spatial, and “parts list” variation via imaging, images have the potential to be a standard data type for biology.

For this vision to become reality, biology needs a new data infrastructure. Imaging methods are of little use if it is too difficult to convert the resulting data into quantitative, interpretable information. New deep learning methods are proving to be essential to reliable interpretation of imaging data. These methods differ from conventional algorithms in that they learn how to perform tasks from labeled data; they have demonstrated immense promise, but they are challenging to use in practice. The expansive training data required to power them are sorely lacking, as are easy-to-use software tools for creating and deploying new models. Solving these challenges through open software is a key goal of the Van Valen lab. In this talk, I describe DeepCell, a collection of software tools that meet the data, model, and deployment challenges associated with deep learning. These include tools for distributed labeling of biological imaging data, a collection of modern deep learning architectures tailored for biological image analysis tasks, and cloud-native software for making deep learning methods accessible to the broader life science community. I discuss how we have used DeepCell to label large-scale imaging datasets to power deep learning methods that achieve human level performance and enable new experimental designs for imaging-based experiments.
Key Locations

**WIFI Instructions:**

- **Choose Network**- “Four Seasons Meeting”
- **Open Browser**- Log in page will auto display
- **Enter PIN**- 618989

Email address for the organizers: coordinator@w-qbio.org

Website for meeting: [http://w-qbio.org](http://w-qbio.org)

Online schedule and abstracts: [https://w-qbio.org/agenda/](https://w-qbio.org/agenda/)

Venue:

Four Seasons Resort O’ahu
92-1001 Olani Street, Kapolei, HI 96707
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