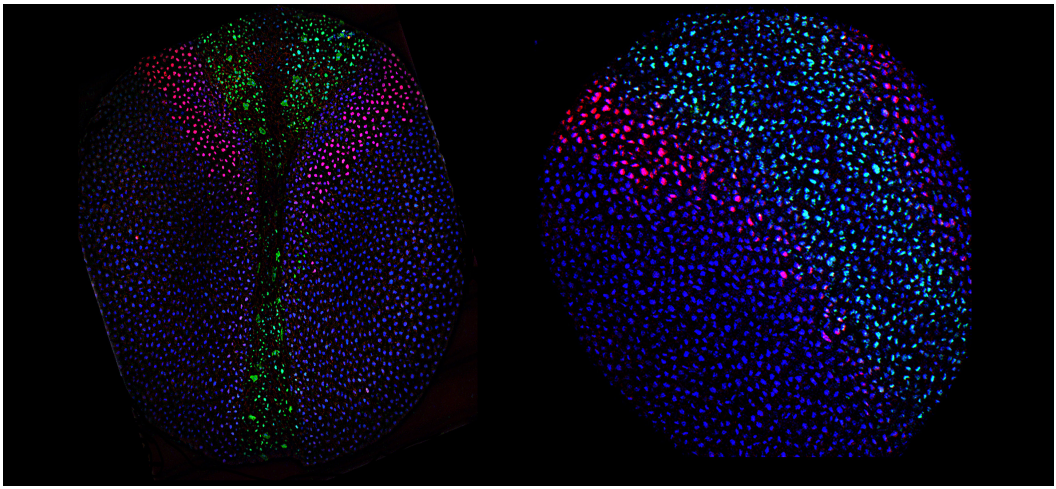
NSF-Simons
Center for Quantitative Biology

1st ANNUAL CONFERENCE

Quantitative Approaches in Biology



November 16-17, 2018
Northwestern University, Evanston, IL

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Northwestern University

The NSF-Simons Center for Quantitative Biology at Northwestern University is an NSF-Simons Research Center for Mathematics of Complex Biological Systems (MathBioSys). The Center is a place where mathematical scientists and developmental biologists intensely work together on a broad range of questions arising from investigations into the biology of animal development.

Our team of investigators is studying high dimensional and dynamic phenomena by using imaging, sequencing, and other technologies. Our aim is to make important new discoveries about the emergent properties of growth and development.

The Center also offers a range of programming that will lay the foundation for collaborations at the intersection of mathematics and biology across the nation and the globe.

Research

The research mission of the NSF-Simons Center for Quantitative Biology is to transform our understanding of animal growth and development by applying mathematical analysis and modeling to this discipline. Five vibrant research programs in the Center are composed of collaborative teams of mathematical and life scientists.

The Center deploys three fundamental mathematical disciplines: dynamical systems theory; stochastic processes; and dimension reduction. These approaches are highly suited to the real-world features of growth and development.

Experimental focus is on established laboratory model organisms, Drosophila melanogaster, Caenorhabditis elegans, Xenopus laevis, and Mus musculus.

CONTENTS \ 3

@QuantBiology

What was the best part of your conference experience?

- Interact with us on social media
- Tell us your conference story
- Share your ah-ha moments
- Conference hashtag **#quantbiology2018**

THANK YOU TO OUR SPONSORS

Zeiss, Molecular Devices, and Nikon!

If you have a moment visit the Zeiss poster,
Correlative Microscopy enables a High Content Cryo Workflow,
at Friday's and Saturday's poster session.

FRIDAY SCHEDULE \ 4

McCormick Auditorium,
Norris University Center
1999 Campus Drive, Evanston, IL

8:30 am	**Registration & Breakfast**
8:50 am – 9:00 am	**Directors' Welcome** Richard Carthew, PhD & William Kath, PhD
9:00 am – 10:00 am	**Illuminating arthropod development with lightsheet microscopy** Tassos Pavlopoulos, PhD
10:15 am – 11:15am	**Single-cell Transcriptomics and Biology using Microfluidics** Anindita (Oni) Basu, PhD
11:30 am – 12:30 pm	**Workshop on Interdisciplinary Team Science** Venue: Louis Room, 2nd Floor
12:30 pm – 1:30 pm	Working Lunch
1:30 pm – 2:15 pm	**Poster Session** Undergraduate Research in Quantitative Biology Posters
2:15 pm – 2:30 pm	**Group Photo** Venue: McCormick Auditorium
2:30 pm – 3:30 pm	**Keynote: Physical Morphogenesis** Boris Shraiman, PhD
3:45 pm – 5:00 pm	**Panel on Team Science**
5:00 pm	**Closing Remarks & Award Ceremony**
5:15 pm – 6:30 pm	**Reception & Networking** Venue: Louis Room, 2nd Floor
6:30 pm	Optional Meet up at Cupitol 812 Grove St, Evanston, IL 60201

Boris Shraiman, PhD

Professor of Physics
Kavli Institute for Theoretical Physics,
University of California - Santa Barbara

Physical Morphogenesis

Understanding how a genetically encoded program of development defines the physical form and structure of a multicellular organism is one of the fundamental problems of biology. Remarkably, thanks to the great advances in developmental biology, we now find ourselves in the situation where we know more about developmental genes than about the physical processes involved in shaping the tissues. Here, Developmental Biology meets the emerging field of Living Matter Physics. This talk will review the physical phenomena involved in morphogenesis and provide some examples of physics ideas, quantitative models and tools that are being used to describe cell and tissue mechanics that underlies morphogenesis. Combination of quantitative experiments with mathematical models helps to uncover hidden simplicity in biological processes. On the flip side, the study of mechanics of morphogenesis enriches Physics with new concepts, models and challenges.

Anindita (Oni) Basu, PhD

Assistant Professor of Genetic Medicine
University of Chicago & Argonne National Laboratory

Single-cell Transcriptomics and Biology using Microfluidics

The basic units of biological structure and function are cells, which exhibit wide variation in regard to both type and state. We assess such variation by simultaneously profiling the transcriptomes of thousands of single mammalian cells (Drop-seq) or nuclei (DroNc-seq), using high-throughput emulsion microfluidics and DNA barcodes. These are accomplished by (a) encapsulating and lysing one cell/nuclei per emulsion droplet, and (b) barcoding RNA contents from each cell/nuclei using unique DNA-barcoded micro-beads, (c) performing Next-Gen Sequencing.

We are using these droplet-based techniques to profile cell types comprising complex tissues in a variety of tissue-types such as the heart and solid tumors in mouse models and human primary tissue. Besides, we are using Drop-seq and DroNc-seq to profile cell-states, particularly cellular heterogeneity in development and differentiation processes using a combination of cell lines, mouse embryonic tissue, in vitro culture, and human induced pluripotent stem cells. We also develop custom microfluidic devices to study phenotypic responses of cells to different environmental stimuli including physical, bio-chemical and pathogenic stimuli.

Tassos Pavlopoulos, PhD

Howard Hughes Medical Institute Fellow
HHMI Janelia Research Campus

Illuminating arthropod development with lightsheet microscopy

The origin of biological form is one of the oldest and most enduring problems in biology. Embryonic tissues and organs change their size and shape during development through patterned cell activities controlled by intricate physico-chemical mechanisms. We have introduced two genetically and optically tractable arthropod species, the beetle insect Tribolium castaneum and the shrimp-like crustacean Parhyale hawaiensis, as powerful and attractive model systems for biologists and biophysicists interested in the molecular, cellular and mechanical control of developmental morphogenesis. Fluorescently labeled embryos are imaged with multi-view light-sheet microscopy at high spatiotemporal resolution over several days of embryogenesis. Quantification of cell behaviors in imaged wild-type or genetically and mechanically perturbed embryos offers a bottom-up cellular perspective of various morphogenetic processes.

In the case of Tribolium, combining imaging of actin and myosin dynamics with physical modeling has provided insights into the cell and tissue interactions and the forces contributing to the flow of the extraembryonic tissue during its epibolic expansion around the gastrulating embryo. In the case of Parhyale, comprehensive reconstructions of fate maps using our open-source software Massive Multi-view Tracker (available as a Fiji/ImageJ plugin) have provided insights into the cell lineage restrictions and differential cell behaviors contributing to limb bud formation and elongation. We anticipate that the comparisons between Tribolium, Parhyale and the well-characterized Drosophila paradigm will shed light on the conservation and divergence of morphogenetic mechanisms during animal evolution.

WORKSHOP \ 7

Interdisciplinary Team Science: Laying a foundation for success

How is research done in Biology and in Math? How should it be combined in a single research project? Discuss research practices and approaches of interdisciplinary team science, where researchers work jointly to develop shared conceptual frameworks that synthesize and integrate discipline-specific theories concepts and methods to create new models to address a common research problem. Explore principles of interdisciplinary team science applied to quantiative biology contexts.

FACILITATORS

Bennett Goldberg, PhD

Assistant Provost for Learning and Teaching; Director of the Searle Center for Advancing Learning and Teaching; Professor of Physics and Astronomy

Denise Drane, PhD

Director, Research and Evaluation, Searle Center for Advancing Learning and Teaching

Fruma Yehiely, PhD

Associate Vice President for Research, Research Associate Professor of Preventive Medicine

PRIZE FOR UNDERGRADUATE RESEARCH IN QUANTITATIVE BIOLOGY \ 8

Please take a moment to welcome our five finalists for the Prize for Undergraduate Research in Quantitative Biology. These undergraduates have traveled across the country to present their research to us to be considered for one of three prizes; first prize of $1000, second prize of $750, and third prize of $500. They were chosen as finalists based on their application and recommendation letter that demonstrated outstanding undergraduate research in quantitative biology.

Those awarded first, second and third prize will be chosen based on both the content and presentation of their research projects and announced at Friday's closing remarks.

Anthony Aportela
Georgia Institute of Technology
Genetic algorithms to quantify model parameters physiologically, from experimental data

Jocelyn Garcia
University of Illinois Chicago
Quantitative Analysis of Notch Signaling-Mediated Olfactory Neurogenesis

Tingshan Liu
Smith College
Beyond binary brain networks: quantifying and boosting reproducibility of centrality measures

Catalina Medina
University of Nevada, Reno
Host-pathogen dynamics: Quantifying process-level variation using a system-specific dynamical model in a non-linear mixed effects modeling framework

Bailey Moers
Gallaudet University
Effective Intracellular Delivery of Large Cell Membrane-Impermeable Cargos

PANEL ON TEAM SCIENCE \ 9

The Panel on Team Science is candid discussion on the benefits and difficulties of truly interdisciplinary collaborations from the viewpoints of senior and junior faculty, postdoctoral student, graduate student, and senior university administration. Feel free to ask at any point of the discussion. Microphones will be provided.

MODERATOR

Nicole Moore, PhD
Director of Northwestern's Office for Research Development

PANELISTS

Richard Carthew, PhD
Director of the NSF-Simons Center for Quantitative Biology; Professor of Molecular Biosciences

Neda Bagheri, PhD
Assistant Professor of Chemical and Biological Engineering; Investigator, NSF-Simons Center for Quantitative Biology

Thomas Stoeger, PhD
Postdoctoral Fellow, Chemical and Biological Engineering, Luis Amaral Research Group

Rachel Bakker
PhD Candidate, Interdisciplinary Biological Sciences Program, Richard Carthew Research Group

SATURDAY SCHEDULE \ 10

Abbott Auditorium,
Pancoe Life Sciences Pavilion
2200 Campus Drive, Evanston, IL

8:30 am	Registration & Breakfast
8:50 am – 9:00 am	**Directors' Welcome** Richard Carthew, PhD & William Kath, PhD
9:00 am – 9:45 am	**Using Gene Expression to Tell Time** Rosemary Braun, PhD
9:45 am – 10:30 am	**Universal Features of Metastable States in Tissues and other Domain Systems** Sascha Hilgenfeldt, PhD
10:45 am – 11:30 am	**Sensing and signaling in cellular communities** Andrew Mugler, PhD
11:30 am – 12:15 pm	**A Circuit Theory for Biology** Milo Lin, PhD
12:15 pm – 2:00 pm	**Lunch & Poster Session** Venue: Pancoe Hall, Second Floor
2:00 pm – 3:00 pm	Lightning Talks
3:00 pm – 3:45 pm	**Emergent metabolic dynamics in microbial communities** Arthur Prindle, PhD
4:00 pm – 4:45 pm	**Controlling Epithelial Cell Shape** Margaret Gardel, PhD
5:00 pm	**Closing Remarks** Richard Carthew, PhD
6:00 pm	Optional Meet up at Prarie Moon 1635 Chicago Ave, Evanston, IL 60201

Rosemary Braun, PhD

Assistant Professor of Preventitative Medicine
Northwestern University

Using Gene Expression to Tell Time

Determining the state of an individual's internal physiological clock has important implications for precision medicine, from diagnosing neurological disorders to optimizing drug delivery. To be useful, such a test must be accurate, minimally burdensome to the patient, and robust to differences in patient protocols, sample collection, and assay technologies. In this talk I will present TimeSignature, a novel machine-learning algorithm to infer circadian time from gene expression in human blood. A powerful feature is TimeSignature's generalizability, enabling it to be applied to samples from disparate studies and yield highly accurate results despite systematic differences between the studies. This quality is unique among expression-based predictors and addresses a major challenge in the development of reliable and clinically useful biomarker tests.

Margaret Gardel, PhD

Associate Professor of Physics
University of Chicago

Controlling Epithelial Cell Shape

I will discuss my lab's recent work to study the biophysical mechanisms regulating control of cell shape in epithelial tissue. In particular, we have used optogenetics to locally regulate Rho activity at cell junctions to uncover how local Rho pulses drive junction contraction and stabilization via a ratcheting mechanism. We find that at short timescales, Rho activation drives junction contraction that reverses upon Rho reduction. Sustained RhoA activity shows a similar initial rapid contraction followed by a slow contractile phase. Upon removal of RhoA activation, the junction does not fully recover back to its original length, similar to junctional ratcheting observed in vivo. We find that this ratchet is dependent on both trans E-cadherin interactions and Formin activity. To understand these data, we model junction length in response to variable tension. In contrast to existing vertex models, our data argues that a junction has a rest length that is determined by the force-dependent junctional remodeling under acute periods of tension. This model then predicts that the slow contractile phase will eventually saturate to limit the amount of junction length changes and this is indeed what we see experimentally. We can overcome this saturation by inducing multiple activation periods, recapitulating junctional ratcheting seen in vivo. Altogether, these data provide insight into the underlying molecular and biophysical mechanisms of junction length changes seen in development.

Sascha Hilgenfeldt, PhD

Professor of Mechanical Science & Engineering
University of Illinois Urbana-Champaign

Universal Features of Metastable States in Tissues and Other Domain Systems

Recent work has demonstrated that the shape of cell domains in quasi-2-D tissue model systems (single-layer confluent tissues) is indicative of mechanical behavior, with a critical perimeter-to-area ratio separating mechanically rigid from "floppy" ground states. However, a given domain system in mechanical equilibrium generally occupies a metastable state in a complex energy landscape above the ground state. Here we show that these metastable-state energies can also be deduced simply and reliably from either geometric or statistical information obtained from the structure. The obtained relationships are robust against changes in the type of energy functional, domain polydispersity, and mechanical parameters. Thus, relevant information on the mechanics of a cellular system can be obtained from visual information of any snapshot.

Milo Lin, PhD

Assistant Professor Cecil H. and Ida Green Center for Molecular, Computational, & Systems Biology,
University of Texas Southwestern Medical Center

A Circuit Theory for Biology

The Boltzmann distribution predicts the collective behavior of systems at thermodynamic equilibrium as a function of their constituent parts. Yet most systems in nature–especially living systems– are not at equilibrium, and a unified theory of their behavior does not currently exist. I will show that the Boltzmann distribution is a special case of a general probability flow equation (PFE) that governs stochastic systems, even if far from equilibrium. The PFE is an analog of the voltage equation governing electronic circuits, where resistors, batteries, node voltages, and path currents correspond to equilibrium rate constants, driven rate constants, probabilities, and probability flows, respectively. I will discuss how this new approach can be used to recapitulate known properties of weakly driven systems as well as provide new insights into strongly-driven systems. These insights include fundamental limits on system performance; experimental data, ranging from cell signaling to kinetic proofreading, show that living systems can operate at those limits. Using system-invariant consequences of the PFE as well as illustrative examples of its application to specific systems, I aim to show the usefulness of this approach in simplifying, predicting, and ultimately controlling the behavior of non-equilibrium systems.

Andrew Mugler, PhD

Assistant Professor of Physics
Purdue University

Sensing and signaling in cellular communities

Communication allows groups of cells to perform behaviors that individual cells could not perform alone. I will discuss two examples of collective behaviors in cellular communities and the quantitative approaches that we are using to understand them. First, I will describe collective gradient sensing in epithelial organoids. Scaling laws from diffusion theory explain how groups of cells surpass single-cell bounds on sensory precision. Then, I will describe long-range electrical signaling in bacterial communities. Predictions from percolation theory explain why not all bacteria signal and why the ones that do are organized in a particular way. These works suggest that simple theories can quantitatively and predictively describe complex phenomena from the molecular to the multicellular scale.

Arthur Prindle, PhD

Assistant Professor of Biochemistry & Molecular Genetics
Northwestern University

Emergent metabolic dynamics in microbial communities

The cell is the unit of life, yet cells usually exist in the context of many others within a community. In this talk, I will describe several of our recent efforts to understand collective functions in bacterial communities known as biofilms. I will describe how a conflict between protection and starvation is resolved through emergence of long-range metabolic co-dependence between peripheral and interior cells. As a result, biofilm growth halts periodically, increasing nutrient availability for the sheltered interior cells and increasing biofilm fitness. I will then describe our recent discovery that bacteria that reside in biofilm communities communicate using electrical signals coordinated by ion channels. These findings revealed an unexpected functional similarity between ion channels in neurons and those in microbes, thereby establishing a prokaryotic paradigm for electrical signaling. Finally, I will describe some of our more recent efforts to understand this phenomenon in more detail.

CENTER INVESTIGATORS \ 15

Life Scientists

Richard Carthew, Director
Professor of Molecular Biosciences

Ravi Allada
Chair and Professor of Neurobiology

Erik Andersen
Assistant Professor of Molecular Biosciences

Carole LaBonne
Chair and Professor of Molecular Biosciences

Alec Wang
Associate Professor of Molecular Biosciences

Mathematical Scientists

William Kath, Co-Director
Professor of Engineering Sciences and Applied Mathematics and Neurobiology

Luis Amaral
Professor of Chemical and Biological Engineering and Molecular Biosciences

Antonio Auffinger
Associate Professor of Mathematics

Neda Bagheri
Assistant Professor of Chemical and Biological Engineering

Rosemary Braun
Assistant Professor of Preventive Medicine and Engineering Sciences and Applied Mathematics

Niall Mangan
Assistant Professor of Engineering Sciences and Applied Mathematics

Madhav Mani
Assistant Professor of Engineering Sciences and Applied Mathematics and Molecular Biosciences

JiPing Wang
Professor of Statistics and Molecular Biosciences

Collaborate with Us!

Visiting Scholars

This program attracts participants from colleges and universities worldwide, and is designed to stimulate creative thinking and interdisciplinary science. The Center has capacity for up to six visitors at a time. Each visitor occupies a shared office embedded near our Center's laboratories and groups, and typically shares the office with a participant from a complementary discipline – e.g. a mathematician and biologist might share an office.

Participants can use their time for a variety of purposes:

1. Initiation and growth of cross-disciplinary collaborations
2. Problem-solving particular issues central to their research
3. Immersion in fields that are unfamiliar but of interest
4. Other professional development activities

In addition, participants can work within the Center's experimental labs, either developing and learning new methods or conducting research. Applications are accepted on a rolling basis, please check the website for further application information.

Pilot Projects

This program supports exploratory pilot projects by investigators outside of the Center. The Center has the capacity to support up to two pilot projects each year. Pilot projects should be high-risk high-reward research, interdisciplinary in nature, and be working at the interface of developmental biology and mathematics. Each project is funded for 12 months with up to $40,000 direct cost support.

Applicants must be independent investigators who are tenure track faculty at an academic institution located within a 160-mile radius of Northwestern University, Evanston. Please check the website for further application information. Round two funding submission deadline: May 31, 2019.

quantitativebiology.northwestern.edu