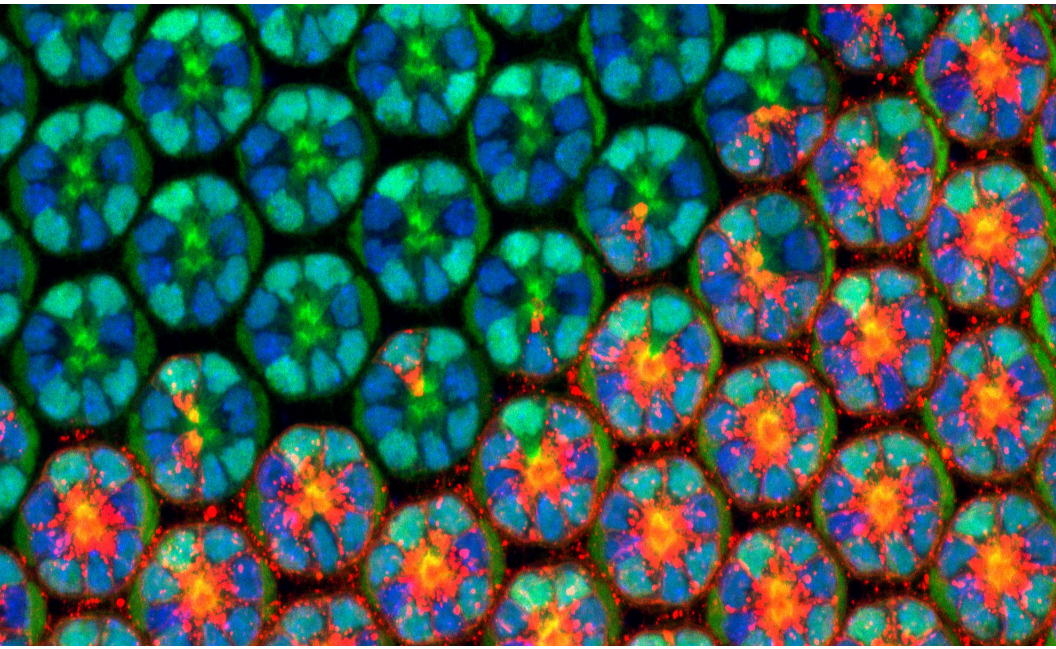
NSF-Simons Center for Quantitative Biology

2nd ANNUAL CONFERENCE

Quantitative Approaches in Biology



October 4-5, 2019
Northwestern University, Evanston, IL

Supported by the
National Science Foundation 1764421
Simons Foundation 597491

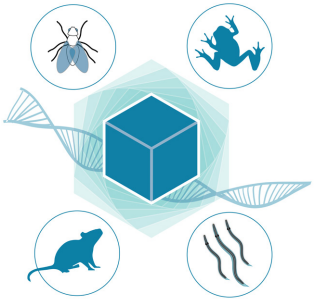
Northwestern University

ABOUT \ 2

The NSF-Simons Center for Quantitative Biology (CQuB) 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.



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.

Investigators

Life Scientists

Richard Carthew, Director
Professor of Molecular Biosciences

Ravi Allada
Chair and Professor of Neurobiology

Erik Andersen
Associate 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

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

www.quantitativebiology.northwestern.edu

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@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 **#quantbiology2019**

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stay GENUINE

FRIDAY SCHEDULE \ 4

LOUIS ROOM
Norris University Center
1999 Campus Drive, Evanston, IL

8:30 am	Registration & Breakfast
8:45 am – 9:00 am	**Welcome** Richard Carthew, PhD
9:00 am – 9:40 am	**Dynamic coupling of cell adhesion, RhoA signaling and force generation encodes a self-propelled zipper that drives neural tube closure** Ed Munro, PhD
9:50 am - 10:30 am	**Ecology, Evolution, and Fine-Scale Microbial Diversity** Daniel S. Fisher, PhD
10:40 am – 11:20 am	**Clocks and Timers in Embryonic Development** Andrew Oates, PhD
11:30 am – 12:30 pm	**Lightning Talks**
12:30 pm – 2:00 pm	**Lunch** (Louis Room) **Poster Session** (Northwestern Room) Prize for Undergraduate Research in Quantitative Biology Finalists Poster Competition
2:00 pm – 2:40 pm	**RNA profiling: Extracting structural signals from noisy distributions** Christine Heitsch, PhD
2:50 pm – 3:30 pm	**Two new computational tools for imaging data** Madhav Mani, PhD
3:40 pm – 4:00 pm	**Remarks** **Undergraduate Prize Announcement**
4:00 pm - 4:45 pm	**Applying to Graduate School at Northwestern** (207 Rock Room)
4:00 pm – 5:30 pm	**Reception** (Northwestern Room)
6:00 pm	**Optional Meet** up at Bangers & Lace

SPEAKERS \ 5

Ed Munro, PhD

Associate Professor of Biological Sciences Division,
Molecular Genetics & Cell Biology
University of Chicago

Dynamic coupling of cell adhesion, RhoA signaling and force generation encodes a self-propelled zipper that drives neural tube closure

A fundamental challenge in developmental biology is to understand how embryos pattern force generation in space and time to shape specific organs and tissues. To address this question, we study how the neural tube zips itself shut in the simple chordate Ciona robusta. During zippering, the neural folds meet and fuse from posterior to anterior, replacing heterotypic junctions between neural and epidermal cells (Ne/Epi junctions) with homotypic (Ne/Ne and Epi/Epi) junctions o separate a closed neural tube from the overlying epidermis. Using live imaging, biophysical manipulations and modeling, we have found that zippering is governed by complex spatiotemporal pattern of actomyosin contractility.

Daniel Fisher, PhD

Professor of Applied Physics
Stanford Univsersity

Ecology, Evolution, and Fine-Scale Microbial Diversity

Recent observations show that biological diversity extends down to the finest scales with spatial coexistence of many strains and sub-strains of single bacterial species. Progress on understanding how such diversity might evolve and be maintained, without necessity of invoking multiple microniches, will be discussed, focussing on simple models and statistical physics approaches.

Andrew Oates, PhD

Professor
École Polytechnique Fédérale de Lausanne (EPFL)

Clocks and Timers in Embryonic Development

Some biological oscillators function throughout the life of an organism, for example the circadian clock, whereas others have a more restricted duration, particularly in embryogenesis. The “segmentation clock” is a multi-cellular patterning system of genetic oscillators thought to control the rhythmic and sequential formation of the vertebrate embryo’s body segments. Individual oscillating cells are synchronized with their neighbors, forming a coherent wave pattern of gene expression. How these wave patterns arise and how they are regulated during embryogenesis is not clear. I will describe recent progress in understanding the behavior of individual cells from the zebrafish as they slow their oscillations and differentiate during segmentation, and discuss how this gives rise to the tissue-level wave patterns. Central to this understanding is the concept of a timer that regulates the duration of a clock. This perspective reveals what part of the oscillatory cycle is changing as the cells slow and stop.

Christine Heitsch, PhD

Professor of Mathematics; Director of the Southeast Center for Mathematics and Biology
Georgia Institute of Technology

RNA profiling: Extracting structural signals from noisy distributions

Accurate RNA structural prediction remains challenging, despite its increasing biomedical importance. Sampling secondary structures from the Gibbs distribution yields a strong signal of high probability base pairs. However, identifying higher order substructures requires further analysis. RNA profiling (Rogers & Heitsch, NAR, 2014) is a novel method which identifies the most probable combinations of base pairs across the Boltzmann ensemble. This combinatorial approach is straightforward, stable, and clearly separates structural signal from thermodynamic noise. Moreover, it can be extended to predict consensus stems for an RNA family with high accuracy via unsupervised clustering of unaligned homologous sequences.

Madhav Mani, PhD

Assistant Professor of Engineering Sciences and Applied Mathematics and Molecular Biosciences; Investigator, NSF-Simons Center for Quantitative Biology
Northwestern University

Two new computational tools for imaging data

The first computational tool is a high precision framework for studying variation in adult form in a landmark-free manner. Using some tricks from complex analysis we are able to produce a precision alignment of images of the drosophila wing, allowing a study of how variation in adult form relates to differences conferred by mutations in signaling systems. The second computational tool is an inference scheme that permits the reconstruction of the approximate force diagram in 2 and 3-dimensional aggregates of cells. Accuracy will be demonstrated in 2D epithelial tissues, and a future goal of reconstructing the entire force diagram of an embryo will be discussed.

PRIZE FOR UNDERGRADUATE RESEARCH IN QUANTITATIVE BIOLOGY \ 7

Please take a moment to welcome our five finalists for the NSF-Simons Center for Quantitative Biology's Prize for Undergraduate Research in Quantitative Biology. These five 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 during Friday's closing remarks.

Nathan Burg

University of Illinois at Chicago

Notch Signaling Regulates Stem Cell Behavior During Ciliated Olfactory Neuron Differentiation

Ciliated olfactory sensory neurons (cOSNs) constitute a primary sensory neuron subtype in the vertebrate olfactory epithelium (OE) that is used to detect volatile odors. The Notch signaling pathway has been shown to play important roles in cell proliferation and differentiation across many developing organ systems, but the possible mechanisms and downstream pathways through which it might regulate the differentiation of cOSNs are relatively unexplored. By analyzing relative mRNA levels using in situ Hybridization Chain Reaction (HCR), we discovered that multiple Notch signaling components are dynamically expressed in the OE during early development. Using both genetic and chemical Notch signaling inhibitors, we found a statistically significant increase in the number of cOSNs and a statistically significant decrease in the number of progenitors in response to inhibition of Notch signaling. We optimized an automated spots analysis feature in commercially available software, Imaris, to count progenitor cells and quantitate immunostaining signal for Dlx3b, a progenitor marker. We then obtained the mean fluorescence intensity levels per cell for both control and Notch signaling inhibited embryos. Analyzing the distribution of protein levels across more than 3,500 cells per condition revealed that the observed decrease in progenitor cell numbers upon Notch signaling inhibition occurs in a distinct subset of the total progenitor cell population. Taken together, our findings suggest that the increase in cOSN numbers upon Notch signaling inhibition may be due to the premature differentiation of specific progenitor cells.

Nicholas Hilgert

Purdue University

Physics of flow-sensing by self-communicating cancer cells

The majority of cancer deaths occur when tumor cells metastasize, or spread throughout the body. Many cancer cells achieve metastasis by detecting the direction of flow in the lymphatic system. A prevailing hypothesis for this mechanism is that these cells self-communicate: they symmetrically emit molecules and asymmetrically re-absorb them after the molecules are displaced by the flow. This hypothesis is supported by experimental evidence [1], shown in Fig. 1A, but a quantitative theory of this process has not yet been constructed. We build a mathematical model founded on the physics of low-Reynolds number hydrodynamics and the mathematics of diffusive processes that sets limits on cellular sensing capabilities, providing a framework for experiments that will illuminate how physics informs the development of cancer.

Gil Parnon

Portland State University

Pattern and Stripe Formation in Zebrafish

Zebrafish (Danio rerio) are fish that live in freshwater and have black stripes and yellow interstripes. The stripes are made of a combination of melanophores, iridophores, and xanthophores, the latter two have both loose and dense forms. This REU project built on the work of a paper by Sandstede and Volkening to extend and develop their model to be both more accurate and applicable onto the fins of the zebrafish as well as implementing skin growth and bones onto a new domain. Previous models only took melanophores and xanthophores into account. Over the course of this project we further developed a 5-cell model in order to advance the biological understanding of how autonomous stripe formation works on zebrafish. We used a series of differential equations to describe interactions between cells, bones, and the edges of the simulated fish body. This work incorporated mutated variations of Danio rerio which were missing certain pigment cell types in order to better replicate a realistic model. By accurately being able to generate mutations as well as the unmutated fish we were able to check for accuracy of the cell-to-cell interactions. We developed a methodology for generating and working with boundaries of different shapes in order to accommodate different fins as well as more realistic bodies, and worked towards biological realism in our model.

Ruchira Ray

Yale University

A new biomechanical mathematical model to predict force effects on actin dynamics during clathrin-mediated endocytosis

During clathrin-mediated endocytosis, a flat membrane invaginates to form a round vesicle. In yeast, actin filaments assemble into a network that generates the force necessary to deform the membrane. Mechanical models have described how endocytic proteins generate force, while biochemical models have described how their composition changes over time. However, the interactions between the mechanical and chemical aspects remain unclear. This study proposes a new biomechanical approach to model how the actin filament network composition responds to different load forces in yeast.

Hannah Scanlon

Wake Forest University

Modeling Blood Flow Regulation and Tissue Oxygenation in the Retina

Glaucoma is a serious ocular disease characterized by damage to retinal ganglion cells that results in irreversible vision loss. While thought primarily to be a disease associated with high intraocular pressure, clinical evidence shows that almost one third of glaucoma patients do not exhibit elevated pressure. Impaired tissue perfusion, blood flow, and oxygenation of retinal tissue have been identified as other important factors that may contribute to retinal ganglion cell death. Theoretical modeling provides a useful tool for predicting the impact of several hemodynamic factors on blood flow regulation and retinal oxygenation. In this study, two mathematical models (compartmental and heterogeneous) are combined into a hybrid model to describe tissue oxygenation in a human retina. A compartment model that represents blood vessels as resistors is adapted to include a wall-derived metabolic signal. This signal is calculated from the partial pressure of oxygen in the blood and assumed to be conducted upstream through the network. The model is used to predict changes in retinal tissue perfusion as tissue oxygen demand is increased or as incoming arterial pressure is varied. A heterogeneous model of the human retinal arterioles is adapted from a mouse model. The heterogeneous model is connected to a compartmental model of the capillaries and venules to create a hybrid model description of the retinal microcirculation. Flow, pressure, and partial pressure of oxygen from the heterogeneous model serve as inputs to the compartmental model, and then the conducted metabolic signal is calculated in the capillaries and venules and relayed back to the heterogeneous arterial network. This hybrid model preserves important spatial information from the arteriolar network while accounting for realistic conducted metabolic responses generated downstream. Ultimately, this model provides an important approach for predicting retinal blood and tissue oxygenation within a realistic human retinal network and understanding the role of these factors in glaucoma.

FRIDAY SURVEY \ 9

Help Shape Future Conferences With Your Feedback!

Why?

Feedback is optional, but your input will help shape future conferences, help improve the Center's activities and will contribute to our understanding of how to support interdisciplinary researchers.

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https://www.surveymonkey.com/r/CQuBConferenceFriday

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NSF-Simons Center for Quantitative Biology

SATURDAY SCHEDULE \ 10

LOUIS ROOM
Norris University Center
1999 Campus Drive, Evanston, IL

8:30 am	**Registration & Breakfast**
8:45 – 9:00 am	**Welcome** William Kath, PhD
9:00 am – 9:30 am	**From molecules to development: understanding how biological oscillators function and coordinate** Qiong Yang, PhD
9:40 am – 10:10 am	**Quantitative Analyses of Bird Songs and Other Learned Behaviors** Nicole Creanza, PhD
10:20 am - 10:30 am	Break
10:30 am – 11:30 am	**Lightning Talks**
11:30 am – 1:25 pm	**Lunch** (Louis Room) **Poster Session** (Northwestern Room)
1:25 pm – 1:35 pm	Group Photo
1:35 pm – 2:05 pm	**Quantitative Analysis of Patterning and Scaling in Planarian Regeneration** Christian Petersen, PhD
2:15 pm – 2:45 pm	**Computational Reconstruction of Gene-Gene Dynamics in Temporal Patterning of Drosophila Medulla Neuroblasts from Single-Cell RNA-Seq** Xin Li, PhD & Dave Zhao, PhD
2:55 pm – 3:25 pm	**Neurotransmitter Receptors as Key Modulators of Drosophila Epithelial Morphogenesis** Jeremiah Zartman, PhD
3:35 pm - 4:05 pm	**Membrane Tethering Force in the Pathology of Alzheimer's Disease** James Lee, PhD
4:10 pm - 4:15 pm	**Closing Remarks** Richard Carthew, PhD
4:30 pm	Optional Meet up at Prairie Moon

Qiong Yang, PhD

Assistant Professor of Biophysics and Physics
University of Michigan

From molecules to development: understanding how biological oscillators function and coordinate

Although most biological oscillators share the same core structure that contains linked positive and negative feedback loops, what peripheral structures drive specific oscillation properties remain elusive. In our computational work, we generated an atlas of oscillators and found that, while certain core topologies are essential for self-sustained oscillations, local structures substantially modulate the degree of robustness, an essential ability of a clock system to function reliably under intrinsic stochasticity and environmental perturbations. Remarkably, two key local structures, incoherent inputs and coherent inputs, can modify a core topology to promote and attenuate its robustness, additively. We further apply this computational framework to search for structures underlying tunability, another crucial property shared by many biological timing systems to adapt their frequencies to environmental changes.

Nicole Creanza, PhD

Assistant Professor of Biological Sciences
Vanderbilt University

Quantitative Analyses of Birdsongs and Other Learned Behaviors

Approximately half of bird species learn their songs, which generally function in territory defense and mate attraction, and the quality of song learning and performance can affect fitness. Most studies of oscine songbirds focus on the significant song variation within a single species, including spatial variation; this variation raises the possibility that the accumulation of cultural changes over millions of years would obscure signals of evolutionary history. Both birds and humans can often use a bird's song to identify its species; however, it remains unknown whether birds' songs preserve evolutionary information beyond the species level. In this talk, I introduce quantitative tools to compare song similarity and genetic relatedness between species; computational analyses with this new software indicates that features of song evolve at different rates. In addition, we detect evolutionary patterns in individual species' songs over decades of recordings and across geographic distance. In birdsong, there is a tension between the selection pressures for vocal virtuosity and for reliable species recognition: a bird's song should demonstrate to potential mates that he is capable of learning and producing an exceptional song, but he must still be immediately recognizable as a member of the correct species. These results suggest that these differing selection pressures might act on different aspects of learned song. To further quantify the evolutionary dynamics of this learned behavior, we have assessed how song evolution responds to different selection pressures and how song co-evolves with the capacity for learning. We also quantify the ability of learned song to act as a cultural barrier to gene flow. Combining a genetic framework with a large-scale quantitative analysis of learned behavior, these experiments offer a quantitative approach to evolution of behavior both within and between species.

Christian Petersen, PhD

Associate Professor of Molecular Biosciences;
CQuB Pilot Project Investigator
Northwestern University

Quantitative Analysis of Patterning and Scaling in Planarian Regeneration

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.

Xin Li, PhD

Assistant Professor of Cell and Developmental Biology;
CQuB Pilot Project Investigator
University of Illinois Urbana-Champaign

Sihai Dave Zhao, PhD

Assistant Professor of Statistics;
CQuB Pilot Project Investigator
University of Illinois Urbana-Champaign

Computational Reconstruction of Gene-Gene Dynamics in Temporal Patterning of Drosophila Medulla Neuroblasts from Single-Cell RNA-Seq

Neural stem cells (neuroblasts) in both vertebrates and invertebrates undergo temporal patterning to sequentially generate a defined order of different neural types as they age. In the Drosophila medulla, part of the visual processing center of the brain, neuroblasts sequentially express a temporal cascade of transcription factors, including Hth, Ey, Slp, D and Tll, which control the sequential generation of different neural types. The temporal transitions between different temporal stages are coupled with cell-cycle progression, but the exact mechanism is not clear. To dissect the complete molecular basis of the genomic regulation of these temporal transitions at the level of single cells, we purified medulla neuroblasts, a mixed population of all temporal stages due to the progressive nature of medulla neurogenesis, by FACS sorting, and performed single-cell RNA-seq analysis. Unsupervised clustering of medulla neuroblasts revealed clusters of cells that corresponded well to neuroblast temporal stages, which were marked by the known temporal factors Hth, Ey, Slp, D and Tll. Differential expression analysis revealed additional genes active only at specific temporal stages. Finally, a novel gene network analysis based on RNA velocity identified new potential regulators of temporal patterning. These new candidate temporal transcription factors and regulators of temporal patterning are being experimentally verified.

Jeremiah Zartman, PhD

Associate Professor of Chemical & Biomolecular Engineering
University of Notre Dame

Mechanisms of cell-cell signal integration during Drosophila wing disc development

Organ development relies on a symphony of signals that are coordinated spatiotemporally. These signals regulate cell processes through key integrators such as calcium ions. However, how calcium signaling is regulated at the tissue level and contributes to organogenesis is still poorly understood. Here, we report new methods to reverse-engineer multiscale signal integration during Drosophila wing disc development, an accessible genetic and biophysical model of morphogenesis.

To do so, we built a geometrically-accurate computational model of multicellular calcium signaling of the wing disc. We show that the spatiotemporal extent of calcium signaling is determined by the class and level of hormonal stimulation. The computational model predicts the regulation of the main classes of calcium signaling dynamics observed in vivo: single-cell calcium spikes, multicellular transient bursts, global intercellular calcium waves, and global fluttering. The tuning of the spatial extent of signaling dynamics from single cells to global waves emerges naturally as a function of global stimulation strength. The generation of global waves depends on the subdivision of the cell population into a small fraction of initiator cells surrounded by a large fraction of standby cells connected by gap junctions.

Further, we performed a RNAi-based screen of candidate upstream regulators that control the distinct spatiotemporal classes of calcium signaling. This quantitative screen employed a new deep learning-based bioimage platform to identify neuropeptide GPCRs as novel regulators of organ growth and morphogenesis. As a specific validation test, we characterized how the serotonin receptor, 5-HT1B, plays critical roles in patterning and growth. These studies provide a high-dimensional mapping of calcium signaling dynamics to morphogenetic phenotypes. The systems analysis of cell-cell signal integration mechanisms provides a critical step toward developing new strategies in engineering multicellular systems for a range of applications ranging from cancer treatments to regenerative medicine.

James Lee, PhD

Associate Professor of Bioengineering
University of Illinois at Chicago

Membrane Tethering Force in the Pathology of Alzheimer's Disease

Membrane-cytoskeleton connectivity (MCC), an apparently continuous adhesion between plasma membrane lipids and cytoskeletal proteins, governs the rates of mechanochemical processes. Our research employs atomic force microscopy (AFM) to measure the force for membrane tether formation (F_{mtf}), as a measure of MCC, and investigates the roles of mechanical pathways in the pathology of Alzheimer's disease (AD), especially amyloid-β peptide (Aβ)-related cellular processes. Aβ is a neurotoxic protein accumulated in AD brains. We find that Aβ increases adhesion probability, but lowers the membrane tether adhesion force mediated by the bonding between p-selectin and sialyl-Lewis^x (sLe^x) at the surface of cerebral endothelial cells (CECs), governing the rolling adhesion in the transmigration of monocytes across the blood-brain barrier (BBB). In another related study, we find that cytosolic phospholipase A_2 facilitates Aβ uptake in microglia via its regulation of MCC.

SATURDAY SURVEY \ 14

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https://www.surveymonkey.com/r/CQuBConferenceSaturday

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NSF-Simons Center for **Quantitative Biology**

Submit your anonymous feedback on the Conference as a whole via our survey using either the URL or QR code provided below. The survey takes 5 minutes.

The feedback we ask for explores several questions about the Conference's success as a vehicle for (a) learning about other disciplines, (b) communicating and making connections across disciplines, (c) interdisciplinary research impacts, and (d) creating & supporting the community of researchers.

https://www.surveymonkey.com/r/CQuBConferenceConclusion

Collaborate with Us!

Visiting Scholars

This program attracts participants from colleges and universities worldwide, including graduate students, postdoctoral fellows, research staff, and faculty; 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:

- Initiation and growth of cross-disciplinary collaborations
- Problem-solving particular issues central to their research
- Immersion in fields that are unfamiliar but of interest
- 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 three funding submission deadline: March 31, 2020.

Undergraduate Summer Research Program

The Quantitative Biology Undergraduate Summer Research Program offers summer research fellowships to undergraduates. This program allows undergraduate students majoring in biology, engineering, mathematics, statistics, or physics to participate in hands-on laboratory or computational research that applies mathematical concepts and methodology to understanding mechanisms in biology. If selected, leadership will match you with a faculty mentor. Please check the website for further application information. Application deadline: March 1, 2020.