Recent Activities of the Center for Data-driven Modeling in Biology

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Prof. Alex Mogilner, Courant Institute of Mathematical Sciences and the Department of Biology, New York University, NYC

This talk is co-sponsored by the Department of Mathematics and Interdisciplinary Center for Data-driven Modeling in Biology.

May 13th, Wednesday, 2026
4:00 - 5:00 p.m.
Skye Hall 284

Colloquium Poster
https://icqmb.ucr.edu/sites/default/files/2026-04/mogilner.pdf

TITLE: Deciphering self-assembly of mitotic spindle

ABSTRACT: Mitotic spindle, a remarkable molecular machine, self-assembles to segregate chromosomes at the onset of cell division. Spindle assembles in phase, one of the earliest and least understood stages of mitosis. We used high-resolution 3D measurements of movements and deformations of chromosomes and spindle in prometaphase coupled with computational modeling to decipher force balances and speed and accuracy of integration of chromosomes into the spindle. I will describe how mathematical models are built from microscopy data and demonstrate that rapid stochastic interactions within the spindle leads to rapid, precise and robust self-assembly of the spindle.

Prof. Daniele E. Schiavazzi**,** Department of Applied and Computational Mathematics and Statistics,
University of Notre Dame, IN

Friday May 1st, 12-1pm, in the MRB Seminar Room (1st floor).

This talk is co-sponsored by RAISE@UCR Institute and Interdisciplinary Center for Data-driven Modeling in Biology.

TITLE: Model Synthesis for Scientific Agents

ABSTRACT: Applications of generative modeling and deep learning in physics-based systems have traditionally focused on building emulators - computationally inexpensive approximations of input-to-output maps. However, the remarkable flexibility data-driven architectures open opportunities to broaden their scope to include model inversion and identifiability analysis. We present InVAErt networks, a framework for data-driven analysis and synthesis of parametric physical systems. Through numerical experiments, we demonstrate the framework's versatility across a wide range of problems, including linear systems of equations, spatio-temporal PDEs, and lumped-parameter physiological models. We further introduce an extension for systems with observational noise, enabling the separation of structural from practical identifiability in complex ill-posed inverse problems. Finally, we discuss recent efforts to integrate InVAErt networks with large language model agents for applications in cardiovascular health.

Pictures taken during the talk.

Prof. James A. Glazier, Department of Intelligent Systems Engineering

Director, Biocomplexity Institute

Indiana University, Bloomington

This talk is co-sponsored by the Department of Mathematics and Interdisciplinary Center for Data-driven Modeling in Biology.

March 10th, Tuesday, 2026
2:00 - 3:00 p.m.
Skye Hall 284

TITLE: Multi-Scale, Multicellular, Agent-Based Virtual-Tissue Simulations of Development, Homeostasis and Disease

Abstract: Multi-scale, Multicellular Agent-Based Virtual-Tissue models are versatile tools for exploring how the complex interactions between cells and their local environment and between that environment and signaling and regulatory control lead to patterning during development, maintenance of tissues during homeostasis and recovery after injury and failure of tissue

organization and function due to damage or disease. This talk explores the evolution and application of multiscale, multicellular agent-based "Virtual Tissues" using the CompuCell3D (CC3D) modeling environment. The CC3D project originated more than 25 years ago in a collaboration between Dr. Glazier, Dr. Mark Alber and others at the University of Notre Dame under an NSF Biocomplexity grant. I will talk a bit about the history of the methodology and its strengths and limitations and then illustrate its use in a variety of contexts new and old, from the simulation of somite formation during development to epithelial homeostasis, vascular invasion and kidney cystogenesis. I will highlight two recent applications of this approach. First, a computational model of neural tube closure defects, demonstrating how transcriptomics-driven perturbations can be mapped onto conserved pathways to enable probabilistic hazard assessment of developmental failure. Second, adult-tissue Virtual-Tissue toxicology models of the cornea (vCornea). I am particularly interested in suggestions for extensions and improvements around the core CPM formalism and for potential novel applications. You can download CompuCell3D from https://compucell3d.org/SrcBin.

15th Annual Southern California Systems Biology Symposium

Saturday, April 25, 2026
9:30 a.m. to 7:00 p.m.
University of California, Los Angeles

The annual symposium, now in its 15th year, brought together researchers from across Southern California—from Santa Barbara to San Diego—to share research, build community, and stimulate collaborations. The Symposium had invited speakers, 10 lightning talks speakers, 73 posters and 192 registered participants.

Participants of the SoCal Sysbio 2026

15th Annual
Southern California Systems Biology Symposium

PROGRAM

UCLA QCBio

9:00am | Welcoming remarks: Alexander Hoffmann, UCLA

9:15am | **Session I chaired by Stacey Deleria Finley**

. Matt Thomson, Caltech: *TBD*
. Judith Kribelbauer, USC: *Constructing synthetic gene loci to learn the cis-regulatory code*
. Arnab Mukherjee, UCSB: *Programming aquaporins to image and modulate biological functions from the cell surface*
. Minji Byun, UCI: *One Mutation, two Diseases, one mechanism? DNMT3A loss-of-function in overgrowth syndromes and clonal hematopoiesis*
. Nagarajan Vaidehi, City of Hope: *Interpretable AI reveals cooperativity and allosteric communication in protein complexes*

10:30am | Coffee break

11:00am | **Session II chaired by Mark Alber**

. Sheng Zhong, UCSD: *Targeting a multifunctional protein for Alzheimer's disease*
. Jia Gou, UCR: *A study of the mechanisms of early epithelial cell clustering and collective motion*
. Parag Katira, SDSU: *Predicting phenotype to mechanotype relationships in migrating cancer cells*
. Carolyn Mills, UCSB: *Cell-free systems for studying and engineering protein assemblies*
. David Ardell, UC Merced: *Evidence for an information genomics approach to predicting tRNA interaction determinants*

12:15pm | **Lightning Talks - Part I**

Haripriya Vaidehi Narayanan, UCLA – Babgen Manookian, City of Hope – Emma Campagnolo, Cedars-Sinai

12:30pm | Lunch and Poster Session I (Posters 1-36)

1:45pm | **Keynote Speaker:** Arthur Lander, UCI: *How do biological systems deal with "exponential" threats?*

2:15pm | **Session III chaired by Adam MacLean**

. Elisa Franco, UCLA, *Programmable artificial RNA condensates in mammalian cells*
. Heather Brooks, Harvey Mudd College: *Modeling the effects of hormonal oral contraceptive dosing on contraceptive efficacy*
. Sharmila Venugopal, CSULB: *Defining functional interactomes in neural systems: toward a systems level framework with AI-augmented analysis*
. Barbara Bailus, Keck Graduate Institute a Member of the Claremont Colleges: *Zip delivery: a new way to deliver therapeutics to the brain*
. Russell Rockne, City of Hope, *Viewing acute myeloid leukemia as an epigenetic system-wide state-transition*

3:30pm | Coffee break

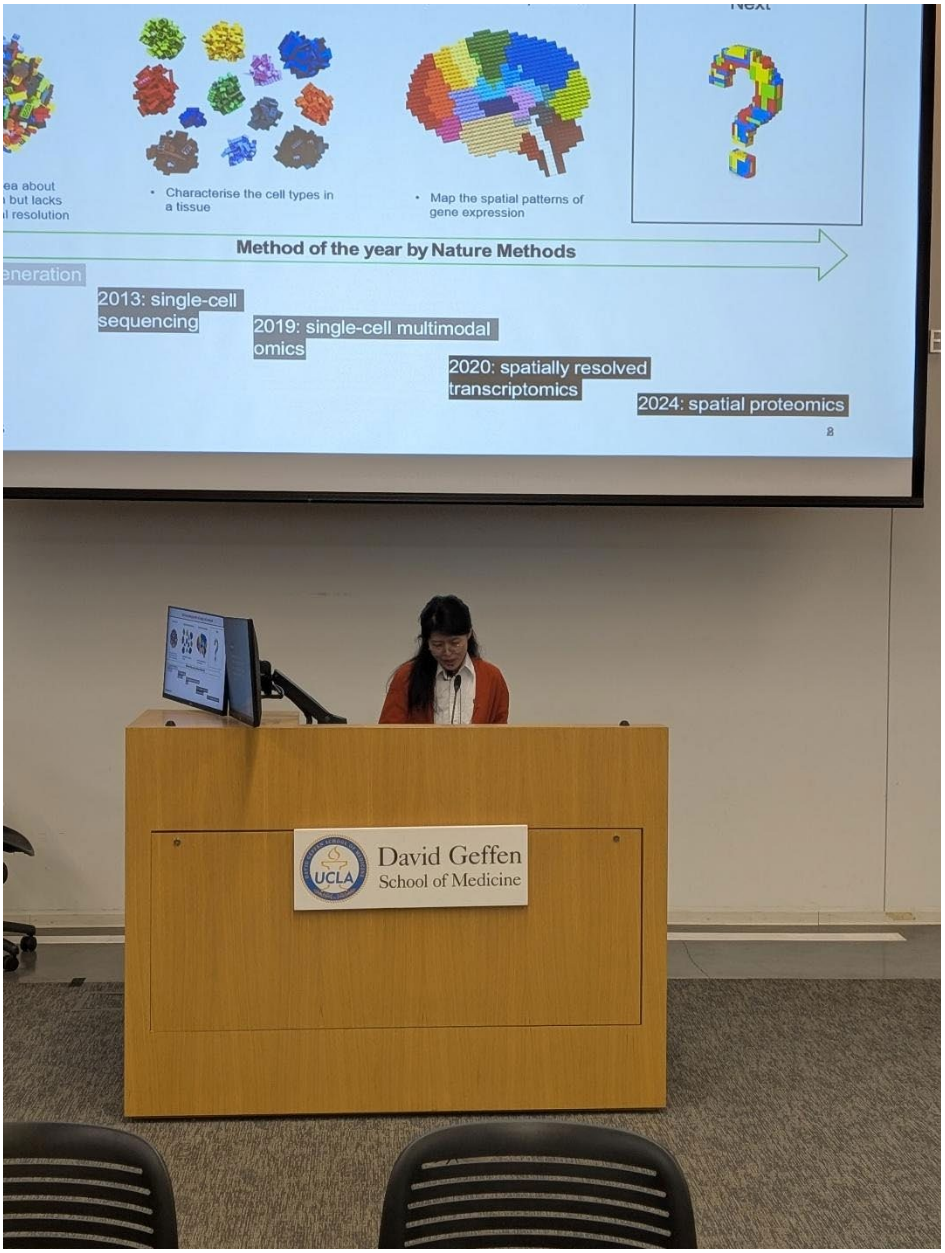
4:00 pm | **Session IV chaired by Weitao Chen**

. Ami Radunskaya, Pomona College: *Focused ultrasound and immunotherapy for brain cancer*
. Seungsoo Kim, UCI: *Combinatorial transcription factor control of cell identity*
. Yue Wu, UCR: *From snapshots to dynamics: tracking cells across time, space, and identity*
. Tainã Coleman, UCSD: *Enabling scientific discovery through workflows and autonomous AI*
. Roy Wollman, UCLA: *An information theory of biological atlases*

5:15pm | **Lightning Talks - Part II**

Jonathan Martinez, USC – Ethan Nowaski, UC Riverside – Dayeon Cheong, UC Irvine – Tyler King, USC – Sai Bavisetty, UCLA

5:30pm | Reception and Poster Session II (Posters 37-71)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Characterise the cell types in a tissue
Map the spatial patterns of gene expression
Method of the year by Nature Methods
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2019: single-cell multimodal omics
2020: spatially resolved transcriptomics
2024: spatial proteomics
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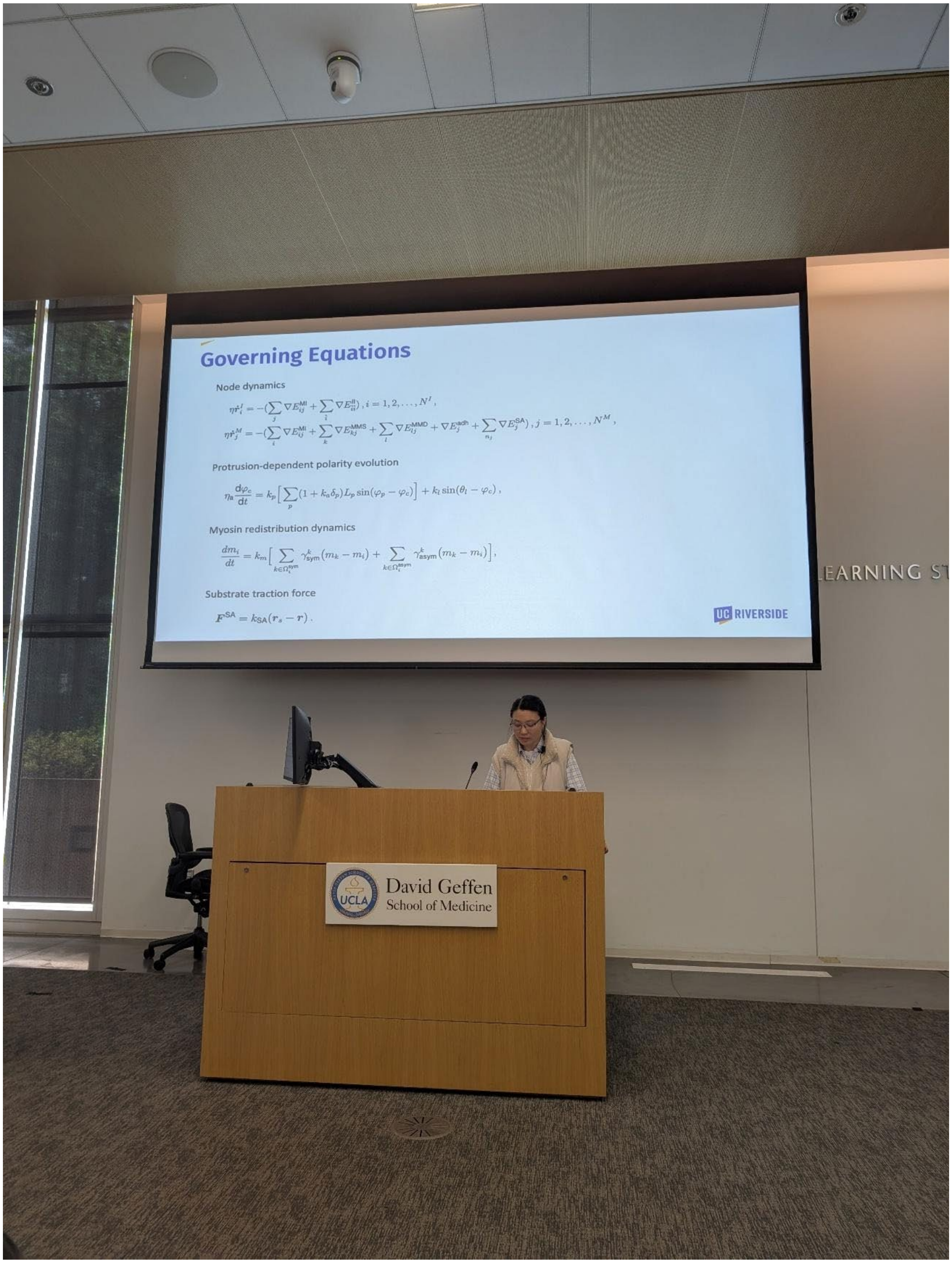
UCLA
David Geffen School of Medicine

Dr. Yue Wu, UCR



Governing Equations

Node dynamics

$$\eta \dot{\boldsymbol{r}}_i^I = -\Big(\sum_j \nabla E_{ij}^{\mathrm{MI}} + \sum_l \nabla E_{il}^{\mathrm{II}}\Big),\, i = 1, 2, \ldots, N^I,$$

$$\eta \dot{\boldsymbol{r}}_j^M = -\Big(\sum_i \nabla E_{ij}^{\mathrm{MI}} + \sum_k \nabla E_{kj}^{\mathrm{MMS}} + \sum_l \nabla E_{lj}^{\mathrm{MMD}} + \nabla E_j^{\mathrm{adh}} + \sum_{n_j} \nabla E_j^{\mathrm{SA}}\Big),\, j = 1, 2, \ldots, N^M,$$

Protrusion-dependent polarity evolution

$$\eta_{\mathrm{a}} \frac{\mathrm{d}\varphi_c}{\mathrm{d}t} = k_p \Big[\sum_p (1 + k_a \delta_p) L_p \sin(\varphi_p - \varphi_c) \Big] + k_l \sin(\theta_l - \varphi_c),$$

Myosin redistribution dynamics

$$\frac{dm_i}{dt} = k_m \Big[\sum_{k \in \Omega_i^{\mathrm{sym}}} \gamma_{\mathrm{sym}}^k (m_k - m_i) + \sum_{k \in \Omega_i^{\mathrm{asym}}} \gamma_{\mathrm{asym}}^k (m_k - m_i) \Big],$$

Substrate traction force

$$\boldsymbol{F}^{\mathrm{SA}} = k_{\mathrm{SA}} (\boldsymbol{r}_s - \boldsymbol{r}).$$

Dr. Jia Gou, UCR

Future Initiatives Sponsored by the Center

14th European Conference on Mathematical & Theoretical Biology

Joint event by the Society for Mathematical Biology (SMB) and The European Society for Mathematical and Theoretical Biology (ESMTB)

13 – 17 July 2026
University of Graz, Austria

Mini symposium: **Recent Development in Digital Twins for Biology and Biomedical Sciences**
https://ecmtb2026.org/contributions/minisymposia/ms176

Organizers: Weitao Chen, University of California, Riverside, and Uduak George, San Diego State University

Abstract

Mathematical modeling has long played a critical role in advancing our understanding of biological systems and disease processes, spanning scales from molecular interactions to population-level dynamics. These approaches provide a principled framework for uncovering mechanisms, integrating heterogeneous data, and generating predictive insight. Recent advances in computational power, high-throughput sequencing, advanced imaging, electronic health records, and artificial intelligence have created unprecedented opportunities for mathematical and computational modeling to fundamentally reshape biomedical research.

This minisymposium brings together applied mathematicians and computational scientists working on diverse forms of digital twins, highlighting both methodological innovations and novel biomedical applications. Our objective is to catalyze new directions in mathematical biology that address pressing, real-world challenges requiring integrative and cross-disciplinary approaches. Through structured presentations and interactive discussion, the minisymposium aims to promote a cultural shift toward deeper, more systematic integration of mathematics into biomedical research and clinical practice.

Chicago, IL, USA

International Workshop: **Mathematical Morphogenesis and Digital Twins Across Scales**

August 2027

Organizing Committee:

Mark Alber, Distinguished Professor of Mathematics, Director of the
Interdisciplinary Center for Data-driven Modeling in Biology, University
of California, Riverside, USA.

Weitao Chen, Associate Professor of Mathematics, Member of the Steering
Committee of the Interdisciplinary Center for Data-driven Modeling in Biology,
University of California, Riverside, USA.

Philip Maini, FRS, Professor and Director, Wolfson Centre for Mathematical
Biology, Mathematical Institute, University of Oxford, UK.

Roeland Merks, Professor of Multiscale Mathematical Biology, Mathematical Institute
and Institute of Biology, Leiden University, Director of Lorentz Center, Leiden,
The Netherlands.

Publications

PLoS Computational Biology Collection, Predictive Modeling in Biology and Medicine: Digital Twins and Multi-scale Modeling, 2026

Editors: Mark Alber, Amber Smith, Reinhard Laubenbacher, Roeland M.H. Merks

This collection contains papers submitted by the plenary and invited speakers at the conference on “Predictive Modeling in Biology and Medicine” held at University of California, Riverside, from November 17th -19th, 2023. Several additional authors contributed as well. The Conference was supported by the National Science Foundation (NSF DMS 2331170**).** The conference focused on the progress in multi-scale mathematical and computational modeling of biological systems, on translational model predictions in biology and medicine, and on data-driven and machine learning methodologies in biology and medicine. The conference brought together researchers at different stages of their career to exchange ideas and novel approaches as well as to promote interdisciplinary collaborations.

Digital Twins. Over the last 10 years, it has been shown that multi-scale modeling approaches combined with machine learning provide a powerful method for developing robust predictive models for studying many biomedical processes and exploring massive data sets [1,2]. Recently, the concept of *digital twins* has gained increasing attention in biology, biomedicine, and healthcare communities. This collection explores the construction of digital twins and multiscale models as they relate to predictive biology and medicine. The concept originated in work at NASA and is broadly used in industry and other fields, such as city planning. In the biological context, a digital twin of a biological system, whether a specific animal or patient, a specific corn field, or the population of a village, is a computational model of some aspect of the system and is calibrated dynamically to evolve together with the system, linking the physical and the digital twin. The digital twin can then be used to identify interventions or features of interest of the physical twin. This approach to "personalized" biology has tremendous potential for biotechnology, ecology, and healthcare in the future, to name just a few application areas. For a comprehensive discussion of this topic see the 2023 report on this topic by the National Academies of Science, Engineering, and Medicine (NASEM) [3] and reviews [4,5].

References

1. Grace C. Y. Peng, Mark Alber, Adrian Buganza Tepole, William R. Cannon, Suvranu De, Salvador Dura-Bernal, Krishna Garikipati, George Karniadakis, William W. Lytton, Paris Perdikaris, Linda Petzold & Ellen Kuhl [2021], Multiscale Modeling Meets Machine Learning: What Can We Learn? *Archives of Computational Methods in Engineering*, 28, pages1017–1037.
2. Mark Alber, Adrian Buganza Tepole, William R. Cannon, Suvranu De, Salvador Dura-Bernal, Krishna Garikipati, George Karniadakis, William W. Lytton, Paris Perdikaris, Linda Petzold & Ellen Kuhl [2019], Integrating machine learning and multiscale modeling - perspectives, challenges, and opportunities in the biological, biomedical, and behavioral sciences, *npj Digital Medicine*, 2:115.
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4. R. Laubenbacher, B. Mehrad, I. Shmulevich, N. Trayanova [2024], Digital twins in medicine [2024], *Nat Comput Sci*. Mar;4(3):184-191.
5. Christoph Sadée, Stefano Testa, Thomas Barba, Katherine Hartmann, Maximilian Schuessler, Alexander Thieme, George M Church, Ifeoma Okoye, Tina Hernandez-Boussard, Leroy Hood, Ilya Shmulevich, Ellen Kuhl, Olivier Gevaert [2025], Medical digital twins: enabling precision medicine and medical artificial intelligence. *Lancet Digit Health*. Jul;7(7):100864.