

PHYSICAL MATH SEMINAR

From statistics to dynamics: emerging trend in data-driven single cell studies



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ABSTRACT:

High-throughput techniques, especially at the single cell level, have greatly expanded our knowledge of cellular processes. With the increasing availability of data, a fundamental question arises: how can we leverage this data to gain mechanistic insights? Unlike static data typically targeted by statistics-based machine learning approaches, single cell data are snapshots from the dynamical state space of a cell having interacting components that dictate the temporal evolution of the system. Consequently, we witness a growing convergence of two disciplines: data science and systems biology¹. The latter seeks to unravel qualitative and quantitative causal relationships among cellular components, as well as their functions within the broader context of cell regulatory networks, all through the lens of dynamical systems theory.

In contrast to molecular systems, cells exhibit more intricate dynamics characterized by numerous highly coupled degrees of freedom, a wide dynamical range without clear time-scale separation, and being out of thermodynamic equilibrium (i.e., violation of detailed balance). During this presentation, I will delve into our recent endeavors focused on deducing the comprehensive governing dynamical equations of cells using both snapshot and time series single-cell data²⁻⁵. Distinguishing our approach from simple data manifold learning, reconstructing a dynamical system imposes additional constraints on the manifold and its associated tangent space. Furthermore, it necessitates dynamical and topological invariance under representation transformation, a fundamental principle in theoretical physics.

If time permits, I will also provide a brief overview of our ongoing research in areas such as selecting the appropriate Hilbert space representation, exploring non-Hermitian physics, and conducting spectral analyses of the cellular dynamical equations.

1. Xing, J. Reconstructing data-driven governing equations for cell phenotypic transitions: integration of data science and systems biology. *Physical Biology* **19**, 061001 (2022).
2. Wang, W., Poe, D., Yang, Y., Hyatt, T. & Xing, J. Epithelial-to-mesenchymal transition proceeds through directional destabilization of multidimensional attractor. *eLife* **11**, e74866 (2022).
3. Wang, W. *et al.* Live-cell imaging and analysis reveal cell phenotypic transition dynamics inherently missing in snapshot data. *Science Advances* **6**, eaba9319 (2020).
4. Qiu, X. *et al.* Mapping Transcriptomic Vector Fields of Single Cells. *Cell* **185**, 690-711 (2022).
5. Zhang, Y. *et al.* Graph-Dynamo: Learning stochastic cellular state transition dynamics from single cell data **to be submitted**(2023).

TUESDAY, OCTOBER 3, 2023

2:30 pm – 3:30 pm

Building 2, Room 449

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