7th Symposium on Biophysics Postgraduate Research in Hong Kong

Event Schedule

Date: Dec 16-18, 2024

Program at a glance

<table>
<tr><th>Time/Date</th><th>16-Dec-24</th><th>17-Dec-24</th><th>18-Dec-24</th></tr>
<tr><td rowspan="5">Morning</td><td rowspan="5">/</td><td>Registration</td><td rowspan="10">Safe trip back to home</td></tr>
<tr><td>Breakfast & Tea</td></tr>
<tr><td>Opening session</td></tr>
<tr><td>Picture Taking</td></tr>
<tr><td>Plenary & Invited speech</td></tr>
<tr><td>Noon</td><td rowspan="5">Registration</td><td>Lunch & Poster session</td></tr>
<tr><td rowspan="4">Afternoon</td><td>Invited speech</td></tr>
<tr><td>Discussion session</td></tr>
<tr><td>Students’ Presentation</td></tr>
<tr><td>Tea Break & Poster Session</td></tr>
<tr><td></td><td>Awarding & Closing</td></tr>
</table>

Technical Program

Morning Session		
8:30 – 9:30	Registration	
8:40 – 9:30	Breakfast & Tea	
9:00 – 9:15	Opening Speech	
9:15 – 9:20	Picture Taking	
9:20 – 10:05	Plenary Talk	
	Jianhua Xing	University of Pittsburgh
	Complex Biology, Simple Physics ----Studying biological physics in the big data era	
10:05 – 2:50	Invited talk	
10:05 – 10:30	**Yanting Wang**	Institute of Theoretical Physics, CAS
	Moderate Point: Balanced Entropy and Enthalpy Contributions in Soft Matter	
10:30 – 10:55	**Jianing Li**	Purdue University
	To be confirmed	
10:55 – 11:20	**Zhiyong Zhang**	University of Science and Technology of China
	To be confirmed	
11:20 – 11:45	**Jhih-Wei Chu**	National Chiao Tung University
	To be confirmed	
11:45 – 12:10	**Jian Zhou**	South China University of Technology

	To be confirmed
12:10 – 2:00	Lunch & Poster Session
Afternoon Session	
2:00 – 2:25	**Weikang Wang** Institute of Theoretical Physics, CAS
	Geometric Quantification of Cell Phenotype Transition Manifolds with Information Geometry
2:25 – 2:50	**Haibing Su** Hong Kong University of Science and Technology
	To be confirmed
2:50 – 3:15	Discussion Topic: to be confirmed
3:15 – 4:00	Students' Presentation
4:00 – 4:30	Tea Break & Poster Session
4:30 – 5:00	Awards for Best Student Poster & Best Student Talk Presenter: To be confirmed

Complex Biology, Simple Physics
----Studying biological physics in the big data era

Jianhua Xing

Department of Computational and Systems Biology, University of Pittsburgh

Abstract:
One main aim of biological physics is to unravel simple physics principles underlying seemingly complex biological processes. Now we are at a big data age. How do the data and the trend of machine learning/AI change or not change biological physics studies?
The importance of using physical intuition to guess the answer has been repetitively stated by many prominent physicists such as Einstein and Feynman. I would like to argue that physical intuition has guided my research bother before (e.g., mechanism of the bacterial flagellar motor, PNAS 2006, olfactory receptor selection, PNAS 2016) and at the big data era. Here I will focus on our recent study on chromosome folding, a fundamental process in cell biology. Nature has evolved a remarkably robust mechanism to fold 46 human chromosomes (with up to ~10^8 monomers and a total length ~ 2 meters) into segregated territories within a nucleus with size ~ 10 microns or less in a few minutes. People have estimated that it would take ~ 1000 years for a random search. The mechanism must work for all the cell types including cancer cells, against distinct cell type-specific chromosome structure and function requirements, unavoidable stochasticity during the folding process and mutations, otherwise cells would not survive. The secret for achieving this mission impossible hides in public domain (HiC and DNA MERFISH) data, but finding it requires seeing the data through the lens of physics.
Einstein stressed that it is more important to know how to formulate a problem than how to solve it. I will share my experience on reconstructing the governing equations of cellular processes. Physics understanding of a process typically ends at mathematical description. While one can directly apply Newton's equations, Schrodinger's equations, and related formulation to molecular systems, how to write down the equations for cell state change? Our previous publications (Sci Adv 2020, eLife 2022, Cell 2022) provide a general data-driven framework for both cellular kinematics and dynamics. I will present our new efforts and examples of applications, with the long-term goal of constructing virtual cell models parallel to molecular force fields as well as simple models revealing essential physics.

Geometric Quantification of Cell Phenotype Transition Manifolds with Information Geometry

Miao Huang[1,2], Junda Ying[3], Yuxuan Wang[4], Haijun Zhou[1,2], Lei Zhang[5], Weikang Wang[1,2]

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[5]Beijing International Center for Mathematical Research, Center for Quantitative Biology, Center for Machine Learning Research, Peking University, Beijing 100871, China.

Cell phenotype transition (CPT) plays a pivotal role in various biological processes like development. Recent advancements in single-cell sequencing techniques have uncovered that cell transition dynamics during development are confined on low-dimensional manifolds. However, existing methods are inadequate for directly quantifying the manifolds from experimental data. Here we present SCIM (single cell information manifolds), a novel geometry-guided method to quantify the CPT manifolds using information geometry. In particular, we convert single cells' high-dimensional gene vectors into probability distributions via Gaussian embedding. The Fisher metric is naturally defined in this embedding space. With the transformed Gaussian distributions, we calculate the coarse Ricci curvature of each single cell. Our analyses reveal that the cells with low curvature are associated with critical transitions. To further examine the invariant characteristics of the manifolds of CPT, we compute the information velocity of each single cell based on RNA velocity. Remarkably, the regions with high information velocity correspond with the low curvature regions, indicating that the geometry can guide the dynamics of single cells on the manifolds. The proposed method not only unveils the invariant characteristics of the CPT manifolds, but also establishes a generic approach for quantifying the intricate dynamics on the CPT manifolds.

References

[1] Miao Huang, Junda Ying, Yuxuan Wang, Haijun Zhou, Lei Zhang, Weikang Wang. doi: https://doi.org/10.1101/2023.12.28.573500.

Moderate Point: Balanced Entropy and Enthalpy Contributions in Soft Matter

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Various soft materials share some common features, such as significant entropic effect, large fluctuations, sensitivity to thermal conditions, and mesoscopic characteristic temporal and spatial scales [1]. Until now, no quantitative definitions have yet been provided for soft matter, and the intrinsic mechanisms leading to their common features are unclear. In this talk, with the aid of an appropriately chosen order parameter, I will define a “moderate point” [2], at which a thermodynamic system has as balanced as possible entropy and enthalpy contributions among its substates. The order parameter fluctuation, the associated response function, and the time and spatial correlation functions all maximize around the moderate point, which explains the characteristics of soft matter mentioned at the beginning. The relation between the moderate point and the so-called “Widom line” [3] as well as a primitive application of this theory to biomachines will also be discussed.

References

[1] R. A. Jones, *Soft Condense Matter* Oxford University Press (2002).
[1] B. He and Y. Wang, *Chinese Physics B* 26, 030506 (2017).
[2] L. Xu et al., *Proceedings of the National Academy of Sciences* 102, 16558 (2005).