

Wai Shing Tang wstangp@gmail.com

Bayesian inference | cryo-EM modeling | statistical ensemble refinement | machine learning for structural biology
Python | C/C++ | CUDA | PyTorch | Bayesian modeling | high-performance computing | molecular simulation

RESEARCH EXPERIENCE	Microsoft Research <i>Senior Researcher, AI4Science</i> <ul style="list-style-type: none">- Incorporated cryo-EM imaging data into generative molecular models for macromolecular structure prediction	May 2025 – Oct 2025
	Flatiron Institute <i>Flatiron Research Fellow, Center of Computational Mathematics (CCM) and Structural Molecular Biophysics group (SMBp)</i> <ul style="list-style-type: none">- Developed Bayesian inference methods for extracting conformational heterogeneity from experimental cryo-EM data, resulting in a new statistical framework for ensemble refinement adopted in ongoing collaborative projects- Implemented high-throughput, high-performance software for processing large-scale cryo-EM data	June 2022 – April 2025
	Brown University <i>Ph.D. research</i> <ul style="list-style-type: none">- Developed advanced statistical inference framework for identifying conformational ensemble differences among protein mutants- Perform large-scale MD simulation on HPC- Developed novel data analytic approach to reveal biophysical insights from large-scale MD simulations	Sept 2017 – May 2022
	Brown University <i>Ph.D. in Physics</i>	Sept 2017 – May 2022
EDUCATION	The Chinese University of Hong Kong <i>B.Sc. in Physics (Enrichment Stream in Physics)</i>	Sept 2013 – June 2017
	SOFTWARE DEVELOPED [1] SINATRA Pro : Protein Structure and Conformation Analysis using Topological Summary Statistics (in Python and C/C++). [2] Ensemble reweighting using Cryo-EM particles . [3] CryoLike : A Python package for Cryo-EM image-to-structure likelihood calculations	
SELECTED PUBLICATION	[1] W. Tang , J. Soules, A. Rangan, P. Cossio (2024). CryoLike: A python package for cryo-electron microscopy image-to-structure likelihood calculations. bioRxiv .	
	[2] W. Tang , D.S. Sánchez, J.G. Barreto, B. Carpenter, S.M. Hanson, A.H. Barnett, E.H. Thiede, P. Cossio (2023). Ensemble reweighting using Cryo-EM particles. Journal of Physical Chemistry B . 127(24), 5410–5421.	
	[3] W. Tang , E.D. Zhong, S.M. Hanson, E.H. Thiede, P. Cossio (2023). Conformational heterogeneity and probability distributions from single-particle cryo-electron microscopy. Current Opinion in Structural Biology . 81, 102626.	
	[4] W. Tang , G.M. da Silva, H. Kirveslahti, E. Skeens, B. Feng, T. Sudijono, K.K. Yang, S. Mukherjee, B. Rubenstein, and L. Crawford (2022). A topological data analytic approach for discovering biophysical signatures in protein dynamics. PLOS Computational Biology . 18(5): e1010045.	
	[5] A.C. Murthy, W. Tang , N. Jovic, A. Janke, D.H. Seo, T. Perdikari, J. Mittal, and N.L. Fawzi (2021). Molecular interactions contributing to FUS SYGQ LC/RGG phase separation and co-partitioning with RNA polymerase II heptads. Nature Structural & Molecular Biology . 28, 923–935.	
	[6] W. Tang , N.L. Fawzi, and J. Mittal (2020). Refining All-Atom Protein Force Fields for Polar-Rich, Prion-like, Low-Complexity Intrinsically Disordered Proteins. Journal of Physical Chemistry B . 124(43): 9505-9512.	