Tong Wang

📞: +1 217-974-5103
✉: sptow@channing.harvard.edu
🔗: wt1005203.github.io/tongwang
G: user=eh1WhmsAAAAJ

EMPLOYMENT

Channing Division of Network Medicine (CDNM)
Brigham and Women's Hospital, Harvard Medical School   Boston, Massachusetts
Postdoctoral Research Fellow in Dr. Yang-Yu Liu's lab   June 2021–Present

EDUCATION

University of Illinois Urbana-Champaign (UIUC)   Urbana, Illinois
Ph.D. in Physics, GPA: 3.97/4.00, Advisor: Dr. Sergei Maslov   August 2014–May 2021
  – *Dissertation title*: "Modeling for microbial communities with cross-feeding and predator-prey interactions"
  – *Committee*: Sergei Maslov, Ido Goldening, James O'Dwyer, and Nigel Goldenfeld (Chair)

University of Science and Technology of China (USTC)   Hefei, Anhui
B.S. in Applied Physics, *summa cum laude*, GPA: 3.98/4.30, Rank: 1/67   September 2010–June 2014

RESEARCH INTERESTS

My research seamlessly blends computational biology, microbiology, ecology, biophysics, and medicine to devise computational methods for complex biological systems. I develop **mathematical models and machine learning methods that integrate multi-omics data to explore diet-microbe-metabolite-disease relationships**, revealing their dynamics and connection to human health.

SCHOLARSHIPS AND AWARDS

- The Les Houches School of Physics "Evolution of Diversity" Program Scholarship   2018
- Guo Moruo Scholarship (the highest honor in USTC)   2014
- UCLA Cross-disciplinary Scholars in Science and Technology (CSST) Summer Research Scholarship   2013
- China National Scholarship   2012
- XinDi Scholarship   2011

FUNDING IN APPLICATION

- Pathway to Independence Award (K99/R00), The National Institutes of Health (NIH), resubmitted in July 2024
- Career Awards at the Scientific Interface (CASI), Burroughs Wellcome Fund (BWF), submitted in August 2024

PUBLICATIONS AND PREPRINTS (*: EQUAL CONTRIBUTION)

First or Co-first

- **Wang T**, George AB, Maslov S. Higher-order interactions in auxotroph communities enhance their resilience to resource fluctuations. *Under Review at **Cell Systems**.* BioRxiv DOI: 10.1101/2024.05.22.595348
- **Wang T**, Holscher HD, Maslov S, Hu FB, Weiss ST, Liu YY. Predicting metabolite response to dietary intervention using deep learning. *In Press at **Nature Communications**.* BioRxiv DOI: 10.1101/2023.03.14.532589

- **Wang T**, Fu Y, Shuai M, Zheng JS, Zhu L, Chan AT, Sun Q, Hu FB, Weiss ST, Liu YY. Microbiome-based correction for random errors in nutrient profiles derived from self-reported dietary assessments. ***Nature Communications***. 2024 Oct 22;15(1):9112. DOI: 10.1038/s41467-024-53567-w

- **Wang T***, Li L*, Figeys D, Liu YY. Pairing metagenomics and metaproteomics to characterize ecological niches and metabolic essentiality of gut microbiomes. ***ISME Communications***. 2024 Jan 1;4(1):ycae063. DOI: 10.1093/ismeco/ycae063

- Li L*, **Wang T***, Ning Z, Zhang X, Butcher J, Serrana JM, Simopoulos CM, Mayne J, Stintzi A, Mack DR, Liu YY, Figeys D. Revealing proteome-level functional redundancy in the human gut microbiome using ultra-deep metaproteomics. ***Nature Communications***. 2023 Jun 10;14(1):3428. DOI: 10.1038/s41467-023-39149-2

- **Wang T**, Wang XW, Lee-Sarwar KA, Litonjua AA, Weiss ST, Sun Y, Maslov S, Liu YY. Predicting metabolomic profiles from microbial composition through neural ordinary differential equations. ***Nature Machine Intelligence***. 2023 Mar;5(3):284-93. DOI: 10.1038/s42256-023-00627-3 — highlighted in IGB Newsletter

- Goyal A*, **Wang T***, Dubinkina V, Maslov S. Ecology-guided prediction of cross-feeding interactions in the human gut microbiome. ***Nature Communications***. 2021 Feb 26;12(1):1335. DOI: 10.1038/s41467-021-21586-6 — highlighted in EurekAlert!; Bik's Picks

- Ping D*, **Wang T***, Fraebel DT, Maslov S, Sneppen K, Kuehn S. Hitchhiking, collapse, and contingency in phage infections of migrating bacterial populations. ***The ISME Journal***. 2020 Aug;14(8):2007-18. DOI: 10.1038/s41396-020-0664-9 — highlighted in Nature Research Microbiology Community; Bik's Picks

- **Wang T***, Goyal A*, Dubinkina V, Maslov S. Evidence for a multi-level trophic organization of the human gut microbiome. ***PLoS Computational Biology***. 2019 Dec 19;15(12):e1007524. DOI: 10.1371/journal.pcbi.1007524 — highlighted in Phys; ScienceDaily; EurekAlert!; Bik's Picks

Co-author

- Wu L, Wang XW, Tao Z, **Wang T**, Zuo W, Zeng Y, Liu YY, Dai L. Data-driven prediction of colonization outcomes for complex microbial communities. ***Nature Communications***. 2024 Mar 16;15(1):2406. DOI: 10.1038/s41467-024-46766-y

- Sun Z, Liu J, Zhang M, **Wang T**, Huang S, Weiss ST, Liu YY. Removal of false positives in metagenomics-based taxonomy profiling via targeting Type IIB restriction sites. ***Nature Communications***. 2023 Sep 1;14(1):5321. DOI: 10.1038/s41467-023-41099-8

- Aparicio A, **Wang T**, Saavedra S, Liu YY. Feasibility in MacArthur's Consumer-Resource Model. ***Theoretical Ecology***. 2023 Sep;16(3):225-38. DOI: 10.1007/s12080-023-00566-0

- George AB, **Wang T**, Maslov S. Functional convergence in slow-growing microbial communities arises from thermodynamic constraints. ***The ISME Journal***. 2023 Sep;17(9):1482-94. DOI: 10.1038/s41396-023-01455-4

- Wang XW, **Wang T**, Schaub DP, Chen C, Sun Z, Ke S, Hecker J, Maaser-Hecker A, Zeleznik OA, Zeleznik R, Litonjua AA, DeMeo DL, Lasky-Su J, Silverman EK, Liu YY, Weiss ST. Benchmarking omics-based prediction of asthma development in children. ***Respiratory Research***. 2023 Feb 26;24(1):63. DOI: 10.1186/s12931-023-02368-8

- Ranoa DR, Holland RL, Alnaji FG, Green KJ, Wang L, Fredrickson RL, **Wang T**,..., Burke MD. Mitigation of SARS-CoV-2 Transmission at a Large Public University. ***Nature Communications***. 2022 Jun 9;13(1):3207. DOI: 10.1038/s41467-022-30833-3 — highlighted in EurekAlert!; MedicalXpress; Chicago Tribune; ScienMag

- Wang Z, Goyal A, Dubinkina V, George AB, **Wang T**, Fridman Y, Maslov S. Complementary resource preferences spontaneously emerge in diauxic microbial communities. ***Nature Communications***. 2021 Nov 18;12(1):6661. DOI: 10.1038/s41467-021-27023-y — highlighted in EurekAlert!; Phys

- Tkachenko AV, Maslov S, **Wang T**, Elbana A, Wong GN, Goldenfeld N. Stochastic social behavior coupled to COVID-19 dynamics leads to waves, plateaus, and an endemic state. ***Elife***. 2021 Nov 8;10:e68341. DOI: 10.7554/eLife.68341 — highlighted in UIUC Physics news; BNL News

- Pilosof S, Alcala-Corona SA, **Wang T**, Kim T, Maslov S, Whitaker R, Pascual M. The network structure and eco-evolutionary dynamics of CRISPR-induced immune diversification. ***Nature Ecology & Evolution***. 2020 Dec;4(12):1650-60. DOI: 10.1038/s41559-020-01312-z — highlighted in EurekAlert!; Phys

- Liao C, **Wang T**, Maslov S, Xavier JB. Modeling microbial cross-feeding at intermediate scale portrays community dynamics and species coexistence. ***PLoS Computational Biology***. 2020 Aug 18;16(8):e1008135. DOI: 10.1371/journal.pcbi.1008135

Research Experience

Postdoctoral Research Fellow June 2021–Present

Dr. Yang-Yu Liu' lab, Brigham and Women's Hospital, Harvard Medical School Boston, MA, USA

- Developed a deep-learning method to predict the metabolome of a microbial community based on its composition
- Created a deep-learning method to forecast metabolic responses to dietary interventions using individual factors
- Formulated a new deep-learning method to correct the random measurement errors in assessed nutrient profiles
- Investigated the relationships between microbes, metabolites, and dietary compounds through network analysis
- Integrated multi-omics data for enhancing disease diagnostics

Invited Visiting Scholar May 2022

Dr. Daniel Figeys' lab, University of Ottawa Ottawa, Canada

- Designed the metric for the gut microbiome, "proteome-level functional redundancy", to diagnose diseases
- Compared the metagenome and metaproteome to assign metabolic and ecological roles of each protein family

Graduate Research Assistant January 2017–May 2021

Dr. Sergei Maslov's lab, University of Illinois Urbana-Champaign Urbana, IL, USA

- Developed an ecological model to stratify the trophic organization of the gut microbiome
- Built mathematical models to predict assembly outcomes of auxotroph microbial communities
- Modeled the spatial infection dynamics of phage P1vir infecting the chemotactic *E. coli*
- Simulated the CRISPR-induced arms-race co-evolutionary dynamics between bacteria and phages
- Developed agent-based COVID-19 infection models and analyzed on-campus infection data for policymaking

Teaching experience

- Invited Lecture: "Application of Machine-Learning Methods in Biology and Medicine". Summer School hosted by the School of Medicine, Peking University, July 2024
- Invited Lecture: "Application of Machine-Learning Methods in Biology and Medicine". Summer School hosted by the School of Medicine, Peking University, July 2023
- Guest Lecture: "Regression Models – predicting metabolomic profiles of microbial communities as an example". Microbiome Data Science, BIO/MIC 494/598, Arizona State University, March 2023
- Graduate Mentor: mentored two students in analyzing the microbiome data and modeling
- Teaching Assistant: Statistical Physics, UIUC PHYS 504, Spring 2017
- Teaching Assistant: Relativity & Math Applications, UIUC PHYS 225, Fall 2016
- Teaching Assistant: Classical Mechanics II, UIUC PHYS 326, Spring 2016
- Teaching Assistant: Classical Mechanics II, UIUC PHYS 326, Fall 2015
- Teaching Assistant: Quantum Mechanics II, UIUC PHYS 581, Spring 2015
- Teaching Assistant: Classical Mechanics II, UIUC PHYS 326, Fall 2014

Invited talks

- Predicting metabolic response to dietary intervention using deep learning. Virtual oral presentation at AI in Biomedicine, Keystone Symposia, May 2024
- Machine learning for precision nutrition. Virtual oral presentation at the Bio-Data Club Seminar, Moffitt Cancer Center, Tampa, FL, January 2024
- Machine learning for precision nutrition. Oral presentation at Circulating Metabolic Intermediates as Fuels and Signals Conference, Keystone Symposia, Salt Lake City, UT, October 2023
- Machine learning for precision nutrition. Oral presentation at the MIT Center for the Physics of Living Systems, Department of Physics, Massachusetts Institute of Technology, Boston, MA, April 2023

- Pairing metagenomics and metaproteomics to pinpoint ecological niches and metabolic essentiality of microbial communities. Oral virtual presentation at the International Workshop on Soft Matter and Biophysics theories, Institute of Theoretical Physics, Chinese Academy of Sciences, Beijing, November 2022
- Pairing metagenomics and metaproteomics to pinpoint ecological niches and metabolic essentiality of microbial communities. Oral presentation at the MIT Center for the Physics of Living Systems, Department of Physics, Massachusetts Institute of Technology, Boston, MA, May 2022
- Pairing metagenomics and metaproteomics to pinpoint ecological niches and metabolic essentiality of microbial communities. Oral presentation at the School of Pharmaceutical Sciences, University of Ottawa, Ottawa, May 2022
- Predicting metabolomic profiles from microbial compositions through neural ordinary differential equations. Oral presentation at the Center for Complex Network Research, Northeastern University, Boston, MA, March 2022

Contributed presentations

- Machine learning for precision nutrition. Oral presentation at Cold Spring Harbor Laboratory Microbiome Meeting, Cold Spring Harbor, NY, October 2024
- Predicting metabolic response to dietary intervention using deep learning. Oral presentation at Microbial Communities, APS March Meeting 2024, Minneapolis, MN, March 2024
- Predicting metabolic response to dietary intervention using deep learning. Poster presentation at Microbial Ecology and Evolution Hub-based Conference 2024, Boston College, Boston, MA, January 2024
- Machine learning for precision nutrition. Poster presentation at IAIFI Summer Workshop, Northeastern University, Boston, MA, August 2023
- Microbiome-based correction of dietary assessment. Oral presentation at Health Professionals Follow-up Study meeting, Harvard Medical School, Boston, MA, May 2023
- Predicting metabolomic profiles from microbial compositions through neural ordinary differential equations. Poster presentation at MIT Microbiome Symposium, Massachusetts Institute of Technology, Boston, MA, April 2023
- Predicting metabolomic profiles from microbial composition through neural ordinary differential equations. Oral presentation at Microbial Communities, APS March Meeting 2023, Las Vegas, NV, March 2023
- Pinpointing ecological niches and metabolic essentiality of microbial communities using both metagenomics and metaproteomics. Oral presentation at Ecological and Evolutionary Biology, APS March Meeting 2022, Chicago, IL, March 2022
- Predicting metabolomic profiles from microbial composition through neural ordinary differential equations. Oral presentation at Channing Microbiome Meeting, Harvard Medical School, Boston, MA, February 2022
- Hitchhiking, collapse, and contingency in phage infections of migrating bacterial populations. Poster presentation at Biocomplexity Theme Review, Carl R. Woese Institute for Genomic Biology, Urbana, IL, October 2019
- CRISPR-induced Red Queen dynamics in the phage-microbial system. Poster presentation at Biocomplexity Theme Review, Carl R. Woese Institute for Genomic Biology, Urbana, IL, October 2019
- Evidence for a multi-level trophic organization of the human gut microbiome. Poster presentation at IGB Fellows Symposium, Carl R. Woese Institute for Genomic Biology, Urbana, IL, April 2019
- Thermodynamic constraints on cross-feeding in bacterial population. Oral presentation at Ecological and Evolutionary Biology, APS March Meeting 2019, Boston, MA, March 2019
- Hitchhiking, collapse, and contingency in phage infections of migrating bacterial populations. Poster presentation at the "Evolution of Diversity" Program, Les Houches Physics School, Les Houches, February 2018

Peer Review

- <u>Scientific Journals</u>: Science, Cell, Nature Communications, PNAS, eLife, PloS Computational Biology, Biophysical Journal, Microbiology Spectrum, PloS One, BMC Medicine, Nutrients, Computational and Structural Biotechnology Journal, peerJ
- <u>Grants</u>: UKRI (United Kingdom Research and Innovation)

Skills

- <u>Programming Languages</u>: Python, R, Matlab, Julia, C, C++
- <u>Machine Learning</u>: PyTorch, TensorFlow, scikit-learn
- <u>Languages</u>: English (full professional proficiency), Chinese (native), Spanish (limited working proficiency)
- <u>Other</u>: Open MPI, Latex, Markdown, Illustrator, ChatGPT