

Dong Wang

– Infectious Disease Modelling | Bayesian Inference | Complex Networks

Postdoctoral researcher with a PhD in Mathematics, specialising in mechanistic and Bayesian approaches for infectious-disease dynamics and evolutionary epidemiology. Experienced in integrating heterogeneous datasets (surveillance, clinical outcomes, mobility/contact networks, and sequence-derived signals) to infer transmission processes, quantify uncertainty, and evaluate interventions. Strong programming skills in R (RStan) and Python; committed to reproducible, open science and collaborative work across disciplines.

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Present academic position:

Post-doctoral Fellow School of Public Health The University of Hong Kong
<https://sph.hku.hk/en/Biography/Wang-Dong>

Educations

2015–2021 Ph.D. of Science
 Major: Mathematics
 School: School of Science
 Institution: Harbin Institute of Technology, Shenzhen, China
2011–2015 Bachelor of Science
 Major: Information and Computing Science
 School: School of Mathematics and Computer Science
 Institution: Northwest Minzu University, Lanzhou, China

Skills

Epidemiology; Mathematical high-order modeling; Complex network analysis; Statistical Modeling and inference; geographic and spatial analytics; Bayesian hierarchical modeling; *phylodynamics*; analysis of collective behavior.

Particularly adept at higher-order infectious disease modeling that synthesizes epidemiological, geographic, phylogenetic, and network approaches to elucidate the impact of viral evolution and human mobility on shaping patterns of disease transmission.

Interests

- Microbial genomics and evolutionary epidemiology; linking genomic/metagenomic patterns to transmission and population dynamics
- Probabilistic modelling and Bayesian hierarchical inference under partial observability
- Pathogen-agnostic analytics and automation for genomic epidemiology workflows
- Higher-order contact and mobility networks; forecasting and intervention evaluation

Softwares

Extensive experience with **R**, including data visualization (*ggplot2*), bioinformatics workflows, and, in particular, mathematical modeling and statistical inference via **RStan**. Proficient in **Python** for data manipulation and analysis (pandas and others), as well as **MATLAB** for numerical computations and algorithmic development.

Project

Reference number	Project title	Capacity (PI / Co-I)	Funding source(s) and amount
22210582	The impact of higher-order interactions in human mobility networks on the transmission of COVID-19 in Hong Kong and mainland China	PI	Health and Medical Research Fund (HMRF) HK\$551,440.00
17100225	Identifying the dynamical interaction among respiratory viruses including influenza and COVID-19, and prediction of their cocirculation burden in the post-pandemic period using multi-stream data	Co-I	General Research Fund (GRF) HK\$1,015,417

Open-source software (selected) <https://github.com/WangDongHKU>

1. [High_order_modelling](#): Higher-order (simplicial / network) transmission modelling integrating mobility + epidemiological data to quantify spatiotemporal heterogeneity.
2. [Chikv_global_dynamic](#): Phylogenetic / phylogeographic workflows to characterise global spread and evolutionary dynamics of three major CHIKV lineages.
3. [Global_covid_dynamics](#): Bayesian (Stan) higher-order modelling pipelines for multi-country COVID-19 transmission dynamics, with analyses across phases/variant periods.
4. [Ensemble_Influenza_Forecasting](#): Reproducible ensemble framework for influenza forecasting in Hong Kong using multi-source surveillance data and temporal cross-validation.

Publishing

- [1] **Dong Wang**, Yiu-Chung Lau, Songwei Shan, Dongxuan Chen, et al Ensemble forecasting of influenza activity and dynamical characteristics during and post-COVID-19 pandemic era in subtropical location, under review, *PLOS Computational Biology*, 2025.
- [2] **Dong Wang et al.** Social reinforcements and the spatiotemporal characteristics for the transmission dynamics of SARS-CoV-2 in mainland China, submitted to *Science Advance*.

Publications

- [1] D. Chen, D.C. Adam, YC Lau, **Dong Wang et al.** Investigating setting-specific superspreading potential and generation intervals of COVID-19 in Hong Kong. *Nat Commun* **16**, 5816 (2025).
- [2] YC Lau, S Shan, **Dong Wang et al.** (2024) Forecasting of influenza activity and associated hospital admission burden and estimating the impact of COVID-19 pandemic on 2019/20 winter

season in Hong Kong. *PLOS Computational Biology* 20(7): e1012311.

[3] **Dong Wang**, Yi Zhao, Jianfeng Luo, Hui Leng, Simplicial SIRS epidemic models with nonlinear incidence rates, *Chaos*, 31(5), 053112 2021.

[4] **Dong Wang**, Michael Small, Yi Zhao, Exploring the optimal network topology for spreading dynamics, *Physica A*, 564, 125535, 2021.

[5] **Dong Wang**, Yi Zhao, Hui Leng, Michael Small. A social communication model based on simplicial complexes, *Physics Letters A*, 384 (35), 126895, 2020.

[6] **Dong Wang**, Yi Zhao, Hui Leng, Dynamics of epidemic spreading in the group-based multilayer networks, *Mathematics*, 8(11), 1895, 2020.

[7] **Dong Wang**, Yi Zhao, Network community detection from the perspective of time series, *Physica A*, 522, 205-214, 2019.

Selected conference presentations

1. Forecasting of influenza activity using multi-stream surveillance data in Hong Kong (Oral). OPTIONS XI, *UK (2022)*

2. Forecasting global influenza activities using multi-stream surveillance data (Poster). EPIDEMIC 9, *Italy (2023)*

3. Prediction of influenza hospital admission rates across age groups in Hong Kong using multi-stream surveillance data (Poster). OPTIONS XII, *Australia (2024)*

4. The COVID-19 transmission dynamics in mainland China: a higher-order spatiotemporal modeling study (Poster). OPTIONS XII, *Australia (2024)*

5. Social reinforcements and the spatiotemporal characteristics for the transmission dynamics of SARS-CoV-2 in mainland China (Oral), EPIDEMIC 10 USA (2025)

6. Disentangling the multifaceted drivers of disease transmission: a bayesian hierarchical model of climate, air quality, and contact patterns in Hong Kong (Poster), EPIDEMIC 10 USA (2025)

Contact information for reference

Prof. Cowling, Benjamin John *bcowling@hku.hk*

Prof. Ali Sheikh Taslim *alist15@hku.hk*

Highly motivated to develop reproducible, pathogen-agnostic modelling and inference frameworks that integrate genomic/metagenomic data with surveillance and experimental readouts to quantify microbial population dynamics and support better prevention and treatment of infectious diseases.