

Tianjian Qin PhD

📍 Netherlands

Computational Biologist & AI/ML Researcher

Postdoctoral Researcher · Wageningen University & Research

✉ tianjian.qin@wur.nl | 🌐 qtj.me | 📄 herdlink.nl | 🌐 [EvoLandEco](https://evolandeco.com) | 🌐 [tjqin](https://tjqin.com)

📞 0000-0003-2540-1778

Computational biology | AI/ML | Infectious disease modelling

Network science | Phylodynamics | One Health | Research software

Computational biologist developing AI/ML methods, stochastic models and research software for complex biological systems. My work connects phylogenetic inference, temporal networks and spatiotemporal modelling. I translate empirical data, scientific questions and stakeholder needs into transparent models, reproducible research pipelines and interactive tools for analysis and decision support.

SELECTED RESEARCH & SOFTWARE

NetForge: synthetic livestock contact networks

[Network science](#) · [Epidemiology](#)

Developed within the IMBIT pandemic preparedness programme, combining stochastic block models with contact history selection to generate synthetic livestock contact networks; benchmarked them against temporal reachability and simulated infection dynamics.

First-author [bioRxiv preprint \(2026\)](#) | [Software and documentation](#)

EvoNN & EVE: neural inference for evolutionary biology

[AI/ML](#) · [Stochastic modelling](#)

Designed ensemble neural networks that learn from tree structure, branching times and summary statistics, alongside stochastic diversification models and high-performance simulators.

First-author articles: [Systematic Biology \(2026\)](#) | [Journal of Theoretical Biology \(2025\)](#)

FEATURED APPLICATION

[HerdLink.nl](#) | [Source code](#)

HerdLink: interactive intervention modelling

Developed within IMBIT and deployed as a public web platform linking Dutch livestock trade networks, geographic views and disease simulations. Implemented dated route and regional movement restrictions, seven scenario presets, and paired baseline and intervention comparisons of epidemic trajectories, regional burden and retained trade for scenario comparison and decision support.

[JavaScript](#) · [React](#) · [D3.js](#) · [Vite](#) · [Automated tests and deployment](#)

RESEARCH EXPERIENCE

2025–present

Postdoctoral Researcher

Wageningen University & Research · Infectious Disease Epidemiology Group

Develop AI and computational methods for One Health and pandemic preparedness, integrating multiplex temporal networks, network-phylodynamic inference, spatio-temporal epidemic modelling, and neural/hybrid AI for future outbreaks. Build reproducible HPC pipelines and interactive web tools. Participate in education and grant writing.

2019–2026

Doctoral Researcher in Theoretical & Computational Biology

University of Groningen · Groningen Institute for Evolutionary Life Sciences

Developed simulation and inference methods for evolutionary diversification; built research packages in R, C++ and Python with CPU/GPU computing, testing, documentation and open releases.

🏆 **Denise Kirschner Best Student Paper Prize, 2025**

[Journal of Theoretical Biology](#)

🗣 **Languages** Chinese: native | English: proficient | Dutch: A2 certified, strong reading | German: A2

Publications & education

PEER-REVIEWED ARTICLES

1. Qin, T., van Benthem, K. J., Valente, L.[†], & Etienne, R. S.[†] (2026). Parameter estimation from phylogenetic trees using neural networks and ensemble learning. *Systematic Biology*, 75(2), 344–365. DOI
2. Qin, T., Valente, L.[†], & Etienne, R. S.[†] (2025). Impact of evolutionary relatedness on species diversification and tree shape. *Journal of Theoretical Biology*, 598, 111992. DOI
3. Sun, K., Liu, X.-S., Qin, T.-J., Jiang, F., Cai, J.-F., Shen, Y.-L., A, S.-H., & Li, H.-L. (2022). Relative abundance of invasive plants more effectively explains the response of wetland communities to different invasion degrees than phylogenetic evenness. *Journal of Plant Ecology*, 15(3), 625–638. DOI
4. Qin, T., Zhou, J., Sun, Y., Müller-Schärer, H., Luo, F., Dong, B., Li, H., & Yu, F.-H. (2020). Phylogenetic diversity is a better predictor of wetland community resistance to *Alternanthera philoxeroides* invasion than species richness. *Plant Biology*, 22(4), 591–599. DOI
5. Wan, J.-Z., Wang, M.-Z., Qin, T.-J., Bu, X.-Q., Li, H.-L., & Yu, F.-H. (2019). Spatial environmental heterogeneity may drive functional trait variation in *Hydrocotyle vulgaris* (Araliaceae), an invasive aquatic plant. *Aquatic Biology*, 28, 149–158. DOI
6. Qin, T.-J.* , Guan, Y.-T.* , Quan, H., Dong, B.-C., Luo, F.-L., Zhang, M.-X., Li, H.-L., & Yu, F.-H. (2019). Growth traits of the exotic plant *Hydrocotyle vulgaris* and the evenness of resident plant communities are mediated by community age, not species diversity. *Weed Research*, 59(5), 377–386. DOI
7. Qin, T.-J., Guan, Y.-T., Zhang, M.-X., Li, H.-L., & Yu, F.-H. (2018). Sediment type and nitrogen deposition affect the relationship between *Alternanthera philoxeroides* and experimental wetland plant communities. *Marine and Freshwater Research*, 69(5), 811–822. DOI
8. Liu, L., Guan, Y.-T., Qin, T.-J., Wang, Y.-Y., Li, H.-L., & Zhi, Y.-B. (2018). Effects of water regime on the growth of the submerged macrophyte *Ceratophyllum demersum* at different densities. *Journal of Freshwater Ecology*, 33(1), 45–56. DOI

PREPRINTS

1. Qin, T., Atamer Balkan, B., Schmid, B. V., & ten Bosch, Q. A. (2026). From Movement to Spread: Generating Livestock Contact Networks that Preserve Infection Dynamics. *bioRxiv*. DOI
2. Qin, T., van Benthem, K., Valente, L.[†], & Etienne, R. S.[†] (2026). Identifying evolutionary relatedness effects on diversification from phylogenies using neural networks. *bioRxiv*. DOI

* Equal contribution. † Joint senior authors.

CONFERENCE PRESENTATION

Qin, T., Atamer Balkan, B., Schmid, B., & ten Bosch, Q. (2026). From Livestock Movements to Infection Dynamics: Mechanism-Informed Learning for Synthetic Contact Networks. 🗣️ Oral presentation, ModAH Conference 2026, Nantes, France, 26 August 2026.

EDUCATION

2019–2026

PhD in Theoretical Biology

University of Groningen, Netherlands

Thesis: *Diversification Models and Neural Inference*. Supervisors: Rampal Etienne, Luis Valente and Koen van Benthem.

2016–2019

MSc in Wetland Ecology

Beijing Forestry University, China

Supervisors: Hongli Li and Feihai Yu. Research on wetland invasion resistance and community assembly, with field surveys across 18 Chinese provinces, controlled experiments, image analysis and phylogenetic workflows.

2012–2016

BSc in Marine Biology

Nanjing Normal University, China

Programmes, software & expertise

RESEARCH PROGRAMMES & FUNDING

NextdAI: Integrated AI-Driven Early Detection System

IN DEVELOPMENT | 2026

NWO KIC: Early Detection of (Emerging) Infectious Disease Outbreaks

Grant writing and work-package design. Co-develop the proposal's AI architecture and data infrastructure for heterogeneous surveillance, anomaly detection, neurosymbolic characterisation, forecasting and decision support.

EUPAHW: hepatitis E across pigs, wild boar and humans

ONGOING | 2026

European Partnership on Animal Health and Welfare · SOA26

Phylogenetic and network research. Develop analyses linking livestock movements, wildlife and landscape data to investigate transmission pathways and inform One Health surveillance.

SSS-mod: Preparedness Package for Future Respiratory Outbreaks

ONGOING | 2026

ZonMw Implementatie-impuls COVID-19 programma

Research software development. Build data preparation, recalibration, model output and interface workflows supporting reuse of a setting-specific respiratory transmission model.

IMBIT: Intervention Modeling & Bayesian Inference of Transmission Routes for Early Pandemic Response

COMPLETED | 2025

ZonMw Kennisprogramma Pandemische Paraatheid

Methods and software development. Developed NetForge and HerdLink.nl for synthetic livestock contact networks and interactive intervention experiments, within a One Health programme coupling multi-route simulation with Bayesian transmission-route inference.

RESEARCH SOFTWARE

EvoNN & evessim

Developer. Neural inference from phylogenies and fast simulation of evolutionary relatedness dependent birth-death processes.

NetSpectra, EvoLab, miniape

Developer. Interactive network dynamics, lineage simulation, tree reconstruction and browser-based phylogenetic data handling.

treestats, DDD, DAISIE

Collaborator. Phylogenetic statistics, data structures, simulation and inference for diversification and island biogeography.

TECHNICAL EXPERTISE

AI & machine learning

Graph, recurrent and dense neural networks; Transformers; ensemble and generative modelling; PyTorch, PyTorch Geometric, model benchmarking and evaluation.

Modelling & inference

Stochastic processes, simulation-based inference, likelihood methods, dynamic and temporal networks, transmission simulation, phylodynamics and phylogenetic analysis.

Programming & data

Python, R, C/C++, JavaScript, SQL; package development, spatiotemporal data integration, GIS and reproducible analysis pipelines.

Research computing

Linux, Bash, CPU/GPU HPC, Docker, Git, GitHub workflows, CI/CD, automated testing, reproducible environments and AI-assisted software development.

Web & visualisation

React, D3.js, Three.js, Vite; interactive scientific interfaces, geospatial visualisation, $\LaTeX$, TikZ and PGFPlots.

SEMINARS, WORKSHOPS, MENTORING & SERVICE

- Mentor BSc/MSc students and junior PhD researchers; pair programming on test-driven development and scientific software design.
- Seminars and workshops at Groningen, WUR and Wageningen Bioveterinary Research on island biogeography, stochastic modelling, phylodynamics, neural networks and network statistics.
- Reviewer for *Systematic Biology*, *PLOS Computational Biology*, *Epidemics*, *BMC Public Health* and *BMC Plant Biology*; open-source contributor.

Academic leadership: Vice President, Graduate Student Council (2017–2018); student representative, Wetland Ecology Group (2016–2019). **University awards:** First-Class Academic Performance Award (2017–2019); Graduate Academic Innovation Award (2018), Beijing Forestry University.