

Jianshu Zhao

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Academic Appointments

2024–2026 **Postdoctoral Researcher**
UNIVERSITY OF CALIFORNIA, SAN DIEGO

Education

2020–2024 **Ph.D. in Bioinformatics**
GEORGIA INSTITUTE OF TECHNOLOGY
2016–2019 **M.S. in Environmental Science and Engineering**
TSINGHUA UNIVERSITY
2012–2016 **B.S. in Environmental Science**
NANJING AGRICULTURAL UNIVERSITY

Research Interests

Large-scale genomics, metagenomics, microbiome analysis, long-read metagenomics, microbial ecology, metatranscriptomics, single-cell genomics, single-cell rRNA sequencing, genome search, biological network embedding, and high-performance scientific software.

Research Software

KEY SOFTWARE AND LIBRARIES

[DartUniFrac](#); [DartMinHash](#); [TurboANI](#); [GSearch](#); [LASH](#); [Annembed](#); [GraphEmbed](#); [Granne](#); [Rust-DiskANN](#); [ExaLogLog](#); [FastCover](#); [SuperBits](#); [Adas](#); [BinDash-rs](#); [Bindashtree](#); [EMDUniFrac](#); [fpcoa](#).

CONTRIBUTED SOFTWARE AND LIBRARIES

[UltraLogLog](#); [succparen](#); [Scikit-bio](#); [BinDash](#).

Publications

* indicates first author or co-first author.

UNDER REVIEW AND PREPRINTS

- [P1] M. Omar Din, Caitriona Brennan, **Jianshu Zhao**^{*}, Renee Oles, Lucas Patel, Amanda Birmingham, Dilara M. Sevilir, Lauren Hansen, Gillian M. Wright, Madison Ambre, Meika Tomita, et al. “Genome-resolved ecology and evolution of the microbiome enabled by quantitative long-read metagenomics”. In: *bioRxiv* (2026). [\[DOI\]](#)
- [P2] **Jianshu Zhao**^{*}, Jean Pierre Both, and Rob Knight. “Ultra-fast and Efficient Network Embedding for Gigascale Biological Datasets”. In: *bioRxiv* (2025). [\[DOI\]](#)
- [P3] **Jianshu Zhao**^{*}, Xiaofei Zhao, Jean Pierre-Both, and Konstantinos T. Konstantinidis. “BinDash 2.0: New MinHash Scheme Allows Ultra-fast and Accurate Genome Search and Comparisons”. In: *bioRxiv* (2024). [\[DOI\]](#)

JOURNAL ARTICLES

- [J1] **Jianshu Zhao**^{*}, Daniel McDonald, Igor Sfiligoi, Manuel E. Lladser, Lucas Patel, Yuhang Weng, Lora Khatib, Samuel Degregori, Antonio Gonzalez, Catherine A. Lozupone, and Rob Knight. “Megascale microbiome analysis with DartUniFrac”. In: *Nature Biotechnology* (2026). [\[DOI\]](#)
- [J2] Lora Khatib, Renee Oles, Alejandra Ríos Hernández, Tyler Myers, **Jianshu Zhao**, Megha Kumar, Ana Laroya, Veronica Tolosa-Enguis, Nobuko Matsunami, Daisuke Suzuki, Nodoka Chiba, et al. “Five-country analysis of geographic and dietary drivers of gut microbiome composition and genomic variation”. In: *Nature Communications* (2026). [\[DOI\]](#)
- [J3] Matthew Aton, Daniel McDonald, Jorge Cañardo Alastuey, Raed Azom, Paarth Batra, Valentyn Bezshapkin, Evan Bolyen, Alexander Cagle, J. Gregory Caporaso, Justine W. Debelius, Kestrel Gorlick, Nirmitha Hamsanipally, Lars Hunger, Aryan Keluskar, Disen Liao, Yang Young Lu, Jose A. Navas-Molina, Anders Pitman, Jai Ram Rideout, Anton Sazonov, Bharath Sathappan, Karen Schwarzbach Lipson, Igor Sfiligoi, Chris Tapo, Yoshiki Vázquez-Baeza, Zijun Wu, Zhenjiang Zech Xu, Mingsong Sam Ye, **Jianshu Zhao**, Rob Knight, James T. Morton, and Qiyun Zhu. “Scikit-bio: a fundamental Python library for biological omic data analysis”. In: *Nature Methods* 23, 274–276 (2026). [\[DOI\]](#)
- [J4] **Jianshu Zhao**^{*}, Genevieve Brandt, Jessica L. Gronniger, Zhao Wang, Jiaqian Li, Dana E. Hunt, Luis M. Rodriguez-R, Janet K. Hatt, and Konstantinos T. Konstantinidis. “Quantifying the contribution of the rare biosphere to natural disturbances”. In: *The ISME Journal* 19, wrf129 (2025). [\[DOI\]](#)
- [J5] **Jianshu Zhao**^{*}, Maria Pachiadaki, Roth E. Conrad, Janet K. Hatt, Laura A. Bristow, Luis M. Rodriguez-R, Ramon Rossello-Mora, Frank J. Stewart, and Konstantinos T. Konstantinidis. “Promiscuous and genome-wide recombination underlies the sequence-discrete species of the SAR11 lineage in the deep ocean”. In: *The ISME Journal* 19, wrf072 (2025). [\[DOI\]](#)
- [J6] Congmin Zhu, Linwei Wu, Daliang Ning, Renmao Tian, Shuhong Gao, Bing Zhang, **Jianshu Zhao**, Ya Zhang, Naijia Xiao, Yajiao Wang, et al. “Global diversity and distribution of antibiotic resistance genes in human wastewater treatment systems”. In: *Nature Communications* 16, 4006 (2025). [\[DOI\]](#)
- [J7] **Jianshu Zhao**^{*}, Jean Pierre Both, Luis M. Rodriguez-R, and Konstantinos T. Konstantinidis. “GSearch: ultra-fast and scalable genome search by combining K-mer hashing with hierarchical navigable small world graphs”. In: *Nucleic Acids Research* 52, e74 (2024). [\[DOI\]](#)

- [J8] **Jianshu Zhao**^{*}, Jean Pierre Both, and Konstantinos T. Konstantinidis. “Approximate nearest neighbor graph provides fast and efficient embedding with applications for large-scale biological data”. In: *NAR Genomics and Bioinformatics* 6, lqae172 (2024). [\[DOI\]](#)
- [J9] Qi Qi, Shijie Ning, Xue Guo, **Jianshu Zhao**, Renmao Tian, Haoran Gui, Jin-Sheng He, Hao Wang, Zhenhua Zhang, Konstantinos T. Konstantinidis, Qun Gao, Yuxin Wang, Shunyi Li, Weishu Zhao, Yunfeng Yang, and Jizhong Zhou. “More sensitive microbial responses to the interactive effects of warming and altered precipitation in subsoil than topsoil of an alpine grassland ecosystem”. In: *Global Change Biology* 30, e17487 (2024). [\[DOI\]](#)
- [J10] Osmar Menezes, Kumru Kocaman, Stanley Wong, Erika E. Rios-Valenciana, Eliot J. Baker, Janet K. Hatt, **Jianshu Zhao**, Camila L. Madeira, Mark J. Krzmarzick, Jim C. Spain, Reyes Sierra-Alvarez, Konstantinos T. Konstantinidis, and Jim A. Field. “Quinone Moieties Link the Microbial Respiration of Natural Organic Matter to the Chemical Reduction of Diverse Nitroaromatic Compounds”. In: *Environmental Science & Technology* 56, 9387–9397 (2022). [\[DOI\]](#)
- [J11] Qi Qi, **Jianshu Zhao**, Renmao Tian, Yufei Zeng, Changyi Xie, Qun Gao, Tianjiao Dai, Hao Wang, Jin-Sheng He, Konstantinos T. Konstantinidis, Yunfeng Yang, Jizhong Zhou, and Xue Guo. “Microbially enhanced methane uptake under warming enlarges ecosystem carbon sink in a Tibetan alpine grassland”. In: *Global Change Biology* 28, 6906–6920 (2022). [\[DOI\]](#)
- [J12] Qi Qi, Yue Haowei, Zhenhua Zhang, Joy D. Van Nostrand, Linwei Wu, Xue Guo, Jiajie Feng, Mengmeng Wang, Sihang Yang, **Jianshu Zhao**, Qun Gao, Qiuting Zhang, Mengxin Zhao, Changyi Xie, Zhiyuan Ma, Jin-Sheng He, Haiyan Chu, Yi Huang, Jizhong Zhou, and Yunfeng Yang. “Microbial Functional Responses Explain Alpine Soil Carbon Fluxes under Future Climate Scenarios”. In: *mBio* 12, e00761–20 (2021). [\[DOI\]](#)
- [J13] Xiaoling Wan, Qun Gao, **Jianshu Zhao**, Jiajie Feng, Joy D. van Nostrand, Yunfeng Yang, and Jizhong Zhou. “Biogeographic patterns of microbial association networks in paddy soil within Eastern China”. In: *Soil Biology and Biochemistry* 142, 107696 (2020). [\[DOI\]](#)
- [J14] **Jianshu Zhao**^{*}, Qun Gao, Jizhong Zhou, Mengmeng Wang, Yuting Liang, Bo Sun, Haiyan Chu, and Yunfeng Yang. “The scale dependence of fungal community distribution in paddy soil driven by stochastic and deterministic processes”. In: *Fungal Ecology* 42, 100856 (2019). [\[DOI\]](#)
- [J15] Qun Gao, Yunfeng Yang, Jiajie Feng, Renmao Tian, Xue Guo, Daliang Ning, Lauren Hale, Mengmeng Wang, Jingmin Cheng, Linwei Wu, Mengxin Zhao, **Jianshu Zhao**, et al. “The spatial scale dependence of diazotrophic and bacterial community assembly in paddy soil”. In: *Global Ecology and Biogeography* 28, 1093–1105 (2019). [\[DOI\]](#)
- [J16] Yan Huang, Li Sun, **Jianshu Zhao**, Rong Huang, Rong Li, and Qirong Shen. “Utilization of different waste proteins to create a novel PGPR-containing bio-organic fertilizer”. In: *Scientific Reports* 5, 7766 (2015). [\[DOI\]](#)
- [J17] Zongzhuan Shen, Shutang Zhong, **Jianshu Zhao**, Jian Zhang, Rong Li, Yunze Ruan, and Qirong Shen. “Effects of ammonia fumigation on soil microflora and banana production in an orchard with serious Fusarium wilt disease”. In: *Acta Ecologica Sinica* 35, 2946–2953 (2015). [\[DOI\]](#)

Selected Publication Notes

- DartUniFrac enables megascale UniFrac computation for microbiome analyses.
- GSearch provides ultra-fast, scalable genome search by combining k-mer hashing and graph-based approximate nearest-neighbor search.
- Rare biosphere work uses population genomes reconstructed from metagenomes to test ecological theory under disturbance.
- Network embedding work accelerates large biological network embedding for genome-scale and single-cell-scale data.

Presentations and Posters

- 2024 Poster: Promiscuous and unbiased recombination underlies the sequence-discrete species of the SAR11 lineage in the deep ocean.
ASM Microbe, Atlanta, GA.
- 2023 Poster: High Performance parallel and concurrent programming for bioinformatics and computational biology.
International Summer School on High Performance Computing, Atlanta, GA.
- 2022 Poster: Time-series metagenomics enables quantification of the rare biosphere to natural disturbances.
ASM Microbe, Washington, DC.

Skills

PROGRAMMING	Rust, Python, Shell, R.
ANALYSIS	GPU programming, statistics, modeling, visualization.
RESEARCH AREAS	Microbial genomics, metagenomics, metatranscriptomics, long-read metagenomics, single-cell genomics, microbiome analysis, biological network embedding.