Xiang Ji, Ph.D.

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Assistant Professor, Department of Mathematics
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Personal Website: http://xiang-ji-ncsu.github.io/
Google Scholar: https://scholar.google.com/citations?user=YH4BbIMAAAAJ&hl=en

EDUCATION

Doctor of Philosophy in Bioinformatics and Statistics (Co-Major) *December 2017*
North Carolina State University, Raleigh, NC
Dissertation: Phylogenetic Approaches for Quantifying Interlocus Gene Conversion
Committee: Jeffrey Thorne, Eric Stone, Nadia Singh, and Sujit Ghosh

Master of Science in Material Science and Engineering *September 2013*
North Carolina State University, Raleigh, NC
Thesis: Laser Interference Lithography for Fabrication of Gas Sensors
Committee: John Muth, Lew Reynolds, Michael Kudenov, and Jon-Paul Maria

Bachelor of Science in Economics (Double Major) *July 2011*
Peking University, Beijing, China

Bachelor of Science in Physics *July 2011*
Peking University, Beijing, China
Advisor: Jia-Sen Zhang

APPOINTMENTS

Faculty Investigator *November 2024 – Present*
Tulane Biostatistics and Bioinformatics Core, Tulane University, New Orleans, LA

Faculty Member *October 2021 – Present*
Cancer Center, Tulane University, New Orleans, LA

Assistant Professor *July 2020 – Present*
Department of Mathematics, Tulane University, New Orleans, LA

Postdoctoral Fellow *January 2018 – July 2020*
University of California, Los Angeles, CA

RESEARCH INTERESTS

Multigene family evolution; cancer systems biology; phylogenetics with large data sets; development of statistical techniques and software

PUBLICATIONS

49. Cong, F., Bao, H., Wang, X., Tang, Y., Bao, Y., Poulton, J., Liu, X., Wong, A., **Ji, X.** and Deng, W. (2025) Gut Bacterial Translocation Promotes Tumor-Associated Mortality by Inducing Immune-Activated Renal Damage. Accepted at *The EMBO Journal*
48. Niu, Q., Jiang, Z., Wang, L., **Ji, X.**, Baele, G., Qin, Y., Lin, L., Lai, A., Chen, Y., Veit, M. and Su, S. (2025) Prevention and control of avian influenza virus: Recent advances in diagnostic technologies and surveillance strategies. *Nature Communications*
47. Baele, G., **Ji, X.**, Hassler, G. W., McCrone, J. T., Shao, Y., Holbrook, A. J., Lemey, P., Drummond, A., Rambaut, A., Suchard, M. A. (2025) BEAST X for Bayesian phylogenetic, phylodynamic and phylogeographic inference. accepted at *Nature Methods*
46. Pekar, J., et al., (2025) The recency and geographical origins of the bat viruses ancestral to SARS-CoV and SARS-CoV-2. Accepted at *Cell*
45. Jiang, Z., Yan, Z., Hou, Y., Tang, J., Zheng, M., Lu, M., **Ji, X.**, Gangavarapu, G., Li, X., and Su, S., (2025). The RodentGPOmics Atlas: a comprehensive database of rodent biology for genomes and pathogens. *Nucleic Acids Research*.
44. Kang, M., Wang, L.F., Sun, B.W., Wan, W.B., **Ji, X.**, Baele, G., Bi, Y.H., Suchard, M.A., Lai, A., Zhang, M., … Su, S., (2024). Zoonotic infections by avian influenza virus: changing global epidemiology, investigation, and control. *The Lancet Infectious Diseases*.
43. Magee, A. F., Holbrook, A. J., Pekar, J. E., Caviedes-Solis, I. W., Matsen IV, F. A., Baele, G., Wertheim, J. O., **Ji, X.**, Lemey, P., and Suchard, M. A., (2024). Random-effects substitution models for phylogenetics via scalable gradient approximations. *Systemic Biology*.
42. Yang, J., Schuemie, M.J., **Ji, X.** and Suchard, M.A., (2024). Massive parallelization of massive sample-size survival analysis. *Journal of Computational and Graphical Statistics*, *33*(1), pp.289-302.
41. Gangavarapu, K., **Ji, X.**, Baele, G., Fourment, M., Lemey, P., Matsen IV, F.A. and Suchard, M.A., (2024). Many-core algorithms for high-dimensional gradients on phylogenetic trees. *Bioinformatics*, *40*(2), p.btae030.
40. Huang, S., He, J., Yu, L., Guo, J., Jiang, S., Sun, Z., Cheng, L., Chen, X., **Ji, X.** and Zhang, Y., (2024). ASTK: A Machine Learning-Based Integrative Software for Alternative Splicing Analysis. *Advanced Intelligent Systems*, p.2300594.
39. Fisher, A., **Ji, X.**, Nishimura, A., & Suchard, M. A. (2023) Shrinkage-based random local clocks with scalable inference. *Molecular Biology and Evolution, 40*(11), msad242.
38. **Ji, X.,** Fisher, A. A., Su, S., Thorne, J. L., Potter, B., Lemey, P., Baele, G., & Suchard, M. A., (2023) Scalable Bayesian divergence time estimation with ratio transformations. *Systematic Biology*, syad039, arXiv preprint arXiv:2110.13298.
37. Yang, Y., Xu, T., Conant, G., Kishino, H., Thorne, J.L. and **Ji, X.**, (2023) Interlocus Gene Conversion, Natural Selection, and Paralog Homogenization. *Molecular Biology and Evolution*, msad198.
36. Matteson, N. L., et al., (2023) Genomic surveillance reveals dynamic shifts in the connectivity of COVID-19 epidemics. *Cell*, 186(26), pp.5690-5704.
35. He, W.T., Li, D., Baele, G., Zhao, J., Jiang, Z., **Ji, X.**, Veit, M., Suchard, M.A., Holmes, E.C., Lemey, P., Boni, M.F. and Su, S., (2023) Newly identified lineages of porcine

hemagglutinating encephalomyelitis virus exhibit respiratory phenotype. *Virus Evolution*, *9*(2), p.vead051.

34. Zhang, Z., Nishimura, A., Trovão, N.S., Cherry, J.L., Holbrook, A.J., **Ji, X.**, Lemey, P. and Suchard, M.A., (2023) Accelerating Bayesian inference of dependency between mixed-type biological traits. *PLOS Computational Biology*, *19*(8), p.e1011419.
33. Zhao, J., Kang, M., Wu, H., Sun, B., Baele, G., He, W.T., Lu, M., Suchard, M.A., **Ji, X.**, He, N. and Su, S., (2023) Risk assessment of SARS-CoV-2 replicating and evolving in animals. *Trends in Microbiology*.
32. Zhao, J., Dellicour, S., Yan, Z., Veit, M., Gill, M.S., He, WT, Zhai, X., **Ji, X.**, Suchard, M.A., Lemey, P. and Su, S., (2023) Early Genomic Surveillance and Phylogeographic Analysis of Getah Virus, a Reemerging Arbovirus, in Livestock in China. *Journal of Virology*, *97*(1), pp.e01091-22.
31. Tsui, L.H., et al., (2023) Genomic assessment of invasion dynamics of SARS-CoV-2 Omicron BA. 1. *Science*, *381*(6655), pp.336-343.
30. Hassler, G.W., Magee, A.F., Zhang, Z., Baele, G., Lemey, P., **Ji, X.**, Fourment, M. and Suchard, M.A., (2023) Data Integration in Bayesian Phylogenetics. *Annual Review of Statistics and Its Application*, 10, pp.353-377.
29. Fisher, A. A., Hassler, G. W., **Ji, X.**, Baele, G., Suchard, M. A., & Lemey, P. (2022) Scalable Bayesian phylogenetics. *Philosophical Transactions of the Royal Society B*, 377.1861(2022): 20210242.
28. Zhao, J., Dellicour, S., Yan, Z., Veit, M., Gill, M.S., He, WT, Zhai, X., **Ji, X.**, Suchard, M.A., Lemey, P. and Su, S., (2022) Early Genomic Surveillance and Phylogeographic Analysis of Getah Virus, a Reemerging Arbovirus, in Livestock in China. *Journal of Virology*, pp.e01091-22.
27. Holbrook, A. J., **Ji, X.**, & Suchard, M. A. (2022) From viral evolution to spatial contagion: a biologically modulated Hawkes model. *Bioinformatics*, 38(7), pp.1846-1856. arXiv:2103.03348 [stat.ME]
26. McCrone, J.T., Hill, V., Bajaj, S. et al. (2022) Context-specific emergence and growth of the SARS-CoV-2 Delta variant. *Nature*, 610(7930), pp.154-160.
25. He, W., et al., (2022). Virome characterization of game animals in China reveals a spectrum of emerging pathogens. *Cell,* 185(7), 1117-1129.
24. Tian, J., Sun, J., Li, D., Wang, N., Wang, L., Zhang, C., Meng, X., **Ji, X.**, Suchard, M. A., Zhang, X., Lai, A., Su, S., & Veit, M. (2022) Emerging viruses: Cross-species transmission of Coronaviruses, Filoviruses, Henipaviruses and Rotaviruses from bats. *Cell Reports*
23. Zhao, J., Sun, J., Li, X., Xing, G., Zhang, Y., Lai, A., Baele, G.*, **Ji, X.*,** Su, S.* (2022). Divergent Viruses Discovered in Swine Alter the Understanding of Evolutionary History and Genetic Diversity of the Respirovirus Genus and Related Porcine Parainfluenza Viruses. *Microbiology Spectrum*,10(3), pp.e00242-22. *Senior author
22. He, W., et al., (2022) Phylogeography reveals association between swine trade and the spread of porcine epidemic diarrhea virus in China and across the world. *Molecular Biology and Evolution, 39(2), msab364*
21. Fan, Y., et al. (2022). Systematic analysis of inflammation and pain pathways in a mouse model of gout. *Molecular Pain*, 18, 17448069221097760.

20. Xie, S., et al. (2022). Disrupted myelination network in the cingulate cortex of Parkinson's disease. *IET Systems Biology*, 16(3-4), pp.98-119.
19. Holbrook, A. J., **Ji, X.**, & Suchard, M. A. (2022) Bayesian mitigation of spatial coarsening for a fairly flexible spatiotemporal Hawkes model. *Annals of Applied Statistics*, 16 (1), 573-595.
18. Holbrook, A. J., Nishimura, A., **Ji, X.**, & Suchard, M. A. (2021). Computational Statistics and Data Science in the Twenty-first Century. *Wiley StatsRef: Statistics Reference Online.* arXiv preprint arXiv:2204.05530.
17. Lemey, P., et al., (2021) Untangling introductions and persistence in COVID-19 resurgence in Europe. *Nature,* 595 (7869), 713-717.
16. Landeros, A., **Ji, X.**, Lange, K., Stutz, T. C., Xu, J., Sehl, M. E., & Sinsheimer, J. S. (2021) An examination of school reopening strategies during the SARS-CoV-2 pandemic. *PloS One*, 16(5), e0251242.
15. Zhang, Z., Nishimura, A., Bastide, P., **Ji, X.**, Payne, R. P., Goulder, P., ... & Suchard, M. A. (2021). Large-scale inference of correlation among mixed-type biological traits with phylogenetic multivariate probit models. *The Annals of Applied Statistics*, 15(1), 230-251.
14. Lindelof, K., Lindo, J. A., Zhou, W., **Ji, X.**, & Xiang, Q. Y. J. (2020) Phylogenomics, biogeography, and evolution of the blue- or white-fruited dogwoods (Cornus) - insights into morphological and ecological niche divergence following intercontinental geographic isolation. *Journal of Systematics and Evolution*, 58(5), pp.604-645.
13. Sun, J., He, W. T., Wang, L., Lai, A., **Ji, X.**, Zhai, X., ... & Veit, M. (2020). COVID-19: epidemiology, evolution, and cross-disciplinary perspectives. *Trends in Molecular Medicine*, 26(5), pp.483-495.
12. He, W.*, **Ji, X.***, He, W. *, Dellicour, S. *, …, & Su, S. (2020) Genomic epidemiology, evolutionary dynamics, and transmission patterns of porcine deltacoronavirus. *Molecular Biology and Evolution*, 37(9), pp.2641-2654. *equal contribution
11. **Ji, X.**, Zhang, Z., Holbrook, A., Nishimura, A., Baele, G., Rambaut, A., Lemey, P., & Suchard, M. A. (2020) Gradients *do* grow on trees: a linear-time O(N)-dimensional gradient for statistical phylogenetics. *Molecular Biology and Evolution*, 37(10), pp.3047-3060. arXiv:1905.12146 [stat.CO]
10. Fisher, A., **Ji, X.**, Zhang, Z., Lemey, P., & Suchard, M. A. (2020) Relaxed random walks at scale. *Systematic Biology*, 70(2), pp.258-267. arXiv:1906.04834[q-bio.PE]
9. Blestsa, M., Suchard, M. A., **Ji, X.**, Gryseels, S., Vrancken, B., Baele, G., Worobey, M., & Lemey, P. (2019) Divergence dating using mixed effects clock modelling: an application to HIV-1. *Virus Evolution*, 5(2), vez036.
8. Li, G., Zhang, W., Wang, R., Xing, G., Wang, S., **Ji, X.**, ... & Zhou, J. (2019). Genetic Analysis and Evolutionary Changes of the Torque teno sus Virus. *International journal of molecular sciences*, 20(12), 2881.
7. Zhou, W., **Ji, X.**, Obata, S., Pais, A., Dong, Y., Peet, R., & Xiang, Q., (2018) Resolving relationships and phylogeographic history of the Nyssa sylvatica complex using data from RAD-seq and species distribution modeling. *Molecular Phylogenetic and Evolution*, 126, 1-16.

6. **Ji, X.** (2017). Phylogenetic approaches for quantifying interlocus gene conversion. Doctoral Dissertation
5. **Ji, X.**, Griffing, A., & Thorne, J. L. (2016). A phylogenetic approach finds abundant interlocus gene conversion in yeast. *Molecular Biology and Evolution*, 33(9), 2469-2476.
4. Wang, K., Yu, S., **Ji, X.**, Lakner, C., Griffing, A., & Thorne, J. L. (2015). Roles of Solvent Accessibility and Gene Expression in Modeling Protein Sequence Evolution. *Evolutionary Bioinformatics*, 11, 85.
3. **Ji, X.** (2013). Laser Interference Lithography for Fabrication of Gas Sensors. Master Thesis
2. Han, X., **Ji, X.**, Wen, H., & Zhang, J. (2012). H-shaped resonant optical antennas with slot coupling. *Plasmonics*, 7(1), 7-11.
1. Xiao, G., **Ji, X.**, Gao, L., Wang, X., & Zhou, Z. (2012). Effect of dipole location on profile properties of symmetric surface plasmon polariton mode in Au/Al2O3/Au waveguide. *Frontiers of Optoelectronics*, 5(1), 63-67.

Articles in Submission and Preparation

4. Baele, G., Carvalho, L. M., Brusselmans, M., Dudas, G., **Ji, X.**, McCrone, J. T., Lemey, P., Suchard, M. A. and Rambaut, A. (2024) HIPSTR: highest independent posterior subtree reconstruction in TreeAnnotator X. *In review with Bioinformatics*
3. Bao, Y., Deng, W., Su, S., Lemey, P., Suchard, M. A., Glatt-Holtz, N.*, & **Ji, X.*** (2024) Reflection Hamiltonian Monte Carlo for divergence time estimations. *Senior author. *In preparation*
2. **Ji, X.**, Redelings, B., Su, S., Deng, W., Thorne, J. L., Lemey, P., & Suchard, M. A. (2024) Branch-specific substitution models for identifying natural selection differences via shrinkage priors. *In preparation*
1. **Ji, X.**, Thorne, J. L. (2024) A phylogenetic approach disentangles the tract length and initiation rate of interlocus gene conversions. *In wait/delay for submission*, arXiv:1908.08608 [q-bio.PE]

TEACHING EXPERIENCE

Assistant Professor

Department of Mathematics, Tulane University, New Orleans, LA

Summary: I regularly teach graduate-level Math 7260 (Linear Models) and Math 7360 (Data Analyses, a Tulane version of statistical learning), and undergraduate-level Math 3070 (Intro to Probability). Periodically, I teach Math 1230 Stats for Scientists, which is designed for students with non-math majors.

- Spring 2025
  - ***Math 6040/7260 Linear Models (3 credits)***
    GitHub site: https://tulane-math-7260-2025.github.io/
    Level: Graduate (Master + Ph.D.)
    Topics: Simple and multiple linear regressions, hypothesis testing, analysis of variance, bootstrap, logistic regression
    Enrollment: 7
- Fall 2024

- ***Math 1230 Stats for Scientists (3 credits)***
  Level: Undergraduate
  Topics: Probability, random variable, discrete and continuous distributions, sampling distributions, one and two-sample estimations, hypothesis testing, simple linear regression
  Enrollment: 62
- ***Math 3070/6070 Intro to Probability (3 credits)***
  GitHub site: https://tulane-math-3070-2024.github.io/
  Level: Undergraduate, Graduate (Master)
  Topics: Axioms of probability, discrete and continuous random variables, multivariate distributions, expectation, limit theorem
  Enrollment: 33

- Spring 2024
  Teaching Relief
- Fall 2023
  - ***Math 7360 Data Analysis (3 credits)***
    GitHub site: https://tulane-math-7360-2023.github.io/
    Level: Graduate (Master + Ph.D.)
    Topics: R, RMarkdown, Rcpp, git, data visualization using ggplot2, web scraping, linear models, generalized linear models, neural network, classification
    Enrollment: 22
  - ***Math 3070/6070 Intro to Probability (3 credits)***
    GitHub site: https://tulane-math-3070-2023.github.io/
    Level: Undergraduate, Graduate (Master)
    Topics: Axioms of probability, discrete and continuous random variables, multivariate distributions, expectation, limit theorem
    Enrollment: 48
- Spring 2023
  - ***Math 6040/7260 Linear Models (3 credits)***
    GitHub site: https://tulane-math-7260-2023.github.io/
    Level: Graduate (Master + Ph.D.)
    Topics: Simple and multiple linear regressions, hypothesis testing, analysis of variance, bootstrap, logistic regression
    Enrollment: 13
  - ***Math 7980 Independent Study (3 credits)***
    Level: Graduate (Master)
    Topics: Item response theory models
    Enrollment: 1
- Fall 2022
  - ***Math 3070/6070 Intro to Probability (3 credits)***
    GitHub site: https://tulane-math-3070-2022.github.io/
    Level: Undergraduate, Graduate (Master)

Topics: Axioms of probability, discrete and continuous random variables, multivariate distributions, expectation, limit theorem
Enrollment: 37

- ***Math 1230 Stats for Scientists (3 credits)***
  Level: Undergraduate
  Topics: Probability, random variable, discrete and continuous distributions, sampling distributions, one and two-sample estimations, hypothesis testing, simple linear regression
  Enrollment: 66
- ***Math 7980 Independent Study (3 credits)***
  Level: Graduate (Ph.D.)
  Topics: Bayesian Phylogenetics
  Enrollment: 1

- Spring 2022
  - ***Math 6040/7260 Linear Models (3 credits)***
    GitHub site: https://tulane-math-7260-2022.github.io/
    Level: Graduate (Master + Ph.D.)
    Topics: Simple and multiple linear regressions, hypothesis testing, analysis of variance, bootstrap, logistic regression
    Enrollment: 16
  - ***Math 7980 Independent Study (3 credits)***
    Level: Graduate (Master)
    Topics: Review of optimization methods
    Enrollment: 1
- Fall 2021
  - ***Math 7360 Data Analysis (3 credits)***
    GitHub sites: https://tulane-math-7360-2021.github.io/
    Level: Graduate (Master + Ph.D.)
    Topics: R, RMarkdown, Rcpp, git, data visualization using ggplot2, web scraping, linear models, generalized linear models, neural network, classification
    Enrollment: 19
- Spring 2021
  - ***Math 6040/7260 Linear Models (3 credits)***
    GitHub site: https://tulane-math-7260-2021.github.io/
    Level: Graduate (Master + Ph.D.)
    Topics: Simple and multiple linear regressions, hypothesis testing, analysis of variance, bootstrap, logistic regression
    Enrollment: 17
- Fall 2020
  - ***Math 7360 Data Analysis (3 credits)***
    GitHub site: https://tulane-math7360.github.io/
    Level: Graduate (Master + Ph.D.)

Topics: R, RMarkdown, Rcpp, git, data visualization using ggplot2, web scraping, linear models, generalized linear models, neural network, classification
Enrollment: 12

STUDENT ADVISING

Co-Supervisor (Doctoral) *2024 – Present*
Department of Microbiology and Immunology, The University of Melbourne
Melbourne, Australia

- Student name: John Tay
- Supervisor: Sebastian Duchene
- Research Title: TBD

Committee Chair (Doctoral) *2023 – Present*
Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Yufei Zou
- Research Title: Evolutionary inference with interlocus gene conversion

Committee Chair (Doctoral) *2022 – Present*
Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Yuwei Bao
- Research Title: Reflective Hamiltonian Monte Carlo method

Prospectus Exam Committee Chair (Doctoral) *2025*
Department of Mathematics, Tulane University, New Orleans, LA

- Student name: John Argentino
- Chair: Michelle Lacey
- Research title: Multivariate Modeling Techniques for Estimating Assistance Impacts from Daily Food Security Surveys

Dissertation Defense Committee Member (Doctoral) *2025*
Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Linh Do
- Chair: Scott McKinley

Research title: Statistical techniques for comparing populations of continuous piecewise-linear stochastic processes

Prospectus Exam Committee Chair (Doctoral) *2024*
Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Yuwei Bao
- Chair: Xiang Ji
- Research title: Scalable Bayesian statistical phylogenetics models

Dissertation Defense Committee Member (Doctoral) *2024*
Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Daniela A. Florez Pineda
- Chair: Ricardo Cortez

Oral Exam Committee Member (Doctoral) *2024*

Department of Mathematics, Tulane University, New Orleans, LA

- Student name: John V. Argentino
- Chair: Michelle Lacey

Prospectus Exam Committee Member (Doctoral) *2024*

Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Daniela A. Florez Pineda
- Chair: Ricardo Cortez
- Research title: Mathematical models for transmission and control of mosquito-borne diseases

Prospectus Exam Committee Member (Doctoral) *2023*

Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Linh Do
- Chair: Scott McKinley
- Research title: Statistical techniques for comparing populations of continuous piecewise-linear stochastic processes

Oral Exam Committee Member (Doctoral) *2023*

Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Moslem Uddin
- Chair: Lisa Fauci

Oral Exam Committee Chair (Doctoral) *2023*

Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Yuwei Bao
- Chair: Xiang Ji

Oral Exam Committee Member (Doctoral) *2023*

Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Sinchita Lahiri
- Chair: Kyle Kun Zhao

Oral Exam Committee Member (Doctoral) *2022*

Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Linh Do
- Chair: Scott McKinley

Oral Exam Committee Member (Doctoral) *2022*

Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Daniela A. Florez Pineda
- Chair: Ricardo Cortez

Independent Study Advisor (Master) *2022*

Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Paul Pluscht
- Project topic: Review of optimization methods

Undergraduate Research Advisor (Undergraduate) *2020 – 2022*

Department of Statistics, North Carolina State University, Raleigh, NC

- Student name: Yixuan Yang
- Co-advisor: Jeffrey L. Thorne
- Research topic: Quantifying interlocus gene conversion and natural selection

Undergraduate Research Advisor (Undergraduate) *2021*

Department of Mathematics, Tulane University, New Orleans, LA

- Student name: Jiayun Ling
- Co-advisor: Xin Jiang
- Research topic: Item response theory model, Add Health data, social science

MENTEE ACHIEVEMENTS

Megan (Jiayun) Ling (undergraduate research advisor) *2021*

- Oral presentation at ASA Louisiana Chapter meeting in 2021
- Graduated from master's program in Data Analytics of Duke University
- Now working as Data Analyst at Blizzard Entertainment

Yuwei Bao (PhD thesis advisor) *2022 – Present*

- Oral presentation at ASA Louisiana Chapter meeting in 2022
- Oral presentation at Tulane Math Graduate Student Colloquium in 2022
- Oral presentation at Evolution Meeting 2023
- Oral presentation at Scientific Computing Around Louisiana Meeting 2023
- Oral presentation at Math for All in Nola meeting 2023
- Poster presentation at New England Statistical Symposium 2024
- Poster presentation at Pharmaceutical Data Science Conference online 2024
- Poster presentation at ASA Conference on Statistical Practice 2024
- Tuition Scholarship & Travel Award at Summer Institute in Statistical Genetics 2023
- Travel Award from Society for Study of Evolution at Evolution Meeting 2023
- Summer Research Fund from Math Department at Tulane University 2023
- Travel Award from Graduate Studies Student Association at Tulane University 2023 & 2024
- Student Poster Award at New England Statistical Symposium 2024
- FDA-OCE-ASA Oncology Educational Fellow 2024
- Internship at Moderna Spring 2025

Yufei Zou (undergraduate research & PhD thesis advisor) *2022 – Present*

- Tuition Scholarship & Travel Award at Summer Institute in Statistical Genetics 2023

AWARDS

HPC Fund Research Cloud Allocation Award[1]	AMD Corporation	2023
NVIDIA Academic Hardware Grant[2]	NVIDIA Corporation	2022

[1] 1,080 node hours (targeting 4 MI100 GPUs/node)
[2] Donation of one A100 80Gb PCIE GPU card

Tuition Scholarship	SISMID[3]	2018
NIEHS Fellowship[4]	North Carolina State University	2015
SAMSI Graduate Fellow	SAMSI[5]	2014
Tuition Scholarship	SISG[6]	2013
University Graduate Fellowship	North Carolina State University	2011

FUNDED PROJECTS

External

Louisiana Board of Regents Research Competitiveness Subprogram 07/01/23 – 06/30/26

- Title: Molecular epidemiology through scalable statistical phylogenetic Modelling
- Principle Investigator: Xiang Ji
- Total Amount: $159,000
- Direct Cost: $159,000

National Science Foundation 05/01/23 – 07/31/24

- Title: Evolutionary inference with interlocus gene conversion
- Principle Investigator: Jeffrey L. Thorne
- Co-Investigator: Xiang Ji
- Award number: DEB1754142
- Total Amount: $564,338
- Shared Amount: $94,351

National Institute of Health 07/01/22 – 03/31/25

- Title: Statistical innovation to integrate sequences and phenotypes for scalable phylodynamic inference
- Principle Investigator: Marc A. Suchard
- Subaward Investigator: Xiang Ji
- Award number: R01AI153044
- Total Amount: $2,321,335
- Shared Amount: $117,259

National Institute of Health 04/01/22 – 03/31/27

- Title: Notch signaling and germline-soma interactions in *Drosophila* ovarian model
- Principle Investigator: Wu-Min Deng
- Co-Investigator: Xiang Ji
- Award number: R01GM072562
- Total Amount: $ 2,432,208
- Shared Amount: $86,460

[3] SISMID: Summer Institute in Statistics and Modeling in Infectious Diseases at the University of Washington at Seattle
[4] The funds were matched through North Carolina State University
[5] SAMSI: The Statistical and Applied Mathematical Sciences Institute
[6] SISG: Summer Institute in Statistical Genetics at the University of Washington at Seattle

National Institute of Health 02/01/20 – 01/31/22

- Title: Consortium for viral systems biology (CViSB)
- Principle Investigator: Robert F. Garry
- Co-Investigator: Xiang Ji
- Award number: U19AI135995
- Total Amount: $1,143,554
- Shared Amount: $51,774

Internal

Tulane University CoR Research Fellowship 05/01/23 – 05/31/24

- Title: Scalable molecular epidemiology models
- Principle Investigator: Xiang Ji
- Total Amount: $5,500

SUBMITTED PROPOSALS

National Institute of Health 2025

- Title: Statistical innovation to integrate sequences and phenotypes for scalable phylodynamic inference
- Principle Investigator: Marc A. Suchard
- Subaward Investigators: Xiang Ji
- Total Amount: $1,833,000
- Shared Amount: $204,805
- Status: Pending

National Institute of Health 2025

- Title: COBRE for Basic and Translational Research in Cancer (BATRIC)
- Principle Investigator: Wu-Min Deng
- Core Co-Director: Xiang Ji
- Total Amount: $11,420,264
- Shared Amount: $86,460
- Status: Pending

National Science Foundation 2025

- Title: FEC: Identifying factors that mitigate the effect of poverty on child brain development using computational neural fingerprinting techniques
- Principle Investigator: Yu-ping Wang
- Co-Investigators: Xiang Ji
- Total Amount: $4,000,000
- Shared Amount: $20,000
- Status: Pending

National Institute of Health 2025

- Title: Scalable statistical advances to quantify interlocus gene conversion in multigene family evolution
- Principle Investigator: Xiang Ji
- Co-Investigators: None
- Total Amount: $1,833,000
- Status: Pending

National Science Foundation 2024

- Title: Scalable phylogenomic inference through massively parallelized action-based BEAGLE library
- Principle Investigator: Xiang Ji
- Co-Investigators: Robert F. Garry and Marc A. Suchard
- Total Amount: $1,600,775
- Status: Pending

National Institute of Health 2024

- Title: Tracking and controlling viral outbreaks through scalable biologically realistic phylodynamic integrations
- Principle Investigator: Xiang Ji
- Co-Investigators: Robert F. Garry and Marc A. Suchard
- Total Amount: $2,693,909
- Status: Pending

National Institute of Health 2024

- Title: Characterizing intra- and inter-host Nov evolution using human challenge study samples
- Principle Investigator: Pengbo Liu
- Subaward Investigators: Xiang Ji
- Shared Amount: $120,018
- Status: Pending

CONFERENCE PRESENTATIONS

Upcoming Conference Presentations

6 **Ji, X.** (2025, October) *Scalable phylogenetic inference with Hamiltonian Monte Carlo method*. Statistics and AI in Precision Health and Biology, AMS Sectional Meeting, Tulane University, New Orleans, LA

5 **Ji, X.** (2025, August) *Quantitative traits on massive trees with many incomplete measurements*. JSM 2025, Nashville, TN

4 **Ji, X.** (2025, June) *Action-based phylogenetic likelihood calculations for large state-space models*. Evolution 2025 Meeting, University of Georgia, Athens, GA

3 **Ji, X.** (2025, June) *Scalable phylogenetic inference with Hamiltonian Monte Carlo method*. 2025 International Indian Statistical Association Conference, University of Nebraska-Lincoln, Lincoln, NE

2 **Ji, X.** (2025, May) *Scalable phylogenetic inference*. STATGEN 2025: Conference on Statistics in Genomics and Genetics, ASA Section on Statistics in Genomics and Genetics, University of Minnesota, Minneapolis, MN

1 **Ji, X.** (2025, May) *Action–based phylogenetic likelihood calculations for large state– space models.* 2025 Spring ASA Louisiana Chapter Meeting, LSU Health Science Center, New Orleans, LA

Oral Presentations

6 **Ji, X.** (2023, June) Scalable phylogenetic inference with Hamiltonian Monte Carlo method. Evolution 2023 meeting, Albuquerque, NM

5 **Ji, X.** (2023, March) *Scalable phylogenetic inference*. SCALA 2023: Scientific Computing Around Louisiana, Tulane University, New Orleans, LA

4 **Ji, X.** (2021, August) *Divergence time estimation with Hamiltonian Monte Carlo sampling and ratio transform*. Invited speaker at 2nd AsiaEvo Conference, Online

3 **Ji, X.** (2021, July) *Divergence time estimation with Hamiltonian Monte Carlo sampling and ratio transform*. Society of Molecular Biology and Evolution Meeting, Online

2 **Ji, X.** (2018, September) *Large-scale molecular epidemiology for viruses: efficient algorithms and new models.* Oral session presented at the Taishan Forum on Viral Infectious Diseases, Taishan Medical University, Tai'an, Shandong Province, China

1 **Ji, X.** (2017, August) *Phylogenetic approaches for quantifying interlocus gene conversion.* Quest for Ortholog 5 Meeting, University of Southern California, Los Angeles, CA

Poster Presentations

2 **Ji, X.** (2017, July). *Phylogenetic approaches for quantifying interlocus gene conversion.* Society of Molecular Biology and Evolution Meeting, Austin, TX

1 **Ji, X.** (2014, June). *A Phylogenetic approach for quantifying interlocus gene conversion.* Evolution Meeting, Raleigh, NC

INVITED TALKS

15	Scalable phylogenetic Hamiltonian Monte Carlo method and its application in molecular epidemiology *Iowa State University, Ames, IA*	03/05/2025
14	Scalable phylogenetic Hamiltonian Monte Carlo method and its application in divergence time estimations *Southeastern Louisiana University, Hammond, LA*	08/29/2024
13	Phylogenetic approach for estimating amounts of interlocus gene conversion in duplications *AMS/AWM at Tulane University, New Orleans, LA*	12/06/2023
12	Scalable phylogenetic inference via Hamiltonian Monte Carlo method *Indiana University, Bloomington, IN*	02/03/2023
11	Scalable phylogenetic algorithm, modeling, and inference *North Carolina State University, Raleigh, NC*	10/10/2022
10	Smooth non-parametric coalescent priors for scalable divergence time estimations	10/05/2022

	AMS/AWM at Tulane University, New Orleans, LA	
9	Scalable modeling and inference for phylogenetics – from interlocus gene conversion to evolving pathogens *Tulane University, New Orleans, LA*	12/04/2019
8	Scalable modeling and inference for phylogenetics – from interlocus gene conversion to evolving pathogens *Louisiana State University, Baton Rouge, LA*	11/04/2019
7	Large-scale molecular epidemiology for viruses *University of California, Los Angeles, CA*	11/08/2018
6	Phylogenetic approaches for quantifying interlocus gene conversion *Zhejiang University, Hangzhou, China*	09/18/2018
5	Phylogenetic approaches for quantifying interlocus gene conversion *Chinese Academy of Sciences, Beijing, China*	09/04/2018
4	Phylogenetic approaches for quantifying interlocus gene conversion *CGM Online*	05/30/2018
3	Phylogenetic approaches for quantifying interlocus gene conversion *Duke University, Durham, NC*	02/15/2018
2	Phylogenetic approaches for quantifying interlocus gene conversion *Temple University, Philadelphia, PA*	04/25/2017
1	Phylogenetic approaches for quantifying interlocus gene conversion *North Carolina State University, Raleigh, NC*	03/24/2017

SOFTWARE

IGCexpansion

- My software for studying interlocus gene conversion.
- Available at https://github.com/xji3/IGCexpansion.

IGC BEAST Tutorial

- A tutorial for the Bayesian method (under development) of quantifying interlocus gene conversion in BEAST.
- Available at https://github.com/xji3/IGC_BEAST_Tutorial.

BEAST X

- I am a developer of the BEAST X software package.
- Available at https://github.com/beast-dev/beast-mcmc.

BEAGLE

- I am a developer of the BEAGLE library.
- Available at https://github.com/beagle-dev/beagle-lib.

Bito

- I collaborate with a group of statisticians and programmers to help them use my linear-time gradient algorithm implementations for their variational Bayesian phylogenetics development.
- Available at https://github.com/phylovi/bito.

SYNERGISTIC ACTIVITIES

Grant Panelist

- I served as a guest panel member for the UK MRC Better Methods, Better Research (BMBR) Panel in 2023.

Professional service

- I serve as an Editorial Board member for *Discover Viruses* by *Springer Nature.*
- I serve as a Review Editor for *Frontiers in Statistical Genetics and Methodology.*
- I have reviewed manuscripts for
    - *Nature Medicine* (2)
    - *Proceedings of National Academy of Sciences* (2)
    - *Molecular Biology and Evolution* (9)
    - *Annals of Applied Statistics* (2)
    - *Journal of Computational and Graphical Statistics (1)*
    - *Theoretical Population Biology (1)*
    - *The American Journal of Human Genetics (1)*
    - *Plos Pathogens (1)*
    - *Microbiology Spectrum (1)*
    - *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (1)
    - *Frontiers in Public Health* (2)
    - *Frontiers in Virology (2)*
    - *BMC Ecology and Evolution (1)*
    - *Evolutionary Bioinformatics* (2)
    - *International Journal of Data Mining and Bioinformatics* (1)
    - *Rapid Reviews: COVID-19* (1)
    - *Open Veterinary Journal (1)*

Departmental service

- I led the development and establishment of a new Master of Science in Data Science program jointly hosted by the Math and Computer Science Departments at Tulane University.
- I served as the Director of Master Programs of the Math Department at Tulane University from Fall 2021 to Spring 2024.
- I served on the Graduate Study Committee of the Math Department at Tulane University from Fall 2021 to Spring 2024.
- I ran a tutorial workshop on building personal website for graduate students in the Math Department on 04/05/2022 (tutorial link: xji3.github.io/Tutorial).
- I served on the College of Science & Engineering Cypress HPC committee as the representative for the Math Department in Spring 2025.

Outreach

- I participated in the LA FIRST Lego League State Championship as a volunteer judge in January 2023.
- I participated in Boys at Tulane in STEM (BATS) and Girls in STEM at Tulane (GIST), organized by Tulane Center for K-12 System Education
    - Volunteer, Boys at Tulane in STEM (BATS), 03/18/2023

    - Volunteer, Boys at Tulane in STEM (BATS), 09/16/2023
    - Volunteer, Girls in STEM at Tulane (GiST), 11/04/2023
    - Volunteer, Girls in STEM at Tulane (GiST), 03/09/2024
    - Volunteer, Boys at Tulane in STEM (BATS), 04/13/2024
    - Volunteer, Boys at Tulane in STEM (BATS), 09/21/2024
    - Volunteer, Girls in STEM at Tulane (GiST), 10/26/2024
    - Volunteer, Boys at Tulane in STEM (BATS), 02/01/2025
    - Volunteer, Girls in STEM at Tulane (GiST), 03/22/2025
- I served as treasurer of the ASSIST[7] Student Leadership Council in 2012 and 2013. I participated in the Magnet Fair at South Raleigh Magnet High School as an ASSIST center graduate representative in 2012.

[7] ASSIST: The NSF Center for Advanced Self-Powered Systems of Integrated Sensors and Technologies at NC State University