

Xiang Ji, Ph.D.

Last Updated on 12/06/2024

Assistant Professor, Department of Mathematics

Tulane University, New Orleans, LA, 70118

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Personal Website: <http://xiang-ji-ncsu.github.io/>

Google Scholar: <https://scholar.google.com/citations?user=YH4BbIMAAAJ&hl=en>



EDUCATION

Doctor of Philosophy in Bioinformatics and Statistics (Co-Major)

December

North Carolina State University, Raleigh, NC

2017

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

North Carolina State University, Raleigh, NC

2013

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 (Double Major)

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

46. Pekar, J., et al., (2024) 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., (2024). The RodentGPOMics Atlas: a comprehensive database of rodent biology for genomes and pathogens. Accepted at *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*. In press.
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.btac030.
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 Respirivirus 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

7. 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*
6. Baele, G., **Ji, X.**, Hassler, G. W., McCrone, J. T., Shao, Y., Holbrook, A. J., Lemey, P., Drummond, A., Rambaut, A., Suchard, M. A. (2024) BEAST X for Bayesian phylogenetic, phylodynamic and phylogeographic inference. *In revision at Nature Methods*
5. Cong, F., Bao, H., Wang, X., Tang, Y., Bao, Y., Poulton, J., Liu, X., Wong, A., **Ji, X.** and Deng, W. (2024) Gut Bacterial Translocation Promotes Tumor-Associated Mortality by Inducing Immune-Activated Renal Damage. *In review with Immunity*
4. Niu, Q., Jiang, Z., Wang, L., **Ji, X.**, Baele, G., Qin, Y., Lin, L., Lai, A., Chen, Y., Veit, M. and Su, S. (2024) Avian influenza virus: recent advances in diagnostics and mitigation strategies. *In revision with Nature Communications*
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.

- 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: 70

- ***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: 35
- 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) <i>Department of Microbiology and Immunology, The University of Melbourne Melbourne, Australia</i> <ul style="list-style-type: none"> • Student name: John Tay • Supervisor: Sebastian Duchene • Research Title: TBD 	2024 – Present
Committee Chair (Doctoral) <i>Department of Mathematics, Tulane University, New Orleans, LA</i> <ul style="list-style-type: none"> • Student name: Yufei Zou • Research Title: Evolutionary inference with interlocus gene conversion 	2023 – Present
Committee Chair (Doctoral) <i>Department of Mathematics, Tulane University, New Orleans, LA</i> <ul style="list-style-type: none"> • Student name: Yuwei Bao • Research Title: Reflective Hamiltonian Monte Carlo method 	2022 – Present
Prospectus Exam Committee Chair (Doctoral) <i>Department of Mathematics, Tulane University, New Orleans, LA</i> <ul style="list-style-type: none"> • Student name: Yuwei Bao • Research title: Scalable Bayesian statistical phylogenetics models 	2024
Dissertation Defense Committee Member (Doctoral) <i>Department of Mathematics, Tulane University, New Orleans, LA</i> <ul style="list-style-type: none"> • Student name: Daniela A. Florez Pineda • Chair: Ricardo Cortez 	2024
Oral Exam Committee Member (Doctoral) <i>Department of Mathematics, Tulane University, New Orleans, LA</i> <ul style="list-style-type: none"> • Student name: John V. Argentino • Chair: Michelle Lacey 	2024
Prospectus Exam Committee Member (Doctoral) <i>Department of Mathematics, Tulane University, New Orleans, LA</i> <ul style="list-style-type: none"> • Student name: Daniela A. Florez Pineda • Chair: Ricardo Cortez • Research title: Mathematical models for transmission and control of mosquito-borne diseases 	2024
Prospectus Exam Committee Member (Doctoral) <i>Department of Mathematics, Tulane University, New Orleans, LA</i> <ul style="list-style-type: none"> • Student name: Linh Do • Chair: Scott McKinley • Research title: Statistical techniques for comparing populations of continuous piecewise-linear stochastic processes 	2023
Oral Exam Committee Member (Doctoral) <i>Department of Mathematics, Tulane University, New Orleans, LA</i> <ul style="list-style-type: none"> • Student name: Moslem Uddin 	2023

<ul style="list-style-type: none"> Chair: Lisa Fauci 	
Oral Exam Committee Chair (Doctoral)	2023
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> Student name: Yuwei Bao Chair: Xiang Ji 	
Oral Exam Committee Member (Doctoral)	2023
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> Student name: Sinchita Lahiri Chair: Kyle Kun Zhao 	
Oral Exam Committee Member (Doctoral)	2022
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> Student name: Linh Do Chair: Scott McKinley 	
Oral Exam Committee Member (Doctoral)	2022
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> Student name: Daniela A. Florez Pineda Chair: Ricardo Cortez 	
Independent Study Advisor (Master)	2022
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> Student name: Paul Pluscht Project topic: Review of optimization methods 	
Undergraduate Research Advisor (Undergraduate)	2020 –
<i>Department of Statistics, North Carolina State University, Raleigh, NC</i>	2022
<ul style="list-style-type: none"> Student name: Yixuan Yang Co-advisor: Jeffrey L. Thorne Research topic: Quantifying interlocus gene conversion and natural selection 	
Undergraduate Research Advisor (Undergraduate)	2021
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> 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
<ul style="list-style-type: none"> Oral presentation at ASA Louisiana Chapter meeting in 2021 Graduated from master's program in Data Analytics of Duke University Now work as Data Analyst at Blizzard Entertainment 	
Yuwei Bao (PhD thesis advisor)	2022 –
<ul style="list-style-type: none"> Oral presentation at ASA Louisiana Chapter meeting in 2022 Oral presentation at Tulane Math Graduate Student Colloquium in 2022 	Present

- 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

Yufei Zou (undergraduate research & PhD thesis advisor)

2022 –

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

AWARDS

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

- Title: Molecular epidemiology through scalable statistical phylogenetic Modelling 06/30/26
- Principle Investigator: Xiang Ji
- Total Amount: \$159,000
- Direct Cost: \$159,000

National Science Foundation 05/01/23 –

- Title: Evolutionary inference with interlocus gene conversion 07/31/24

¹ 1,080 node hours (targeting 4 MI100 GPUs/node)

² Donation of one A100 80Gb PCIE GPU card

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

- 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
- Co-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

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 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: Scalable statistical advances to quantify interlocus gene conversion in multigene family evolution
- Principle Investigator: Xiang Ji
- Co-Investigators: None
- Total Amount: \$1,872,750
- Status: In preparation

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
- Co-Investigators: Xiang Ji
- Shared Amount: \$120,018
- Status: Pending

CONFERENCE PRESENTATIONS

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

14	Scalable phylogenetic Hamiltonian Monte Carlo method and its application in divergence time estimations <i>Southeastern Louisiana University, Hammond, LA</i>	08/29/2024
13	Phylogenetic approach for estimating amounts of interlocus gene conversion in duplications <i>AMS/AWM at Tulane University, New Orleans, LA</i>	12/06/2023
12	Scalable phylogenetic inference via Hamiltonian Monte Carlo method <i>Indiana University, Bloomington, IN</i>	02/03/2023
11	Scalable phylogenetic algorithm, modeling, and inference <i>North Carolina State University, Raleigh, NC</i>	10/10/2022
10	Smooth non-parametric coalescent priors for scalable divergence time estimations <i>AMS/AWM at Tulane University, New Orleans, LA</i>	10/05/2022
9	Scalable modeling and inference for phylogenetics – from interlocus gene conversion to evolving pathogens <i>Tulane University, New Orleans, LA</i>	12/04/2019
8	Scalable modeling and inference for phylogenetics – from interlocus gene conversion to evolving pathogens <i>Louisiana State University, Baton Rouge, LA</i>	11/04/2019
7	Large-scale molecular epidemiology for viruses <i>University of California, Los Angeles, CA</i>	11/08/2018
6	Phylogenetic approaches for quantifying interlocus gene conversion <i>Zhejiang University, Hangzhou, China</i>	09/18/2018
5	Phylogenetic approaches for quantifying interlocus gene conversion <i>Chinese Academy of Sciences, Beijing, China</i>	09/04/2018
4	Phylogenetic approaches for quantifying interlocus gene conversion <i>CGM Online</i>	05/30/2018
3	Phylogenetic approaches for quantifying interlocus gene conversion <i>Duke University, Durham, NC</i>	02/15/2018
2	Phylogenetic approaches for quantifying interlocus gene conversion <i>Temple University, Philadelphia, PA</i>	04/25/2017
1	Phylogenetic approaches for quantifying interlocus gene conversion <i>North Carolina State University, Raleigh, NC</i>	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

- I am a developer of the BEAST software.
- 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/bit0>.

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)
 - *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)

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.

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
- I served as treasurer of the ASSIST⁷ 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 Center for Advanced Self-Powered Systems of Integrated Sensors and Technologies