

Xiang Ji

Department of Mathematics

Tulane University

New Orleans, LA, 70118

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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

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

Affiliations

Faculty Member

October 2021 – Present

Cancer Center, Tulane University, New Orleans, LA

Research Interests

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

Publications

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40. Fisher, A., Ji, X., Nishimura, A., & Suchard, M. A. (2021) Shrinkage-based random local clocks with scalable inference. *Molecular Biology and Evolution*, accepted
 39. 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.
 38. 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.

37. Matteson, N. L., et al., (2023) Genomic surveillance reveals dynamic shifts in the connectivity of COVID-19 epidemics. *Cell*, accepted.
36. 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.
35. Zhang, Z., Nishimura, A., Tróvão, 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.
34. 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*.
33. Yang, J., Schuemie, M.J., **Ji, X.** and Suchard, M.A., (2023) Massive parallelization of massive sample-size survival analysis. *Journal of Computational and Graphical Statistics*, (just-accepted), pp.1-23.
32. Zhao, J., Dellicour, S., Yan, Z., Veit, M., Gill, M.S., He, W.T., 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, W.T., 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., Hou, X., Zhao, J., Sun, J., He, H., Si, W., ... & Su, S. (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.

in submission

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- Ji, X.**, Thorne, J. L. (2019) A phylogenetic approach disentangles the tract length and initiation rate of interlocus gene conversions. *in submission*, arXiv:1908.08608 [q-bio.PE]
- Gangavarapu, K., **Ji, X.**, Baele, G., Fourment, M., Lemey, P., Matsen IV, F. A. and Suchard, M. A. (2023) Many-core algorithms for high-dimensional gradients on phylogenetic trees. arXiv:2303.04390 [stat.CO] *in revision*
- Magee, A., 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. (2023) Random-effects substitution models for phylogenetics via scalable gradient approximations. arXiv:2303.13642 [q-bio.PE] *in revision*

Huang, S., He, J., Guo, J., Sun, Z., Cheng, L., **Ji, X.** and Zhang, Y. (2023) ASTK: a software for comprehensive analysis of alternative splicing.

Teaching Experience

Assistant Professor

Department of Mathematics, Tulane University, New Orleans, LA

- Fall 2023
Math 7360 Data Analysis (3 credits), GitHub site: <https://tulane-math-7360-2023.github.io/>
Math 3070 Intro to Probability (3 credits), GitHub site: <https://tulane-math-3070-2023.github.io/>
- Spring 2023
Math 7260 Linear Models (3 credits), GitHub site: <https://tulane-math-7260-2023.github.io/>
- Fall 2022
Math 3070 Intro to Probability (3 credits), GitHub site: <https://tulane-math-3070-2022.github.io/>
Math 1230 Stats for Scientists (3 credits)
- Spring 2022
Math 7260 Linear Models (3 credits), GitHub site: <https://tulane-math-7260-2022.github.io/>
- Fall 2021
Math 7360 Data Analysis (3 credits), GitHub sites: <https://tulane-math-7360-2021.github.io/>
- Spring 2021
Math 7260 Linear Models (3 credits), GitHub site: <https://tulane-math-7260-2021.github.io/>
- Fall 2020
Math 7360 Data Analysis (3 credits), GitHub site: <https://tulane-math7360.github.io/>

Awards

HPC Fund Research Cloud Allocation Award	AMD Corporation	2023
CoR Research Fellowship	Tulane University	2023
NVIDIA Academic Hardware Grant	NVIDIA Corporation	2022
Tuition Scholarship	SISMID ¹	2018
NIEHS Fellowship ²	North Carolina State University	2015
Graduate Fellow	SAMSI ³	2014
Tuition Scholarship	SISG ⁴	2013
University Graduate Fellowship	North Carolina State University	2011

Funding

Louisiana Board of Regents Research Competitiveness Subprogram grant (PI)	07/01/23 – 06/30/26
NIH R01GM072562 Deng (PI) / Ji (Co-Investigator)	04/01/22 – 03/31/27
NSF DEB1754142 Thorne (PI) / Ji (Subcontract Co-Investigator)	05/01/23 – 07/31/24
NIH 5R01AI153044-03 Suchard (PI) / Ji (Subcontract Co-Investigator)	10/01/23 – 03/31/24
NIH 5R01AI153044-02 Suchard (PI) / Ji (Subcontract Co-Investigator)	07/01/22 – 09/30/22
NIH 5U19AI135995-03 Garry (PI) / Ji (Subcontract Co-Investigator)	02/01/21 – 01/31/22
NIH 5U19AI135995-03 Garry (PI) / Ji (Subcontract Co-Investigator)	02/01/20 – 01/31/21

Conference Presentations

Oral Presentations

¹ SISMID: Summer Institute in Statistics and Modeling in Infectious Diseases at the University of Washington at Seattle

² The funds were matched through North Carolina State University

³ SAMSI: The Statistical and Applied Mathematical Sciences Institute

⁴ SISG: Summer Institute in Statistical Genetics at the University of Washington at Seattle

- Ji, X.** (2023, June) Scalable phylogenetic inference with Hamiltonian Monte Carlo method. Evolution 2023 meeting, Albuquerque, NM
- Ji, X.** (2023, March) *Scalable phylogenetic inference*. SCALA 2023: Scientific Computing Around Louisiana, Tulane University, New Orleans, LA
- Ji, X.** (2021, August) *Divergence time estimation with Hamiltonian Monte Carlo sampling and ratio transform*. Invited speaker at 2nd AsiaEvo Conference, Online
- Ji, X.** (2021, July) *Divergence time estimation with Hamiltonian Monte Carlo sampling and ratio transform*. Society of Molecular Biology and Evolution Meeting, Online
- 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
- 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

- Ji, X.** (2017, July). *Phylogenetic approaches for quantifying interlocus gene conversion*. Society of Molecular Biology and Evolution Meeting, Austin, TX
- Ji, X.** (2014, June). *A Phylogenetic approach for quantifying interlocus gene conversion*. Evolution Meeting, Raleigh, NC

Invited Talks

Scalable Phylogenetic Inference via Hamiltonian Monte Carlo Method <i>Indiana University, Bloomington, IN</i>	02/03/2023
Scalable Phylogenetic Algorithm, Modeling, and Inference <i>North Carolina State University, Raleigh, NC</i>	10/10/2022
Smooth Non-Parametric Coalescent Priors for Scalable Divergence Time Estimations <i>AMS/AWM at Tulane University, New Orleans, LA</i>	10/05/2022
Scalable Modeling and Inference for Phylogenetics – from Interlocus Gene Conversion to Evolving Pathogens <i>Tulane University, New Orleans, LA</i>	12/04/2019
Scalable Modeling and Inference for Phylogenetics – from Interlocus Gene Conversion to Evolving Pathogens <i>Louisiana State University, Baton Rouge, LA</i>	11/04/2019
Large-scale Molecular Epidemiology for Viruses <i>University of California, Los Angeles, CA</i>	11/08/2018
Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>Zhejiang University, Hangzhou, China</i>	09/18/2018
Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>Chinese Academy of Sciences, Beijing, China</i>	09/04/2018
Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>CGM Online</i>	05/30/2018
Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>Duke University, Durham, NC</i>	02/15/2018
Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>Temple University, Philadelphia, PA</i>	04/25/2017
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

Professional service

- I have reviewed manuscripts for
 - *Nature Medicine* (1)
 - *Proceedings of National Academy of Sciences* (2)
 - *Molecular Biology and Evolution* (9)
 - *Annals of Applied Statistics* (2)
 - *Plos Pathogens* (1)
 - *Microbiology Spectrum* (1)
 - *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (1)
 - *Frontiers in Public Health* (2)
 - *Frontiers in Virology* (2)
 - *Evolutionary Bioinformatics* (2)
 - *International Journal of Data Mining and Bioinformatics* (1)
 - *Rapid Reviews: COVID-19* (1)
- I serve as a Review Editor for *Frontiers in Statistical Genetics and Methodology*.

Departmental service

- I have served as the Director of Master Programs of the Math Department at Tulane University since Fall 2021.
- I have served on the Graduate Study Committee of the Math Department at Tulane University since Fall 2021.
- I led the proposal and development of a new Master of Science in Data Science program jointly hosted by the Math and Computer Science Departments at Tulane University.

Outreach

- I served as treasurer of the ASSIST⁵ 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.

⁵ ASSIST: The Center for Advanced Self-Powered Systems of Integrated Sensors and Technologies