

Xiang Ji

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EDUCATION

Doctor of Philosophy in Bioinformatics and Statistics (Co-Major) <i>North Carolina State University, Raleigh, NC</i> Dissertation: Phylogenetic approaches for quantifying interlocus gene conversion Committee: Jeffrey Thorne, Eric Stone, Nadia Singh, and Sujit Ghosh	<i>December 2017</i>
Master of Science in Material Science and Engineering <i>North Carolina State University, Raleigh, NC</i> Thesis: Laser interference lithography for fabrication of gas sensors Committee: John Muth, Lew Reynolds, Michael Kudenov, and Jon-Paul Maria	<i>September 2013</i>
Bachelor of Science in Economics (Double Major) <i>Peking University, Beijing, China</i>	<i>July 2011</i>
Bachelor of Science in Physics <i>Peking University, Beijing, China</i> Advisor: Jia-sen Zhang	<i>July 2011</i>

Appointments

Assistant Professor Department of Mathematics, Tulane University	<i>July 2020 – Present</i>
Postdoctoral Fellow University of California, Los Angeles	<i>January 2018 – July 2020</i>

Affiliations

Faculty Member Cancer Center, Tulane University	<i>October 2021 – Present</i>
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RESEARCH INTERESTS

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

PUBLICATIONS

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.

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.

- 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.
- 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.
- 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*.
- 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.
- 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.
- Tsui, L.H., et al., 2023. Genomic assessment of invasion dynamics of SARS-CoV-2 Omicron BA. 1. *Science*, 381(6655), pp.336-343.
- 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. *bioRxiv*, pp.2023-01.
- 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.
- 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.
- 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.
- 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]
- 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.
- 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.
- 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*
- Zhang, Z., Nishimura, A., **Ji, X.**, Lemey, P., & Suchard, M. A. (2022). Hamiltonian zigzag speeds up large-scale learning of direct effects among mixed-type biological traits. arXiv preprint arXiv:2201.07291. *submitted*
- 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
- 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
- Fan, Y., et al. (2022). Systematic analysis of inflammation and pain pathways in a mouse model of gout. *Molecular Pain*, 18, 17448069221097760.
- 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.
- 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.
- 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.
- Fisher, A., **Ji, X.**, Nishimura, A., & Suchard, M. A. (2021) Shrinkage-based random local clocks with scalable inference. *in revision*

- Lemey, P., et al., (2021) Untangling introductions and persistence in COVID-19 resurgence in Europe. *Nature*, 595 (7869), 713-717.
- 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.
- 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.
- 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.
- 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.
- 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
- 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]
- 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]
- Bleetsa, 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.
- 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]
- 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.
- 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.
- Ji, X.** (2017). Phylogenetic approaches for quantifying interlocus gene conversion. Doctoral Dissertation
- 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.
- 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.
- Ji, X.** (2013). Laser Interference Lithography for Fabrication of Gas Sensors. Master Thesis
- Han, X., **Ji, X.**, Wen, H., & Zhang, J. (2012). H-shaped resonant optical antennas with slot coupling. *Plasmonics*, 7(1), 7-11.
- 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.

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

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

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
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

- Ji, X.** (2023, June) Scalable phylogenetic inference with Hamiltonian Monte Carlo method. Evolution 2023 meeting, Albuquerque, NM, US
- Ji, X.** (2023, March) *Scalable phylogenetic inference*. SCALA 2023: Scientific Computing Around Louisiana, Tulane University, New Orleans, LA, US
- 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, US

POSTER PRESENTATIONS

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

Invited Talks

<i>Scalable phylogenetic inference via Hamiltonian Monte Carlo method</i>	Indiana University	02/03/2023
<i>Scalable phylogenetic algorithm, modeling, and inference</i>	N. C. State University	10/10/2022
<i>Smooth non-parametric coalescent priors for scalable divergence time estimations</i>	AMS/AWM at Tulane	10/05/2022
<i>Scalable Modeling and Inference for Phylogenetics</i> -from Interlocus Gene Conversion to Evolving Pathogens	Tulane University	12/04/2019
<i>Scalable Modeling and Inference for Phylogenetics</i> -from Interlocus Gene Conversion to Evolving Pathogens	Louisiana State University	11/04/2019

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 University of Washington at Seattle

<i>Large-scale molecular epidemiology for viruses</i>	UCLA	11/08/2018
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	Zhejiang University	09/18/2018
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	Chinese Academy of Sciences	09/04/2018
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	CGM online	05/30/2018
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	Duke University	02/15/2018
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	Temple University	04/25/2017
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	N.C. State University	03/24/2017

Software

- My software for studying interlocus gene conversion is freely available at <https://github.com/xji3/IGCexpansion>.
- A tutorial for the Bayesian method (under development) of quantifying interlocus gene conversion in BEAST is available at https://github.com/xji3/IGC_BEAST_Tutorial
- I'm a developer of the BEAST (<https://github.com/beast-dev/beast-mcmc>) software and the BEAGLE (<https://github.com/beagle-dev/beagle-lib>) library.
- 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 at <https://github.com/phylovi/bito>.

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)
 - *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 serve as the Director of Master Programs of the Math Department at Tulane University since Fall 2021.
- I serve on the Graduate Study Committee of the Math Department at Tulane University since Fall 2021.
- I lead the proposal and development of a new Master of Science in Data Science program jointly hosted by the Math and CS departments at Tulane University.

Outreach

- I served as treasurer on 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