

Xiang Ji

Department of Mathematics

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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

Postdoctoral Fellow

January 2018 – July 2020

University of California, Los Angeles

Affiliations

Faculty Member

October 2021 – Present

Cancer Center, Tulane University

RESEARCH INTERESTS

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

PUBLICATIONS

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. *medRxiv*, pp.2023-01.

- 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.
- 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.
- Hassler, G. W., Magee, A. F., Zhang, Z., Baele, G., Lemey, P., **Ji, X.**, Fourment, M., & Suchard, M. A. (2022). Data Integration in Bayesian Phylogenetics. *Annual Review of Statistics and Its Application*, 10.
- Holbrook, A. J., **Ji, X.**, & Suchard, M. A. (2022) From viral evolution to spatial contagion: a biologically modulated Hawkes model. *Bioinformatics*, 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*
- 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*
- Ji, X.**, Fisher, A. A., Su, S., Thorne, J. L., Potter, B., Lemey, P., Baele, G., & Suchard, M. A. (2022). Scalable Bayesian divergence time estimation with ratio transformations. arXiv preprint arXiv:2110.13298. *in revision*
- 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*, *Senior author
- Holbrook, A. J., Nishimura, A., **Ji, X.**, & Suchard, M. A. (2022). Computational Statistics and Data Science in the Twenty-first Century. arXiv preprint arXiv:2204.05530.
- 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*.
- 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.
- 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*

- 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*.
- 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*, *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*, arXiv:1905.12146 [stat.CO]
- Fisher, A., **Ji, X.**, Zhang, Z., Lemey, P., & Suchard, M. A. (2020) Relaxed random walks at scale. *Systematic Biology*, 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

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

NIH R01GM072562 Deng (PI) / Ji (Co-Investigator)	04/01/22 – 03/31/27
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

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

CONFERENCE PRESENTATIONS

ORAL PRESENTATIONS

- 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
<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*.

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