Xiang Ji

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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

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.

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 Respirovirus 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*

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.*

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]

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.

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

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 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. (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

Scalable phylogenetic algorithm, modeling, and inference	N. C. State University	10/10/2022

[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

Scalable divergence time estimations with coalescent priors	Tulane University	10/03/2022
Scalable Modeling and Inference for Phylogenetics -from Interlocus Gene Conversion to Evolving Pathogens	Tulane University	12/04/2019
Scalable Modeling and Inference for Phylogenetics -from Interlocus Gene Conversion to Evolving Pathogens	Louisiana State University	11/04/2019
Large-scale molecular epidemiology for viruses	UCLA	11/08/2018
Phylogenetic approaches for quantifying interlocus gene conversion	Zhejiang University	09/18/2018
Phylogenetic approaches for quantifying interlocus gene conversion	Chinese Academy of Sciences	09/04/2018
Phylogenetic approaches for quantifying interlocus gene conversion	CGM online	05/30/2018
Phylogenetic approaches for quantifying interlocus gene conversion	Duke University	02/15/2018
Phylogenetic approaches for quantifying interlocus gene conversion	Temple University	04/25/2017
Phylogenetic approaches for quantifying interlocus gene conversion	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* (8)
  - *Annals of Applied Statistics* (2)
  - *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 ASSIST[5] 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.

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