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

RESEARCH INTERESTS

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

PUBLICATIONS

He, W., et al., (2021) Phylogeography finds association between swine trade and the spread of porcine epidemic diarrhea virus in China and across the world. *submitted*

Fisher, A., **Ji, X.**, Nishimura, A., & Suchard, M. A. (2020) 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.*

Holbrook, A. J., **Ji, X.**, & Suchard, M. A. (2021) Bayesian mitigation of spatial coarsening for a fairly flexible spatiotemporal Hawkes model. *Annals of Applied Statistics, in press*

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.*

Holbrook, A. J., **Ji, X.**, & Suchard, M. A. (2020) From viral evolution to spatial contagion: a biologically modulated Hawkes model. *Submitted*, arXiv:2103.03348 [stat.ME]

He, W., Liao, M., Zhao, W., Sun, J., Zhao, J., Wang, L., Meng, X., Zhou, J., **Ji, X.**, Suchard, M. A., Zhang, X., Su, S., & Veit, M. (2020) Cross-species transmission of viruses from bats. Submitted to *Cell Reports*

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

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

[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

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/libsbn.

Synergistic Activities

Professional service

- I have reviewed manuscripts for *Nature Medicine*, *Proceedings of National Academy of Sciences*, *Molecular Biology and Evolution, Annals of Applied Statistics*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, *Frontiers in Public Health*, and *Evolutionary Bioinformatics*.

- 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