

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

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*
- 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
- 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. *Molecular Biology and Evolution*, 39(2), msab364
- 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*.
- 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*
- 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]
- 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

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 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

<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

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

<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/libsbm>.

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)
 - *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