**Xiang Ji**

Department of Mathematics

Tulane University

New Orleans, LA 70118

xji4@tulane.edu · <http://xiang-ji-ncsu.github.io/> · [Github:@xji3](https://github.com/xji3)

**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]

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**

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| --- | --- | --- |
| NVIDIA Academic Hardware Grant | NVIDIA Corporation | 2022 |
| Tuition Scholarship | SISMID[[1]](#footnote-1) | 2018 |
| NIEHS Fellowship[[2]](#footnote-2) | North Carolina State University | 2015 |
| Graduate Fellow | SAMSI[[3]](#footnote-3) | 2014 |
| Tuition Scholarship | SISG[[4]](#footnote-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**

*Scalable Modeling and Inference for Phylogenetics* Tulane University 12/04/2019

-from Interlocus Gene Conversion to Evolving Pathogens

*Scalable Modeling and Inference for Phylogenetics* Louisiana State University 11/04/2019

-from Interlocus Gene Conversion to Evolving Pathogens

*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* (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 ASSIST[[5]](#footnote-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.

1. SISMID: Summer Institute in Statistics and Modeling in Infectious Diseases at University of Washington at Seattle [↑](#footnote-ref-1)
2. The funds were matched through North Carolina State University [↑](#footnote-ref-2)
3. SAMSI: The Statistical and Applied Mathematical Sciences Institute [↑](#footnote-ref-3)
4. SISG: Summer Institute in Statistical Genetics at University of Washington at Seattle [↑](#footnote-ref-4)
5. ASSIST: The Center for Advanced Self-Powered Systems of Integrated Sensors and Technologies [↑](#footnote-ref-5)