**Xiang Ji**

Department of Mathematics

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**Education**

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| **Doctor of Philosophy in Bioinformatics and Statistics (Co-Major)**  *North Carolina State University, Raleigh, NC*  Dissertation: Phylogenetic Approaches for Quantifying Interlocus Gene Conversion  Committee: Jeffrey Thorne, Eric Stone, Nadia Singh, and Sujit Ghosh | *December 2017* |
| **Master of Science in Material Science and Engineering**  *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 | *September 2013* |
| **Bachelor of Science in Economics (Double Major)**  *Peking University, Beijing, China* | *July 2011* |
| **Bachelor of Science in Physics**  *Peking University, Beijing, China*  Advisor: Jia-sen Zhang | *July 2011* |

**Appointments**

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| **Assistant Professor**  *Department of Mathematics, Tulane University, New Orleans, LA* | *July 2020 – Present* |
| **Postdoctoral Fellow**  *University of California, Los Angeles, CA* | *January 2018 – July 2020* |

**Affiliations**

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| **Faculty Member**  *Cancer Center, Tulane University, New Orleans, LA* | *October 2021 – Present* |

**Research Interests**

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

**Publications**

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| **39.** | **Ji, X.**, Fisher, A. A., Su, S., Thorne, J. L., Potter, B., Lemey, P., Baele, G., & Suchard, M. A., (2023) Scalable Bayesian divergence time estimation with ratio transformations. *Systematic Biology*, syad039, arXiv preprint arXiv:2110.13298. |
| **38.** | Yang, Y., Xu, T., Conant, G., Kishino, H., Thorne, J.L. and **Ji, X.**, (2023) Interlocus Gene Conversion, Natural Selection, and Paralog Homogenization. *Molecular Biology and Evolution*, msad198. |
| 37. | Matteson, N. L., et al., (2023) Genomic surveillance reveals dynamic shifts in the connectivity of COVID-19 epidemics. *Cell*, accepted. |
| 36. | He, W.T., Li, D., Baele, G., Zhao, J., Jiang, Z., **Ji, X.**, Veit, M., Suchard, M.A., Holmes, E.C., Lemey, P., Boni, M.F. and Su, S., (2023) Newly identified lineages of porcine hemagglutinating encephalomyelitis virus exhibit respiratory phenotype. *Virus Evolution*, *9*(2), p.vead051. |
| 35. | Zhang, Z., Nishimura, A., Trovão, N.S., Cherry, J.L., Holbrook, A.J., **Ji, X.**, Lemey, P. and Suchard, M.A., (2023) Accelerating Bayesian inference of dependency between mixed-type biological traits. *PLOS Computational Biology*, *19*(8), p.e1011419. |
| 34. | Zhao, J., Kang, M., Wu, H., Sun, B., Baele, G., He, W.T., Lu, M., Suchard, M.A., **Ji, X.**, He, N. and Su, S., (2023) Risk assessment of SARS-CoV-2 replicating and evolving in animals. *Trends in Microbiology*. |
| 33. | Yang, J., Schuemie, M.J., **Ji, X.** and Suchard, M.A., (2023) Massive parallelization of massive sample-size survival analysis. *Journal of Computational and Graphical Statistics*, (just-accepted), pp.1-23. |
| 32. | Zhao, J., Dellicour, S., Yan, Z., Veit, M., Gill, M.S., He, WT, 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. |
| 31. | Tsui, L.H., et al., (2023) Genomic assessment of invasion dynamics of SARS-CoV-2 Omicron BA. 1. *Science*, *381*(6655), pp.336-343. |
| 30. | 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, pp.353-377. |
| 29. | 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. |
| 28. | Zhao, J., Dellicour, S., Yan, Z., Veit, M., Gill, M.S., He, WT, 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. |
| 27. | Holbrook, A. J., **Ji, X.**, & Suchard, M. A. (2022) From viral evolution to spatial contagion: a biologically modulated Hawkes model. *Bioinformatics*, 38(7), pp.1846-1856. arXiv:2103.03348 [stat.ME] |
| 26. | McCrone, J.T., Hill, V., Bajaj, S. et al. (2022) Context-specific emergence and growth of the SARS-CoV-2 Delta variant. *Nature*, 610(7930), pp.154-160. |
| 25. | 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. |
| 24. | 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* |
| 23. | 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*,10(3), pp.e00242-22. \*Senior author |
| 22. | 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* |
| 21. | Fan, Y., et al. (2022). Systematic analysis of inflammation and pain pathways in a mouse model of gout. *Molecular Pain*, 18, 17448069221097760. |
| 20. | Xie, S., et al. (2022). Disrupted myelination network in the cingulate cortex of Parkinson’s disease. *IET Systems Biology*, 16(3-4), pp.98-119. |
| 19. | 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. |
| 18. | Holbrook, A. J., Nishimura, A., **Ji, X.**, & Suchard, M. A. (2021). Computational Statistics and Data Science in the Twenty-first Century. *Wiley StatsRef: Statistics Reference Online.* arXiv preprint arXiv:2204.05530. |
| 17. | Lemey, P., et al., (2021) Untangling introductions and persistence in COVID-19 resurgence in Europe. *Nature,* 595 (7869), 713-717*.* |
| 16. | 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. |
| 15. | 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. |
| 14. | 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*, 58(5), pp.604-645. |
| 13. | 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*, 26(5), pp.483-495. |
| **12.** | 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*, 37(9), pp.2641-2654. \*equal contribution |
| **11.** | **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*, 37(10), pp.3047-3060. arXiv:1905.12146 [stat.CO] |
| 10. | Fisher, A., **Ji, X.**,Zhang, Z., Lemey, P., & Suchard, M. A. (2020) Relaxed random walks at scale. *Systematic Biology*, 70(2), pp.258-267. arXiv:1906.04834[q-bio.PE] |
| 9. | 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. |
| 8. | 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. |
| 7. | 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. |
| **6.** | **Ji, X.** (2017). Phylogenetic approaches for quantifying interlocus gene conversion. Doctoral Dissertation |
| **5.** | **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. |
| 4. | 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. |
| **3.** | **Ji, X.** (2013). Laser Interference Lithography for Fabrication of Gas Sensors. Master Thesis |
| 2. | Han, X., **Ji, X.**, Wen, H., & Zhang, J. (2012). H-shaped resonant optical antennas with slot coupling. *Plasmonics*, 7(1), 7-11. |
| 1. | 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. |

*in submission*

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|  | **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] | |
|  | | Gangavarapu, K., **Ji, X.**, Baele, G., Fourment, M., Lemey, P., Matsen IV, F. A. and Suchard, M. A. (2023) Many-core algorithms for high-dimensional gradients on phylogenetic trees. arXiv:2303.04390 [stat.CO] *in revision*  Magee, A., Holbrook, A. J., Pekar J. E., Caviedes-Solis I. W., Matsen IV, F. A., Baele, G., Wertheim, J. O., **Ji, X.,** Lemey, P. and Suchard, M. A. (2023) Random-effects substitution models for phylogenetics via scalable gradient approximations. arXiv:2303.13642 [q-bio.PE] *in revision*  Fisher, A., **Ji, X.**, Nishimura, A., & Suchard, M. A. (2021) Shrinkage-based random local clocks with scalable inference. *in revision* |
|  | | 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. |

**Teaching Experience**

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| **Assistant Professor**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Fall 2023   Math 7360 Data Analysis (3 credits), GitHub site: <https://tulane-math-7360-2023.github.io/>  Math 3070 Intro to Probability (3 credits), GitHub site: <https://tulane-math-3070-2023.github.io/>   * Spring 2023   Math 7260 Linear Models (3 credits), GitHub site: <https://tulane-math-7260-2023.github.io/>   * Fall 2022   Math 3070 Intro to Probability (3 credits), GitHub site: <https://tulane-math-3070-2022.github.io/>  Math 1230 Stats for Scientists (3 credits)   * Spring 2022   Math 7260 Linear Models (3 credits), GitHub site: <https://tulane-math-7260-2022.github.io/>   * Fall 2021   Math 7360 Data Analysis (3 credits), GitHub sites: <https://tulane-math-7360-2021.github.io/>   * Spring 2021   Math 7260 Linear Models (3 credits), GitHub site: <https://tulane-math-7260-2021.github.io/>   * Fall 2020   Math 7360 Data Analysis (3 credits), GitHub site: <https://tulane-math7360.github.io/> |

**Awards**

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| HPC Fund Research Cloud Allocation Award | AMD Corporation | 2023 |
| CoR Research Fellowship | Tulane University | 2023 |
| 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**

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| Louisiana Board of Regents Research Competitiveness Subprogram grant (PI) | 07/01/23 – 06/30/26 |
| NIH R01GM072562 Deng (PI) / Ji (Co-Investigator) | 04/01/22 – 03/31/27 |
| NSF DEB1754142 Thorne (PI) / Ji (Subcontract Co-Investigator) | 05/01/23 – 07/31/24 |
| NIH 5R01AI153044-03 Suchard (PI) / Ji (Subcontract Co-Investigator) | 10/01/23 – 03/31/24 |
| 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 |

**Cconference Presentations**

**Oral Presentations**

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| **Ji, X.** (2023, June) Scalable phylogenetic inference with Hamiltonian Monte Carlo method. Evolution 2023 meeting, Albuquerque, NM |
| **Ji, X.** (2023, March)*Scalable phylogenetic inference*.SCALA 2023: Scientific Computing Around Louisiana, Tulane University, New Orleans, LA |
| **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 |

**Poster Presentations**

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| **Ji, X.** (2017, July). *Phylogenetic approaches for quantifying interlocus gene conversion.* Society of Molecular Biology and Evolution Meeting, Austin, TX |
| **Ji, X.** (2014, June). *A Phylogenetic approach for quantifying interlocus gene conversion.* Evolution Meeting, Raleigh, NC |

**Invited Talks**

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| Scalable Phylogenetic Inference via Hamiltonian Monte Carlo Method  *Indiana University, Bloomington, IN* | 02/03/2023 |
| Scalable Phylogenetic Algorithm, Modeling, and Inference  *North Carolina State University, Raleigh, NC* | 10/10/2022 |
| Smooth Non-Parametric Coalescent Priors for Scalable Divergence Time Estimations  *AMS/AWM at Tulane University, New Orleans, LA* | 10/05/2022 |
| Scalable Modeling and Inference for Phylogenetics – from Interlocus Gene Conversion to Evolving Pathogens  *Tulane University, New Orleans, LA* | 12/04/2019 |
| Scalable Modeling and Inference for Phylogenetics – from Interlocus Gene Conversion to Evolving Pathogens  *Louisiana State University, Baton Rouge, LA* | 11/04/2019 |
| Large-scale Molecular Epidemiology for Viruses  *University of California, Los Angeles, CA* | 11/08/2018 |
| Phylogenetic Approaches for Quantifying Interlocus Gene Conversion  *Zhejiang University, Hangzhou, China* | 09/18/2018 |
| Phylogenetic Approaches for Quantifying Interlocus Gene Conversion  *Chinese Academy of Sciences, Beijing, China* | 09/04/2018 |
| Phylogenetic Approaches for Quantifying Interlocus Gene Conversion  *CGM Online* | 05/30/2018 |
| Phylogenetic Approaches for Quantifying Interlocus Gene Conversion  *Duke University, Durham, NC* | 02/15/2018 |
| Phylogenetic Approaches for Quantifying Interlocus Gene Conversion  *Temple University, Philadelphia, PA* | 04/25/2017 |
| Phylogenetic Approaches for Quantifying Interlocus Gene Conversion  *North Carolina State University, Raleigh, NC* | 03/24/2017 |

**Software**

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| **IGCexpansion**   * My software for studying interlocus gene conversion. * Available at <https://github.com/xji3/IGCexpansion>. |
| **IGC BEAST Tutorial**   * A tutorial for the Bayesian method (under development) of quantifying interlocus gene conversion in BEAST. * Available at <https://github.com/xji3/IGC_BEAST_Tutorial>. |
| **BEAST**   * I am a developer of the BEAST software. * Available at <https://github.com/beast-dev/beast-mcmc>. |
| **BEAGLE**   * I am a developer of the BEAGLE library. * Available at <https://github.com/beagle-dev/beagle-lib>. |
| **bito**   * 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. * Available at <https://github.com/phylovi/bito>. |

**Synergistic Activities**

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| **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.* |
| **Departmental service**   * I have served as the Director of Master Programs of the Math Department at Tulane University since Fall 2021*.* * I have served on the Graduate Study Committee of the Math Department at Tulane University since Fall 2021. * I led the proposal and development of a new Master of Science in Data Science program jointly hosted by the Math and Computer Science Departments at Tulane University. |
| **Outreach**   * I served as treasurer of 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 the 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 the 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)