**Xiang Ji**, Ph.D.

*Last Updated on 05/22/2024*

A qr code on a white background

Description automatically generatedAssistant Professor, Department of Mathematics

Tulane University, New Orleans, LA, 70118

[xji4@tulane.edu](mailto:xji4@tulane.edu) • [GitHub @ xji3](https://github.com/xji3)

Personal Website: <http://xiang-ji-ncsu.github.io/>

Google Scholar: <https://scholar.google.com/citations?user=YH4BbIMAAAAJ&hl=en>

**EDUCATION**

|  |  |
| --- | --- |
| **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**

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

**RESEARCH INTERESTS**

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

**PUBLICATIONS**

|  |  |
| --- | --- |
| 43. | Magee, A. F., 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., (2024). Random-effects substitution models for phylogenetics via scalable gradient approximations. *Systemic Biology*. In press. |
| 42. | Yang, J., Schuemie, M.J., **Ji, X.** and Suchard, M.A., (2024). Massive parallelization of massive sample-size survival analysis. *Journal of Computational and Graphical Statistics*, *33*(1), pp.289-302. |
| 41. | Gangavarapu, K., **Ji, X.**, Baele, G., Fourment, M., Lemey, P., Matsen IV, F.A. and Suchard, M.A., (2024). Many-core algorithms for high-dimensional gradients on phylogenetic trees. *Bioinformatics*, *40*(2), p.btae030. |
| 40. | Huang, S., He, J., Yu, L., Guo, J., Jiang, S., Sun, Z., Cheng, L., Chen, X., **Ji, X.** and Zhang, Y., (2024). ASTK: A Machine Learning‐Based Integrative Software for Alternative Splicing Analysis. *Advanced Intelligent Systems*, p.2300594. |
| 39. | Fisher, A., **Ji, X.**, Nishimura, A., & Suchard, M. A. (2023) Shrinkage-based random local clocks with scalable inference. *Molecular Biology and Evolution, 40*(11), msad242. |
| 38. | **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. |
| 37. | 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. |
| 36. | Matteson, N. L., et al., (2023) Genomic surveillance reveals dynamic shifts in the connectivity of COVID-19 epidemics. *Cell*, 186(26), pp.5690-5704. |
| 35. | 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. |
| 34. | 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. |
| 33. | 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*. |
| 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., et al., (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. |

**Articles in Submission and Preparation**

|  |  |
| --- | --- |
| 5. | Bao, Y., Deng, W., Su, S., Lemey, P., Suchard, M. A., Glatt-Holtz, N.\*, & **Ji, X.**\* (2024) Reflection Hamiltonian Monte Carlo for divergence time estimations. \*Senior author. *in preparation* |
| 4. | **Ji, X.**, Redelings, B., Su, S., Deng, W., Thorne, J. L., Lemey, P., & Suchard, M. A. (2024) Branch-specific substitution models for identifying natural selection differences via shrinkage priors. *in preparation* |
| 3. | Baele, G., **Ji, X.**, Hassler, G. W., McCrone, J. T., Shao, Y., Holbrook, A. J., Lemey, P., Drummond, A., Rambaut, A., Suchard, M. A. (2024) BEAST X for Bayesian phylogenetic, phylodynamic and phylogeographic inference. *in submission* |
| 2. | Kang, M., Wang, L., Sun, B., Wan, W., **Ji, X.**, Baele, G., Bi, Y., Suchard, M. A., Lai, A., Zhang, M., Wang, L., Zhu, Y., Ma, L., Li, H., Haerheng, A., Qi, Y., Wang, R., & Su, S. (2024) Zoonotic infections by avian influenza virus: Changing global epidemiology, investigation and control. *in review at Lancet Infectious Diseases* |
| 1. | **Ji, X.**, Thorne, J. L. (2024) A phylogenetic approach disentangles the tract length and initiation rate of interlocus gene conversions. *in submission*, arXiv:1908.08608 [q-bio.PE] |

**TEACHING EXPERIENCE**

|  |
| --- |
| **Assistant Professor**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Spring 2023   Teaching Relief   * Fall 2023 * ***Math 7360 Data Analysis (3 credits)***   GitHub site: <https://tulane-math-7360-2023.github.io/>  Level: Graduate (Master + Ph.D.)  Topics: R, RMarkdown, Rcpp, git, data visualization using ggplot2, web scraping, linear models, generalized linear models, neural network, classification  Enrollment: 22   * ***Math 3070/6070 Intro to Probability (3 credits)***   GitHub site: <https://tulane-math-3070-2023.github.io/>  Level: Undergraduate, Graduate (Master)  Topics: Axioms of probability, discrete and continuous random variables, multivariate distributions, expectation, limit theorem  Enrollment: 48   * Spring 2023 * ***Math 6040/7260 Linear Models (3 credits)***   GitHub site: <https://tulane-math-7260-2023.github.io/>  Level: Graduate (Master + Ph.D.)  Topics: Simple and multiple linear regressions, hypothesis testing, analysis of variance, bootstrap, logistic regression  Enrollment: 13   * ***Math 7980 Independent Study (3 credits)***   Level: Graduate (Master)  Topics: Item response theory models  Enrollment: 1   * Fall 2022 * ***Math 3070/6070 Intro to Probability (3 credits)***   GitHub site: <https://tulane-math-3070-2022.github.io/>  Level: Undergraduate, Graduate (Master)  Topics: Axioms of probability, discrete and continuous random variables, multivariate distributions, expectation, limit theorem  Enrollment: 37   * ***Math 1230 Stats for Scientists (3 credits)***   Level: Undergraduate  Topics: Probability, random variable, discrete and continuous distributions, sampling distributions, one and two-sample estimations, hypothesis testing, simple linear regression  Enrollment: 66   * ***Math 7980 Independent Study (3 credits)***   Level: Graduate (Ph.D.)  Topics: Bayesian Phylogenetics  Enrollment: 1   * Spring 2022 * ***Math 6040/7260 Linear Models (3 credits)***   GitHub site: <https://tulane-math-7260-2022.github.io/>  Level: Graduate (Master + Ph.D.)  Topics: Simple and multiple linear regressions, hypothesis testing, analysis of variance, bootstrap, logistic regression  Enrollment: 16   * ***Math 7980 Independent Study (3 credits)***   Level: Graduate (Master)  Topics: Review of optimization methods  Enrollment: 1   * Fall 2021 * ***Math 7360 Data Analysis (3 credits)***   GitHub sites: <https://tulane-math-7360-2021.github.io/>  Level: Graduate (Master + Ph.D.)  Topics: R, RMarkdown, Rcpp, git, data visualization using ggplot2, web scraping, linear models, generalized linear models, neural network, classification  Enrollment: 19   * Spring 2021 * ***Math 6040/7260 Linear Models (3 credits)***   GitHub site: <https://tulane-math-7260-2021.github.io/>  Level: Graduate (Master + Ph.D.)  Topics: Simple and multiple linear regressions, hypothesis testing, analysis of variance, bootstrap, logistic regression  Enrollment: 17   * Fall 2020 * ***Math 7360 Data Analysis (3 credits)***   GitHub site: <https://tulane-math7360.github.io/>  Level: Graduate (Master + Ph.D.)  Topics: R, RMarkdown, Rcpp, git, data visualization using ggplot2, web scraping, linear models, generalized linear models, neural network, classification  Enrollment: 12 |

**STUDENT ADVISING**

|  |  |
| --- | --- |
| **Co-Supervisor (Doctoral)**  *Department of Microbiology and Immunology, The University of Melbourne*  *Melbourne, Australia*   * Student name: John Tay * Supervisor: Sebastian Duchene * Research Title: TBD | *2024 – Present* |
| **Committee Chair (Doctoral)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Yufei Zou * Research Title: Evolutionary inference with interlocus gene conversion | *2023 – Present* |
| **Committee Chair (Doctoral)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Yuwei Bao * Research Title: Reflective Hamiltonian Monte Carlo method | *2022 – Present* |
| **Oral Exam Committee Member (Doctoral)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: John V. Argentino * Chair: Michelle Lacey | *2024* |
| **Prospectus Exam Committee Member (Doctoral)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Daniela A. Florez Pineda * Chair: Ricardo Cortez * Research title: Mathematical models for transmission and control of mosquito-borne diseases | *2024* |
| **Prospectus Exam Committee Member (Doctoral)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Linh Do * Chair: Scott McKinley * Research title: Statistical techniques for comparing populations of continuous piecewise-linear stochastic processes | *2023* |
| **Oral Exam Committee Member (Doctoral)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Moslem Uddin * Chair: Lisa Fauci | *2023* |
| **Oral Exam Committee Chair (Doctoral)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Yuwei Bao * Chair: Xiang Ji | *2023* |
| **Oral Exam Committee Member (Doctoral)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Sinchita Lahiri * Chair: Kyle Kun Zhao | *2023* |
| **Oral Exam Committee Member (Doctoral)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Linh Do * Chair: Scott McKinley | *2022* |
| **Oral Exam Committee Member (Doctoral)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Daniela A. Florez Pineda * Chair: Ricardo Cortez | *2022* |
| **Independent Study Advisor (Master)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Paul Pluscht * Project topic: Review of optimization methods | *2022* |
| **Undergraduate Research Advisor (Undergraduate)**  *Department of Statistics, North Carolina State University, Raleigh, NC*   * Student name: Yixuan Yang * Co-advisor: Jeffrey L. Thorne * Research topic: Quantifying interlocus gene conversion and natural selection | *2020 - 2022* |
| **Undergraduate Research Advisor (Undergraduate)**  *Department of Mathematics, Tulane University, New Orleans, LA*   * Student name: Jiayun Ling * Co-advisor: Xin Jiang * Research topic: Item response theory model, Add Health data, social science | *2021* |

**AWARDS**

|  |  |  |
| --- | --- | --- |
| HPC Fund Research Cloud Allocation Award[[1]](#footnote-1) | AMD Corporation | 2023 |
| NVIDIA Academic Hardware Grant[[2]](#footnote-2) | NVIDIA Corporation | 2022 |
| Tuition Scholarship | SISMID[[3]](#footnote-3) | 2018 |
| NIEHS Fellowship[[4]](#footnote-4) | North Carolina State University | 2015 |
| Graduate Fellow | SAMSI[[5]](#footnote-5) | 2014 |
| Tuition Scholarship | SISG[[6]](#footnote-6) | 2013 |
| University Graduate Fellowship | North Carolina State University | 2011 |

**FUNDED PROJECTS**

|  |  |
| --- | --- |
| **External** |  |
| **Louisiana Board of Regents Research Competitiveness Subprogram**   * Title: Molecular epidemiology through scalable statistical phylogenetic Modelling * Principle Investigator: Xiang Ji * Total Amount: $159,000 * Direct Cost: $159,000 | 07/01/23 – 06/30/26 |
| **National Science Foundation**   * Title: Evolutionary inference with interlocus gene conversion * Principle Investigator: Jeffrey L. Thorne * Co-Investigator: Xiang Ji * Award number: DEB1754142 * Total Amount: $564,338 * Shared Amount: $94,351 | 05/01/23 – 07/31/24 |
| **National Institute of Health**   * Title: Statistical innovation to integrate sequences and phenotypes for scalable phylodynamic inference * Principle Investigator: Marc A. Suchard * Co-Investigator: Xiang Ji * Award number: R01AI153044 * Total Amount: $2,321,335 * Shared Amount: $89,724 | 07/01/22 – 03/31/25 |
| **National Institute of Health**   * Title: Notch signaling and germline-soma interactions in *Drosophila* ovarian model * Principle Investigator: Wu-Min Deng * Co-Investigator: Xiang Ji * Award number: R01GM072562 * Total Amount: $ 2,432,208 * Shared Amount: $86,460 | 04/01/22 – 03/31/27 |
| **National Institute of Health**   * Title: Consortium for viral systems biology (CViSB) * Principle Investigator: Robert F. Garry * Co-Investigator: Xiang Ji * Award number: U19AI135995 * Total Amount: $1,143,554 * Shared Amount: $51,774 | 02/01/20 – 01/31/22 |
| **Internal** |  |
| **Tulane University CoR Research Fellowship**   * Title: Scalable molecular epidemiology models * Principle Investigator: Xiang Ji * Total Amount: $5,500 | 05/01/23 – 05/31/24 |

**SUBMITTED PROPOSALS**

|  |  |
| --- | --- |
| **National Institute of Health**   * Title: Scalable evolutionary inference with interlocus gene conversion * Principle Investigator: Xiang Ji * Co-Investigators: None * Total Amount: $1,872,750 * Status: Pending | 2024 |
| **National Institute of Health**   * Title: Scalable phylogenomic inference through massively parallelized action-based BEAGLE library * Principle Investigator: Xiang Ji * Co-Investigators: Robert F. Garry and Marc A. Suchard * Total Amount: $2,693,909 * Status: Not Funded | 2023 |
| **National Institute of Health**   * Title: Characterizing intra- and inter-host Nov evolution using human challenge study samples * Principle Investigator: Pengbo Liu * Co-Investigators: Xiang Ji * Shared Amount: $120,018 * Status: Not Funded | 2023 |

**CONFERENCE PRESENTATIONS**

**Oral Presentations**

|  |  |
| --- | --- |
| 6 | **Ji, X.** (2023, June) Scalable phylogenetic inference with Hamiltonian Monte Carlo method. Evolution 2023 meeting, Albuquerque, NM |
| 5 | **Ji, X.** (2023, March)*Scalable phylogenetic inference*.SCALA 2023: Scientific Computing Around Louisiana, Tulane University, New Orleans, LA |
| 4 | **Ji, X.** (2021, August)*Divergence time estimation with Hamiltonian Monte Carlo sampling and ratio transform*.Invited speaker at 2nd AsiaEvo Conference, Online |
| 3 | **Ji, X.** (2021, July) *Divergence time estimation with Hamiltonian Monte Carlo sampling and ratio transform*. Society of Molecular Biology and Evolution Meeting, Online |
| 2 | **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 |
| 1 | **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**

|  |  |
| --- | --- |
| 2 | **Ji, X.** (2017, July). *Phylogenetic approaches for quantifying interlocus gene conversion.* Society of Molecular Biology and Evolution Meeting, Austin, TX |
| 1 | **Ji, X.** (2014, June). *A Phylogenetic approach for quantifying interlocus gene conversion.* Evolution Meeting, Raleigh, NC |

**INVITED TALKS**

|  |  |  |
| --- | --- | --- |
| 13 | Phylogenetic approach for estimating amounts of interlocus gene conversion in duplications  *AMS/AWM at Tulane University, New Orleans, LA* | 12/06/2023 |
| 12 | Scalable phylogenetic inference via Hamiltonian Monte Carlo method  *Indiana University, Bloomington, IN* | 02/03/2023 |
| 11 | Scalable phylogenetic algorithm, modeling, and inference  *North Carolina State University, Raleigh, NC* | 10/10/2022 |
| 10 | Smooth non-parametric coalescent priors for scalable divergence time estimations  *AMS/AWM at Tulane University, New Orleans, LA* | 10/05/2022 |
| 9 | Scalable modeling and inference for phylogenetics – from interlocus gene conversion to evolving pathogens  *Tulane University, New Orleans, LA* | 12/04/2019 |
| 8 | Scalable modeling and inference for phylogenetics – from interlocus gene conversion to evolving pathogens  *Louisiana State University, Baton Rouge, LA* | 11/04/2019 |
| 7 | Large-scale molecular epidemiology for viruses  *University of California, Los Angeles, CA* | 11/08/2018 |
| 6 | Phylogenetic approaches for quantifying interlocus gene conversion  *Zhejiang University, Hangzhou, China* | 09/18/2018 |
| 5 | Phylogenetic approaches for quantifying interlocus gene conversion  *Chinese Academy of Sciences, Beijing, China* | 09/04/2018 |
| 4 | Phylogenetic approaches for quantifying interlocus gene conversion  *CGM Online* | 05/30/2018 |
| 3 | Phylogenetic approaches for quantifying interlocus gene conversion  *Duke University, Durham, NC* | 02/15/2018 |
| 2 | Phylogenetic approaches for quantifying interlocus gene conversion  *Temple University, Philadelphia, PA* | 04/25/2017 |
| 1 | Phylogenetic approaches for quantifying interlocus gene conversion  *North Carolina State University, Raleigh, NC* | 03/24/2017 |

**SOFTWARE**

|  |
| --- |
| **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**

|  |
| --- |
| **Grant Panelist**   * I served as a guest panel member for the UK MRC Better Methods, Better Research (BMBR) Panel in 2023.   **Professional service**   * I serve as an Editorial Board member for *Discover Viruses* by *Springer Nature* * I serve as a Review Editor for *Frontiers in Statistical Genetics and Methodology.* * 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)   + *Journal of Computational and Graphical Statistics (1)*   + *Theoretical Population Biology (1)*   + *Plos Pathogens (1)*   + *Microbiology Spectrum (1)*   + *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (1)   + *Frontiers in Public Health* (2)   + *Frontiers in Virology (2)*   + *BMC Ecology and Evolution (1)*   + *Evolutionary Bioinformatics* (2)   + *International Journal of Data Mining and Bioinformatics* (1)   + *Rapid Reviews: COVID-19* (1) |
| **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 participated in the LA FIRST Lego League State Championship as a volunteer judge in January 2023. * I participated in Boys at Tulane in STEM (BATS) and Girls in STEM at Tulane (GIST), organized by Tulane Center for K-12 System Education in 2023 and 2024. * I served as treasurer of the ASSIST[[7]](#footnote-7) 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. 1,080 node hours (targeting 4 MI100 GPUs/node) [↑](#footnote-ref-1)
2. Donation of one A100 80Gb PCIE GPU card [↑](#footnote-ref-2)
3. SISMID: Summer Institute in Statistics and Modeling in Infectious Diseases at the University of Washington at Seattle [↑](#footnote-ref-3)
4. The funds were matched through North Carolina State University [↑](#footnote-ref-4)
5. SAMSI: The Statistical and Applied Mathematical Sciences Institute [↑](#footnote-ref-5)
6. SISG: Summer Institute in Statistical Genetics at the University of Washington at Seattle [↑](#footnote-ref-6)
7. ASSIST: The Center for Advanced Self-Powered Systems of Integrated Sensors and Technologies [↑](#footnote-ref-7)