

# Xiang Ji, Ph.D.

*Last Updated on 05/08/2024*

Assistant Professor, Department of Mathematics

Tulane University, New Orleans, LA, 70118

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

Google Scholar: <https://scholar.google.com/citations?user=YH4BbIMAAAJ&hl=en>



## EDUCATION

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### Doctor of Philosophy in Bioinformatics and Statistics (Co-Major)

*December*

*North Carolina State University, Raleigh, NC*

*2017*

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*

*North Carolina State University, Raleigh, NC*

*2013*

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

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### Faculty Member

*October 2021 – Present*

*Cancer Center, Tulane University, New Orleans, LA*

### Assistant Professor

*July 2020 – Present*

*Department of Mathematics, Tulane University, New Orleans, LA*

### Postdoctoral Fellow

*January 2018 – July 2020*

*University of California, Los Angeles, CA*

## 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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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.btac030.
  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, W.T., 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 Gethah 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 Respirivirus 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/Al<sub>2</sub>O<sub>3</sub>/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

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### 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

<b>Committee Chair (Doctoral)</b>	2023 –
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	<i>Present</i>
<ul style="list-style-type: none"> <li>• Student name: Yufei Zou</li> <li>• Research Title: Evolutionary Inference with Interlocus Gene Conversion</li> </ul>	
<b>Committee Chair (Doctoral)</b>	2022 –
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	<i>Present</i>
<ul style="list-style-type: none"> <li>• Student name: Yuwei Bao</li> <li>• Research Title: Reflective Hamiltonian Monte Carlo method</li> </ul>	
<b>Oral Exam Committee Member (Doctoral)</b>	2024
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> <li>• Student name: John V. Argentino</li> <li>• Chair: Michelle Lacey</li> </ul>	
<b>Prospectus Exam Committee Member (Doctoral)</b>	2024
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> <li>• Student name: Daniela A. Florez Pineda</li> <li>• Chair: Ricardo Cortez</li> <li>• Research title: Mathematical Models for Transmission and Control of Mosquito-borne Diseases</li> </ul>	
<b>Prospectus Exam Committee Member (Doctoral)</b>	2023
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> <li>• Student name: Linh Do</li> <li>• Chair: Scott McKinley</li> <li>• Research title: Statistical Techniques for Comparing Populations of Continuous Piecewise-linear Stochastic Processes</li> </ul>	
<b>Oral Exam Committee Member (Doctoral)</b>	2023
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> <li>• Student name: Moslem Uddin</li> <li>• Chair: Lisa Fauci</li> </ul>	
<b>Oral Exam Committee Chair (Doctoral)</b>	2023
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> <li>• Student name: Yuwei Bao</li> <li>• Chair: Xiang Ji</li> </ul>	
<b>Oral Exam Committee Member (Doctoral)</b>	2023
<i>Department of Mathematics, Tulane University, New Orleans, LA</i>	
<ul style="list-style-type: none"> <li>• Student name: Sinchita Lahiri</li> <li>• Chair: Kyle Kun Zhao</li> </ul>	
<b>Oral Exam Committee Member (Doctoral)</b>	2022

*Department of Mathematics, Tulane University, New Orleans, LA*

- Student name: Linh Do
- Chair: Scott McKinley

**Oral Exam Committee Member (Doctoral)**

2022

*Department of Mathematics, Tulane University, New Orleans, LA*

- Student name: Daniela A. Florez Pineda
- Chair: Ricardo Cortez

**Independent Study Advisor (Master)**

2022

*Department of Mathematics, Tulane University, New Orleans, LA*

- Student name: Paul Pluscht
- Project topic: Review of optimization methods

**Undergraduate Research Advisor (Undergraduate)**

2020 -

*Department of Statistics, North Carolina State University, Raleigh, NC*

2022

- Student name: Yixuan Yang
- Co-advisor: Jeffrey L. Thorne
- Research topic: Quantifying Interlocus Gene Conversion and Natural Selection

**Undergraduate Research Advisor (Undergraduate)**

2021

*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

## AWARDS

HPC Fund Research Cloud Allocation Award <sup>1</sup>	AMD Corporation	2023
NVIDIA Academic Hardware Grant <sup>2</sup>	NVIDIA Corporation	2022
Tuition Scholarship	SISMID <sup>3</sup>	2018
NIEHS Fellowship <sup>4</sup>	North Carolina State University	2015
Graduate Fellow	SAMSI <sup>5</sup>	2014
Tuition Scholarship	SISG <sup>6</sup>	2013
University Graduate Fellowship	North Carolina State University	2011

## FUNDED PROJECTS

### External

**Louisiana Board of Regents Research Competitiveness Subprogram**

07/01/23 –

- Title: Molecular Epidemiology through Scalable Statistical Phylogenetic Modelling
- Principle Investigator: Xiang Ji

06/30/26

<sup>1</sup> 1,080 node hours (targeting 4 MI100 GPUs/node)

<sup>2</sup> Donation of one A100 80Gb PCIe GPU card

<sup>3</sup> SISMID: Summer Institute in Statistics and Modeling in Infectious Diseases at the University of Washington at Seattle

<sup>4</sup> The funds were matched through North Carolina State University

<sup>5</sup> SAMSI: The Statistical and Applied Mathematical Sciences Institute

<sup>6</sup> SISG: Summer Institute in Statistical Genetics at the University of Washington at Seattle



- Total Amount: \$159,000
- Direct Cost: \$159,000

**National Science Foundation**

05/01/23 –  
07/31/24

- 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

**National Institute of Health**

07/01/22 –  
03/31/25

- 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

**National Institute of Health**

04/01/22 –  
03/31/27

- 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

**National Institute of Health**

02/01/20 –  
01/31/22

- 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

**Internal**

**Tulane University CoR Research Fellowship**

05/01/23 –  
05/31/24

- Title: Evolutionary Inference with Interlocus Gene Conversion
- Principle Investigator: Xiang Ji
- Total Amount: \$5,500

## SUBMITTED PROPOSALS

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**National Institute of Health**

2024

- Title: Scalable Evolutionary Inference with Interlocus Gene Conversion
- Principle Investigator: Xiang Ji
- Co-Investigators: None
- Total Amount: \$1,872,750
- Status: Pending

**National Institute of Health**

2023

- 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

**National Institute of Health**

2023

- 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

## CONFERENCE PRESENTATIONS

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### 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

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13	Phylogenetic approach for estimating amounts of interlocus gene conversion in duplications <i>AMS/AWM at Tulane University, New Orleans, LA</i>	12/06/2023
12	Scalable Phylogenetic Inference via Hamiltonian Monte Carlo Method <i>Indiana University, Bloomington, IN</i>	02/03/2023
11	Scalable Phylogenetic Algorithm, Modeling, and Inference <i>North Carolina State University, Raleigh, NC</i>	10/10/2022
10	Smooth Non-Parametric Coalescent Priors for Scalable Divergence Time Estimations <i>AMS/AWM at Tulane University, New Orleans, LA</i>	10/05/2022
9	Scalable Modeling and Inference for Phylogenetics – from Interlocus Gene Conversion to Evolving Pathogens <i>Tulane University, New Orleans, LA</i>	12/04/2019
8	Scalable Modeling and Inference for Phylogenetics – from Interlocus Gene Conversion to Evolving Pathogens <i>Louisiana State University, Baton Rouge, LA</i>	11/04/2019
7	Large-scale Molecular Epidemiology for Viruses <i>University of California, Los Angeles, CA</i>	11/08/2018
6	Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>Zhejiang University, Hangzhou, China</i>	09/18/2018
5	Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>Chinese Academy of Sciences, Beijing, China</i>	09/04/2018
4	Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>CGM Online</i>	05/30/2018
3	Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>Duke University, Durham, NC</i>	02/15/2018
2	Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>Temple University, Philadelphia, PA</i>	04/25/2017
1	Phylogenetic Approaches for Quantifying Interlocus Gene Conversion <i>North Carolina State University, Raleigh, NC</i>	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](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/bit0>.

## **SYNERGISTIC ACTIVITIES**

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### **Grant Panelist**

- I served as a guest panel member for the UK MRC Better Methods, Better Research (BMBR) Panel in 2023.

### **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)
  - *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)
- 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 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<sup>7</sup> 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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<sup>7</sup> ASSIST: The Center for Advanced Self-Powered Systems of Integrated Sensors and Technologies