# Xiang Ji, Ph.D.

*Last Updated on 05/08/2024*

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

## EDUCATION

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

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

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
  Course release
- 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

- o ***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

- o ***Math 7980 Independent Study (3 credits)***

  Level: Graduate (Ph.D.)

  Topics: Bayesian Phylogenetics

  Enrollment: 1

- Spring 2022
  - o ***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

  - o ***Math 7980 Independent Study (3 credits)***

    Level: Graduate (Master)

    Topics: Review of optimization methods

    Enrollment: 1

- Fall 2021
  - o ***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
  - o ***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
  - o ***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

| | |
|---|---|
| **Committee Chair (Doctoral)** | *2023 –* |
| *Department of Mathematics, Tulane University, New Orleans, LA* | *Present* |

- Student name: Yufei Zou
- Research Title: Evolutionary Inference with Interlocus Gene Conversion

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| **Committee Chair (Doctoral)** | *2022 –* |
| *Department of Mathematics, Tulane University, New Orleans, LA* | *Present* |

- Student name: Yuwei Bao
- Research Title: Reflective Hamiltonian Monte Carlo method

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| **Oral Exam Committee Member (Doctoral)** | *2024* |
| *Department of Mathematics, Tulane University, New Orleans, LA* | |

- Student name: John V. Argentino
- Chair: Michelle Lacey

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| **Prospectus Exam Committee Member (Doctoral)** | *2024* |
| *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

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| **Prospectus Exam Committee Member (Doctoral)** | *2023* |
| *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

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|---|---|
| **Oral Exam Committee Member (Doctoral)** | *2023* |
| *Department of Mathematics, Tulane University, New Orleans, LA* | |

- Student name: Moslem Uddin
- Chair: Lisa Fauci

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|---|---|
| **Oral Exam Committee Chair (Doctoral)** | *2023* |
| *Department of Mathematics, Tulane University, New Orleans, LA* | |

- Student name: Yuwei Bao
- Chair: Xiang Ji

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|---|---|
| **Oral Exam Committee Member (Doctoral)** | *2023* |
| *Department of Mathematics, Tulane University, New Orleans, LA* | |

- Student name: Sinchita Lahiri
- Chair: Kyle Kun Zhao

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|---|---|
| **Oral Exam Committee Member (Doctoral)** | *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[1] | AMD Corporation | 2023 |
| NVIDIA Academic Hardware Grant[2] | NVIDIA Corporation | 2022 |
| Tuition Scholarship | SISMID[3] | 2018 |
| NIEHS Fellowship[4] | North Carolina State University | 2015 |
| Graduate Fellow | SAMSI[5] | 2014 |
| Tuition Scholarship | SISG[6] | 2013 |
| University Graduate Fellowship | North Carolina State University | 2011 |

## FUNDED PROJECTS

| **Louisiana Board of Regents Research Competitiveness Subprogram** | 07/01/23 – |
|---|---|
| - Title: Molecular Epidemiology through Scalable Statistical Phylogenetic Modelling | 06/30/26 |
| - Principle Investigator: Xiang Ji | |
| - Total Amount: $159,000 | |

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[1] 1,080 node hours (targeting 4 MI100 GPUs/node)
[2] Donation of one A100 80Gb PCIE GPU card
[3] SISMID: Summer Institute in Statistics and Modeling in Infectious Diseases at the University of Washington at Seattle
[4] The funds were matched through North Carolina State University
[5] SAMSI: The Statistical and Applied Mathematical Sciences Institute
[6] SISG: Summer Institute in Statistical Genetics at the University of Washington at Seattle

- Direct Cost: $159,000

**National Science Foundation** <span style="float:right">05/01/23 – 07/31/24</span>
- 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

**Tulane University CoR Research Fellowship** <span style="float:right">05/01/23 – 05/31/24</span>
- Title: Evolutionary Inference with Interlocus Gene Conversion
- Principle Investigator: Xiang Ji
- Total Amount: $5,500

**National Institute of Health** <span style="float:right">07/01/22 – 03/31/25</span>
- 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** <span style="float:right">04/01/22 – 03/31/27</span>
- 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** <span style="float:right">02/01/20 – 01/31/22</span>
- 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

## SUBMITTED PROPOSALS

**National Institute of Health** <span style="float:right">2024</span>
- 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

**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    12/06/2023

| | | |
|---|---|---|
| | *AMS/AWM at Tulane University, New Orleans, LA* | |
| 12 | Scalable Phylogenetic Inference via Hamiltonian Monte Carlo Method | 02/03/2023 |
| | *Indiana University, Bloomington, IN* | |
| 11 | Scalable Phylogenetic Algorithm, Modeling, and Inference | 10/10/2022 |
| | *North Carolina State University, Raleigh, NC* | |
| 10 | Smooth Non-Parametric Coalescent Priors for Scalable Divergence Time Estimations | 10/05/2022 |
| | *AMS/AWM at Tulane University, New Orleans, LA* | |
| 9 | Scalable Modeling and Inference for Phylogenetics – from Interlocus Gene Conversion to Evolving Pathogens | 12/04/2019 |
| | *Tulane University, New Orleans, LA* | |
| 8 | Scalable Modeling and Inference for Phylogenetics – from Interlocus Gene Conversion to Evolving Pathogens | 11/04/2019 |
| | *Louisiana State University, Baton Rouge, LA* | |
| 7 | Large-scale Molecular Epidemiology for Viruses | 11/08/2018 |
| | *University of California, Los Angeles, CA* | |
| 6 | Phylogenetic Approaches for Quantifying Interlocus Gene Conversion | 09/18/2018 |
| | *Zhejiang University, Hangzhou, China* | |
| 5 | Phylogenetic Approaches for Quantifying Interlocus Gene Conversion | 09/04/2018 |
| | *Chinese Academy of Sciences, Beijing, China* | |
| 4 | Phylogenetic Approaches for Quantifying Interlocus Gene Conversion | 05/30/2018 |
| | *CGM Online* | |
| 3 | Phylogenetic Approaches for Quantifying Interlocus Gene Conversion | 02/15/2018 |
| | *Duke University, Durham, NC* | |
| 2 | Phylogenetic Approaches for Quantifying Interlocus Gene Conversion | 04/25/2017 |
| | *Temple University, Philadelphia, PA* | |
| 1 | Phylogenetic Approaches for Quantifying Interlocus Gene Conversion | 03/24/2017 |
| | *North Carolina State University, Raleigh, NC* | |

## 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 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[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.

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[7] ASSIST: The Center for Advanced Self-Powered Systems of Integrated Sensors and Technologies