

# Xiang Ji

xji4@tualne.edu · <http://xiang-jj-ncsu.github.io/> · Github: @xji3

## EDUCATION

---

<b>Doctor of Philosophy in Bioinformatics and Statistics (Co-Major)</b> <i>North Carolina State University, Raleigh, NC</i> Dissertation: Phylogenetic approaches for quantifying interlocus gene conversion Committee: Jeffrey Thorne, Eric Stone, Nadia Singh, and Sujit Ghosh	<i>December 2017</i>
<b>Master of Science in Material Science and Engineering</b> <i>North Carolina State University, Raleigh, NC</i> Thesis: Laser interference lithography for fabrication of gas sensors Committee: John Muth, Lew Reynolds, Michael Kudenov, and Jon-Paul Maria	<i>September 2013</i>
<b>Bachelor of Science in Economics (Double Major)</b> <i>Peking University, Beijing, China</i>	<i>July 2011</i>
<b>Bachelor of Science in Physics</b> <i>Peking University, Beijing, China</i> Advisor: Jia-sen Zhang	<i>July 2011</i>

## RESEARCH INTERESTS

---

Multigene family evolution; phylogenetics with large data sets; development of statistical techniques and software

## RESEARCH EXPERIENCE

---

<b>Postdoc Project</b> <i>Advisor: Marc Suchard</i> <i>Department of Biomathematics and Human Genetics</i> <i>University of California, Los Angeles, CA</i> <ul style="list-style-type: none"><li>Phylogenetic analysis of large viral (and other) data sets via linear time scalable algorithm for calculating likelihood gradient</li><li>Hamiltonian Monte Carlo methods</li><li>C implementation in BEAGLE with CPU and GPU versions</li><li>Java implementation in BEAST</li></ul>	<i>Spring 2018 – Summer 2020</i>
<b>Dissertation Project</b> <i>Advisor: Jeffrey Thorne</i> <i>Bioinformatics Research Center and Department of Statistics</i> <i>North Carolina State University, Raleigh, NC</i> <ul style="list-style-type: none"><li>Developed the first statistical phylogenetic model that can quantify interlocus gene conversion in multigene family evolution</li><li>Found that high proportion of nucleotide substitutions in multigene families originated with interlocus gene conversion rather than point mutation</li><li>Implementation in Python of the approaches into freely available software</li><li>Resulted in a successful NSF grant award (DEB 1754142)</li></ul>	<i>Fall 2013 – Fall 2017</i>

**Consulting Project***Spring 2016**Employer: Jenny (Qiu-yun) Xiang**Bioinformatics Research Center and Department of Statistics**North Carolina State University, Raleigh, NC*

- De novo assembly of genotyping-by-sequencing reads into DNA sequences
- Population structure analysis
- Species distribution study of past and future over North America

**Collaborative Project***Fall 2013 – Spring 2014**Collaborator: Kuangyu Wang**Bioinformatics Research Center and Department of Statistics**North Carolina State University, Raleigh, NC*

- Data mining of solvent accessibility information from protein coding genes in several species

**Master Thesis***Fall 2011 – Spring 2013**Advisor: John Muth**Department of Material Science and Engineering**North Carolina State University, Raleigh, NC*

- Derivation of laser interference lithography theory and Matlab implementation of simulation
- Experimental setup of the laser interference lithography in cleanroom
- Fabrication of ozone gas sensor
- Gas sensor characterization

**Undergraduate Thesis Project***Fall 2010 – Fall 2011**Advisor: Zhiping Zhou**School of Electronics Engineering and Computer Science**Peking University, Beijing, China*

- Optimization of surface plasmon source doping location inside a waveguide

**Undergraduate Research Project***Fall 2009 – Fall 2011**Advisor: Jia-sen Zhang**School of Physics**Peking University, Beijing, China*

- Fortran implementation of 3D surface plasmon light scattering simulation
- Plasmonic lens design with rectangular-shaped slots for sharp focus
- Fabrication of the lens on 200nm gold thin film on glass
- Experimental characterization

**WORKING & TEACHING EXPERIENCE**

---

**Postdoc Researcher***January 2018 – Present**Advisor: Marc Suchard**Department of Biomathematics and Human Genetics**University of California, Los Angeles, CA*

- Develop and implement novel phylogenetic algorithms
- Mentor Ph.D. students in the Department of Biomath and the Department of Biostatistics
- Collaborative work in Center for Viral Systems Biology (<https://cvisb.org/>) and Artic Network (<http://artic.network/>)

## Research Assistant

Fall 2013 – Fall 2017

Advisor: Jeffrey Thorne

Bioinformatics Research Center and Department of Statistics

North Carolina State University, Raleigh, NC

- Development of phylogenetic approaches for quantifying interlocus gene conversion in multigene family evolution
- Mentored two undergraduate summer research assistants (one on ancestral sequence reconstruction and one on the evolutionary alignment of protein tertiary structure)

## Research & Teaching Assistant

Fall 2011 – Summer 2013

Department of Material Science and Engineering

North Carolina State University, Raleigh, NC

- Develop Interference laser lithography in Dr. John Muth's lab
- Teach computational laboratory on thin-film interference to MSE undergraduates
- Help design a new MSE undergraduate course on data analysis and experimental design

## PUBLICATIONS

---

- He, W., et al., (2021) Phylogeography finds association between swine trade and the spread of porcine epidemic diarrhea virus in China and across the world. *submitted*
- Lemey, P., et al., (2021) SARS-CoV-2 European resurgence foretold: interplay of introductions and persistence by leveraging genomic and mobility data. *submitted*
- Fisher, A., **Ji, X.**, Nishimura, A., & Suchard, M. A. (2020) Shrinkage-based random local clocks with scalable inference. *in prep*
- Lemey, P., **Ji, X.**, Membrebe, J. V., Martin, D., & Suchard, M. A. (2020) Reconciling fast Hepatitis B evolutionary rates with ancient co-divergence. *in prep*
- Holbrook, A. J., **Ji, X.**, & Suchard, M. A. (2020) Bayesian mitigation of spatial coarsening for a fairly flexible spatiotemporal Hawkes model. *Submitted*, arXiv:2010.02994[stat.ME]
- He, W., Liao, M., Zhao, W., Sun, J., Zhao, J., Wang, L., Meng, X., Zhou, J., **Ji, X.**, Suchard, M. A., Zhang, X., Su, S., & Veit, M. (2020) Cross-species transmission of viruses from bats. Submitted to *Cell Reports*
- Lindelof, K., Lindo, J. A., Zhou, W., **Ji, X.**, & Xiang, Q. Y. J. (2020) Phylogenomics, biogeography, and evolution of the blue - or white - fruited dogwoods (Cornus) - insights into morphological and ecological niche divergence following intercontinental geographic isolation. *Journal of Systematics and Evolution*
- Sun, J., He, W. T., Wang, L., Lai, A., **Ji, X.**, Zhai, X., ... & Veit, M. (2020). COVID-19: epidemiology, evolution, and cross-disciplinary perspectives. *Trends in Molecular Medicine*.
- He, W. \*, **Ji, X. \***, He, W. \*, Dellicour, S. \*, ..., & Su, S. (2020) Genomic epidemiology, evolutionary dynamics, and transmission patterns of porcine deltacoronavirus. *Molecular Biology and Evolution*, \*equal contribution
- Zhang, Z., Nishimura, A., Bastide, P., **Ji, X.**, Payne, R. P., Goulder, P., Lemey, P., & Suchard, M. A. (2020) Large-scale inference of correlation among mixed-type biological traits with phylogenetic multivariate probit models. *Annals of Applied Statistics*, arXiv:1912.09185 [stat.ME]
- Ji, X.**, Zhang, Z., Holbrook, A., Nishimura, A., Baele, G., Rambaut, A., Lemey, P., & Suchard, M. A. (2020) Gradients do grow on trees: a linear-time O(N)-dimensional gradient for statistical phylogenetics. *Molecular Biology and Evolution*, arXiv:1905.12146 [stat.CO]
- Fisher, A., **Ji, X.**, Zhang, Z., Lemey, P., & Suchard, M. A. (2020) Relaxed random walks at scale. *Systematic Biology*, arXiv:1906.04834[q-bio.PE]
- Bleetsa, M., Suchard, M. A., **Ji, X.**, Gryseels, S., Vrancken, B., Baele, G., Worobey, M., & Lemey, P. (2019) Divergence dating using mixed effects clock modelling: an application to HIV-1. *Virus Evolution*, 5(2), vez036.

- Ji, X.,** Thorne, J. L. (2019) A phylogenetic approach disentangles the tract length and initiation rate of interlocus gene conversions. *in submission*, arXiv:1908.08608 [q-bio.PE]
- Li, G., Zhang, W., Wang, R., Xing, G., Wang, S., **Ji, X.**, ... & Zhou, J. (2019). Genetic Analysis and Evolutionary Changes of the Torque teno sus Virus. *International journal of molecular sciences*, 20(12), 2881.
- Zhou, W., **Ji, X.**, Obata, S., Pais, A., Dong, Y., Peet, R., & Xiang, Q., (2018) Resolving relationships and phylogeographic history of the Nyssa sylvatica complex using data from RAD-seq and species distribution modeling. *Molecular Phylogenetic and Evolution*, 126, 1-16.
- Ji, X.** (2017). Phylogenetic approaches for quantifying interlocus gene conversion. Doctoral Dissertation
- Ji, X.**, Griffing, A., & Thorne, J. L. (2016). A phylogenetic approach finds abundant interlocus gene conversion in yeast. *Molecular Biology and Evolution*, 33(9), 2469-2476.
- Wang, K., Yu, S., **Ji, X.**, Lakner, C., Griffing, A., & Thorne, J. L. (2015). Roles of Solvent Accessibility and Gene Expression in Modeling Protein Sequence Evolution. *Evolutionary Bioinformatics*, 11, 85.
- Ji, X.** (2013). Laser Interference Lithography for Fabrication of Gas Sensors. Master Thesis
- Han, X., **Ji, X.**, Wen, H., & Zhang, J. (2012). H-shaped resonant optical antennas with slot coupling. *Plasmonics*, 7(1), 7-11.
- Xiao, G., **Ji, X.**, Gao, L., Wang, X., & Zhou, Z. (2012). Effect of dipole location on profile properties of symmetric surface plasmon polariton mode in Au/Al<sub>2</sub>O<sub>3</sub>/Au waveguide. *Frontiers of Optoelectronics*, 5(1), 63-67.

## Awards

Tuition Scholarship	SISMID <sup>1</sup>	2018
NIEHS Fellowship <sup>2</sup>	North Carolina State University	2015
Graduate Fellow	SAMSI <sup>3</sup>	2014
Tuition Scholarship	SISG <sup>4</sup>	2013
University Graduate Fellowship	North Carolina State University	2011

## CONFERENCE PRESENTATIONS

### ORAL PRESENTATIONS

- Ji, X.** (2018, September). *Large-scale molecular epidemiology for viruses: efficient algorithms and new models*. Oral session presented at the Taishan Forum on Viral Infectious Diseases, Taishan Medical University, Tai'an, Shandong Province, China
- Ji, X.** (2017, August). *Phylogenetic approaches for quantifying interlocus gene conversion*. Quest for Ortholog 5 Meeting, University of Southern California, Los Angeles, CA, US

### POSTER PRESENTATIONS

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

## Invited Talks

<i>Scalable Modeling and Inference for Phylogenetics</i> -from Interlocus Gene Conversion to Evolving Pathogens	Tulane University	12/04/2019
<i>Scalable Modeling and Inference for Phylogenetics</i> -from Interlocus Gene Conversion to Evolving Pathogens	Louisiana State University	11/04/2019

<sup>1</sup> SISMID: Summer Institute in Statistics and Modeling in Infectious Diseases at University of Washington at Seattle

<sup>2</sup> The funds were matched through North Carolina State University

<sup>3</sup> SAMSI: The Statistical and Applied Mathematical Sciences Institute

<sup>4</sup> SISG: Summer Institute in Statistical Genetics at University of Washington at Seattle

<i>Large-scale molecular epidemiology for viruses</i>	UCLA	11/08/2018
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	Zhejiang University	09/18/2018
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	Chinese Academy of Sciences	09/04/2018
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	CGM online	05/30/2018
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	Duke University	02/15/2018
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	Temple University	04/25/2017
<i>Phylogenetic approaches for quantifying interlocus gene conversion</i>	N.C. State University	03/24/2017

## Funding

---

My dissertation project leads to an NSF grant award (DEB 1754142)

## Software

---

- My software for studying interlocus gene conversion is freely available at <https://github.com/xji3/IGCexpansion>.
- A tutorial for the Bayesian method (under development) of quantifying interlocus gene conversion in BEAST is available at [https://github.com/xji3/IGC\\_BEAST\\_Tutorial](https://github.com/xji3/IGC_BEAST_Tutorial)
- I'm a developer of the BEAST (<https://github.com/beast-dev/beast-mcmc>) software and the BEAGLE (<https://github.com/beagle-dev/beagle-lib>) library.
- I collaborate with a group of statisticians and programmers to help them use my linear-time gradient algorithm implementations for their variational Bayesian phylogenetics development at <https://github.com/phylovi/libsbm>.

## Synergistic Activities

---

### Professional service

- I have reviewed manuscripts for *Molecular Biology and Evolution*, *Annals of Applied Statistics*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, and *Evolutionary Bioinformatics*.

### Outreach

- I served as treasurer on the ASSIST<sup>5</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.

---

<sup>5</sup> ASSIST: The Center for Advanced Self-Powered Systems of Integrated Sensors and Technologies