

Xiang Ji

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EDUCATION

Doctor of Philosophy in Bioinformatics and Statistics (Co-Major) <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>
Master of Science in Material Science and Engineering <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>
Bachelor of Science in Economics (Double Major) <i>Peking University, Beijing, China</i>	<i>July 2011</i>
Bachelor of Science in Physics <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

Postdoc Project <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">Phylogenetic analysis of large viral (and other) data sets via linear time scalable algorithm for calculating likelihood gradientHamiltonian Monte Carlo methodsC implementation in BEAGLE with CPU and GPU versionsJava implementation in BEAST	<i>Spring 2018 – Summer 2020</i>
Dissertation Project <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">Developed the first statistical phylogenetic model that can quantify interlocus gene conversion in multigene family evolutionFound that high proportion of nucleotide substitutions in multigene families originated with interlocus gene conversion rather than point mutationImplementation in Python of the approaches into freely available softwareResulted in a successful NSF grant award (DEB 1754142)	<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

- 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*
- 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. (2019) Large-scale inference of correlation among mixed-type biological traits with phylogenetic multivariate probit models. Revised and resubmitted to *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. (2019) 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.**, Lemey, P., & Suchard, M. A. (2019) Relaxed random walks at scale. Accepted by *Systematic Biology*, arXiv:1906.04834[q-bio.PE]
- 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.
- 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/Al₂O₃/Au waveguide. *Frontiers of Optoelectronics*, 5(1), 63-67.

Awards

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

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

² The funds were matched through North Carolina State University

³ SAMSI: The Statistical and Applied Mathematical Sciences Institute

⁴ SISG: Summer Institute in Statistical Genetics at University of Washington at Seattle

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
- 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 ASSIST⁵ 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.

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