**Xiang Ji**

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**EDUCATION**

**Doctor of Philosophy in Bioinformatics and Statistics (Co-Major)** *December 2017*

*North Carolina State University, Raleigh, NC*

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 2013*

*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

**Bachelor of Science in Physics** *July 2011*

*Peking University, Beijing, China*

Advisor: Jia-sen Zhang

**Bachelor of Science in Economics (Double Major)** *July 2011*

*Peking University, Beijing, China*

**RESEARCH INTERESTS**

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

**RESEARCH EXPERIENCE**

**Postdoc Project**  *Spring 2018 – Present*

*Advisor: Marc Suchard*

*Department of Biomathematics and Human Genetics*

*University of California, Los Angeles, CA*

* Phylogenetic analysis of large viral (and other) data sets via linear time scalable algorithm for calculating likelihood gradient
* Hamiltonian Monte Carlo methods
* C implementation in BEAGLE with CPU and GPU versions
* Java implementation in BEAST

**Dissertation Project** *Fall 2013 – Fall 2017*

*Advisor: Jeffrey Thorne*

*Bioinformatics Research Center and Department of Statistics*

*North Carolina State University, Raleigh, NC*

* Developed the first phylogenetic model that can quantify interlocus gene conversion in multigene family evolution
* Found that high proportion of nucleotide substitutions in multigene families originated with interlocus gene conversion rather than point mutation
* Implementation in Python of the approaches into freely available software
* Resulted in a successful NSF grant award (DEB 1754142)

**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/) (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**

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*

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. submitted 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. in revision, submitted to *Molecular Biology and Evolution*, arXiv:1905.12146 [stat.CO]

Fisher, A., **Ji, X.,** Lemey, P., & Suchard, M. A. (2019) Relaxed random walks at scale. *in review*, 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**

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| Tuition Scholarship | SISMID[[1]](#footnote-1) | 2018 |
| NIEHS Fellowship[[2]](#footnote-2) | North Carolina State University | 2015 |
| Graduate Fellow | SAMSI[[3]](#footnote-3) | 2014 |
| Tuition Scholarship | SISG[[4]](#footnote-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**

*Scalable Modeling and Inference for Phylogenetics* Tulane University 12/04/2019

-from Interlocus Gene Conversion to Evolving Pathogens

*Scalable Modeling and Inference for Phylogenetics* Louisiana State University 11/04/2019

-from Interlocus Gene Conversion to Evolving Pathogens

*Large-scale molecular epidemiology for viruses* UCLA 11/08/2018

*Phylogenetic approaches for quantifying interlocus gene conversion* Zhejiang University 09/18/2018

*Phylogenetic approaches for quantifying interlocus gene conversion* Chinese Academy of Sciences 09/04/2018

*Phylogenetic approaches for quantifying interlocus gene conversion* CGM online 05/30/2018

*Phylogenetic approaches for quantifying interlocus gene conversion* Duke University 02/15/2018

*Phylogenetic approaches for quantifying interlocus gene conversion* Temple University 04/25/2017

*Phylogenetic approaches for quantifying interlocus gene conversion* 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>
* 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/libsbn>.

**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[[5]](#footnote-5) 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. SISMID: Summer Institute in Statistics and Modeling in Infectious Diseases at University of Washington at Seattle [↑](#footnote-ref-1)
2. The funds were matched through North Carolina State University [↑](#footnote-ref-2)
3. SAMSI: The Statistical and Applied Mathematical Sciences Institute [↑](#footnote-ref-3)
4. SISG: Summer Institute in Statistical Genetics at University of Washington at Seattle [↑](#footnote-ref-4)
5. ASSIST: The Center for Advanced Self-Powered Systems of Integrated Sensors and Technologies [↑](#footnote-ref-5)