Alexander T. Xue

Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory

One Bungtown Road, Cold Spring Harbor, NY 11724

516-367-8395; xanderxue@gmail.com; http://www.xanderxue.com

POSITIONS

- Computational Postdoctoral Fellow; Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory; Supervisor: Adam C. Siepel; 2018-Present
- Post-Doctoral Associate; Human Genetics Institute of New Jersey and Department of Genetics, Rutgers University; Supervisor: Andrew D. Kern; 2017-2018

EDUCATION

- Ph.D. in Biology (Ecology, Evolutionary Biology, and Behavior); Graduate Center and City College of the City University of New York; Advisor: Michael J. Hickerson; 2012-2017
- M.S. for Teachers in Adolescent Education; Pace University; Advisor: James F. Kilbane; 2009-2011
- B.S. in Conservation and Resource Studies; University of California, Berkeley; Advisor: Jeffrey L. Boore; 2005-2007

PUBLICATIONS

- **Xue AT**, Schrider DR, Kern AD, Ag1000G Consortium. 2021. *Discovery of ongoing selective sweeps within Anopheles mosquito populations using deep learning*. Molecular Biology and Evolution. 38(3) 1168-1183.
- Bertola LD, Boehm JT, Putman NF, **Xue AT**, Robinson JD, Harris S, Baldwin CC, Overcast I, Hickerson MJ. 2020. *Asymmetrical gene-flow in five co-distributed syngnathids explained by ocean currents and rafting propensity*. Proceedings of the Royal Society B: Biological Sciences. 287(1926) 20200657.
- **Xue AT**, Hickerson MJ. 2020. *Comparative phylogeographic inference with genome-wide data from aggregated population-pairs*. Evolution. 74(5) 808-830.
- Thom G, **Xue AT**, Sawakuchi AO, Ribas CC, Hickerson MJ, Aleixo A, Miyaki C. 2020. *Quaternary climate changes as speciation drivers in the Amazon Floodplains*. Science Advances. 6(11), eaax4718.
- Myers EA, **Xue AT**, Gehara M, Cox CL, Davis Rabosky AR, Lemos-Espinal J, Martínez-Gómez JE, Burbrink FT. 2019. *Environmental heterogeneity and not vicariant biogeographic barriers generate community-wide population structure in desert-adapted snakes*. Molecular Ecology. 28(20), 4535-4548.
- **Xue AT**, Ruggiero RP, Hickerson MJ, Boissinot S. 2018. *Differential effect of selection against LINE retrotransposons among vertebrates inferred from whole-genome data and demographic modeling*. Genome Biology and Evolution. 10(5), 1265-1281.
- Potter S, **Xue AT**, Bragg JG, Rosauer DF, Roycroft EJ, Moritz C. 2018. *Pleistocene climatic changes drive diversification across a tropical savanna*. Molecular Ecology. 27(2), 520-532.

- Mastretta-Yanes A, **Xue AT**, Moreno-Letelier A, Jorgensen TH, Alvarez N, Piñero D, Emerson BC. 2018. *Long-term in situ persistence of biodiversity in tropical sky islands revealed by landscape genomics*. Molecular Ecology. 27(2), 432-448.
- **Xue AT**, Hickerson MJ. 2017. *Multi-DICE: R package for comparative population genomic inference under hierarchical co-demographic models of independent single-population size changes.* Molecular Ecology Resources. 17(6), e212-e224.
- Prates I, **Xue AT**, Brown JL, Alvarado-Serrano DF, Rodrigues MT, Hickerson MJ, Carnaval AC. 2016. *Inferring responses to climate dynamics from historical demography in neotropical forest lizards.* Proceedings of the National Academy of Sciences. 113(29), 7978-7985.
- Harris SE, **Xue AT**, Alvarado-Serrano D, Boehm JT, Joseph T, Hickerson MJ, Munshi-South J. 2016. *Urbanization shapes the demographic history of a native rodent (the white-footed mouse, Peromyscus leucopus) in New York City.* Biology Letters. 12(4), 20150983.
- **Xue AT**, Hickerson MJ. 2015. *The aggregate site frequency spectrum for comparative population genomic inference.* Molecular Ecology. 24(24), 6223-6240.

SOFTWARE PACKAGES

- **Xue AT**, Schrider DR, Kern AD. *partialS/HIC: Python software for detecting selective sweeps, including partial hard sweeps and partial soft sweeps.*
- **Xue AT**. *Multi-DICE: R package for constructing hierarchical co-demographic models and simulating multi-taxa summary statistic vectors*.

INVITED PRESENTATIONS

- **Xue AT**. 2019. *Comparative population genomic inference of demography and selection*. Keynote Speaker at Mexico Population Genomics Meeting.
- **Xue AT**. 2018. *Comparative population genomic inference: detecting partial selective sweeps with deep learning and hierarchical co-demographic modeling*. Seminar at Cold Spring Harbor Laboratory.
- **Xue AT**. 2018. *Comparative population genomic inference: hierarchical co-demographic models and detecting partial selective sweeps.* Seminar at Temple University.
- **Xue AT**. 2016. *Comparative phylogeographic and population genomic inference under hierarchical models.* Seminar at Harvard University.
- **Xue AT**, Hickerson MJ. 2015. *Novel method for next-generation comparative phylogeography and population genomics.* Atlantic Forest Dimensions of Biodiversity Meeting.
- **Xue AT**. 2014. *What can we do with our personal genomic data?* National Genographic and American Museum of Natural History New York City Student Ancestry Event.

CONTRIBUTED PRESENTATIONS

- **Xue AT**, Huang YF, Siepel A. 2021. *ASSESS: Estimating a complex trait's genome-wide distribution of selection coefficients and effect sizes from GWAS summary statistics under a likelihood model*. Cold Spring Harbor Laboratory Simons Center for Quantitative Biology Bioinformatics and Computational Biology Seminar.

- **Xue AT**, Huang YF, Siepel A. 2020. *Likelihood model that uses GWAS summary statistics to estimate strength of polygenic selection underlying a complex trait*. New York Area Population Genomics Workshop.
- **Xue AT**, Huang YF, Siepel A. 2019. *Estimating distribution of fitness effects (DFE) from GWAS statistics within a likelihood framework*. The Biology of Genomes Meeting. (Poster)
- **Xue AT**, Schrider DR, Kern AD. 2018. *Probing the genomic signatures of insecticide resistance in the malaria vector Anopheles gambiae via deep learning*. GSA Population, Evolutionary, and Quantitative Genetics Conference. (Poster)
- **Xue AT**, Hickerson MJ. 2016. *Comparative phylogeographic and population genomic inference under hierarchical multi-taxa co-divergence models.* Evolution Meeting.
- **Xue AT**, Hickerson MJ. 2015. *Novel method for next-generation comparative phylogeography and population genomics.* Evolution Meeting.
- **Xue AT**, Hickerson MJ. 2015. *New method for demographic inference of comparative population genomic data.* New York Area Population Genomics Workshop.
- **Xue AT**, Hickerson MJ. 2014. *The multi-species allele frequency spectrum (msAFS) for next-generation comparative phylogeography.* Evolution Meeting.
- **Xue AT**, Hickerson MJ. 2014. *Using the multi-species allele frequency spectrum (AFS) for community-level demographic inference.* International Biogeography Society Early Career Conference.
- **Xue AT**, Hickerson MJ. 2013. *Detecting melting pots and hotspots among Australian communities.* Software and Statistical Methods for Population Genetics. (Poster)

AWARDS, GRANTS, AND FELLOWSHIPS

- City University of New York Science Scholarship; Tuition and Stipend; 2012-2017
- Segal AmeriCorps Education Award; $4,725 toward educational expenses; 2009-2010
- New York City Teaching Fellowship; Tuition and Salary; 2009-2011

TEACHING EXPERIENCE – WORKSHOPS

- Multi-DICE R package: Hierarchical co-demographic inference for comparative phylogeography; CompPhylo Workshop, University of Oslo; Summer 2019
- Hierarchical co-demographic inference with Multi-DICE R package; Universidad Nacional Autónoma de México; Spring 2019
- Demographic modeling and population genomic inference; University of Texas, Arlington; Spring 2017
- Model-based demographic inference using sub-genomic data for comparative phylogeography; University of Adelaide; Fall 2015
- Model-based statistical inference of demographic histories for comparative phylogeographic purposes using Next-Generation Sequencing data; Australian National University; Fall 2015

TEACHING EXPERIENCE – COURSES

- Biological Foundations II; City College of the City University of New York; Fall 2016 (2 sections), Spring 2015, Fall 2014
- Evolution (Guest Lecture); Graduate Center of the City University of New York; Fall 2015

- Statistical Inference in Phylogeography (Guest Lecture); Graduate Center of the City University of New York; Fall 2014
- Anthropological Genomics; City College of the City University of New York; Spring 2014
- Licensed and Certified Secondary School Teacher; New York City Department of Education: Frederick Douglass Academy, International High School at Prospect Heights; 2009-2011
  - Special education mathematics and special education science (middle school); biology, ELL (English Language Learners) science, and English (high school)

POPULAR PRESS

- BreakThru Radio. 2014. *Finding Human Identity Through Genomics - Identity Week.* http://www.breakthruradio.com/#/post/?blog=72&post=36017.

STUDENTS MENTORED

- Malouf, Georgio; Undergraduate (City College of the City University of New York); 2015-2017

GRANT PROPOSALS REVIEW

- *The Great Lakes Fishery Commission*

PEER REVIEW

- *Molecular Biology and Evolution*
- *Methods in Ecology and Evolution*
- *Systematic Biology*
- *TREE*
- *Molecular Ecology*
- *PLOS ONE* (3)