

Jeffrey R. Adrion

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PROFESSIONAL SUMMARY

- ♦ Nine years of experience in project design, statistical problem solving, data analysis, and code development
- ♦ Strong communication skills demonstrated by numerous presentations and publications in leading journals

EXPERIENCE

University of Oregon

August 2018-Present

Postdoctoral research associate

Eugene, OR

- ♦ Design machine learning software for population genomic analyses
- ♦ Identify methods to improve robustness for deep learning applications
- ♦ Optimize statistical data analysis pipelines for genome-size datasets
- ♦ Team-develop genomic simulation models for comparative methods testing
- ♦ Manage TB-scale datasets and analysis pipelines across HPC clusters

Indiana University

August 2012-July 2018

PhD student researcher

Bloomington, IN

- ♦ Developed software for the population genomic analysis of transposable elements
- ♦ Designed and managed multi-year projects with numerous remote collaborators
- ♦ Analyzed genomic sequence data from natural populations using HPC clusters
- ♦ Tested theoretical predictions and compared statistical models

North Carolina State University

May 2011-July 2012

Research assistant

Raleigh, NC

- ♦ Designed experiments, collected and analyzed data, and developed PCR primers
- ♦ Prepared samples for sequencing and performed gel electrophoresis
- ♦ Sampled animals from nature and performed field surveys of rare butterflies

EDUCATION

Indiana University, *PhD in Biology*

Bloomington, IN

North Carolina State University, *BS summa cum laude in Zoology*

Raleigh, NC

University of Central Florida, *BS in Psychology*

Orlando, FL

TECHNICAL SKILLS

- ♦ **Coding languages:** Python, R, Bash, C++
- ♦ **Technologies:** Unix, Vim, Git, PyPI, HSI, HPCs, HPSS, Tensorflow, Keras, Conda, Snakemake, Numpy, Pandas, scipy, sklearn, scikit-allel, cleverhans, msprime, SLiM, LaTeX, jupyter, Microsoft office
- ♦ **Laboratory skills:** genomic sequencing preparations, primer design, gel electrophoresis, microinjection
- ♦ **Other skills:** project design and management, large-scale data management, cloud computing, technical writing, student training and supervision

SOFTWARE

i-Against-i A deep learning software pipeline that predicts population expansions using adversarial training
<https://github.com/jradrion/i-against-i>

ReLERNN A deep learning software pipeline that uses recurrent neural networks to infer the genome-wide landscape of recombination rates directly from raw polymorphism data
<https://github.com/jradrion/ReLERNN>

TEFLoN A software pipeline that uses paired-end Illumina sequence data to discover novel transposable element insertions and estimate their allele frequencies
<https://github.com/jradrion/TEFLoN>

- simpoolTE** A program that simulates the insertion and deletion of transposable elements in a pooled population of chromosomes
<https://github.com/jradrion/simpoolTE>
- PopSim** A community-maintained library of standardized population genetic simulation models
<https://github.com/popsim-consortium>

PUBLICATIONS

- Adrion, J.R.**, C.B. Cole, N. Dukler, J.G. Galloway, A.L. Gladstein, G. Gower, C.C. Kyriazis, A.P. Ragsdale, G. Tsambos, F. Baumdicker, J. Carlson, R.A. Cartwright, A. Durvasula, B.Y. Kim, P. McKenzie, P.W. Messer, E. Noskova, D. Ortega-Del Vecchyo, T.J. Struck, S. Gravel, R.N. Gutenkunst, P.L. Ralph, D.R. Schrider, A. Siepel, J. Kelleher, and A.D. Kern. (2020). A community-maintained standard library of population genetic models. *eLife*. doi:10.7554/eLife.54967
- Adrion, J.R.**, J.G. Galloway, and A.D. Kern. (2020). Prediction the landscape of recombination using deep learning. *Molecular Biology and Evolution*. doi:10.1093/molbev/msaa038
- Alcalay, Y., S. Fuchs, R. Galizi, F. Bernardini, R.E. Haghghat-Khah, D.B. Rusch, **J.R. Adrion**, M.W. Hahn, P. Tortosa, and P.A. Papatathanos. (2019). The potential for a released autosomal X-shredder becoming a driving-Y chromosome and invasively suppressing wild populations of malaria mosquitoes. *bioRxiv*. doi:10.1101/860551
- Wepprich, T., L. Ries, J. Wiedmann, **J.R. Adrion**, N.M. Haddad. (2019). Butterfly abundance declines over 20 years of systematic monitoring in Ohio, USA. *PLOS One*. 14(7). doi:10.1371/journal.pone.0216270
- Adrion, J.R.**. (2018). *The roles of spatially varying selection and constraint in shaping genomic variation* (Doctoral dissertation). Indiana University. Bloomington, IN.
- Adrion, J.R.**, D.J. Begun, and M.W. Hahn. (2019). Patterns of transposable element variation and clinality in *Drosophila*. *Molecular Ecology*. 28(6): 1523-1536. doi:10.1111/mec.14961
- Adrion, J.R.**, M.J. Song, D.R. Schrider, M.W. Hahn, and S. Schaack. (2017). Genome-wide estimates of transposable element insertion and deletion rates in *Drosophila melanogaster*. *Genome Biology and Evolution*. 9(5): 1329-1340. doi:10.1093/gbe/evx05
- Adrion, J.R.**, P.S. White, and K.L. Montooth. (2016). The roles of compensatory evolution and constraint in aminoacyl tRNA synthetase evolution. *Molecular Biology and Evolution*. 33(1): 151-162. doi:10.1093/molbev/msv206
- Adrion, J.R.**, M.W. Hahn, and B.S. Cooper. (2015). Revisiting classis clines in *Drosophila melanogaster* in the age of genomics. *Trends in Genetics*. 31(8): 434-444. doi:10.1016/j.tig.2015.05.006
- Adrion, J.R.**, A. Kousathanas, M. Pascual, H.J. Burrack, N.M. Haddad, A. Bergland, H. Machado, T. Sackton, T. Schlenke, M. Watada, D. Wegmann, and N.D. Singh. (2014). *Drosophila suzukii*: the genetic footprint of a recent, worldwide invasion. *Molecular Biology and Evolution*. 31(12): 3148-3163. doi:10.1093/molbev/msu246

PRESENTATIONS

- ♦ The Allied Genetics Conference. (2020). *Poster presentation*. Virtual
- ♦ Society for Molecular Biology and Evolution. (2019). *Symposium speaker*. Manchester, United Kingdom
- ♦ Population, Evolutionary, and Quantitative Genetics. (2018). *Poster presentation*. Madison, WI
- ♦ Society for Molecular Biology and Evolution. (2017). *Symposium speaker*. Austin, TX
- ♦ Evolution. (2016). *Symposium speaker and Poster presentation*. Austin, TX
- ♦ Midwest Ecology and Evolution Conference. (2015). *Poster presentation*. Bloomington, IN
- ♦ 56th Annual *Drosophila* Research Conference. (2015). *Poster presentation*. Chicago, IL
- ♦ Evolution. (2014). *Symposium speaker*. Raleigh, NC
- ♦ Society for Molecular Biology and Evolution. (2014). *Symposium speaker*. San Juan, Puerto Rico
- ♦ Evolution. (2013). *Poster presentation*. Snowbird, UT
- ♦ 53rd Annual *Drosophila* Research Conference. (2012). *Poster presentation*. Chicago, IL

FELLOWSHIPS, GRANTS & AWARDS

National Science Foundation Graduate Research Fellowship (est. \$150,000)	2013-2018
Society for the Study of Evolution Rosemary Grant Award (\$2100)	2013
NIH Training Grant in Genetics, Cellular, and Molecular Science (\$100,000)	2013-2015