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 fellow   *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 candidate   *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++, C
- **Technologies:** Unix, Vim, Git, PyPI, HSI, HPCs, HPSS, Tensorflow, Keras, Conda, Snakemake, Numpy, Pandas, scipy, sklearnn, 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 leaning 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*. dio:10.1093/molbev/msaa038

Alcalay, Y., S. Fuchs, R. Galizi, F. Bernardini, R.E. Haghighat-Khah, D.B. Rusch, **J.R. Adrion**, M.W. Hahn, P. Tortosa, and P.A. Papathanos. (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). dio: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**