Curriculum Vitae

Keaka Farleigh, Ph.D.

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WEBSITES AND SOCIAL MEDIA

Coding Repository:	https://github.com/kfarleigh
Research profiles:	Google Scholar ResearchGate
Website:	https://kfarleigh.github.io

PROFESSIONAL POSITIONS

Sep 2024	NSF Postdoctoral Research Fellow Project: *Investigating contact zones to understand the genomic and environmental underpinnings of reproductive isolation and adaptive introgression* Research Advisors: Dr. Drew Schield, Dr. Jesse Meik University of Virginia, Department of Biology
Sep 2019-Aug 2024	NSF Graduate Research Fellow Project: *Identifying genomic adaptations to diverse climates and habitats in Dipodomys microps populations* Research Advisor: Dr. Tereza Jezkova Miami University, Department of Biology
Aug 2018-Aug 2019	Graduate Assistant Miami University, Department of Biology
June 2017-July 2017	NSF Student Researcher Project: *Variability in development rate within and between clutches from individual female copepods (Pseudodiaptomas forbesi)* Research Advisor: Dr. Wim Kimmerer San Francisco State University, BREED REU Program

EDUCATION

August 2024	**Ph.D Ecology, Evolution, and Environmental Biology**. Miami University Dissertation title: *Exploring the genetic basis of local adaptation* Advisor: Tereza Jezkova

May 2018 **B.A. Biology.** Capital University
Advisor: Christine Anderson

PUBLICATIONS

18. **Farleigh, K.**, Highland, D. K., Alderman, M. G., Francioli, Y., Hirst, S. R., Faber, E. M., ... & Schield, D. R. (2026). Evolution of genome-wide barriers to gene flow during complex speciation in rattlesnakes. *Proceedings of the National Academy of Sciences*, *123*(21), e2609058123.

17. Bist, B. S., **Farleigh, K.**, Jiménez, F. A., Nielsen, C. K., & Jezkova, T. (2026). Phylogeographic structure and signals of selection provide insight into the range expansion of the Mexican Long-nosed Armadillo (*Dasypus mexicanus*). *Journal of Mammalogy*, gyag032.

16. **Farleigh, K.**, Murphy, M. O., Blair, C., & Jezkova, T. (2026). PopGenHelpR: An R Package to Streamline and Facilitate Informed Population Genomic Analyses and Visualization of Genetic Ancestry, Diversity and Differentiation. *Molecular Ecology Resources*, *26*(4), e70142.

15. Prange, S., **Farleigh, K.**, & Anderson, C.S. Evaluation of genetic diversity, inbreeding, and gene flow in declining populations of the gray fox (*Urocyon cinereoargenteus*) in Ohio. *Accepted at Ohio Journal of Science.*

14. Blair, C., Pavón-Vázquez, C., Rana, Q., **Farleigh, K.**, Crispo, E., Panzera, T., ... & Vazquez, U. G. (2025). Isolation and divergence of Greater Earless Lizards (Phrynosomatidae: *Cophosaurus*) in western North America support multiple diversification processes and indicate a cryptic species complex. *Molecular Phylogenetics and Evolution,* 108442.

13. Schield, D.R., Carter, J.K., Alderman, M.G., **Farleigh, K.**, Highland, D.K., & Safran, R.J. (2025). Selection shapes repeated genomic landscapes of divergence across the speciation continuum in swallows (*Hirundo*). *Molecular Ecology*, *34*(22), e70074.

12. Murphy, M.O., **Farleigh, K.**, Jezkova T., Peterman, W.E., & Boone, M.D. (2025). Land-cover patterns differentially affect population genetic structure and connectivity of two anurans. *Landscape Ecology*, 40(74).

11. Bernstein, J.M., Francioli, Y.Z., Schield, D.R., Adams., R.H., Perry, B.W., **Farleigh, K.**, … & Castoe, T.A. (2025). Disentangling a genome-wide mosaic of conflicting phylogenetic signals in Western Rattlesnakes. *Molecular Phylogenetics and Evolution*, 108309.

10. Hein, S. R., **Farleigh, K.**, & Berg, D. J. (2024). Riverscape genomics of the endangered freshwater mussel *Lampsilis rafinesqueana*. *Freshwater Biology*, 69, 1438–1453.

9. Pavón-Vázquez, C. J., Rana, Q., **Farleigh, K.**, Crispo, E., Zeng, M., Liliah, J., ... & Blair, C. (2024). Gene Flow and Isolation in the Arid Nearctic Revealed by Genomic Analyses of Desert Spiny Lizards. *Systematic Biology*, syae001.

8. Brunton, A.J., **Farleigh, K.**, Ogbourne, S.M., Rossetto, M., Schoeman, D.S., Conroy, G.C. (2024). The geno-geo-climate nexus: contributions of geographic and ecological factors in shaping the genomic divergence of two closely related threatened rainforest species of Fontainea Heckel (*Euphorbiaceae*). *Landscape Ecology,* 39(11).

7. **Farleigh, K.**, Ascanio, A., Farleigh, M.E., Schield, D.R., Card, D.C., Leal, M., Castoe, T.A., Jezkova, T., Rodriguez-Robles, J.A. (2023). Signals of differential introgression in the genome of natural hybrids of Caribbean anoles. *Molecular Ecology*, 32(22), 6000-6017.

6. **Farleigh, K.**, & Jezkova, T. (2023). Genetic signals of local adaptation in a desert rodent that occupies diverse climates and habitats. *Landscape Ecology,* 38, 3269-3284.

5. Koochekian, N., Ascanio, A., **Farleigh, K.**, Card, D. C., Schield, D. R., Castoe, T. A., & Jezkova, T. (2022). A chromosome-level genome assembly and annotation of the desert horned lizard, *Phrynosoma platyrhinos*, provides insight into chromosomal rearrangements among reptiles. *GigaScience*, 11.

4. Finger, N., **Farleigh, K.**, Bracken, J. T., Leaché, A. D., François, O., Yang, Z., ... & Blair, C. (2022). Genome-Scale Data Reveal Deep Lineage Divergence and a Complex Demographic History in the Texas Horned Lizard (*Phrynosoma cornutum*) throughout the Southwestern and Central United States. *Genome biology and evolution*, 14(1), evab260.

3. **Farleigh, K.**, Vladimirova, S. A., Blair, C., Bracken, J. T., Koochekian, N., Schield, D. R., ... & Jezkova, T. (2021). The effects of climate and demographic history in shaping genomic variation across populations of the Desert Horned Lizard (*Phrynosoma platyrhinos*). *Molecular Ecology*, 30(18), 4481-4496.

2. Santibáñez-López, C. E., **Farleigh, K.**, Cushing, P. E., & Graham, M. R. (2021). Restriction enzyme optimization for RADseq with camel spiders (Arachnida: *Solifugae*). *The Journal of Arachnology*, 48(3), 346-350.

1. **Farleigh, K.** (2018). Genetic estimates of migration for white-footed mice (*Peromyscus leucopus)* at the Primmer Outdoor Learning Center. *2018 NCUR Proceedings*.

Manuscripts in Review

Amoroso, J., **Farleigh, K.**, Crispo, E., & Blair, C. Genome-wide signatures of reproductive isolation shape the varied genomic landscape of the roundtail horned lizard (*Phrynosoma modestum*). *In review at Genome Biology and Evolution*.

Brunton, A., **Farleigh, K.**, Brunton, E., Cristescu, R., Hohweiler, K., Holmes, B., Kozakiewicz, C., Levengood, A., Schoeman, D., Ogbourne, S., & Conroy, G. Around the world in 1500 SNPs:

cross-kingdom genomics across global taxa highlights optimised sampling for accurate genetic diversity assessments. *In revision.*

PRESENTATIONS

2026	**Farleigh, K.**, Highland, D.K., Alderman, M.G., Francioli, Y.Z., Hirst, S.R., Perry, B.W., Holding, M.L., Margres, M.J., Mackessy, S.P., Meik, J.M., Castoe, T.A., Schield, D.R. Evolution of genome-wide barriers to gene flow during complex speciation in rattlesnakes. Oral Presentation. University of Virginia Computational Biology Ph.D. Program, Charlottesville, VA.
2025	Schield, D.R., **Farleigh, K.**, Highland, D.K., Alderman, M.G., Francioli, Y., Hirst, S.R., Perry, B.W., Holding, M.L., Margres, M., Mackessy, S.P., Meik, J.M., & Castoe, T.A. Detecting the genomic footprints of introgression during rattlesnake speciation. Oral Presentation. Biology of Pitvipers 5. Rodeo, NM.
2025	Alderman, M.G., **Farleigh, K.**, Highland D.K., & Schield, D.R. Repeat element proliferation on the caenophidian W chromosome. Poster Presentation. Biology of Pitvipers 5. Rodeo, NM.
2025	Highland, D.K., **Farleigh, K.**, Alderman, M.G., Perry, B.W., Hirst, S.R., Margres, M.J., Holding, M.L., & Schield, D.R. Population genomics of venom genes in speckled rattlesnakes. Poster Presentation. Biology of Pitvipers 5. Rodeo, NM.
2025	**Farleigh, K.**, Highland, D.K., Alderman, M.G., Francioli, Y.Z., Hirst, S.R., Perry, B.W., Holding, M.L., Margres, M.J., Mackessy, S.P., Meik, J.M., Castoe, T.A., Schield, D.R. Genome-wide signatures of selection and introgression during rattlesnake speciation. Oral Presentation. Evolution 2025. Athens, GA.
2025	Alderman, M.G., **Farleigh, K.**, Highland, D.K., & Schield, D.R. Repeat element proliferation on the caenophidian W chromosome. Poster Presentation. Evolution 2025. Athens, GA.
2025	Highland, D.K., **Farleigh, K.**, Alderman, M.G., Perry, B.W., Hirst, S.R., Margres, M.J., Holding, M.L., & Schield, D.R. Population genomics of venom genes in speckled rattlesnakes. Poster Presentation. Evolution 2025. Athens, GA.
2025	**Farleigh, K.,** Genome-wide signatures of selection and introgression during rattlesnake speciation. Oral Presentation. Annual Biological Sciences Research Symposium. University of Virginia. Charlottesville, VA.
2025	**Farleigh, K.,** Exploring signals of local adaptation and plasticity in desert horned lizards. Oral Presentation. EEbio Seminar. University of Virginia. Charlottesville, VA.

2024	**Farleigh, K.,** Exploring the genetic basis of local adaptation. Oral Presentation. Dissertation Defense. Miami University. Oxford, OH.
2024	**Farleigh, K.,** & Jezkova, T., Local adaptation in desert horned lizards (*Phrynosoma platyrhinos*). Oral Presentation. Herpetology (BIO 409). Miami University. Oxford, OH.
2023	Jezkova, T., & **Farleigh, K.**, Genomic approaches to detecting signals of local adaptation. Oral Presentation. Central Ohio Phylogeography Extravaganza. Columbus, OH.
2022	Koochekian, N., Ascanio, A., **Farleigh, K.**, Card, D.C., Schield, D.R., Castoe, T.A., Jezkova, T. A chromosome-level genome assembly and annotation of the desert horned lizard, *Phrynosoma platyrhinos*, provides insight into chromosomal rearrangements among reptiles. Oral Presentation. Evolution 2022.
2022	**Farleigh, K.,** & Jezkova, T. Genetic signals of local adaptation in a desert rodent that occupies diverse climates and habitats. Evolution 2022. Oral Presentation. Virtual.
2022	**Farleigh, K.,** & Jezkova, T. Exploring signatures of differential selection and local adaptation across climate and habitat in the chisel-toothed kangaroo rat (*Dipodomys microps*). Oral Presentation. International Biogeography Society Meeting. Virtual.
2021	Koochekian, N., Ascanio, A., **Farleigh, K.**, Card, D.C., Schield, D.R., Castoe, T.A., Jezkova, T. The genome of *Phrynosoma platyrhinos.* Oral Presentation. Virtual Evolution 2021. Virtual.
2021	**Farleigh, K.,** & Jezkova, T. Identifying genomic adaptations in *Dipodomys microps*. Oral Presentation. American Society of Mammalogists 100th Annual Meeting. Virtual.
2021	**Farleigh, K.** Identifying genomic adaptations in *Dipodomys microps*. Oral Presentation. Miami University Ecolunch. Virtual.
2020	Jezkova, T., & **Farleigh, K.** Detecting genomic signals of population adaptation. City University of New York Bioinformatics Bootcamp for Ecology and Evolution. Oral Presentation. Virtual.
2019	Blair, C., Finger, N., Jezkova, T., François, O., Williams, D., Leachè, A.D., Charran, T., **Farleigh, K.,** Bracken, J.T. Genomic data reveal deep lineage divergence and molecular adaptation in the Texas horned lizard (*Phrynosoma cornutum*), Poster Presentation. Annual Evolution Meeting. Providence, RI.

2019 **Farleigh, K.,** & T. Jezkova. Identifying genomic adaptations to diverse environments in the Chiseled-Toothed Kangaroo Rat (*Dipodomy microps*). Oral presentation. American Society of Mammalogists 99th Annual Meeting. Washington D.C.

2018 **Farleigh, K.,** Ignoffo, T., & W.J. Kimmerer. Variability in development rate within and between clutches from individual females copepods (*Pseudodiaptomus forbesi*). Oral Presentation. Capital University Symposium for Undergraduate Research. Columbus, OH.

2018 **Farleigh, K.,** & C.S. Anderson. Population Genetics and Migration of *Peromyscus leucopus,* a Lyme disease reservoir species. Poster Presentation. Capital University Symposium for Undergraduate Research. Columbus, OH.

2018 **Farleigh, K.,** & C.S. Anderson. Population Genetics and Migration of *Peromyscus leucopus,* a Lyme disease reservoir species. Poster Presentation. Ohio Academy of Science (OAS) 127th Annual Meeting. Bowling Green, OH.

2018 **Farleigh, K.,** & C.S. Anderson. Conservation genetics and migration of Lyme disease reservoir species. Poster Presentation. National Conference on Undergraduate Research. Edmond, OK.

2018 **Farleigh, K.,** & C.S. Anderson. Bioinformatics in Conservation of Lyme disease reservoir species *Peromyscus leucopus*. Poster Presentation. Ohio Fish and Wildlife Management Association Conference. Columbus, OH.

2017 **Farleigh, K.,** Ignoffo, T., & W.J. Kimmerer. Variability in development rate within and between clutches from individual females copepods (*Pseudodiaptomus forbesi*). Poster Presentation. Coastal and Estuarine Research Foundation Biennial Convention. Providence, RI.

2017 **Farleigh, K.,** Ignoffo, T., & W.J. Kimmerer. Variability in development rate within and between clutches from individual females copepods (*Pseudodiaptomus forbesi*). Oral Presentation. Romberg Tiburon Research Symposium. San Francisco, CA.

2017 **Farleigh, K.,** Ignoffo, T., & W.J. Kimmerer. Variability in development rate within and between clutches from individual females copepods (*Pseudodiaptomus forbesi*). Oral Presentation. Summer Research Symposium at San Francisco State University. San Francisco, CA.

2017 **Farleigh, K.,** & C.S. Anderson. Genetic estimates of migration of white-footed mice (*Peromyscus leucopus*) between two habitats at Primmer Outdoor Learning Center. Poster Presentation. Capital University Symposium for Undergraduate Research. Columbus, OH.

2017 **Farleigh, K.,** Mcknight, M., Rios, B., & K. Cheesman. Nitrate Consumption of *Chlorella vulgaris* and *Ulothrix*. Poster Presentation. Capital University Symposium for Undergraduate Research. Columbus, OH.

GRANTS AND AWARDS

2024 NSF DBI-2409958 – Postdoctoral Research Fellowship in Biology: *Investigating contact zones to understand the genomic and environmental underpinnings of reproductive isolation and adaptive introgression* (**$240,000**)
2023 Dissertation Scholarship – Miami University (**$11,000**)
2022 Thesis and Dissertation Research Support – Miami University: *Identifying genomic adaptations of Ambystoma salamanders using whole exome sequencing* (**$600**)
2020 Theodore Roosevelt Memorial Grant Program – American Museum of Natural History: *Identifying genomic adaptations to diverse climates and habitats in Dipodomys microps* (**$2,000**).
2020 NSF Graduate Research Fellowship Program: *Identifying genomic adaptations to diverse climates and habitats in Dipodomys microps populations* (**$147,000**).
2018 Diversity Enhancement Pathway (DEP) Graduate Assistantship
2018 Graduate School Scholar Assistantship
2018 Magna Cum Laude
2017 Boyd Fund Memorial Grant – Capital University: *Bioinformatics in Conservation of Lyme disease reservoir species Peromyscus leucopus* (**$1,000**).
2017 Beta Beta Beta Research Grant: *Bioinformatics in Conservation of reservoir species Peromyscus leucopus* (**$500**).
2017 NSF REU Travel Grant: *Variability in development rate within and between clutches from individual female copepods (Pseudodiaptomas forbesi)* (**$1,000**).
2017 President's List, Capital University
2014-2017 Capital Grant Award
2014-2017 Presidential Scholarship
2014-2017 Discover Cap Grant
2014-2017 Rev. Rufus Tarrant Grant
2014-2017 HWCIA Scholarship
2014-2016 Dean's List, Capital University

SOFTWARE AND DATA REPOSITORIES

PopGenHelpR (https://kfarleigh.github.io/PopGenHelpR):
An R package to estimate commonly used population genomic statistics and to generate publication quality figures.

HybridFindR (https://github.com/kfarleigh/HybridFindR):
An R package to detect signals of differential introgression in hybrid individuals (see publication #7).

GEApermutation (https://github.com/kfarleigh/GEApermutation)

A statistical test to identify differential patterns of local adaptation linked to environmental conditions (see publication #6).

Bioinformatics Bootcamp 2020 (https://github.com/kfarleigh/BioinformaticsBootcamp_2020):

A tutorial to perform genome-environment association analysis using data published in Farleigh et al., (2021; see publication #3). This tutorial was presented at the City University of New York Bioinformatics Bootcamp in the Summer of 2020.

Moments (https://github.com/kfarleigh/Moments):

Python scripts and demographic models used to model the demographic history of 3 and 4 populations. Models were originally published in Farleigh et al., (2021; see publication #3).

STUDENT ADVISING AND TRAINING

As a Ph.D. student in the laboratory of Dr. Jezkova at Miami University, I assisted Dr. Jezkova in mentoring eight undergraduate researchers and one high school researcher. I have trained students in molecular laboratory techniques, including parts of next-generation library construction, and have trained students in bioinformatic techniques as well as the use of Geographic Information Systems (GIS) programs.

TEACHING EXPERIENCE

Guest Lecturer Spring 2026

Computational Biology I – University of Virginia, Charlottesville, VA
Prepared and taught the lecture and lab portions of the Molecular Phylogenetics and Evolution unit, introducing students to phylogenetics and their underlying algorithms.

Founder, Organizer, and Instructor Summer 2025

Foundations in R – University of Virginia, Charlottesville, VA
Organized workshop, developed curriculum, and instructed classes, introducing participants to R, how to perform data wrangling, basic analysis, and data visualization.

Instructor Summer 2023

Lambda Biological Data Analysis Workshop – Miami University, Oxford, OH
Instructor for Genetic Data with R, focusing on population genomics, phylogenetics, and differential gene expression.

Assistant Instructor Summer 2019, 2021

Computer Science in Modern Biology – Miami University, Oxford, OH
Assistant instructor for introduction to R and data visualization classes.

Instructor Summer 2020

Bioinformatics Boot Camp for Ecology and Evolution – The City University of New York, New York, NY

Instructor for a tutorial demonstrating how to use genetic and environmental data to perform genome-environment association analyses.

Graduate Teaching Assistant Fall 2018
Miami University, Oxford, OH
Laboratory instructor for semester long course Biological Concepts: Ecology, Evolution, Genetics, and Diversity (BIO 115).

PROFESSIONAL SOCIETIES

Member	Beta Beta Beta, National Biological Honor Society
Member	Society for the Study of Evolution

SERVICES

2025	Judge, Covenant School Science Fair
2025	Panelist, Finding Funding, University of Virginia GSPA
2024	Reviewer, NSF GRFP Speed Dating, University of Virginia
2017-2018	Treasurer, Beta Beta Beta, Capital University
2018	Participant, Student Leadership Conference, Capital University
2017	Presenter, Science Visit Day, Capital University
2017	Judge, Horizon Science Academy Science Fair
2017	Panelist, Capital University Student Science Opportunities Panel
2017	Student Coordinator, Capital University Primmer Property Cleanup and BBQ
2017	Beta Beta Beta National Biological Honor Society, Capital University
2017	Volunteer, Relay for Life, Capital University

SKILLS AND LANGUAGES

R: High proficiency;
- Datacamp certified Data Scientist in R
- Ability to develop and publish packages to CRAN
- Ability to implement standard and advanced statistical processes
- Machine Learning (Supervised, Unsupervised, Reinforcement)
- Data Cleaning, Mining, and Modeling
- GIS Mapping
- Function Writing
- Data Visualization

Python: Working proficiency;
- Ability to implement standard statistical processes
- Function Writing
- Data Cleaning, Mining, and Modeling
- Data Visualization

Git: Working proficiency;
- Version control

Bash: Working proficiency;

  Shell scripting
ArcGIS: High proficiency;
  Spatial Analysis – proficient
Microsoft: High proficiency;
  PowerPoint
  Word
  Excel
Spanish: Beginner
