# NATHAN L. BROUWER PHD

**Computational ecologist specializing in complex datasets**

I am a computational ecologist, data scientist and educator with 15 years of experience extracting insights from messy data and communicating the results. I specialize in using generalized-linear mixed models (GLMMs) to analyze data from long-term observational studies. Since my PhD I have also taught myself key aspects of bioinformatics, phylogenetics, machine learning and population genomics.

## EDUCATION

2002 — **Seattle Pacific University**
B.S. in Biology, with Honors

2015 — **University of Pittsburgh**
Phd in Biological Sciences - Ecology & Evolution

Dissertation: *Applying multilevel longitudinal models to plant demographic processes: novel insights into the long-term impacts of invasive species and overabundant herbivores.*

## RESEARCH & PROFESSIONAL EXPERIENCE

2019 | present — **Associate Teaching Professor - General & Quantitative Biology**
Unv. of Pittsburgh Dept. of Biological Sciences
- **R Programming** Develop & deliver curriculum for updated **Computational Biology** course (4 semesters)
- **Data analysis** Instructor for **biostatistics** (1 semester) & consult on statistics curriculum development for lab classes.
- **Science communication**: Teach scientific writing, non-majors biology, intro biology lecture & labs.

2015 | 2019 — **Post-doctoral Research Associate - Avian Conservation**
National Aviary of Pittsburgh
- **GLMMS**: Analyze decade-long tropical bird population & community datasets.
- **Data Cleaning**: Clean & merge diverse datasets of environmental data & organism traits.
- **R packages**: Implement models on migratory birds as reproducible software,
- **Computational Statistics**: Develop sensitivity and uncertainty analyses methods for for migration models.

2018-2019 (Fall & Winter) — **Adjunct Professor - Biology**
La Roche College, Pittsburgh
- Co-taught intro to research course (fall) & scientific writing (spring)
- Developed new lab and data analysis activities

## CONTACT INFO


brouwern@gmail.com
github.com/brouwern
517-898-5440


## RELEVANT SKILLS

**STATISTICAL MODELING**: Multiple publications employing **GLMMs** & **GAMMs**.

**DATA VIZUALIZATION**: Expert at visualizing complex data with `ggplot2`.

**DATA CLEANING**: Expert in **data manipulation** & cleaning, including use of **Tidyverse**.

**UNSUPERVISED MACHINE LEARNING**: Skilled with identifying patterns in **high-dimensional data** with ordination & cluster analysis.

**SCIENTIFIC COMMUNICATION**: Excellent written, verbal & graphical communication skills.

**R PACKAGES**: Experience using R packages to distribute scientific software and organize complex analyses.

**REPRODUCIBLE WORKFLOWS**: Large portfolio of **RMarkdown** products, including books & package documentation.

2016-2017

**Adjunct Professor - Biological Data Analysis**
Dusquesne Unv. & California Unv. of PA

- **R programming & data analysis**: Teach graduate (Dusquesne, Spring 2017) & undergraduate data analysises courses (CalU, Fall 2016 & 2017)

2010 | 2015

**Graduate Research Assistant**
Department of Biological Sciences, University of Pittsburgh

- **Data Cleaning**: Update, clean and manage decade-long plant demographic experiment.
- **GLMMs**: Determine appropriate model structures and analyze data.
- **Field work**: Design & carry out research on plant demography.

2004 | 2006

**Peace Corps Volunteer - Agroforestry Outreach**
National Agricultural Research Institute, The Gambia, West Africa

- Assist in staff development, including data analysis & experimental design,
- Conducted outreach and training on agroforestry & sustainable agriculture

2002 | 2004

**Infecious Disease Research Scientist**
University of Washington Department of Allergy & Infectious Disease

- **Lab work**: Conduct experiments on pathogen cell-adhesion proteins.

## PUBLICATIONS - SCIENCE EDUCATION

2022

**Computational Biology for All! An open access book for bioinformatics & computational biology vs 0.9**
Open-access computational biology textbook.
**Brouwer**

2022

**A Little Book of R for Bioinformatics vs. 2.0**
Open-access bioinformatics primer.
Coghlan (au.) & **Brouwer** (ed., au)

**Foundations of Biology and Environmental Science: An Open-Access Encyclopedia**
Compilation of Open-Access resources on general biology, computational biology, and environmental science.
**Brouwer** (ed., au.)

## PASSIONS

**BAYESIAN STATISTICS**: Bayesian approaches have always been apparent to me as the optimal way to approach complex ecological data. Having recently made the time to start using `rstan`, I'm excited to explore the possibilities of working directly in `Stan`.

**MACHINE LEARNING**: While working through Kaggle exercises this summer to prepare for my most recent Computational Biology class, the beauty and power of supervised ML methods were revealed to me.

**REPRODUCIBLE WORKFLOWS**
…

## R PACKAGES

**Population Modeling: redstart: An R package for Periodic Full-Annual Cycle Avian Population Models and Monte-Carlo simulation.**
R implementation & replication of Runge & Marra (2005) Modeling Seasonal Interactions in the Population Dynamics of Migratory Birds.
**Brouwer** *et al.*

• Website & Tutorials: brouwern.github.io/FACavian/index.html

Brouwer & Coghlan

**Computational Biology: combio4all: A repository of data & lessons introducing key concepts related to computational biology.**

## PUBLICATIONS

2019

**Population Models: Direct effects of a non-native invader erode native plant fitness in the forest understory**
Journal of Ecology 108:189–198
Bialic-Murphy, **Brouwer** & Kaliz.

Data & Code: Dryad

2019

**NMDS: Stream acidification & reduced availability of pollution-sensitive aquatic insects are associated with dietary shifts in a stream-dependent Neotropical migratory songbird.**
PeerJ 6:e5141
Trevelline, Nuttle, Porter, **Brouwer** *et al.*

Data & Code

2018

**NMDS: DNA metabarcoding reveals the importance of aquatic prey subsidies & the structure of dietary niches in a community of breeding riparian songbirds.**
Oecologia 187: 85-98
Trevelline, **Brouwer** *et al.*

2018

**GLMM: Avian community characteristics & demographics reveal how conservation value of regenerating tropical dry forests changes with forest age**
PeerJ 6: e5217
Latta, **Brouwer** *et al.*

Data & Code: GitHub

2017

**GLMM: Long-term monitoring reveals an avian species credit in secondary forest patches of Costa Rica**
PeerJ 6: e3539
Latta, **Brouwer** *et al.*

Data & Code: Harvard Dataverse

2017

**GAMM: Increased photosynthetic performance of an invasive forest herb mediated by deer overabundance.**
AoB Plants 9: plx011
Heberling, **Brouwer** & Kalisz.

2015

**GLMM: Mutualism-disrupting allelopathic invader drives carbon stress & vital rate decline in a forest perennial herb.**
AoB Plants 7: plv014
**Brouwer**, Hale & Kalisz.

GAMM Code: GitHub Data & Code:AoB Plants