*Last updated in Apr 2026*

# Joshua C. Macdonald

Computational Scientist

jmacdo16@jh.edu Baltimore, Maryland, USA jcmacdonald.dev jc-macdonald joshuacmacdonald
0000-0002-3643-6266

## Research Profile

Computational scientist developing methods, scientific AI/ML, and research software for partially observed systems across earth, environmental, and health sciences. My work integrates generative modeling (mechanistic, statistical, and hybrid), Bayesian inference, uncertainty quantification, and scientific computing to build defensible inference under structural incompleteness — where the full system state is never directly observed and prediction alone is not enough. Current application areas include infectious disease dynamics and forecasting, host–pathogen and comparative health systems, marine and terrestrial ecology, environmental hazards, and computational tools for decision support.

## Education

**PhD** **University of Louisiana at Lafayette**, Mathematics — Lafayette, Louisiana, USA, 2017 – 2022
- Advisor: Hayriye Gulbudak
- Dissertation: *Population Dynamics Under Disturbance in Ecology and Epidemiology*

**MS** **University of Louisiana at Lafayette**, Mathematics — Lafayette, Louisiana, USA, 2017 – 2020

**BA** **University of North Carolina Asheville**, Mathematics — Asheville, North Carolina, USA, 2014 – 2016

**BA** **University of North Carolina Greensboro**, Archaeology — Greensboro, North Carolina, USA, 2008 – 2013

## Appointments

**Johns Hopkins Bloomberg School of Public Health**, Postdoctoral Scholar — Baltimore, Maryland, USA, 2024 – present
International Vaccine Access Center, Department of International Health. Mentor: Shaun Truelove. Research focus: infectious disease modeling and inference, scientific computing, decision support systems, and research software engineering.

**Tel Aviv University**, Zuckerman STEM Leadership Postdoctoral Fellow — Tel Aviv, Israel, 2022 – 2024
School of Zoology. Mentor: Yoav Ram. Research drew directly on archaeological training in the study of material culture diversity and cultural transmission, applying Bayesian dimensionality reduction and multivariate data analysis to cultural datasets.

## Published Papers

**Within-host viral growth and immune response rates predict FMDV transmission dynamics for African buffalo** — 2024
***J.C. Macdonald***, H. Gulbudak, B. Beechler, E. Gorsich, S. Gubbins, E. Perez, A. Jolles
10.1086/730703 (The American Naturalist)

**Cultural transmission, networks, and clusters among Austronesian-speaking peoples** — 2024
***J.C. Macdonald***, J. Blanco-Portillo, M.W. Feldman, Y. Ram
10.1017/ehs.2024.45 (Evolutionary Human Sciences)

**Forward hysteresis and Hopf bifurcation in an NPZD model with application to harmful algal blooms** 2023
***J.C. Macdonald***, H. Gulbudak
10.1007/s00285-023-01969-7 (Journal of Mathematical Biology)

**First and second wave outbreak size with reactive quarantine measures: a COVID-19 model applied to an epidemic in China** 2022
C.J. Browne, H. Gulbudak, J.C. Macdonald
10.1016/j.jtbi.2021.110919 (Journal of Theoretical Biology)

**Modeling COVID-19 outbreaks in the United States with distinct testing, lockdown speed, and fatigue rates** 2021
***J.C. Macdonald***, C.J. Browne, H. Gulbudak
10.1098/rsos.210227 (Royal Society Open Science)

## Papers Under Review

**An immuno-epidemiological model of foot-and-mouth disease in African buffalo with carrier transmission** 2026
S. Atkins, H. Gulbudak, S. Welker, H. Smith, ***J.C. Macdonald***, B.R. Beechler, A.E. Jolles
(Under review, Bulletin of Mathematical Biology)

## Preprints

**Bayesian estimation of the number of significant principal components for cultural data** 2024
***J.C. Macdonald***, J. Blanco-Portillo, M.W. Feldman, Y. Ram
10.48550/arXiv.2409.12129

## Manuscripts in Preparation

**Lawful learning: a scientific machine learning approach to dynamical systems inference** 2026
***J.C. Macdonald***
(In preparation for SIAM Journal on Scientific Computing)

**Structured observables: a physics-based approach to dynamical systems inference** 2026
***J.C. Macdonald***
(In preparation for SIAM Journal on Applied Dynamical Systems)

**Shapelet analysis of infectious disease forecasts reveals heterogeneity across epidemic phases** 2026
K. Roosa, L.A. White, T.M. Leon, ***J.C. Macdonald***, A. Srivastava, S. Truelove
(In preparation for Epidemics)

## Research Support

**CDC-RFA-FT-23-0069 (NU38FT000012)** 2023 – present
Atlantic Coast Center for Infectious Disease Dynamics and Analytics (ACCIDDA). Postdoctoral Scholar (60% FTE). Insight Net center for infectious disease forecasting and outbreak analytics. Research role: operational modeling, forecasting pipeline development, and computational infrastructure.

**USDA-NIFA AFRI US–UK Collaboration (Award #1032897)** 2025 – 2028
Quiescence to emergence: nairovirus diversity loss and disease transmission. Collaborator (40% FTE). Research role: mathematical model parameterization, data analysis, and advising on mathematical and statistical methods.

**USDA-ARS Cooperative Agreement (3022-32000-021-018-S)** 2025 – present

Investigating the Epidemiology of CCHFV in an Endemic Setting: Uganda. PIs: Bree Beechler and Anna Jolles (Oregon State University). Collaborator. Research role: mathematical modeling of cross-species CCHFV transmission dynamics, surveillance design optimization, and advising on mathematical and statistical methods for decision support.

**NSF EEID / UKRI UK–US Collaboration Grant ($4.05M / 5 years)** 2022 – 2027

Multi-scale infection dynamics from cells to landscapes: FMD in African buffalo. Senior Personnel (from 2024). Research role: mathematical model development and parameterization of within-host viral and immune dynamics.

**Zuckerman Postdoctoral Scholarship ($120K total)** 2022 – 2024

Co-evolution of Cultural and Genetic Traits. Principal Investigator. Competitive postdoctoral fellowship; authored and defended research proposal.

**National One Health Mission India ($1M / 3 years)** 2026 – 2029

Development of an Integrated One Health Disease Modelling and Digital Health Program in Human, Livestock, and Wildlife. Co-Investigator (pending). Research role: mathematical model parameterization and data analysis; mechanistic modeling for HPAI and anthrax in India; stakeholder training in modeling; and supervision of postdoctoral and doctoral trainees.

## Operational Modeling

**Flu Scenario Modeling Hub** 2024 – present

ACCIDDA. Lead Model Developer. Operational modeling and forecasting pipeline development. Leading scientific overhaul of ACCIDDA flu model in advance of 2026/27 operational round.

**COVID-19 Scenario Modeling Hub** 2025 – 2025

ACCIDDA. Support. Data cleaning and assimilation in support of ACCIDDA's health heterogeneities COVID-19 round.

**Hib Vaccination Modeling (Navajo Nation)** 2026 – present

ACCIDDA. Technical supervisor managing PhD students in implementation of an age- and immune-status-structured Hib model for the Navajo Nation to evaluate the impact of long-running vaccination programs.

## Research Software – Lead Developer

**OP System (Operator-Partitioned System)** 2026 – present

ACCIDDA. Declarative governing equation specification compiler for structured dynamical systems. Transforms YAML model definitions into callable numerics consumed by OP Engine or other solvers.

- github.com/ACCIDDA/op_system

**pp-eigentest** 2026 – present

Posterior predictive eigenvalue testing framework for determining signal rank in covariance and Gram matrices. Supports ordered hypothesis testing, family-wise error-rate control, and false discovery rate control.

- github.com/jcm-sci/pp-eigentest

**model-criticism** 2026 – present

Observable-based model calibration and criticism framework. Uses model worlds with known ground truth to tune inference pipelines—scoring rules, observable weights, and model settings—so that when applied to real data where latent structure is unobserved, the pipeline transfers reliably.

- github.com/jcm-sci/model-criticism

**OP Engine (Operator-Partitioned Engine)** 2025 – present

ACCIDDA. Numerical simulation engine for mechanistic models of biological and epidemiological systems. Supports ODE, PDE, and hybrid operator-splitting solvers with pluggable backends.

- github.com/ACCIDDA/op_engine

**vbpca-py** 2024 – present

Variational Bayesian PCA for incomplete data with native missing-data handling, uncertainty quantification, and C++-accelerated kernels; compatible with scikit-learn.

- pypi.org/project/vbpca-py/

## Research Software – Collaborative Infrastructure

**FlepiMoP2 (Flexible Epidemic Modeling Pipeline 2)** 2025 – present

ACCIDDA. Core contributor to the redesign of a modular epidemic modeling and simulation pipeline for forecasting and scenario analysis.

**TabularEpi** 2025 – present

UNC / ACCIDDA. Rule-based tabular epidemic simulator. Conducted systematic performance benchmarking that identified critical architectural bottlenecks, motivating an ongoing refactor to a vectorized backend.

**FlepiMoP (Flexible Epidemic Modeling Pipeline)** 2024 – 2025

Hopkins IDD / ACCIDDA. Developed modular ODE solver interfaces; implemented PyMC-based Bayesian inference module for operational influenza modeling; benchmarking identified vectorization-driven performance gains of 5–20x, informing FlepiMoP2 architecture.

## Invited Talks and Seminars

**Cross-Scale Feedback Motifs: Structure-Preserving Models and Computational Tools for Complex Systems** Mar 2026

Biological Oceanography Seminar, Woods Hole Oceanographic Institution, Woods Hole, Massachusetts

**Decision-Support Modeling for One Health Pathogens** Mar 2026

Differential Equations Seminar, University of Maryland Baltimore County, Baltimore, Maryland

**Modeling long-term viral infections** 2025

Mathematics Seminar, Shippensburg University, Shippensburg, Pennsylvania

**Scenario and forecast modeling for respiratory viruses** 2025

Navajo Nation Epidemiology Center Data Summit, Window Rock, Arizona

**Impacts of host behavior and viral life history on infectious disease transmission** 2024

Department of Mathematics, Virginia Tech; Infectious Disease Dynamics Group, Johns Hopkins University

**Within-host viral life histories predict FMDV transmission dynamics for African buffalo** 2024

Hawlena Lab, Ben-Gurion University, Midreshet Ben Gurion, Israel

**Modeling process-based effects of harmful algal blooms** 2023 – 2024

University of Essex (2024); Tel Aviv University (2023); Israel Oceanographic and Limnological Research, Haifa (2023); Inter-University Institute for Marine Sciences, Eilat (2023)

**Patterns of cultural variation in the Austronesian expansion** 2023

Fortunato Lab, University of Oxford (virtual)

**Consilience in FMDV ecology** 2022
Gresham Lab, New York University; Obolski Lab, Tel Aviv University

## Selected Conference Presentations

**Decision-Support Modeling for One Health Pathogens: Using Mechanistic Models for Surveillance and Forecast Design** 2026
Society for Mathematical Biology Annual Meeting, Graz, Austria; mini-symposium talk

**Recovering Ecological Geometry: A Trait- and Depth-Structured IPDE Model of Plankton Dynamics** 2025
Society for Mathematical Biology Annual Meeting, Edmonton, Alberta, Canada; mini-symposium talk

**Biologically Grounded Surrogate-Driven Parameter Inference for Sparsely Observed Dynamical Systems** 2025
Symposium on Biomathematics and Ecology Education and Research (BEER), Fairfax, Virginia; contributed talk

**Forward hysteresis and Hopf bifurcation in an NPZD model with application to harmful algal blooms** 2023
Society for Mathematical Biology Annual Meeting, Columbus, Ohio; mini-symposium talk

**Within-host viral growth and immune response rates predict FMDV transmission dynamics for African buffalo** 2022 – 2023
SIAM TXLA, Lafayette, Louisiana (2023); SMB Epidemiology-Immunology Midyear Meeting (2022, virtual)

**Dengue immunodynamics: antibody-dependent enhancement, cross-reactive immunity, and model–data confrontation** 2022 – 2023
SIAM TXLA (2023); Mathematical Perspectives on Immuno-Biology, Bulgaria (2023); Center for Combatting Pandemics, Tel Aviv (2023); European Conference on Theoretical and Mathematical Biology, Heidelberg (2022)

**Disease dynamics necessarily operate across scales** 2021
SIAM TXLA, South Padre Island, Texas; mini-symposium talk

**Modeling COVID-19 outbreaks in the United States with distinct testing, lockdown speed, and fatigue rates** 2021
Society for Mathematical Biology Annual Meeting (virtual); contributed talk

## Teaching

**Johns Hopkins University**, Teaching Assistant — Baltimore, Maryland, USA
June 2025 – Aug 2025
Teaching assistant for *Topics in Infectious Disease Epidemiology* with Shaun Truelove and Sara Loo.

**University of Louisiana at Lafayette**, Teaching Assistant and Instructor of Record — Lafayette, Louisiana, USA
2017 – 2020
Instructor of record for elementary statistics (3 sections), survey of calculus (2 sections), precalculus (2 sections), and college algebra (2 sections). Teaching assistant for calculus, linear algebra, differential equations, and basic statistics.

**McDowell County Schools / Memorial University / UNC Asheville**, Teaching and Tutoring 2016 – 2017
Instructor of record for North Carolina Math III / Algebra II (2017). Mathematics and statistics tutoring at Memorial University of Newfoundland (2016–2017) and University of North Carolina Asheville (2016).

## Mentoring

**Mentoring students and postdoctoral researchers** 2021 – present

- Jolles and Beechler Labs, Oregon State University (2025–present)
- Society for Mathematical Biology (2022–present)
- Association for Women in Mathematics (2023–2025)
- Ram Lab, Tel Aviv University (2022–2024)
- MIDAS Network (2021–2022)
- Gulbudak Group, University of Louisiana at Lafayette (2021–2022)

**Undergraduate Research Supervision: Shany Naim** 2024

Tel Aviv University. Supervised undergraduate research project: initial translation of the VBPCApy variational Bayesian PCA codebase from MATLAB to Python.

## Community Outreach

**Science communication and research dissemination** 2021 – 2022

- University of Louisiana R1 Showcase: selected to present COVID-19 modeling research at the university-wide showcase (2022)
- Ocean View United Methodist Church, Oak Island, NC: community discussion on vaccines and COVID-19, with on-site pharmacist for vaccination (2021)

## Professional Service

**SMB Diversity, Equity, and Inclusion Committee** 2023 – 2025

Member

**Session Chair / Leader** 2021 – 2023

- SMB Early Career Workshop: Applying for postdoctoral funding (2023)
- SMB Epidemiology-Immunology Midyear Meeting: Contributed talks (2022)
- SMB Annual Meeting: CT04-MEPI contributed talks in mathematical epidemiology (2021)

**Mini-symposium Co-organizer** 2019 – 2023

- SIAM TXLA: Data-driven mathematical and statistical modeling approaches to population biology (2023)
- SMB Annual Meeting: Disease Dynamics Across Scales (2023)
- SMB/ESTMB Joint Meeting: Multi-scale and data-driven modeling approaches in ecology, immunology, and epidemiology (2022)
- SIAM TXLA: Reproducibility, reliability, and robustness: confronting models from across mathematical biology with data (2021)
- SIAM TXLA: Population Dynamics in Ecology and Epidemiology (2019)

**Secretary, University of Louisiana AMS Graduate Student Chapter** 2021 – 2022

## Journal Reviewing

**2022–present:** *PLOS ONE*, *Journal of Biological Systems*, *Journal of Biological Dynamics*, *Frontiers in Public Health*, *Frontiers in Veterinary Science*, *Computational and Applied Mathematics*, *Mathematical Biosciences*, *Scientific Reports*, *PLOS Computational Biology*, and *BMC Infectious Diseases*.

## Honors and Awards

**Travel Awards** 2019 – 2022

SIAM, Society for Mathematical Biology, and University of Louisiana Graduate Research Association

**Rhodes Outstanding Graduate Assistant Award** 2021

Department of Mathematics, University of Louisiana at Lafayette. Awarded to two graduate students annually (approximately 50 graduate students total).

**Outstanding Contributed Talk Award (Mathematical Epidemiology)** 2021
Society for Mathematical Biology Annual Meeting

**Three Minute Thesis Competition, Finalist** 2019
Louisiana Sea Grant

## Computational Expertise

**Modeling:** Generative models (ODE/PDE/stochastic/hybrid); compartmental and agent-based models; scientific AI/ML (physics-embedded surrogates, lawful learning); multivariate data analysis and dimensionality reduction; stability, bifurcation, and sensitivity analysis; parameter identifiability and inverse problems

**Inference:** Bayesian hierarchical models; variational and simulation-based inference; data assimilation; uncertainty quantification; model calibration and validation; proper scoring rules and forecast evaluation

**Computing:** Python, Julia, C++, Stan, R, MATLAB. Scientific computing; high-performance numerical solvers; operator splitting; data pipelines and exploratory analysis; reproducible workflows (Git, CI/CD, containerization)

## Professional Affiliations

Society for Mathematical Biology; Society for Industrial and Applied Mathematics; International Society for Bayesian Analysis; United States Research Software Engineer Association; MIDAS Network; Association for Women in Mathematics; Institute of Industrial and Systems Engineers; Society for Health Systems (SHS/IISE); and Healthcare Information and Management Systems Society (HIMSS).