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Nathan Layman, PhD

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Experience

EcoHealth Alliance — Remote
Research Scientist — *Nov 2021 – Current*

- **OutCast: A disease Outbreak forecasting application**: A webapp used for forecasting early-day epidemiological outbreaks. Developed a novel hybrid machine-learning / mechanistic forecasting method. Designed and maintained a database of time-series outbreak events, including details about the location, pathogen, host, and biological, socio-economic, and environmental context of the outbreak. Built the backend using R and a versioned SQL database called DOLT. Used Shiny to create an appealing frontend.
- **Wild disease Ssrveillance sensitivity analysis**: Developed a pipeline to perform an automated literature search to extract and structure outbreak event details from scientific literature using natural language processing and large language models. Extracted 4,000 outbreak events from 100,000 articles and used them to evaluate the sensitivity of the World Organisation for Animal Health's wildlife animal surveillance system.
- **Western Asian Bat Research Network CoV prevalence analysis**: Developed a comprehensive machine learning pipeline for analyzing disease prevalence using Bayesian Additive Regression Trees (BART) and Elastic Net logistic regression. Implemented automated hyper-parameter optimization, final model evaluation, and feature importance analysis using DALEX to predict the drivers of CoV prevalence in bats in Western Asia.
- **Endorheic culicine mosquitoes demography analysis**: Performed statistical analysis of mosquito recapture data from a mark-release-recapture study, estimating population sizes and dispersal distances using nonlinear least squares to fit a Gaussian diffusion model. Analyzed data in R to determine diffusion coefficients for different mosquito subgenera, providing insights into the potential spread of Rift Valley fever vectors.

University of Idaho — Moscow, ID
Postdoctoral Research Scientist — *Jan 2020 – May 2020*

- **MuSe: A web application for estimating the strength of mutation and selection**: Developed a user-friendly web application to estimate the strength of selection acting against antigenic inserts in Lassa fever virus. The application provided researchers with real-time visualizations and computational tools to assess the evolutionary pressures on viral antigens, aiding in vaccine development and epidemiological studies.
- **Zoonotic reservoir prediction via computer vision**: Developed a method using neural networks to segment aerial imagery for predicting zoonotic disease reservoir distributions. Segmented images were linked to extracted environmental features and reservoir presence/absence data using boosted regression trees. Demonstrated the approach with the Lassa virus reservoir, *Masstomys natalensis*, in Sierra Leone and Guinea, enhancing spatial disease risk forecasting.
- **Spatial distribution of pathogen genetic diversity**: Developed innovative methods to map the spatial distribution of the genetic diversity of Lassa fever virus. The approach combined genetic sequencing data with spatial analysis techniques, providing insights into the evolution and spread of the virus across different geographical areas, crucial for understanding transmission dynamics and guiding public health responses.

Education

Washington State University — Pullman, WA
PhD in Biology, GPA: 4.0/4.0 — *Aug 2012 – May 2018*

University of Washington — Seattle, WA
Bachelor of Science in Biology and Environmental Studies — *Aug 2001 – March 2011*

Skills

Research: Evolutionary and ecological modeling, Statistics, Phylogenetics, Machine-Learning, Individual-based modeling, Time-series analysis, Spatial analysis

Technologies: R, Python, SQL, C++, Stan, Docker, GIS, SQL, Git, AWS, Pipeline management (e.g. targets), Web application development (e.g. shiny), Data management (e.g. arrow)

Project Management: Grant writing, Cross-discipline collaboration, Budgeting, Mentoring, International travel, Academic publication