

Nathan Layman, PhD

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Experience

EcoHealth Alliance

Research Scientist (40 hrs/week)

Remote

Nov 2021 – Current

- **OutCast: A disease outbreak forecasting application:** Engineered a Shiny-based web application for forecasting early-day epidemiological outbreaks, employing a novel hybrid machine-learning and mechanistic forecasting method. Designed and maintained a database of time-series outbreak events, including details about the outbreak's location, pathogen, host, and biological, socio-economic, and environmental context.
- **Wildlife disease surveillance sensitivity analysis:** Developed a pipeline for automating literature searches to extract and structure details of outbreak events from scientific publications. Leveraged natural language processing and large language models to reduce costs tenfold compared to manual extraction methods. Identified 4,000 outbreak event data by processing 100,000 journal articles. Used the resulting data to evaluate the sensitivity of the World Organisation for Animal Health's wildlife animal surveillance system.
- **Western Asian Bat Research Network CoV prevalence analysis:** Created 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 with 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, providing insights into the potential spread of Rift Valley fever vectors.

University of Idaho

Postdoctoral Research Scientist (40 hrs/week)

Moscow, ID

Aug 2018 – Oct 2021

- **MuSe: A web application for estimating the strength of mutation and selection:** Created a web application to determine maximum likelihood estimates of the strength of selection acting against antigenic inserts in the Lassa fever virus. The application served as a computational tool for researchers to assess evolutionary pressures on viral antigens, supporting vaccine development and epidemiological studies.
- **Zoonotic reservoir prediction via computer vision:** Implemented 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, *Mastomys natalensis*, in Sierra Leone and Guinea.
- **Spatial distribution of pathogen genetic diversity:** Combined genetic sequencing data with spatial analysis techniques to map the spatial distribution of the genetic diversity of Lassa fever virus.

Education

Washington State University

PhD in Biology; Focus on Computational Biology; GPA: 4.0/4.0

Pullman, WA

Aug 2012 – May 2018

University of Washington

Bachelor of Science in Biology and Environmental Studies

Seattle, WA

Aug 2001 – March 2011

Skills

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

Programming & 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 & Leadership: Grant writing, Cross-discipline collaboration, Budgeting, Mentoring, International travel, Academic publication