**BOB WEEK**

Computational Biologist

I am interested in applying my background in mathematical and computational methods to solve difficult problems faced by industry. My experience makes me uniquely positioned to develop and analyze simulations and models used to optimize industrial processes.

**Software:**

Julia, Python, R, Linux, Mathematica, SLURM, C/C++, Matlab

**Math:**

Linear Algebra, Dynamical Systems,Harmonic Analysis, Stochastic Processes

**Statistics:**

Modeling, Analysis, Inference  
(e.g., GLM, PCA, MCMC, KDE, ABC, GRF)

2022 – Current Postdoctoral Research Fellow B.J.M. Bohannan Lab, University of Oregon

Developed a novel mathematical framework to understand microbiome-mediated host evolution This is the first time such a genralization has been formally carried out **Conceptually novel** approach formally generalizing biological inheritance using path analysis Developed individual-based **simulations** to test the mathematical framework Chose Julia for fast implementation, JIT-compilation, and ease of parallelization Implented **multi-threading** on a computational cluster in Julia to compare theory and simulations Multi-threading was necessary to overcome time constraints Mathematical framework and associated simulation model are under review at [The Royal Society B](https://royalsocietypublishing.org/journal/rspb) Code for the simulation model is available at [github.com/bobweek/host-microbe-sims](https://github.com/bobweek/host-microbe-sims) Developed a novel genetically-explicit spatial host-microbe simulation model in Julia The model is novel by adding explicit genome evolution and host spatial structure Chose Julia for fast implementation, JIT-compilation, and ease of parallelization Used **sparse matrices** for representing genomic data to improve simulation performance Code for this simulation model is available at [github.com/bobweek/spatial-genetic-host-microbe](https://github.com/bobweek/spatial-genetic-host-microbe)

2020 – 2022 Postdoctoral Researcher G. Bradburd Lab, Michigan State University

Developed an individual-based model of spatial host-parasite coevolution Implemented this model using the SLiM simulation framework [(messerlab.org/slim)](https://messerlab.org/slim/) Used this model to derive an **SPDE** model and analytical results using **Fourier analysis** Applied **SVD** (singular value decomposition) to simulate multivariate Gaussian fields in Julia This provided a numerical method to sample equilibrium solutions of the SPDE model Chose SVD instead of **Cholesky** because high numerical stability was required Chose Julia because of fast implementation The SPDE model is published at [doi.org/10.1086/727470](https://doi.org/10.1086/727470) Used **SLURM** to schedule large-scale simulations on a High-Performance Computing Cluster Applied **FFT** in NumPy to analyze coherence of simulated genomic data Chose this approach to identify the spatial signature of coevolution on genomic data Chose **NumPy** because Python also has tools for efficient analysis of genomic data Code for the simulation model is available at [github.com/bobweek/genomic-sign-coev-cont-sp](https://github.com/bobweek/genomic-sign-coev-cont-sp)

2015 – 2020 Doctoral Student S.L. Nuismer Lab, University of Idaho

Developed heuristics to calculate population-level models from individual-based models This is useful for **analyzing simulations** and deriving mechanistic analytical models Developed heuristics using infinite-dimensional **stochastic analysis** to calculate SDE from SPDE Applied the above heuristics to generalize existing eco-evolutionary mathematical frameworks This framework is published at [doi.org/10.1016/j.jtbi.2021.110660](https://doi.org/10.1016/j.jtbi.2021.110660) Developed numerical methods to solve associated SPDE and simulate rescaled processes Associated code is available at [github.com/bobweek/white.noise.community.ecology](https://github.com/bobweek/white.noise.community.ecology) Developed a model-based **maximum likelihood** method to measure species coevolution This required developing a model of coevolution yielding a tractable likelihood function Implemented this method in R to make it accessible for empirical biologists This project is published at [doi.org/10.1111/ele.13231](https://doi.org/10.1111/ele.13231) Modeled the coevolutionary maintence of mutualism, published at [doi.org/10.1086/714274](https://doi.org/10.1086/714274)

2023 The Evolution of Microbiome-Mediated Traits    [github.com/bobweek/host-microbe-sims](https://github.com/bobweek/host-microbe-sims) Analytical and simulation models of host trait evolution mediated by microbiome transmission 2023 Host-Parasite Coevolution in Continuous Space [zenodo.org/records/8008017](https://zenodo.org/records/8008017) A stochastic partial differential equation model for spatial analysis of host-parasite coevolution 2022 The Genomic Signature of Coevolution [github.com/bobweek/genomic-sign-coev-cont-sp](https://github.com/bobweek/genomic-sign-coev-cont-sp) Individual-based simulations of coevolution and spatial analysis of simulated genomic data 2021 White Noise Evolutionary Ecology [github.com/bobweek/white.noise.community.ecology](https://github.com/bobweek/white.noise.community.ecology) An application of infinite-dimensional stochastic calculus to unify eco-evolutionary models 2019 Measuring Coevolution [github.com/bobweek/measuring.coevolution](https://github.com/bobweek/measuring.coevolution) A maximum likelihood method to measure coevolution using spatial trait data

2020 PhD Bioinformatics & Computational Biology S.L. Nuismer Lab, University of Idaho Dissertation focused on modeling eco-evolutionary processes and developing statistical methods 2015 BS Mathematics University of Idaho Traditional math degree with electives Digital Logic, Signals & Systems, Physics, and Numerical Methods

2018 – 2019 Bioinformatics & Computational Biology Fellowship IBEST, University of Idaho Project aimed to model the duration of coevolutionary associations 2017-2018 Bioinformatics & Computational Biology Fellowship IBEST, University of Idaho Project aimed to develop a method to measure coevolution in continuous space 2017 Paul Joyce Memorial BCB Fellowship Endowment IBEST, University of Idaho Nominated by Professor Scott Nuismer because of my “love for mathematics and helping others to appreciate how it can be used to understand biological processes” 2013-2015 Undergraduate Research in Biology & Mathematics IBEST, University of Idaho Efforts focused on developing a method to measure coevolution in discrete space