BOB WEEK

Computational Biologist

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SUMMARY

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.

SKILLS

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)

EXPERIENCE

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

- I 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** by formally generalizing biological inheritance using path analysis
  - Requisite background is basic calculus, which facilitates **communication** with biologists
- I developed microbially-explicit individual-based **simulations** to test the mathematical framework
  - I chose Julia for fast implementation, JIT-compilation, and ease of parallelization
- I implented **multi-threading** on a computational cluster in Julia to compare theory and simulations
  - Multi-threading was necessary to overcome time constraints
- The mathematical framework and associated simulation model is under review at *RoySocB*
  - Code for the simulation model is available *here*
- I 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
  - I chose Julia for fast implementation, JIT-compilation, and ease of parallelization
  - To improve simulation performance, I used **sparse matrices** to represent genomic data
  - Code for this simulation model is available *here*

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

- Applied **SVD** (singular value decomposition) to simulate multivariate Gaussian fields in Julia
  - I chose SVD instead of **Cholesky** because high numerical stability was required
  - I chose Julia because of fast implementation
- I applied **FFT** in NumPy to analyze coherence of simulated genomic data
  - I chose this approach to identify the spatial signature of coevolution on genomic data
  - I chose **NumPy** because Python also has tools for efficient analysis of genomic data
- I used **SLURM** to schedule large-scale simulations on a High-Performance Computing Cluster
- I developed an individual-based model of spatial host-parasite coevolution
  - I then implemented this model using the *SLiM* simulation framework
  - I also used this model to derive an **SPDE** model and analytical results using **Fourier analysis**
- I published the SPDE model in a recent paper available *here*
- Code for the simulation model is available *here*

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

- I developed heuristics to calculate population-level models from individual-based models
  - This is useful for **analyzing simulations** and deriving mechanistic analytical models
- I developed heuristics using infinite-dimensional **stochastic analysis** to calculate SDE from SPDE
- I applied the above heuristics to generalize existing eco-evolutionary mathematical frameworks
  - I published this framework *here*
  - Code associated with this framework is available *here*
- I developed a model-based **maximum likelihood** method to measure species coevolution
  - This required developing a model of coevolution yielding a tractable likelihood function
  - I implemented this method in R to make it accessible for empirical biologists
  - I published this project *here*
- I applied my framework to study the coevolutionary maintence of mutualism, published *here*

SELECTED PROJECTS

2023	**The Evolution of Microbiome-Mediated Traits**	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
	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
	Individual-based simulations of coevolution and spatial analysis of simulated genomic data	

2021	**White Noise Evolutionary Ecology**	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
	A maximum likelihood method to measure coevolution using spatial trait data	

EDUCATION

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	

AWARDS

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	