Ford Fishman

contact

913 E. Grimes LN
Bloomington, IN 47401
847-637-7334
fordfishman@gmail.com
github.com/fordfishman
fordfishman.github.io

skills

Machine learning
Dimension reduction
Data imputation
Data cleaning
Feature selection
Multiprocessing
Agent-based modeling
Simulation modeling
Network modeling
HPC job submission

programming languages

Python (NumPy, Pandas, Scikit-learn, Matplotlib)
R (ggplot2, tidyverse)
SQL
Bash
Git
Java
HTML, CSS
Markdown, LaTeX

relevant coursework

Applied Machine Learning
Applied Statistical Methods
Bayesian Data Analysis
Multivariable Calculus
Software Design
Mathematical Biology
Quantitative Biodiversity

hobbies

basketball analytics
book reviews
sci-fi and fantasy fiction

objective

Biology graduate student passionate about computational problem-solving. I am eager to contribute to data science teams using my quantitative skills for positions starting this summer.

education

2019–Present	**Master's** in Evolution, Ecology and Behavior (3.96/4.00)	Indiana University, Bloomington, IN

Carl H. Eigenmann Biology Scholarship, NSF Graduate Research Fellowship Honorable Mention

2015–2019	**BS** Biology, Mathematics Minor (3.98/4.00)	Hope College, Holland, MI

Summa cum laude, Phi Beta Kappa, Patterson Memorial Prize in Biology, Sigma Xi, Beta Beta Beta Biological Honor Society, Hope College Presidential Scholarship
Study Abroad Semester – University of Queensland, Brisbane, QLD, Australia

relevant experience

2019–Present	**Graduate Researcher**	Indiana University, Bloomington, IN

- Modeled constraints on microbial diversity using simulation modeling in R
- Collected ancient genomic data including over 700 sequences from 30 studies
- Constructed object-oriented agent-based models of complex bacterial interactions in Python and showed how they promote coexistence
- Designed and assembled publication-ready plots and figures
- Regularly presented research to colleagues in different fields

2017 Summer	**Research Intern**	Duke University Marine Laboratory, Beaufort, NC

- Utilized Shannon entropy to cluster bacterial DNA sequences to analyze the effects of distance from shore on marine diversity using R and Python
- Used canonical correspondence analysis to determine that distance from the shore and nutrient available were the largest contributors to changes in diversity

2016–2019	**Undergraduate Researcher**	Hope College, Holland, MI

- Determined the efficacy of the local watershed restoration project and analyzing E. coli genomics to find efficient methods to classify potential pathogens and fecal contamination
- Created R-shiny web application to automate data preprocessing and run linear regressions on complex output for chemical analyte concentrations in water samples
- Built Python, R and Bash pipelines to analyze genomic data

additional experiences

2021–Present	**EcoLunch Seminar Committee Chair**	Indiana University, Bloomington, IN
2019–Present	**Associate Instructor: Microbiology Lab**	Indiana University, Bloomington, IN
Spring 2019	**Teaching Assistant: Microbiology Lab**	Hope College, Holland, MI
Fall 2016	**Peer Tutor for Biology and Chemistry**	Hope College, Holland, MI