

SARAH TEICHMAN

CONTACT INFORMATION	Email: steichma@fredhutch.org GitHub: https://github.com/svteichman Webpage: svteichman.github.io
EMPLOYMENT	Fred Hutchinson Cancer Center , Seattle, WA Postdoctoral Research Fellow in the Data Science Lab, January 2026–Present <ul style="list-style-type: none">• Developing training materials for data science education. University of Washington , Seattle, WA Research Scientist in Biostatistics Department, January 2025–December 2025 <ul style="list-style-type: none">• Statistical methods development with applications in microbiome science.
EDUCATION	University of Washington , Seattle, WA Ph.D. Statistics, December 2024 <ul style="list-style-type: none">• Dissertation: Statistical methods development with applications in microbiome science.• Advisor: Amy Willis Amherst College , Amherst, MA B.A. Statistics (magna cum laude), May 2018
PUBLICATIONS	Sarah Teichman , Michael D Lee, and Amy Willis (2023) “Analyzing microbial evolution through gene and genome level phylogenies.” <i>Biostatistics</i> . Pauline Trinh, Sarah Teichman , Marilyn C Roberts, Peter M Rabinowitz, and Amy D Willis (2024) “A cross-sectional comparison of gut metagenomes between dairy workers and community controls.” <i>BMC Genomics</i> .
SUBMITTED MANUSCRIPTS	David S Clausen, Sarah Teichman , and Amy D Willis (2025) “Estimating Fold Changes from Partially Observed Outcomes with Applications in Microbial Metagenomics.”
MANUSCRIPTS IN PREPARATION	Sarah Teichman and Amy D Willis “Scalable differential abundance analysis for microbial metagenomics.” Zinka Bartolek, Amy Willis, Sarah Teichman , and E. Virginia Armbrust “Functional patterns of microbial interaction in the North Pacific revealed through statistical modeling of environmental metatranscriptomes” Grant Hopkins, Ellen Graham, Sarah Teichman , and Amy Willis “Nonparametric identification and estimation of microbial differential abundance parameters”
TECHNICAL REPORTS	Sarah Teichman “Associations between Periodontal Disease and Pregnancy Outcomes in the Microbiota and Preterm Birth study cohort”
INVITED CONFERENCE PRESENTATIONS	Sarah Teichman , Michael D Lee, and Amy Willis. “Visualizing Gene Trees to Investigate Gene and Genome Level Evolution.” In <i>ENAR Spring Meeting</i> , Houston, TX, March 2022.
CONTRIBUTED CONFERENCE PRESENTATIONS	Sarah Teichman , Rachel Heath, and Tyler McCormick. “Decomposing Wage Variance in Low-Resource Settings.” In <i>Joint Statistical Meetings</i> , virtual, August 2020. (Poster presentation)

OTHER TALKS AND
PRESENTATIONS

Sarah Teichman, Michael D Lee, and Amy Willis. “Analyzing microbial evolution through gene and genome level phylogenies.” *Microbiome Virtual International Forum*, Virtual (December 2023).

SOFTWARE

groves. [R package](#) implementing a gene-level phylogeny visualization method.

- Primary developer, 124 commits

fastEmu. [R package](#) implementing fast differential abundance analysis for large datasets.

- Primary developer, 77 commits

breakaway. [R package](#) estimating species richness.

- Contributor, 73 commits

corncob. [R package](#) modeling relative abundance from high throughput sequencing data.

- Contributor, 62 commits

DivNet. [R package](#) estimating and testing alpha and beta diversity for microbiome analyses.

- Contributor, 35 commits

enviromtx. [R package](#) modeling gene expression relative to species abundance.

- Contributor, 32 commits

happi. [R package](#) modeling gene presence in pangenomics.

- Contributor, 16 commits

radEmu. [R package](#) for differential abundance estimation and inference.

- Contributor, 155 commits

raoBust. [R package](#) for performing robust score tests for generalized linear models.

- Contributor, 40 commits

rigr. [R package](#) implementing regression, inference, and general data analysis tools.

- Contributor, 10 commits

TEACHING
EXPERIENCE

Marine Biological Laboratory, Woods Hole, MA

Teaching Assistant, July 2022, July 2023, July 2024, July 2025

- Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS)
- Taught statistical and computational methods to microbiome scientists

University of Washington, Seattle, WA

Predoctoral instructor, Winter 2022, Spring 2022

- Statistics 302: Statistical Computing
- Topics: programming fundamentals, data manipulation and visualization, debugging, version control and git

University of Washington, Seattle, WA

Predoctoral instructor, Summer 2021

- Statistics 303: Introduction to the ethics of algorithmic decision making
- Co-developed curriculum and course materials.
- Topics: ethics in statistical analyses, bias and fairness, facial recognition, privacy

University of Washington, Seattle, WA

Teaching Assistant, Fall 2018, Winter 2018, Spring 2019, Winter 2021

- Statistics 221: Statistical Concepts & Methods for the Social Sciences
- Statistics 311: Elements of Statistical Methods

Amherst College, Amherst, MA

Statistics Fellow, May 2015–May 2018

- Held weekly drop-in sessions available to students in all statistics classes
- Planned and led R tutorials open to the Five College community

MENTORSHIP

University of Washington, Seattle, WA

Statistics Undergraduate Directed Reading Program, January 2020–Present

- Mentored five students in quarter long projects

Amherst College, Amherst, MA

Amherst Women in Science Mentorship Program, January 2017–May 2018

HONORS AND
AWARDS

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| 2023 | Best Selected Talk
<i>(Microbiome Virtual International Forum, Session 24)</i> |
| 2018 | Blalock Fellowship
<i>(Center for Statistics and Social Sciences, University of Washington)</i> |
| 2018 | Top Scholar Award
<i>(Department of Statistics, University of Washington)</i> |
| 2018 | Five College Statistics Award
<i>(Department of Statistics, Amherst College)</i> |

SKILLS

R & Statistical Programming: Expert in R, including RMarkdown, package development, the tidyverse suite, and debugging.

Version Control & Software Development: Proficient with Git/Github and workflows including unit testing, code coverage checks, and GitHub Actions

High-performance computing: Experience with remote computing environments and SLURM job scheduling for large-scale analyses

Bioinformatics Tools: Some experience with bioinformatics tools for microbial genomics: Anvi'o, GToTree, DADA2.

Other Programming Languages: Experience using Python, MATLAB, Java, and Stan.

Scientific Writing: Skilled in LaTeX.

SERVICE

- Statistics camp for high school students with UW GEAR UP organizer (2022)
- UW StatCom consultant (2022)
- UW Statistics Department PhD student peer mentor (2021–2023)
- StatsPhD.com graduate student panel organizer (2021–2022)
- UW Statistics Department Graduate Student Representative (2020–2021)
- UW Statistics Department Admissions Screening Committee (2020, 2021)
- UW Statistics Department Directed Reading Program Organizing Committee (2020–2022)
- UW Statistics Department Diversity Equity and Inclusion Committee (2019–2023)
- UW Statisticians and Biostatisticians from Underrepresented Genders Organizing Committee (2019–2022)