

Michael J. Sieler Jr.

Microbiome Scientist | Data Enthusiast | PhD Candidate at OSU
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SUMMARY

- Microbiome scientist with 5+ years of experience developing molecular, computational, and statistical research methods
- Robust data analytic skills in multivariate statistics and machine learning to drive research experiments forward
- Demonstrated abilities to collaborate and take leadership in multi-laboratory experiments
- Experienced in written, oral and visual communication across scientific and public audiences

EDUCATION

Oregon State University

Ph.D. in Microbiology, minor in Biological Data Science*

Expected 2025

Oregon State University

B.Sc. in Bioresource Research, options in Bioinformatics and Genomics

2020

WORK EXPERIENCE

Phd Bioinformatics and Data Science Intern

2023-2024

Research focus in metabolomic data science and bioinformatics

Pacific Northwest National Laboratory

MJSieler Consulting - Owner

May 2022-Present

- Data science and life sciences solutions, specializing in coding, statistics, research, experimental design, and analysis
- Educational software used to fulfill research grant deliverables for communicating science to the public
- Tools used: R, Python, C#, Unity, Adobe Photoshop/Illustrator

RESEARCH EXPERIENCE

Developed high-throughput molecular biological and statistical pipelines to interrogate gut microbiome

- Designed and implemented procedures to process 1,000+ zebrafish embryos to analyze their microbiomes
- Tools used: DADA2 (16S sequencing), R (data cleaning, statistical analysis, visualization)

Measure resilience of gut microbiome to chronic exposure of antibiotics, temperature and parasites

- Exposed 720 adult zebrafish to consecutive disturbances to interrogate gut microbiome stability and resilience
- Tools used: DADA2 (16S sequencing), R (data cleaning, statistical analysis, visualization)

Investigate the joint interaction effects of pathogen exposure and diet on gut microbiome succession

- Fed 180 zebrafish three commonly used laboratory diets and exposed half to a common pathogen
- Tools used: DADA2 (16S sequencing), R (data cleaning, statistical analysis, visualization)

Meta-analysis of zebrafish gut microbiomes phylogeny

- Identified relevant studies and datasets to include in meta-analysis
- Tools used: Python (data cleaning)

Evaluated common batch effect correction algorithm performance for small molecule data

- Evaluated 12 common batch effect correction algorithms and contributed to bioinformatic packages
- Tools used: R (data cleaning, statistical analysis, visualization), GitHub (version control)

Technical Skills

- **Programming Languages:** R, Python, C# (Unity), Git, HTML, CSS, C++, UNIX/LINUX
- **Statistics and Data Analytics:** multivariate regression, machine learning, model building and selection, data viz
- **Bioinformatics:** 16S sequencing, batch effect correction algorithms, DADA2, Phyloseq, Mothur, HMMER, FastTree
- **Molecular Biology:** zebrafish husbandry, DNA extraction, PCR, gel electrophoresis
- **Other:** Microsoft Office Suite, Adobe Photoshop and Illustrator

For a full list of my publications, please see michaelsieler.com/en/latest/Publications/publications.html

