

# Michael J. Sieler Jr.

Microbiome Data Scientist | PhD Candidate at OSU

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## SUMMARY

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- Microbiome scientist with 5+ years of experience developing molecular, computational, and statistical research methods
- Robust data analytic skills in multivariate statistics 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

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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

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*Phd Bioinformatics and Data Science Intern*

2023-2024

Pacific Northwest National Laboratory

- Research focus in small molecule, metabolomic data science and bioinformatics

*MJSieler Consulting - Owner*

May 2022-Present

- Data science and life sciences solutions, specializing in bioinformatics, data science, and data viz
- 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

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

- Designed and implemented germ-free 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*

- Longitudinally exposed 720 adult zebrafish to 8 pairwise combinatorial stressors to interrogate gut microbiome stability
- 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 analyzed datasets to include in meta-analysis
- Tools used: Unix and Python (data wrangling and cleaning)

*Evaluated common batch effect correction algorithm performance for small molecule data*

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

## Technical Skills

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- **Programming Languages:** R, Python, C# (Unity), Git, HTML, CSS, C++, UNIX/LINUX
- **Statistics and Data Analytics:** multivariate regression, model building and selection, data viz (Ggplot, Plotly, R shiny)
- **Bioinformatics:** 16S sequencing, multi-omic analysis, DADA2, Phyloseq, Mothur, HMMER, FastTree
- **Molecular Biology:** zebrafish husbandry, DNA extraction, PCR, gel electrophoresis
- **Other:** Microsoft Office Suite, Adobe Photoshop and Illustrator, German (B2)

For a full list of my publications, please see [michaelsieler.com/en/latest/Publications/publications.html](https://michaelsieler.com/en/latest/Publications/publications.html)

