# Michael J. Sieler Jr.

Microbiome Data Scientist | PhD Candidate at OSU
MichaelSieler.com | sielerjm@oregonstate.edu | GitHub: sielerjm | LinkedIn: mjsielerjr

## SUMMARY

- **Microbiome scientist** with 7+ years of experience developing molecular, computational, & statistical research methods
- **Strong analytical expertise** in multivariate statistical methods, guiding experimental research and data interpretation
- **Proven collaborator and leader**, managing projects across multi-laboratory teams & interdisciplinary groups
- **Experienced communicator**, skilled in conveying scientific concepts to both scientific and lay audiences
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## 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
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

*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

- **Programming Languages**: R, Python, C# (Unity), Git, HMTL, CSS, C++, UNIX/LINUX
- **Statistics and Data Analytics**: multivariate regression, model building and selection, data viz (Ggplot, Plotly, R shiny)
- **Bioinformatics**: 16S sequencing, metagenomics, transcriptomics, metabolomics, DADA2, HPC, command line tools
- **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