Michael J. Sieler Jr.
Microbiome Data Scientist | PhD

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SUMMARY

- **Microbiome scientist** with 8+ 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   *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