**Michael J. Sieler Jr.**

Microbiome Scientist | Data Enthusiast | 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 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** | | |
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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 | |

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| **WORK EXPERIENCE** | |
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| *Phd Bioinformatics and Data Science Intern*  Research focus in metabolomic data science and bioinformatics  Pacific Northwest National Laboratory | 2023-2024 |
| *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 | |

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| **RESEARCH EXPERIENCE** |
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| *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 |
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| **Technical Skills** |
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| * **Programming Languages**: R, Python, C# (Unity), Git, HMTL, 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 |