

Elizabeth McDaniel, PhD

Computational Biologist

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I am a computational biologist with a generalist mindset to problem-solving and specialized skills in microbial metagenomics and multi-omics approaches. I received a PhD in Microbiology and have published research on the microbial ecology of engineered water systems and novel computational methods for exploring multi-omics data. I am passionate about open science and reproducibility, designing scrappy solutions to applied problems, and helping others with their analytical challenges.

Skills

Code: R, python, bash, Nextflow, unix

Bioinformatics: Metagenomic assembly (short- and long-read technologies), metagenomic binning, genome annotation and evaluation, protein structure analysis, transcriptomics, 16S rRNA gene amplicon analysis, phylogenomics, variant calling

Computing: SLURM, HT-Condor, AWS Batch, Nextflow Tower, Docker, git/GitHub

Wet-lab: Aseptic technique, DNA/RNA extraction, PCR, qPCR, HPLC, lab-scale bioreactor operation

Education

University of Wisconsin - Madison

2016-2021

Ph.D., Microbiology

University of Arkansas

2012-2016

B.S., Biology

Professional and Research Experience

Computational Scientist - Oct. 2022-Aug. 2024

Arcadia Science

- Created reproducible computational workflows for bespoke analyses and production-ready solutions deployed on AWS Batch using Nextflow/Nextflow Tower.
- Assisted scientists with their analytical challenges for pilot projects on quick timescales.
- Communicated the development of open-source tools and scientific results through a non-journal-based publishing platform.

Postdoctoral Researcher - Nov. 2021-Aug. 2022

Ziels and Hallam Labs - Departments of Civil Engineering and Microbiology and Immunology, University of British Columbia, Vancouver, BC

- Explored the composition and metabolic activity of microbial communities underlying anaerobic digestion systems using genome-resolved metagenomics, metaproteomics, and stable-isotope probing techniques.

Graduate Research Assistant - Jan. 2017-Aug. 2021

McMahon Lab - Departments of Civil and Environmental Engineering and Bacteriology, University of Wisconsin - Madison, Madison, WI

- Dissertation on the ecology and evolution of enrichment microbial communities simulating enhanced biological phosphorus removal using genome-resolved metagenomics and metatranscriptomics.
- Assisted other researchers with high-throughput mining and annotation of microbial metagenomes.
- Taught workshops on reproducible coding skills with R, python, git/GitHub as a Certified Carpentries Instructor.

Undergraduate Research Assistant - Aug. 2013-Aug. 2016

Lewis Lab - Department of Biology, University of Arkansas, Fayetteville, AR

- Investigated the natural variation of stress defense mechanisms of lab and wild strains of the budding yeast *S. cerevisiae*.

Selected Publications and Preprints Full list of publications on Google Scholar: <https://scholar.google.com/citations?user=QJFxBWMAAAJ&hl=en>

denotes equal contribution

Pubs from Arcadia Science are not published in traditional journals and contributing authors are listed alphabetically.

Discovering shared protein structure signatures connected to polyphosphate accumulation in diverse bacteria. Avasthi P., Celebi F.M., McDaniel E.A. Arcadia Science. Oct. 2023. DOI: 10.57844/arcadia-ac10-23e7

Diverse electron carriers drive syntrophic interactions in an enriched anaerobic acetate-oxidizing consortium. McDaniel E.A., Scarborough M., Mulat G.M., Lin X., Sampara P.S., Olson H.M., Young R.P., Eder E.K., Attah I.K., Markillie L.M., Hoyt D.W., Lipton M.S., Hallam S.J., Ziels R.M. ISMEJ. Oct. 2023. DOI: 10.1038/s41396-023-01542-6.

Quickly preprocessing and profiling microbial community sequencing data with a Nextflow workflow for metagenomics. Dutton R.J., McDaniel E.A. Arcadia Science. May 2023. DOI: 10.57844/arcadia-7etp-pj24

TbasCO: Trait-based Comparative 'Omics Identifies Ecosystem-Level and Niche-Differentiating Adaptations of an Engineered Microbiome. McDaniel E.A.#, van Steenbrugge J.J.M.#, Noguera D.R., McMahon K.D., Raaijmakers J.M., Medema M.H., Oyserman B.O. *bioRxiv*. Dec. 2021. DOI: 10.1101/2021.12.04.471239

Expanded Phylogenetic Diversity and Metabolic Flexibility of Mercury-Methylating Microorganisms. McDaniel E.A., Peterson B., Stevens S.L.R., Tran P.Q., Anantharaman K., McMahon K.D. *mSystems*. Aug. 2020. DOI: 10.1128/mSystems.00299-20