Andrew Morris

Postdoctoral Scholar

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Education

- 2022 PhD Biology, University of Oregon, Eugene, OR.
- 2017 MS Soil Science, Penn State University, State College, PA.
- 2014 BS Plant Sciences, Cornell University, Ithaca, NY.

Experience

2022–present **Postdoctoral Scholar**, *University of Oregon*, Eugene, OR.

- Developed a novel framework for understanding microbiome heritability in humans and animals, manuscript in prep.
- Submitted a first-author publication to ISME Communications.
- Presented original research on the heritability and function of the microbiome at the International Society of Microbial Ecology meeting in Lausanne, Switzerland.

2017–2022 **NSF Graduate Research Fellow**, *University of Oregon*, Eugene, OR.

- Assembled microbial genomes and performed comparative genomics across ecosystems using micro-
- Engineered microbiomes that consume greenhouse gases at high rates using laboratory selection experiments.
- Published a first-author paper on integrating quantitative genetics with microbiome science in Philosophical Transactions of the Royal Society.
- Awarded multiple grants and fellowships including the National Science Foundation Graduate Research Fellowship and named an ARCS Scholar by the Oregon chapter of the ARCS Foundation.
- Presented research to members and potential donors at the Oregon ARCS Foundation meeting.

2015–2017 Graduate Research Assistant, Penn State University, State College, PA.

- Demonstrated a new approach to reducing the impact of agriculture on climate change by decreasing microbiome-mediated nitrous oxide emissions.
- Led field teams and mentored undergraduate research assistants.
- Collaborated with a team of over 14 scientists and industry partners.
- Presented research at scientific meetings including The Ecological Society of America and the Soil Science Society of America.
- Communicated results to non-science audiences including farmers, technicians, and extension educators.

Skills

Formal Training.

- Advanced biostatistics coursework with both frequentist and Bayesian inference using R and Stan.
- Training in bioinformatics at the Marine Biology Laboratory in Woods Hole, MA using R, Python, and QIIME2 to analyze next-generation sequencing data.
- Intensive workshop in machine learning for image analysis using deep neural networks with Keras and TensorFlow through the University of Oregon Data Science Initiative.

Microbiome Analysis.

- 16S rRNA gene amplicon analyses using R, phyloseq, and QIIME2.
- Short-read shotgun metagenomic analyses including read recruitment, gene calling, taxonomic and functional annotation, contig assembly, genome binning, and comparative genomics.
- Statistical analyses in R including linear mixed effects models with crossed, nested, and repeated measures designs as well as non-parametric tests (Kruskal-Wallis, Wilcoxon, etc.).
- Microbiome analyses including ecological dissimilarity metrics (Bray-Curtis, Jaccard, UniFrac, etc.),
 PCoA and NMDS ordinations, PERMANOVA, Mantel tests, and differential abundance tests.

Tools R, Bash, Python, git, Github, Linux, Unix, high-performance computing, cloud computing

Selected Publications

- 2023 **Morris, AH** and Bohannan, BJM. Artificial ecosystem selection reveals relationships between microbiome composition and ecosystem function. In review at *ISME Communications*
- 2021 **Morris, AH**, Isbell, SA, Saha, D and Kaye, JP. Mitigating nitrogen pollution with under-sown legume-grass cover crop mixtures in winter cereals. *Journal of Environmental Quality*
- 2020 Meyer, KM, **Morris, AH**, Webster, K, Klein, A, Kroegerv, ME, Meredith, LK, et al. Belowground changes to community structure alter methane-cycling dynamics in Amazonia. *Environment International*
- 2020 Meyer, KM, Hopple, AM, Klein, A, **Morris, AH**, Bridgham, SD, and Bohannan, BJM. Community structure–ecosystem function relationships in the Congo Basin methane cycle depend on the physiological scale of function. *Molecular Ecology*
- 2020 **Morris, AH**, Meyer, KM, and Bohannan, BJM. Linking microbial communities to ecosystem functions: what we can learn from genotype–phenotype mapping in organisms. *Philosophical Transactions of the Royal Society B: Biological Sciences*

Selected Presentations

- 2022 **Morris, AH**, Bohannan, BJM. Artificial ecosystem selection reveals relationships between microbiome composition and ecosystem function. *ISME Meeting*. Lausanne, Switzerland.
- 2019 **Morris, AH**, Meyer, KM, Bohannan, BJM. Linking microbial communities to ecosystem functions: what we can learn from genotype-phenotype mapping in organisms. *Achievement Rewards for College Scientists Annual Luncheon*. Portland, OR.
- 2017 **Morris, AH**, Isbell, S, Kaye, JP. Improving nitrogen retention of agroecosystems using interseeded cover crops. *Ecological Society of America Meeting*. Portland, OR.
- 2016 Morris, AH, Isbell, S, Kaye, JP. Managing Inter-Seeded Cover Crops and Tillage to Decrease Nitrate Leaching and Nitrous Oxide Emissions from Agricultural Soils. Soil Science Society of America Meeting. Phoenix, AZ.

Teaching

- 2018 Faculty, Juneau Icefield Research Program: Geobotany and Ecology
- 2018 Guest Lecture on Evolutionary Processes, University of Oregon: Ecology and Evolution
- 2018 Teaching Assistant, University of Oregon: Ecology and Evolution, Genetics and Molecular Biology, Cells
- 2017 Teaching Assistant, Penn State University: Soil Science