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.
- Submitted a first-author publication to *The ISME Journal*.
- 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 microbiome metagenomic data.
- o 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 prestigious National Science Foundation Graduate Research Fellowship and named an ARCS Scholar by the Oregon chapter of the Achievement Rewards for College Scientists 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.
- 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 deep marker gene and metagenomic 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.
- o Short-read shotgun metagenomic analyses including data preparation (BBTools), read recruitment (bowtie2), gene calling (prodigal), taxonomic and functional annotation (Kaiju, KEGG), contig assembly (MEGAHIT), and genome binning and comparative genomics (Anvi'o).
- Statistical analyses in R including linear mixed effects models with crossed, nested, and repeated
 measures designs as well as case-control and continuous outcomes and non-parametric tests (KruskalWallis, Wilcoxon, etc.).
- Microbiome analyses including ecological dissimilarity metrics (Bray-Curtis, Jaccard, UniFrac, etc.),
 PCoA and NMDS ordinations, PERMANOVA, Mantel tests, and differential abundance tests (DESeq2, ALDEx2, etc.).

Typesetting LATEX, R Markdown, Jupyter

Coding R, Bash, Python

Computing Linux, Unix, HPC, Slurm

Collaboration git, Github, Slack, Zoom

Selected Publications

- 2023 **Morris, AH** and Bohannan, BJM. Artificial ecosystem selection reveals relationships between microbiome composition and ecosystem function. In review at *The ISME Journal*
- 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.

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