

Nathaniel Fisher, MS

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EDUCATION

- 2024 M.S. in Bioinformatics. Boston University, Boston, MA
Grade: 4.0
- 2019 B.A. in Biological Sciences. (*magna cum laude*) Cornell University, Ithaca, NY
Grade: 3.87
Honors Thesis: Nutrient Limitations to Denitrification in Northeastern Hardwood Forests
- 2021 CHEM 271, Chemical Biology. University of California, Berkeley, CA
Grade: A+

RESEARCH EXPERIENCE

- 2024- Bioinformatician, Boston University School of Medicine, Boston, MA
- Member of iCaMP Lab (Integrative Cardiovascular Metabolism and Pathophysiology)
 - Developed tools to simulate mitochondrial read datasets and evaluate features of different mitochondrial variant calling pipelines to optimize variant call accuracy for single nucleotide variants, indels, and structural variants
 - Researched mitochondrial genetic variation across tissue sites of the human body, culminating in first-author publication (in revision)
 - Deployed [Mitoproximal Protein Database](#) and collaborated on team to develop the interface and back-end search functions
 - Automated mtDNA WGS and RNA-seq mitochondrial variant calling pipelines, reducing manual runtime 5x and improved organization of run and error logs
 - Developed data-driven variant filtering method to call mitochondrial variants with high accuracy (FDR < 15%) from RNA-seq data
 - Adapted and wrote bash scripts to perform quality control and variant calling of 15,000+ WGS and RNA-Seq samples
 - Collaborated with computer scientists to parallelize and enable batch processing of whole genome sequencing (WGS) analysis pipeline and reduce runtime by 50x
 - Adapted a WGS analysis pipeline for identifying nuclear embedded sequences to remove false positive mitochondrial reads and flag contaminated positions
- 2022-2023 Senior Research Associate, DNA Process Development, Moderna, Norwood, MA
- Completed strain engineering projects and independently designed new plasmid-based approach for DNA production based on a novel genetic system
 - Planned a project and executed experiments to onboard new gene editing technologies
 - Collaborated with the operations team to test and implement new processes for optimizing plasmid production
- 2020-2022 Strain Engineer, Microbial Engineering, Joyn Bio LLC, Boston, MA
- Automated data processing and analysis of a high-throughput CRISPR PAM library interference next-generation sequencing assay

- Automated data processing and analysis from a high throughput RedOx assay
- Developed a method for site-specific, marker-less genome integration and identified and characterized two endogenous Type I CRISPR/Cas systems in a novel agriculturally important Gram+ prokaryote
- Performed sequence analysis of a plasmid library and compared with transformation data to identify active restriction modification systems in novel Gram+ prokaryotes
- Designed and coordinated RNA-Seq experiments with multiple internal departments and contract research organizations
- Designed and implemented protein engineering projects to deregulate nitrogen fixation
- Designed and ran metabolic engineering experiments to improve biological nitrogen fixation and evaluate the association between non-symbiotic plant growth promoting microbes and agriculturally important cereal crops

2016-2019 Research Assistant, Goodale Lab, Cornell University, Ithaca, NY

- Adapted an existing denitrification enzymatic assay, assayed 135 soil samples at 3 time points using gas chromatography, and analyzed the results using R
- Studied the effects of nutrient limitations on microbial denitrification activity in northeastern forest soils
- Designed and implemented an independent research project studying the effects of nutrient limitations on fine root biomass
- Led a field crew in the installation of 120 root cores at 3 forest sites

2018-2019.1 Undergraduate Researcher, Thies Lab, Cornell University, Ithaca, NY

- Isolated chromium-resistant bacterial strains from contaminated soils
- Inoculated cowpea seedlings with chromium-resistance strains to study their effects on plant grown in the presence of chromium

2018 Research Assistant, Baars Lab North Carolina State University, Raleigh, NC

- Worked on methods development for the extraction and quantitation of small molecules from soils using LC-MS and analyzed data in R and MZmine

DEIA STATEMENT

I am committed to questioning existing hierarchies and uplifting underrepresented perspectives to improve research and work towards a more just society. In one effort to increase DEI awareness and action at my previous company, I organized and facilitated three rounds of small discussion groups for my company, each of which followed a larger training on a core component of DEI. In these discussions, coworkers voiced concerns and provided ideas for the future, which were documented for continued initiatives.

DEI efforts require consistent commitment at multiple scales. In my daily interactions, I focus on active listening, maintaining an open mind, and recognizing all that I do not know before drawing conclusions. I also intend to advance equity and accessibility through my work as a volunteer English language tutor with ELNOR, an organization that provides English language education to students living in refugee camps and contexts. I am glad for the efforts to raise awareness of DEI and look forward to continuing to participate in putting words to action. I want to help create environments where everybody is included, and diverse perspectives are valued.

GRANTS, HONORS, AND AWARDS

2019 Granted Honors in Biological Sciences

2019 Graduated with Distinction in all subjects (Top 30% of class)

- 2018 Awarded NSF REU Summer Fellowship in Basic and Environmental Soil Science Training
- 2017 Writing in the Majors Prize Honorable Mention for: “Towards an Understanding of the Genetic and Morphological Consequences of Tar Sands Pollutants on Lake Trout (*Salvelinus namaycush*) Populations in Lake Athabasca”
- 2016 Member of Cornell delegation to UN Framework Convention on Climate Change COP 22. Presented research on climate change to an international audience.

TECHNICAL SKILLS AND EXPERIENCE

Computational: R, Python, Linux, Snakemake, Git, SQL, AWS, Google Cloud, High performance computing, Next Generation Sequencing analysis pipelines, Shiny, Web Development (HTML, JavaScript, CSS), Adobe Illustrator

Molecular Biology: RNA-Seq, Whole Genome Sequencing, PCR, qPCR, Golden Gate Assembly, Gibson Assembly, nucleic acid extraction, protein purification, cell-free systems

Microbiology: Microbial culturing, non-model bacterial transformation (electroporation, conjugation, natural competence, and chemical competence), genetic toolkit development for undomesticated bacteria

PUBLICATIONS

Orcid: 0009-0005-7497-411X

1. V Rai, **N Fisher**, OW Duckworth, O Baars, 2020. Extraction and Detection of Structurally Diverse Siderophores in Soil. *Frontiers in Microbiology* 11, 1–13. doi:10.3389/fmicb.2020.581508 PMID:33042099 PMCID:PMC7527475
2. JD Moreira-Bouchard, J Cunha, BS Tao, H Kim, J Lepson, EJ Nessen, ZJ Milstone, **N Fisher**, N Clinton, LM Roberts, MA Serrano, DM Gopal, EJ Benjamin, K So-Armah, JL Fetterman, 2024. Creating diversity, equity, inclusion, and accessibility statements for your CV: a resource guide to effectiveness and comprehensiveness. *American Journal of Physiology-Heart and Circulatory Physiology* 327, H1376–H1383. doi:10.1152/ajpheart.00610.2024 PMID:39485298
3. ZJ Milstone, JD Moreira-Bouchard, KK Smith, A Gower, Y Alekseyev, J Cunha, **N Fisher**, J Lepson, A Lamason, BS Tao, C Williams, EJ Benjamin, D Levy, R Mitchell, RF Padera, SH Choi, DM Gopal, N Tucker, JL Fetterman, 2024. Site-Specific Transcriptomic Patterns and Cell Types Associated with Hypertension. *Circulation* 150, A4141486-A4141486. doi:10.1161/circ.150.suppl_1.4141486
4. ZJ Milstone, JD Moreira-Bouchard, KK Smith, A Anilkumar, AC Gower, Y Alekseyev, JA Cunha, **N Fisher**, L Legler, J Lepson, BS Tao, C Williams, EJ Benjamin, D Levy, RN Mitchell, RF Padera, H Shah, SH Choi, DM Gopal, NR Tucker, JL Fetterman, 2025. Multiomics investigation of the female hypertensive human heart. *Physiological Reports* 13, e70586. doi:10.14814/phy2.70586 PMID:41036600 PMCID:PMC12489463
5. **N Fisher***, L Xue*, KK Smith, B Tao, J Cunha, S Ladenheim, JD Moreira-Bouchard, ZJ Milstone, A Zhebrun, X Zhang, GR Jun, TD Stein, TFA Ang, LA Farrer, MG Farb, RF Padera, EJ Benjamin, D Levy, DM Gopal, RS Isaac, ME Lenburg, SH Choi, JL Fetterman, 2025. Mitochondrial Genetic Variation Across Tissues of the Human Body. (*under revision*)

CONFERENCE PRESENTATIONS

A. Oral Presentations

1. **Fisher N.** Controls on Denitrification at Three Soil Depths West of Watershed 6. Hubbard Brook Ecosystem Study, 56th Annual Cooperator's Meeting, Woodstock, NH, July 2019.

B. Poster Presentations

1. **N Fisher***, L Xue*, KK Smith, B Tao, J Cunha, S Ladenheim, JD Moreira-Bouchard, ZJ Milstone, A Zhebrun, X Zhang, GR Jun, TD Stein, TFA Ang, LA Farrer, MG Farb, RF Padera, EJ Benjamin, D Levy, DM Gopal, RS Isaac, ME Lenburg, SH Choi, JL Fetterman. Mitochondrial Genetic Variation Across Tissues of the Human Body. Boston University Department of Medicine Evans Days. Boston, MA. October 2025
2. **N Fisher***, L Xue*, X Sun, JD Moreira-Bouchard, Y Li, KK Smith, J Cunha, BS Tao, ZJ Milstone, RF Padera, ME Lenburg, D Levy, EJ Benjamin, S Ladenheim, DM Gopal, C Liu, SH Choi, JL. Fetterman. Methods for Studying Heteroplasmic Mitochondrial Genetic Variation Using RNA-Seq Datasets from Human Tissues. Boston University Department of Medicine Evans Days. Boston, MA. October 2024
3. **N Fisher***, L Xue*, X Sun, JD Moreira-Bouchard, Y Li, KK Smith, J Cunha, BS Tao, ZJ Milstone, RF Padera, ME Lenburg, D Levy, EJ Benjamin, S Ladenheim, DM Gopal, C Liu, SH Choi, JL. Fetterman. Mitochondrial Genetic Variation Across Human Tissues. Bioinformatics Student Organized Symposium. Boston, MA. June 2024
4. **N Fisher** and C Goodale. Controls on Denitrification at Three Depths in a Northeastern Hardwood Forest. Hubbard Brook LTER Mid-Term Review. Woodstock, NH. June 2019.
5. **N Fisher**, S Liu, TG Gardner, and O Baars Relationships between Nutrient Content, Microbial Communities, and Presence of Siderophores in North Carolina Soils. SSSA International Soils Meeting. San Diego, CA. January 2019.

*denotes equal contributions to project

PROFESSIONAL ORGANIZATIONS

Student Member, American Society of Microbiology (2021- 2022)

Student Member, Soil Science Society of America (2018-2019)

GENERAL RESEARCH INTERESTS

human disease genomics, mitochondrial genetics, parallel computing, quantum computing, computational biology technologies applied to metabolic engineering, regulatory circuit redesign, and protein engineering, developing computational tools to improve design and data analysis of experiments, environmental applications for biotechnology