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**CURRENT POSITION**

<b>The Ohio State University</b> Graduate Research Associate	Columbus, OH 2020-Present
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**EDUCATION**

<b>The Ohio State University</b> PhD Candidate, Environmental Sciences (Focus: Engineering/Environmental Health/Microbial Genomics) Dissertation: Microbial function and volatile emissions as markers of indoor environmental microbial exposures.	Columbus, OH Expected Spring 2026
<b>Purdue University</b> MS, Civil Engineering (Focus: Environmental Engineering)	West Lafayette, IN 2020
<b>Anna University</b> B.Tech, Chemical Engineering	Chennai, India 2018

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**FELLOWSHIPS AND AWARDS**

<b>Graduate Mentor Award, Microbiome Sciences, Midwest Microbiome</b> For having mentored and directed the projects of undergraduates (15+ students) through the NSF REU and Student Experience and Engagement Delegates (SEEDs) programs in environmental microbiome sciences.	May 2025
<b>National Science Foundation (NSF) INTERN awardee, \$47,000</b> Microbial Genomics and Bioinformatics INTERN fellow at Abbott Nutrition (Jan 2025-Jun 2025)	July 2024
<b>Doctoral University Fellow</b> The Ohio State University Graduate School	2020-2021

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**RESEARCH EXPERIENCE**

<b>Abbott</b> Food Safety group, Nutrition Division, NSF INTERN fellow & Abbott Research Park Intern	Columbus, OH Jan 2025-Present
<ul style="list-style-type: none"><li>Implemented and validated Whole Genome Sequencing pipelines consisting of metagenomics, AMR &amp; virulence profiling, Single Nucleotide Polymorphism (SNP), cg- &amp; wg-Multi Locus Sequence Typing to support foodborne pathogen monitoring efforts.</li><li>Built version-controlled bioinformatics workflows with containerization and orchestration technologies including Docker, Kubernetes and Gitlab for streamlined and reproducible application deployment on local, cluster (HPC), and cloud computing environments (AWS).</li><li>Optimized containerized workflows and bioinformatics pipelines for business use cases by implementing custom NextFlow, Bash, and Python scripts enabling custom deployment, data management, and visualization solutions.</li><li>Designed and executed laboratory feasibility studies assessing long-read sequencing technology for R&amp;D and operational use cases, gaining applied microbiology and NGS library preparation experience.</li><li>Collaborated with cross-divisional cloud infrastructure engineers and bioinformatics teams for best practices in DevOps, cloud-native deployments, automation and containerization.</li><li>Cultivated business &amp; regulatory awareness and strategic communication skills by engaging with cross-functional teams, presenting innovation updates to key stakeholders, and managing project documentation and knowledge transfer for business alignment and continuity.</li></ul>	
<b>The Ohio State University</b> Graduate Research Associate; Advisor: Karen C. Dannemiller	Columbus, OH 2020-Present
<ul style="list-style-type: none"><li>Metatranscriptomics to identify fungal gene markers of water damage in homes and in the International Space Station (ISS) to provide insights into human and astronaut exposures and health outcomes. (4 first-author manuscripts: 2 published (Microbiome &amp; Scientific Reports), 2 under revision)</li></ul>	

- Led R&D studies to profile microbial communities and gene expression patterns in indoor environments, contributing to respiratory health risk assessment and exposure quantification.
- Designed and executed RNA-seq pipeline for functional metatranscriptomic analysis, leveraging Trinity, Bash scripting, DESeq2, and KEGG/GO enrichment tools on HPC infrastructure (Ohio Supercomputer).
- Translated the lab's end to end RNAseq pipeline into Nextflow with containerized processes on the HPC for complete reproducibility, scalability and automation.
- Automated data workflows in R to standardize annotation sources (BLAST, GO, KEGG) across datasets and merge with gene expression outputs, streamlining downstream biological insights and reproducibility.
- Developed scripts in R to perform statistical analysis and visualization for dimensionality reduction (PCA, PCoA), differential analysis, and hypothesis testing of -omics datasets.
- Applied multi-omics data integration techniques (WGCNA, HALLA) to reveal correlated microbial functions and metabolic pathways across transcriptomic and metabolomic (PTR-ToF-MS) datasets.
- Developed and performed manual and automated RNA and DNA isolation assays for complex low-biomass indoor environmental samples such as dust from swabs, carpet samples, ISS HVAC filters and pure bacterial and filamentous fungal cultures.
- Designed and developed RT-qPCR assays for fungal target genes, utilizing novel absolute quantification standards developed from purified and sequenced amplicons.
- Contributed to SARS-CoV-2 environmental surveillance through targeted viral RNA isolation and RT-qPCR quantification in built environment samples.

**Purdue University**  
Graduate Researcher

West Lafayette, IN  
2018-2020

- Modeled pollutant transport and inhalation exposure using an eddy transport model and Monte Carlo simulations in MATLAB to estimate breathing zone concentrations.
- Involved in collecting participant exhaled breath for tetrachloroethylene analysis and analyzed metabolite levels measured by ICP-MS in workers exposed to heavy metals and solvents.

**Indian Institute of Technology Madras**  
Research Intern, Department of Chemical Engineering  
Fluorescence microscopy-based quantification of fungal spores using image detection tools and maintained pure fungal cultures of *P. chrysogenum*.

Chennai, India  
Summer 2016

**Anna University**  
Research Assistant, Department of Chemical Engineering  
Kinetic modeling, reactor design and experiments to determine efficacy of pretreatment of lignocellulosic biomass using coffee grounds.

Chennai, India  
Summer 2016

## TEACHING EXPERIENCE

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**Purdue University**  
Graduate Teaching Assistant, Thermal Sciences (Thermodynamics)  
Graduate Teaching Assistant, Air Quality Control

West Lafayette, IN  
Spring 2021  
Spring 2021

## RELATED PROFESSIONAL EXPERIENCE

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- Mentored and directed the projects of groups undergraduates (15+ students total) through NSF REU and Student Experience and Engagement Delegates (SEEDs) programs. (2021-Present)
- Member, International Scientific Advisory Committee for the conference, Indoor Air 2024.
- Podium Presentation: Indoor Air 2024 conference. Honolulu, Hawaii. July 7-11, 2024.
- Invited talk: Scientific Governing Body for Next Generation Sequencing, Abbott (division-wide)
- Podium presentations: AEESP 2025 (Metatranscriptomics of mold in homes), May 20-22, Midwest Microbiome 2025 (Metatranscriptomics of ISS HVAC filter dust).

## TECHNICAL SKILLS

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<b>Molecular Biology &amp; Microbiology</b>	DNA/RNA isolation (manual & automated), QC methodologies (Bioanalyzer, Qubit, Nanodrop), PCR (reverse transcription, digital & quantitative), Liquid handlers programming, NGS library preparation and sequencing, Microbial culturing (BSL-2), Fluorescence microscopy
<b>Bioinformatics &amp; Omics</b>	Bacterial source tracing with WGS   RNA-Seq   Shotgun, 16S & ITS rRNA Metagenomics   Multi-omics integration   Visualizations   Statistics <ul style="list-style-type: none"> <li>• <i>Select tools &amp; methods:</i> CSP2, Trinity, DESeq2, Kraken2, DADA2, WGCNA, sPLS, ggplot2, ggTree, matplotlib, seaborn, MATLAB, Cytoscape, Inkscape, Illustrator, ArcGIS, Reads QC (fastp, trimmomatic)</li> <li>• <i>Select databases:</i> NCBI, ENA, BLAST, KEGG, Uniprot</li> </ul>
<b>Bioinformatics DevOps</b>	Workflow tools: Nextflow, Bash, Make, Git/GitHub/GitLab Containerization: Docker, Apptainer, Kubernetes Platforms: HPC (Unix/Linux), AWS (Batch, EKS, HealthOmics) Languages: Python, R, DSL2 (Nextflow), SQL, MATLAB

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## PEER-REVIEWED PUBLICATIONS AND CONFERENCE PROCEEDINGS

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**Balasubrahmaniam, N., King, J. C., Hegarty, B., & Dannemiller, K. C. (2024).** Moving beyond species: Fungal function in house dust provides novel targets for potential indicators of mold growth in homes. *Microbiome*, 12(1), 231. <https://doi.org/10.1186/s40168-024-01915-9> **(Note: Patent filed on this work)**

**Balasubrahmaniam, N., Nastasi, N., Hegarty, B., Horack, J. M., Meyer, M. E., Haines, S. R., & Dannemiller, K. C. (2025).** Exposure to elevated relative humidity in laboratory chambers alters fungal gene expression in dust from the International Space Station (ISS). *Scientific Reports*, 15(1), 28366.

Nastasi, N., Anderson, M. Z., **Balasubrahmaniam, N.**, Bope, A., ... & Dannemiller, K. C. (2022). Application of Emerging Innovations in Microbiome Science to Space Development and Settlement Systems. In *Proceedings of the International Astronautical Congress, IAC* (Vol. 2022). International Astronautical Federation, IAF.

Nastasi, N., Renninger, N., Bope, A., Cochran, S. J., Greaves, J., Haines, S. R., **Balasubrahmaniam, N.**, ... & Dannemiller, K. C. (2022). Persistence of viable MS2 and Phi6 bacteriophages on carpet and dust. *Indoor air*, 32(1), e12969.

Renninger, N., Nastasi, N., Bope, A., Cochran, S. J., Haines, S. R., **Balasubrahmaniam, N.**, ... & Dannemiller, K. C. (2021). Indoor Dust as a Matrix for Surveillance of COVID-19. *Msystems*, 6(2), 10-1128.

**Balasubrahmaniam, N., King, J., Hegarty, B. & Dannemiller, K. C.** Quantitative reverse transcription assays of novel targets for potential indicators of mold growth in homes. (*In submission*)

- **For the complete and updated list, please see:**  
<https://scholar.google.com/citations?user=XJMt9RMAAAAJ&hl=en&oi=ao>

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## REFERENCES

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1. Dr. Karen Dannemiller, Associate Professor (PhD Thesis advisor, The Ohio State University)  
Email: [dannemiller.70@osu.edu](mailto:dannemiller.70@osu.edu)
2. Dr. Bridget Hegarty, Assistant Professor (Collaborator faculty), Case Western Reserve University  
Email: [beh53@case.edu](mailto:beh53@case.edu)
3. Dr. Lexie Blalock, Senior Scientist, Microbial Genomics, R&D Microbiology & Allergen group, Nutrition Division, Abbott  
Email: [lexie.blalock@abbott.com](mailto:lexie.blalock@abbott.com)
4. Dr. Sarah Haines, Assistant Professor (Collaborator faculty), University of Toronto  
Email: [s.haines@utoronto.ca](mailto:s.haines@utoronto.ca)