

## EDUCATION

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- 2024      **Doctor of Philosophy (Molecular, Cellular and Integrative Biosciences)**  
*The Pennsylvania State University, University Park, PA*  
• Concentration in functional, computational, and evolutionary genomics with an emphasis in gene-environment interactions and parent-of-origin effects
- 2019      **Bachelor of Science (Neuroscience)**  
*The University of Nebraska at Omaha, Omaha, NE*

## RESEARCH AND WORK EXPERIENCE

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- July 2024 – Present      **Postdoctoral Data Scientist**  
*The University of Texas MD Anderson Cancer Center, Houston, TX (Remote)*  
*Institute for Data Science in Oncology, Department of Epidemiology*  
• Leveraged isoform-level transcriptome-wide association study framework integrating multi-tissue GTEx RNA-seq data (N>20,000) with population-scale cancer GWAS to identify genetic risk mechanisms  
• Assembled comprehensive tissue-specific transcriptome references across multiple human tissues using Oxford Nanopore and PacBio long-read RNA-seq with orthogonal multi-omic validation datasets, identifying thousands of novel high-confidence isoforms and reducing inferential uncertainty in short-read quantification by 30%  
• Developed computational frameworks leveraging multi-omics integration to study environmental exposure effects on birth outcomes mediated through developmental gene regulation in international birth cohorts  
• Conducted comparative analyses of RNA-seq quantification methods and transcriptomic annotations to assess reproducibility of eQTL detection, transcriptome-wide association study and colocalization results  
• Designed simulation software for causal inference using generative adversarial networks and multi-omic negative controls to calibrate confounding bias in environmental epidemiology studies  
• Mentors: Dr. Arjun Bhattacharya and Dr. Paul Scheet
- June – August 2024      **Data, AI & Genome Sciences Intern**  
*Merck Research Laboratories, Boston, MA*  
• Developed methods for differentiating hematopoietic and tumor mutations in liquid biopsies leveraging KEYTRUDA™ keynote study genomics data  
• Mentors: Dr. Minita Shah and Dr. Razvan Cristescu
- 2019 – 2024      **National Science Foundation Graduate Research Fellow**  
2019 – 2022      **Integrative Pollinator Ecology Graduate Training Fellow**  
2019 – 2020      **Penn State University Graduate Fellow**  
*The Pennsylvania State University, Huck Institutes of the Life Sciences, University Park, PA*  
• Generated multi-omics datasets and leveraged statistical genomics, unsupervised clustering and machine-learning methods to study molecular mechanisms of parental conflicts underlying plasticity in bee behaviors  
• Analyzed tissue-specific gene expression profiles to investigate environmentally sensitive phenotypic plasticity  
• Designed production-grade metagenomics software to assess species biodiversity in environmental samples  
• Mentors: Dr. Christina Grozinger and Dr. Michael Axtell
- 2018 – 2019      **Research Assistant**  
*University of Nebraska at Omaha, Department of Mathematics, Omaha, NE*  
• Developed a network model of macrophage protein interactions to study HIV infection
- 2017 – 2019      **Research Assistant**  
*University of Nebraska at Omaha, Department of Biology, Omaha, NE*  
• Used CRISPR/Cas9 to investigate the genetic basis of stress coping behaviors in zebrafish

## AWARDS AND HONORS

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2025	American Society of Human Genetics (ASHG 2025) – Travel Award	\$1,500
2023	Huck Institutes of the Life Sciences – Graduate Travel Award	\$2,250

## RESEARCH SUPPORT

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### Completed Support

2019 – 2024	National Science Foundation Graduate Research Fellowship Program	\$173,000
2019 – 2022	Integrative Pollinator Ecology Graduate Training Fellowship Program	\$58,000
2019 – 2020	Penn State University Graduate Fellowship	\$19,500
2017 – 2018	UNO ORCA – Funds for Undergraduate Scholarly Experiences Grant	\$2,500

### Submitted Support

#### **R21 (Co-I: Bresnahan, S. T.)**

*Identifying PFAS-Induced Disruption of Placental Imprinting and Neurodevelopment Through Multi-Omic Negative Control Calibration*

Sponsor: National Institute of Environmental Health Sciences

Funding period: 04/01/2026 – 03/31/2028

Total costs: \$500,000

Co-Is: Bhattacharya, A., Huang, J., Fry, R., O’Shea, M.

#### **MERP (Key personnel: Bresnahan, S. T.)**

*The effects of burn pit and toxicant exposure to lung cancer risk and progression via alternative splicing and transcript-isoform expression moderation*

Sponsor: Office of Research and Development, U.S. Dept. of Veterans Affairs

Funding period: 04/01/2026 – 03/31/2031

Total costs: \$2,000,000

MPIs: Bhattacharya, A. & Shin, D.

#### **R01 (Key personnel: Bresnahan, S. T.)**

*Dissecting genetic and environmental effects on the placental transcriptome in gestational complications*

Sponsor: National Institute of Child Health and Human Development

Funding period: 04/01/2026 – 03/31/2031

Total costs: \$2,000,000

MPIs: Bhattacharya, A., Huang, J., Fry, R., Santos, H.

## PUBLICATIONS

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### Publications in Peer-Reviewed Journals

1. Chang, Y. H., **Bresnahan, S. T.**, Head, S. T., Harrison, T., Yu, Y., Huff, C. D., Pasaniuc, B., Lindström, S., & Bhattacharya, A. Isoform-level analyses of 6 cancers uncover extensive genetic risk mechanisms undetected at the gene level. *Br J Cancer*. 133, 874-885. <https://doi.org/10.1038/s41416-025-03141-y>
2. **Bresnahan, S. T.**, Mahony, S., Anton, K., Harpur, B., & Grozinger, C. M. (2025). Intragenomic conflict underlies extreme phenotypic plasticity in queen-worker caste determination in honey bees (*Apis mellifera*). *Genome Biology*. 26(171). <https://doi.org/10.1186/s13059-025-03628-0>
3. **Bresnahan, S. T.**, Ma, R., Galbraith, D., Rangel, J., & Grozinger, C. M. (2023). Beyond conflict: Kinship theory of intragenomic conflict predicts individual variation in altruistic behaviour. *Molecular Ecology*. 32(21), 5823-5837. <https://doi.org/10.1111/mec.17145>
4. **Bresnahan, S. T.**, Lee, E., Clark, L., Ma, R., Rangel, J., & Grozinger, C. M. (2023). Examining parent-of-origin effects on transcription and RNA methylation in mediating aggressive behavior in honey bees (*Apis mellifera*). *BMC Genomics*. 24, 315. <https://doi.org/10.1186/s12864-023-09411-4>
5. Crone, M., Boyle, N., **Bresnahan, S. T.**, Biddinger, D., & Grozinger, C. M. (2023). More than mesolectic: Characterizing the nutritional niche of *Osmia cornifrons*. *Ecology and Evolution*. 13, e10640. <https://doi.org/10.1002/ece3.10640>
6. **Bresnahan, S. T.**, Döke, M. A., Giray, T., & Grozinger, C. M. (2021). Tissue-specific transcriptional patterns underlie seasonal phenotypes in honey bees (*Apis mellifera*). *Molecular Ecology*. 31(1), 174-184. <https://doi.org/10.1111/mec.16220>

## Under Review/Revision for Publication in Peer-Reviewed Journals

1. **Bresnahan, S. T.**, Yong, H., Wu, W. H., Lopez, S., Chan, J. K. Y., White, F., Jacques, P.-É., Hivert, M.-F., Chan, S.-Y., Love, M. I., Huang, J. Y., & Bhattacharya, A. (2025). Long-read transcriptome assembly reveals vast transcriptional complexity in the placenta associated with metabolic and endocrine function. *bioRxiv; in review at Nature Communications*. <https://doi.org/10.1101/2025.06.26.661362>
2. Head, S. T., Bresnahan, S. T., Cole, N., Wu, W., Bhattacharya, B. (2025). Quantification method affects replicability of eQTL analysis, colocalization, and TWAS. *bioRxiv; in review at Nature Genetics*. <https://doi.org/10.1101/2025.08.20.671303>

## Non-Refereed Articles

1. **Bresnahan, S. T.** (2023). [\*Metacleaner: Automated curation of barcode sequence databases for metabarcoding and metagenomics\*](#).
2. **Bresnahan, S. T.** (January – April 2022). [\*Entomologist of the Month Factsheets\*](#). Penn State Insect Biodiversity Center, College of Agricultural Sciences.
3. **Bresnahan, S. T.** (2020). [\*Mind the Bees – Ralf Nauen and Colleagues Protect Pollinators Through Neonicotinoid Research\*](#). Penn State College of Agricultural Sciences News.
4. **Bresnahan, S. T.** (2020). [\*The “Hidden” World of Colony-Level Impacts of Neonicotinoids on Social Pollinators\*](#). Penn State College of Agricultural Sciences News.

## PRESENTATIONS AND POSTERS

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### Oral Presentations

#### International and National Presentations

1. **Bresnahan, S. T.**, Wu, W., Huang, J., & Bhattacharya, A. (2025). *Long-read transcriptome assembly reveals vast transcriptional complexity in the placenta associated with metabolic and endocrine function*. ASHG 2025, Boston, MA.
2. **Bresnahan, S. T.**, Wu, W., Huang, J., & Bhattacharya, A. (2025). *Long-read assembly of the placenta reduces inferential uncertainty and unveils novel isoforms associated with gestational diabetes mellitus*. Biology of Genomes, Cold Spring Harbor Laboratory, Long Island, NY.
3. **Bresnahan, S. T.**, Mahony, S., Anton, K., Harpur, B., & Grozinger, C. M. (2024, **invited**). *Investigating the molecular mechanisms of intragenomic conflict in honey bees*. Biology and Genomics of Social Insects, Cold Spring Harbor Laboratory, Long Island, NY.
4. **Bresnahan, S. T.**, & Grozinger, C. M. (2024, **invited**). *Investigating the molecular mechanisms of intragenomic conflict in honey bees*. Plant and Animal Genomics Annual Meeting, San Diego, CA.
5. **Bresnahan, S. T.**, Hines, H., Zayed, A., Rangel, J., Li-Byarlay, H., & Grozinger, C. M. (2022, **invited**). *Intragenomic conflict and its epigenetic basis in honey bees*. International Union for the Study of Social Insects, San Diego, CA.
6. **Bresnahan, S. T.**, Axtell, M., & Grozinger, C. M. (2022, **invited**). *Evaluating piRNAs as a mechanism of intragenomic conflict in honey bees*. Plant and Animal Genomics Annual Meeting, San Diego, CA.
7. **Bresnahan, S. T.**, Li-Byarlay, H., Rangel, J., Ma, R., Galbraith, D., & Grozinger, C. M. (2021). *Evaluating intragenomic conflict in altruistic, pheromone-mediated honey bee behaviors*. Biology and Genomics of Social Insects, Cold Spring Harbor Laboratory, Long Island, NY.

#### State, Regional, and Local Presentations

1. **Bresnahan, S. T.** (2025, **invited**). *Long-read assembly and analysis of breast tissue and tumor*. The University of Texas MD Anderson Cancer Center, Department of Epidemiology Trainee Works in Progress Seminar Series, Houston, TX.
2. **Bresnahan, S. T.**, Döke, M. A., Giray, T., & Grozinger, C. M. (2021, **invited**). *Tissue-specific transcriptional patterns underlie seasonal phenotypes in honey bees*. Penn State University Center for Pollinator Research Symposium, University Park, PA.

### Poster Presentations

1. **Bresnahan, S. T.**, Ma, R., Galbraith, D., Rangel, J., & Grozinger, C. M. (2023). *Kinship theory of intragenomic conflict predicts altruistic and selfish behaviors in honey bees*. International Conference on Pollinator Biology, Health, and Policy, University Park, PA.
2. **Bresnahan, S. T.**, Axtell, M., & Grozinger, C. M. (2020). *Evaluating the role of PIWI/piRNAs in intragenomic conflict in honey bees*. Regulatory and Non-Coding RNAs, Cold Spring Harbor Laboratory, Long Island, NY.

## TEACHING EXPERIENCE

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2024 – Present	MDACC Epidemiology Trainee Works in Progress biweekly meetings
Fall 2021	Honey Bees and Humans, Penn State, ENT 222 (TA), 90 students
Spring 2020	RNA-seq Analysis, workshop through the Penn State University Library, 20 participants
Fall 2018	Introduction to Neuroscience, UNO, NEUR 1520 (TA), 50 students

## SERVICE

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### Ad Hoc Journal Reviewer

*Nature; Heredity; Cell Genomics; Scientific Reports; BMC Genomics; G3 (Genes/Genomes/Genetics); Genome Biology and Evolution; Molecular Ecology; Insect Molecular Biology*

### Student Mentorship

*Mentoring responsibilities include providing training on molecular biology laboratory techniques, computational genomics and statistical methods, study design, data analysis, and presentations*

#### **Graduate Students**

2025 – Present	<u>Yung-Han Chang</u> , Doctoral Student, Department of Epidemiology, The University of Texas MD Anderson Cancer Center, UTHHealth Houston Graduate School
2025 – Present	<u>Sierra Lopez</u> , Masters Student, Global Environmental Science, The University of Hawai'i at Mānoa (mentored through Dr. Jonathan Huang's lab)
2024 – Present	<u>Robbie Kelly</u> , Doctoral Student, Huck Institutes of the Life Sciences, PSU
2023 – 2024	<u>Avi Eliyahu</u> , Doctoral Student, Department of Entomology, The Hebrew University of Jerusalem (mentored at Penn State through the US-Israel Binational Agricultural Research and Development Fund Graduate Fellowship Program)

#### **Undergraduate Students**

2025 – Present	<u>Aryun Nemanji</u> , Department of BioSciences, Rice University (mentored through Dr. Bhattacharya's lab)
2025 – Present	<u>William Wu</u> , Department of BioSciences, Rice University (mentored through Dr. Bhattacharya's lab)
2023 – 2024	<u>Owen Christopher</u> , Department of Biology, Penn State University
2023	<u>Mariam Taninabe</u> , Department of Biology, Penn State University

## LABORATORY SKILLS

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- Nucleic acid extraction and quality control, PCR, qPCR, CRISPR/Cas9, RNAi, bacterial cell culture
- Chromatin prep. and immunoprecipitation (ChIP), assay for transposase-accessible chromatin (ATAC)
- Sequencing library preparation, Illumina sequencing, Oxford Nanopore sequencing

## COMPUTING SKILLS

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- Advanced: R (including software development), Unix, HPC environments, AWS
- Intermediate: Python, MatLab, Nextflow, C++, Rust

## SOFTWARE

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*I maintain and contribute to several R packages, all available on GitHub*

1. scAmbi: mapping ambiguity overdispersion correction and BCV analysis for scRNA-seq
2. Metacleaner: automated curation of sequence databases for metabarcoding and metagenomics
3. SQANTI3: tool for the quality control of long read defined transcriptomes