

Sean T. Bresnahan, PhD
MD Anderson Cancer Center Epidemiology
Postdoctoral Data Scientist

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EDUCATION

- 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
• Mentors: Dr. Christina Grozinger and Dr. Michael Axtell
- 2019 **Bachelor of Science (Neuroscience)**
The University of Nebraska at Omaha, Omaha, NE

RESEARCH AND WORK EXPERIENCE

- 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
• Biomarkers of cancer survivorship across diverse populations and environments
• Placental genomic signatures mediating maternal exposures and pregnancy complications
• Mentors: Dr. Arjun Bhattacharya and Dr. Paul Scheet
- June – August 2024 **Data, AI & Genome Sciences Intern**
Merck Research Laboratories, Boston, MA
• Analyzed KEYTRUDA™ keynote study genomics data for collaborative projects
• Developed method for differentiating hematopoietic and tumor mutations in liquid biopsies
• 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 used advanced statistical methods to study molecular mechanisms of parental conflicts underlying plasticity in honey bee behaviors
• Used complex data collection designs and analyzed tissue-specific gene expression profiles to investigate environmentally sensitive plasticity in honey bee colonies
• Designed 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
• Advisor: Dr. Jim Rogers
- 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
• Advisor: Dr. Ryan Wong

AWARDS AND HONORS

2025	American Society of Human Genetics (ASHG 2025) – Travel Award	\$1,500
2023	Huck Institutes of the Life Sciences – Graduate Travel Award	\$2,250
2019	UNO ORCA Student Research and Creative Activity Fair – Outstanding New Research	NA

RESEARCH SUPPORT

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

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). Intragenic 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

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

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

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

LABORATORY SKILLS

- 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

- Advanced: R (including software development), Bash, Unix, HPC environments
- Intermediate: Python, MatLab

SOFTWARE

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