Curriculum Vitae
Sean T. Bresnahan, PhD
MD Anderson Cancer Center Epidemiology
Associate Data Scientist & Bioinformatics Data Science Contractor

Updated: April 29th, 2026
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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
2019	**Bachelor of Science (Neuroscience)** *The University of Nebraska at Omaha, Omaha, NE*

RESEARCH AND WORK EXPERIENCE

March 2026 – Present;

Previously: Assistant Data Scientist, July 2024 – March 2026

Associate Data Scientist
The University of Texas MD Anderson Cancer Center, Houston, TX (Remote)
Institute for Data Science in Oncology, Department of Epidemiology

- Applied isoform-resolution transcriptome-wide association study (TWAS) framework integrating multi-tissue GTEx RNA-seq with population-scale GWAS across cancer indications, integrating ENCODE datasets to identify molecular mechanisms associated with lead isoQTLs
- Assembled tissue-specific transcriptome references using Oxford Nanopore and PacBio long-read RNA-seq, novel isoforms and reducing short-read quantification uncertainty; demonstrated improved eQTL detection and TWAS accuracy in colocalization studies
- Conducted systematic comparative analyses of RNA-seq quantification methods and transcriptomic annotations affecting replicability of eQTL detection, TWAS, and colocalization results
- Established multi-ancestry placental genomics resource across multiple birth cohorts to investigate gene-environment interactions underlying childhood metabolic disease, including genome-wide GxE scans testing how gestational diabetes and PFAS exposure modify fetal genetic regulation
- Characterized parent-of-origin-specific (genomic imprinting) regulation at isoform level using trio genotypes, revealing allele-specific expression disruption by environmental exposures and demonstrating that natural variation in transplacental transfer efficiency exposes distinct transcriptional networks mediating PFAS effects on birth outcomes
- Developed SCENIC R package implementing causal inference approaches using generative adversarial networks to systematically compare negative control debiasing methods under unmeasured confounding, with mediation frameworks testing pathways from prenatal exposures through placental mechanisms to child health outcomes

March 2026 – Present

Bioinformatics Data Science Contractor
Vindhya Data Science (Remote)

- Conducted pan-cancer genomic analyses across TCGA cohorts and DepMap CRISPR screens to evaluate therapeutic target candidates across multiple cancer indications

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

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 statistical genomics and machine-learning methods to study molecular mechanisms of parental conflicts underlying plasticity in bee behaviors
- Analyzed tissue-specific gene expression profiles to investigate phenotypic plasticity
- Designed metagenomics software to assess species biodiversity in environmental samples

RESEARCH AND WORK EXPERIENCE (cont.)

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

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

Submitted Support

R21 (MPI: Bresnahan, S. T.)
Title: *Understanding how maternal metabolic environment moderates fetal genetic regulation of the placental transcriptome underlying childhood metabolic traits*
Sponsor: National Institute of Environmental Health Sciences
Funding period: 04/01/2027 – 03/31/2029
Total costs: $500,000
MPI: Bhattacharya, A. Huang, J.

R21 (Co-I: Bresnahan, S. T.)
Title: *Identifying PFAS-Induced Disruption of Placental Imprinting and Neurodevelopment Through Multi-Omic Negative Control Calibration*
Sponsor: National Institute of Environmental Health Sciences
Funding period: 09/01/2026 – 08/31/2028
Total costs: $500,000
PI: Bhattacharya, A.
Co-I: Huang, J., Fry, R., O’Shea, M.

R01 (Co-I: Bresnahan, S. T.)
Title: *Dissecting genetic and environmental effects on the placental transcriptome in gestational complications*
Sponsor: National Institute of Child Health and Human Development
Funding period: 04/01/2027 – 03/31/2032
Total costs: $2,000,000
MPI: Bhattacharya, A, Huang, J., Fry, R., Santos, H.

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

PUBLICATIONS

Publications 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. (2026). Long-read transcriptome assembly reveals vast transcriptional complexity in the placenta associated with metabolic and endocrine function. *Nature Communications*. https://doi.org/10.1038/s41467-026-71303-4

Publications in Peer-Reviewed Journals (cont.)

2. 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. *British Journal of Cancer*. *133*, 874-885. https://doi.org/10.1038/s41416-025-03141-y
3. **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
4. **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
5. **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
6. 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
7. **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

Publications Under Review/Revision in Peer-Reviewed Journals

1. Head, S. T., **Bresnahan, S. T.**, Cole, N., Wu, W., Bhattacharya, B. (2025). Quantification method affects replicability of eQTL analysis, colocalization, and TWAS. *bioRxiv* [preprint]; *in revision* at *Nature Genetics*. https://doi.org/10.1101/2025.08.20.671303
2. **Bresnahan, S. T.**, Yong, H. E. J., Drelichman, M. G., Campbell, S. N., Trapse, A. E., Romo, G. R., Cellini, C. M., Lopez, S., Yen Chan, J. K., Chan, S. Y., Elkin, E. R., Bhattacharya, A., & Huang, J. Y. (2026). Natural variation in transplacental transfer efficiency exposes distinct transcriptional network architectures of PFAS effects on birth weight and gestational age. *bioRxiv* [Preprint]. https://doi.org/10.64898/2026.03.23.712893
3. Head, S. T., Nemani, A., Chang, Y. H., Harrison, T. A., **Bresnahan, S. T.**, Rothstein, J. H., Sieh, W., Lindström, S., & Bhattacharya, A. (2026). Improving isoform-level eQTL and integrative genetic analyses of breast cancer risk with long-read RNA transcript assemblies. *bioRxiv* [Preprint]. https://doi.org/10.64898/2026.03.22.713514

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.**, Xiong, C., Bhattacharya, A., Huang, J. (2026, **invited**). *Negative controls and instrumental variables for identifying PFAS effects on placental gene regulation and developmental outcomes*. Society for Epidemiological Research, Phoenix, AZ.
2. **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, Boston, MA.
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.

International and National Presentations (cont.)

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.**, Xiong, C., Huang, J., & Bhattacharya, A. (2026, **invited**). *A negative control framework for causal inference in genomic mediation: application to PFAS-induced placental imprinting and neurodevelopment*. STATGEN, Atlanta, GA.
2. **Bresnahan, S. T.**, Huang, J., Fry, R. C., & Bhattacharya, A. (2026). *Effects of PFAS exposure during pregnancy on placental gene regulation and infant neurodevelopment*. Society for Reproductive Investigation, San Juan, PR.
3. **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.
4. **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.
5. **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	Yung-Han Chang, Doctoral Student, Department of Epidemiology, The University of Texas MD Anderson Cancer Center, UTHealth Houston Graduate School
2025 – Present	Sierra Lopez, Masters Student, Global Environmental Science, The University of Hawai‘i at Mānoa (mentored through Dr. Jonathan Huang's lab)
2024 – 2025	Robbie Kelly, Doctoral Student, Huck Institutes of the Life Sciences, PSU

Graduate Students (cont.)

2023 – 2024	Avi Eliyahu, 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

2026 – Present	Charis Xiong, Department of Biostatistics, Rice University (mentored through Dr. Bhattacharya's lab)
2025 – Present	Aryun Nemani, Department of BioSciences, Rice University (mentored through Dr. Bhattacharya's lab)
2025 – Present	William Wu, Department of BioSciences, Rice University (mentored through Dr. Bhattacharya's lab)
2023 – 2024	Owen Christopher, Department of Biology, Penn State University
2023	Mariam Taninabe, 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, HPC environments, AWS
- Intermediate: Python, MatLab, C++

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