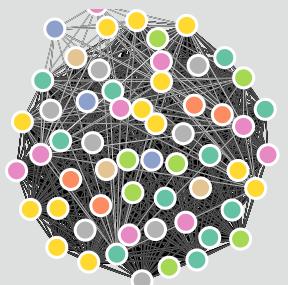


BRENDAN F. MILLER

Post-doctoral research fellow developing computational pipelines for analysis of single-cell and spatial-omics data. Molecular biologist with strong background in clinical diagnostics and cancer biology.



CURRENT POSITION

Current
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2020

- **Post-Doctoral Fellow in Computational Biology**
Johns Hopkins University
Department of Biomedical Engineering
 JEFworks Lab
Supervisor - Dr. Jean Fan
 - Development of open-source computational pipelines and statistical software to characterize and visualize cell type spatial organizational patterns in tissues.
 - Directly analyzed and extracted meaningful cell type spatial relationships from leading-edge technologies such as Visium, MERSCOPE, Slide-Seq, DBiT-Seq.
 - Annotated cell types and quantified their spatial co-localization changes across immune tissues using CODEX highly multiplexed spatial protein expression data.
 - Applied convolutional neural networks to segment cells in H&E images to increase the resolution of Visium datasets.
 - Developed statistical software packages in R and Python. Performed extensive high-throughput analyses with a high-performance Linux cluster.
 - Characterizing spatial gene expression heterogeneity in spatially resolved single-cell transcriptomic data with nonuniform cellular densities | *Genome Res* 2021
 - Reference-free cell type deconvolution of multi-cellular pixel-resolution spatially resolved transcriptomics data | *Nat Commun* 2022

Baltimore, MD

CONTACT

- bmill3r@gmail.com
 <https://github.com/bmill3r>
 <https://bmill3r.github.io/>
 [brendan-f-miller](#)
 Google Scholar

EDUCATION

2020
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2014

- **Ph.D., Molecular Biology**
Johns Hopkins University
National Institutes of Health Graduate Partnership Program
Advisor - Dr. Laura Eltsitski
 - Dissertation: Investigating Blood-based Biomarkers and Patterns of DNA Methylation in Tumors
 - Optimized single molecule detection assay to quantify rare fragments of methylated cell-free DNA in patient plasma. Developed computational machine learning algorithms leveraging heterogeneous methylation patterns to optimize liquid biopsy cancer diagnostics.
 - Developed pipeline to process cell-free DNA from hundreds of patient plasma samples. Samples were analyzed using ddPCR and qPCR.
 - Bisulfite sequencing analysis of extracted cell-free DNA to detect rare methylated DNA variants.
 - Assessing ZNF154 methylation in patient plasma as a multicancer marker in liquid biopsies from colon, liver, ovarian and pancreatic cancer patients | *Sci Reports* 2021
 - Leveraging locus-specific epigenetic heterogeneity to improve the performance of blood-based DNA methylation biomarkers | *Clin Epigenetics* 2020
 - The emergence of pan-cancer CIMP and its elusive interpretation | *Biomolecules* 2016
- **B.S., Biochemistry | Pharmacology minor**
University of Vermont
 - Burlington, VT

2012
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2008

EXPERTISE

- Biology**
Assay optimization
Cancer diagnostics
Cell-free DNA
droplet digital PCR
DNA Methylation
Epigenetics and chromatin
Gene expression variability

Data Analysis

- Bisulfite sequencing
Differential Gene Expression
Cell type deconvolution
Gene set enrichment analysis
Machine learning models
Single-cell multi-omics
Spatial transcriptomics

Software/Coding

- R/RStudio
Python
Bash scripting
Linux High-Performance Computing

Data Visualization

- ggplot2
jupyter notebook
markdown
matplotlib
R Shiny

Version Control

- Bioconductor
git/GitHub
PyPI

Scientific Communication

- High impact publications
Invited conference speaker

AWARDS AND HONORS

- 2022 • **Johns Hopkins Whiting School of Engineering Excellence in Research Trainee Award**
Johns Hopkins University  Baltimore, MD
• "Reference-free cell-type deconvolution of multi-cellular pixel resolution spatially resolved transcriptomics data"
- 2020 • **National Human Genome Research Institute Intramural Research Award**
National Institutes of Health  Bethesda, MD
• Project: "Detection of Methylated Cancer Biomarkers in Cell-free DNA"
- 2020 • **National Institutes of Health Fellows Award for Research Excellence**
National Institutes of Health  Bethesda, MD
• Abstract: "A Methylation Density Binary Classifier for Predicting and Optimizing the Performance of Methylation Biomarkers in Clinical Samples"
- 2019 • **National Institutes of Health Graduate Student Research Award**
National Institutes of Health  Bethesda, MD
• 15th Annual NIH Graduate Student Research Symposium
• Section: Pharmacology and Clinical and Translational Science
- 2017 • **National Institutes of Health Fellows Award for Research Excellence**
National Institutes of Health  Bethesda, MD
• Abstract: "Digital Droplet PCR Liquid Biopsy Assay for Detecting Circulating Tumor DNA in Patient Plasma"
- 2013 • **National Institutes of Health Post-Baccalaureate Outstanding Poster Award**
National Institutes of Health  Bethesda, MD
- 2012 • **National Institutes of Health Post-Baccalaureate Training Award**
National Institutes of Health  Bethesda, MD
- 2012 • **John Thanassi Research Award for Outstanding Achievements in Biochemistry**
University of Vermont  Burlington, VT
- 2000 • **Geography Bee Winner**
East Kingston Elementary School  East Kingston, NH
• Winner of the 5th grade Geography Bee at the Elementary School level

RESEARCH EXPERIENCE

- 2020 | 2014 • **Graduate Research Fellow**
Translational and Functional Genomics Branch  Bethesda, MD
• Advisor: **Dr. Laura Elnitski**
• Project 1: "Detection of Methylated Cancer Biomarkers in Cell-free DNA"
• Project 2: "Elucidation of Molecular Commonalities in CpG Island Methylator Phenotype Tumors Across Cancer-types"

2014

- **Graduate Research Fellow**

Research Rotation
Carnegie Institution of Washington
Department of Embryology

📍 Baltimore, MD

- Advisor: **Dr. Alex Bortvin**
- Project: "Quantitation of transposable element abundance in RNA-seq data"
- Comparison and benchmarking of multiple bioinformatic pipelines for taxonomic classification and quantification of DNA transposable elements in biological samples.
- Preprocessing, alignment, and filtering of NGS RNA-seq reads followed by quantitation of genomic feature overlaps using combination of `bowtie`, `bedtools`, and custom `Python` scripts

2014

- **Post-Baccalaureate Research Fellow**

Genomic Structure and Function Section

📍 Bethesda, MD

- Advisor: **Dr. Anthony Furano**
- Project: "Factors that Determine Strand Selection During Repair of T/G Mismatches"

2012

- **Undergraduate Researcher**

Department of Pharmacology

📍 University of Vermont

- Advisor: **Dr. Wolfgang Dostmann**
- Project: "Purification and Long-term Storage of Toxoplasma gondii PKGII Protein"

2011

- **Undergraduate Researcher**

Department of Biochemistry

📍 University of Vermont

- Advisor: **Dr. Anne B. Mason**
- Project: "Identification of Key Residues of Human Transferrin and Transferrin Receptor"

2007

- **Research Assistant**

Department of Biological Sciences

📍 University of Massachusetts, Lowell, MA

- Advisor: **Dr. Brian Bettencourt**
- Project: "Variation in Hsp70 Expression During Natural Thermal Stress Drives Differential Suppression of poly-Q Toxicity"



TEACHING EXPERIENCE

2016

- **Lecturer - Research Tools for Studying Disease**

National Institutes of Health

📍 Bethesda, MD

- Developed syllabus, overall course structure, and administered grades for "Proteins I" and "Computational Biology" lectures

2015

- **Teaching Assistant - General Biology**

Johns Hopkins University

📍 Baltimore, MD

- Managed laboratory section, which included experimental setup, development of instructional lectures, and administration of assignments and exams

2014

- **Program Leader**

Health Education Outreach Program

📍 Bethesda, MD

- Taught topics in medicine and healthcare to underprivileged and underrepresented communities

2012

- **Tutor - General Chemistry and Organic Chemistry**

University of Vermont

📍 Burlington, VT

- Established and oversaw individual and group tutoring sessions

MENTORSHIP

- 2022 • **High School Summer Student**
Johns Hopkins University  Baltimore, MD
• Efficient Detection of Gene Expression Patterns in Large Spatially Resolved Single-Cell Transcriptomics Datasets with Pseudospot Aggregation
• Mayling Chen
- 2022 | 2021 • **Undergraduate Research Assistant**
Johns Hopkins University  Baltimore, MD
• STdeconvolve Computational Performance Benchmarking
• Feiyang

INVITED SPEAKER

- 2022 • **Reference-free cell-type deconvolution of multi-cellular pixel resolution spatially resolved transcriptomics data**
NYU Langone Single Cell Club  Virtual
- 2022 • **Reference-free cell-type deconvolution of multi-cellular pixel resolution spatially resolved transcriptomics data**
 Bioengineering Solutions for Biology and Medicine  Munich, Germany
- 2022 • **Reference-free cell-type deconvolution of multi-cellular pixel resolution spatially resolved transcriptomics data**
 CNS Research Showcase at Indiana University  Virtual
- 2021 • **Reference-free cell-type deconvolution of multi-cellular pixel resolution spatially resolved transcriptomics data**
 University of Sydney Bioinformatics Seminar Series  Virtual
- 2019 • **A methylation density binary classifier for predicting and optimizing the performance of methylation biomarkers in clinical samples**
Circulating Nucleic Acids/Liquid Biopsy Interest Group  Virtual
- 2018 • **Advancement in ovarian carcinoma detection using circulating cell-free DNA from patient plasma samples**
National Human Genome Research Institute Symposium  Bethesda, MD
- 2018 • **Detecting DNA methylation patterns in patient plasma to improve cancer diagnostics**
NIEHS Inflammation Faculty Workshop  Research Triangle Park, NC
- 2018 • **Detecting DNA methylation patterns in patient plasma to improve cancer diagnostics**
3rd Annual Liquid Biopsy Summit  San Francisco, CA

SELECTED POSTER PRESENTATIONS

- 2020 • **A methylation density binary classifier for predicting and optimizing the performance of methylation biomarkers in clinical samples**
Advances in Genome Biology and Technology  Marco Island, FL
- 2017 • **Detecting DNA methylation in blood for cancer diagnostics**
Next Generation Diagnostics Summit  Washington, DC
- 2017 • **Detecting DNA methylation in blood for cancer diagnostics**
EMBO Chromatin and Epigenetics Meeting  Heidelberg, Germany

2013

- Factors that determine strand selection during repair of T/G mismatches
13th Annual Postbac Poster Day

📍 Bethesda, MD

📎 PREPRINT PUBLICATIONS

2015

- Building genomic analysis pipelines in a hackathon setting with bioinformatician teams: DNA-Seq, Epigenomics, Metagenomics, and RNA-Seq

🔗 bioRxiv 018085

- Ben Busby, Allissa Dillman, Claire L. Simpson, Ian Fingerman, Sijung Yun, David M. Kristensen, Lisa Federer, Naisha Shah, Matthew C. LaFave, Laura Jimenez-Barron, Manjusha Pande, Wen Luo, **Brendan Miller**, Cem Mayden, Dhruba Chandramohan, Kipper Fletez-Brant, Paul W. Bible, Sergej Nowoshilow, Alfred Chan, Eric JC Galvez, Jeremy Chignell, Joseph N. Paulson, Manoj Kandpal, Suhyeon Yoon, Esther Asaki, Abhinav Nellore, Adam Stine, Robert Sanders, Jesse Becker, Matt Lesko, Mordechai Abzug, Eugene Yaschenko

📘 SELECTED PUBLICATIONS

2022

- Reference-free celltype deconvolution of multi-cellular pixel-resolution spatially resolved transcriptomics data

🔗 Nat Commun 13, 2339 (2022)

- **Brendan F. Miller**, Feiyang Huang, Lyla Atta, Arpan Sahoo, Jean Fan
- Software: **🔗 STdeconvolve**

2021

- Characterizing spatial gene expression heterogeneity in spatially resolved single-cell transcriptomics data with nonuniform cellular densities

🔗 Genome Res. 2021. 31: 1843-1855

- **Brendan F. Miller**, Dhananjay Bambah-Mukku, Catherine Dulac, Xiaowei Zhuang, Jean Fan
- Software: **🔗 MERINGUE**

2021

- Assessing ZNF154 methylation in patient plasma as a multicancer marker in liquid biopsies from colon, liver, ovarian and pancreatic cancer patients

🔗 Sci Rep 11, 221 (2021)

- **Brendan F. Miller**, Hanna M. Petrykowska, Laura Elnitski

2020

- Leveraging locus-specific epigenetic heterogeneity to improve the performance of blood-based DNA methylation biomarkers

🔗 Clin Epigenet 12, 154 (2020)

- **Brendan F. Miller**, Thomas R. Pisanic II, Gennady Margolin, Hanna M. Petrykowska, Pornpat Athamanolap, Akosua Osei-Tutu, Tza-Huei Wang, Christina Annunziata, Laura Elnitski
- Software: **🔗 EpiClass**

2019

- Identification of human silencers by correlating cross-tissue epigenetic profiles and gene expression

🔗 Genome Research. 2019 March; 29(3):1-11

- Di Huang, Hanna M. Petrykowska, **Brendan F. Miller**, Laura Elnitski, Ivan Ovcharenko

2018

- Transient reduction of DNA methylation at the onset of meiosis in male mice

🔗 Epigenetics and Chromatin. 2018 April; 11:15

- Valeriya Gaysinskaya, **Brendan F. Miller**, Godfried W. van der Heijden, Kasper D. Hansen, Alex Bortvin

2016

- The emergence of pan-cancer CIMP and its elusive interpretation

🔗 Biomolecules. 2016 Nov; 6(4):45

- **Brendan F. Miller**, Francisco Sanchez-Vega, Laura Elnitski

2014

- **Repair of naturally occurring mispairs can induce mutations in flanking DNA**

🔗 eLife 2014;3:e02001

• Jia Chen, **Brendan F. Miller**, Anthony V. Furano

2012

- **Structure-based Mutagenesis Reveals Critical Residues in the Transferrin Receptor Participating in the Mechanism of pH-induced Release of Iron from Human Serum Transferrin**

🔗 Biochemistry. 2012 Feb; 51(10):2113-21

• Ashley N. Steere, N. Dennis Chasteen, **Brendan F. Miller**, Valerie C. Smith, Ross T. A. MacGillivray, Anne B. Mason

2012

- **Ionic Residues of Human Serum Transferrin that Affect Binding to the Transferrin Receptor and Iron Release from the Complex**

🔗 Biochemistry. 2012 Dec; 51(2):686-94

• Ashley N. Steere, **Brendan F. Miller**, Samantha E. Roberts, Shaina L. Byrne, N. Dennis Chasteen, Valerie C. Smith, Ross T. A. MacGillivray, Anne B. Mason.

SOFTWARE

2021

- **STdeconvolve**

🔗 <https://jef.works/STdeconvolve/>

• Unsupervised machine learning approach to deconvolve multi-cellular pixel resolution spatial transcriptomics datasets in order to recover the putative transcriptomic profiles of cell-types and their proportional representation within spatially resolved pixels without reliance on external single-cell transcriptomics references.

2021

- **MERINGUE**

🔗 <https://jef.works/MERINGUE/>

• MERINGUE characterizes spatial gene expression heterogeneity in spatially resolved single-cell transcriptomics data with non-uniform cellular densities.

2020

- **EpiClass**

🔗 <https://pypi.org/project/EpiClass/>

• Optimizing and predicting performance of DNA methylation biomarkers using sequence methylation density information.

SERVICE

Current
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2019

- **The Liquid Biopsies (LB) Scientific Interest Group (SIG)**

Research Webinar Committee Co-Leader

• The aims of the Liquid Biopsies Interest Group are to: (1) foster scientific exchange; (2) communication of research (3); working towards establishing standard practices for circulating nucleic acids studies; (4) sharing and optimization of techniques.

2021

- **Journal Reviewer - Nature Protocols**

🔗 Prioritization of cell-types responsive to biological perturbations in single-cell data with Augur. Nat Protoc 16, 3836-3873 (2021)

2019

- **Journal Reviewer - Epigenomics**