

# BRENDAN F. MILLER


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



## CURRENT POSITION

Current  
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2020

### Post-doctoral Research Fellow

*Johns Hopkins University*  *Baltimore, MD*  
*Department of Biomedical Engineering*  
*JEFworks Lab*

- Supervisor: **Dr. Jean Fan**
- Project: "Reference-free deconvolution of multi-cellular spatially resolved transcriptomics data"



## EDUCATION

2020  
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2014

### Ph.D., Molecular Biology

*Johns Hopkins University*  *Baltimore, MD*

- Supervisor: **Dr. Laura Elnitski**
- Dissertation: "Investigating Blood-based Biomarkers and Patterns of DNA Methylation in Tumors"
- Part of the National Institutes of Health and Johns Hopkins University Graduate Partnership Program

2012  
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2008

### B.S., Biochemistry (minor in Pharmacology)

*University of Vermont*  *Burlington, VT*



## AWARDS AND HONORS

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

## CONTACT

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

## PROFICIENCIES

### Computational Biology

Python, R, git, Unix

### Data Analysis

Spatial transcriptomics  
Single-cell sequencing

### Diagnostics and Sequencing

Droplet-digital PCR  
Bisulfite sequencing  
Cell-free DNA

### Molecular Biology

DNA methylation  
Cell culture  
DNA cloning  
Nucleic acid purification  
siRNA knockdowns

- 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*



## RESEARCH EXPERIENCE

- 2020  
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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  
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2012 ● **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  
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2011 ● **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  
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2015

### 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  
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2012

### Program Leader

*Health Education Outreach Program* 📍 *Bethesda, MD*

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

2012  
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2010

### Tutor

*General Chemistry and Organic Chemistry* 📍 *Burlington, VT*

- Established and oversaw individual and group tutoring sessions



## INVITED SPEAKER

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

- 2021 ● **Reference-free cell-type deconvolution of pixel-resolution spatially resolved transcriptomics data**  
*bioRxiv 448381*  
**Brendan F. Miller**, Lyla Atta, Arpan Sahoo, Feiyang Huang, Jean Fan  
Software: STdeconvolve
- 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, Dhruva 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

- 2021 ● **Characterizing spatial gene expression heterogeneity in spatially resolved single-cell transcriptomics data with nonuniform cellular densities**  
*Genome Research in press*  
**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

### Circulating Nucleic Acids/Liquid Biopsy Interest Group

*Research Webinar Committee Co-Leader*

- The aims of the circulating nucleic acid/liquid biopsy interest group are (1) working towards establishing standard practices for CNA studies; (2) sharing and optimization of DNA techniques; (3) communication of CAN research

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



## REFERENCES

### Dr. Jean Fan

*Johns Hopkins University  
Department of Biomedical Engineering  
jeanfan@jhu.edu*

### Dr. Laura Elniski

*National Institutes of Health  
National Human Genome Research Institute  
elnitski@nih.gov*

### Dr. Thomas Pisanic II

*Johns Hopkins University  
Department of Mechanical Engineering  
tpisani1@jhu.edu*