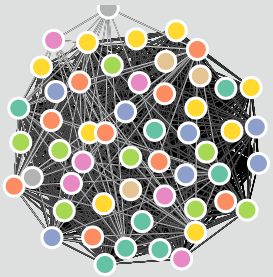
BRENDAN F. MILLER

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



CONTACT

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CURRENT POSITION

Current | 2020

Post-doctoral Research Fellow

Johns Hopkins University
Department of Biomedical Engineering
JEFworks Lab

Baltimore, MD

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

EDUCATION

2020 | 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 | 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

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

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

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 | 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 | 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 | 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 inn Hsp70 Expression During Natural Thermal Stress Drives Differential Suppression of poly-Q Toxicity"

TEACHING EXPERIENCE

2016 | 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 adminstration of assignments and exams

2014 | 2012 • **Program Leader**
Health Education Outreach Program — Bethesda, MD

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

2012 | 2010

Tutor - General Chemistry and Organic Chemistry
University of Vermont — Burlington, VT
• Established and oversaw individual and group tutoring sessions

INVITED SPEAKER

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, 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

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

BUGSS Volunteer

Current | 2019

Liquid Biopsies Scientific Interest Group

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

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