

# BRENDAN F. MILLER

Molecular Biologist | Computational Biology | Statistical Programming

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



## CURRENT POSITION

Current  
|  
2020

### Post-Doctoral Research Fellow

Johns Hopkins University  
Department of Biomedical Engineering  
JEFworks Lab  
Supervisor - Dr. Jean Fan

📍 Baltimore, MD

- 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*
- Cell type annotation and quantitation of co-localization changes across immune tissues using CODEX data

## EDUCATION

2020  
|  
2014

### Ph.D., Molecular Biology

Johns Hopkins University  
National Institutes of Health Graduate Partnership Program  
Advisor - Dr. Laura Elnitski

📍 Baltimore, MD

- Dissertation: "Investigating Blood-based Biomarkers and Patterns of DNA Methylation in Tumors"
- 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*

## STATISTICAL SOFTWARE

2022

### STdeconvolve

<https://jef.works/STdeconvolve/>  
Available on Bioconductor

- 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.

## CONTACT

✉ [bmill3r@gmail.com](mailto:bmill3r@gmail.com)

🌐 <https://github.com/bmill3r>

🌐 <https://bmill3r.github.io/>

in [brendan-f-miller](#)

## SOFTWARE CODING

R

Python

Linux command line

High-Performance

Computing

## AREAS OF EXPERTISE

### Biology

Cell-free DNA

Liquid biopsy

Cancer diagnostics

Epigenetics

Gene expression variability

### Data Analysis

Bisulfite sequencing

Cell type deconvolution

Spatial transcriptomics

Single-cell sequencing

Targeted sequencing

### Data Visualization

ggplot2

matplotlib

### Package Development

Bioconductor

devtools

Git/GitHub

PyPI

### Scientific Communication

High impact publications

Invited speaker

*Last updated on 2022-05-10*