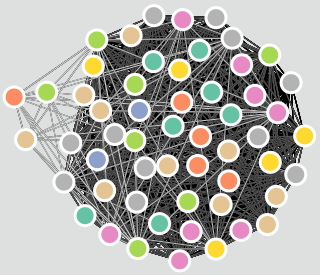
# BRENDAN F. MILLER

**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 and cancer biology.



## CURRENT POSITION

Current | 2020

### Post-Doctoral Research Fellow

Baltimore, MD

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

- Development of open-source computational pipelines and statistical software to characterize, cluster, and visualize cell type spatial organizational patterns in tissues.
- 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 protein expression data | ***in progress***

## EDUCATION

2020 | 2014

### Ph.D., Molecular Biology

Baltimore, MD

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

- 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*

## ADDITIONAL RESEARCH

2014

### Graduate Research Fellow

Baltimore, MD

Research Rotation
Carnegie Instituion of Washington
Department of Embryology
Advisor - Dr. Alex Bortvin

- Project: "Quantitation of transpoable element abundance in RNA-seq data"
- Comparison and benchmarking of multiple bioinformatic pipelines for identification of transosable elements
- 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

## CONTACT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https://bmill3r.github.io/
brendan-f-miller
Google Scholar


## EXPERTISE

**Biology**

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

**Data Analysis**

- Bisulfite sequencing
- Differential 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`

**Package Development**

- `Bioconductor`
- `git/GitHub`
- `PyPI`

**Scientific Communication**

- High impact publications
- Invited conference speaker

## 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.