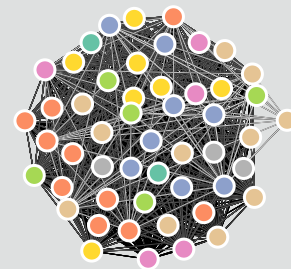# BRENDAN F. MILLER

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

📍 Baltimore, MD

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

- 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 | *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*

💻 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
🔗 https://github.com/bmill3r
🌐 https://bmill3r.github.io/
in brendan-f-miller

SOFTWARE CODING

```
R/RStudio
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 conference speaker

Last updated on 2022-05-11