

# Matthew Montierth

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## Education

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**Baylor College of Medicine** Houston, TX  
*Ph.D. in Quantitative and Computational Biosciences* October 2025

**Brigham Young University** Provo, UT  
*B.S. in Genetics and Biotechnology, Minor in Statistics* 2019

- Full academic scholarship

## Research & Professional Experience

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**Data Scientist - MD Anderson Cancer Center** Houston, TX  
*Bioinformatics & Cancer Genomics Analysis* October 2025 – present

- Managed large-scale genomics datasets on high-performance computing (HPC) infrastructure, ensuring efficient storage, access control, and versioning
- Analyzed single-cell RNA-seq datasets to identify immune correlates with tumor evolutionary states
- Supported multiple translational and computational oncology projects by designing and implementing reproducible bioinformatics pipelines in R and Python

**PhD Researcher - Wang Lab, MD Anderson Cancer Center** Houston, TX  
*Computational Biology & Cancer Genomics* 2019 – 2025

- Designed and executed pan-cancer subclonal reconstruction across 9,000+ samples and 32 cancer types, surfacing prognostic biomarkers
- Benchmarked and deployed DeMixNB (sparse-data deconvolution method) across bulk and spatial tumor datasets in real patient cohorts
- Performed multiomic integration of ATAC-seq and RNA-seq data to identify tumor signature genes across cancer types
- Optimized somatic mutation calling pipeline processing 5,000+ whole exomes
- Applied Bayesian risk prediction models to identify *de novo* BRCA mutations in high-risk pedigrees

**Research Mentor - Indigo Research** Remote  
*Scientific Mentorship & Education* 2023 – Present

- Mentor pre-collegiate researchers in computational biology, teaching statistical analysis and scientific programming

**Bioinformatics Associate - Genentech** South San Francisco, CA  
*GWAS Analysis & Data Integration* 2018 – 2019

- Harmonized multi-source GWAS datasets and performed meta-analyses identifying novel ocular disease variants
- Collaborated with software teams to develop clinical trial data exploration platforms

**Life Sciences Tutor - Brigham Young University** Provo, UT  
*Academic Support & Education* 2017 – 2018

- Tutored core life sciences courses (100–300 level) and held bi-weekly exam prep lectures in genetics, molecular biology, and developmental biology

**Research Assistant - Davis Lab, Brigham Young University** Provo, UT  
*Multiple Sclerosis Genomics Research* 2016 – 2019

- Performed Mendelian randomization studies of causal factors in multiple sclerosis
- Identified variants influencing multiple sclerosis comorbidities via GWAS
- Developed random forest classification model for multiple sclerosis subtypes using blood panel test data
- Managed peers and mentored fellow students as senior lab manager

## Technical Skills

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**Genomics & Bioinformatics:** Mutation calling (MuSE, GATK, Strelka2), RNA-seq/ATAC-seq analysis, single-cell, GWAS, deconvolution, subclonal reconstruction, variant annotation, spatial transcriptomics

**Programming & Computing:** R, Python, Unix/Linux, SQL, LaTeX, High-performance computing (HPC)

**Workflow & Reproducibility:** Snakemake, Docker, Git

**Statistical Methods:** Machine learning, survival analysis, Bayesian modeling, feature selection

**Data Management & Visualization:** MySQL, DuckDB, Shiny, Quarto, Observable JS, Adobe Illustrator

**Languages:** English (native), Spanish (fluent)

## Publications

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### Journal Articles

**Montierth, M.D.**, Jiang, Y., Yu, K., et al. (2024). Subclonal mutation load predicts survival and response to immunotherapy in cancers with low to moderate tumor mutation burden. *bioRxiv*. doi: 10.1101/2024.07.03.601939

Dai, Y., Pan, X., Guo, S., Ji, S., Cao, S., **Montierth, M.D.**, Jiang, Y., Chang, J.T., Shi, L., Shalpour, S., Echeverria, G.V., Yates, L., Staaf, J., Lim, B., Yuan, Y., Wang, W. (2026). Tumor microenvironment transcriptional activity enables robust stratification of chemotherapy response in triple-negative breast cancer. *Cell Reports Medicine*.

Dai, Y., Guo, S., Pan, Y., Castignani, C., **Montierth, M.D.**, Van Loo, P., Wang, W. (2025). A guide to transcriptomic deconvolution in cancer. *Nature Reviews Cancer*.

**Montierth, M.D.**, Yan, H., Xie, L., Wang, W. (Under revision). "Deconvolution of Sparse-count RNA Sequencing Data for Tumor Cells Using Embedded Negative Binomial Distributions." *Genome Biology*.

Cermakova, K., et al. including **Montierth, M.D.** (2024). Reactivation of the G1 enhancer landscape underlies core circuitry addiction to SWI/SNF. *Nucleic Acids Research*.

Wang, J.R., **Montierth, M.D.**, Xu, L., et al. (2022). Impact of somatic mutations on survival outcomes in patients with anaplastic thyroid carcinoma. *JCO Precision Oncology*, 6, e2100504.

Cao, S., Wang, J.R., et al. including **Montierth, M.D.** (2022). Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression. *Nature Biotechnology*.

Miller, J.M., Beales, J.T., **Montierth, M.D.**, et al. (2021). The impact of multiple sclerosis disease status and subtype on hematological profile. *International Journal of Environmental Research and Public Health*.

Johnson, D.K., Reynolds, K.M., Poole, B.D., **Montierth, M.D.**, et al. (2021). Contribution of viral infection to risk for cancer in SLE and MS. *PLOS ONE*.

Gao, F., Pan, X., Dodd-Eaton, E.B., Recio, C.V., **Montierth, M.D.**, et al. (2020). A pedigree-based prediction model identifies carriers of deleterious *de novo* mutations in Li-Fraumeni syndrome families. *Genome Research*.

## Books and Chapters

Ji, S., **Montierth, M.D.**, Wang, W. (2022). MuSE: A novel approach to mutation calling with sample-specific error modeling. In *Variant Calling: Methods and Protocols*. Springer.

## Conference Presentations

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### Oral Presentations

Scalable subclonal reconstruction of cancer cells via penalized likelihood. *RECOMB Satellite on Computational Cancer Biology (RECOMB-CCB)*, 2026.

Subclonal mutation load predicts survival and response to immunotherapy in cancers with low to moderate TMB. *Baylor College of Medicine Graduate School Symposium*, 2025.

### Posters

Subclonal mutation load predicts survival and response to immunotherapy in cancers with low to moderate TMB. *American Association for Cancer Research*, 2025.

TmiS: A Prognostic Indicator for Prostate Cancer Survival Based on Total Tumor Cell miRNA Levels. *Leading Edge Cancer Symposium*, 2024.

DeMixMir: Deconvolution of microRNA sequencing data from heterogeneous tumor samples. *AACR*, 2023.

Estimating total tumor-specific microRNA content in human tissues using computational deconvolution. *ASHG*, 2022.

Integration of tumor-specific miRNA and mRNA using computational deconvolution methods. *RECOMB*, 2022.

The impact of multiple sclerosis disease status and subtype on hematologic profile. *ASM*, 2018.

Contribution of known risk variants to multiple sclerosis age of onset. *ASM*, 2018.

Effect of genetic variants associated with uric acid on multiple sclerosis: a Mendelian randomization study. *ASM*, 2017.

## Professional Development & Affiliations

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### Additional Training

NCI Spring School on Algorithmic Cancer Biology, National Cancer Institute, 2023

Computational Genomics Summer Institute (CGSI), 2022

Advanced Statistics for Data Science Specialization, Coursera, 2022

### Professional Affiliations

American Association for Cancer Research, 2022–2025

American Society of Human Genetics, 2017–2022

## Leadership, Service & Volunteering

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### Full-time Volunteer - Church of Jesus Christ of Latter-Day Saints

Taught English as Second Language (ESL) course to immigrant and refugee parents with Spring Branch ISD

Participated in city-wide flood recovery, translating for city services and American Red Cross

Volunteered as translator for Saving Smiles initiative, educating children from low-income schools about dental hygiene

### Team Lead - Niche Navigators, Allison Institute Hackathon

Led team to a 5th-place finish at MD Anderson's [Allison Institute Colin Stroud Hackathon](#), a computational oncology team competition

### Vice President - BYU Genetics Club

Organized social activities for 200+ club members

Planned career and networking events with industry professionals in healthcare and biotech

## References

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*Available upon request*