Matthew Montierth

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Education

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

Data Scientist - MD Anderson Cancer Center   Houston, TX
Computational Biology & Cancer Genomics   *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*

— Led largest-ever subclonal reconstruction study analyzing tumor evolution across 9,000+ patient samples and 32 cancer types, identifying novel prognostic biomarkers

— Contributed to development team for DeMixNB, a novel computational tool for deconvolution of sparse expression data including spatial datasets; benchmarked performance and deployed in real patient datasets

— 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

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

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

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

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

Workflow Management: Snakemake, Docker, Git

Languages: English (native), Spanish (fluent)

Publications

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., Shalapour, 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.*

Jiang, Y., Yu, K., Shin, S.J., **Montierth, M.D.**, et al. (2021). CliP: Subclonal architecture reconstruction using a penalized likelihood model. *Genome Research.*

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

Oral Presentations

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

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

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

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

Available upon request