Matthew D. Montierth

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Houston, TX

Education

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

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

- Full academic scholarship

Research & Professional Experience

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

- Identified novel prognostic biomarker in largest subclonal reconstruction study analyzing tumor evolution across 9,000+ patient samples and 32 cancer types
- Developed and benchmarked methods for deconvolution of tumor miRNA proportions from bulk miRNAseq data
- 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

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

- Led initiative to download and harmonize public GWAS data to common standard for subsequent analysis
- Performed meta-analysis combining in-house data with public data to identify novel ocular disease variants
- Collaborated with software development team to create exploratory portal for clinical trial data

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

- On-site tutor in life sciences student help center for all core life sciences courses from 100-300 level
- Held test preparation lectures bi-weekly for genetics, molecular biology, and physical and developmental biology courses

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

- Performed Mendelian randomization studies to examine the relationship between potential causal factors and multiple sclerosis
- Identified variants influencing multiple sclerosis comorbidities via genome-wide association scan
- Developed random forest multiple sclerosis subtype classification model using blood panel test data
- Managed peers and mentored fellow students' ongoing projects as senior lab manager

Technical Skills

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

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

Statistical Methods: Machine learning, survival analysis, Bayesian modeling, meta-analysis, feature selection, dimensionality reduction, Mendelian randomization

Data Management & Visualization: MySQL, DuckDB, ggplot2, Shiny, plotly, Observable JS, Seaborn, Matplotlib, Adobe Illustrator

Workflow Management: Snakemake, Docker, version control (Git), reproducible research practices

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.

Cermakova, K., Tao, L., Sala, M., **Montierth, M.D.**, Chan, Y.S., Patel, I., Chambers, C., Loeza Cabrera, M., Hoffman, D., Parchem, R.J., Wang, W., Nencka, R., Barbieri, E., Hodges, H.C. (2024). "Reactivation of the G1 enhancer landscape underlies core circuitry addiction to SWI/SNF." *Nucleic Acids Research* PMID: 37993417.

Wang, J.R., **Montierth, M.D.**, Xu, L., Goswami, M., Zhao, X., Cote, G., 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., Ji, S., Yang, P., Dai, Y., Guo, S., **Montierth, M.D.**, et al. (2022). "Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression." *Nature Biotechnology*, 40(11), 1624-1636.

Jiang, Y., Yu, K., Ji, S., Shin, S.J., Cao, S., **Montierth, M.D.**, et al. (2021). "CliP: Subclonal architecture reconstruction of cancer cells in DNA sequencing data using a penalized likelihood model." *Genome Research*, 31(10), 1868-1879.

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*, 18(6), 3318.

Johnson, D.K., Reynolds, K.M., Poole, B.D., **Montierth, M.D.**, et al. (2021). "Contribution of viral infection to risk for cancer in systemic lupus erythematosus and multiple sclerosis." *PLOS ONE*, 16(1), e0243150.

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 families with Li-Fraumeni syndrome." *Genome Research*, 30(8), 1170-1180.

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* (pp. 21-27). 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." *American Association for Cancer Research*, 2023.

"Estimating total tumor-specific microRNA content in human tissues using computational deconvolution." *American Society of Human Genetics*, 2022.

"Integration of tumor-specific miRNA and mRNA using computational deconvolution methods." *Research in Computational Molecular Biology*, 2022.

"The impact of multiple sclerosis disease status and subtype on hematologic profile." *American Society of Microbiologists*, 2018.

"Contribution of known risk variants to multiple sclerosis age of onset." *American Society of Microbiologists*, 2018.

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

Professional Development & Affiliations

Additional Training

NCI Spring School on Algorithmic Cancer Biology, National Cancer Institute (NCI), 2023.

Summer Short Program, 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 as school program 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