

# Matthew Montierth

✉ montiert@bcm.edu    🐦 @mattmontierth  
🌐 <https://mattmontierth.quarto.pub/>  
🌐 <https://www.linkedin.com/in/matthew-montierth/>



## Education

- Anticipated 2024    📖 **Ph.D., Baylor College of Medicine** Quantitative and Computational Biosciences.  
2019    📖 **B.S., Brigham Young University** Genetics and Biotechnology.  
Minor: Statistics  
*full academic scholarship*

## Conference Presentations

### Posters

- 2024    "Evaluating prognostic utility of TmiS for Gleason 7 and Gleason 8 prostate cancer" *American Association for Cancer Research*
- 2023    "TmiS: A Prognostic Indicator for Prostate Cancer Survival Based on Total Tumor Cell miRNA Levels" *Leading Edge Cancer Symposium*
- 2023    "DeMixMir: deconvolution of microRNA sequencing data from heterogeneous tumor samples" *American Association for Cancer Research*
- 2022    "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*
- 2018    "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*
- 2017    "Effect of genetic variants associated with uric acid on multiple sclerosis: a mendelian randomization study" *American Society of Microbiologists*

## Research Publications

### Journal Articles

- 1    Cermakova, K., Tao, L., Dejmek, M., Sala, M., Montierth, M. D., Chan, Y. S., ... Hoffman, D. et al. (2024). Reactivation of the g1 enhancer landscape underlies core circuitry addiction to swi/snf. *Nucleic acids research*, 52(1), 4–21.
- 2    Jiang, Y., Montierth, M. D., Yu, K., Ji, S., Guo, S., Tran, Q., ... Li, R. et al. (2024). Pan-cancer subclonal mutation analysis of 7,827 tumors predicts clinical outcome. *bioRxiv*, 2024–07.
- 3    Cermakova, K., Tao, L., Dejmek, M., Sala, M., **Montierth, M. D.**, Chan, Y. S., ... Hodges, H. C. (2023). Reactivation of the g1 enhancer landscape underlies core circuitry addiction to swi/snf. *Nucleic Acids Research*, in press. [doi:10.1093/nar/gkad1081](https://doi.org/10.1093/nar/gkad1081)

- 4 Cao, S., Wang, J. R., Ji, S., Yang, P., Dai, Y., Guo, S., ... Chen, J. et al. (2022). Estimation of tumor cell total mRNA expression in 15 cancer types predicts disease progression. *Nature biotechnology*, 1–10.
- 5 Wang, J. R., **Montierth, M. D.**, Xu, L., Goswami, M., Zhao, X., Cote, G., ... Busaidy, N. L. et al. (2022). Impact of somatic mutations on survival outcomes in patients with anaplastic thyroid carcinoma. *JCO Precision Oncology*, 6, e2100504.
- 6 Jiang, Y., Yu, K., Ji, S., Shin, S. J., Cao, S., **Montierth, M. D.**, ... Wang, W. (2021). CliP: Subclonal architecture reconstruction of cancer cells in DNA sequencing data using a penalized likelihood model. *BioRxiv (preprint)*. [doi:10.1101/2021.03.31.437383](https://doi.org/10.1101/2021.03.31.437383)
- 7 Miller, J. M., Beales, J. T., **Montierth, M. D.**, Briggs, F. B., Frodsham, S. F., & Davis, M. F. (2021). The impact of multiple sclerosis disease status and subtype on hematological profile. *International Journal of Environmental Research and Public Health*, 18(6), 3318. [doi:10.3390/ijerph18063318](https://doi.org/10.3390/ijerph18063318)
- 8 Johnson, D. K., Reynolds, K. M., Poole, B. D., **Montierth, M. D.**, Todd, V. M., Barnado, A., & Davis, M. F. (2021). Contribution of viral infection to risk for cancer in systemic lupus erythematosus and multiple sclerosis. *PLOS ONE*, 16(1), e0243150. [doi:10.1371/journal.pone.0243150](https://doi.org/10.1371/journal.pone.0243150)
- 9 Gao, F., Pan, X., Dodd-Eaton, E. B., Recio, C. V., **Montierth, M. D.**, Bojadzieva, J., ... Wang, W. (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. [doi:10.1101/gr.249599.119](https://doi.org/10.1101/gr.249599.119)

## Books and Chapters

- 1 Ji, S., **Montierth, M. D.**, & Wang, W. (2022). MuSE: A novel approach to mutation calling with sample-specific error modeling. In *Variant calling* (pp. 21–27). Springer.

## Research and Employment History

2019 – present    ◇ **PhD student**, Wang Lab - MD Anderson Cancer Center, Houston, TX.

- Applied bayesian risk prediction methods to identify *de novo* BRCA mutations in pedigree cohort
- Integrated ATACseq data to pan-cancer analysis for more than 5,000 samples from The Cancer Genome Atlas
- Refined, documented, and implemented somatic mutation calling pipeline to characterize landscape of mutations in pan-cancer studies
- Characterized subclonality of mutations and relationship with clinical outcomes in pan-cancer study of over 7,000 samples and 32 cancer types
- Developed DeMixMir, a computational tool for deconvolution of miRNA expression from mixed tumor samples
- Analyzed tumor evolutionary dynamics in largest ever subclonal reconstruction study across 7,708 patient samples.

2023 – present    ◇ **Research mentor** Indigo Research

- Taught principles of scientific inquiry to pre-collegiate researchers
- Guided literature search, hypothesis generation, and study design
- Directed learning of statistical and coding skills to scientific analysis

## Research and Employment History (continued)

- 2018 – 2019   ◇ **Bioinformatics Associate** Genentech, South San Francisco, CA.
- Lead 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
- 2017 – 2018   ◇ **Life Sciences Tutor** Brigham Young University, Provo, UT.
- On-site tutor in life sciences student help center.
  - Tutored students 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
- 2016 – 2019   ◇ **Research assistant** Davis Lab - Brigham Young University, Provo, UT.
- 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

## Skills

Languages	◇ English: native speaker, Spanish: Fluent
Coding	◇ R, Python, Unix, $\LaTeX$
Databases	◇ MySQL, DuckDB
Data visualization	◇ ggplot, Shiny, plotly, Observable JS, Seaborn, Matplotlib, Adobe Illustrator
Pipeline management	◇ Snakemake
Bioinformatics	◇ Mutation calling, RNAseq analysis, deconvolution, single cell analysis, ATACseq analysis, subclonal reconstruction, GWAS, mendelian randomization
Data analysis	◇ Statistical machine learning, survival analysis, feature selection

## Affiliations and Training

### Additional training

- 2023   ◇ **NCI Spring School on Algorithmic Cancer Biology**, National Cancer Institute (NCI).
- 2022   ◇ **Summer short program**, Computational Genomics Summer Institute (CGSI).
- 2022   ◇ **Advanced Statistics for Data Science Specialization**, Coursera.

## **Affiliations and Training (continued)**

---

### **Professional Affiliations**

- 2017-2022   ◇   **American Society of Human Genetics**
- 2022-2024   ◇   **American Association for Cancer Research**

## **Volunteering and Service**

---

### **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 on Request