

Atlanta, GA
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Hope Mumme

GitHub: [hmumme](#)

A PhD student at Emory University whose research specialties are bioinformatics, biomedical informatics, and machine learning. I have experience with (i) performing omics analysis of pediatric cancers, and (ii) development of and (iii) application of bioinformatics tools and methods.

EDUCATION

PhD Computer Science and Informatics

Aug 2021 - May 2025 (Exp.)

(Concentration in Biomedical Informatics)

Emory University (Atlanta, GA)

BSc Biomedical Engineering

Aug 2016 - Dec 2020

Georgia Institute of Technology (Atlanta, GA)

RESEARCH

Graduate Researcher, Bhasin Lab

Aug 2021 - Current

Emory University

Atlanta, GA

- Performed pediatric Pan-Leukemia transcriptomic analysis to identify 9 genes dysregulated in leukemia and over-expressed at diagnosis in AML, ALL, and MPAL
- Developed [PedSCAtlas](#), first interactive tool for analyzing compiled datasets of pediatric single-cell RNA-seq cancer datasets for pediatric cancer subtypes
- Performed single-cell RNA-seq analysis of pediatric mixed phenotype acute leukemia (MPAL), and comparison to other acute leukemia subtypes
- Validated our group's 7-gene signature for identification of AML malignant blast cells using external single-cell and bulk RNA-seq datasets
- Assisted with various bioinformatics projects in the lab, such as the development and maintenance of the web resource [Survival Genie](#), single-cell analysis of T-cell acute lymphoid leukemia immune microenvironment, and the single-cell analysis of diabetic foot ulcer healing

Undergraduate Researcher, Jo Lab

Dec 2019 - Dec 2020

Georgia Institute of Technology

Atlanta, GA

- Performed scRNA-seq, scATAC-seq, and lncRNA analysis to study endothelial cell reprogramming in the carotid artery

Data Analysis Internship

June 2018 - Aug 2018

Open Medicine Institute

Mountain View, CA

- Developed a single-cell RNA sequencing protocol for their patient data

PUBLICATIONS

- **Mumme HL**, Raikar SS, Bhasin SS et al. Single-cell RNA sequencing distinctly characterizes the wide heterogeneity in pediatric mixed phenotype acute leukemia. *Genome Med* 15, 83 (2023). <https://doi.org/10.1186/s13073-023-01241-z>
- **Mumme H**, Thomas BE, Bhasin SS et al. Single-cell analysis reveals altered tumor microenvironments of relapse- and remission-associated pediatric acute myeloid leukemia. *Nat Commun* 14, 6209 (2023). <https://doi.org/10.1038/s41467-023-41994-0>
- Bhasin SS, Thomas BE, Summers RJ, Sarkar D, **Mumme H** et al. Pediatric T-cell acute lymphoblastic leukemia blast signature and MRD associated immune environment changes defined by single cell transcriptomics analysis. *Sci Rep* 13, 12556 (2023). <https://doi.org/10.1038/s41598-023-39152-z>

- Dwivedi B, **Mumme H**, Satpathy S *et al.* Survival Genie, a web platform for survival analysis across pediatric and adult cancers. *Sci Rep* 12, 3069 (2022). <https://doi.org/10.1038/s41598-022-06841-0>
- Theocharidis G, Thomas BE, Sarkar D, **Mumme HL** *et al.* Single cell transcriptomic landscape of diabetic foot ulcers. *Nat Commun* 13, 181 (2022). <https://doi.org/10.1038/s41467-021-27801-8>
- Andueza A, Kumar S, Kim J, Kang DW, **Mumme HL** *et al.* Endothelial Reprogramming by Disturbed Flow Revealed by Single-Cell RNA and Chromatin Accessibility Study. *Cell Rep* 33, 11 (2020). <https://doi.org/10.1016/j.celrep.2020.108491>
- Mankoul-Mansour MM, El-Beyrouthy JB, **Mumme HL**, Freeman, EC. Photopolymerized microdomains in both lipid leaflets establish diffusive transport pathways across biomimetic membranes. *Soft Matter* 15, 43 (2019). <https://doi.org/10.1039/C9SM01658A>

PRESENTATIONS

- Poster Presentation, [Atlanta Workshop on Single-cell Omics](#), April 2023. "Single Cell RNA Sequencing Driven Characterization of Pediatric Mixed Phenotype Acute Leukemia"
- Oral Presentation, American Society of Hematology, Dec 2022. "A Single Cell Atlas and Interactive Web-Resource of Pediatric Cancers and Healthy Bone Marrow", <https://doi.org/10.1182/blood-2022-169153>
- Oral Presentation, [Atlanta Workshop on Single-cell Omics](#), April 2022. "Pediatric Cancer Cell Atlas"
- Poster Presentation, American Society of Hematology, Dec 2021. "Pediatric Single Cell Cancer Atlas: An Integrative Web-Based Resource for Single Cell Transcriptome Data from Pediatric Leukemias", <https://doi.org/10.1182/blood-2021-154282>
- Poster Presentation, American Society of Hematology, Dec 2021. "Single Cell RNA Sequencing Driven Characterization of Rare B/Myeloid and T/Myeloid Mixed Phenotype Acute Leukemia", <https://doi.org/10.1182/blood-2021-153776>

TEACHING AND ACTIVITIES

- Emory CS 170, Graduate TA (Fall 2021)
- Atlanta Workshop on Single-cell Omics, Planning Committee (April 2022)
- Emory CS 170, Graduate TA (Fall 2022)
- Emory CS 470, Graduate TA (Spring 2023)

WORKSHOPS

- NCI Human Tumor Atlas Network (HTAN) Data Jamboree (Dec 2023)
 - download, process, and map immune infiltration of HTAN spatial transcriptomics (ST) data (using scRNA-seq as reference for immune signatures)
 - gained experience with analyzing 10X Visium data and pancreatic ductal adenocarcinoma (PDAC)
 - HTAN Immune Infiltration [Github](#) with our code and results

AWARDS

- Best Poster, [Atlanta Workshop on Single-cell Omics](#) (April 2023)

SKILLS

Programming

R, Python, L^AT_EX, Matlab, MarkDown, Java, Bash

Omics Analysis

scRNA-seq, scATAC-seq, CITE-seq, bulk RNA-seq, Spatial transcriptomics (Visium)

AI

scikit-learn, tensorflow, pytorch

Web Tool Dev.

R shiny, Python dash, HTML

Other

Github, Microsoft Office