# Hope Mumme

Atlanta, GA
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GitHub: hmumme

I'm a PhD candidate at Emory University specializing in bioinformatics, biomedical informatics, and machine learning. My expertise includes (i) performing omics analysis of pediatric leukemias, and (ii) development of and (iii) application of bioinformatics tools and methods.

## EDUCATION

**PhD Computer Science and Informatics**　　　　　　　　　　　　　　　　**May 2025 (Exp.)**
*Concentration: Biomedical Informatics*
*Emory University (Atlanta, GA)*

**MSc Computer Science and Informatics**　　　　　　　　　　　　　　　　　　　**May 2024**
*Interim Masters*
*Emory University (Atlanta, GA)*

**BSc Biomedical Engineering**　　　　　　　　　　　　　　　　　　　　　　　　**Dec 2020**
*Georgia Institute of Technology (Atlanta, GA)*

## RESEARCH

**Graduate Researcher, Bhasin Lab**　　　　　　　　　　　　　　　**Aug 2021 - Current**
*Emory University*　　　　　　　　　　　　　　　　　　　　　　　　　　　*Atlanta, GA*

- Developing CAR-T target identification platform using single-cell RNA sequencing data from leukemia and vital tissues. Identifying targets or pairs of targets, including for logic-gated CARs.
- 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, 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 Internsip**　　　　　　　　　　　　　　　　　　**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

## PRESENTATIONS

- Poster Presentation, Atlanta Workshop on Single-cell Omics, April 2024. "CAR-Machine: Resource for Single-Cell Guided CAR-T Target Identification and Testing for Hematological Childhood Cancers"
- Poster Presentation, Atlanta Workshop on Single-cell Omics, April 2024. "Single-cell Profile of Prostate Cancer PBMCs Before and After Androgen Deprivation Therapy"
- Poster Presentation, St. Jude National Graduate Student Symposium, March 2024. "Single Cell RNA Sequencing Driven Characterization of Pediatric Mixed Phenotype Acute Leukemia"
- 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 Workship 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

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| **Programming** | R, Python, Bash, Matlab, MarkDown, Java, LATEX, Git |
| **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 |