Swethasree Bhattaram November 12, 2025
PhD Student - School of CSE @ Georgia Tech sbhattaram6@gatech.edu

RESEARCH INTERESTS

I specialize in designing and scaling computational algorithms to solve problems at the intersection of biology and high-performance computing. My work leverages parallel computing to analyze large-scale, complex, high-dimensional single cell genomics datasets. This includes developing novel methods for integrating diverse, multi-modal data types, such as gene expression and chromatin accessibility. By creating these scalable frameworks, my research aims to uncover complex cellular relationships and provide deeper insights into biological systems.

EDUCATION

- **Georgia Institute of Technology** Atlanta, GA
  Doctor of Philosophy (PhD), School of CSE. Advised by Prof. Srinivas Aluru. *2023 – 2026 (expected)*
  Master of Science (MS) in Bioinformatics. Advised by Prof. Rishikesan Kamaleswaran. *2021 – 2022*
- **University of Illinois at Urbana-Champaign** Champaign, IL
  Bachelor of Science (BS) in Bioengineering, Minor in Computer Science. *2017 – 2021*

WORK EXPERIENCE

- **Georgia Institute of Technology** Atlanta, GA
  Graduate Researcher *August 2021 – Present*
    - (PhD) Parallelizing the Gromov Wasserstein algorithm for large scale single-cell data of multiple modalities.
    - (PhD) Developed a scalable single-cell integration method for gene expression and chromatin accessibility profiles using a Gromov–Wasserstein optimal transport approach with dynamic Dijkstra sampling and matrix-safe joint embeddings, enabling integration of over a million cells.
    - (MS) Collaborated on early-stage PDAC detection by correlating sequencing data with radiological and histopathological image patterns using CNNs.
    - (MS) Designed and implemented an NLP pipeline to identify acute respiratory distress syndrome and sepsis severity from doctors' notes.
- **Exact Sciences** San Diego, CA
  Research Intern *May 2025 - Present*
    - Building cancer classification models based on short variant assay data to identify early stage cancer
    - Analyzing effects of degradation of certain proteins on classifier predictions.
- **Oak Ridge National Laboratory** Knoxville, TN
  Graduate Researcher *May 2024 – Present*
    - Developed a knowledge-guided framework that augments hidden markov model based protein homology search and alignment with query-specific adaptation to local sequence context.
    - Implemented end-to-end GPU implementations of the HMMER suite (HMMBuild, HMMAlign, HMMSearch).
- **University of Maryland School of Medicine** Baltimore, MD
  Bioinformatics Research Intern *May 2022 - August 2022*
    - Implemented graph models of liver and kidney cellular data (gene network, and omics data analysis) to identify patterns representing organ rejection post transplant.

PUBLICATIONS

- **Bhattaram, S.**, Bhowmik, D., Kannan, R.
  CAHS: Context Aware Homology Search
  Under Review: IEEE International Conference on Data Engineering, 2026

RELEVANT GRADUATE COURSEWORK

High Perfomance Computing, Artifical Intelligence, Multivariate Statistic Analysis, Machine Learning Biosciences, Computational Genomics

RELEVANT SKILLS

Python, C++, R, MPI, OpenMP, PyTorch, spaCy, NLTK, Statistics/Probability Distributions

REFERENCES

Prof. Srinivas Aluru (Georgia Tech; aluru@cc.gatech.edu)
Dr. Ramakrishnan Kannan (Oak Ridge National Lab; kannanr@ornl.gov)