Abhishek Murti

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Professional Summary

Computational biologist with 4+ years of experience building single-cell and spatial transcriptomics pipelines for liver disease research, with deep domain expertise across NAFLD, hepatoblastoma, autoimmune hepatitis, and porphyria. Designed and trained LiverTransformer, a liver-specific foundation model pre-trained on 1.04M human cells, bridging biological domain knowledge and transformer-based ML to contribute meaningfully to the virtual cell modeling space. Experienced in leading cross-institutional collaborations, with contributions to high-impact publications in *Nature Biotechnology*, *Nature Communications*, and *eLife*.

Experience

University of California, San Francisco — Bioinformatician *Dec 2021 – Present*

- Analyzed large-scale **single-cell**, **single-nuclei**, and **spatial transcriptomics** datasets totaling **1M+ cells** using `Seurat`, `Scanpy`, and `Squidpy` to investigate immune-mediated diseases and tumor microenvironments.
- Developed parallel single-cell and single-nuclei RNA sequencing pipelines for **20 hepatoblastoma patients**, identifying tumor signatures for risk stratification and **expanding cohort size by 40%** through inclusion of archived biobanked samples.
- Implemented and validated SNP-based consensus **demultiplexing algorithms** for single-nuclei workflows, achieving a **66% reduction in sequencing costs** through improved sample multiplexing efficiency.
- Led autoimmune hepatitis study integrating bulk, single-nuclei RNA sequencing, and spatial transcriptomics data from **8 patient biopsies**, uncovering a **novel autoantigen** and a **therapeutically targetable** immune pathway from minimal tissue input.
- Contributed to multi-organ, cross-institutional atlas projects (**COVID Tissue Atlas** and **Tabula Sapiens 2.0**) encompassing **85,000+ cells** from **20+ human organs**, leading the liver data analysis to identify systemic disease responses and establish reference cell-type profiles.

Selected Technical Projects

- **LiverTransformer: Human Liver Foundation Model for Single-Cell Genomics**
  Designed and trained a liver-specific transformer (~23.6M parameters) pre-trained via **masked gene prediction** on **1.04M human liver cells** (36K genes, 6 diseases, 125 cell types) from CellxGene Census. Achieved **91% cell type classification** across 15 classes via linear probing of frozen embeddings. Validated cross-platform generalization on spatial transcriptomics data (MERFISH, Xenium): **84–86% hepatocyte zonation accuracy** from frozen embeddings, despite training on dissociated cells with no spatial signal. Earlier mouse model (82K cells) achieved **87.1% three-way disease classification**. Built with `PyTorch`.
- **spatialzones: Spatial Tumor-Region Assignment Package**
  Built and released an open-source `Python` package (`spatialzones`) that computes **inside/interface/outside tumor regions** from spatial transcriptomics data using nearest-neighbor spatial context, with built-in visualization of region assignments and gene expression. Validated across **31 TMA cores** spanning multiple hepatoblastoma subtypes, including cases with **multiple subtypes within the same core**, and integrated with scRNA-seq and snRNA-seq for tumor–immune microenvironment analysis.
- **AI Scientist Framework**
  Built an end-to-end `Python` pipeline using **LLMs** to classify hepatoblastoma subtypes from single-cell transcriptomics and generate biologically interpretable hypotheses with supporting literature, accelerating experimental prioritization.
- **Julia Transcriptomics Toolkit (scAM.jl)**
  Created an open-source `Julia` package for NGS data analysis with complete workflows from preprocessing through clustering and differential expression, **implementing 15+ core functions** (UMAP, QC, visualization) as a high-performance alternative to existing R/Python tools.

Technical Skills

Programming: Python (PyTorch, Scanpy, Squidpy, Pandas, NumPy), R (Seurat, tidyverse, ggplot2), Bash, Julia
Machine Learning & AI: Transformer architectures, self-supervised pre-training, masked language modeling, deep learning, LLM applications
Bioinformatics: Single-cell & single-nuclei RNA-seq, Spatial Transcriptomics, Clustering, Dimensionality Reduction (UMAP, PCA), Pathway Analysis, Gene Ontology, GWAS
Infrastructure: HPC, Docker, Git, Google Cloud Platform, Nextflow
Visualization: Matplotlib, Seaborn, Plotly

Education

Cornell University, NY — MS *Aug 2019 – Jul 2021*
Chemical and Biomolecular Engineering, GPA: 3.77/4
Thesis: Mechanistic Modeling of a Cell-Free Glucose Biosensor for Therapeutic Applications

BITS Pilani, India — BE *Aug 2015 – Jul 2019*
Major: Chemical Engineering, Minor: Finance, GPA: 9.21/10

Publications

- Kim, J.J., Kurial, S.N., Choksi, P.K., ... **Murti, A.**, 2025. AAV capsid prioritization in normal and steatotic human livers maintained by machine perfusion. *Nature Biotechnology*, pp.1–13.
- Crowley, G., **Tabula Sapiens Consortium**, and Quake, S.R., 2025. Benchmarking cell type and gene set annotation by large language models with AnnDictionary. *Nature Communications*, 16, 9511.
- Quake, S.R. and **Tabula Sapiens Consortium**, 2024. Tabula Sapiens reveals transcription factor expression, senescence effects, and sex-specific features in cell types from 28 human organs and tissues. *bioRxiv*.
- Alkhani, A., Baskaran, S., **Murti, A.**, et al., 2024. Perinatal liver inflammation is associated with persistent elevation of CXCL10 and its canonical receptor CXCR3 on common myeloid progenitors. *bioRxiv*.
- Granados, A.A., Bucher, S., ... and **COVID Tissue Atlas Consortium**, 2023. Single-nuclei characterization of pervasive transcriptional signatures across organs in response to COVID-19. *eLife*, 12, p.e81090.
- Liu, J., Tran, V., ... **Murti, A.**, et al., 2023. Concordance of MERFISH spatial transcriptomics with bulk and single-cell RNA sequencing. *Life Science Alliance*, 6(1).
- Adhikari, A., **Murti, A.**, et al., 2023. Modeling and Analysis of a Cell-Free Gluconate Responsive Biosensor. *bioRxiv*.

Posters & Presentations

- **Murti, A.**, et al. "Effects of Intravenous Heme and Placebo on Gene Expression in Patients with Acute Hepatic Porphyria Attacks." **Oral presentation and poster**, *International Porphyrias Symposium*; Oct 2025. *Awarded one of the 3 best talks*.
- **Murti, A.**, et al. "Single-Cell and Single-Nuclei Transcriptomics Reveal Hepatoblastoma Tumor Signatures for Precision Oncology." **Poster**, *5th International Pediatric Liver Tumor Research Meeting*; Jun 2025.
- **Murti, A.**, et al. "Single-Cell and Single-Nuclei Transcriptomics Reveal Hepatoblastoma Tumor Signatures for Precision Oncology." **Oral presentation**, *UCSF Annual Liver Center Symposium*; May 2025.
- **Murti, A.**, et al. "A single nuclei RNA sequencing approach to characterize autoimmune hepatitis biology." **Oral presentation**, *UCSF Annual Liver Center Symposium*; May 2024.
- **Murti, A.**, et al. "Harnessing the Power of Next Generation Sequencing to Understand Liver Pathophysiology." **Poster**, *UCSF Annual Liver Center Symposium*; May 2023.