SRI HARSHA MEGHADRI

Computational Biologist | Single-Cell, Spatial and Bulk Transcriptomics | Lung Disease

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SUMMARY

Computational biologist (PhD thesis submitted, defense December 2026) working on single-nucleus, spatial and bulk transcriptomics of chronic lung disease at the German Center for Lung Research. Combines analysis depth (150,000+ nuclei, three previously undescribed cell populations, a first-author deconvolution method) with bench experience, including building the 10x Genomics Chromium platform from scratch at Sahlgrenska University Hospital. Also owns the roadmap of a Nextflow RNA-seq diagnostics platform and develops open-source single-cell software in Rust and Python.

CORE SKILLS

Single-cell and spatial: snRNA-seq and scRNA-seq (10x Chromium, Flex), Xenium spatial transcriptomics, Seurat, clustering and annotation, pySCENIC regulon inference, cell-type deconvolution (MuSiC and own published framework)

Bulk and translational: DESeq2, limma-voom, edgeR, pathway enrichment (EnrichR), STRING networks, L1000/Connectivity Map drug repurposing, TCGA, GEO, Ensembl, UCSC Genome Browser, comparative genome alignment

Programming and infrastructure: R (advanced; Bioconductor, package development with Roxygen2), Python (pandas, NumPy), Nextflow DSL2, Docker, Git, Linux, AWS, SQL (basic), AI-assisted development (Claude Code)

Wet lab and NGS: 10x Chromium library preparation, TruSeq, Ion Torrent, amplicon and custom capture panels, UMI-barcoded multiplex PCR, qPCR, digital PCR, primary and patient-derived cell culture, FACS, immunofluorescence and confocal microscopy, molecular cloning, protein purification

Working familiarity: ACMG variant classification, variant-calling pipeline architecture

EXPERIENCE

PhD Candidate, Computational Biology

Hannover Medical School (MHH), DZL-BREATH, Hannover, Germany *Jan 2020 – Present*

DZL-BREATH is the Hannover site of the German Center for Lung Research (DZL), Germany's national network for translational research on chronic lung disease.

- **Single-nucleus atlas:** Lead computational analyst on a 150,000+ nucleus snRNA-seq dataset (10x Flex) of pulmonary arterial hypertension versus control lung; identified three previously undescribed cell populations, including an EndoMT-associated transitional endothelial state (manuscript in preparation).
- **Regulatory programmes:** Inferred the transcription factor networks behind the disease-associated populations with pySCENIC regulon analysis.
- **Spatial validation:** Implementing Xenium spatial transcriptomics workflows to localise the new populations in intact lung tissue.
- **Methods:** Developed a framework that extends cell-type-specific pathway analysis to bulk RNA-seq through deconvolution (first author, bioRxiv 2024).
- **Drug repurposing:** Ranked candidate small molecules for idiopathic pulmonary fibrosis using L1000/Connectivity Map perturbational signatures.
- **Knockout model:** Led the transcriptomic analysis of Serpina1-deficient mice, including pathway enrichment and STRING network analysis (first author, Int. J. Mol. Sci. 2022).
- **Pipelines:** Built reproducible, version-controlled Nextflow and R pipelines for snRNA-seq and bulk RNA-seq processing.

Transcriptomics Product Owner (Remote)

newGenia AB, Stockholm, Sweden *Feb 2021 – Present*

Pre-seed startup building a cloud-based clinical RNA-seq diagnostics platform ahead of clinical deployment.

- **Platform roadmap:** Own the roadmap for a Nextflow DSL2 RNA-seq platform on AWS covering STAR alignment, GATK variant calling, DESeq2 differential expression, and a module linking classified variants to aberrant expression (OUTRIDER), allele-specific expression and aberrant splicing (FRASER2).
- **Technical audit:** Led an audit of the differential-expression and variant-expression modules; turned findings on strandedness, reproducibility and model-formula safeguards into a 25-ticket backlog across five sprints.
- **Requirements:** Translate scientific and product requirements into pipeline priorities with the engineering team.

Assistant Researcher, NGS Laboratory

Sahlgrenska University Hospital, Gothenburg, Sweden *Jun 2018 – Nov 2019*

Sweden's largest university hospital, combining clinical diagnostics and translational research.

- **Platform build:** Set up the 10x Genomics Chromium single-cell platform from scratch: wrote protocols, validated workflows and trained 5+ researchers in library preparation and instrument operation.

- **Single-cell oncology:** Applied 10x scRNA-seq to EBV-associated post-transplant lymphoproliferative disorder (PTLD) across multiple patient samples.
- **Clinical assay:** Designed and validated a UMI-barcoded multiplex PCR assay (SiMSen-seq) for melanoma mutation detection.
- **Clinical metagenomics:** Built a metagenomic NGS pipeline for pathogen detection in cerebrospinal fluid (Scientific Reports 2022).
- **Library preparation:** Prepared TruSeq, Ion Torrent, amplicon and custom capture libraries; ran qPCR and digital PCR; co-supervised a Master's thesis.

Earlier Research Positions

DKFZ Heidelberg, Karolinska Institute, University of Gothenburg *2012 – 2017*

- **Research Associate, Oncology, University of Gothenburg (2017):** patient-derived cancer cell lines, plasmid construction, fluorescence microscopy; survival and differential expression analysis of TCGA DLBCL cohorts.
- **Research Assistant, University of Gothenburg (Sep 2015 – Sep 2016):** mammalian meiosis; molecular cloning, protein purification, protein interaction assays, yeast genetics screen.
- **Research Assistant, Karolinska Institute (Sep 2012 – Jul 2013):** regulation of a cellular E3 ligase by an EBV-encoded microRNA (acknowledged, PLoS Pathogens 2016).
- **Master's Thesis, DKFZ Heidelberg (Feb – Aug 2012):** mitotic phenotypes of EBV-infected B cells using immunofluorescence, histochemistry, FACS and primary cell culture.

INDEPENDENT PROJECTS

- **CREST (github.com/harshameghadri/CREST):** open-source single-cell RNA-seq toolkit with Rust kernels behind a scanpy-style Python API; streams counts in chunks to bound memory; published on PyPI as crest-sc.
- **medgemma-spatial (github.com/harshameghadri/medgemma-spatial):** prototype linking Visium spatial analysis (Scanpy, Squidpy) to a quantised MedGemma model for draft pathology summaries.

PUBLICATIONS

Meghadri SH, et al. Discovery of novel cell types in pulmonary arterial hypertension through large-scale snRNA-seq. Manuscript in preparation.

Meghadri SH, et al. Extending deconvolution capabilities for cell type-specific pathway analysis of bulk RNA-seq data. bioRxiv, 2024. doi:10.1101/2024.07.30.605740

Meghadri SH, et al. Loss of Serpina1 in mice leads to altered gene expression in inflammatory and metabolic pathways. Int. J. Mol. Sci., 2022. doi:10.3390/ijms231810425

Co-author. Optimization of CSF microbial DNA metagenomic sequencing diagnostics. Scientific Reports, 2022. doi:10.1038/s41598-022-07260-x

Acknowledged. Bernhardt K, et al. A viral microRNA cluster regulates the expression of PTEN, p27, and of a Bcl-2 homolog. PLoS Pathogens, 2016.

EDUCATION AND CERTIFICATION

PhD, Computational Biology, Hannover Medical School (MHH), DZL-BREATH (thesis submitted) 2020 – Dec 2026

MSc, Genomics and Systems Biology, University of Gothenburg, Sweden 2015 – 2020

MSc, Infection Biology, Uppsala University, Sweden (thesis at DKFZ Heidelberg) 2010 – 2012

BTech, Biotechnology, Anna University, Chennai, India 2006 – 2010

FELASA Category B, laboratory animal science, University of Gothenburg

LEADERSHIP, COMMUNICATION AND LANGUAGES

- **Leadership:** President, ISCB Regional Student Group Gothenburg (2018 – 2020); organised bioinformatics workshops and industry talks.
- **Science communication:** author of the Weekly Bioinformatics newsletter; talks and posters at DZL Annual Meetings (2022, 2023), BIOMEDAS and AACR Shenzhen (2019).
- **Awards:** TRAIN Academy Stipend (2023), FF Donations Board Scholarship (2018), Adelbert Foundation Scholarship (2017).
- **Languages:** English (fluent); German (A2); Swedish (A2); Telugu, Tamil and Hindi (native or fluent).