Mallikarjuna Thippana, PhD

Computational Biologist | Single-Cell and Spatial Multi-Omics | Bioinformatics Data Science
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Location: Solna, Stockholm, Sweden | Available for relocation | Open to remote

PROFESSIONAL SUMMARY

Results-driven computational biologist and bioinformatics data scientist with a PhD in Computational Systems Biology and 7+ years of experience delivering multi-omics analysis, NGS pipeline development, and machine learning solutions in cancer research and translational genomics. Expert in single-cell RNA sequencing (scRNA-seq), spatial transcriptomics, ATAC-seq, bulk RNA-seq, and multi-omics data integration using Python and R, with a consistent track record of translating complex biological datasets into actionable insights in collaboration with experimental scientists and cross-functional teams. Experienced in building reproducible, scalable bioinformatics pipelines using Snakemake, Git, and Linux HPC environments, with strong software development practices including version control, modular code, and documentation. 9 peer-reviewed publications; manuscript under revision at Nucleic Acids Research (impact factor approximately 23.5). Motivated to apply deep computational expertise to industry research and development programmes in oncology, precision medicine, single-cell biology, or spatial genomics.

TECHNICAL SKILLS

Single-cell and spatial genomics: scRNA-seq, snRNA-seq, scATAC-seq, multiome, spatial transcriptomics (10x Visium); Scanpy, Seurat; full workflow from raw data QC to biological interpretation

Multi-omics integration: Harmony, scVI, BBKNN, MOFA+, WNN; cross-modal factor analysis across transcriptomic, epigenomic, and proteomic data layers

Bulk NGS analysis: RNA-seq (STAR, DESeq2, edgeR, GSEA), ATAC-seq (MACS2, deepTools, ArchR, Signac), GRO-seq, WGS and WES variant calling (GATK, bcftools, ANNOVAR); QC tools (FastQC, MultiQC, Trim Galore)

Machine learning and statistics: scikit-learn, SciPy; supervised and unsupervised learning, predictive modeling, dimensionality reduction (PCA, UMAP, t-SNE), clustering, feature selection, regression, classification

Bioinformatics pipeline development: Snakemake, Git and GitHub, Linux and Unix HPC (SLURM), Docker (familiar), Nextflow (familiar); reproducible, documented, scalable workflow engineering

Programming languages: Python (pandas, NumPy, scikit-learn, SciPy, matplotlib, seaborn, Scanpy, NetworkX, Biopython), R (Seurat, Bioconductor, DESeq2, edgeR, ggplot2, WGCNA, igraph, Monocle3), Bash and Unix shell scripting

Data visualisation and reporting: ggplot2, matplotlib, Plotly (interactive dashboards), seaborn, IGV; CellxGene for interactive single-cell data exploration; R Shiny (familiar)

Regulatory network analysis: SCENIC and pySCENIC for gene regulatory network inference, TF motif enrichment, cell-cell communication (CellChat, LIANA), trajectory inference (Monocle3, scVelo)

Databases and data resources: TCGA, GEO, EGA, GTEx, Ensembl, Human Protein Atlas, Human Cell Atlas, STRING, BioGRID, KEGG, Reactome, DrugBank, UniProt, cBioPortal

PROFESSIONAL EXPERIENCE

Postdoctoral Researcher, Computational Cancer Epigenomics | December 2024 to Present | Karolinska Institutet, Solna, Sweden

- Deliver multi-omics analytical solutions across three concurrent cancer research programmes, integrating ATAC-seq, GRO-seq, RNA-seq, and snRNA-seq data to generate biological insights that directly inform experimental decisions
- Built and maintain reproducible Snakemake pipelines on Linux HPC for large-scale NGS data processing, with Git version control and team-accessible documentation
- Led snRNA-seq analysis of a 17-donor clinical patient cohort (EGA: EGAD50000001017, 10x Genomics): delivered full pipeline from QC through multi-donor Harmony integration, cell type annotation, pseudobulk differential expression, expression variability analysis, and CTCF regulatory enrichment testing (Fisher exact test, odds ratio quantification)

- Characterised genome-wide chromatin accessibility changes and transcription factor activity shifts driving invasive cancer cell states using differential ATAC-seq analysis and SCENIC regulon inference
- Contributed to manuscript under revision at Nucleic Acids Research (impact factor approximately 23.5): MYC gene gating and CTCF-mediated expression plasticity through a negative feed-forward regulatory loop
- Trained and supported experimental team members in bioinformatics analysis methods; collaborated across multi-PI interdisciplinary teams

IoE Postdoctoral Fellow, Computational Drug Discovery | July 2024 to November 2024 | University of Hyderabad, India

- Delivered a Python-based target-to-compound discovery pipeline integrating molecular docking, pharmacophore modeling, and ADMET profiling to identify and rank anti-cancer tyrosine kinase inhibitor candidates
- Collaborated with synthetic chemistry team to align computational predictions with experimental feasibility, accelerating compound shortlisting

PhD Researcher, Cancer Multi-Omics and Algorithm Development | 2019 to 2024 | University of Hyderabad, India (ICMR-funded)

- Designed and validated two original computational gene prioritisation algorithms in Python and R — a fractal and chaos game representation method (Theory in Biosciences, 2024) and a moment of inertia tensor approach (Proteins, 2022) — both peer-reviewed, open-source, and validated on TCGA cancer datasets
- Integrated transcriptomic, genomic, and protein interaction network data from TCGA and GEO to identify cancer driver genes and therapeutic targets; applied PPI network analysis, WGCNA co-expression, and pathway enrichment
- Published 5 first or co-author papers; presented research at ISMB/ECCB 2023 (Lyon), SACB 2022 (Woods Hole), and GIW/ISCB-Asia 2022; supervised 5 master's dissertation students

EDUCATION

PhD, Biotechnology, Specialisation in Computational Systems Biology | August 2018 to May 2024 | University of Hyderabad, India

Supervisor: Professor Vaibhav Vindal

Master of Technology, Bioinformatics | 2015 to 2017 | University of Hyderabad, India

GATE 2015 qualified (Biotechnology)

Integrated Master of Science, Biotechnology and Bioinformatics | 2008 to 2013 | Yogi Vemana University, India

SELECTED PUBLICATIONS (9 PEER-REVIEWED TOTAL, 2 PREPRINTS)

1. Gao C, and colleagues including Thippana M, and Gondor A. A distal CTCF-binding site drives MYC expression plasticity in a negative feed-forward loop. **Nucleic Acids Research, 2026.** *Reviewer comments received | impact factor approximately 23.5*

2. Dwivedi A, Thippana M, and colleagues. Unraveling the gender-specific molecular landscape of lung squamous cell carcinoma. **Journal of Biomolecular Structure and Dynamics, 2025.** *Impact factor 3.4*

3. Mallikarjuna T, and colleagues. Prioritizing cervical cancer candidate genes using chaos game and fractal-based time series approach. **Theory in Biosciences, 2024.** *Impact factor 1.8*

4. Thippana M, and colleagues. Identification of key molecular players in cervical squamous cell carcinoma through network analysis. **Proteins, 2023.** *Impact factor 3.8*

5. Thummadi NB, Thippana M, and colleagues. Prioritizing candidate genes related to cervical cancer using the moment of inertia tensor. **Proteins, 2022.** *Impact factor 3.8*

Full publication list available on request or at Google Scholar and ORCID profiles.

AWARDS AND HONOURS

June 2023: DST-SERB International Travel Support, ISMB/ECCB 2023, Lyon, France

May 2023: ISCB Travel Fellowship, ISMB/ECCB 2023, Lyon, France

April 2023: NUS-Temasek Foundation Travel Grant, RNA Society Annual Meeting, Singapore

October 2022: DBT-CTEP Travel Grant, SACB 2022, Marine Biological Laboratory, Woods Hole, USA

June 2019: ICMR Senior Research Fellowship, Indian Council of Medical Research, Government of India

LANGUAGES

English: fluent | Swedish: basic, actively developing | Telugu: native | Hindi: basic