

Harshini Suresha

Research Interests: Bulk/Single-cell Transcriptomics, ML for RNA therapeutic design, Explainable AI, Drug discovery

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Education

King's College London

2026 – Present

MSc, Applied Bioinformatics

PES University, Bangalore

2022 – 2026

B.Tech (Bachelor of Technology) in Biotechnology – Converted Degree Class: UK 2:1

Advisor: Dr. Reshma S V

Minor in Computer Science – Converted Degree Class: UK First Class Honours

Research Experience

National Centre for Biological Sciences (NCBS) – KoshKey

Jun 2026 – Sep 2026

Bioinformatics Scientist (Supervised by Dr. Tanay Bhatt)

Bangalore, India

- Built a **single-pass mechanism-arbitration platform** spanning **41 RNA therapeutic mechanisms** across 9 therapeutic goals, with 19 mechanism-specific features to generate ranked candidate oligos.
- Benchmarked **7 ML models across 12 controlled experiments** on RNase H, splice-switching, siRNA oligos and validated the workflow with 84 arbitration, 11 feature-level tests; **submitted to ICLR 2027 and sent for patent.**
- Profiled **mouse fibroblast heterogeneity in scleroderma** with 10x Genomics scRNA-seq (Seurat batch-aware integration, Monocle3 trajectories, CellPhoneDB) and supported **primer design** for follow-up.

Indian Institute of Science (IISc)

Jun 2025 – Jun 2026

Project Trainee, B.Tech Internship Dissertation (Advised by Dr. Payel Roy)

Bangalore, India

- Analysed **bulk/single-cell RNA-seq of human and mouse T-cell populations** in chronic Atherosclerosis disease.
- Built a reproducible pipeline for **FastQC, MultiQC, FastP, STAR, edgeR, DESeq2, Seurat, WGCNA & COMPASS** for QC, differential expression, cellular heterogeneity, trajectory/pseudotime and Th17 metabolic modelling.
- Received the **Research Excellence Honour** for research contributions among the final-year cohort; manuscript submitted to the Journal of Immunology (American Association of Immunologists), for consideration.

Dept. of Biochemistry, Indian Institute of Science (IISc)

Oct 2025 – Mar 2026

Research Student (Advised by Prof. Dipankar Nandi; Co-advised by Dr. Payel Roy)

Bangalore, India

- Utilised **CellRanger, FeatureCounts, Salmon-Alevin** for stimulation-resolved cardiovascular and immune cohorts (CD3, CD28, PMA, P3971 panels), with Harmony/scVI batch correction and Scrublet doublet removal.
- Identified stimulated T-cell signatures using limma-voom, MAST & GLMMs; performed **MiXCR TCR/BCR clonotype profiling**, and built reproducible HPC workflows on SLURM using Snakemake, Nextflow & Docker.

Plant Tissue Culture Lab, PES University

Feb 2024 – Jun 2025

Research Intern (Advised by Dr. Reshma S V)

Bangalore, India

- **In vitro:** plant tissue culture, inoculation and hardening; quorum-quenching assays and SEM on *P. aeruginosa*.
- **In silico:** virtual screening, docking and GROMACS MD with MMPBSA of phytochemicals against QS targets.
- **Outcome:** Honours thesis integrating *In vitro* and *In silico* ranked in the **top 10% of the graduating cohort.**

Center for Innovation and Entrepreneurship (CIE), Bangalore

Jul 2024 – Dec 2024

Research Student (Advised Dr. Kavitha S H; Co-advised by Prof. Sathya Prasad)

Bangalore, India

- Designed **Kavach, a deepfake authentication platform** that detects manipulated content; built **MATLAB kinetic models of *S. cerevisiae* bioethanol production** across diverse feedstocks, backed by 250+ sources.
- Optimised ***A. awamori* cellulase production** (Plackett–Burman, RSM, R^2 0.9878): **87% of peak titre in 58% of the time.** Selected as **one of only 120 participants among 1,500 applicants** in the CIE programme that year.

Dept. of Computer Science, PES University

Nov 2024 – Jul 2025

Research Student (Advised by Prof. Sunil K C; Co-advised by Prof. Badri Prasad V R)

Bangalore, India

- Developed **TriggerNet**, an **explainable AI framework** combining Grad-CAM, RISE, FullGrad and TCAV in a hierarchical pipeline; reached **97.3% accuracy on plant images**, 94.2% on PathMNIST and 92.8% on CIFAR-10.
- **First-authored at NeurIPS 2025 workshops (SPIGM, Reliable ML from Unreliable Data)**, recognised among the **top papers**; presented at ICCET, with a **21.4% p-score gain** and **16.7% lower Brier score** over baselines.

Select Projects (See GitHub profile for more)

GenomeSearch | Python, PostgreSQL | github.com/Harshini-Suresha/genome-search Jan 2026 – May 2026

- Built an integrated system for **indexing, searching and processing DNA/protein sequences**: k-mer index, trie, Smith–Waterman alignment, a DAG workflow scheduler and a PostgreSQL store; designed a **multi-process execution engine** with a dependency-aware scheduler starting longest ready task first.
- **Benchmarked end to end on real NCBI RefSeq data** (154 kb *Arabidopsis* chloroplast genome, 9.6 kb *Yersinia pestis* plasmid) and a **32-task, six-stage bioinformatics workflow**, with critical-path analysis.

RouteOpt | Python, JavaScript | github.com/Harshini-Suresha/routeopt Jun 2024 – Aug 2024

- Designed a **graph-based navigation system** on grid maps of 36 to 100 locations, comparing **Dijkstra, A*, Bellman–Ford** and **BFS** on nodes visited with a **Trie for O(k) prefix autocomplete**, hash table for O(1) lookup.
- **Benchmarked all four algorithms across 630 location pairs**, with scaling measured from **25 to 900 nodes in Python** and up to **6,400 nodes live in the browser**, all datasets exported as CSV for biological network analysis.

AlgoBench | Python, Scikit-learn, SciPy | github.com/Harshini-Suresha/algobench Sep 2024 – Dec 2024

- Implemented algorithms across **eight paradigms** (greedy, backtracking, branch and bound) including knapsack, TSP, max-flow and N-Queens, with a protocol that **checks every algorithm against a reference before timing**.
- **14 benchmark suites**; fitted measured performance to theoretical complexity on a **162-point dataset** (R^2 , empirical exponents), profiled memory with `tracemalloc`, quantified **knapsack quality against DP optimum**.

DataSphere | MySQL, MongoDB, Neo4j | github.com/Harshini-Suresha/datasphere-ml Sep 2024 – Dec 2024

- Designed a **polyglot architecture** (orders in MySQL, documents in MongoDB, network in Neo4j), with 3NF/BCNF modelling, CTEs, window functions, triggers, ACID transactions and EXPLAIN-verified indexing.
- **Benchmarked MySQL, MongoDB and Neo4j** side by side on **median/p95/p99 latency, cold vs warm cache, throughput, indexing and storage overhead**, with execution plans verified using EXPLAIN and PROFILE.

KernelSim | C/C++ | github.com/Harshini-Suresha/kernelsim Jun 2024 – Aug 2024

- Built a **modular OS simulator in C/C++** covering CPU scheduling (FCFS, SJF, Priority, Round Robin, MLFQ), paging with FIFO/LRU/Optimal replacement (reproducing Belady’s anomaly), and IPC operations.
- **POSIX-thread concurrency with deadlock detection and avoidance** (Banker’s algorithm), indexing **all 20 interleavings of a 3-step counter increment**; scheduling ideas behind **HPC & workflows used in bioinformatics**.

Technical Skills

- **Languages**: Python, C++, C, Java, R, JavaScript, TypeScript, PHP, Perl, Bash/Shell, HTML5, CSS3, Linux/Unix.
- **Platforms**: Docker, Git/GitHub, Google Colab, Conda, Jupyter Notebook, MATLAB, MySQL, Neo4j, MongoDB
- **Bioinformatics Tools**: Galaxy, Cutadapt, KEGG, Bowtie2, EMBOSS, AutoDock, SwissDock, PyMOL, STRING, Chimera, Rosetta, limma, STAR, FeatureCounts, DESeq2, edgeR, IGV, fastp, WGCNA, COMPASS, MiXCR, Monocle3, Seurat, MAST, clusterProfiler, SAMtools, BamTools, Trimmomatic, CellRanger, Salmon-Alevin.

Select Publications (First author Preprints and Conference Proceedings)

- **PathSymetic: Neuro-Symbolic Causal Hypothesis Generation for Mechanistic Pathway Discovery in Genomic Systems**. *AAAI Workshops on Bridge-LM Reasoning, AI4Science for Research, and SPARTA 2026, Singapore*
- **A Multi-Method Interpretability Framework for Probing Cognitive Processing in Deep Neural Networks Across Vision & Biomedical Domains** *NeurIPS Workshops (SPIGM & Reliable ML from Unreliable Data), 2025, USA*
- **Evaluating a Comprehensive Set of Machine Learning Algorithms for Classifying Red Palm Mite-Affected Plants and Detecting Infestations Using Leaf Images**. *ICCET 2025, Chennai*
- **TriggerNet: A Novel Explainable AI Framework for Red Palm Mite Detection and Multi-Model Comparison and Heuristic-Guided Annotation**. *arXiv*
- **Innovative Bioethanol Production from Tropical Fruit Residues Using Biomaterial Catalysts and Yeast Bioagents**. *ICRAES 2024, MSRIT, Bangalore*