Liyana Saleem

+44 (0)7554463425 | liyanaps17@gmail.com | Linked-in : Liyana Saleem | LinkedIn

MSc Bioinformatics graduate (Distinction, University of Glasgow) with strong expertise in computational biology, multi-omics integration, single-cell and bulk transcriptomics and network biology. Experienced in NGS analysis, bioinformatics pipeline development, HPC computing and translational research. Skilled in Python, R, SQL, Bash and Linux/Unix environments. Strong collaborator with experience in mentoring and cross-disciplinary team projects.

Education

MSc Bioinformatics (Distinction), University of Glasgow, Glasgow, UK (2024-2025)

- Developed skills in Linux environments, Bash scripting and bioinformatics workflow design,
- Advanced data analysis in single-cell and bulk RNA-seq, GWAS, and multi-omics integration.

B. Tech Biotechnology with Genetic Engineering (Distinction) , Bharath University, Chennai, Tamil Nadu, India (2020-2024)

- Final Project: Network pharmacology analysis of the anti-inflammatory properties of *Phyllanthus niruri*.
- Gained hands-on experience in PCR, gel electrophoresis, flow cytometry, molecular cloning and strengthened skills applied statistics.

Research & Relevant Experience

Graduate Teaching Assistant & Demonstrator | University of Glasgow | 09/2025 – present

- Supporting MSc Bioinformatics students (cohort of ~48) in lab sessions.
- Guiding students through coding, data analysis and problem-solving.
- Explaining advanced computational biology concepts in accessible ways.
- Strengthened ability to communicate complex technical concepts clearly.

Msc Project | *Integrative single-cell analysis to elucidate leukemic stem cell persistence and therapeutic resistance in CML* | Wolfson Wohl cancer research centre | 06//2025 – 09/2025

- Integrated six public scRNA-seq datasets using ScanPy (Python) and Harmony to investigate leukemic stem cell persistence and TKI resistance mechanisms in CML.
- Strengthened expertise in single-cell analysis, Python programming, network biology, and reproducible workflow development for large-scale omics data.
- Applied data harmonisation, metadata management, and combined transcriptomic and functional network data (STRING) to uncover resistance pathways, demonstrating translational insight.
- Built a foundation for multi-omics integration (proteomic and clinical data) while enhancing collaboration and communication skills through teamwork and presentations

Academic Projects | University of Glasgow | 2024 - 2025

- Developed bioinformatics pipelines for large-scale omics datasets

- Analysed transcriptomic changes in mitochondria-depleted senescent IMR90 fibroblasts, identifying dysregulated metabolic and stress-response pathways and developing insights into mitochondrial biology and cellular ageing
- Performed GWAS using *PLINK*, applying regression models, multiple testing corrections and visualized results with Manhattan/QQ plots
- Applied statistical analyses to understand the transcriptional differences in Gout and septic arthritis
- Designed SQL schemas for multi-omics data integration and efficient querying
- Conducted single-cell and bulk transcriptomics analyses in *R (Seurat)* and *Python (ScanPy)*
- Executed sequence preprocessing, QC (FastQC)**,** trimming (Trim Galore, Trimmomatic)**,** assembly (SPAdes, HISAT) and alignment (Bowtie)
- Performed multi-omics (genomics, proteomics, metabolomics) analysis to study Amphotericin B resistance in *Leishmania mexicana*.

Laboratory Intern | Bionyme Laboratories, India | 2023 – 2024

- Operated instruments including GC/MS**,** flow cytometer and chromatography systems**.**
- Trained new interns and assisted with experimental design**,** data handling and report preparation**.**
- Ensured compliance with GLP and lab safety standards**.**
- Contributed to reports and client presentations.

Key Skills

- **Bioinformatics & Data Analysis:** scRNA-seq, bulk RNA-seq, GWAS, WGS, QC and preprocessing , bioinformatics pipeline development, network biology (STRING, Networkx), biomarker discovery, multi-omics data analysis and integration (transcriptomics, genomics, metabolomics, proteomics)
- **Programming & Computing:** Python, R, SQL, Bash, Git, Linux/Unix, HPC cluster computing.
- **Statistical analysis :** Differential expression, regression models, correlation, multiple testing correction, clustering, dimensionality reduction, statistical tests, enrichment analysis.
- **Bioinformatics Tools:** PyMOL, NCBI, BLAST, Galaxy, FastQC, Trim Galore, SPAdes, VCFtools, Bowtie, SnpEff, IGV, Cytoscape, Molecular docking(AutoDock, SwissDock).
- **Molecular Biology:** PCR, gel electrophoresis, flow cytometry, GC/MS, molecular cloning techniques.
- **Data Visualisation:** ggplot2, matplotlib, seaborn, ScanPy plotting tools.
- **Research Communication:** Scientific writing, conference presentations, teaching , peer support.
- **Transferable Skills:** Collaboration, project management, critical thinking, problem-solving, translational insight.

Additional Roles

Class Representative |University of Glasgow | 2024 – 2025

- Represented the MSc student cohort in meetings and served as liaison between students and staff.