

Single-Cell Omics Analysis & Integration — Hands-on

Gain expertise in single-cell omics analysis and integration: scRNA-seq and scATAC-seq QC, clustering, annotation, cross-modal integration, trajectories, and velocity.

Single-Cell Omics Analysis & Integration

[Help Desk](#) · [WhatsApp](#)

Session Index

[Session 1 — scRNA-seq QC & Preprocessing](#) [Session 2 — Clustering, Annotation & DE](#) [Session 3 — Multi-omics, Trajectories & Velocity](#) [Session 4 — Mini Capstone: scOmics Pipeline](#)

Session 1

Fee: Rs 6300 [Apply Now](#)

scRNA-seq QC & Preprocessing

Read processing, mapping and quantification choices

[Cell Ranger](#) [STARsolo](#) [Alevin-fry](#)

QC metrics, filtering and ambient RNA removal

[genes/cell](#) [UMIs/cell](#) [MT%](#) [SoupX](#)

Doublet detection and normalization strategies

[Scrublet](#) [DoubletFinder](#) [SCTransform](#) [log-normalize](#)

Session 2

Fee: Rs 8400 [Apply Now](#)

Clustering, Annotation & DE

Dimensionality reduction and community detection

PCA **UMAP/t-SNE** **Leiden/Louvain** **Scanpy/Seurat**

Automated cell-type annotation and marker discovery

SingleR **Azimuth** **CellTypist** **FindMarkers**

Differential expression and enrichment overlays

rank_genes_groups **GSEA/ORA** **KEGG/Reactome**

Session 3

Fee: Rs 11200 Apply Now

Multi-omics, Trajectories & Velocity

scATAC-seq QC, peaks and gene activity matrices

FRiP/TSS enrichment **MACS2** **Signac/ArchR**

Cross-modal integration and joint embeddings

Seurat WNN **Harmony** **LIGER**

Trajectory inference and RNA velocity views

Monocle 3 **Slingshot** **PAGA** **scVelo**

Session 4

Fee: Rs 14000 Apply Now

Mini Capstone: scOmics Pipeline

Design a reproducible scRNA-seq/scATAC-seq workflow with provenance

Theory

Automate ingest→QC→cluster→annotate→integrate→trajectory with reports

Snakemake **Conda/Mamba** **Quarto/JupyterLab**

Deliver annotated objects, dashboards and submission-ready metadata

Seurat/Scanpy **pandas** **plotly**