Single Cell & Spatial Data to GRN & Signaling Models — Hands-on

Learn how to turn single cell and spatial omics readouts into mechanistic insight. This module walks through QC and clustering of scRNA-seq, spatial transcriptomics and imaging data, mapping cell states onto pathways and networks, and building GRN and signaling models that explicitly account for cell to cell variability and spatial organisation.

Single Cell & Spatial Data to GRN & Signaling Models

Help Desk · WhatsApp

Session Index

Session 1

Fee: Rs 8800 Apply Now

Single Cell & Spatial Omics Foundations

scRNA-seq, spatial transcriptomics and imaging assays overview

- droplet and plate based scRNA-seq
- Visium and related platforms
- multiplexed imaging readouts

Basic processing, QC and clustering pipelines

- quality metrics and filtering
- normalisation and HVG selection
- dimension reduction and clustering

Defining cell types, states and trajectories for modelling

marker based annotation pseudotime and lineage concepts link to GRN and signaling questions

Session 2

Fee: Rs 11800 Apply Now

GRN Inference from Single Cell Data

Regulons, TF activity and GRN building from scRNA-seq

co-expression and motif based links SCENIC / GRNBoost concepts cell state specific networks

Dynamic and trajectory aware GRN inference ideas

pseudotime and RNA velocity inputs cause effect hints along trajectories limitations and robustness checks

From inferred GRN to mechanistic model sketches

selecting key regulators and targets encoding interactions in ODE style choosing levels of model detail

Session 3

Fee: Rs 14800 Apply Now

Spatial Context, Ligand–Receptor & Signaling Maps

Adding spatial coordinates to cell states and networks

spatial transcriptomics mapping image based segmentation and features neighbourhood definitions

Ligand–receptor analysis and intercellular signaling networks

databases (CellPhoneDB, NicheNet ideas) cell type communication graphs prioritising key signaling routes

Embedding spatial and communication info into models

compartments and cell populations | diffusing signals vs direct contacts | link to ODE / ABM frameworks

Session 4
Fee: Rs 18800 Apply Now

Mini Capstone: Single Cell / Spatial Driven Mechanistic Model

Select a single cell or spatial dataset for a pathway question

Theory + Practical

Derive a GRN or signaling sketch and encode a simple model

cell states and communication edges | basic ODE or compartment model | simulate baseline and perturbations

Deliverables: processed data, model files and short report

notebook with analysis steps | SBML / script for the model | figures and interpretation summary