Learn how to turn pathway cartoons and phospho-omics readouts into quantitative signaling networks. This module focuses on reconstructing, calibrating and analyzing signaling networks so that feedback, crosstalk and intervention points can be systematically explored for systems biology and network medicine projects.

Signaling Network Reconstruction & Analysis

Help Desk · WhatsApp

Session Index

Session 1 — Signaling Pathways & Network Motifs   Session 2 — Network Reconstruction from Omics & Literature   Session 3 — Dynamic Signaling Models & Simulation   Session 4 — Mini Capstone: Phospho Data to Signaling Network

Session 1
Fee: Rs 8800   Apply Now
Signaling Pathways & Network Motifs

Architecture of canonical signaling cascades

RTK–MAPK   PI3K–AKT–mTOR   JAK–STAT / NF-κB

Dynamic motifs in signaling networks

feedforward and feedback loops   bistability and switches   oscillations and pulses

From pathway diagrams to networks

nodes, edges and layer types   activating vs inhibitory

edges cross-talk between pathways

Session 2
Fee: Rs 11800 Apply Now

Network Reconstruction from Omics & Literature

Data sources for signaling network building

phospho-proteomics time course perturbation data PPI / pathway databases

Integrating prior knowledge and data driven edges

KEGG / Reactome priors sign-dependent edge annotation confidence scoring of interactions

Practical network assembly workflows

Cytoscape based curation scripted assembly in R / Python export to SBML / SBGN

Session 3
Fee: Rs 14800 Apply Now

Dynamic Signaling Models & Simulation

Choosing modeling formalisms for signaling

ODE based models logic / Boolean approximations hybrid approaches

Parameterisation from dose–response and time course data

fitting simple rate laws handling scale differences basic identifiability checks

Simulating interventions and perturbations

ligand and inhibitor dosing node knockdown/knockout scenarios reading time course outputs

Session 4
Fee: Rs 18800 Apply Now

Mini Capstone: Phospho Data to Signaling Network

From phospho dataset to curated signaling graph

Theory + Practical

Qualitative and quantitative analysis of the network

centrality and bottleneck nodes **path tracing from receptor to response** **candidate intervention points**

Deliverables: model files, figures and README

SBML/SBGN or network files **Cytoscape visualisations** **methods + assumptions document**