

Protein Network Topology & Interfaces — Hands-on

Learn how to connect protein structure, interfaces and interaction data into coherent network based views. From building and annotating protein interaction graphs through mapping structural interfaces, hotspots and allosteric paths, you will use network topology and graph measures to prioritize residues, partners and regions that matter for function, mechanism and design.

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Session Index

Session 1 — Interaction Data, Networks & Graph Basics Session 2 — Structural Interfaces & Hotspot

Annotation Session 3 — Network Topology, Paths & Communities Session 4 — Workflows, Integration & Reporting

Session 1

Fee: Rs 12320 Apply Now

Interaction Data, Networks & Graph Basics

Protein interaction data sources and QC

experimental vs predicted interactions confidence
scores and filtering ideas binary vs complex level
interactions

Graph representation of protein networks

nodes, edges and edge weights concepts directed,
undirected and bipartite views network building from
interaction tables

Basic network descriptors and plots

components and subgraphs simple layouts and visual cues

Session 2

Fee: Rs 16520 Apply Now

Structural Interfaces & Hotspot Annotation

Mapping interactions to structural interfaces

using complexes and docking models buried surface area and contact residues interface type and geometry views

Interface hotspot and energy contributions (concepts)

conserved and central interface residues alanine scanning ideas electrostatic and hydrophobic contributions

From residue level features to interface level labels

annotating edges with interface types critical residues and mutation sensitivity linking structural details to network edges

Session 3

Fee: Rs 20720 Apply Now

Network Topology, Paths & Communities

Centrality and importance measures

degree, betweenness and closeness ideas

eigenvector and pagerank style views node and edge centrality for PPIs

Paths, communication routes and allostery (concepts)

shortest paths and path ensembles connecting

binding sites via residue networks simple models of information flow

Communities, modules and sub networks

clustering and community detection ideas functional modules and complexes mapping communities back to structures

Session 4

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Workflows, Integration & Reporting

End to end network and interface workflows

from interaction tables to graphs and interfaces
combining centrality, communities and hotspots
shortlisting residues, proteins and complexes

Integration with omics and structural projects

overlaying expression and variant data linking to docking, MD and free energy outputs pathway and disease module mapping

Figures, tables and project ready summaries

network diagrams with highlighted hubs interface
and hotspot panels on structures ranked lists with
clear interpretation notes