Biological Networks, Graphs & Topology — Hands-on

Learn how biological systems are represented as networks, how topology shapes function, and how to extract key nodes, edges and modules from large omics graphs. This module builds the graph theory foundations required for downstream systems biology, network medicine and pathway dynamics work.

Biological Networks, Graphs & Topology

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Session Index

Session 1

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Biological Networks and Graph Basics

Representing biological systems as graphs

PPI networks **gene regulatory networks** **metabolic and signaling maps**

Graph terminology and network types

nodes and edges **directed vs undirected** **weighted, signed, bipartite**

Network data sources and file formats

edge lists and adjacency matrices **SIF, GraphML,**

GML import to Cytoscape and Python

Session 2

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Topological Measures and Motifs

Degree based and centrality measures

degree and hubs betweenness and closeness eigenvector centrality

Global topology and paths

shortest paths diameter and average path length clustering coefficient

Network motifs in biology

triads and feedforward loops feedback motifs motifs and function hypotheses

Session 3

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Communities, Modules and Visualization

Community detection algorithms

Louvain and Leiden spectral clustering modularity concepts

Biological interpretation of modules

functional enrichment hub genes and bottlenecks disease modules overview

Visual analytics of networks

layout algorithms edge and node styling Cytoscape and Gephi basics

Session 4

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Mini Capstone: Disease or PPI Network Analysis

Build a PPI or co expression network from a dataset

Theory plus guided practical

Run centrality and community analysis

networkx or igraph | Cytoscape workflows | basic report tables and plots

Deliverables: network file, notebook and summary slides

GraphML or SIF file | Python or R notebook | PPT or PDF summary