Pathway Knowledgebases & Curation Practices — Hands-on

Learn how to navigate, curate and operationalise major pathway knowledgebases. This module focuses on KEGG, Reactome, BioCyc and allied resources, covering practical curation, identifier mapping and enrichment workflows that feed directly into systems biology and network medicine analyses.

Pathway Knowledgebases & Curation Practices

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Session Index

Session 1

Fee: Rs 8800 Apply Now

Landscape of Pathway Databases & Ontologies

Major pathway resources and their strengths

KEGG **Reactome** **BioCyc / WikiPathways**

Ontology ecosystem around pathways

GO Biological Process **Reactome hierarchy** **disease and phenotype ontologies**

Access models and APIs

web interfaces REST APIs R / Python clients

Session 2

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Curation, Annotation & Identifier Mapping

Curation workflows from literature and omics hits

evidence grading inclusion and exclusion criteria versioned change logs

Identifier harmonisation across resources

Ensembl / Entrez / UniProt HGNC gene symbols mapping tables and pitfalls

Annotation templates and data models

pathway membership tables metadata fields (PMID, species, tissue) FAIR annotation guidelines

Session 3

Fee: Rs 14800 Apply Now

Pathway Enrichment & Network-Level Analytics

Over representation and GSEA style methods

ORA / hypergeometric tests GSEA style workflows multiple testing control

Pathway topology and network aware scores

centrality measures bottlenecks and hubs subnetwork extraction

Toolchain for enrichment and visualisation

clusterProfiler / fgsea g:Profiler / Enrichr Cytoscape maps

Session 4

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Mini Capstone: Curated Pathway Panel for a Study

Select and refine a pathway panel for a real dataset

Theory + Practical

Build enrichment ready gene set files and metadata

GMT / GPML style exports version and provenance tracking documentation of assumptions

Deliverables for downstream systems biology modeling

curated pathway list and mapping tables enrichment summary plots FAIR oriented README