Perturbation Screens & Causal Inference (CRISPR/RNAi) — Hands-on

Learn how to process and interpret functional genomic perturbation screens using CRISPR and RNAi technologies. This module walks through pooled and arrayed screen design, NGS-based readouts, raw count processing, normalization, hit calling, enrichment analysis, and causal interpretation using pathways and networks. You will implement hands-on workflows in Python/R inspired by tools like MAGeCK, and convert screen results into mechanistic and actionable hypotheses for drug discovery and systems biology.

Perturbation Screens & Causal Inference (CRISPR/RNAi)

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Session Index

Session 1

Fee: Rs 8800 Apply Now

Screen Modalities, Libraries & Readouts

Pooled vs arrayed perturbation screens

- pooled dropout & enrichment
- arrayed plate based formats (overview)
- phenotypic vs reporter readouts

CRISPR and RNAi technologies

CRISPRko, CRISPRi, CRISPRa (concept level) sgRNA/shRNA library structure on target vs off target considerations

Screen design & experimental context

MOI, coverage and replicates (concepts) baseline, treatment & time points NGS based barcode/sgRNA readouts

Session 2
Fee: Rs 11800 Apply Now

Count Processing, QC & Hit Calling

From FASTQ to sgRNA count matrices

barcode/sgRNA extraction (concept level) alignment vs direct counting (overview) building count tables per sample

QC & normalization of screen data

library representation & dropout checks size factor / median ratio style normalization replicate concordance & controls

Hit calling workflows (MAGeCK style concepts)

sgRNA level statistics & ranking gene level aggregation & FDR control Python/R code notebooks for hit calling

Session 3
Fee: Rs 14800 Apply Now

Enrichment, Networks & Causal Interpretation

Pathway & functional enrichment of hits

GO / KEGG / Reactome sets over representation & GSEA style concepts phenotype specific signatures

Network and causal context for screen hits

mapping hits to PPI and pathway graphs identifying hubs, modules & synthetic interactions linking to upstream regulators & effectors (concepts)

Causal inference & mechanism of action hypotheses

perturbation logic & direction of effect integrating screens with omics and prior knowledge prioritizing targets and pathways for follow up

Session 4
Fee: Rs 18800 Apply Now

Mini Capstone: From Raw Reads to Causal Hypotheses

End-to-end mini project on a CRISPR/RNAi screen dataset (or mock)

Theory + Practical

From counts to hits, pathways & causal stories

processing & hit calling workflow enrichment & network overlays constructing a mechanism of action narrative

Deliverables

PDF/HTML screen analysis report R/Python notebooks and result tables environment.yml / requirements.txt