Proteogenomics Integration — Genome to Protein — Hands-on

Learn how to integrate NGS and mass spectrometry based proteomics into coherent proteogenomic workflows. From building variant aware protein databases using genome / exome and RNA seq data, through searching MS/MS spectra, mapping peptides back to genomic coordinates and interpreting variant and splice specific events, you will design analyses that reveal genome to protein links for oncology, rare disease and systems biology applications.

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Session Index

Session 1

Fee: Rs 12320 Apply Now

Concepts, Study Design & Data Sources

Proteogenomics foundations and use cases

linking variants to peptide evidence **oncology, infection and rare disease views** **advantages and limitations vs genomics alone**

Study design and sample tracking

tumor–normal and cohort layouts | metadata and identifiers for multi omics | batching, randomization and QC ideas

Core data types and formats

FASTA, GTF/GFF, VCF basics | mzML, mzIdentML, RAW overview | RNA seq counts and junction files (concepts)

Session 2

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Variant Aware Protein Database Construction

From VCF to custom protein FASTA

SNPs, indels and frameshifts | somatic vs germline variants | annotation with gene and transcript IDs

Incorporating RNA seq and novel junctions

alternative splicing and isoforms | junction peptides and novel exons | expression filters to control database growth

Database size, decoys and FDR awareness

canonical + variant concatenation strategies | decoy generation concepts | impact of large search spaces on sensitivity

Session 3

Fee: Rs 20720 Apply Now

MS/MS Search, Peptide Mapping & Variant Calls

Searching spectra against custom databases

search engine parameter choices | separating canonical and variant hits | handling multiple search passes

PSM filtering and FDR in proteogenomics

global vs local FDR thinking **stringency for variant specific peptides** **manual review of key spectra (concepts)**

Mapping peptides back to genome and transcripts

genomic coordinate mapping views **exon, junction and reading frame context** **variant, splice and fusion peptide flags**

Session 4

Fee: Rs 26320 Apply Now

Biological Interpretation, Workflows & Reporting

Biological themes from proteogenomic events

neoantigens, splice isoforms and truncations **co occurrence with PTMs (concepts)** **pathway and network level integration ideas**

Workflow patterns and automation options

from raw data to event tables **pipeline scripting / workflow engine concepts** **re running analyses for new cohorts**

Figures, tables and multi omics reporting

variant peptide evidence panels **integrated heatmaps and oncoprint style views** **checklists for manuscripts and collaborators**