Sample-to-Report Pipelines for WES & WGS — Hands-on

Learn how to build and operate robust sample-to-report pipelines for whole exome and whole genome sequencing. This module walks through each step from FASTQ to annotated VCF and report handoff, emphasizing QC, validation mindset and integration with downstream clinical interpretation teams.

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Help Desk · WhatsApp

Session Index

Session 1

Fee: Rs 8800 Apply Now

WES/WGS Data Flow & QC Foundations

From sequencer to FASTQ: layouts and metadata

paired-end libraries | read groups | lane and sample tracking

FASTQ QC and trimming strategy

quality profiles | adapter contamination | read length & depth expectations

Panel vs WES vs WGS — pipeline implications

capture design | coverage targets | turnaround and cost

Session 2

Fee: Rs 11800 Apply Now

Alignment, Coverage & BAM-Level QA

Short-read alignment and reference builds

BWA-MEM / alternatives GRCh37 vs GRCh38 alt contigs and decoys

BAM post-processing and best practices

sorting and indexing duplicate marking BQSR mindset

Coverage, depth and callable regions

on-target vs off-target uniformity metrics QC thresholds for clinical use

Session 3

Fee: Rs 14800 Apply Now

Variant Calling, Filtering & Annotation

Germline and somatic variant calling strategies

single sample vs family tumor-normal pairs joint calling overview

Filtering, hard and soft thresholds

depth and quality population frequency panel of normals mindset

Annotation and pipeline outputs

gene and transcript models clinical databases hooks VCF + tabular exports

Session 4

Fee: Rs 18800 Apply Now

Mini Capstone: End-to-End Pipeline Run

Run a WES/WGS pipeline from FASTQ to annotated VCF

Theory + Practical

Generate QC snapshot and pipeline audit trail

multi-sample summary **logs and run metadata** **versioned config files**

Prepare handoff package for clinical interpretation

VCF + summary tables **coverage report** **pipeline README snapshot**