

Tumor–Normal & Liquid Biopsy Bioinformatics — Hands-on

Master bioinformatics for oncology across tissue and plasma. This module covers tumor–normal and tumor-only study designs, low-VAF somatic calling with UMIs, ctDNA/fragmentomics and MRD tracking, CHIP filtering, and clinical reporting (TMB/MSI, actionability) with robust QC for audits.

Tumor–Normal & Liquid Biopsy Bioinformatics

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[Session 1](#)

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Study Designs: Tumor–Normal vs Tumor-Only

Design choices & trade-offs

[matched normals](#) [panel-of-normals \(PoN\)](#) [tumor-only](#)
[caveats](#)

Somatic vs germline disambiguation

[population AF, gnomAD](#) [artifact & CHIP flags](#)

clonality cues

Tumor content & purity

purity/ploidy impacts | sampling/FFPE effects | QC checkpoints

Session 2

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Somatic Calling & Low-VAF/UMI Pipelines

Callers & error suppression

Mutect2 / Strelka2 / VarDict | UMI consensus & duplex artifact blacklists

Low VAF tuning & QC

depth, LOD, filters | strand bias & context | PoN & orientation

TMB/MSI & signatures (overview)

coverage constraints | panel calibration | report thresholds

Session 3

Fee: Rs 24320 | Apply Now

Liquid Biopsy (ctDNA), MRD & Fragmentomics

ctDNA pipelines & metrics

UMI depth & family size | limit of detection | plasma QC

MRD strategies

tumor-informed vs naive | track sets & thresholds | time-series QC

Fragmentomics & CHIP filtering

fragment length patterns | DNase footprints (overview)

CHIP gene lists & normals

Session 4

Fee: Rs 29920 [Apply Now](#)

Reporting, QC & Longitudinal Tracking

Clinical reporting (somatic)

tiers & actionability **TMB/MSI notes** **limitations/LOQ**

QC, validation & audits

precision/accuracy **LoD/MRD thresholds**

documentation/SOPs

Longitudinal dashboards

time-series trends **alerting rules** **EHR integration**
(FHIR)