

Genome Assembly, Variant Calling & Annotation — Hands-on

Gain expertise in genome assembly, variant calling, and functional annotation with end-to-end, reproducible hands-on labs.

Genome Assembly, Variant Calling & Annotation

[Help Desk](#) · [WhatsApp](#)

Session Index

[Session 1 — Assemblies & Polishing](#) [Session 2 — Mapping & Preprocessing](#) [Session 3 — Variant Calling & Annotation](#) [Session 4 — Mini Capstone: AVA Pipeline](#)

Session 1

Fee: Rs 6300 [Apply Now](#)

Assemblies & Polishing

De novo vs reference-guided assembly strategies

Theory

Short/long-read assemblers & hybrid approaches

SPAdes **MEGAHIT** **Flye** **Canu**

Polishing, scaffolding & assembly QC

Pilon **Racon** **QUAST** **BUSCO**

Session 2

Fee: Rs 8400 Apply Now

Mapping & Preprocessing

Read alignment for short/long reads; primary metrics

BWA-MEM2 **Bowtie2** **minimap2**

SAM/BAM processing: sorting, indexing, duplicates, calibration

samtools **Picard** **GATK BQSR**

Coverage, insert-size & library complexity checks

mosdepth **RSeQC** **preseq**

Session 3

Fee: Rs 11200 Apply Now

Variant Calling & Annotation

SNP/indel callers, joint calling & cohort VCFs

GATK HaplotypeCaller **bcftools** **FreeBayes**

Filtering, normalization & quality models

GATK VQSR **Hard filters** **bcftools norm**

Functional effects & structural variants

SnpEff **VEP** **Manta/Delly**

Session 4

Fee: Rs 14000 Apply Now

Mini Capstone: AVA Pipeline

Design end-to-end assembly→variants→annotation workflow

Theory

Automate mapping, calling, filtering & reports

Snakemake **Conda/Mamba** **MultiQC**

Deliver VCFs, annotated tables & dashboards

pandas **JupyterLab** **Quarto**