

Shotgun Metagenomics: Assembly & Binning (MAGs) — Hands-on

Build robust, reproducible shotgun metagenomics pipelines from raw reads to high-quality MAGs. You'll perform host/read QC, assemble (single/co-assembly), compute coverage, bin & refine genomes, and validate MAG quality against MIMAG standards. Finish with dereplication and lightweight annotation for downstream comparative analyses.

Shotgun Metagenomics: Assembly & Binning (MAGs)

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Session 1

Fee: Rs 8800 [Apply Now](#)

Read QC, Host Depletion & Strategy

Data intake & quality control

[FastQC / MultiQC](#) [fastp / Trimmomatic](#) [adapter/quality trimming](#)

Host/contaminant read removal

[Bowtie2 / BWA](#) [KneadData / BMTagger](#) [human/host genome filters](#)

Assembly planning

per-sample vs co-assembly **memory/CPU budgeting**
metadata & reproducibility

Session 2

Fee: Rs 11800 Apply Now

Assembly & Contig Quality

Assembly workflows

MEGAHIT / metaSPAdes **SPAdes (hybrid)** **contig**
filtering (length/coverage)

Assembly evaluation

QUAST / metaQUAST **N50, L50, NGA50** **k-mer spectra**
checks

Gene calling for bin support

Prodigal / MetaGeneMark **HMMs for markers**

Session 3

Fee: Rs 14800 Apply Now

Coverage, Binning & Refinement

Coverage estimation

Bowtie2 / Minimap2 **SAMtools /**
jgi_summarize_bam_contig_depths **depth tables**

Binning algorithms

MetaBAT2 / MaxBin2 / CONCOCT **coverage +**
composition **co-assembly multi-sample bins**

Refinement & contamination checks

DASTool integration **manual curation (Anvi'o)**
split/merge strategies

Session 4

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MAG QA/QC, Dereplication & Annotation

Quality assessment & standards

CheckM / GUNC / MIMAG tiers

Dereplication & redundancy control

dRep / ANI clustering **representative MAG set**

Lightweight annotation & export

Prokka / DRAM (overview) **FASTA/GBK + reports**
ready for downstream profiling