

Metagenome Assembly and Binning MAGs — Hands-on

Learn how to go from cleaned shotgun metagenomic reads to assembled contigs and high quality metagenome assembled genomes (MAGs). You will compare assembly strategies, configure binning and refinement workflows, and produce MAG reports aligned with community quality guidelines.

Metagenome Assembly and Binning MAGs

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Session 1

Fee: Rs 8800 [Apply Now](#)

Metagenome Assembly Concepts & Strategies

Assembly goals in metagenomics

[contigs and scaffolds](#) [MAG recovery](#) [strain and plasmid context](#)

Assembly paradigms and graph concepts

[de Bruijn graphs](#) [k mer spectra](#) [complexity and repeats](#)

Per sample vs co assembly strategies

[when to co assemble cohorts](#) [heterogeneity and](#)

coverage **resource and runtime trade offs**

Session 2

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Assembly Workflows, Parameters & QC

Short and long read assembly workflows

short read only assemblies **hybrid assembly**
concepts **resource planning and parallelism**

Parameter selection and optimization thinking

k mer size choices **minimum contig length** **coverage**
filters and heuristics

Assembly QC metrics and interpretation

N50 and L50 **assembly size vs expected** **misassembly**
and contamination signals

Session 3

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Binning Strategies, Refinement & MAG Curation

Binning based on composition and coverage

tetranucleotide composition **differential coverage**
profiles **co assembly coverage matrices**

Combining and refining bins from multiple tools

consensus and dereplication logic **manual curation**
workflows **avoiding chimeric bins**

Initial MAG curation and tracking

naming conventions **versioned bin sets** **metadata for**
downstream QA tools

Session 4

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Mini Capstone: MAGs from Reads

End to end assembly and binning on a cohort

Theory plus guided practical

MAG selection, QC summary and basic annotation view

completeness and contamination metrics **basic**

taxonomic placement **prioritizing MAGs for**

downstream analysis

Deliverables: assemblies, bin sets and methods text

FASTA assemblies and MAGs **QC tables and plots**

reproducible workflow description