Metagenome Assembly, Binning & MAG Quality Assessment — Hands-on

Learn how to assemble metagenomes from host depleted reads, recover metagenome assembled genomes (MAGs), and evaluate their quality using current community standards. This module walks through assemblers, binners, refinement strategies and reporting practices that support robust ecological and AMR focused microbiome studies.

Metagenome Assembly, Binning & MAG Quality Assessment

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Session Index

Session 1

Fee: Rs 8800 Apply Now

Metagenome Assembly Fundamentals

From host depleted reads to assembly ready inputs

- read depth and complexity checks
- sample pooling options
- co assembly versus per sample

Assembly algorithms and parameter choices

- de Bruijn graph overview
- MEGAHIT, metaSPAdes, others
- kmer sizes and presets

Assembly evaluation and cleanup

N50 and length distributions contig filtering thresholds basic contamination checks

Session 2

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Binning Strategies & Tools

Principles of genome binning from metagenomes

coverage profiles tetranucleotide frequencies single sample versus multi sample binning

Common binning tools and workflows

MetaBAT, MaxBin, CONCOCT Semi bin and other options coverage matrix generation

Consensus binning and refinement systems

DASTool and similar approaches integrating multiple binners tracking bin provenance

Session 3

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MAG Quality Assessment & Refinement

Assessing completeness and contamination

CheckM and single copy marker genes quality thresholds for MAGs basic versus high quality criteria

Standards and reporting for MAGs

MIMAG guidelines genome statistics tables annotations and taxonomic placement

Refining bins and removing contamination

manual curation strategies **rebinning and splitting bins** **re assembly and polishing overview**

Session 4

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Mini Capstone: MAGs from Reads to Reports

Designing a small metagenome assembly and binning workflow

guided theory plus practical

Running assembly, binning and quality assessment on a teaching dataset

clean reads to contigs **bins to MAG quality metrics** **basic annotation preview**

Deliverables and FAIR oriented documentation

workflow diagram and parameter log **MAG summary tables** **metadata for future dereplication modules**