

Data Standards, Repositories & FAIR Practices for Microbiome Studies — Hands-on

Learn how to turn microbiome projects into FAIR, repository-ready datasets. This module covers data and metadata standards, MIxS-style checklists, major repositories for amplicon and shotgun studies, and practical steps to design submission-ready packages with clear provenance, documentation and re-use potential.

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Session 1

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Standards, Checklists & Metadata Foundations

Why standards and metadata matter in microbiome work

[reproducibility and comparability](#) [long term reuse and meta analysis](#) [journals, funders and repository expectations](#)

Core microbiome standards and checklists (concept level)

[sample and sequencing minimal information ideas](#)

amplicon vs shotgun metadata requirements
environment, host and technical fields overview

Metadata templates, controlled terms and codebooks

spreadsheet templates for samples and runs
controlled vocabularies and consistent coding **data**
dictionaries and readme files

Session 2

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Public Repositories & Submission Workflows

Repository landscape for microbiome data

sequence archives for amplicon and shotgun reads
analysis oriented resources (concepts only) **when to**
choose which repository

Preparing files for submission

FASTQ organisation and naming conventions **sample**
sheets, run tables and manifests **project, sample and**
experiment identifiers overview

Submission portals, releases and accession tracking

interactive vs scripted submission concepts
embargo, release and update strategies **storing**
accession IDs for papers and reports

Session 3

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FAIR Data Management, Provenance & Reuse

FAIR principles in microbiome projects

findable via identifiers and searchable metadata
accessible under clear conditions **interoperable and**
reusable in downstream work

Project structure, identifiers and versions

organising raw, intermediate and final folders **stable IDs for samples and subjects** **versioning of code, configs and outputs (concepts)**

Capturing provenance and workflow details

logs for tools, parameters and versions **workflow files and container images (idea level)** **linking results back to raw data and methods text**

Session 4

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Mini Capstone: Repository-Ready Microbiome Package

Designing a FAIR data package for one study

guided theory plus practical

Building a submission bundle

organised FASTQ and metadata sheets **readme, methods summary and code pointers** **choosing a target repository and accession plan**

Deliverables: zipped submission folder and FAIR summary

folder structure plus example files **metadata template and codebook** **short FAIR and reuse statement for papers or reports**