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Workshop 2: Running microbiome analyses on CloWM

Thursday 2 October 2025 10:45 (1h 30m)

High-throughput sequencing has made metagenomics routine, but turning raw reads into biologically meaningful insights still requires considerable computational expertise, and resources. NFDI4Microbiota’s Cloud-based Workflow Manager (CloWM) aims to lower this barrier by providing end-to-end metagenomic analyses in the cloud, empowering researchers to focus on biology rather than infrastructure - no installation required, free for academic use.

What we will cover:
-Navigating CloWM’s interface
-Managing data within CloWM’s data buckets
- Exploring & executing best-practice metagenomic workflows (SPIRE workflow, nHUMAnN, SameStr)
- Accessing & downloading outputs
- Interpreting results & planning next steps

Presenter: PODLESNY, Daniel (EMBL)

Session Classification: From Bench to Browser: Microbiome Analysis Without Coding Skills