NFDI4Microbiota Annual Conference 2025 - "From Lab to Publication: Bridging the Gap with Best Practices"

Report of Contributions

Welcome and Introduction

Contribution ID: 1

Type: not specified

Welcome and Introduction

Tuesday 30 September 2025 13:30 (15 minutes)

Presenter:FÖRSTNER, Konrad (NFDI4Microbiota Speaker, ZB MED)Session Classification:Opening and Closing

tba

Contribution ID: 2

Type: not specified

tba

Tuesday 30 September 2025 13:45 (1h 30m)

Presenter: SMIRNOV, Alexandre (University of Strasbourg - CNRS) **Session Classification:** Keynotes

tba

Contribution ID: 3

Type: not specified

tba

Wednesday 1 October 2025 09:00 (1h 30m)

Session Classification: Keynotes

tba

Contribution ID: 4

Type: not specified

tba

Thursday 2 October 2025 08:45 (1h 30m)

Session Classification: Keynotes

Type: not specified

Workshop 1: Managing your 16S Amplicon Data: An Introduction to Qiita

Tuesday 30 September 2025 15:45 (2 hours)

Taking the step from running experiments in the wet lab, and generating samples, to analyzing your own 16S Amplicon sequencing data can be quite daunting. Thus, in this workshop, we aim to introduce you to Qiita, a microbial study management platform used to manage and compute studies with 16S microbiome data. This framework establishes an easily accessible way for non-computational scientists to analyse their own data with the option of using pre-defined workflows or building their own. We will give you a compact overview on what you need to get started, possible pitfalls when it comes to data preparation, and show you how to use Qiita for your needs.

Presenters: REHM, Anna (Justus-Liebig-University Giessen); JANSSEN, Stefan (Justus-Liebig-University Giessen)

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

Workshop 2: Running microbiome ...

Contribution ID: 6

Type: not specified

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

Type: not specified

Workshop 3: GSC standards, where to find them and how to use them

Tuesday 30 September 2025 15:45 (2 hours)

Standardised and well annotated metadata are a cornerstone of the FAIR data principles. In this workshop, we will begin with the metadata standards developed and maintained by the Genomic Standards Consortium (GSC), which provides checklists and extensions for a variety of environments and biological context proposed by the NFDI4Microbiota consortium, built on the GSC framework. Next, you'll learn how to choose biome-specific ontologies and use the Ontology Lookup Service (OLS) to annotate your metadata, including how to record the value NULL. Finally, we will move to the NMDC Sandbox submission portal (ORCID required), to validate your tables with DataHarmonizer and export compliant, annotated metadata. By the end of the workshop, participants will be able to create reusable metadata annotations that enhance the reach and impact of their data.

Presenter: BOLE, Martin (Helmholtz Centre for Environmental Research)

Workshop 4: Notebook 2.0: How t...

Contribution ID: 8

Type: not specified

Workshop 4: Notebook 2.0: How to switch to ELNs in your lab

Wednesday 1 October 2025 13:30 (1h 30m)

Discover how Electronic Lab Notebooks (ELNs) enhance reproducibility, collaboration, and FAIR compliance in microbiota workflows. We will demonstrate best practices in eLabFTW - a free and open source favorite in the field - by covering its interface, metadata features, and integrations, then guide you through a hands-on exercise to create and manage a sample project. By the end, you'll be ready to implement ELNs in both wet-lab and bioinformatics settings.

Presenter: THÖLKEN, Clemens (Philipps-Universität Marburg)

Workshop 5: RDM Basics: Writing ...

Contribution ID: 9

Type: not specified

Workshop 5: RDM Basics: Writing DMPs and Applying Metadata Standards

Wednesday 1 October 2025 15:30 (1 hour)

This workshop covers fundamental research data management (RDM) practices, including drafting a Data Management Plan (DMP) and working with common metadata standards. Through brief interactive examples, participants will learn how to structure a DMP and tag datasets using existing schemas.

Presenter: THÖLKEN, Clemens (Philipps-Universität Marburg)

Type: not specified

Workshop 6: Using the virus database VirJenDB to access metadata and sequences for bioinformatics analyses

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

Virus research depends on accurate sequence and metadata, but is often hampered by errors in user-submitted data and a lack of standardized metadata practices. Viral genomes are small and highly variable and current challenges in their organization are compounded by inconsistencies in related metadata (e.g., taxonomy, segment nomenclature, lifecycle definitions). VirJenDB (VJDB; virjendb.org) aims to provide a platform to address these challenges with a metadata-driven, integrative virus sequence database. Virus metadata and sequences from primary and secondary sources such as NCBI Virus, ENA, BVBRC, and community standards like MIGS-VI and ENA Sample Checklists have been merged and harmonized into an integrated dataset. The integrated dataset is used to enable development of metadata schema extensions and through different applications supports virus researchers throughout the data lifecycle. The VJDB dataset is accessible through the web portal, and provides input to bioinformatics webtools (future feature). In this demo, we will start with an overview of virus resources and demonstrate how to use currently available features of the VJDB portal: searching and refining results, downloading data, and exploring metadata schemas. Note that the demo content is subject to change depending on user demands.

Presenter: Dr CASSMAN, Noriko

Type: not specified

Workshop 7: Identifying Identifiers: Harnessing StrainInfo's tools to find and resolve strain designations in literature and metadata

Tuesday 30 September 2025 15:45 (2 hours)

Extracting meaningful biological entities (e.g. sequence accession numbers and species names) from unstructured text is an essential yet complex task. In microbiology, the identification is further complicated by the use of different designations (e.g. DSM 20543 and LMG 28910) for the same strain. Learn how to identify strain designations in literature and sequence metadata by leveraging StrainInfo's API and libraries. A workshop ideal for bioinformaticians, data scientists and researchers with a beginner-level understanding of Python, where participants will be guided through hands-on exercises. By the end of the workshop, attendees will have written a script capable of extracting strain identifiers from both literature and sequence metadata. This script will utilize the StrainInfo API to identify these strains and collect key information such as alternative designations, type strain status, taxonomy and more.

Presenter: LISSIN, Artur (DSMZ)

Type: not specified

Workshop 8: Federated and FAIR: Scalable Data Management with Aruna v3 (Part I)

Wednesday 1 October 2025 13:30 (1h 30m)

Modern microbiome research, as addressed by NFDI4Microbiota, depends on scalable and interoperable infrastructures. Aruna v3 introduces a federation-first approach to research data management, eliminating central coordination while preserving institutional autonomy. Built on peerto-peer technologies, Aruna ensures secure and efficient metadata replication, data locality-aware compute integration, and governance across distributed domains.

The attendees of this workshop will be introduced to the Aruna Version 3 architecture and its new features. Furthermore, the presentation will comprise a demonstration of practical applications within the field, in addition to the provision of a set of guidelines on the establishment of FAIR-compliant data pipelines for the management of research data that is both scalable and secure.

Presenters: HOCHMUTH, Jannis (Justus-Liebig-University Giessen); BREHM, Lukas (Justus-Liebig-University Giessen)

Type: not specified

Workshop 9: CAMI benchmarking portal: towards standards and best practices in computational metagenome analyses

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

We invite you to a hands-on workshop on the CAMI Benchmarking Portal (https://cami-challenge.org, Meyer et al., NAR 2025), an online platform that automates comprehensive evaluation and ranking of software for metagenomic analyses. The portal builds upon the metrics, datasets, and best practices established by the community-driven initiative for Critical Assessment of Metagenome Interpretation (CAMI).

This workshop will cover:

- An overview of the CAMI resources available to the community, including benchmark datasets, standards, and integrated evaluation software

- Exploring and interpreting results from CAMI benchmarking challenges and other users, and how to use the performance rankings to derive software recommendations, such as for integration in workflows

- Submitting your own metagenome assembly, genome and taxonomic binning, and taxonomic profiling results on CAMI datasets for benchmarking

The workshop is intended for researchers, developers, or anyone interested in microbiome analysis, metagenomics, and bioinformatics tool development, as well as good benchmarking principles.

Presenter: MEYER, Fernando (Helmholtz Centre for Infection Research)

Contribution ID: 14

Type: not specified

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Wednesday 1 October 2025 11:00 (1h 30m)

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Session Classification: Panel Discussion

Poster presentation

Contribution ID: 15

Type: not specified

Poster presentation

Wednesday 1 October 2025 16:30 (3h 30m)

Session Classification: Poster Session

Closing Plenary and Take-home R...

Contribution ID: 16

Type: not specified

Closing Plenary and Take-home Recommendations

Thursday 2 October 2025 12:15 (15 minutes)

 Presenter:
 FÖRSTNER, Konrad (NFDI4Microbiota Speaker, ZB MED)

 Session Classification:
 Opening and Closing

Wrap-up of the Conference

Contribution ID: 17

Type: not specified

Wrap-up of the Conference

Thursday 2 October 2025 13:30 (30 minutes)

only for NFDI4Microbiota Consortium Members

Session Classification: NFDI4Microbiota Internal Meeting

Type: not specified

Workshop 8: Federated and FAIR: Scalable Data Management with Aruna v3 (Part II)

Wednesday 1 October 2025 15:30 (1 hour)

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Presenters: HOCHMUTH, Jannis (Justus-Liebig-University Giessen); BREHM, Lukas (Justus-Liebig-University Giessen)