

# Working with Microbiome Data?



If you work with **microbial communities**, you likely face these challenges:

- Which microbes are present in my samples – and in what abundance?
- How do community compositions shift across conditions or treatments?
- Which metabolic functions and pathways are enriched or depleted?
- How can I generate reproducible, publication-ready visualizations at scale?

This flyer shows which de.NBI tools can help analyse your microbiome data, step by step.



GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE



## de.NBI - Trusted Tools for Analysing Life Science Data

### Get started:

Training



Services



E-Learning



### What we Offer

- ✓ Curated tools for genomics, pangenomics, metagenomics, proteomics and more
- ✓ Training, documentation and expert support
- ✓ Access to the de.NBI Cloud
- ✓ Free of charge for academic users

[www.denbi.de](http://www.denbi.de) →  
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de.NBI – German Network for Bioinformatics Infrastructure  
Coordination Office: Forschungszentrum Jülich (FZJ)

## Microbiome Analysis Made Easy - with de.NBI Tools & Training

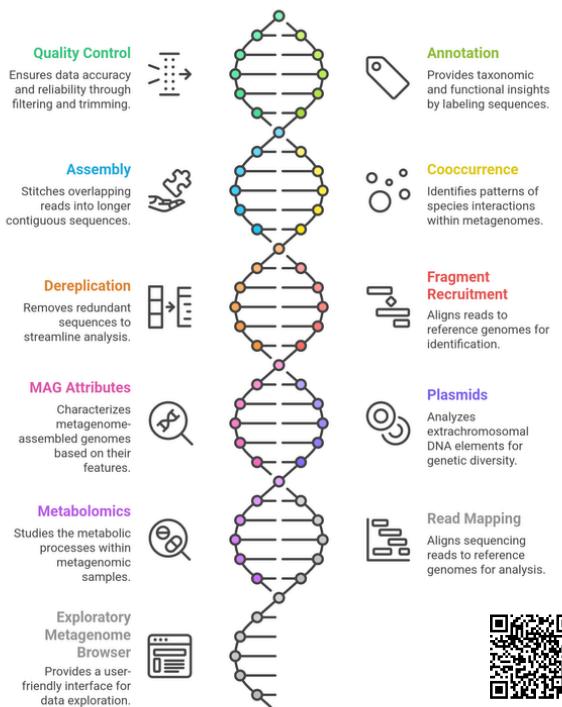
Free for academic life scientists



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# Metagenomics- Toolkit MG-tk

The Metagenomics-toolkit combines novel and established methods for taxonomic and functional microbiome profiling in a reproducible and modular workflow suite.



# microGalaxy



Browser-based workflows for microbial genomics and microbiome analysis – no installation needed, fully powered by the de.NBI Cloud.

# Microbiome Analysis Toolbox



Tools and resources for analysing and interpreting microbiome data. From identifying and quantifying microorganisms to exploring cellular pathways, phylogenetic relationships and microbial community structure.

Microbiome Analysis Toolbox tools:

- NGLess: Workflows for (meta-)genomics data processing
- proGenomes: Taxonomic and functional annotation of prokaryotes
- mOTUs: Metagenomic species profiling
- eggNOG: Resource for orthologous genes
- iPATH: Cellular pathway mapping tool
- Interactive Tree Of Life (iTOL): Interactive tree visualization
- Enterotyping: Gut microbial community typing
- SIAMCAT: Statistical analysis of microbiome data

# Training Opportunities

## Metagenomics Training Courses

Hands-on workshops covering the full workflow from raw reads to biological insights and best practices for reproducible microbiome research.

## E-learning: Metagenomics Media Library

Self-paced learning with videos, practical examples and workflow guides to strengthen your skills anytime.

## Learn from the experts

All courses are developed and taught by researchers who build and maintain de.NBI tools – ensuring accuracy and relevance.

## Build your network

Training events offer direct exchange with fellow microbiome researchers across Germany, providing a platform for collaboration and peer support.



Find a training course for microbiome analysis here:



To the de.NBI E-learning library:



- Easy access: Run analyses directly in the browser.
- Reproducible & scalable: Standardized workflows on de.NBI Cloud infrastructure.

