## Welcome

Dear Reader,

With our second NFDI4Microbiota newsletter, we would like to share news about our community activities such as the ambassador program or conferences we have participated in. In this issue, you can also read about Use Cases which will be implemented this year and about our recently published articles. Moreover, we continue presenting upcoming training courses, report on the release of our new web portal and much more.
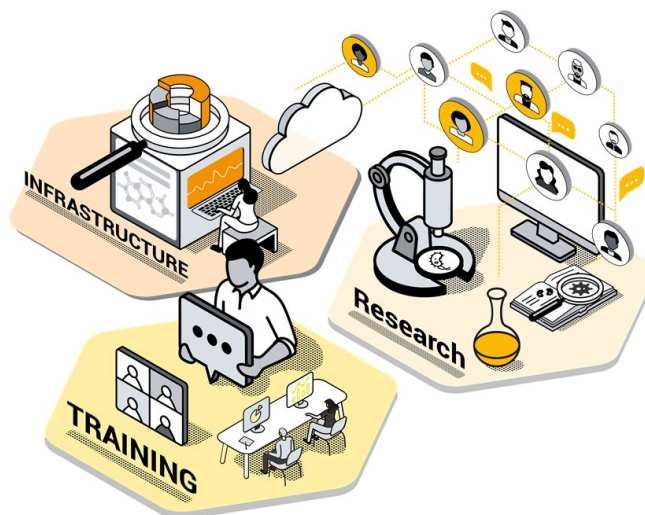
Let us know if you are interested in additional topics that we should cover. We are happy to hear from you!

Enjoy reading the newsletter!

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Community and Training

Ambassador program: Monthly Coffee Talks series has started!

Our mission is to be the central hub in Germany for supporting the microbiology community with access to data, analysis services, data/meta data standards and training. Therefore, the connection and interaction with the German microbiology community is key for our success and the goal of the NFDI4Microbiota ambassador program. The ambassadors will help to efficiently assess and communicate the needs of their community and provide them with suitable solutions generated by the consortium. A bilateral exchange with the ambassadors as well as presentations on different topics take place during the monthly Coffee Talk series. More information and the registration link for the ambassador program can be found here.
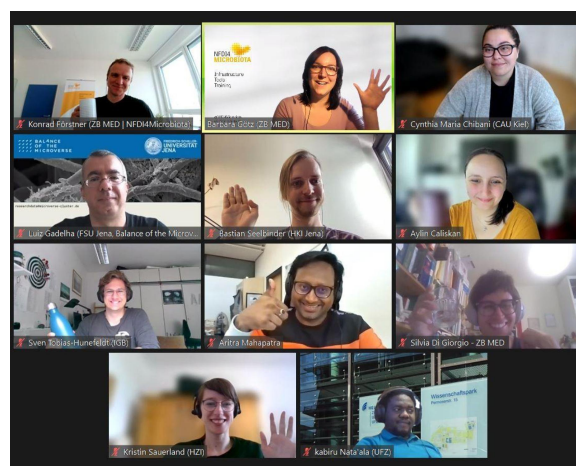
Screenshot of the 1st Coffee Talk

Conferences

NFDI4Microbiota has presented our activities at various conferences, including ISMB, ISME, GCB, ECCB, Targeting Microbiota and DGHM. Moreover, together with representatives of other NFDI consortia, namely NFDI4Health, NFDI4Biodiversity, and KonsortSWD, we participated in the panel discussion 'Everything FAIR and Open? Restrictions on data publications' at JCDL 2022.

NFDI4Microbiota workshop at DGHM
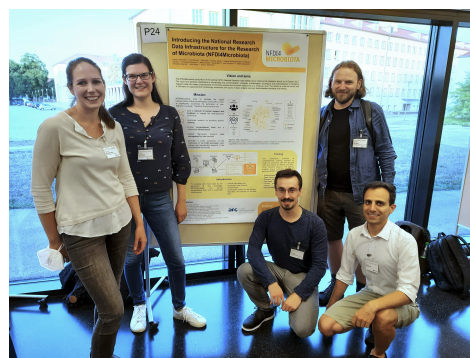
Poster presentation at GCB

Upcoming training and events

Within NFDI4Microbiota the support of the community by education and training is an important goal. Therefore, the consortium offers training on several topics and for different disciplines. Moreover, we are regularly organizing or attending events such as the first BioHackathon Germany. The workshop 'Extending the NFDI4Microbiota Knowledge Base' will be held during that event from 12th to 16th December 2022 in Wittenberg. NFDI4Microbiota has initiated a dedicated Knowledge Base that will contain information on Research Data Management and Reproducible Data Analysis in the broad field of microbiology. The Knowledge Base is developed in an open, collaborative process on GitHub and offered under a permissive license (CC-BY 4.0). Several NFDI4Microbiota members will participate in the BioHackathon and use that time as a content spring. The BioHackathon will offer a great opportunity to engage in discussions with other participants on various topics such as best practices, bioinformatical tools, Electronic Lab Notebooks and privacy issues.

Registration is open for the following workshops and courses:

Title	Location	Date	Link
Lecture on Research Data Management	Online	2022-11-03, 9.00 to 11.00 a.m.	Information and registration
Single Cell Workshop	Online	2022-11-21 to 2022-11-22	Information and registration
Training Course on Metagenome Analysis	Bielefeld University	2022-11-23 to 2022-11-25	Information and registration

1st BioHackathon Germany - Extending the NFDI4Microbiota Knowledge Base	Lutherstadt Wittenberg - Leucorea	2022-12-12 to 2022-12-16	Information and registration

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Networking and Collaborations

Use Cases

We are pleased to announce that NFDI4Microbiota currently has six active Use Cases:

MULTI: Integration of multi-omics data of microbial species

AmpliBench: Replacement or Extension: Systematic Assessment of Differences in Taxonomic Profiling Between Amplicon Sequencing Variants and Operational Taxonomic Units

MetaProt: Functional profiling and routine diagnosis of humane microbiomes by metaproteomics

Strain-ID: Collecting and matching microbial strain identifiers

GUT: Crowd-sourcing high-quality descriptions of novel taxa

MetaENVO (preliminary name): Metagenomic databases

Learn more about the individual Use Cases and how you can contribute on our web portal or look forward to the Use Case showcase during the NFDI4Microbiota Conference on 9ᵗʰ of November. Here, the project background and core aims of each Use Case will be shortly presented thereby providing the opportunity to give feedback, brainstorm further cooperation and discuss integration possibilities within NFDI4Microbiota.

Publications

Next steps after 15 stimulating years of human gut microbiome research – Published in microbial biotechnology

Gut microbiome research has bloomed over the past 15 years. We have learned a lot about the complex microbial communities that colonize our intestine. Promising avenues of research and microbiome-based applications are being implemented, with the goal of sustaining host health and applying personalized disease management strategies. Despite this exciting outlook, many fundamental questions about enteric microbial ecosystems remain to be answered. Organizational measures will also need to be taken to optimize the outcome of discoveries happening at an extremely rapid pace. This article highlights our own view of the field and perspectives for the next 15 years. READ MORE

Publication of the feedback from NFDI4Health, GHGA and NFDI4Microbiota on the positions and recommendations of the German Council of Science and Humanities

NFDI4Health, GHGA and NFDI4Microbiota particularly welcome the positions and recommendations of the German Council of Science and Humanities on digitization and data use for health research and care and have formulated a joint response to this. Here, the consortia appreciate the strategic goal of establishing a decentralized, research-compatible, networked and interoperable health data infrastructure with a central health research data portal. The plea of the German Council of Science and Humanities for a data protection compliant facilitation of data access with the possibilities of the opt-out procedure is explicitly supported by the participating NFDI consortia. Additionally, improved possibilities for the linkage of different data sources (record linkage) on a national level are pleaded for. READ MORE (German)

NFDI4Microbiota - Enabling data-heavy research on microorganisms and their communities – Published in de.NBI brochure (pages 38-41)

Our consortium is engaged in the support of microbiome research and for this builds on the high-performance cloud infrastructure provided by de.NBI. The de.NBI computational infrastructure supplies the network with computational resources on the one hand and massive storage capacities on the other. Furthermore, de.NBI and other partners work together to develop best practices and standards for metadata, training programs and community building. In conclusion, the de.NBI network represents a key component in the provision of NFDI4Microbiota's solution. READ MORE

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Services and Infrastructure

New Release of the NFDI4Microbiota web portal

A new version of the NFDI4Microbiota portal has been released in August 2022. The NFDI4Microbiota services and useful information about the consortium appear in a new design and with an improved structure. New exiting features are an overview of the current Use Cases and our help desk. Currently, our developer team works on a Content Hub that will function as a Knowledge Base in the future. Here, important resources on research data management and for reproducible data analysis will be available.
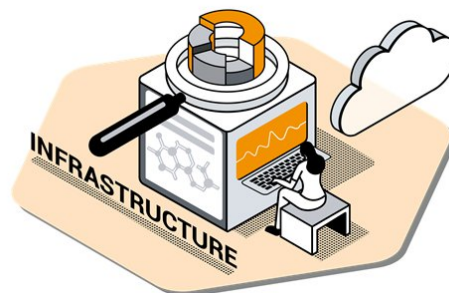
Survey on the use of Electronic Lab Notebooks

Electronic Lab Notebooks (ELNs) play an important role in documenting research data: they provide clear documentation of experiment planning and implementation and of data generation and processing. One of our aims is is to ensure research data are captured as early in the process as possible in order to feed them directly into the analysis pipeline. In order to understand why or why not researchers use an ELN, and what are/were their hurdles in implementing or using an ELN, we conducted a survey on the use of ELNs which was intended for NFDI4Microbiota partners and participants. Only around 26% of respondents are currently using a ELN indicating a clear need to build awareness. Moreover, the ELNs being used varies greatly and are in need of improvements. To further support the use of ELNs and identify the needs of our community, we will soon organise a workshop. Ultimately, we would like to recommend a single ELN and guide researchers in the selection and implementation of the appropriate ELN for their research.

The FAIR annotation of bacterial genomes

The annotation of microbial genomes is a key task in bioinformatics and a requirement for many genome-based downstream analyses. Available contemporary command line annotation software tools, however, only provide mere functional descriptions for coding genes instead of linking known sequences to their related public database records. In particular, for proteins of unknown functions, i.e. hypothetical proteins, public databases can provide useful additional information. To address these challenges and to foster FAIR principles in general, the new software tool Bakta systematically assigns database accession numbers from e.g. UniRef and RefSeq to known protein sequences and related UniRef protein clusters as well as functional categories like COG, KEGG Orthology and GO. Recently, even Torsten Seemann, the developer of the famous Prokka tool, endorsed Bakta. It has been published in Microbial Genomics and is available via Docker and Conda as well as online here.

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Social links and Contact

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Questions or suggestions?

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