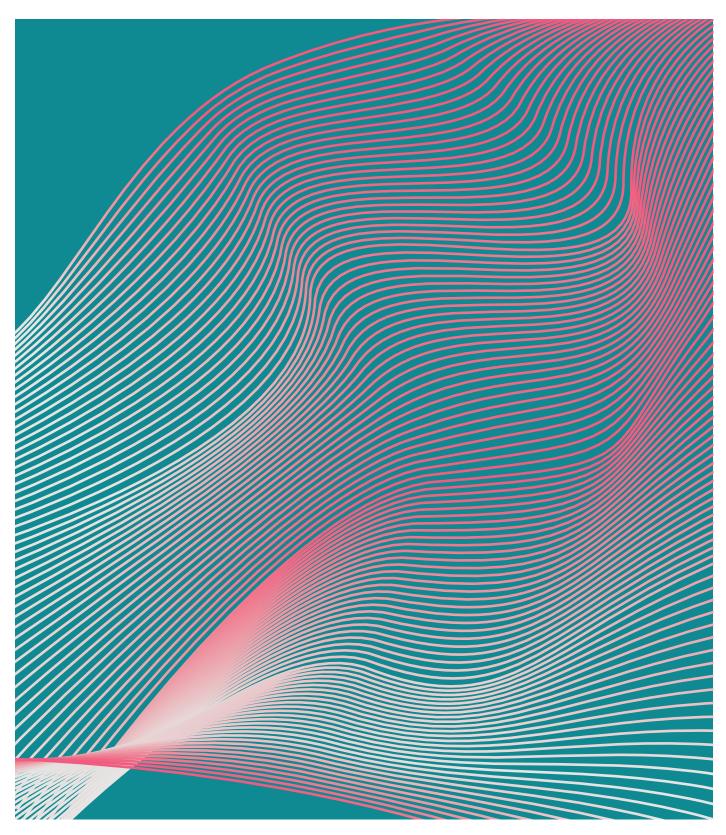


## Long Live Research Data

Book of Abstracts, National EOSC CZ Conference 2025





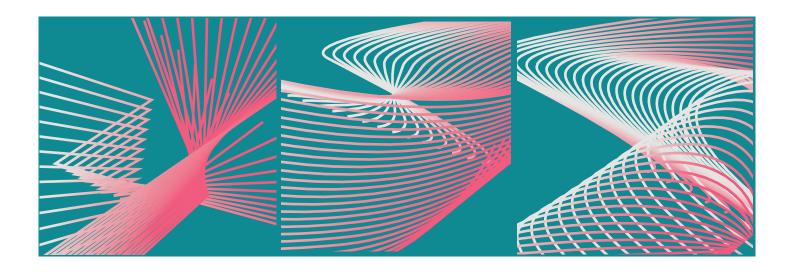




## Long Live Research Data

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Ostrava, 2-3 December 2025



Masaryk University Press Brno 2025





Abstracts were submitted in three categories:

Category 1: Use case of secondary use of research data

Category 2: Own FAIR research data

Category 3: Use case of developing / using / promoting

National Data Infrastructure (NDI) tools and services

Long Live Research Data

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### PROGRAMME OF THE CONFERENCE (2 DECEMBER 2025)

9.00-10.00	Registration
10.00-10.10 10.10-10.30	Opening Remarks by VSB – Technical University of Ostrava and EOSC CZ Research Data in Czech Republic Matej Antol (Masaryk University)
Tools for Data Ma	anagement (Chair: Luděk Matyska (CESNET, Masaryk University))
10.30-11.00 Keynote	COnnecting REpositories (CORE - core.ac.uk) – An Open Scholarly Infrastructure by Researchers for Researchers Petr Knoth (Knowledge Media Institute The Open University)
11.00-12.00	Flash talks and moderated discussion  No persistent Identifiers (PIDs)? No data management!  Petra Černohlávková (National Library of Technology)  Repository for Human and Animal Imaging and Physiological Multimodal Data  Jan Fousek (CEITEC Masaryk University)  OneData Platform  Antonín Fejfar (Institute of Physics of the CAS)  Building Repositories: From Infrastructure to User  Illyria Brejchová (Institute of Computer Science Masaryk University)

#### 12.00-13.00 Lunch

### Stories of Data (Re-)Use (Chair: Jaroslav Juráček (Masaryk University)

13.00-13.30	Health Data Stories
Keynote	Martin Komenda (Institute of Health Information and Statistics of the CR)
13.30-14.30	Flash talks and moderated discussion
	Using and Reusing Single-Cell RNA Sequencing Data Jaroslav Ol'ha (Faculty of Medicine Masaryk University) Experience with Data Sharing and Reuse in the Field of Computer Science Monika Čechová (Faculty of Informatics Masaryk University) I found it - Automation Accelerated Data Sharing Marek Cebecauer (J. Heyrovsky Institute of Physical Chemistry CAS) Data Use Cases at CEITEC Adrián Rošinec (CEITEC Masaryk University)

#### 14.30-15.00

17.00-17.45

Coffee Break

Poster Session

### Advancing Data Skills (Chair: Matej Antol (Masaryk University))

15.00-15.30 Keynote	Data Matters - and Data Matter Ladislav Krištoufek (Vice-Rector for Research Charles University)
15.30-16.30	Flash talks and moderated discussion
	Introduction to the Data Steward Certificate Course at the University of Vienna Michael Feichtinger (University of Vienna) The Data Steward Microcertificate Course at the Charles University Jan Dvořák (Faculty of Arts Charles University) Developing Data Literacy: Personal Insights from Practice Tomáš Marek (Faculty of Arts Masaryk University) Building RDM and OS Skills from the Ground Up Jan Vališ (National Library of Technology) The Role of a Data Steward in Educational Processes Georgia Koutentaki (Faculty of Information Technology Czech Technical University in Prague)

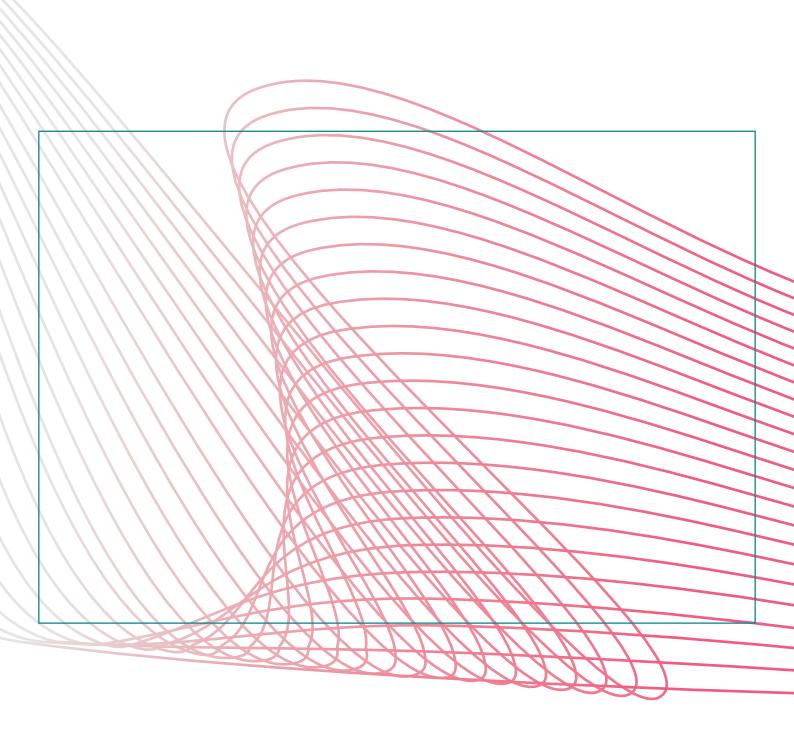
### PROGRAMME OF THE WORKSHOP REPO BUILDERS (3 DECEMBER 2025)

8.30-9.00	Registration
	ing a New Repository
9.00-9.40	The Process of Cre Tutor: Illyria Brejch
9.40-10.10	Core NRP Reposito Tutors: Illyria Brejcl
10.10-10.30	Legal and Licensin Tutor: Daniel Mikšíl
10.30-11.00	Coffee Break
	ces and Tools for Repo
11.00-11.40	UX, Testing, and M Tutors: Illyria Brejcl
11.40-12.00	FAIR Principles in N Tutor: Milan Janíče
12.00-12.15	AAI and the Service
12.15-12.30	Tutors: Eliška Blažk Repository System
12.10	Q&A Session Partic Eliška Blažková   Da
12.30-13.30	Lunch Break
BLOCK 3: Metao 13.30-13.50	data I Czech Core Metada
	Tutor: Michal Med
13.50-14.35	Domain Specific M Tutors: Petra Černo
14.35-15.00	National Metadata Tutor: Michal Klodr
15.00-15.30	Coffee Break
BLOCK 4: Metac	
15.30-16.00	National Catalogue Tutor: Alexandr Kud
16.00-16.30	Persistent Identifie Tutor: Hana Hering

### PROGRAMME OF THE WORKSHOP YOUNG RESEARCHERS (3 DECEMBER 2025)

	8.30-9.00	Registration
BLOCK 1: My Data 9.00-9.45		<ul> <li>Basic Data Stewa</li> <li>FAIR on the First Tr</li> <li>Tutor: Michal Růžič</li> </ul>
	9.45-10.30	Persistent Identifier Tutor: Hana Hering
	10.30-11.00	Coffee Break
	BLOCK 2: My Data 11.00-11.30	<ul> <li>Management and How I Learned to S Tutor: Antonín Zita</li> </ul>
	11.30-12.00	Where to with it? Do Tutor: Jan Vališ
	12.30-13.30	Lunch Break
	BLOCK 3: My Data 13.00-14.30	- Processing and Ar Data analysis with Tutor: David Chudá
	14.30-15.00	Computing Time ar Tutor: Kateřina Mar
	15.00-15.30	Coffee Break
	BLOCK 4: Case Stu 15.30-16.30	ıdies Your FAIR Data / Us Speaker: Jan Fišer

## Abstracts



# A COMPREHENSIVE PROBIT ANALYSIS: MODELING COGNITIVE, ECONOMIC AND SOCIAL FACTORS OF SUSTAINABLE FASHION CONSUMPTION

#### ALEX NEUBAUER \*\*

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The global economic transition towards environmental sustainability requires a fundamental shift in consumer behaviour1. We analyse the impact of cognitive, product-based, socio-economic and demographic factors on sustainable consumer behaviour (SBC) using survey data from the ET CASE project and a probit regression model2. Our findings indicate that engagement with sustainability concepts, demographic profile and willingness to bear associated costs substantially increase the propensity for sustainable behaviour.

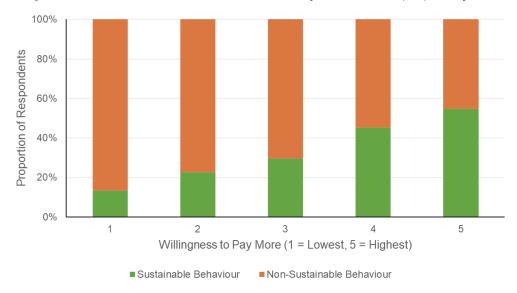


Fig. 1. Sustainable Behaviour by Willingness to Pay More

We establish demographics as the strongest driver of SBC, as being a female is associated with the biggest increase in probability of taking part in sustainable practices. Cognitive engagement also plays a significant role, as literacy of circular economy concepts increases SCB. Lastly, economic and value perceptions create a trade-off: willingness to pay more positively influences SBC, yet importance of the brand acts as a counterweight.

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- 2. ALVES, Márcia; Carlos SEIXAS; Alberto Castro a Alexandra Leitão. Promoting the Transition to a Circular Economy: A Study about Behaviour, Attitudes, and Knowledge by University Students in Portugal. In Sustainability. 2024, 16(1).

# A FAIR DATASET FOR ASSESSING MICROCENTRIFUGAL FILTER REUSABILITY USING FT-IR SPECTROSCOPY AND CUSTOM PIPELINE

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The Fourier Transformed Infrared spectroscopy (FT-IR) is an analytical technique that requires little to no sample preparation. FT-IR shows great potential for diagnosis of biofluids like human serum. Serum, however, contains high-molecular-weight components that have minimal diagnostic value, but significantly affect the spectral profile. To reduce this complexity, single-use microcentrifugal filters are employed. However, for economic and environmental reasons, these filters are commonly reused several times. The aim of this study was to investigate whether such practice is actually feasible. To begin with, we used two sets of 100 kDa filters repeatedly – up to 4 times – to process a sample of human pooled serum (Fig. 1). Each filtrate was subsequently measured 9 times using FT-IR spectrometer. The filter reusability was analysed using a pipeline which included normalisation and classification. To make our dataset findable, we published it with rich metadata¹. The proprietary format SPA was converted to CSV to ensure interoperability, and to enhance reusability, ReadMe file and open licence was provided. Adhering to the FAIR principles, facilitated seamless collaboration between researchers, improved transparency and dataset reusability. Our results indicate that repeated use of microcentrifugal filters has a measurable impact on spectra, thus suggesting this practice should be abandoned.

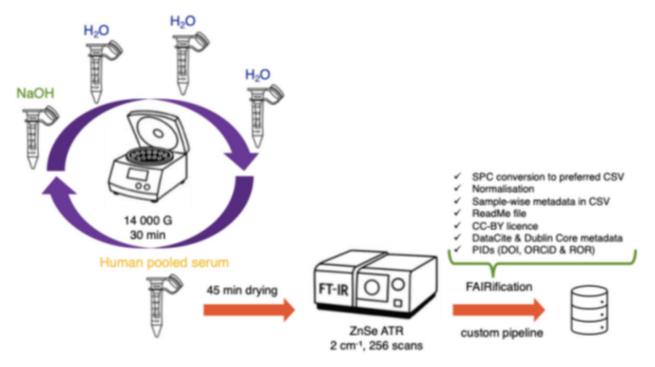


Fig. 1. Sample preparation (purple), measurement of FT-IR spectra, and data processing (red).

This work was supported by grants of Specific University Research [A2-FCHI-2025-018, A1-FCHI-2025-002, and A1-FCHI-2025-005].

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# ALPHAFIND 2.0 – ENHANCED STRUCTURAL SIMILARITY SEARCH FOR ALPHAFOLD DATABASE

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Four years after the breakthrough of Al-powered protein structure prediction with AlphaFold, databases of protein structures continuously evolve, as evidenced by the recent (October, 2025) enrichment of AlphaFold Database with additional 20+ million structures in version 6 of the data. However, to keep this vast data ecosystem useful for researchers, students, and other domain experts, specialized systems are needed to provide analytics on top of it. AlphaFind 2.0 is an advanced similarity search engine for protein structures of the AlphaFold Database. Building upon its predecessor (https://alphafind.fi.muni.cz/), a new version of this tool allows users to search in the structures of protein chains, focus on the high-confidence regions of these chains, and also the domains from https://ted.cathdb.info/. Users can search by uploading a structure, providing protein ID or via protein name. The system employs state-of-the-art embedding models for quick filtering in the vector space to achieve scalable, high-speed retrieval and uses TM-Align to report on the biological similarity metrics such as TM-Score and RMSD. A redesigned web interface integrates Mol\*, providing interactive 3D visualization, shows useful attributes such as organism or CATH annotation, domainlevel alignment inspection, and real-time query refinement. Architecturally, the application allows researchers to quickly find similar protein structures from various structural perspectives and visualize the alignment of similar AlphaFold-predicted structures, connecting users to this vast resource of data.

NIKOLA SIXTOVÁª\*, VLADIMÍR ULMAN<sup>b</sup>, EMMA STROUHALOVÁª, MICHAL TARANAª, MICHAL MED°, MICHAL KOZUBEK<sup>b</sup>. MAREK CEBECAUERª

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We are establishing a new repository for FAIR-sharing of biological image data, representing a National Data Infrastructure (NDI) use case service. Initiated with the Czech Biolmaging community, it will eventually serve all researchers in the Czech Republic. The repository will be registered with the National Repository Platform and will offer Persistent Identifiers. We have adopted the Czech Core Metadata Model1 (CCMM) to ensure consistent harvesting into the "National Catalogue of Open Data" and interoperability with other national systems. We have extended CCMM¹ with domain-specific elements based on the Recommendations for Metadata in Biological Imaging², utilizing the Dataspecer³ tool to maintain the linked data approach for semantic web operability. In this poster, we demonstrate our use case experience with the key steps for building a new NDI-compatible repository.

This output was developed with financial contributions from the EOSC CZ initiative through the National Repository Platform for Research Data project (CZ.02.01/00/23\_014/0008787), funded by the Operational Programme Johannes Amos Comenius of the Ministry of Education, Youth and Sports of the Czech Republic.

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# DATA MANAGEMENT TOOLS CATALOGUE: SUPPORTING FAIR RESEARCH

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Researchers face increasing challenges managing research data due to the growing number and diversity of available tools. Identifying suitable solutions for each phase of the data lifecycle can be time-consuming, especially when some tools are region-specific or limited to certain infrastructures.

To support researchers, we developed the Data Management Tools Catalogue<sup>1</sup>, a centralized overview that collects and categorizes tools by their role in the data lifecycle. It provides a structured guide to navigate solutions, including those available exclusively in the Czech Republic, and highlights resources accessible through the National Data Infrastructure (NDI) for easier discovery and comparison.

The current beta version covers all major lifecycle phases. Planned enhancements include subject-specific filters and broader tool coverage to support diverse research domains. By presenting tools in an organized, transparent manner, the catalogue helps researchers make informed choices, promotes standardized practices, and fosters FAIR-compliant data management.

This contribution will present the catalogue's structure, demonstrate its beta functionalities, and outline the development roadmap, emphasizing its role as a practical resource for simplifying data management.

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# DEVELOPMENT OF THE CZECH FEGA NODE FOR SECURE GENOMIC DATA MANAGEMENT

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The European Genome-phenome Archive (EGA) provides a secure infrastructure for storage, sharing, and controlled access of sensitive genomic and phenotypic data. Its primary goal is to ensure data confidentiality while enabling authorized researchers to access information in a compliant and traceable manner. Within this initiative, national nodes (FEGA – Federated EGA) are being established to support data management in accordance with the legal and technical requirements of individual countries.

The Czech national FEGA node is currently under development and builds upon the Sensitive Data Archive software implementation. The system is deployed on a Kubernetes platform to ensure scalability and reliability. Data storage is provided through an object storage service compatible with the S3 protocol, while metadata is managed by the central EGA node (CEGA). Sensitive data are encrypted using the Crypt4GH standard, which enables efficient re-encryption of files for specific recipients without processing their entire content. This approach maintains a high level of data security while simplifying access management. The current implementation is in the prototype phase and is integrated into the EGA test infrastructure.

Future development foresees integration into the Genomic Data Infrastructure (GDI), which aims to enable secure federated computation across sensitive datasets.

# EMPOWERING OPEN SCIENCE THROUGH EOSC AI: SCALABLE, SECURE, AND RESEARCH-READY INFRASTRUCTURE AT CERIT-SC.

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Artificial Intelligence (AI) is transforming scientific research by enabling advanced data analysis, knowledge discovery, and communication. To support this shift within the European Open Science Cloud (EOSC) ecosystem, CERIT-SC—a core component of e-INFRA CZ—is developing an on-premise AI environment that provides researchers with secure, high-performance, and interoperable tools. This ecosystem empowers innovation while ensuring compliance with FAIR principles and open science.

Our infrastructure features cutting-edge NVIDIA DGX H100 and DGX B200 systems, enabling efficient large-scale model training and inference. It hosts open large language and generative models—including DeepSeek R1, Qwen3-Coder-480B, Gemma3, and GPT-OSS-120B—accessible via an Open WebUI interface or OpenAI-compatible APIs. This facilitates seamless integration into research workflows and EOSC services.

Beyond conversational AI, the ecosystem supports AI-augmented workflows through JupyterHub with preconfigured Notebook Intelligence plugins for local model interaction and the DeepSite web application for generative design of websites, visuals, and presentations. An AI-powered documentation portal further enhances contextual assistance across e-INFRA CZ and EOSC resources.

All services operate within e-INFRA CZ's trusted infrastructure, guaranteeing data privacy, reproducibility, and regulatory compliance. Researchers retain full control to fine-tune or train custom models locally, fostering community-driven Al development aligned with EOSC's federated vision.

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In this project, we processed a neuroimaging dataset originally collected in 2019 by Jan Štrobl. The dataset was converted to the Brain Imaging Data Structure (BIDS) format, a recognized community standard for organizing and describing neuroimaging data and associated metadata. To support reproducibility and reusability, we developed a conversion pipeline for transforming data from the European Data Format (EDF) to BIDS. The implementation will be made openly available on GitHub. Following conversion and verification, the dataset was deposited in the National Repository Platform for Research Data, enhancing its accessibility and compliance with the FAIR data principles—Findable, Accessible, Interoperable, and Reusable. This work demonstrates a practical example of applying data standardization and open science practices to ensure long-term usability of neuroimaging data.

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# FAIRIFICATION IN A MULTIMODAL IN-VIVO IMAGING CENTRE: APPLYING REMBI-STRUCTURED METADATA AND FAIR WIZARD WORKFLOW IN PRACTICE

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Implementing FAIR data principles within preclinical in vivo imaging is challenging. Research infrastructures routinely generate heterogeneous datasets across MRI, CT-PET/SPECT, ultrasound and optical imaging, where interoperability and metadata standardisation are often limited. We present the FAIRification workflows developed at the Center for Advanced Preclinical Imaging (CAPI), a Czech-BioImaging and Euro-BioImaging Node. Using the FAIR Wizard platform to create Data Management Plans and internal guidelines aligned with the REMBI metadata model, we standardised documentation of imaging studies and their experimental context.

FAIR principles were introduced gradually — starting with study-level metadata and researcher training. This incremental approach improved data findability, metadata completeness and internal interoperability. Pragmatic FAIRification based on REMBI and structured DMP planning enhances transparency and reusability in complex imaging environments.

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# FROM CHAOS TO FAIR, BECAUSE WE CARE: ENVI DATA IN ARCHAEOLOGY

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The Environmental Department was established in 2023 as part of the Center for Field Archaeology (CETA) at the University of Hradec Králové<sup>1</sup>. Our mission is to apply a comprehensive approach to studying the past anthropogenic environment — from field sampling through laboratory analysis to data interpretation. The laboratory's core activities focus on geochemical, hyperspectral, and luminescence (portable OSL) analyses. The resulting datasets of various dimensionality and metadata characteristics follow a standardized structure, with each sample assigned an internal persistent identifier to ensure consistent traceability. The laboratory aims to gradually implement the FAIR data principles. The poster presents the current status of our datasets and outlines our planned approach to enhance data management through the implementation of an electronic lab notebook.



Fig. 1. Our data originate in the field, beginning with sample collection. Foto: Anna Horáková

#### **RFFFRFNCFS**

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# FROM MAP TO ROADMAP: LAUNCHING FAIR DATA MANAGEMENT AT CZU

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In 2025, the Data Management Competence Centre (DMCC) at the Czech University of Life Sciences Prague (CZU) conducted a comprehensive institutional survey to map how researchers create, store, and share their data across the university. The questionnaire comprised 58 items and received 227 responses from academic staff and doctoral students. It aimed to identify current practices, needs, and barriers throughout the entire research data lifecycle — from planning and collection to preservation, sharing, and reuse.

The resulting dataset and accompanying analysis have been openly published on Zenodo and the Open Science Framework (OSF), including metadata, documentation files, and a clearly defined licensing structure. This makes the mapping of research data management at CZU a FAIR-ready institutional dataset and a reproducible example of FAIR data production within the Czech academic environment.

The survey reveals significant systemic gaps in research data management, marked by limited awareness of institutional rules and low engagement in preparing Data Management Plans. While many respondents rely on insecure local storage, there is an overwhelming call for centralized institutional support — including clear guidelines, training, and a secure long-term repository.

By making this dataset openly available, the mapping provides a robust evidence base for advancing FAIR implementation at CZU and offers a scalable model for other universities seeking to assess and enhance their own data management maturity.

# FROM OPEN DATA TO OPEN KNOWLEDGE. WHY DIAMOND OPEN ACCESS MATTERS

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Diamond Open Access (DOA) is a vital missing piece in the Open Science ecosystem, especially where research data and publications intersect. While FAIR data and infrastructures like EOSC enable sharing and reuse, much of the scientific record remains locked behind subscriptions or APC-funded publishing models. This limits both access and participation, even when data are openly available.

The poster outlines four key issues: prohibitive publication costs, market concentration, the privatization of publicly funded research, and the inaccessibility of articles linked to open datasets. Diamond OA addresses these challenges by eliminating costs for both authors and readers and by relying on institutional, public, or cooperative funding. This shifts scholarly communication back into the public sphere and supports equity, bibliodiversity, and academic autonomy.

Recent EU projects—DIAMAS, CRAFT-OA, and PALOMERA—have developed standards, tools, and infrastructure to support this shift. Their joint outcome, the European Diamond Capacity Hub (EDCH), now coordinates capacity-building and policy alignment across Europe, including the emerging Czech National Centre for Diamond OA.

By aligning open publications with open data, Diamond OA strengthens the societal mission of science and ensures that research outputs serve the public good rather than commercial interests.

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# GLOBALFUNGI AND GLOBALAMFUNGI: A FAIR ATLAS FOR REUSING GEOREFERENCED FUNGAL METABARCODING SAMPLES

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The advent of high-throughput sequencing has revolutionised our ability to monitor fungal biodiversity and biogeography across ecosystems and continents. To make published observations interoperable and reusable, we established two FAIR-compliant, open-access repositories: GlobalFungi (https://globalfungi.com) and GlobalAMFungi (https://globalamfungi.com). GlobalFungi currently compiles over 4.5 billion ITS1/ITS2 metabarcoding observations from 84 972 samples (Fig. 1.) reported in 846 studies, spanning soils, litter, air, aquatic habitats, plant material and decomposing wood¹. GlobalAMFungi harmonises nearly 90 million Glomeromycotinian amplicons from 8 464 environmental samples across 108 countries, integrating data from SSU rRNA, ITS2 and LSU rRNA markers². Both platforms provide intuitive interfaces for searching, visualising distributions and downloading sequences with rich environmental metadata. They promote community submissions, transparent provenance and automatic versioning, thereby ensuring reproducibility. These atlases have already enabled global biodiversity maps, richness estimates, assessments of environmental constraints and drivers of community turnover, as well as conservation prioritisation. By consolidating scattered sequencing records into coherent and georeferenced datasets, GlobalFungi and GlobalAMFungi deliver unprecedented resources for studying fungal ecology, evolution and ecosystem functioning, while maximising the secondary use of research data.

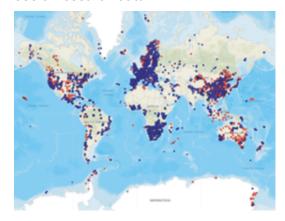


Fig. 1. Sample distribution in GlobalFungi. Previous version samples (red); newly added samples (blue).

We acknowledge support from Talking microbes – understanding microbial interactions within One Health framework (CZ.02.01.01/00/22\_008/0004597) and ELIXIR CZ.

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# GROMACS METADUMP: AUTOMATED METADATA EXTRACTION FOR FAIR MOLECULAR DYNAMICS DATA

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Molecular dynamics (MD) simulations generate vast datasets that are increasingly shared through public repositories, yet fragmentation and inconsistent metadata hinder their reuse. We present GROMACS MetaDump, a software tool that automatically extracts, structures, and annotates metadata from GROMACS simulation files. Using the simulation input file (.tpr) as the foundation, and optionally incorporating topology (.top) and structure (.gro) files, the tool produces human- and machine-readable outputs in JSON or YAML. GROMACS MetaDump is accessible as a web application, API, and command-line utility, facilitating integration into diverse research workflows.

The tool introduces the GROMACS MetaDump Schema, capturing key descriptors such as simulation parameters, system setup, macromolecule identifiers (PDB, UniProt, PubChem), and administrative details. We validated the approach on 4,364 publicly available GROMACS simulations, demonstrating robust extraction and highlighting discrepancies between reported and deposited simulation parameters.

By standardising metadata extraction, GROMACS MetaDump improves findability, accessibility, and reusability of MD data, directly supporting FAIR principles and initiatives such as MDDB. This platform-independent tool represents a practical step toward more transparent, interoperable, and reusable simulation data.

This work was supported by the Ministry of Education, Youth and Sports of the Czech Republic (ELIXIR-CZ, Grant No. LM2023055 and ELIXIR CZ: Capacity extension Grant No. CZ.02.01.01/00/23\_015/0008210).

# INTEGRATIVE ANALYSIS OF SINGLE-CELL RNA-SEQ DATA FROM CEREBRAL ORGANOIDS ACROSS STUDIES

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Cerebral organoids are three-dimensional neural tissues grown from stem cells, which can serve as a powerful model for studying human brain development and disease in vitro. One of the most essential ways to analyze their internal function is single-cell RNA sequencing (scRNA-seq), which measures gene expression profiles and reveals which cell types and cellular programs are present within an organoid. These datasets are extremely information-rich, and any single analysis can only capture a fraction of their potential insight—making them prime candidates for data re-use and secondary analysis.

However, integrating scRNA-seq data across studies is non-trivial – experiments are affected by severe batch effects and produce high-dimensional, complex data. In this project, we explore the integration of healthy cerebral organoid datasets generated by multiple laboratories, using approaches such as canonical correlation analysis (CCA), conditional variational autoencoders (cVAEs), and cluster similarity spectrum (CSS) methods across a range of parameter settings and gene selection strategies. Our goal is to identify reproducible biological patterns across datasets and establish robust integration workflows, so that we can validate our organoid models against fetal brain data and uncover disease-specific expression patterns in brain organoids affected by Alzheimer's disease.

This project has received funding from the European Union's Horizon Europe program under the grant agreement No. 101087124), the CESNET development fund (project no. 779/2025) and by the funds from the Faculty of Medicine, Masaryk University (MUNI/A/1738/2024).

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The poster presents the current state of development in the field of data management for plant phenotyping. With the growing complexity and volume of phenotypic data, standardised and interoperable approaches are essential to ensure data consistency, sharing, and reproducibility. The presentation introduces key community standards such as MIAPPE1 (Minimum Information About a Plant Phenotyping Experiment) and BrAPI2 (Breeding API), which define common frameworks for describing experiments and exchanging data between phenotyping databases and software tools. Furthermore, it highlights existing data platforms designed to handle and integrate multi-source phenotypic and environmental datasets. The poster also outlines pipelines for data processing and analysis, illustrated by examples such as crop growth modelling using the APSIM (Agricultural Production Systems sIMulator) tool, and workflows for processing 2D and 3D data acquired from field measurements and automated phenotyping platforms. These examples demonstrate how standardised data models, interoperable APIs, and modelling tools can significantly improve the efficiency, transparency, and reusability of phenotyping data in modern plant science and digital agriculture.

The results and knowledge included herein have been obtained owing to support from the following institutional grant. Internal grant agency of the Faculty of Economics and Management, Czech University of Life Sciences Prague, grant no. IGA 2023B0005.

This research was carried out under the project: "Precizní zemědělství a digitalizace v ČR" (Precision Agriculture and Digitalization in Czech Republic), reg. no. QK23020058.

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# PRIVACY-PRESERVING DATA QUALITY ASSESSMENT FOR FEDERATED HEALTH DATA NETWORKS

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Assessing data quality in federated health data networks remains a major challenge due to privacy constraints that prevent centralised data access. Traditional quality assessment methods require visibility of raw data, which conflicts with legal and ethical requirements for data sovereignty.

This work presents a privacy-preserving framework for evaluating data quality in federated environments using differential privacy. The approach enables local computation of quality metrics—such as accuracy, completeness, and consistency—while sharing only aggregated, noise-obfuscated results. This ensures that sensitive information about individual patients or small cohorts cannot be inferred from reported metrics.

A proof-of-concept implementation demonstrates the feasibility of the method on synthetic health datasets modelled after common clinical data standards. Each local node executes standardised data quality checks under a fixed privacy budget, and the results are aggregated to provide a federated overview of data quality.

The framework is data-model agnostic and applicable across diverse biomedical domains. It illustrates how differential privacy can enable trustworthy, decentralised data quality assessment and supports scalable, privacy-compliant quality transparency within the European Open Science Cloud and other federated research infrastructures.

This project has received funding from Czech Ministry of Health (MMCI, 00209805), Czech Ministry of Education, Youth and Sports (BBMRI.cz no. LM2023033) and European Union's Horizon Europe research and innovation programme (EvolveBBMRI, no. 1101131701)

# THE MAP AND DATA CENTRE: MANAGING AND REUSING GEOGRAPHICAL RESEARCH DATA AT THE GEOGRAPHICAL INSTITUTE, FACULTY OF SCIENCE, CHARLES UNIVERSITY

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Our contribution introduces the Map and Data Centre of the Faculty of Science, Charles University, a specialised facility dedicated to the management and sharing of geographical research data as well as cartographic outputs. After introducing the centre's mission and development, we focus on practical examples of research data reuse, primarily applications in education activities. We will also outline the centre's next steps, particularly its integration with the National Repository Platform and National Data Infrastructure through the OP JAK Open Science II grant, which will enable enhanced data accessibility, cross-institutional collaboration, and automated data management workflows.

# THE WORKFLOW FOR SHARING SENSITIVE DATA AT FNUSA: THE EXAMPLE OF KARDIOVIZE STUDY

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Research data obtained in epidemiological studies are important for generating new knowledge in medical research. When the data is managed according to the FAIR¹, their value enhances significantly². However, in the health data environment, it is also necessary to establish a clear data collecting and sharing process as part of comprehensive data management, addressing legal and ethical risks and ensures compliance with the GDPR³. The process was created and implemented in cooperation of several departments of St. Anne's University Hospital.

The hospital organizes responsible data sharing through a transparent workflow. Requests are submitted via the REDCap<sup>4</sup> web application and goes through a structural approval process. The Kardiovize Brno population study<sup>5</sup> serves as a pilot dataset for testing and validating process. The implemented procedure is flexible, accomodating large cohort studies and smaller projects that maintain data in an exportable format with a corresponding codebook.

A transparent and auditable procedure for exchanging sensitive data is the main advantage of this process. The active involvement of the Data Protection Officer and legal experts guarantees adherence to all relevant regulations. REDCap provides a reliable, cost-effective solution. Cooperation with the Biostatistics Department provides extensive methodological support to researchers throughout the entire data management lifecycle.

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# WEB PORTAL FOR A RECURRING CRYPTOCURRENCY INVESTMENT SYSTEM

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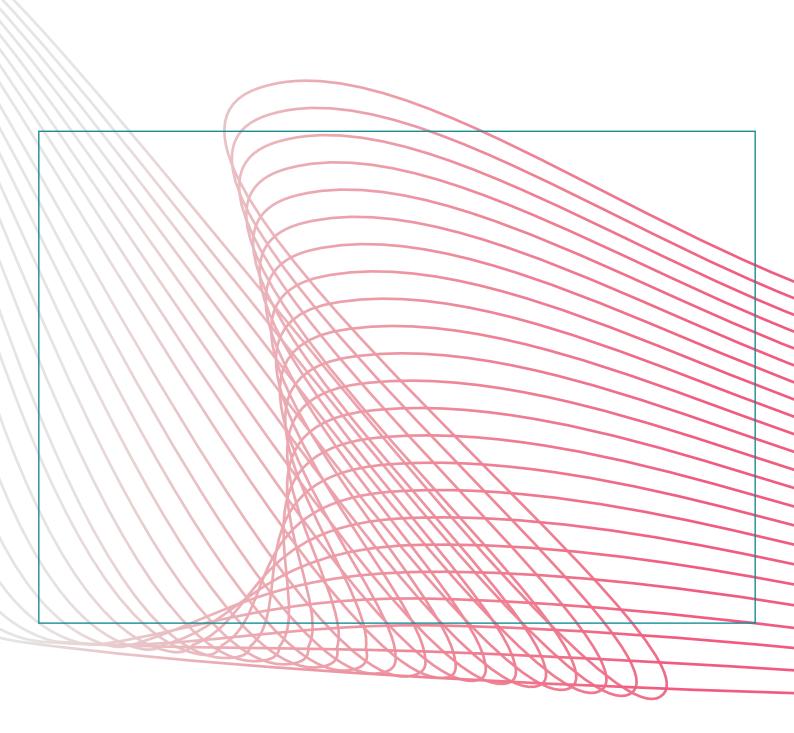
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We present a web portal that combines education for novice investors with analytical tools for cryptocurrency markets. The system combines educational articles, step-by-step guides, and a glossary of terms with interactive visualizations of portfolio development and individual coins. Users can export their overviews and results to common formats (CSV/JSON, PDF).

Technically, the portal uses React for the front-end and PHP/MariaDB for the back-end. Computationally demanding data is generated on a separate computing server and automatically migrated to web hosting. System administration is divided into editorial and administrative sections. The editor manages articles, including their multilingual variants, comments, and sharing on social networks. Content managers have complete control over achievements, feedback, forms, analytical data, and advanced tools. Administrators can manage user data beyond the scope of the manager.

The resulting platform connects education with market analysis and helps to understand data and put it to practical use.

## Meet&Greet



# AUTHENTICATION AND AUTHORIZATION INFRASTRUCTURE (AAI) AS A KEY ELEMENT OF OPEN SCIENCE IN THE CZECH REPUBLIC

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Authentication and Authorization Infrastructure (AAI) is a key tool in open science, as it ensures secure, uniform, and trustworthy access for researchers to web services and data resources across institutions, significantly shaping their cooperation. Within the e-Infrastructure e-INFRA CZ has been developing and operating the national AAI through the edulD.cz federation for a long time and thanks to its participation in the EOSC CZ initiative, it is also integrated into the international identity federation. Its importance is growing with the need for effective and repeated use and processing of research information in accordance with the FAIR principles, including ensuring the protection of sensitive data.

The poster therefore presents the basic principles of AAI, the main benefits for users, identity providers, and service providers, as well as specific examples of use within the National Repository Platform (NRP). The aim is to raise awareness of the possibilities of AAI, support its wider adoption in the academic environment, and demonstrate how to utilize it for effective access to the tools of various services that process and reuse data and metadata in accordance with the FAIR data principles.

# METACENTRUM: THE CZECH NATIONAL DISTRIBUTED COMPUTING INFRASTRUCTURE FOR EOSC-POWERED RESEARCH

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MetaCentrum, jointly operated by CESNET and CERIT-SC within e-INFRA CZ, represents the Czech national distributed infrastructure for cross-disciplinary computational and data-intensive research. It integrates high-performance computing (HPC), cloud, Kubernetes, and AI services, providing access to over 53,000 CPU cores, more than 500 GPUs, and 20 PB of storage for over 3,700 active users.



Fig. 1. Geographical Distribution of Cluster Installations in MetaCentrum

Beyond providing raw computing power, MetaCentrum offers an integrated ecosystem that links data repositories with computational workflows while ensuring adherence to FAIR principles and interoperability with the European Open Science Cloud (EOSC). Through a unified single sign-on interface, users gain access to interactive computational environments (Jupyter Notebooks, RStudio), specialized tools (AlphaFold), commercial software (MATLAB, Ansys), and workflow management systems (Galaxy, Kubernetes, Open OnDemand).

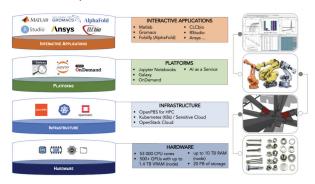


Fig. 2. Hiearchical Services in MetaCentrum

The infrastructure's capabilities are further extended through collaboration with the National Data Infrastructure (NDI), enabling integration between the National Repository Platform (NRP) and computing services. This integration supports end-to-end research workflows encompassing data analysis, preservation, and reuse. Representative applications include repository-linked Galaxy pipelines, scalable data processing on dedicated NRP Kubernetes clusters, and MDDash—a virtual environment for molecular dynamics that leverages EOSC-compliant repository-based data exchange.

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Long Live Research Data

Poster booklet, National EOSC CZ Conference 2025

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