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Turňa Ján,

Slovak Centre of Scientific and Technical Information, Bratislava, Slovakia,
ORCID: 0000-0001-5813-566X, e-mail: jan.turna@cvtisr.sk

Gavurníková Gabriela,

Slovak Centre of Scientific and Technical Information, Bratislava, Slovakia,
ORCID: 00000-0001-7096-6378, e-mail: gabriela.gavurnikova@cvtisr.sk

Zendulková Danica,

Slovak Centre of Scientific and Technical Information, Bratislava, Slovakia,
ORCID: 0000-0003-2487-0177, e-mail: danica.zendulkova@cvtisr.sk

Radvák Peter,

Slovak Centre of Scientific and Technical Information, Bratislava, Slovakia,
ORCID: 0000-0002-7421-3522, e-mail: peter.radvak@cvtisr.sk

Budiš Jaroslav,

Slovak Centre of Scientific and Technical Information, Bratislava, Slovakia,
ORCID: 0000-0002-8667-6655, e-mail: jaroslav.budis@cvtisr.sk

OPEN SCIENCE INFRASTRUCTURE IN SLOVAKIA AND ITS USE IN THE LIFE SCIENCES

ABSTRACT. *Open Science infrastructure provides researchers with digital services, computational resources and data environments supporting the FAIR principles and enabling effective sharing and reuse of research outputs. This paper presents the development of Open Science infrastructure in Slovakia and demonstrates its application in the life sciences through pathogen genomics and antimicrobial resistance (AMR) surveillance. Particular attention is paid to the Slovak node of the European Open Science Cloud (EOSC), the NarCoS bioinformatics platform and their role in processing and analysing large-scale genomic datasets. The paper describes a federated approach to cross-border cooperation between the Slovak and Polish EOSC nodes, in which harmonised workflows enable analysis while sensitive data remain under local control. The presented use case demonstrates how federated Open Science infrastructure can support interoperable genomic analysis, strengthen data sovereignty and contribute to more effective cross-border surveillance of infectious pathogens and antimicrobial resistance.*

KEYWORDS: *Open Science infrastructure, EOSC, Life Sciences, Antimicrobial Resistance, NarCoS.*

INTRODUCTION. At the beginning of June 2021, The National Strategy for Open Science 2021–2028, with its first Action Plan 2021–2022, was adopted by the Slovak government. The creation of the National Strategy is an integral part of the Action Plan of the Open Government Partnership Initiative 2020–2021. The National Strategy aims to create a sustainable paradigm of participation of all stakeholders interested in science and research in Slovakia in the implementation of open science global principles in disseminating, mutual sharing, reusing, and making research outputs available in Slovakia, and thus to support the development of domestic and international scientific collaboration. The implementation of Open Science principles into the Slovak research and development (R&D) environment is connected with a whole complex of legal instruments that constitute a legislative framework for the regulation and management of the existence and scope of individual parts of the R&D sector structure and other specific measures such as copyright.

In this article, we focus on the use of IT systems and modern bioinformatics tools for the management and analysis of large-scale data generated by sequencing technologies (highly parallel sequencing or Next Generation Sequencing, NGS) in monitoring the development and transmission of antimicrobial resistance (AMR) pathogens. Enriching genomic data with high-quality metadata allows for a better understanding of

ongoing epidemics and enables modeling of their development. We point out the cross-border cooperation of the Slovak EOSC node with the Polish EOSC national node in supporting open science and strengthening European data sovereignty and Europe's competitiveness in the global knowledge economy.

Current situation

The implementation of open science principles is one of the fundamental pillars of science policy across the European Union. Broad theoretical foundations, current science policy trends and proven practice form the basis for activities in the field of open science support.

In the Recommendation on Open Science (2021), UNESCO¹ defines open science as an approach to the research process based on collaboration, sharing and open dissemination of knowledge through the optimal use of digital technologies and the application of the principles of openness in every aspect of the research cycle. It includes open access, focused on the free availability of publications.

The Open Science Infrastructure is a set of shared digital services, tools, repositories and platforms that allow researchers to collect, store, process and share scientific publications, research data and software free of charge. We understand it as an ecosystem of interconnected components, which mainly includes: repositories of scientific publications and research data, information systems on science and research, computing and data infrastructure, services for persistent identifiers, metadata, interoperability and linking of research objects and services for Research Data Management (RDM) and the implementation of the FAIR principles.

These four basic principles: findability, accessibility, interoperability and reusability help to maximize the added value obtained from current, formal scientific digital publishing. They are a guide on how to organize and manage research data so that they are long-term findable, available under clearly defined conditions, interoperable and reusable (Wilkinson, 2016).

In Slovakia, the development of this infrastructure is a key part of the ecosystem of state support for research and development (Zendulková et al, 2026) and the policy documents of the National Strategy for Open Science (VAIA, 2023) and the current Action Plan for Open Science for 2026–2028 (VAIA, 2026). The main coordinator of the activities is the Slovak Centre of Scientific and Technical Information (SCSTI).

The documents are based on pan-European policies. One of the main pan-European initiatives to support open science and open innovation is the European Open Science Cloud (EOSC). It represents a network of organizations and infrastructures from different countries and communities that supports the open creation and dissemination of knowledge and scientific data. The EOSC aims to group together existing scientific data infrastructures, which are currently fragmented between individual scientific disciplines and EU Member States.

A number of international projects funded by the EU have been implemented in the field of development and implementation of open science. For example, projects focused on the practical implementation of open science FOSTER (2014–2016) and FOSTER+ (2017–2019), the project focused on the development of EOSC: EOSC Focus (2022–2025) and others. However, we were mainly inspired by the PATHOS project and its outputs focused, among other things, on the economic benefits of open science (Tsipouri et al, 2025; The Economic Benefits of Open Science, 2026) and on the impact of open science in the field of innovation (Caputo, A. et al, 2025).

Research carried out using open science infrastructures has the potential to inspire the scientific community to openness in any field of research. A specific “success story” is dedicated to bioinformatics research in the field of life sciences.

¹ United Nations Educational, Scientific and Cultural Organization

Use case: pathogen genomics and antimicrobial resistance

Antimicrobial Resistance (AMR) is a growing global health threat, with the WHO's Director-General describing it as outpacing advances in modern medicine and threatening the health of families worldwide (United Nations, 2025). This threat is prompting the scientific community and public health authorities to respond through strengthened international surveillance systems, coordinated “One Health” strategies spanning human, animal, and environmental health, and global commitments — including a 2024 UN General Assembly political declaration setting the first international targets to reduce AMR-related deaths (World Health Organization, 2025). Slovakia is no exception regarding rising AMR, and public health authorities and scientific communities recognise it as a major health problem. Despite having an approved national action plan since 2019, Slovakia was one of only two countries in the WHO European region that still had above-median AMR-attributable mortality, even though they had developed, approved, financed, and implemented national AMR action plans. Countries with such plans were otherwise in the lower half of the region for AMR mortality (Mestrovic T., 2022). This complex issue is also fuelled by prescribing patterns that lean unusually hard on broad-spectrum drugs. Slovakia had the lowest share of WHO “Access”-category antibiotics of any EU/EEA country in 2024 at 38.6%, against an EU-wide average of 60.3% and roughly 4.7 percentage points below the 2030 target of over 65% (European Centre for Disease Prevention and Control, 2025). Hospital-level surveys have documented real overuse, with around 31% of surveyed patients on antibiotics at any given time, rising to 54% in ICUs, and excessive use of broad-spectrum antibiotics, prolonged surgical prophylaxis, and frequent unnecessary intravenous (IV) antibiotic use flagged as ongoing problems (Štefkovičová M. et al, 2016). As a result, resistant organisms are well established, with MRSA accounting for 25–30% of invasive staphylococcal isolates in Slovakia between 2016 and 2020 (Tkadlec J. et al, 2023) and a growing hospital burden of multidrug- and extensively drug-resistant ESBL-producing bacteria (Jalali, Y., 2024). The clinical stakes are severe, as one Slovak university hospital study of hospital-acquired bloodstream infections found an in-hospital case-fatality rate of 36.7% overall, rising to 43.3% in ICU patients, with Enterobacteriaceae as the most common causative pathogens (Garabasova, M. et al, 2015).

Several groups in Slovakia are focusing on this important public health threat, including the Genomic Centre Laboratory at Comenius University Science Park (CU SP), together with the Slovak Centre of Scientific and Technical Information (SCSTI), ESMO Žilina, a.s., and Slovgen s.r.o. These public and private biological and IT laboratories are joined together in the project (Integration of genomic data sources for national security in the human, food and environmental areas; acronym: GenSafe) to facilitate the integration of AMR pathogens and their genomic data for national security across the human, food and environmental domains. The project is collaborating closely with the Public Health Authority of the Slovak Republic and other key public entities. The main approach is to generate sequencing data using whole-genome shotgun sequencing (WGS) for surveillance of multidrug-resistant bacteria (e.g., *Klebsiella pneumoniae*, *Escherichia coli*, *Enterobacter hormaechei*, *Acinetobacter baumannii*) from different regions and sources. Large genomic datasets will be analysed within a national computational bioinformatics platform, NarCoS (Národné COVID-19 Sekvenovanie—National COVID-19 sequencing). This can be briefly described as a process, where DNA is extracted from pathogens, fragmented and tagged with genetic “barcodes” (a step called library preparation), so it can be read by a sequencing platform (Illumina NextSeq 2000), which reads DNA from both ends of each fragment for greater accuracy. Once sequenced, specialised software combines the fragments of DNA reads into complete genomes. The finished genomes are then run through a series of tools to answer different questions which are tightly connected to the epidemic of spreading AMR resistant pathogens. Analysis of pathogen genomes is giving us the missing answers to which species and strains are spreading within the population, which antibiotic-resistance and disease-causing (virulence) genes they carry, and which plasmids they bear. A more detailed strain-typing method can be applied to determine how closely related the bacterial samples are to one another.

The NarCoS system has developed into a platform that analyses different biological samples. The bioinformatic system evolution is heading toward capturing samples and collecting information on antibiotic resistance across different sectors. This approach generates large datasets for several reasons. Also, the analysis (assembly, MLST/cgMLST comparisons, and building relatedness trees across many isolates) is computationally demanding, especially for vast samples collected during an outbreak, so laboratories benefit from shared cloud/HPC resources. In addition, patient-linked genomic data is sensitive information, so a lab can't simply email FASTQ files to a partner country. SCSTI, as a project partner, is actively involved in several European research initiatives within the European Research Area, including the European Open Science Cloud (EOSC), so the project GenSafe is an example of how EOSC infrastructure can be utilised.

An EOSC federated setup lets each site interested in interconnecting genomic data keep raw data local and export only standardised, de-identified outputs like resistance profiles or cluster IDs. This only works if everyone uses common standards (shared pipelines, metadata schemas, and persistent identifiers), so that a resistance-gene call or cgMLST type produced in a Slovak genomic lab is directly comparable to one produced elsewhere in Europe, rather than being a one-off local result. Finally, outbreak investigations often need to compare a new isolate against strains from years earlier, which requires curated, persistently stored reference datasets rather than data that disappears once a grant project ends.

EOSC Federation and cross-border cooperation

On November 3, 2025, during the EOSC Symposium, the European Open Science Cloud (EOSC) took a significant step towards its consolidation as a European space for research and innovation data. The 14 coordinators of the first wave of EOSC Federation nodes, including the Slovak node, presented a Memorandum of Understanding (MoU), which is a decisive step towards a borderless European research ecosystem. It supports open science while strengthening European data sovereignty and Europe's competitiveness in the global knowledge economy. SCSTI is part of the EOSC Federation and aims to use all its scientific services and data to achieve the ambitious goals of the federation. Participation in the first wave of the federation represents a self-funded commitment to build trust and shared practices that will anchor the EOSC Federation as a core research infrastructure across disciplines and borders in Europe.

The EOSC Federation offers a technical solution to connect these sources and analyse them with harmonized workflows. The federated analysis of pathogen genomes science case outlines a federated, cross-border capability for timely analysis of pathogen genomes that brings computation to the data instead of copying sensitive datasets across institutions. The objective is to shorten time-to-insight for outbreak detection, source attribution, and antimicrobial-resistance (AMR) surveillance while preserving data sovereignty and meeting European legal and ethical requirements. Experience from COVID-19 showed that sequencing at scale can transform public-health decision-making.

A recent example of this connection: EOSC has a dedicated "Federated analysis of pathogen genomes" pilot that pairs Slovakia's national EOSC node with Poland's, built specifically for cross-border outbreak detection and AMR surveillance using a federated model. This brings computation to the data rather than copying sensitive datasets across institutions, aiming to speed up outbreak detection, source attribution, and AMR surveillance while preserving data sovereignty and meeting European legal and ethical requirements. In this pilot, the Slovak national EOSC node supplies workflows, datasets, computational infrastructure, and domain expertise, while the Polish node contributes technical support and its own datasets. The two were chosen partly for their geographic proximity, making them an ideal cross-border test case (EOSC Association AISBL, 2026). The design principle is deliberate: establish a federation of trusted sites, run harmonised workflows locally at each site, and share only the minimum results needed for action — rather than shipping raw patient-linked sequencing data across borders.

Operationally, the effort starts with two neighbouring nodes of the EOSC Federation—the Slovakian national node providing workflows, datasets, computational infrastructure and domain expertise, and the

Polish national node (via Poland's National Science Centre (NCN) and a scientific repository service) supplying key technical support and their own datasets.

Technical solutions

Technically, the system will leverage the EOSC Federation's e-infrastructure backbone. Identity and access control will rely on the EOSC Federation Authentication and Authorization Infrastructure (AAI), integrating with research identity providers to support fine-grained authorization, auditability and policy enforcement across Nodes. The immediate focus of the use case is to use already-public repositories to prove the technical foundation since timely clinical data are sensitive, embargoed and legally complex to share. Once trust is established, the use case envisions carefully governed links to authorities' private repositories. In other words, "build the plumbing first", then invite data owners to experience the advantages of sharing data.

Scientific outcomes

Establishing a federation of trusted sites for sharing of sensitive data can increase critical data sharing on the advance of AMR and improve cross-border surveillance of pathogen genomes. The use case proposes unified, reusable workflows running across existing European infrastructures to expand the view beyond application domains and national borders, improving outbreak tracing and providing insights into how pathogens spread and evolve. The approach began with *Salmonella*, but in principle can support any organism sequenced with standard technologies such as *Klebsiella* and *Listeria*. The use case utilizes published workflows used in Slovak national surveillance, including pipelines for antimicrobial resistance, to demonstrate interoperability so others can plug in the workflows of their choice.

CONCLUSION. The development of Open Science infrastructure in Slovakia is gradually moving from policy frameworks towards practical services that support research collaboration, data sharing and the implementation of FAIR principles. The Slovak participation in the EOSC Federation represents an important step in this process, providing opportunities to connect national research infrastructures with a broader European ecosystem of data, computational resources and scientific services.

The use case presented in this paper demonstrates the potential of such infrastructure in the life sciences, particularly in pathogen genomics and antimicrobial resistance surveillance. Large-scale genomic analyses require substantial computational and storage capacities, harmonised workflows, high-quality metadata and mechanisms for the secure handling of sensitive data. The NarCoS platform and related activities provide a national basis for addressing these requirements, while integration into the EOSC Federation extends their potential beyond national boundaries.

The federated cooperation between the Slovak and Polish EOSC nodes illustrates a model in which computation can be brought to the data rather than requiring sensitive datasets to be transferred between institutions or countries. Harmonised analytical workflows, common metadata standards, persistent identifiers, authentication and authorisation mechanisms can enable interoperable analysis while supporting data sovereignty and compliance with legal and ethical requirements.

The presented approach also demonstrates that Open Science does not necessarily imply unrestricted access to all research data. Particularly in the life sciences, openness must be balanced with data protection, security and responsible access. Federated infrastructures can help reconcile these requirements by enabling collaboration and reuse while maintaining appropriate control over sensitive information.

Further development should focus on strengthening interoperability between national and European infrastructures, establishing trusted mechanisms for access to sensitive genomic data, expanding harmonised workflows and metadata standards, and involving additional data providers and public health authorities. Experience gained from the Slovak–Polish pilot may subsequently contribute to broader cross-border applications within the EOSC Federation.

The practical value of Open Science infrastructure therefore lies not only in making research outputs openly available, but also in creating trusted environments in which data, computational resources, tools and expertise can be shared and reused across institutional, disciplinary and national boundaries. In the field of pathogen genomics and AMR surveillance, such cooperation has the potential to improve cross-border surveillance and contribute to a better understanding of the spread and evolution of infectious pathogens.

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Турна Ян,

Словацький центр наукової та технічної інформації,
Братислава, Словаччина,
ORCID: 0000-0001-5813-566X, e-mail: jan.turna@cvtisr.sk

Гавурнікова Габрієла,

Словацький центр наукової та технічної інформації,
Братислава, Словаччина,
ORCID: 0000-0001-7096-6378, e-mail: gabriela.gavurnikova@cvtisr.sk

Зендулкова Даніца,

Словацький центр наукової та технічної інформації,
Братислава, Словаччина,
ORCID: 0000-0003-2487-0177, e-mail: danica.zendulkova@cvtisr.sk

Радвак Петер,

Словацький центр наукової та технічної інформації,
Братислава, Словаччина,
ORCID: 0000-0002-7421-3522, e-mail: peter.radvak@cvtisr.sk

Будіш Ярослав,

Словацький центр наукової та технічної інформації,
Братислава, Словаччина,
ORCID: 0000-0002-8667-6655, e-mail: jaroslav.budis@cvtisr.sk

ІНФРАСТРУКТУРА ВІДКРИТОЇ НАУКИ В СЛОВАЧЧИНІ ТА ЇЇ ВИКОРИСТАННЯ В НАУКАХ ПРО ЖИТТЯ

АНОТАЦІЯ. Інфраструктура відкритої науки надає дослідникам цифрові послуги, обчислювальні ресурси та середовища даних, що підтримують принципи FAIR та забезпечують ефективний обмін та повторне використання результатів досліджень. Представлено розвиток інфраструктури відкритої науки в Словаччині та демонструється її застосування в науках про життя через патогенну геноміку та спостереження за стійкістю до антимікробних препаратів (AMR). Особлива увага приділяється словацькому вузлу Європейської хмари відкритої науки (EOSC), біоінформатичній платформі NarCoS, та їхній ролі в обробці та аналізі великомасштабних наборів геномних даних. У статті описано федеративний підхід до транскордонної співпраці між словацьким та польським вузлами EOSC, за якого гармонізовані роботи

процеси дозволяють проводити аналіз, водночас зберігаючи конфіденційні дані під локальним контролем. Представлений приклад використання демонструє, як федеративна інфраструктура відкритої науки може підтримувати сумісний геномний аналіз, зміцнювати суверенітет даних та сприяти ефективнішому транскордонному спостереженню за інфекційними патогенами та стійкістю до антимікробних препаратів.

КЛЮЧОВІ СЛОВА: слова Інфраструктура відкритої науки, EOSC, Науки про життя, стійкість до антимікробних препаратів, NarCoS.