

# Annual Report 2025

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## Introduction

NBIS (National Bioinformatics Infrastructure Sweden) is a distributed national research infrastructure, hosted by Uppsala University. NBIS constitutes the SciLifeLab Bioinformatics Platform. NBIS is formed by 11 partners: Uppsala universitet (hosting NBIS), Chalmers tekniska högskola AB, Göteborgs universitet, Karolinska Institutet, Kungl. Tekniska högskolan, Linköpings universitet, Lunds universitet, Naturhistoriska riksmuseet, Stockholms universitet, Sveriges lantbruksuniversitet, and Umeå universitet.

Funding is provided from the Swedish Research Council (VR), Knut and Alice Wallenberg Foundation, Science for Life Laboratory (SciLifeLab), Swedish universities, and user fees. In addition, we have funding from EU, ELIXIR, NordForsk (NeIC), and Chan Zuckerberg Initiative (CZI).

NBIS expanded 1 Jan 2021 with the SciLifeLab BioImage Informatics Facility (BIIF) and the AIDA Data Hub in Linköping joining us. These are funded outside the VR grant 2021–2024 with resources from SciLifeLab and other sources.

## Vision and Mission

Enable world-class life science research and maximise scientific and societal impact of collected data by:

- Providing expert knowledge, innovative data integration, advanced training, efficient data publication for open science, and access to high-performance data analysis methods
- Coordinating bioinformatics support within Sweden and making bioinformatics easily accessible for life science researchers
- Swiftly responding to changes in support needs as new techniques are developed and utilised
- Forming the Swedish ELIXIR node and participating in relevant international projects

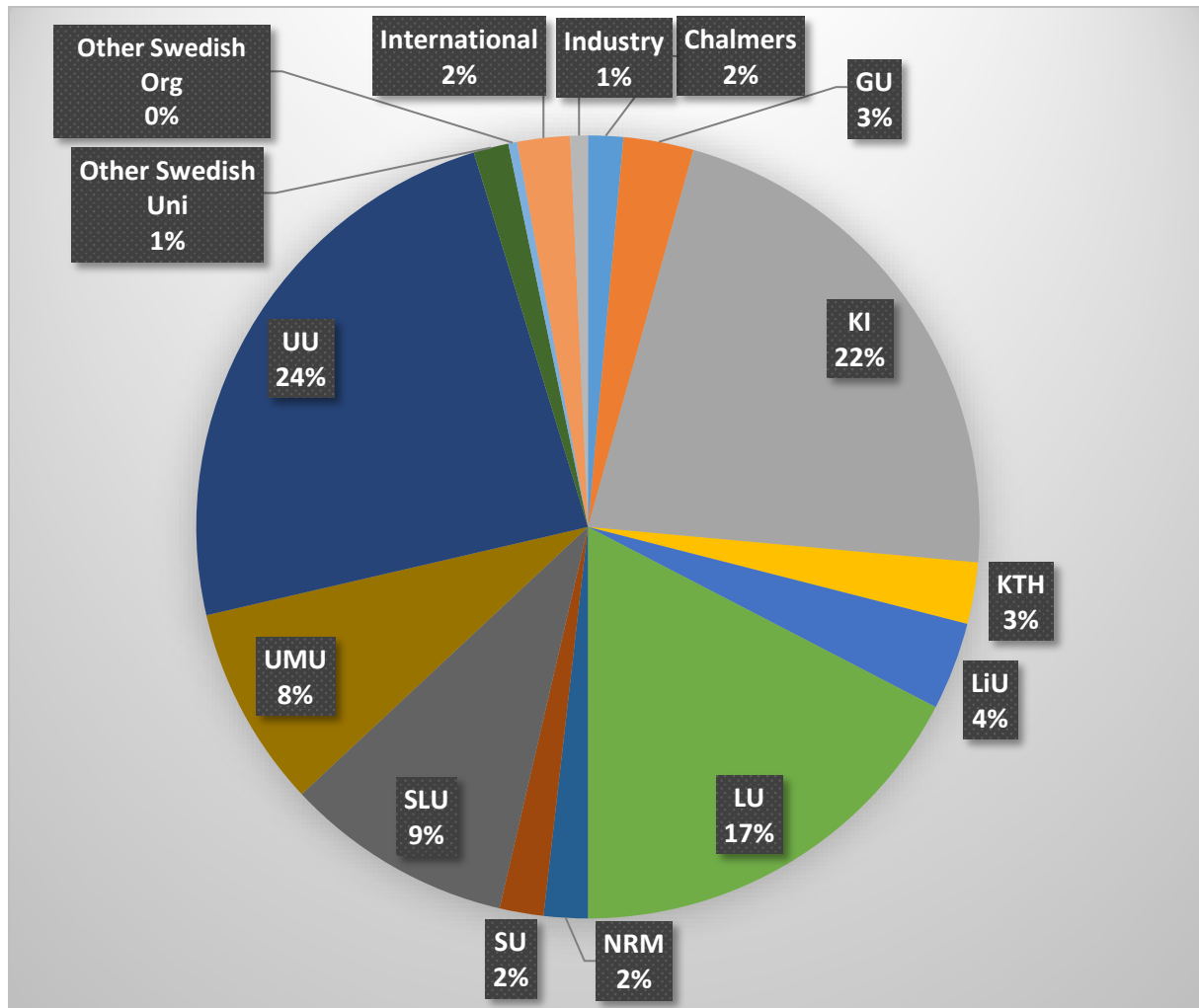
## Support

One of the major activities is support, where our staff helps researchers with bioinformatics tasks in various projects. Currently, NBIS provides expertise in many areas within bioinformatics: genome assembly, genome annotation, genetic variation, comparative genomics, phylogenomics, transcriptomics, proteomics, metabolomics, epigenomics, metagenomics, systems biology, single-cell/spatial biology, structural biology, biostatistics, machine learning and multi-omics integration.

In the current funding landscape, the universities need to contribute a substantial part of infrastructure funding, in proportion to the utilisation of NBIS by the respective university. This is reflected in the increased university contributions from 2018 and onwards. NBIS obtains user fees on direct project-related support, with the exception of the KAW-funded peer review support track (LTS; cf. below). It is not feasible to apply user fees on the infrastructure, outreach and training activities, staff education and project management.

NBIS serves users at all major universities. In 2025, NBIS provided support to **277 PIs** (106 female, 166 male, 5 no info), which is an increase by ~8% compared to 2024. The distribution of the supported PIs is shown in Figure 1. The top three universities using NBIS are as previously Uppsala University, Karolinska Institutet and Lund University. The total number of active support projects

were 333, and in addition to those NBIS has also provided 52 study design consultations, 11 data management projects and 6 partner projects. Number of active support projects have increased considerably during 2025 compared to previous years.



*Distribution of PIs that have received support during 2025*

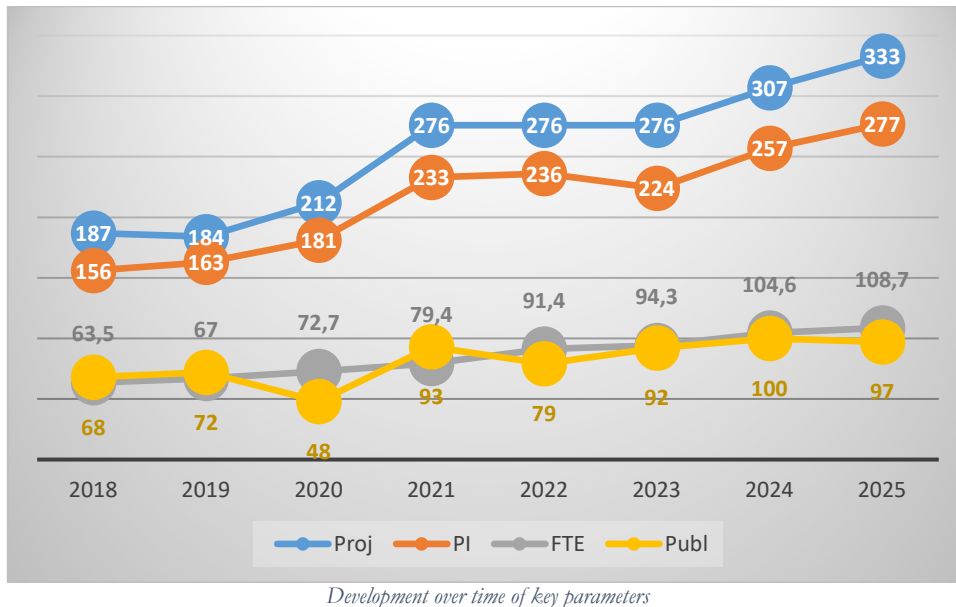
In 2025, our user fee support track had 184 active projects and our peer review support track had 99 active projects. In addition, the BioImage Informatics unit provided support and consultations to 44 projects, and the AIDA Data Hub unit has provided AI support in 6 projects. A wide variety of projects were supported, with no clear single category dominating. We rather see several methodology areas of equal importance, such as statistics, single-cell-RNA, assembly and annotation, pipeline development, metagenomics, proteomics, and more. This highlights the need to maintain a wide array of competences in the organisation. About half of all support is provided from one site to another, emphasising the importance of a national infrastructure. During 2025, we had six international projects in AI4Life, cf. below in the BioImage Informatics section.

Our weekly drop-in sessions plus on-site drop-in in Stockholm, Göteborg and Lund are very popular. A survey shows that 99.9% of the users would recommend this service to a colleague (837 accumulated responses).

Analysed data were from a range of sequencing-based methods, and also other large-scale data, such as proteomics, metabolomics and cell imaging. Projects including single-cell RNA sequencing (scRNA-seq) and metagenomic data remain in high demand of support, while emerging areas

include pipeline development, multiple novel spatial omics technologies, cell image analysis, and protein structure prediction methods.

Below is a diagram showing how development has been since 2018 regarding number of projects, number of unique PIs, number of FTEs in NBIS, and number of publications. We see a clear increase over the years in all parameters.



### Examples of important achievements from NBIS support projects

**Low-Dose Aspirin for PI3K-Altered Colorectal Cancer (CRC):** The Phase III ALASCCA randomized clinical trial aided researchers in validating a common, inexpensive drug as a potent, targeted precision therapy for cancer. Published in *The New England Journal of Medicine (NEJM)*, the study demonstrated that low-dose daily aspirin reduced the cancer recurrence risk by approximately 50% in Stage I–III CRC patients whose tumours harbour specific PI3K pathway mutations. This work confirms the potential of using widely available therapeutics as a precision strategy, set to immediately impact clinical guidelines and improve patient outcomes globally. <https://doi.org/10.1056/NEJMoa2504650>

**Early Germline Sequestration in a Basidiomycete Fungus:** Published in *Science*, this study on the fairy ring fungus *Marasmius oreades* challenged the assumption of late germline definition in fungi. Using whole-genome sequencing over seven years, researchers found that the spore-producing germline is sequestered early in the mycelium. This key finding showed that the germline accumulates significantly fewer mutations than sterile (non-spore-producing) tissues, suggesting that early germline sequestration, a fundamental mechanism for protecting genetic fidelity, is more prevalent across multicellular life. <https://www.science.org/doi/10.1126/science.adu8580>

**Genome Analyses Suggest Recent Speciation and Postglacial Isolation in the Norwegian Lemming:** Published in *PNAS*, this study provided a high-quality genome assembly and resequencing data for the Norwegian lemming (*Lemmus lemmus*). The analysis showed that the species diverged from its sister taxon, the Western Siberian lemming, shortly before the Last Glacial Maximum, confirming it as one of the youngest known mammalian species. Crucially, the absence of gene flow suggests the two species remained fully isolated after the last glaciers, contrasting with many recently diverged mammalian taxa. <https://doi.org/10.1073/pnas.2424333122>

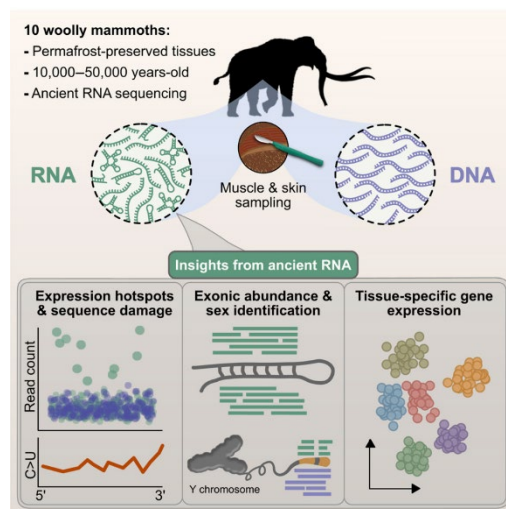
**Identification of proliferating neural progenitors in the adult human hippocampus:**

Published in *Science*, this study resolved a long-standing debate using single-nucleus RNA sequencing to analyze the human hippocampus across the lifespan. Researchers conclusively identified proliferating neural progenitor cells in the dentate gyrus of adult brains. This key finding confirms that neurogenesis is an ongoing process in humans well into late adulthood, contributing to the understanding of brain plasticity and informing future regenerative therapies. <https://www.science.org/doi/10.1126/science.adu9575>

**MSP-tracker:** A powerful new AI-based tool developed to significantly improve Multiple Sclerosis (MS) diagnostics. This machine learning model, trained on over 22,000 patient records, accurately identifies the crucial transition to secondary progressive MS. The tool achieves ~90% accuracy and provides diagnosis earlier than standard clinical methods, allowing for timely treatment adjustments. Developed with support from SciLifeLab NBIS and resources from the SciLifeLab Data Centre, the model is openly available on the SciLifeLab Serve platform for research use. <https://github.com/caramba-uu/MSP-tracker> <https://doi.org/10.1038/s41746-025-01616-z>

**Ancient RNA expression profiles from the extinct woolly mammoth:**

Published in *Cell* (2026), this study reports the first tissue-specific transcriptional profiles from Late Pleistocene woolly mammoths, using RNA sequenced from permafrost-preserved skin and muscle. Researchers recovered hundreds of protein-coding transcripts and numerous microRNAs related to muscle metabolism and contraction, with expression patterns consistent with slow-twitch muscle function. The work demonstrates that RNA can persist in permafrost for tens of thousands of years and establishes a methodological framework for “paleotranscriptomics,” enabling integrative paleo-studies that combine genomics, proteomics and transcriptomics to investigate the biology and adaptations of extinct species. <https://doi.org/10.1016/j.cell.2025.10.025>



**Precise mapping of single-stranded DNA breaks by sequence-templated erroneous DNA polymerase end-labelling:**

Published in *Nature Communications*, this study introduces a sequencing-based method to map single-stranded DNA breaks genome-wide at high resolution. Using a designed DNA polymerase reaction that incorporates erroneous nucleotides at break ends in a sequence-templated manner, the authors create a distinctive molecular signature that can be captured and read out by next-generation sequencing. This approach enables precise localization and characterization of endogenous and induced DNA nicking events, providing new insights into DNA damage patterns, repair pathway usage, and the cellular responses to genotoxic stress. <https://doi.org/10.1038/s41467-025-62512-4>

**Optimizing Xenium In Situ data utility by quality assessment and best-practice analysis workflows:**

Published in *Nature Methods*, this study benchmarks Xenium spatial transcriptomics across 25 datasets from multiple tissues and species, evaluating cell segmentation, normalization and analysis tools. The authors systematically benchmark cell-segmentation strategies, preprocessing pipelines and tools for spatially variable gene and domain detection, showing that segmentation choices and normalization/scaling parameters strongly influence clustering and downstream biological interpretation. From these analyses, they derive a recommended end-to-end workflow—including Baysor-based segmentation with Xenium nuclei priors, library-size

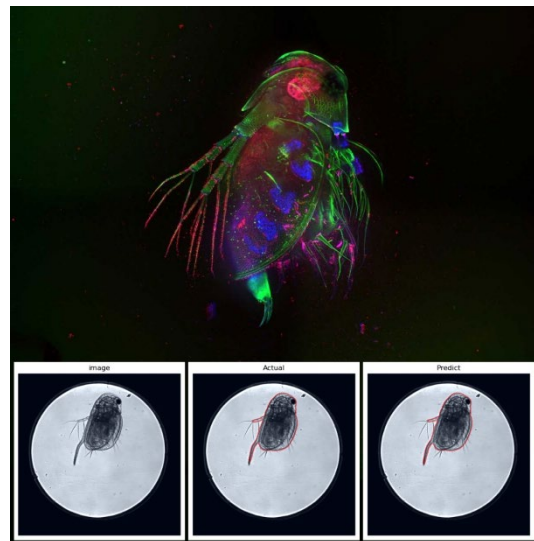
normalization and graph-based clustering—that maximizes data quality and reproducibility, offering practical guidelines for researchers to extract robust biological insights from Xenium experiments. <https://doi.org/10.1038/s41592-025-02617-2>

**Biodiversity Genomics Europe (BGE)** The Evolution and Biodiversity support team has in the last year assembled the genomic sequence of 26 European eukaryote species in the BGE-project, corresponding to a genome size of 39 GB (~13 human genomes). The species represent very diverse organism groups, including insects, birds, fungi, spiders, and mammals. All are selected from biodiversity hotspots or for being of specific interest to researchers in Europe, and many are considered threatened. These genomes constitute an essential resource in the further studies of these species and will directly underlie decisions on conservation. <https://biodiversitygenomics.eu/>

## BioImage Informatics

The Bioimage Informatics team (BIIF) provides expertise and open-source solutions for image analysis in the life science field. The field of bioimage analysis is rapidly evolving in terms of AI usage, increasing complexity of the analysis needed, as well as increasing needs of compute resources and image data sizes. In 2025, BIIF implemented deep Learning-based and AI-models for image analysis, e.g. we handled user projects involving LLMs for the analysis of hand-written slide labels and deep learning based segmentation. BIIF also continued contributing to the EU-funded AI4Life project. For delivery of the pipelines to life scientists, the field moves increasingly to the use of pipelines on HPC. BIIF contributed to the development of a nextflow analysis pipeline for in-situ-sequencing data. Increasing image data sizes lead to the community-driven development of the new file format, OME-Zarr. A member of BIIF is an active contributor to this development. Nextflow and OME-Zarr were among the topics covered by the EMBO practical course “Advanced Methods for Bioimage Analysis”, co-organized by BIIF, which ran during September. The course was very well received, with 180 applicants on 26 spots. BIIF is currently further developing the TissUUmapper viewer (<https://tissuumaps.github.io/>), and supports researchers in making their spatial omics data visualized within TissUUmapper on the SciLifeLab serve platform (see for example

<https://hdca-spinalbrain.serve.scilifelab.se/web/index.html>)



The AI4Life projects (<https://ai4life.eurobioimaging.eu/>) aims to democratise the availability of AI-based image analysis methods to life scientists. The BioImage Informatics team contributed to “Open call” of the AI4Life project. In one project, the provided support allowed AI-based identification of wood in tree rings and with that to describe the wood quality of trees in the Boubín Forest nature reserve, the largest indigenous forest in Central Europe (<https://biifsweden.github.io/projects/2025/05/05/8202/>). In another project, the provided support allowed the identification of nuclear pore complexes in super-resolution microscopy images (<https://biifsweden.github.io/projects/2025/05/05/8203/>).

*Development of an image-based analysis method for studying toxicological effects in *Daphnia magna*.* BIIF built a GUI that allows deep-learning based segmentation of the body and head of the daphnia. More information on <https://biifsweden.github.io/projects/2024/11/06/OskarKarlsson2024-1/>

NBIS has a total of **97 publications** in 2025 from our direct project support work (excluding Compute & Storage), listed in the Annex. A few achievements are shortly highlighted here.

## User Fees

NBIS has five support tracks:

- Study Design Consultation ( $\leq 3$ h)
- User Fee Support (SMS)
- Partner Projects (PP, part of SMS)
- Peer Review Support (LTS)
- BioImage Informatics (BIIF)

For User Fee Support, PP and BIIF, NBIS charges user fees, while Peer Review Support is provided for free according to the funding requirements by the Knut and Alice Wallenberg foundation. In 2025, the income from user fees was 18.3 MSEK, thus a substantial increase compared with 2024.

## Data Management and Open Science Support

During 2025, the Data management unit consisted of ten data stewards and two managers (totalling 10 FTEs during 2025).

NBIS has continued its mission to provide data management support and training, in collaboration with key national and international stakeholders to enable Swedish life science researchers to apply good data management practices so that the research outputs produced are available to the global research community, and to society at large, according to the principles of Open Science, Reproducible Research, and FAIR (Findable, Accessible, Interoperable, Reusable). A continuously updated strategy for the Data management unit operations and activities going forward, is published at <https://doi.org/10.17044/scilifelab.27604476>.

On the support side, we have continued providing Data Management Planning (DMP) support, as well as FAIRification and data publication support to research projects. A large focus has been put on submission of genome sequence data to support the international evolution and biodiversity efforts that NBIS and NGI are engaged in. Together with the SciLifeLab Data Centre, activities have been focused on developing and improving tools functionality for data management, such as the Data Stewardship Wizard for DMPs. Throughout 2025, NBIS has further advanced Sweden's national infrastructure and expertise for the secure management of sensitive human data. Following the successful launch of FEGA Sweden, the national repository has matured operationally, with several universities entering data. During this period, the repository also initiated its first two access requests, which are currently being processed for completion in early 2026. To help scale and broaden the reach of this infrastructure, two additional universities reached the final stages of the formal onboarding procedure by the end of 2025. These institutions are now positioned to begin their first pilot submissions in early 2026. In October, strategic knowledge exchange was enhanced during an interactive full-day meeting between the FEGA Sweden Helpdesk and Australian BioCommons in connection with the GA4GH conference in Uppsala. Our international

collaborations around sensitive human data have also advanced through the European Genomic Data Infrastructure (GDI) and Genome of Europe (GoE) projects. During the year, increased technical maturity enabled deeper synergy between these two initiatives, allowing us to successfully reach all milestones for the tasks we lead in GoE and deliver data demonstrating GDI's capabilities. Notably, NBIS coordinated the FitSM (federated IT service management) planning within GDI to enable coherent service management across participating countries. This included organizing two FitSM foundation training sessions for node representatives, with a follow-up workshop scheduled for January 2026. Continued contributions have also been made to TEHDAS2, an EU project focused on shaping the European Health Data Space.

On the training side, we have continued to provide the course on Introduction to Data Management practices. During the fall we did this in collaboration with the [Graduate Research School in Integrative Biology](#) in Lund. It was also delivered to the DDLS Research School students as an integral part of the course Principles and tools for FAIR research practices. By collaborating with research schools, we can more efficiently reach researchers early in their careers, which is a prioritized target group for RDM training. A large number of outreach events have also been performed, nationally and internationally, among them two-day RDM Roadshow events at the Linköping and Gothenburg SciLifeLab sites in collaboration with the SciLifeLab Data Centre and local data management staff at the sites. During 2025 NBIS Data management has together with the SciLifeLab Data Centre and the SciLifeLab Training Hub established a forum regarding the coordination of Open Science activities across the whole of SciLifeLab. The regular online seminar series (now named the [SciLifeLab Open Science seminar series](#)) arranged together with the Data Centre and Training Hub has grown in number of seminars and participants. Together we have also delivered a course in collaboration with Swedish National Data Service (SND) on the topic of Open Science in the Swedish context. Together with the SciLifeLab Data Centre we have also continued to develop and improve the joint support portal and guideline knowledge-base for research data management for Swedish life science (<https://data.guidelines.scilifelab.se/>). The Data management unit has also been involved in coordinating and contributing to the SciLifeLab Integrated Data Services (IDS) initiated consultation meetings for multimodal research projects.

In the European landscape, NBIS has continued to lead the activities of the ELIXIR Research Data Management Community, which functions as a pan-European competence network for research data management in the life sciences with over 250 RDM professionals in over 20 participating national nodes. This competence community has a focus on knowledge sharing, capacity building, and training for data management. During 2025, the two year DATAREX project was concluded, where NBIS was a key contributor to the establishment of a [Handbook and a Maturity model](#) for Data management service providing professionals and organisations. NBIS has also continued to lead activities in ELIXIR's Scientific Programme 2024–2028, including ELIXIR's Data and Interoperability Platforms and the ELIXIR-STEERS project, while aligning with relevant activities at SciLifeLab. In broader international collaborations, the data management team has continued its contributions as a voice for life science data infrastructure in EOSC. Notably, stepping forward to lead a newly formed subgroup of EOSC Association's Health Data Task Force and establishing a new shared leadership structure for the EOSC Opportunity Area Expert Group on Metadata, Ontologies and Interoperability to focus on supporting interactions with the EOSC Federation and solutions for thematic research use cases. The team has also continued its commitments in the Research Data Alliance (RDA) Life Science Data Infrastructures Interest Group, RDA's Technical Advisory Board, and ELIXIR's global RDA collaboration. Here, taking initiative to organise joint workshops with the Global Alliance for Genomics and Health (GA4GH), Euro-BioImaging, BioFAIR-UK, GO-FAIR Foundation, World Data Systems (WDS) and CODATA to promote global alignment and continued collaboration with national and European initiatives.

## Human Genomics Data

The human data team enables qualified Swedish users to make available and access large quantities of high-quality omics data to the benefit of research, healthcare, and the society.

This is achieved by building and operating technical infrastructure supporting the storage and access and by providing professional data steward support, often in collaboration with Swedish authorities and international research infrastructures, including SoS, E-hälsomyndigheten, Genomic Medicine Sweden, and ELIXIR. The work within Human data is performed by staff in the data management and systems development teams.

The Swedish node of the Federated European Genome-phenome Archive (FEGA Sweden), <https://fega.nbis.se/>, is an NBIS service for making biomedical research data available for research. The software is a result of our long-standing collaborative development with the Nordic ELIXIR Nodes, EMBL-EBI and CRG (Centre for Genomic Regulation (Spain), through the NeIC Tryggve and NeIC Heilsa Tryggvedottir projects. It has been in operation since 2022. During 2025, agreements were established with several universities about the governance model for FEGA users to access data from them, making it possible to submit and re-use datasets from these universities in a harmonised manner. As such, the number of datasets submitted is increasing.

To support the **European 1+Million Genomes Initiative** (1+MG), EU funding has been obtained for related projects. In 2025, NBIS has been engaged in all three current projects. The largest effort is in the implementation project **GDI** (Genomic Data Infrastructure), having a total budget of 40 MEUR for Nov 2022 – Jan 2027. Furthermore, B1MGplus aims to prepare the legal framework and increase contacts with clinicians during 2025–2027 and here NBIS also collaborates with GMS (Genomic Medicine Sweden). Finally, we are part of Genome of Europe (GoE) during 2024–2028, the most extensive EU-funded programme on population genomics to date.

NBIS works for the establishment of a Genome EDIC (European Digital Infrastructure Consortium) as the legal body for the 1+MG and has the governmental mandate to represent Sweden in the negotiations.

A major part of the GDI project is construction of the human genomic data infrastructure, led by NBIS as ELIXIR-SE together with ELIXIR-FI, building on experience from B1MG and FEGA. Focus this year has been on defining the scope of the work of the last year of the project. For example, NBIS has organised an on-site technical workshop for preparing for collaboration between GDI and Genome of Europe, and identifying the Maximum attainable product during the GDI time period. This workshop engaged more than 100 European project members.



*GDI workshop in Paris*

**Genome of Europe (GoE)**, was officially launched in October 2024 and will provide a unique data resource for the Life Science community. 27 countries join forces to establish a unique pan-European reference database containing 100,000 genomes representative of European citizens. This will deepen our understanding of variations in the human genome and be of benefit for personalised health care and research. NBIS is leading the international work on developing submission tracks to feed the data into the European Genomic Data Infrastructure (GDI), and the NBIS data stewards will collaborate with NGI, who coordinates the Swedish data generation.

**Bigpicture** is a European flagship project for establishing a Petabyte platform for digital pathology AI, engaging partners from academia, healthcare and industry. The Bigpicture platform is now receiving contributions from the pharmaceutical industry partners, on track to reach the end goal of storing 3 million digital pathology slides, which will amount to 4.5 Petabytes. We are utilising the same technologies as used in the Federated EGA (and GDI) setup, demonstrating the versatility of the underlying software we developed, that it can be repurposed for several data sharing applications across research fields.

**EUCAIM** is a 4-year 36 MEUR EU project started in 2023 in order to build a European cancer image federation similar to GDI. From NBIS, human genomic data staff from the systems development unit and the AIDA Data Hub are involved. One focus is interoperability with GDI.

## Human Protein Atlas (HPA)

In November a new version 25 of the open-access Human Protein Atlas (HPA) resource was published at the HUPO World Congress in Toronto. The updated Atlas expands the Blood resource to contain pan-disease blood profiling data for in total 71 diseases, including Olink Explore HT and SomaScan data across 32 cohorts. The addition of new tissues resulted in the Single cell resource now comprising 154 different cell types, thus representing the majority of the cell types found in the human body. Predicted structures for 23000 protein-protein interactions was also introduced.



*Human Protein Atlas team*

A lot of focus has been around the development of AI, and in May the HPA director Mathias Uhlen was interviewed in GenomeWeb regarding the new Alpha Cell project, an effort funded by the Knut and Alice Wallenberg Foundation with the aim to combine AI and existing data to generate three-dimensional cell models to map and track cellular components and processes over time.

During 2025 HPA reached 1000 published peer-reviewed articles including "A human pan-disease blood atlas of the circulating proteome" in Science, "Intrinsic heterogeneity of primary cilia revealed through spatial proteomics." in Cell, "Multimodal cell maps as a foundation for structural and functional genomics." in Nature, and "Single-cell spatial transcriptomic atlas of the whole mouse brain" in Neuron.

We are grateful for all feedback from the scientific community and for the continuously growing interest in the Human Protein Atlas reflected by the around 500 000 monthly visits and the about 3000 publications citing us last year.

## Computational Infrastructure

A fundamental part of NBIS is the formation of a sustainable compute infrastructure for life sciences, consisting of access to tools and data. The infrastructure is typically constructed as domain-specific supporting layers utilising resources from the national e-infrastructure providers NAISS and SUNET. Our computational and storage needs are set up in close collaboration with these infrastructures, in order to avoid duplication of efforts and to benefit from the competences within NAISS and SUNET.

### Computational Resources

The AIDA Data Hub provides a Data Science Platform (DSP) based on Bigpicture / GDI technologies such as SDA, REMS, Beacon network, and Life Science Login. These technologies,

originally developed for genetics and extended in Bigpicture to support also pathology, will thereby be further extended to also support use cases in radiology using for example Grand-Challenge.org software components, and open standards health data using OpenEHR (ASHA). The original AIDA Data Hub Sensitive Data Services are tailored to suit the needs of leading-edge national expert AI researchers. However, the plans for DSP include feature additions to make the service more usable by further user competence profiles (such as clinicians) and other usage patterns (such as through a locked-down EHDS conformant remote desktop, or project private SaaS web applications like an open-source or Sectra PACS).

## **Computational Support**

Almost all areas of life science depend on high-performance computers for bioinformatics in some form. Much of the hardware is provided by NAISS, at a national level, but there are also some smaller or regional systems not managed by them. Making best use of these resources can be a daunting thing for many researchers, especially in areas without traditional connections to high performance computing. However, it is also daunting for a traditional HPC centre to have all these new users and softwares with vastly different requirements and demands to cater for.

Thanks to SCoRe, over 1300 bioinformatics-related software packages are installed and maintained on NAISS compute clusters Dardel at ParallellDatorCentrum (PDC, Royal Institute of Technology) and, for sensitive data, Bianca at UPPMAX, Uppsala University. Support for Computational Resources also administers resource allocations and participates in help-desk support at the major national compute clusters, handling 2637 omics research projects with 1086 unique PIs in 2025.

During 2025, NBIS has formed a closer collaboration with other support providers within NAISS and other infrastructures, including work on documentation, user training, and software provisioning. This promising start will be expanded upon in the coming year, notably through the tighter integration of PReSTO. The software environment at UPPMAX has largely been converted into a system that will make it more portable to new systems, such as the upcoming Arrhenius and Arrhenius SENS systems, which will replace Dardel.



*S-CoRe and invited guests from the bioinformatics IT Support community met in March 2025 to discuss coordination and cooperation between all sites that provide HPC resources for bioinformatics, and plan to continue to do so at least annually.*

## Systems Development & Tools

The systems development team at NBIS is dedicated to supporting the life science community by deploying tools and facilitating large scale analyses. They develop custom-made tools for researchers and user-friendly pipelines for stable and efficient analysis. The team works towards promoting reproducible research through the deployment of stable workflow systems and compute environments. They follow the scrum methodology in managing both internal and external projects and aim to make cutting-edge bioinformatics accessible to all.

The combination of bioinformatics experts, who can appraise the scientific value and usefulness of tools, with developers who have the capability of making tools stable and accessible, allows us to develop projects for the scientific community in a better way, since we can understand the needs of the user and provide our unique set of knowledge to help them. The development team also assists in internal development projects, *e.g.* for integrating data services with other initiatives. Furthermore, the team is active in the Global Alliance for Genomic and Health (GA4GH), working with technical standards and frameworks. The system development teams also serve NBIS infrastructure internally.

NBIS maintains a software repository for internal purposes and also public repositories for programs and scripts that are developed by our staff in order to get them to spread to the scientific community. For the latter, we have an organisational account on GitHub. We are also in charge of registration of relevant tools developed by Swedish research groups into the ELIXIR Tools

Registry. Apart from the work described under Human Data, we list a number of resources developed by NBIS.

**PLUPP** – the collaboration between NBIS and the Swedish Museum of Natural History (NRM) is continuing to create a single, comprehensive platform for pollen data. The new Open Pollen API (<https://api.pollenrapporten.se/docs>) developed during 2023 was published in early 2024. Enhanced with new functionality, we have seen it being frequently used by third-party developers during 2024's pollen season. The API enables its users to incorporate real-time pollen forecasts into a wide range of applications, national media among them, making a big impact for allergic people and other interested users all over the country. PLUPP's advanced pollen prognosis system is currently also being incorporated into NRM's newly relaunched website to make it even more accessible for the broad public. This work also includes enhancements to the pollen level graphs. During 2024, the pollen prognosis system had 190 000 unique users.

**Bird Ringing** – another collaboration between NBIS and NRM was initiated during 2025, where the systems development unit is building a new system for the Bird Ringing centre. The initial work concerns the distribution of bird ringing licenses and permits. The plan for this collaboration is to continue during the next years, with ultimate goal the modernization of the IT systems used by the Bird Ringing centre, by creating a platform that would serve as a template for similar organisations even outside of Sweden.

**RDA-GORC-IM** – The systems development team worked on the visualisation of the Research Data Alliance (RDA) Global Open Research Commons (GORC) International Model (IM), a collection of attributes that allow Commons developers to compare features across science clouds and commons. The team worked on an interactive web-based tool that allows navigation of the GORC (IM), including its profiles, slices, and other associated deliverables. It supports dynamic content updates from the GORC II Working Group (WG) and provide advanced capabilities for knowledge graph visualisations.

NBIS is also developing a range of tools and workflows for other data types. For example, our workflows for metabolomics and metagenomics are openly available and have been applied in many projects (see <https://www.nbis.se/about/resources/tools>).

The AIDA Data Hub provides compute services for AI research on sensitive personal data in diagnostic imaging. Among many resulting publications, one example is an effort on self-supervised learning for pathology. Moreover, the infrastructure is providing policy support and other guidance for the domain. Current developments include plans to be a strategic collaborator to the SCAPIS project for data sharing of their unique imaging data collections.

The AIDA Data Hub has supported a Region Skåne led AIDA project aiming at constructing a database facilitating AI research and innovation in mammography. This collaboration served as one of the cornerstones for the AIDA led and VINNOVA funded incubator for validation environments for clinical imaging diagnostic AI (VAI), where AI providers can install tools that national healthcare providers can then evaluate in private using real clinical data. The VAI-B mammography environment is in production, and working to transition to sustainable operations mode, potentially as a national quality register.

AIDA Data Hub has also supported a Region Skåne led AIDA project aiming to develop and evaluate an AI algorithm for automatic identification of gold fiducial markers in an MRI-only prostate radiotherapy workflow. In an extension to this project, Region Skåne transitioned to an

MRI-only workflow in its clinical practice for prostate radiotherapy, obviating the need for complementary CT-scans and reducing the time and complexity of the clinical workflow.

AIDA Data Hub has provided secure storage and GPU processing to a LiU-led AIDA project aiming to develop AI algorithms for automatic time-resolved cardiovascular segmentation of 4d flow MRI. This project is ongoing, and is currently receiving AI development support from the AIDA Data Hub, where initial results using 2D Generative Adversarial Networks are promising and were accepted to ISMRM 2024.

## Advanced Training

Training is a core pillar of NBIS, reflecting the breadth and depth of bioinformatics and data science expertise within our staff. Beyond individual training integrated into the majority of our project-related support, empowering researchers to effectively utilize new tools and enhance their existing skills, NBIS leverages its unique concentration of expertise to deliver cutting-edge advanced training. This positions NBIS at the forefront of bioinformatics training in Sweden, supporting life-wide learning within the life sciences. Training activities, engaging the majority of NBIS staff, comprise approximately 12% of our overall effort. This encompasses our own NBIS training program, collaborative training ventures (e.g. supporting the SciLifeLab/KAW-funded DDLS program and the AIDA community), and contributions as invited lecturers and speakers at external training events. Furthermore, NBIS extends its training impact internationally, actively participating in initiatives like ELIXIR. These international efforts involve not only delivering training but also developing frameworks and guidelines for educators and learners alike, promoting FAIR and Open training practices within the broader life science research infrastructure.

In 2025, NBIS regularly delivered training events on-site, online and in a multi-site hybrid format, where there are on-site classrooms with teaching assistants present at several locations which are virtually connected. During this year, the multi-site hybrid format has been refined and lectures are now streamed from each site in a rotating manner. This hybrid model has proven highly effective in expanding the reach and accessibility of our training programs and it also reduces the carbon footprint since it requires less travelling.

Beyond our traditional multi-day courses, we provide shorter 1–2 hour workshops focused on specific topics designed to address the growing demand for targeted training as well as recorded webinars which also enhances accessibility and creates opportunities for on-demand training.

Our training catalogue caters to graduate students, post-docs, researchers and staff scientists while also welcoming participants from the non-academic sector. We organised 2 new courses this year; *Machine Learning for life sciences* and *Hands On Course in Epigenomics*, the latter organised in collaboration with National Genomics Infrastructure (NGI). This collaboration allowed us to combine wet-lab experiments to produce data and bioinformatics analysis on the data produced in the same course. Further, we have established a collaboration with the DDLS Research School and delivered one of the first curriculum courses *Principles and tools for FAIR research practices*. This course will be recurring annually and we will extend our contributions to the Research school with the course *Machine Learning for life sciences* in 2026.

In total, NBIS held 54 training events, comprising 16 courses within the NBIS training program, 8 workshops and 30 collaborative efforts (see table below). Across all these training activities in 2025, we had 997 participants. Specifically within the NBIS training program, we saw 353 participants with a 72% acceptance rate. Gender distribution among accepted participants was nearly equal,

with 54% female representation. In addition NBIS staff were invited to 23 additional training events with 618 participants.

The PhD advisory mentor programme in bioinformatics is a long-term initiative in NBIS with an increasing demand and is highly appreciated in the life science community. PhD students get bioinformatics mentorship guidance from NBIS experts over a period of 2 years.

Course	From date	To date	Location	Participants
<b>NBIS Training Programme (16 events, 353 participants)</b>				
<b>Introduction to Bioinformatics Using NGS Data</b>	2025-03-24	2025-03-28	online	42
<b>Single Cell RNASeq Data Analysis</b>	2025-03-31	2025-04-03	online	30
<b>Introduction to Data Management Practices</b>	2025-04-01	2025-04-03	Stockholm	13
<b>Introduction to Biostatistics and Machine Learning</b>	2025-04-07	2025-04-11	Uppsala	17
<b>Programming Formalisms</b>	2025-05-05	2025-05-09	online	7
<b>Open Science in the Swedish context</b>	2025-05-05	2025-05-09	Stockholm	20
<b>Advanced Data Visualization</b>	2025-05-13	2025-05-15	Lund	15
<b>RaukR - R Beyond the Basics</b>	2025-06-08	2025-06-19	Visby	27
<b>Machine Learning for life sciences</b>	2025-06-09	2025-06-13	Uppsala	25
<b>Introduction to Data Management Practices</b>	2025-09-09	2025-09-11	Lund	27
<b>Population Genomics in Practice</b>	2025-09-15	2025-09-19	Uppsala	22
<b>Epigenomics Data Analysis: from Bulk to Single Cell</b>	2025-09-22	2025-09-26	online	27
<b>Programming Formalisms</b>	2025-10-23	2025-10-29	online	6
<b>Introduction to Bioinformatics Using NGS Data</b>	2025-11-17	2025-11-21	Uppsala	16
<b>Python Programming with applications to bioinformatics</b>	2025-11-24	2025-11-28	Uppsala/Umeå/Lund	32
<b>R Programming Foundations for Data Analysis</b>	2025-12-01	2025-12-05	Uppsala, Umeå	27
<b>Workshops organised by NBIS (8 events, 188 participants)</b>				
<b>AIDA days technical workshop federated machine learning</b>	2025-09-16	2025-09-16	online	21
<b>AIDA days technical workshop on distributed training with Ray</b>	2025-02-05	2025-02-05	online	14
<b>AIDA days technical workshop on generative AI</b>	2025-02-06	2025-02-06	online	15
<b>DMP workshop for research infrastructure units</b>	2025-03-14	2025-03-14	Lund	18
<b>RDM roadshow Workshop on Data Management Plans</b>	2025-04-24	2025-04-24	Linköping	25
<b>RDM roadshow Workshop on Data submission to public repositories</b>	2025-05-21	2025-05-21	Göteborg	35
<b>RDM roadshow Workshop on GDPR for life science research</b>	2025-05-21	2025-05-21	Göteborg	35
<b>RDM roadshow Workshop on Working with human data</b>	2025-04-24	2025-04-24	Linköping	25
<b>AIDA days technical workshop federated machine learning</b>	2025-09-16	2025-09-16	online	21

Co-organised training events (30 events, 456 participants)				
Advanced Data Visualization	2025-06-16	2025-06-17	online	8
AI Course for Radiologists and Pathologists	2025-05-15	2025-05-15	Linköping	20
AIDA days technical workshop MAIA collaborative platform	2025-09-17	2025-09-17	online	24
Awk workshop	2025-01-16	2025-01-17	online	19
Awk workshop	2025-08-28	2025-08-29	Uppsala	4
Best Practices in Reference Genome Generation workshop	2025-05-13	2025-05-13	Uppsala	74
Bianca workshop, basic	2025-09-15	2025-09-15	online	10
Bianca workshop, basic	2025-03-19	2025-03-19	online	10
Bianca workshop, intermediate	2025-05-23	2025-05-23	online	10
Command Line 201	2025-06-02	2025-06-03	online	10
EMBO practical course Advanced Methods in BioImage Analysis	2025-09-14	2025-09-19	Heidelberg, Germany	26
Hands On Course in Epigenomics	2025-11-10	2025-11-14	Uppsala	8
HPC Python, day 1	2025-10-14	2025-10-14	online	10
HPC Python, day 1	2025-04-24	2025-04-24	online	10
HPC Python, day 1	2025-03-04	2025-03-04	online	10
HPC Python, day 2	2025-04-25	2025-04-25	online	10
Image Analysis, Bioimaging and Cell Analysis	2025-09-09	2025-09-10	Uppsala	30
Intro to UPPMAX	2025-10-15	2025-10-15	online	10
Intro to UPPMAX	2025-08-25	2025-08-25	online	10
Intro to UPPMAX	2025-02-10	2025-02-10	online	10
Principles and tools for FAIR research practices (DDL Research school)	2025-09-24	2025-10-23	Stockholm, online	32
R, MATLAB and Julia in HPC, advanced day	2025-10-10	2025-10-10	online	1
R, MATLAB and Julia in HPC, R day	2025-10-06	2025-10-06	online	10
R, MATLAB and Julia in HPC, R day	2025-03-24	2025-03-24	online	10
Spatial omics data analysis course	2025-01-21	2025-01-24	Lausanne, Switzerland	31
Training Materials made FAIR by design	2025-10-21	2025-10-22	Ghent, Belgium	9
Transferring files to/from HPC Clusters	2025-11-14	2025-11-14	online	10
Transferring files to/from HPC Clusters	2025-09-05	2025-09-05	online	10
Transferring files to/from HPC Clusters	2025-05-16	2025-05-16	online	10
Transferring files to/from HPC Clusters	2025-03-07	2025-11-14	online	10
Invited lectures/University courses (23 events, 618 participants)				
14th NorMIC Imaging Workshop	2025-11-27	2025-11-27	Oslo, Norway	30
Advanced bioinformatics	2025-09-01	2025-10-30	Linköping	33
AI tools in biology: AI and BioImage Analysis	2025-02-19	2025-02-19	Uppsala, Sweden	30
Bioinformatics	2025-04-14	2025-04-14	Uppsala	15
Bioinformatics	2025-09-01	2025-10-30	Linköping	58

<b>Bioinformatics and Sequence Analysis</b>	2025-09-01	2025-09-25	Lund	26
<b>Clinical research school in molecular medicine</b>	2025-03-31	2025-03-31	Stockholm	20
<b>Deep Learning for Image Analysis</b>	2025-05-08	2025-05-08	online	20
<b>Genome Analysis</b>	2025-05-21	2025-05-21	Uppsala	40
<b>Genome Analysis</b>	2025-03-24	2025-03-24	Uppsala	40
<b>Genomic and Epigenomic Medicine</b>	2025-01-20	2025-03-31	Uppsala	28
<b>Intro to mermaid</b>	2025-10-02	2025-10-02	online	10
<b>Intro to mermaid</b>	2025-04-10	2025-04-10	online	10
<b>Intro to R</b>	2025-04-04	2025-04-04	online	10
<b>Intro to R</b>	2025-10-03	2025-10-03	online	10
<b>Introduction to Molecular Epidemiology</b>	2025-10-06	2025-10-10	Umeå	10
<b>Joint's Master Programme in Health informatics</b>	2025-09-18	2025-09-18	Stockholm	40
<b>Molecular Genetics of Eukaryotes</b>	2025-09-01	2025-10-31	Lund	20
<b>Omics - Analysis of large-scale biomolecular datasets</b>	2025-11-03	2026-01-09	Lund	30
<b>Protein Structure, Function and Disease</b>	2025-09-18	2025-12-04	Stockholm	12
<b>Systems Biology Masters course lecture.</b>	2025-10-06	2025-10-06	Göteborg	40
<b>Workshop on Genomics 2025</b>	2025-01-05	2025-01-18	Cesky Krumlov, Czechia	61
<b>Zidas2025</b>	2025-07-08	2025-07-08	Basel, Switzerland	25

To address the growing demand for bioinformatics knowledge and skills, NBIS employs a training co-production model. This involves collaborating with other training providers, both nationally and internationally, to deliver comprehensive training programs. This model not only enhances capacity and knowledge building for researchers but also fosters valuable networking opportunities for both infrastructure staff and course participants, connecting them across different research infrastructures and organizations.

During 2025, we have co-organised several international courses, both together with other ELIXIR nodes; Spatial omics data analysis course (Switzerland) and Training Materials made FAIR by design (Belgium), and with EMBO; EMBO practical course Advanced Methods in BioImage Analysis (Germany).

Internal training is also a vital component of NBIS training efforts, facilitating knowledge transfer within the organization. In 2025, a RSE Tools Tech group for knowledge-transfer within and beyond NBIS was established. This group deploys a collaborative and transparent method where a research software engineering tool useful for bioinformatics is demonstrated in a short walkthrough and documented in a blog post for future reference.

SciLifeLab Training Hub remains an important collaboration partner with NBIS. Much of what the Training Hub at SciLifeLab will offer and provide will be built collaboratively with the NBIS Training team. Also, Training Hub will make use of the open source and open educational resources established by ELIXIR, where NBIS plays a significant role. During 2025 the course co-developed by ELIXIR-BE on how to make Training material FAIR by design was delivered in Ghent.

NBIS Training members are leading contributors to the ELIXIR Training Platform Work Programme 24–26, co-leading several activities. In 2025, their focus has centered on the active development and improvement of two important resources: ELIXIR Training SPLASH, a centralized digital environment serving as a "one-stop-shop" for ELIXIR Training Platform resources, and the new version of ELIXIR Training Metrics Database. NBIS also continues its active engagement and contributions to the Train-the-Trainer instructor network.

NBIS has during 2025 continued to strengthen the connection to the Open Science scene in Sweden and with EOSC in particular. This is done in collaboration with SciLifeLab Training Hub and the SciLifeLab Data Centre. In 2024, a collaboration with the Swedish National Data Service (SND) to co-create a national course on Open Science in the Swedish context which was successfully delivered in May 2025. This led to continued collaboration with the aim of delivering this course annually.

NBIS remains actively engaged in the EOSC association brain pool network, contributing to both Opportunity Areas and Task Forces which aims to provide crucial expertise for EOSC implementation and to support the development of the EOSC ecosystem.

## Outreach

Outreach activities have proven important to inform the scientific community about the support that NBIS can provide, to increase collaborations and to increase the number of users and quality of projects. The activities consist of involvement in local community initiatives that provide the possibility to meet staff representing our wide variety of competences, presentations at events and conferences and weekly Bioinformatics Drop-in sessions enabling face-to-face contact between researchers and our experts, which many times is the first contact in a support case.

During 2025, we arranged 37 national drop-ins via Zoom, as well as many physical drop-ins in Stockholm, Gothenburg and Lund. The Gothenburg drop-in is newly established at Chalmers, bi-weekly with an additional monthly joint drop-in with SciLifeLab at their offices. The Zoom drop-ins were visited by roughly 200 unique researchers and have a mean rating of 9.42/10 from 147 respondents in 2025.

Within the SciLifeLab IDS (Integrative Data Support) effort, NBIS has organised monthly user meetings for multi-modal research projects.

New outreach materials were designed and procured during 2025 for official representation and to be distributed with the help of NBIS training during courses to students. Each NBIS site coordinator will have physical outreach materials and rollups.

The NBIS affiliates program has grown significantly in 2025 and now has 40 affiliates. There is a Slack channel with information about the perks of being an affiliate and for information to flow between NBIS experts and the affiliates.

NBIS has expanded its established AI efforts, together with the Scilifelab Data Centre, to form the Scilifelab AI Network, supporting the SciLifeLab AI lead's work towards an AI strategy for SciLifeLab. The network is public and comprise a chat forum and discussion groups providing a community space to share experiences and get peer support around using and developing AI tools, as well as the Scilifelab AI seminar series – in 2025, there were 8 AI seminars, with presenters from

KI, LiU, LU, UU, Oxford University and 2 international companies, which drew an average audience of 48 persons (range=20–121).

NBIS is engaged in multiple local activities across the country.

In Umeå, NBIS was represented at SciLifeLab infrastructure meetings and participated in local bioinformatics gatherings. NBIS also had posters at KBC days, UPSC day, EMBL-SciLifeLab-MIMS conference and UCMR day. Finally, NBIS joined the “Bioinformatics in Umeå” retreat to talk about our internal technology training initiative.

In Gothenburg, NBIS is involved in managing the local bioinformatics network GOTBIN. NBIS is also active in the SciLifeLab Gothenburg site and provides input in the advisory board for the Core Facilities at University of Gothenburg and Sahlgrenska Academy.

In Linköping, NBIS is active in the SciLifeLab Linköping site and in the Research Infrastructure Specialists (RIS) Network in Linköping with focus on Life Science. This year we co-organized a workshop for the RIS network with a focus on communication and outreach based on the SESAM handbook. NBIS also participated in [“Forskningens dag i Region Östergötland”](#), a seminar day with a focus on collaboration between academia and health care in Region Östergötland.

In Stockholm, we presented NBIS services at a SciLifeLab outreach event for KI junior group leaders and postdocs. Also, we had a poster presentation at SciLifeLab Solna Science Talks, an annual meeting about the research at SciLifeLab Stockholm. In addition, we started discussions with Clinicum – a KI support function for advice on study design, biostatistics and bioinformatics – about joint outreach, joint consultation meetings and referring users between NBIS and Clinicum.

Finally, NBIS has a community coordinator to oversee and plan NBIS outreach activities and five local site coordinators. NBIS has an internal Outreach group which maintains a GitHub repository and a google drive area of outreach materials and presentations as well as discuss NBIS outreach strategy, visual profile and more.

## Collaboration with industry

In 2025, we conducted three industry consultations (totalling 11 hours) and delivered three industry support projects (205 ordered hours, 204 completed in 2025). Of these, three support projects and one consultation remain ongoing, while one support project has been completed. We also had 7 participants from Industry attending our courses.

We continued to strengthen awareness of NBIS services among industry stakeholders. Notably, we participated in Nordic Life Science Days 2025, where we delivered several presentations and held targeted meetings with facilitators and representatives of small and medium-sized enterprises (SMEs). As concrete outcomes of these efforts, we established strong communication channels with Medicon Village Fastighets AB in Lund, STUNS Life Science in Uppsala, Umeå Biotech Incubator AB, LEAD in Linköping, as well as with numerous SME partners with potential interest in our services.

As part of the SciLifeLab platform, we remained active participants in the SciLifeLab External Relations group. Within the framework of the SciLifeLab Industry Access Project, we contributed to the development of industry access surveys for SciLifeLab unit heads. We also engaged in

discussions with NVIDIA to explore collaboration opportunities and ensure SciLifeLab's access to cutting-edge tools and technologies for sequencing data processing.

As the Swedish ELIXIR node, we continued our involvement in the Industry and Innovation Focus Group, providing insights into the evolving landscape of the Swedish biotech industry.

## International

NBIS is the Swedish node in the European infrastructure ELIXIR. NBIS also aims at strengthening the Nordic collaborations, and since 2011, we have regular meetings between the Nordic ELIXIR Heads of Nodes. During the period 2013–2024, we have had funding from NeIC (Nordic eInfrastructure Collaboration) for development and provision of infrastructure for sensitive data (current project NeIC Heilsa Tryggvedottir). On the bioimage analysis side, the BIIF unit of NBIS is involved in Euro-Bioimaging, GloBIAS, AI4Life, and Chan-Zuckerberg image analysis initiatives, as well as in the international initiatives driving the standardisation of file formats (OME-NGFF) and usage of pipelines (e.g. nf-core) in image analysis.

ELIXIR is unique in Europe encompassing all European national bioinformatics infrastructures into a coordinated distributed research infrastructure with currently 23 partners and more expected to join.

During 2025, ELIXIR-SE has continued maintaining and updating the Human Protein Atlas – which is officially named as an ELIXIR Core Data Resource – in the ELIXIR landscape.

ELIXIR-SE has been very active in the systems development for and coordination and support of Federated EGA (FEGA) in collaboration with other Nordic ELIXIR nodes, ELIXIR-Spain and ELIXIR-EBI. Since February 2024, the Swedish FEGA node is in production.

Furthermore, NBIS as ELIXIR-SE has been active in multiple EU projects (as described above), e.g. GDI (Genomic Data Infrastructure), Bigpicture for digital pathology, EUCAIM providing infrastructure for cancer image data, and PHENET (where NBIS provides training on the European level).

## Staff

In total, NBIS staff has now increased to 145 persons. The table shows the number of staff in FTE (full time equivalents) during 2025 for the different functions in NBIS. Gender balance is 63% male and 37% female (which is an increase of female compared to 2024). Number of FTEs has increased from 104.6 in 2024 to 110.1 in 2025.

NBIS	Staff (FTE)
1 Central functions, incl. management	8.1
2A User fee Support (SMS)	30.0
2B Peer review Support (LTS)	15.3
2C Bioimage informatics Support	6.4
3A Data management	3.1
3B Human data	17.5
4A Systems dev. incl. pipelines & tools	5.7
4B AIDA Data Hub	2.2
5 Support for Computational Resources	4.0
6 Training	13.8
7 ELIXIR	4.2
<b>TOTAL</b>	<b>110.1</b>

## Economy report for 2025

NBIS	2025	Result 2025	Budget 2025	Result 2024
Incomes	VR Infrastructure grant	17 870 577	17 720 000	24 536 232
	VR grant EGA-SE	1 905 592	1 404 000	3 449 765
	VR grant Biodiversity	0	0	612 975
	SciLifeLab National	32 133 915	35 000 000	30 809 896
	Universities + SciLifeLab SFO	23 654 847	20 000 000	20 142 000
	KAW	34 513 858	33 535 000	27 328 242
	Vinnova (incl. Co-funding EU-proj.)	9 260 979	5 390 000	4 597 703
	EU + ELIXIR	26 567 196	18 511 000	12 953 672
	NeIC NordForsk	0	0	932 405
	Chan-Zuckerberg	0	0	1 000 000
	User fees	18 348 519	15 948 000	12 015 495
	Other	390 426	0	
	Balance from 2023 and earlier	0	0	3 810 714
	<b>SUM Incomes</b>	<b>164 645 909</b>	<b>147 508 000</b>	<b>142 189 099</b>
Expenses	Personnel	106 836 269	109 273 048	95 408 400
	Equipment	13 021 738		5 408 164
	Travel	2 608 395		2 050 996
	Other costs	4 212 098		5 021 415
	Office space	6 703 859	38 434 952	5 917 933
	Indirect costs	31 263 549		28 382 191
	<b>SUM Expenses</b>	<b>164 645 909</b>	<b>147 708 000</b>	<b>142 189 099</b>

**Distribution of costs on the different NBIS activities**

<b>Activity</b>	<b>kSEK</b>	<b>Budget</b>
1 - Central functions	12 270	15 110
2A – User fee Support (SMS)	39 625	32 763
2B – Peer review Support (LTS)	20 535	38 118
2C – Bioimage informatics Support	8 183	4 200
3A – Data management	5 069	8 050
3B – Human data	34 728	10 158
4A – Systems dev. incl. pipelines & tools	7 309	11 600
4B – AIDA Data Hub	3 438	7 570
5 – Support for Computational Resources	5 158	5 891
6 – Training & Nat networking	19 739	7 238
7 – ELIXIR	8 591	7 010
<b>SUM</b>	<b>164 646</b>	<b>147 708</b>

## Annex – Key performance indicators

### 1. Number of projects

During 2025, we have worked on 333 support projects and provided 52 consultations, involving a total of 277 unique PIs (106 female, 166 male, 5 no info).

### 2. Number of PIs distributed on universities

Univ	# Unique PI
Chalmers	4
GU	8
KI	61
KTH	7
LiU	10
LU	48
NRM	5
SU	5
SLU	26
UMU	23
UU	66
Other Swedish Uni	4
Other Swedish Org	1
International	6
Industry	2

### 3. Number of projects distributed on SCB codes

SCB SCB code and subject	
102 Computer and Information Sciences	6
105 Earth and Related Environmental Sciences	3
106 Biological Sciences	120
107 Other Natural Sciences	6
209 Industrial Biotechnology	3
211 Other Engineering and Technologies	2
301 Basic Medicine	59
302 Clinical Medicine	55
303 Health Sciences	20
304 Medical Biotechnology	7
305 Other Medical and Health Sciences	5
403 Veterinary Science	2
501 Psychology	1

### 4. Gender balance

A total of 277 unique PIs have received support and/or consultations, of which 106 female (39%) and 166 male (61%).

### 5. Number of users that have applied for access but not being prioritised

Here we show numbers from the LTS part of NBIS, since other users have the option of paying user fees as long as their project is technically feasible and NBIS has capacity. In 2025, there were a total of 77 applicants of which 25 were granted peer review (LTS) support (32%). Female: 36 applicants of which 13 were granted (36%). Male: 41 applicants of which 12 were granted (29%). Thus, there was during 2025 a somewhat lower success rate among male PIs. The number of PIs are small, and it varies from year to year (in 2024, there was a somewhat higher success rate for male PIs), but we will keep monitoring if there is a systematic bias over time. As a side note, as of 2025, we have implemented a new and more formally regulated process of appointing the members of the evaluation committee (currently 5 men and 5 women).

## 6. Publications

A total of 97 publications in 2025 have been published from our direct project support work (excluding Compute & Storage); DOIs provided in the table below.

10.37044/osf.io/5uhwz_v2	10.1038/s41598-025-89823-2	10.1101/2025.07.16.664580
10.1093/g3journal/jkaf002	10.1111/mec.70094	10.1007/s00011-025-02101-9
10.1038/s41597-025-04758-7	10.1007/s43440-025-00707-8	10.1016/j.molp.2025.01.008
10.1038/s41592-024-02493-2	10.1073/pnas.2424333122	10.1016/j.jocmr.2025.101920
10.1093/molbev/msaf065	10.1128/mra.01300-24	10.1038/s41598-025-22369-5
10.1093/nar/gkaf005	10.1007/s00253-025-13556-5	10.1021/acscchemneuro.4c00636
10.21203/rs.3.rs-5594800/v1	10.1111/nph.70392	10.1016/j.immuno.2024.100046
10.1158/1538-7445.am2025-6469	10.1016/j.bone.2025.117594	10.1111/mec.17788
10.1093/gigascience/giaf049	10.1371/journal.pcbi.1013558	10.1002/ece3.72163
10.1016/j.cell.2025.08.003	10.47248/hpgg2505010002	10.1242/dev.204421
10.1016/j.cell.2025.10.025	10.1016/j.watres.2025.123154	10.1101/2025.07.11.662357
10.1038/s44161-025-00655-9	10.1126/science.adu9575	10.1038/s41598-024-83775-9
10.1093/cvr/cvaf037	10.3233/SHTI251037	10.1038/s41588-025-02352-6
10.1038/s41467-025-57172-3	10.1093/gigascience/giaf108	10.1016/j.stem.2024.11.013
10.1186/s40164-025-00682-z	10.1016/j.bbamcr.2025.119955	10.1101/2025.05.04.652145
10.1038/s41598-025-17093-z	10.1002/acr2.70009	10.1007/s00294-025-01325-w
10.1038/s41467-025-58989-8	10.1038/s41586-024-08247-6	10.1093/ismeco/ycaf183
10.1016/j.vaccine.2025.127792	10.1056/NEJMoa2504650	10.1093/zoolinlean/zlaf078
10.1038/s41746-025-01616-z	10.1016/j.gene.2025.149539	10.1186/s12879-024-10279-2
10.1186/s12864-025-11861-x	10.1186/s12951-025-03659-6	10.1038/s41588-025-02101-9
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