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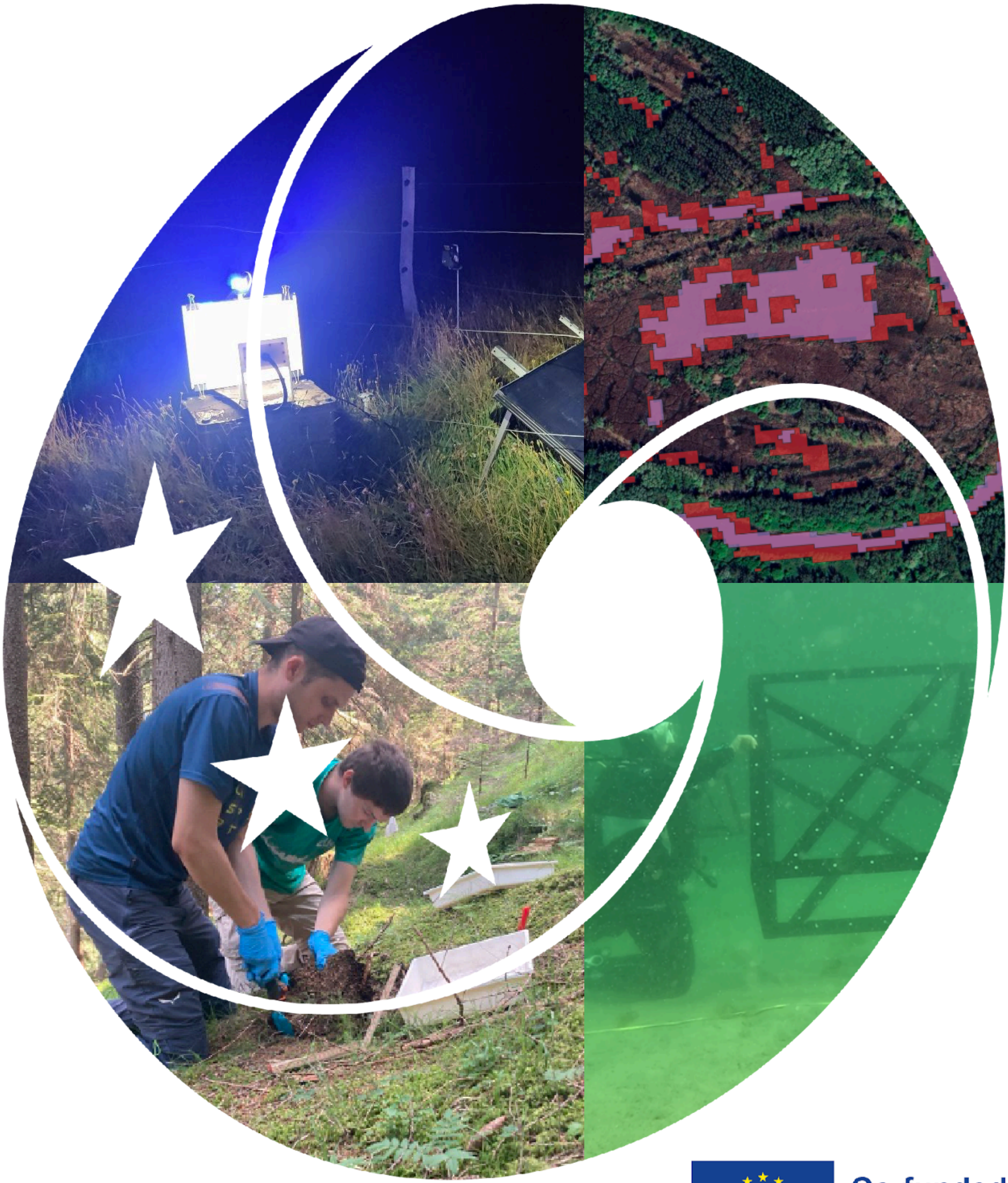
European Biodiversity Partnership

EUROPEAN PARTNERSHIP

Recommendations on the outcomes of the pilots



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What is Biodiversa+

The European Biodiversity Partnership, Biodiversa+, supports excellent research on biodiversity with an impact for policy and society. Connecting science, policy and practice for transformative change, Biodiversa+ is part of the European Biodiversity Strategy for 2030 that aims to put Europe's biodiversity on a path to recovery by 2030. Co-funded by the European Commission, Biodiversa+ gathers partners from research funding, programming and environmental policy actors in European and associated countries to work on 5 main objectives:

1. Plan and support research and innovation on biodiversity through a shared strategy, annual joint calls for research projects and capacity building activities
2. Set up a network of harmonised schemes to improve monitoring of biodiversity and ecosystem services across Europe
3. Contribute to high-end knowledge for deploying Nature-based Solutions and valuation of biodiversity in the private sector
4. Ensure efficient science-based support for policy-making and implementation in Europe
5. Strengthen the relevance and impact of pan-European research on biodiversity in a global context.

More information at: https://www.biodiversa.eu/

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List of acronyms

ABMS	Automated Biodiversity Monitoring Stations
AI	Artificial Intelligence
AMI	Automated Malaise Insect (traps)
BRUV	Baited Remote Underwater Video
EBVs	Essential Biodiversity Variables
eDNA	Environmental DNA
EASIN	European Alien Species Information Network
EBOCC	European Biodiversity Observation Coordination Centre
ERDA	Electronic Research Data Archive (Aarhus University)
EU	European Union
GBIF	Global Biodiversity Information Facility
HELCOM	Helsinki Commission (Baltic Marine Environment Protection Commission)
IAS	Invasive Alien Species
LiDAR	Light Detection and Ranging
MSFD	Marine Strategy Framework Directive
OSPAR	Convention for the Protection of the Marine Environment of the North-East Atlantic
RS	Remote Sensing
UVC	Underwater Visual Census

1. Introduction

This report describes the outcomes of the pilots launched in the second instalment as well as the two pilots launched during the first instalment that are still ongoing.

The three pilots were initiated under the Biodiversa+ European Biodiversity Partnership to address critical gaps in transnational biodiversity monitoring. The **ABMS** pilot was launched to evaluate the potential of automated sensors and AI for scalable monitoring of birds, bats, and nocturnal insects across Europe. Its aims included deploying multi-taxa sensor stations, developing centralized and open-source data processing pipelines, and creating tools for visualizing species observations, thereby testing the feasibility of a coordinated sensor network for Essential Biodiversity Variables (EBVs). The **EuRockFish** pilot was designed to harmonize monitoring of rocky reef fish communities, which are ecologically vital yet poorly studied at the European scale. It aimed to develop and validate standardized protocols combining traditional visual census and video methods with innovative eDNA techniques, ensuring interoperable data collection and optimized sampling designs across partner countries. The **Habitat** pilot focused on grassland and wetland habitats, exploring how remote sensing (RS) could complement field-based monitoring. Its objectives were to test RS-based methods for habitat condition indicators, inundation mapping, vegetation structure assessment, and grassland typology validation, ultimately providing recommendations for harmonized protocols and scalable monitoring frameworks aligned with EU biodiversity policy needs. The **Soil** biodiversity pilot was initiated to develop common protocols for sampling and laboratory work, evaluate the applicability of eDNA for soil invertebrates, and link monitoring outputs to Essential Biodiversity Variables and EU policy frameworks. It aimed to compare traditional and molecular methods and assess governance for a future European soil biodiversity monitoring network. The **Invasive Alien Species** (IAS) pilot was designed to explore image-based technologies for monitoring invasive plants and insects across biogeographical regions. Its objectives included implementing coordinated camera-based monitoring schemes, improving AI-driven species recognition, and establishing centralized data workflows for rapid detection and reporting. Both pilots sought to demonstrate scalable, cost-efficient solutions that can feed into long-term, harmonized monitoring systems at the European level.

The EuRockFish and the Soil Biodiversity pilots will continue in 2026 and the Invasive Alien Species pilot will continue through to the end of 2027 due to extensions and additional insights will follow from detailed analyses of the data collected in these pilots.

This report consists of a brief overview describing which partners were involved with each pilot and what roles they had. We summarize key recommendations from each pilot and refer to more in-depth reporting in each individual pilot report attached as appendices to the deliverable. This structure is decided in agreement with the pilot coordinators to maximize the dissemination of the individual reports to the respective stakeholder networks.

2. Partners and their roles in each pilot

Pilot	Focus	Coordinator	Partners / Contributors	Additional
ABMS (Automated Biodiversity Monitoring Stations)	Transnational sensor network for birds, bats & nocturnal insects using acoustic sensors, insect cameras, and AI pipelines	Aarhus University	Belgium, Bulgaria, Croatia, Czech Republic, Denmark, Finland, Ireland, Italy (Bolzano), Netherlands, Slovakia, Spain, Sweden	
EuRockFish	Harmonized monitoring of rocky reef fish using UVC, BRUV, and eDNA	OFB (French Biodiversity Agency)	France (PatriNat), Norway (Institute of Marine Research), Denmark (Aarhus University), Spain (Instituto Español de Oceanografía), Turkey (TAGEM), Israel (Israel Oceanographic & Limnological Research)	
Habitat Pilot	Remote sensing-based monitoring of grassland & wetland habitats (inundation, vegetation structure, grassland mapping)	Finnish Environment Institute (SYKE) & Swedish Environmental Protection Agency (SEPA)	Finland (SYKE, MoE_FI), Sweden (SEPA), Belgium (VL-O), Italy (Bolzano), Czech Republic (NCA CZ), Slovakia (SAS), Croatia (MESD) Limited: Spain (Catalonia), Bulgaria, Ireland	
Soil Biodiversity Pilot	Monitoring soil biodiversity in protected, near-natural forests; testing harmonized protocols and	Autonomous Province of Bolzano (Italy) through Eurac Research (BOZEN)	Italy (BOZEN), Belgium (VL O), Denmark (MoE_DK), France (OFB), Germany (BMUV), Israel	Catalonia (DACC) with one site; External contractors: ÖKOTEAM (Austria) for morphology, biome-ID

	eDNA methods for soil invertebrates		(MoEP), Portugal (FRCT – Azores), Slovakia (SAS), Sweden (SEPA), Turkey (TAGEM)	(Germany) for eDNA; Aarhus University for image-based biomass estimation
Invasive Alien Species (IAS) Pilot	Image-based monitoring of invasive alien plants and insects using AI-driven camera systems and insect traps	Ministry of Environment Denmark (MoE_DK) through Aarhus University	Italy (BOZEN), Denmark (MoE_DK), France (OFB), Sweden (SEPA), Czech Republic (NCA CZ), Slovakia (SAS), Bulgaria (ExEA), Croatia (MESD), Portugal (FRCT – Azores), Belgium (VL O), Israel (MoEP)	Technical collaborators: Pl@ntNet (plant recognition), The AI Lab (CamAlien system), UKCEH (AMI insect traps); Data infrastructure: ERDA (Aarhus University), GBIF & EASIN for data publishing

For the habitat pilot, the following partners were involved with each of the subtasks:

- **Indicators for Habitat Condition Monitoring:** Finland, Flanders, Czech Republic, Bolzano, Sweden, Slovakia, Croatia;
- **Inundation Mapping:** Finland, Flanders, Czech Republic, Bolzano, Sweden, Slovakia;
- **European Grassland Watch Validation:** Flanders, Czech Republic, Sweden, Denmark, Croatia, Slovakia, Bolzano;
- **Mapping of Open Grassland Habitats:** Finland ;
- **Vegetation Height & Cover (Drone LiDAR):** Denmark, Sweden, Belgium ;
- **Habitat Segmentation & Classification (NaturaSat):** Flanders, Czech Republic, Denmark, Slovakia, Sweden;
- **Super-resolution Enhancement:** Flanders, Bolzano, Sweden, Denmark.

3. Key recommendations to move towards a transnational biodiversity monitoring scheme

3.1. ABMS Pilot (Automated Biodiversity Monitoring Stations)

- **Centralized AI processing is essential** for scalability and consistency in sensor-based monitoring. Partners strongly favored having centralized data management and processing solutions to ensure repeatable and accurate outputs.
- **Local processing options should also be supported** to empower partners and foster equitable participation across regions.
- Investment in **open-source tools for visualization and annotation** (e.g., AnnFlux) is recommended to streamline expert verification and improve AI model performance.
- Coordination with broader communities in image and sound processing is needed to converge on **standardized, repeatable solutions** for biodiversity monitoring.

3.2. EuRockFish Pilot (Rocky Reef Fish Monitoring)

- Develop **harmonized, interoperable protocols** combining traditional (UVC, BRUV) and novel (eDNA) methods to ensure comparability across countries.
- Integrate these protocols into **regional and national monitoring frameworks** to strengthen coherence between science and policy.
- Promote **multi-method approaches** for robust ecological assessments and reporting under EU directives (e.g., MSFD, Habitats Directive) and regional sea conventions (OSPAR, HELCOM).
- Ensure **long-term collaboration and resource allocation** for expert teams in each country to maintain continuity and quality of monitoring.

3.3. Habitat Pilot (Grassland & Wetland Monitoring)

- Establish **harmonized methodological frameworks** for habitat segmentation, hydrological time-series indicators, and RS–in situ data integration.
- Create **shared validation protocols** and centralized technical infrastructure for data preprocessing, gap-filling, and FAIR-compliant data management.
- Scale up monitoring through **cloud-based platforms** (e.g., openEO) and ensure capacity building via training and technical workshops.
- Implement **annual hydrological indicators** and operationalize inundation models for large-scale monitoring.
- Integrate outputs into **EU reporting systems** (e.g., Article 17, Nature Restoration Law) and maintain a **permanent coordination structure** for consistency and transparency.
- Develop **open-source models for advanced methods** (e.g., super-resolution, drone-based LiDAR) to ensure reproducibility and long-term sustainability.

3.4. Soil Biodiversity Pilot

- **Develop harmonized protocols** for field sampling and laboratory work across countries to ensure comparability.
- **Refine eDNA methods** for soil biodiversity monitoring, including:
    - Improved primers for key soil taxa (annelids, arthropods).
    - Increased soil sample size for DNA extraction.
    - Standardized sample storage (preferably frozen in the field).
- **Invest in taxonomic reference libraries** to improve species-level identification from molecular data.
- **Decide on taxonomic resolution** (species vs. family level) and sampling frequency for long-term monitoring.
- **Integrate EBVs** (Essential Biodiversity Variables) and link monitoring outputs to EU and global policy frameworks.
- **Combine traditional and molecular methods** during transition to fully scalable molecular approaches.

3.5. Invasive Alien Species (IAS) Pilot

- **Centralize data management and processing** to ensure scalability and cost-efficiency.
- **Standardize image-based monitoring protocols** for plants (roadside cameras) and insects (AMI traps).
- **Develop robust AI models** for species identification using global image datasets and regional fine-tuning.
- **Ensure FAIR-compliant data infrastructure** and publish data to GBIF and EASIN for interoperability.
- **Explore real-time data transfer and processing** (on-device AI) to reduce delays from observation to actionable information.
- **Maintain shared infrastructure** for image recognition and data visualization under a European coordination center (e.g., EBOCC).
- **Plan for complementary approaches** (e.g., drones for plants) to expand coverage beyond transport corridors.

4. Appendixes

- IAS 2024 report
- Soil 2024 report
- ABMS report
- EURockFish report
- Habitat pilot report

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European Biodiversity Partnership

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Invasive Alien Species pilot second year draft report

Transnational image-based monitoring schemes for invasive alien species

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Authors	Toke Thomas Høye, Lars Dalby, Kavi Mellerup (MoE of DK)
Contributors	Jacopo Breschi (BOZEN), Barbora Šingliarová (SAS), Alix d'Audeville (OFB), Arnaud Albert (OFB), Afonso Prestes (FRCT), Lars B. Pettersson (SEPA), Zdeněk Račanský (NCA CZ), Bram D'hondt (VL O); Petteri Vihervaara (MoE_FI)
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More information at: https://www.biodiversa.eu/

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List of acronyms

AMI traps	“Automated Monitoring of Insects” traps based on a prototype from a research team at Aarhus University, Denmark and further developed into a standardised hardware system by UKCEH
API	Application Programming Interface
CamAlien	Camera system for monitoring invasive alien plant species along roadside verges. Produced by The AI Lab (https://theailab.dk/)
EUNIS	European Nature Information System (https://eunis.eea.europa.eu/)
ERDA	Electronic Research Data Archive, an open science data storage facility at Aarhus University, Denmark (https://www.erda.au.dk/)
EUNIS	European Nature Information System (https://eunis.eea.europa.eu/)
GBIF	Global Biodiversity Information Facility (https://www.gbif.org/)
GDPR	General Data Protection Regulation. Regulation (EU) 2016/679
IAS	Invasive Alien Species
JRC	Joint Research Centre
STING	Science and Technology for Pollinating Insects
SPRING	European project on “Strengthening pollinator recovery through indicators and monitoring”

Executive Summary

Biodiversa+ is testing ways of harmonising biodiversity monitoring at a pan-European scale. This work is conducted through some pilots. In line with the Biodiversa+ priority on "Invasive Alien Species", the Biodiversa+ pilot on “Monitoring invasive alien species with image-based methods” was launched in 2023. It aims to develop and evaluate scalable methods using novel technologies for monitoring invasive alien species on a continental scale. This report describes the outcomes of work done during 2024 as well as some initial perspectives for long term monitoring.

During 2024, the pilot involved 11 active partners across Europe. These included all partners from the first year of the pilot and VL O (Government of Flanders, Belgium), represented by INBO. All partners participated in the plant module and the insect module of the pilot. Both modules employ image-based monitoring approaches to the monitoring of invasive alien species. The plant module trials a camera system (CamAlien) mounted on a car to map invasive alien plant species along roads, while the insect module trials insect camera traps (AMI traps) for monitoring invasive alien moth species attracted to light. During the 2024 season, each partner has collected data in their own country. The data collection in the plant module has mostly progressed as planned and the most relevant subset of the resulting data has been processed using a data management and data processing pipeline developed in collaboration with Pl@ntNet. Data collection in the insect module has also progressed well in 2024. In October 2024, it was decided to further extend the IAS pilot for three more years (2025-2027). A plan for potential implementation of these tools in transnational monitoring of invasive alien plant and insect species will be developed as part of this 2nd extension of the pilot.

The pilot was coordinated by the Ministry of the Environment Denmark through Aarhus University as third party, and was conducted with ten active partners: The Autonomous Province of Bolzano, Italy (BOZEN); Denmark (MoE_DK); France (OFB); Sweden (SEPA); Czech Republic (NCA CZ); Slovakia (SAS); Bulgaria (ExEA); Croatia (MESD); Autonomous Region of the Azores, Portugal, (FRCT); Flanders Region, Belgium (VL O); and Israel (MoEP).

1. Introduction

Evidence is mounting of widespread biodiversity decline across the globe. This gives a stark warning for the perilous state of our planet, yet the evidence base remains biased to a few regions and a few species groups which are feasible to monitor. General conclusions on the status of biodiversity are complex given their diverse ecologies and high variability between and within taxon groups, over time and geographic regions. Repeatable sampling methods that can automate and expand the extent and resolution of biodiversity monitoring are urgently needed to provide robust estimates of long-term trends. Closing the knowledge gap has never been more important.

Biodiversa+ aims at promoting and supporting transnational biodiversity monitoring, by building a transnational network of harmonised biodiversity monitoring schemes on specific priority topics. One of these Biodiversa+ priorities focuses on invasive alien species (IAS) (Basille et al. 2023). As a way of supporting this harmonisation work on this priority, the Biodiversa+ partners agreed to launch in January 2023 a pilot on monitoring invasive alien species with image-based methods. The project was initially planned for one year (2023), then extended one more year (2024) and in October 2024 extended for three more years (2025-2027)[1]. This report concerns the work done in year 2 (2024). The pilot gathers 11 countries: Italy - Autonomous Province of Bolzano with BOZEN, Denmark with MoE_DK, France with OFB, Sweden with SEPA, Czech Republic with NCA CZ, Slovakia with SAS, Bulgaria with ExEA, Croatia with MESD, Portugal - Autonomous Region of the Azores with FRCT, Belgium with VL O, and Israel with MoEP.

The aim of this pilot is to pave the way for and evaluate scalable methods using novel technologies for monitoring invasive alien species at the geographical scale of the partnership. More specifically, the pilot will: a) Implement a coordinated international image-based monitoring scheme for invasive alien plant and insect species across biogeographical regions, b) Improve image recognition for invasive alien plant and insect species, c) Map benefits and constraints to real-time mapping of invasive alien plant and insect species and presentation in decision support tools, and d) showcase the workflow of image-based monitoring for early detection of invasive alien species.

In the context of Biodiversa+, this task is particularly linked to Biodiversa+ work on the harmonisation of protocols, methods and databases and promotion of novel technologies to monitor biodiversity.

The specific objectives of the second year (2024) of the pilot were:

- Each active partner has collected ten hours of image data along road sections with known occurrences of invasive alien plant species during the 2024 growing season.
- Each active partner has had three insect camera traps in operation for at least three months during the 2024 growing season.
- A database hosting all image data and associated metadata is available by the end of the project.
- An automated upload and image-processing workflow to localise and identify plant species and macro moths of invasion concern across the countries involved in the pilot project.
- Visualisations of the locations, identity, and time of observation of at least 100 plant and insect species have been prepared by the end of the project.

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[1] Biodiversa+ biodiversity monitoring pilot: https://www.biodiversa.eu/biodiversity-monitoring/pilot/

- Dialogue with rail, road, and river shipping authorities in at least five countries have been established and trials applying the image recording platform (CamAlien) on trains and or boats in at least three countries have been carried out.
- A data partnership agreement has been established with the EASIN (https://alien.jrc.ec.europa.eu/easin) for publishing data from the pilot scheme in their database.

This 2024 interim report describes the implementation steps taken in this pilot towards the transnational monitoring of invasive alien species, including a description of the equipment, taxonomic focus, site selection, data collection and image analysis. Further, the report summarises data management practices in the project and gives an overview of the first results and lessons learnt. The report ends with sections on the perspectives for implementation in long-term transnational monitoring. This report complements the living document describing the data management plan and the work plan for the 2nd extension of the project during 2025-2027.

2. Implementation

The IAS pilot consists of two modules: a plant module and an insect module. Both modules employ image recognition using computer vision and deep learning models for cost efficient and rapid detection of species of concern. These methods rely on training data of the species of concern to function effectively. Such data is available in the Global Biodiversity Information Facility (GBIF) as well as in databases of various national and regional pilot projects. The pilot program will be relevant in the context of introduction sites as well as for the collection of additional training data to improve image recognition models.

2.1. Equipment

Invasive alien plants are monitored with a custom-built camera system mounted on a car. During driving, the camera records continuously and is capable of recording images without motion blur at driving speeds up to 110 km/h. A web application accessible on a smartphone can be used to monitor camera settings in real time and view photos. An earlier version of the system used in the pilot is described in Dyrmann et al. (2021). The equipment used in this project is named CamAlien and is produced by the company The AI Lab. In addition, a series of Youtube videos give detailed descriptions of the operation of the system.

Insects are monitored with Automated Monitoring of Insects (AMI) traps, which are standardised camera-enabled light traps described by Bjerge et al. (2021) and https://www.insectmonitoring.org/. The AMI insect camera trap attracts nocturnal insects with UV light (LepiLED) and records insects landing on a white board. The AMI traps can be deployed with grid power or using solar panels and batteries. The traps run automatically on a predetermined schedule. The AMI trap images provide a rich basis for large-scale species inventories and abundance time series.

2.2. Taxonomic focus and site selection

2.2.1. Plant module

The recording of images at high speed requires that focal plants are clearly visible and identifiable from images recorded at a distance of 5–10 metres. This has led to a primary focus in the pilot on larger herbaceous or climbing, shrubby or woody species. Each partner was asked to provide a list of relevant plant species for their region. This was done to focus efforts on a manageable number of species. During the first year of the project, a collaboration with Pl@ntNet was established to build the image recognition pipeline around their facility.

The CamAlien camera system is designed for roadside verge monitoring. This is relevant in the context of the establishment and spread of invasive alien plant species, as roads and other transport networks are considered one of their primary dispersal routes. The camera system is capable of recording images along any road, but for consistency in the pilot scheme it was recommended to focus data collection on highways. During the 2024 field season, tests were also made using CamAlien to perform recordings from trains and along canals and rivers.

2.2.2. Insect module

The project is developing a broad taxon classifier as well as a species-level classifier for Lepidoptera. The classification models will allow for the species identification of moth species, which are identifiable from images recorded with the AMI trap cameras. This constrained the taxonomic focus to the subset of Lepidoptera species often referred to by naturalists as macro moths. These are typically, but not always, larger and with more distinct morphological traits.

Regarding site selection, there is limited knowledge about the distribution of invasive alien insect species. As such, the AMI traps have the potential to reveal the occurrence of species not known to the region. Ideally, potential establishment sites for invasive alien species should be selected for the deployment of AMI traps. At the same time, there are logistical considerations with the deployment of AMI traps as they require a power source (e.g. grid or solar) and they are costly equipment with a risk of unwanted interference with the traps or even theft. Given these considerations, the work plan specified that primary sites should be botanical gardens or ports. For some partners, it was necessary to widen the scope to include other potential introduction sites for invasive alien insect species, such as plant nurseries or urban sites.

2.3. Data collection

2.3.1. Plant module

Each partner collects images during continuous recording for ten hours of driving. While driving, an expert in identification of invasive alien plant species (not the driver of the car) scans the roadside verge for the invasive alien plant species of concern. The camera equipment allows for tagging of image sequences when species of concern are observed. By pressing a button, a tag is added to images recorded during the previous few seconds. By tagging subsets of the images with observed species of interest, the co-pilot can help drastically minimise the search for data to evaluate model performance and ultimately feed additional data to the training of better image recognition models. Once satisfactory model performance has been achieved, future monitoring of invasive alien plant species will only require the driver and no expert in plant identification and can thus be deployed at scale.

2.3.2. Insect module

Each active partner deploys three AMI traps. The AMI traps record images automatically every night on a predefined schedule (see section 3.1). During the 2024 field season, the ecologically relevant context of each AMI trap location was characterized through vegetation surveys. The goal was to assess the vegetation and habitats from each site with an AMI trap in three steps (at 5 m, all species; 25 m, woody species; 100 m, EUNIS habitats).

2.4. Image analysis

2.4.1. Plant module

The data upload and image analysis pipeline have been integrated in the data management system of the pilot to ensure that all images uploaded by the partners are managed automatically and in a consistent manner. First, the partners upload their data to the Electronic Research Data Archive (ERDA, erda.au.dk) at Aarhus University (AU). After the user has uploaded an image, an API developed by the pilot coordinators is called and as a first step it will determine if the image name is parsable. Next, the metadata is stored in the database and the image moved to storage. Lastly, a call to Pl@ntNet is made and the results returned are written to the database. A detailed flow diagram of the steps involved in this process is presented in Fig. 1. Collaborators at Pl@ntNet have prepared a dedicated adaptation of the Pl@ntNet application programming interface (API) involving custom-adapted parameters. This pilot was the only user of this facility, but since its start there have been additional requests and it is likely to be maintained in the future. This process involves calling the API several hundred times for each image to assess the likelihood of occurrence of the species of interest in multiple regions of each image and summarising the outcomes of these calls into image-level metrics of confidence scores as the maximum score across all calls to the API.

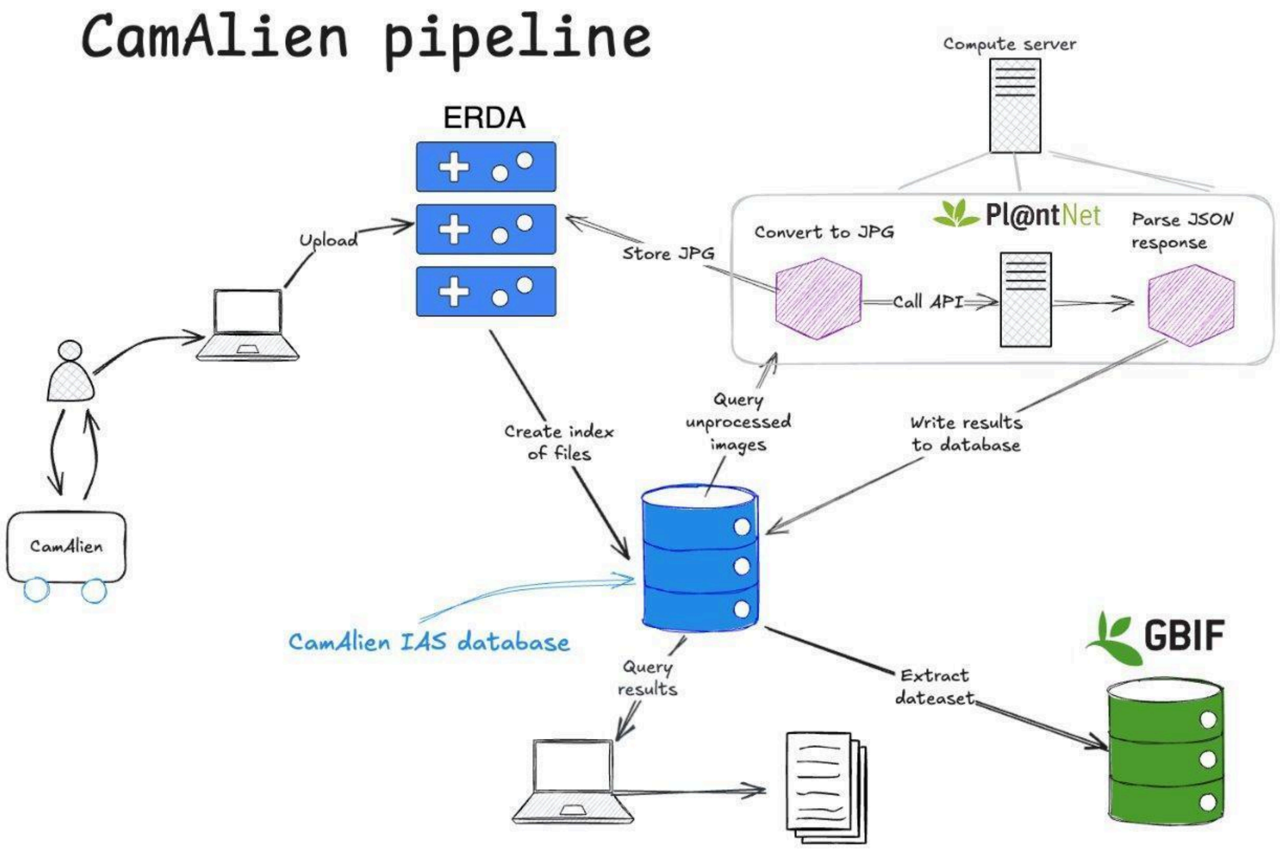

Figure 1: Analysis pipeline for the plant module, describing the process for each image recorded with the CamAlien system from the plant module uploaded to the Electronic Research Data Archive (ERDA) at Aarhus University and the interaction with the Pl@ntNet API.

2.4.2. Insect module

The extraction of species level data from the AMI trap images involves three key steps: localisation, broad taxon classification and species level classification. All three steps of the pipeline are complex tasks for which currently three different deep learning models are involved. Like for the plant module, partners upload their data to the Electronic Research Data Archive (ERDA)[2] at Aarhus University. After the user has uploaded an image, it is indexed and the path to the image and its metadata is written to our AMI database. Through a selection of localisation and classification models, images can be processed and the results are again written to the AMI database. A detailed flow diagram of the steps involved in this process is presented in Fig. 2.

The localisation model is assumed to work generically for images from any region, but the current set of classification models are specific to particular biogeographic regions. For this project, additional work on improving the localisation model is carried out and a new regional classification model has been developed. A first version of both models is now available. The new localisation algorithm (“Flatbug”; Svenning et al. in prep.) for use on the AMI trap images is a YOLOv8 instance segmentation model. It has been pre-trained on images from several other automatic insect localization projects. To improve its

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[2] ERDA: https://erda.au.dk/

performance, all insects from >150 AMI trap images have been manually annotated and used to train this model. The model will be further improved but is already very promising (Fig. 3). Using instance segmentation for insect localization offers a major advantage compared to bounding boxes. When two or more insects are close to each other, bounding boxes can end up containing several insects. It is especially the case for the largest ones. Using polygons allows to extract each insect more precisely, which at the end, will facilitate the classification process.

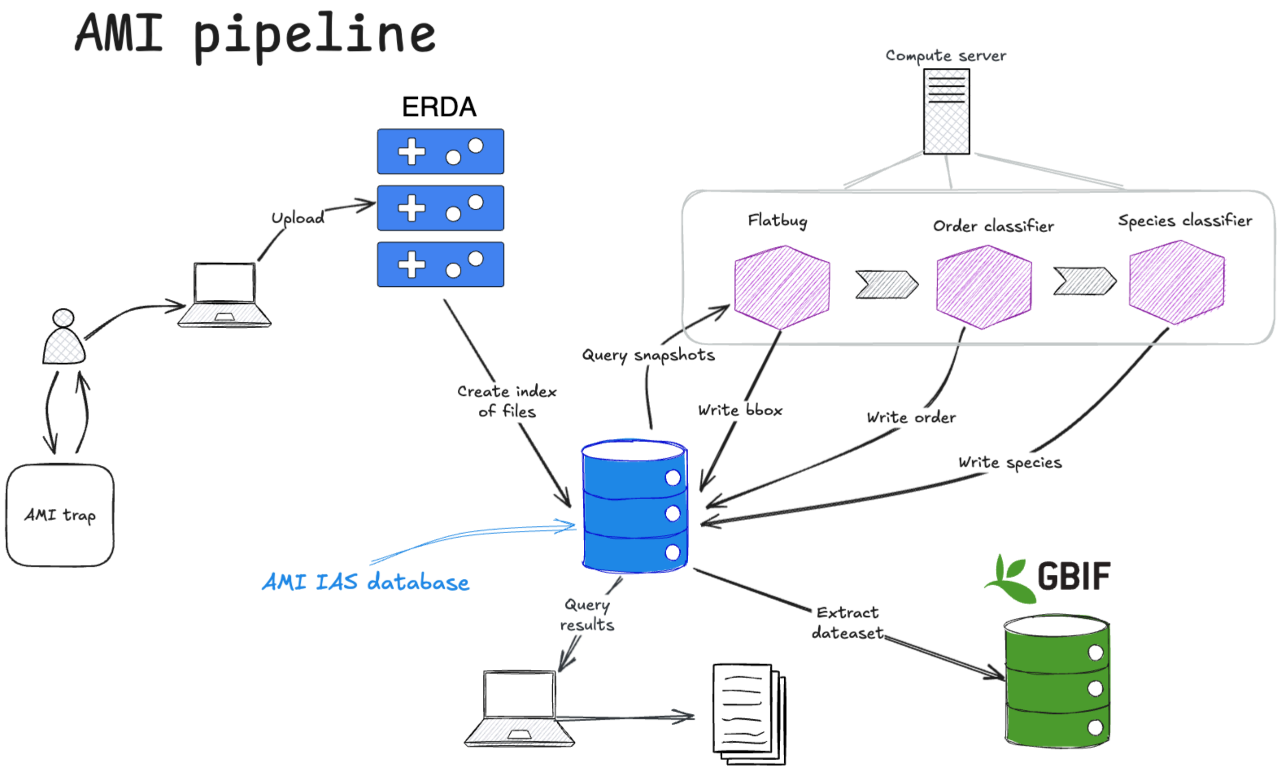

Figure 2: Analysis pipeline for the insect module, describing the process for each image recorded with the AMI system from the insect module uploaded to the Electronic Research Data Archive (ERDA) at Aarhus University and the use of custom-built deep learning models developed as part of the pilot.

For the localisation tasks, a key advantage is that the insects found in the AMI trap images are also represented in global citizen science databases and GBIF. Although these images have many different inherent biases and are taken with different cameras against different backgrounds, they offer an important resource when training image recognition models. In this project, we use five steps to create the species classification model: (1) choosing a backbone model, here we used EfficientNet (Tan & Le 2019), (2) applying an appropriate classification head, (3) collecting and training on citizen science images of the species-of-interest from GBIF, (4) manual annotations of a small number of localised objects from the AMI images and (5) fine-tuning on the manually annotated objects from the AMI images.

The GBIF dataset currently used is based on a list, kindly provided by the Dutch Butterfly Conservation, containing 3235 distinct macro-moth species found in Europe, and records of the countries, which are considered within their range. After conservative name resolution with the GBIF Backbone Taxonomy (i.e. the taxonomic reference that GBIF uses to consistently name species from multiple sources), the GBIF database was queried for observations (with images) for every species-range combination, yielding at least one observation for 2331 of the 3235 moth species and a total of 2,574,470 observations. This dataset was then filtered to exclude images of larvae, pupae, or large images where the moth takes up a small proportion of the image. The remaining dataset consisted of 1,873,998 observations of clearly visible adult moths. Lastly, the distribution of species frequencies was capped to remove the excessive amount of observation related to a few common and charismatic species: we chose to limit the maximum number of observations to 5,648 (from 41,117), leading to a retention of 80 % of the images and a final dataset size of 1,499,199 images.

The recently published CamTrap DP model (see: Bubnicki et al. 2023) is being adapted to accommodate the output format of the machine observed data from this pilot. A collaboration between INBO and AU has been established to publish datasets from the pilot to GBIF. The plan is to publish datasets from one partner at a time to GBIF during 2025 to allow each partner to adapt their license conditions.

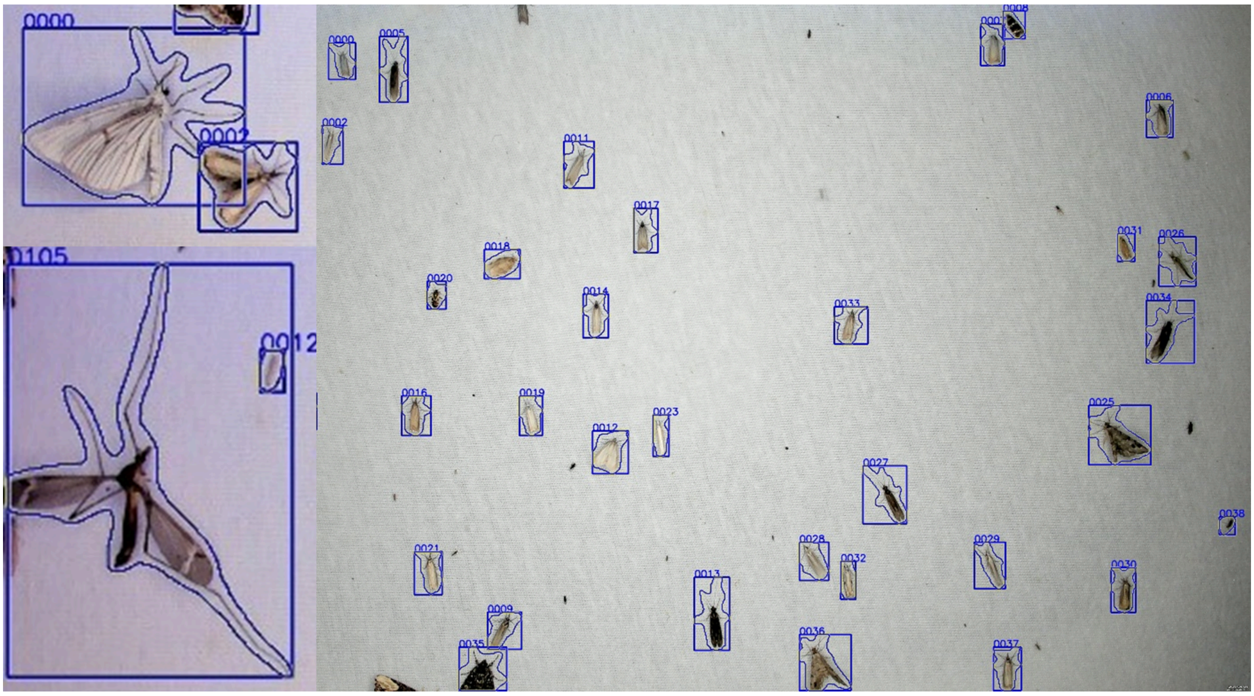

Figure 3: Example of an image recorded with the AMI trap. The new localisation model for AMI trap images draws a segmentation polygon as well as the rectangular bounding box around each detected animal. These are also shown in the main image as well as in two insets of zoomed in details from a similar image highlighting details for individual animals (Svenning et al., unpublished data).

3. Data management

3.1. Data description

For both modules, the species lists provided by the partners included GBIF IDs to ensure smooth integration with classification algorithms using these same GBIF IDs for training and prediction species identities.

The CamAlien system records images (4096 × 3000 pixels in tiff format as well as a compressed version of each image in jpg format) in two different user defined modes. During the IAS pilot, the recording is continuous when the system is powered on. It is also possible to run the system in a mode, where recording is only done when a remote-control button is pushed. Following a software update of the CamAlien system, the recording frequency (frame rate) is now adapted to the driving speed. This means that more images are recorded per second as driving speed increases. The maximum frame rate is five images are recorded per second, but when driving slowly, the frame rate is reduced to minimize the capture of redundant data generated by recording the same road section multiple times. Each image is stored in a buffer on the computer, which is part of the system. The location (latitude, longitude and altitude), speed during recording, exposure time, gain, date and time of recording are stored as part of the filename of each image. In addition, the user can add a tag stored in the filename to indicate the presence of invasive alien species by pressing a button on a remote control. The CamAlien system can inadvertently record images of people or registration plates of cars. During the recording process a software installed on the system directly processes each image and blocks out detected people, bikes and cars to comply with the General Data Protection Regulation of the European Union (GDPR).

The AMI traps record images (4096 × 2160 pixels in jpg format) based on a user defined schedule. During operation, the camera records a snapshot image every 10 minutes. The system also runs a motion detection software and evaluates if motion has happened in the past two seconds and records an additional image if this was the case (Bjerge et al. 2021). The date and time of recording are stored as part of the filename of each image.

3.2. Ensuring the FAIR data principle

All image data collected as part of the IAS pilot is stored in the Electronic Research Data Archive (ERDA) at Aarhus University, Denmark and will be made publicly available through a Danish implementation of the dataverse.

All data created in the pilot study will be made openly available at the end of the pilot. During the first year, the project has worked directly with the European Alien Species Information Network (EASIN) to ensure image-based species observations will be presented through EASIN’s data portal, and associated with appropriate measures of uncertainty. The intention is to submit species occurrences to the Global Biodiversity Information Facility (GBIF), and through tagging allow EASIN to present the data directly on their species occurrence portal.

4. Results and lessons learnt

4.1. Equipment orders, delivery and functionality

During the 2024 season, the CamAlien system has functioned mostly without problems. The software update to the CamAlien was implemented ahead of the field season in the beginning of the year. The main feature of the software update was the addition of the adaptive recording schedule, where the recording frame rate is controlled by the driving speed. The software update also allowed users to choose more flexibly whether to record uncompressed (TIFF) images, compressed (JPG) images or both. In connection with experiments with recording images from trains and other vehicles, in certain situations CamAlien was powered by external 12V batteries. Although this is logistically challenging, it turned out to be possible.

Several partners had experienced that the SSD hard drives in the CamAlien would stop working properly following hard shutdowns of the systems during the previous field season. Following substantial testing by The AI Lab using the Danish partner equipment, it was not possible to reproduce the problem and during 2024 following the software update, no partner has experienced this problem again.

A thorough evaluation of AMI trap issues has been carried out with the supplier UKCEH in the beginning of 2024. Still, some AMI traps have continued to cause problems during 2024. A few key issues affected multiple partners. First, the real-time clock batteries supporting the RockPI were depleted more quickly than anticipated. This does not seem to be a problem for AMI traps installed with Raspberry PI computers. Another recurrent problem was that RockPI computers would stop working. Several partners were supplied with new Raspberry PI computers and had to change their real-time clock batteries. Still, some AMI traps did not work as expected and a few traps completely failed to operate during the 2024 field season.

4.2. Data collection and data transfer

During the 2024 field season, data collection in the plant module went well. By implementing the adaptive recording, we managed to drastically reduce the amount of redundant data collected. All partners expressed enthusiasm about this new feature, which also made data handling much easier than during the previous field season. The CamAlien system produces approximately 2.57 GB of image data per kilometre driven with continuous recording. In 2024, we relied on the SFTP clients FileZilla for data upload and partners were asked to only record and upload the uncompressed TIFF files. This reduced the amount of data to upload substantially.

During the 2024 season, several partners established dialogues with train operators in their respective countries to explore options for using CamAlien to monitor invasive alien plant species along railway lines. In France, the CamAlien was deployed on SNCF trains, whereas in the Autonomous Province of Bolzano (Italy) on SAD trains. During these operations, it became clear that it is more difficult to identify plants from the side windows of trains because of the speed (trains travel at up to 140/160 km/h), whereas images from the front view could be available from other collection pictures tools, but would require a different data analysis. In addition, there is not enough space in the driver's cab to install the CamAlien.

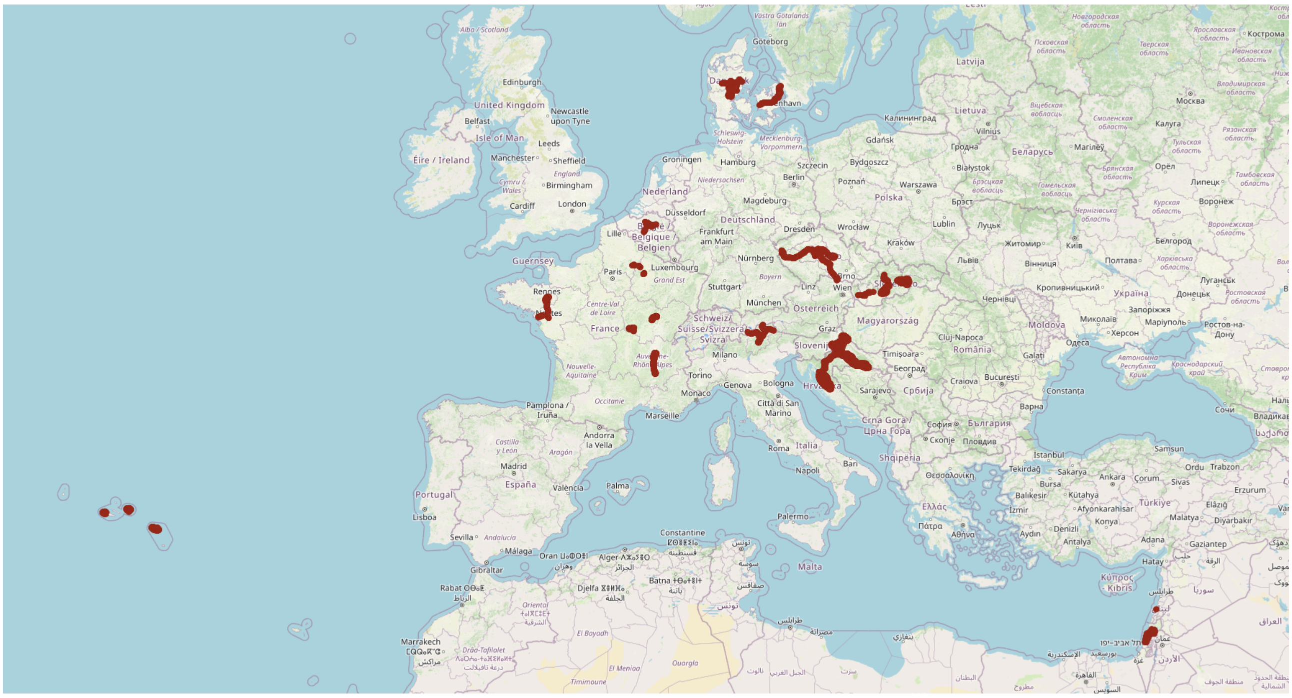

Figure 4: Map of all locations in the database of data recorded with CamAlien during the 2024 field season. Data was also collected in Bulgaria and will be added to the database.

However, the CamAlien image quality was still good and reflections from the side windows did not cause any problems. Unfortunately, it was not possible to get a reliable GPS signal inside the train with the current hardware configuration. For this reason, the images recorded in trains could not be geolocated at present. Through dialogue with The AI Lab – the providers of CamAlien – it seems that a stronger GPS antenna may solve the problem. We will explore this option during 2025.

In France and Belgium, the partners also experimented with taking photos with the CamAlien along rivers and canals. The camera was mounted on a car travelling along the road parallel to the river. From the French experience, It turned out that it was difficult to take a photo of both sides of the river and of the river itself (for terrestrial and aquatic plants) because of the width of the channels (from 5 to around 10 metres). It was also difficult to see aquatic plants because of the reflection of herbaceous plants and trees on the water. One idea would be to fit the camera with a polarisation filter. The speed of the car should be 30 km/h, as the path along the rivers is used by cyclists and walkers. This could be slow enough to monitor invasive alien species in an automated process.

For the insect module, the AMI traps produced much more data during the 2024 field season than was the case in 2023. Most partners managed to cover at least three months of the field seasons, although data gaps are common (Fig. 5). The AMI trap data was uploaded to the ERDA data storage facility at Aarhus University using the file handling software FileZilla. This system facilitates efficient transfer of data but does not allow users to add additional metadata related to the raw data. As such, it introduces a risk of loss of key information related to the raw data such as hardware metadata and location of the AMI trap during deployment. To allow efficient handling of data from multiple partners, it is also critical that the data follows a consistent structure. A customized upload module could ensure this more efficiently than the current approach using partner-specific upload sites (sharelinks) and the generic file transfer software Filezilla. In 2025, it is planned to trial a system of online communication between one AMI trap per partner and the data storage facility. In the future, this may further streamline the process of standardised data structures and efficient collection of deployment metadata.

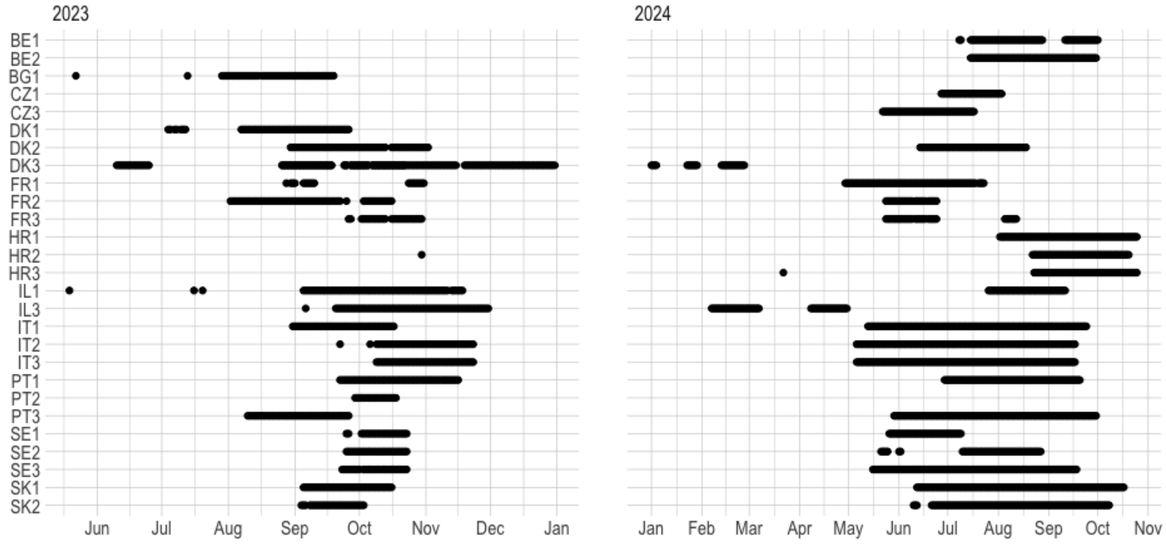

Figure 5: Recording activity for each AMI trap in 2023 and 2024. Data from a few traps deployed during 2024 have not yet been uploaded.

4.3. Image processing and annotations

4.3.1. Plant module

Each image recorded with CamAlien is divided into several hundred subsections or tiles of different sizes and each tile is classified with the Pl@ntNet algorithm. For each tile, the algorithm returns a confidence score for each detection of a plant species. We summarise these scores for a given CamAlien image by taking the maximum confidence score for each of the selected plant species in the project. However, translating the confidence scores to a probability of occurrence is not straightforward. This is particularly true because the Pl@ntNet classifier was not trained on images from CamAlien but typically on close-up images of a single plant or even just parts of a plant.

To establish relationships between confidence values from the classification models and probability of occurrence in the images, we selected images with scores along a gradient from 0.1 to 1 (the maximum possible value) and conducted expert review of the detections in 2023. The selection of images was done in a strategic manner to include images with varying probability of occurrence of the relevant plant species for the project.

During 2024, additional image review of CamAlien images was performed by the partners as it was clear after annotation in 2023 that annotation of images with scores from 0 to 0.1 was needed, particularly for some species that otherwise would have flat curves where a threshold could not be determined. Specifically, we selected up to 20 images per species and partner from images with scores from 0 to 0.1. As the number of target species varies greatly among partners, so does the number of images sampled. Annotation has been done voluntarily hence the annotated dataset is not perfectly stratified across partners and species. Nevertheless, it is possible to estimate the threshold where a detection is true in 50% of the cases across the entire dataset (Fig. 6).

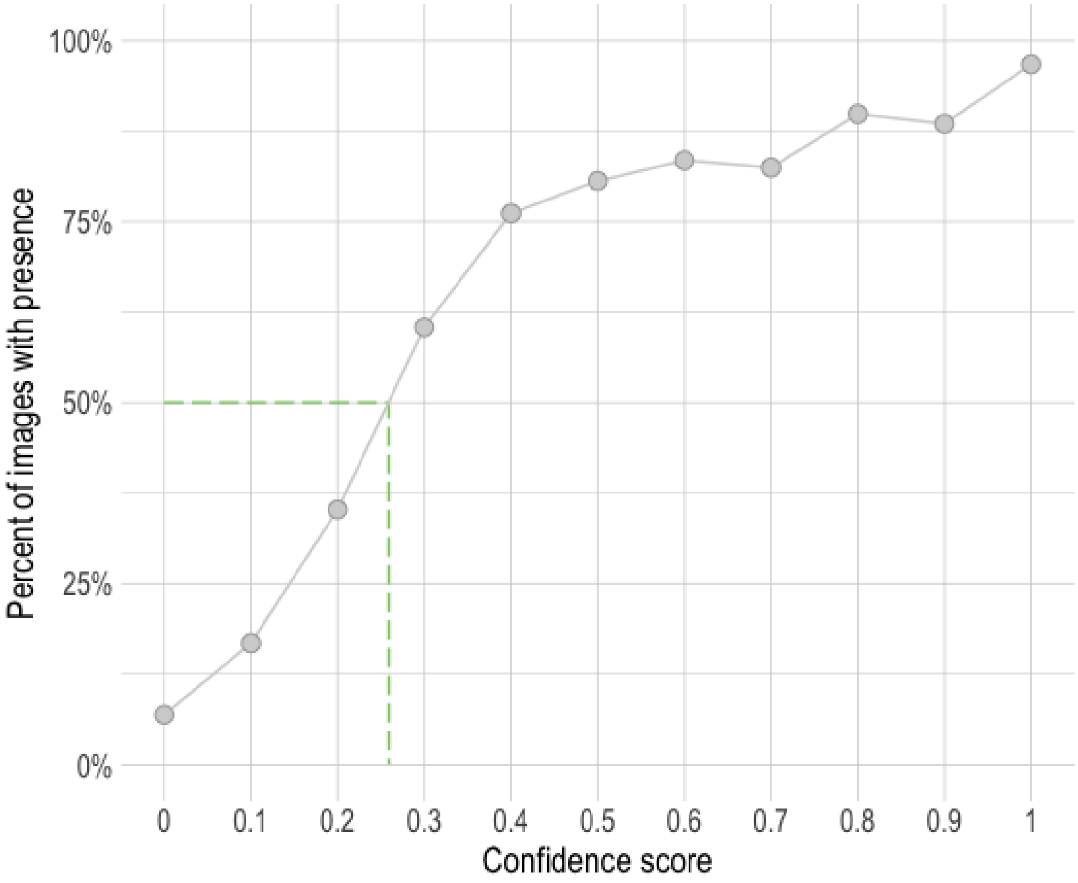

Figure 6: Threshold derived from annotated dataset. Relationship between the percent of the images with the focal species correctly detected by the Pl@ntNet algorithm and the confidence score from the model. Dashed green line shows the threshold confidence score across all focal species at a threshold of 50% (Threshold 0.259). Sample size: 4047.

It is possible that the TIFF images capture details of importance for species recognition that are lost if the image is compressed to jpg format. On the other hand, a small compression of the original file can greatly reduce the amount of storage space needed for the dataset. To understand if image compression resulted in a reduced ability to correctly locate and identify invasive alien plants in the images, we conducted an experiment on the entire set of expert labelled images. This dataset consisted of a total of 4047 images (2469 images with the evaluated plant species present and 1578 images where it was absent). For each image, where the occurrence of a particular invasive alien species was evaluated, we compressed the image to each of the following percentages of original image quality: 95%, 90%, 85%, 80%, 70% and 50%. We then ran all versions of each image through the classification pipeline and evaluated the maximum confidence score for the relevant plant species. This allowed us to evaluate the proportion of images which would be misclassified as a function of varying the confidence value threshold used to determine if the species would be considered detected or not in the image (Fig. 7).

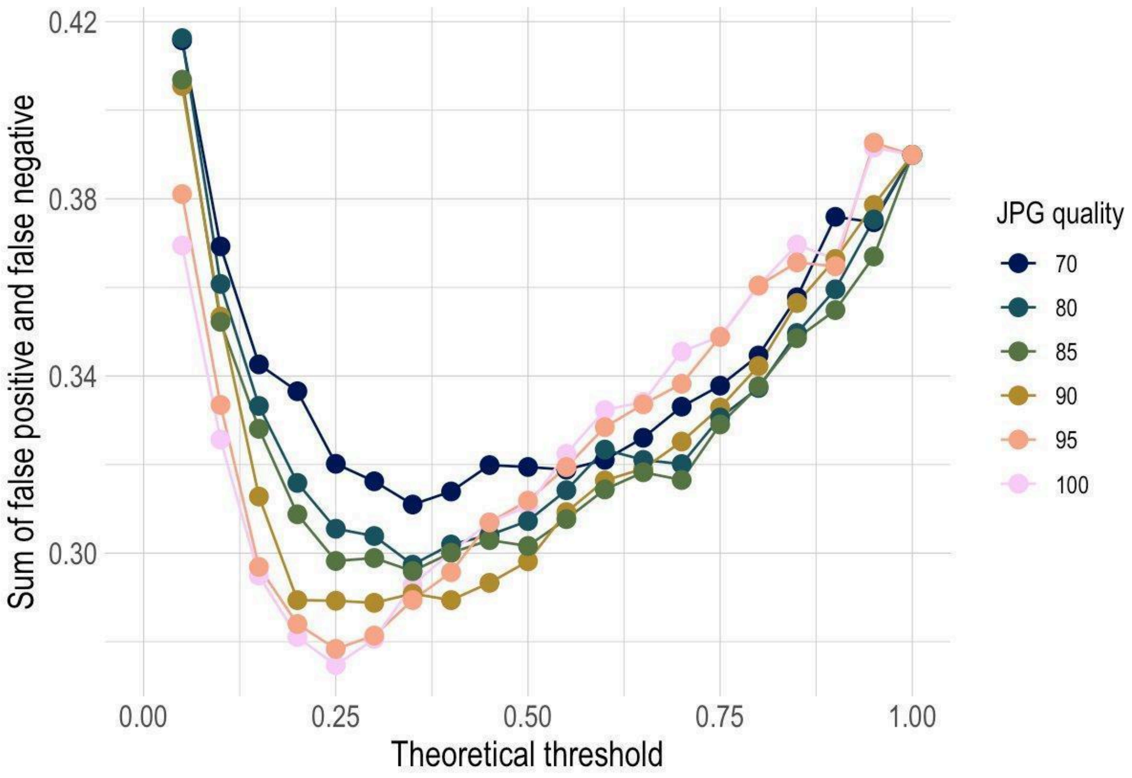

Figure 7: Proportion of the sum of false positives and false negatives across all images in the expert-reviewed dataset of images from CamAlien as a function of different confidence level thresholds. Each colour represents images in either original quality or a reduced image quality due to JPG compression. The figure illustrates that the false classifications are minimized when species receiving a maximum confidence level of 0.25 from the classification algorithm are assumed to be present in the images. The figure likely masks substantial species level variation.

4.3.2. Insect module

An overview of the AMI images recorded during the 2024 field season that have been uploaded to the ERDA facility and processed with the AMI pipeline is presented in Fig. 2. Data from some additional traps are still awaiting upload and could not be taken into account in these first analyses. The currently available dataset includes a total of 56,933 images recorded by 24 deployed AMI traps under the time lapse based schedule (one image every ten minutes). All traps have been running a motion-detection based recording schedule as well. Past experience suggests that the number of images recorded under the motion detection based recording schedule is 50-100 times higher than the time lapse based recording schedule. This means that the total number of images probably exceeds 5 million images. All of these have been uploaded to the ERDA facility, but only the images from the time lapse based schedule have been processed with the AMI pipeline so far (Fig. 2). Among the processed images, 597,676 arthropod detections have been made (Fig. 8). Following the same logic, it is possible that in the entire dataset from 2024, >50 million arthropod detections are likely. The largest number of detections (n=71,634) from a single trap was made from trap BE1 from Flanders (Belgium), while the largest average number of detections per image was made from trap FR1 from France (Table 1).

Table 1: Number of detections and images and average number of detections per images from AMI trap images recorded during the 2024 field season.

Trap ID	Detections	Images	Detections per image
BE1#2024	71634	5264	13.61
BE2#2024	40151	3027	13.26
CZ1#2024	8263	1269	6.51
CZ3#2024	9439	1146	8.24
DK2#2024	20484	1470	13.93
DK3#2024	7121	1634	4.36
FR1#2024	59585	1863	31.98
FR2#2024	4781	344	13.90
FR3#2024	5654	414	13.66
HR1#2024	64099	3120	20.54
HR2#2024	17075	1787	9.56
HR3#2024	12899	2262	5.70
IL1#2024	2089	1123	1.86
IL3#2024	13246	3270	4.05
IT1#2024	35270	2624	13.44
IT2#2024	10612	2343	4.53
IT3#2024	25398	2877	8.83
PT1#2024	18734	3086	6.07
PT3#2024	47363	4143	11.43
SE1#2024	5716	1642	3.48
SE2#2024	21097	1903	11.09
SE3#2024	51478	5518	9.33
SK1#2024	28741	2519	11.41
SK2#2024	16747	2285	7.33

The most abundant insect order detected in the processed images were Diptera with 285,448 (47.8%) of all detections. Lepidoptera made up 100,592 (16.8%) of all detections. This taxonomic group is the focus of the insect module, where species level identification is most feasible. Knowledge about invasive alien insect species is limited and so is the available training data for many taxa and the data collection in this project is facilitating better models for detection of invasive alien insect species in the future.

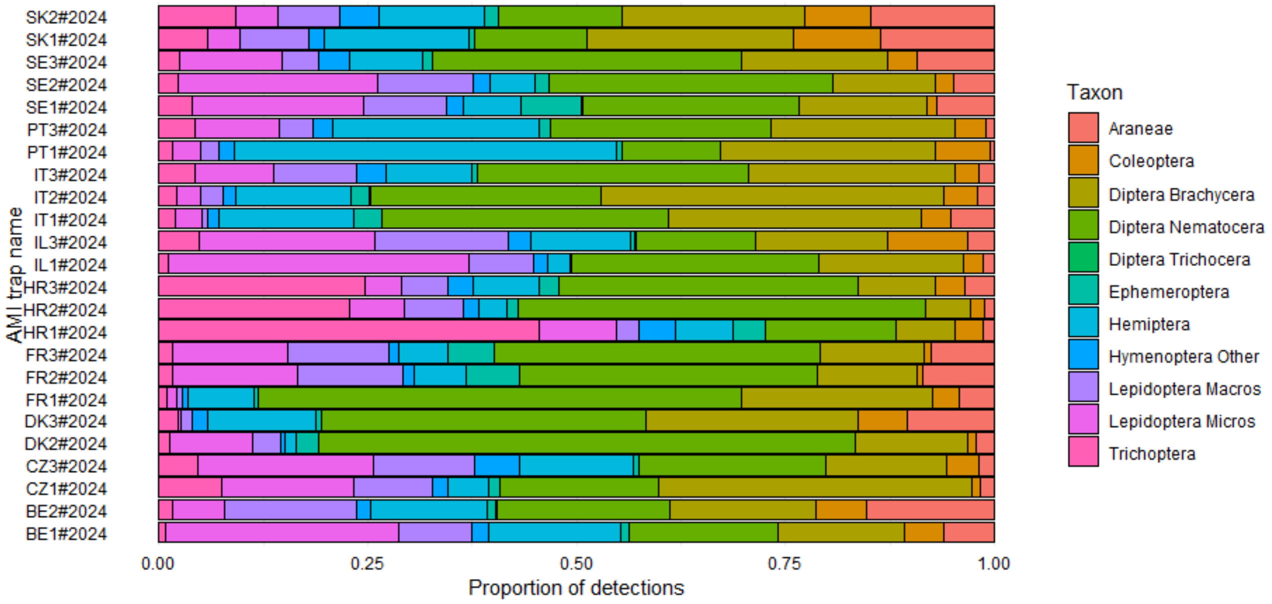

Figure 8: Proportion of detections in images from each AMI trap classified to each taxon by the broad taxon classifier. Detections classified as Diptera Tipulidae, Diptera Trichoceridae, Hymenoptera Vespidae, Opiliones, Neuroptera or as vegetation, were excluded from the graph as these classes were rare compared to the shown classes. The figure illustrates that macro moths (Lepidoptera Macros) make up a rather small proportion of the insects detected at the traps. The figure is based on a total of 597,676 detections.

During the 2023 field season, it became clear that the box tree moth (*Cydalima perspectalis*) is commonly observed in images recorded by the AMI traps and found in all partner-represented countries except for Israel. For the 2024 data, we have used our current species-level classification model for moths to examine how well our pipeline is able to identify this species. Across the nearly 600K detections, 989 were assigned to *C. perspectalis*.

We manually reviewed all predictions made to the species class *C. perspectalis.* From the verified images, it was clear that the species was detected by 15 of the 24 traps for which we have data. We found a false positive rate of 9.7% but only 0.3% were actually moths and the rest of the false predictions were mostly tiny insects that could not easily be identified even to the order level. A simple size criteria could easily filter these false detections out in the future. By further processing of the motion-detection images, we expect to be able to include more species of invasive alien insect species in the training data for future species-level classification models to accurately and efficiently detect such species when recorded at the traps.

5.

6. Perspectives for long-term transnational monitoring

Invasive alien species are, by definition, a problem that needs to be addressed at the transnational scale (IPBES 2023). The data from each module can feed directly into a transnational database and image processing pipeline for generation of transnationally standardised and automated monitoring data.

The image recognition tools developed in this pilot are highly scalable and should be of great value at the transnational scale. The central data processing and management makes it straightforward to add partners to the project. This was evidenced by the addition of Belgium (V LO) to the pilot in 2024 and a smooth integration in the data collection, processing and management. The monitoring goals and taxonomic focus may vary among partners. For example, through the collaboration with Pl@ntNet and the application of a general-purpose plant identification model, we can easily meet the needs of the community for distribution of plant species of interest. One important perspective is that the tools can be used to monitor the spread of species already introduced to the country. Another important perspective is that models of species found in one country can be used for early detection of species as they may become introduced in other countries. This is possible, because the image recognition model does not rely on locally collected training data but lends its strength from a global collection of curated images of >50,000 plant species. Similarly, the insect classification models can cover continental scale and be trained on globally available image data. Finally, the economic burden of maintaining the digital infrastructure for databases and image-recognition will be much smaller for each active partner, if shared at a Pan-European scale. At the moment, this is made possible through the funding for the pilot. In the future, the system could be maintained through modest funding to the data management infrastructure as a component of a transnational unit e.g. under the European Biodiversity Observation Coordination Centre (EBOCC). In such a scenario, each partner will only need to maintain their equipment and take care of data collection and interpretation of results. By centralising the data management, it is also possible to build dashboards for interaction with and visualisation of the outcomes of the data analysis. This part will be further elaborated in the final stage of this pilot.

In the long-term, the image-based approaches offer highly cost-effective means to map and monitor the distribution of invasive alien species and can substantially shorten the time from an observation is made until it enters databases and decision support systems on which management decisions are taken. A dual approach is planned, where detections of invasive alien species are automatically published to the Global Biodiversity Information Facility and EASIN and also ingested in a bespoke database for efficient visualisation and synthesis of the data.

There are still some challenges on the road to implementation in transnational monitoring. One element relates to the delay caused by transfer of data from camera systems to the image recognition models and the time involved with the processing of the image data. In the final stage of the pilot, we will explore options for moving the image recognition models onto the camera systems to further reduce the time delay from observation to actionable information. Also, this pilot focuses entirely on the transport infrastructures. For managers, these are important areas for establishment of invasive alien species, but to fully map the distribution area of populations of invasive alien species, complementary approaches should also be considered e.g. drone surveys for plants. However, this will be outside the scope of the pilot project.

The pilot delivers new ways of standardised and cost-efficient monitoring of species with automated image recognition. Reliable data on the natural environment is fundamental to support science on species conservation in human-modified landscapes. The pilot results can further be used to evaluate if adapted systems could be used to monitor additional taxa of invasive alien species with image-based tools (e.g., mammals often observed as road kills, such as raccoon *Procyon lotor*; arboreal nests of the Asian hornet *Vespa velutina* in fall; fruit flies or other day-active insect species using attractants).

A number of research infrastructures and international projects can support the implementation of these tools in long-term transnational monitoring. Here, we list a few:

- The EASIN information network established by the JRC provides collated information from EU member states as well as regional initiatives such as NOBANIS and ESENIAS. None of these sites present information about monitoring invasive alien species.
- Pl@ntNet is an identification system that helps with the identification of plants through images. It is a research and a citizen science project, initially supported by Agropolis Foundation, and developed since 2009. The Pl@ntNet system works by comparing visual patterns transmitted by users via photos of entire plants or plant organs (e.g. flowers, fruits, leaves) that they seek to determine. These images are analysed and compared to an image database produced collaboratively. Pl@ntNet is governed by a consortium composed of four research organisations: CIRAD, Inria, INRAE, IRD and the Agropolis Foundation. The management of the consortium is part of the InriaSOFT program, a program to perpetuate the digital achievements of Inria and its partners.
- The AMI traps represent one of the recommended tools from the STING expert group appointed by the European Commission Joint Research Centre. Among other tasks, STING develops recommendations on novel technology for pollinator monitoring, which should be tested at European scale for moth monitoring (Potts et al. 2024).
- The Cost Action InsectAI launched in November 2023 will be engaged in the insect module regarding image analysis. In the longer term, this network can also contribute to the further development of improvements and tests of hardware and software and standards for deployments and model training as well as through the collection of additional training data.
- Horizon Europe projects MAMBO (2022-2026), OneSTOP (2025-2028) and BMD (2025-2028) will provide additional technical expertise on image recognition, invasive alien species and early warning systems and will specifically contribute to the continued development of deep learning models.

The challenge over the coming years is to transform this pilot study into long term monitoring and to integrate it into a network of national and transnational biodiversity monitoring schemes.

7. Next steps

To facilitate the implementation of transnational monitoring of invasive alien plant and insect species with image-based methods, this pilot aims to estimate of the costs, refine the protocols, analysis pipelines, data infrastructure and work with the visualisation and synthesis of data into Essential Biodiversity Variables and the flow of actionable information to end users.

Specifically, a well-performing and stable infrastructure for users to collect, process and manage data is needed. The core functionality of this system is already in place, but further system development is needed to consolidate the IT infrastructure back-end and front-end to make it more user friendly and less dependent on specialised expertise. Processing of data from partners will continue and steps will be taken to estimate and minimise the costs of image analysis and data management for future users. The coordinators will also support partners in maintaining and operating their equipment and data uploads.

Secondly, reducing the costs and time-lag involved in translating field observations into actionable knowledge for decision makers is critical. This will partly be achieved by fitting a subset of the AMI traps with new mini-computers for online communication and deep learning models, so they can send occurrence data of invasive alien species in real-time to centralised servers for publishing to GBIF and EASIN and EBV datasets to the Geo-BON portal. To achieve this, we will finalise the revision of data publishing models with GBIF for CamAlien and AMI. Workshops during 2024 with GBIF and data scientists behind the Camera Trap Data Package (CamTrap DP) have revealed that further adaptations of existing standards are needed. This dialogue will be continued to reach consensus and best practice guidelines.

Thirdly, knowledge transfer around distributed, scalable IAS monitoring approaches is needed for the implementation of transnational monitoring. We will connect to partners’ national networks of managers, researchers and authorities as well as EU initiatives (such as the upcoming EBOCC) and projects (such as the Horizon Europe projects MAMBO, GUARDEN, B-CUBED, Biodiversity Meets Data and OneSTOP) to identify ways the pilot project can add value and complement ongoing activities. The coordinator is already in close dialogue with the coordinators of the mentioned Horizon Europe projects. Dialogue meetings will be held with all of these projects. In addition, two in person workshops focussed on coordination and capacity building with EPAs will be organised and participation in relevant conferences and events will be organised.

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EUROPEAN PARTNERSHIP

Soil Biodiversity Pilot second year draft report

Methodological challenges and lessons learnt

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Authors	Julia Seeber (BOZEN)
Contributors	Helene Blasbichler (BOZEN), Ane Kirstine Brunbjerg (MoE_DK, Aarhus University), Miroslav Caboň (SAS), Rémi Gerber (OFB), Sam Lambrechts (INBO, Ghent University), Dilek Kaya Özdoğan (TAGEM), Çağlar Sagun (TAGEM), Afonso Prestes (FRCT).
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What is Biodiversa+

The European Biodiversity Partnership, Biodiversa+, supports excellent research on biodiversity with an impact for policy and society. Connecting science, policy and practice for transformative change, Biodiversa+ is part of the European Biodiversity Strategy for 2030 that aims to put Europe's biodiversity on a path to recovery by 2030. Co-funded by the European Commission, Biodiversa+ gathers partners from research funding, programming and environmental policy actors in European and associated countries to work on 5 main objectives:

11. Plan and support research and innovation on biodiversity through a shared strategy, annual joint calls for research projects and capacity building activities
12. Set up a network of harmonised schemes to improve monitoring of biodiversity and ecosystem services across Europe
13. Contribute to high-end knowledge for deploying Nature-based Solutions and valuation of biodiversity in the private sector
14. Ensure efficient science-based support for policy-making and implementation in Europe
15. Strengthen the relevance and impact of pan-European research on biodiversity in a global context.

More information at: https://www.biodiversa.eu/

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List of acronyms

ASV	Amplicon Sequence Variant
DNA	Deoxyribonucleic Acid
eDNA	Environmental Deoxyribonucleic Acid
EU	European Union
EBV	Essential Biodiversity Variable
FAO	Food and Agricultural Organisation of the United Nations
GLOSOLAN	Global Soil Laboratory Network
GPS	Global Positioning System
HTS	High-throughput Sequencing
LUCAS	Land Use/Cover Area frame Survey
MBAG	Monitoring Network for Biodiversity in the Agricultural area of Flanders
NETSOB	International Network on Soil Biodiversity
OTU	Operational Taxonomic Unit
PCR	Polymerase Chain Reaction
RMQS	Le Réseau de Mesures de la Qualité des Sols
SDG	Sustainable Development Goals
SISEBIO	Catalan Plot System for Terrestrial Biodiversity Monitoring
SoilBON	Soil Biodiversity Observation Network

Table of abbreviations of forest types

Code	Category
FDB	Beech forests of the nemoral and Alpine region
FDC	Broadleaved forests of the Black Sea region
FDE	Oak forests of Continental and Atlantic Europe
FDS	Thermophilous deciduous forest (supramediterranean)
FEH	Broadleaved evergreen forest of the Mediterranean region
FEL	Broadleaved evergreen forest of Macaronesian region
FCM	Coniferous forests of the Mediterranean, Anatolian and Macaronesian region
FCP	Boreal and Alpine spruce forests
FCL	Alpine Swiss pine and larch forests
FCY	Boreal and hemi-boreal Scots pine forests

Executive Summary

Biodiversa+ has established a series of pilots as a proof of concept for its tasks leading to the establishment of a transnational network of biodiversity monitoring systems. In line with one of the priorities of Biodiversa+, the pilot on "Soil biodiversity in protected semi-natural forests" was launched in January 2023.

The aims of the pilot are:

- To develop a feasible experimental design and to define common protocols for field and laboratory work;
- To test the applicability and requirements of eDNA methods in such a scheme to obtain high resolution taxonomic data;
- To test the applicability of EBVs related to soil biodiversity to such monitoring schemes;
- To link the pilot to international and EU policies;
- To evaluate the coordination, cooperation and governance of a transnational soil biodiversity monitoring.

This report focuses on the methodological challenges of transnational monitoring and describes the advantages and limitations of suitable methods (established traditional methods and molecular methods). It also compares the results of the pilot for both methods. The applicability of molecular (eDNA) methods for soil invertebrate monitoring is still limited and problems and possible solutions are discussed.

The pilot was coordinated by the Autonomous Province of Bolzano (Italy) through Eurac Research as third party, and was conducted with ten active partners: Autonomous Region of the Azores (Portugal - FRCT), Belgium (VL O), Denmark (MoE_DK), France (OFB), Germany (BMUV), Israel (MoEP), Province of Bolzano (Italy - BOZEN), Slovakia (SAS), Sweden (SEPA), and Turkey (TAGEM).

1. Introduction

Biodiversa+ aims at promoting and supporting transnational biodiversity monitoring by building a transnational network of harmonised biodiversity monitoring schemes on specific priority topics[3]. One of these Biodiversa+ priorities focuses on soil biodiversity.

To advance such a transnational soil biodiversity monitoring scheme, the aims of the pilot are:

- To develop a feasible experimental design and to define common protocols for field and laboratory work;
- To test the applicability and requirements of eDNA methods in such a scheme to obtain high resolution taxonomic data and compare the results with results obtained by traditional methods;
- To test the applicability of EBVs related to soil biodiversity to such monitoring schemes;
- To link the pilot to international and EU policies;
- To evaluate the coordination, cooperation and governance of a transnational soil biodiversity monitoring.

The results of the pilot should not only contribute to a better understanding of soil biodiversity, but also identify ways to take action in order to conserve or restore it. In this way, the pilot supports actions for the forthcoming European Commission's Biodiversity Strategy for 2030 and the Soil Monitoring Law. On an international level, the pilot is relevant for the SDG framework, the recently adopted Kunming-Montreal Global Biodiversity Framework (United Nations, 2015; United Nations Convention on Biological Diversity, 2022), the International Network on Soil Biodiversity (NETSOB), and the Global Soil Laboratory Network (GLOSOLAN), all of which aim at providing the biological and ecosystem information needed to implement sustainable management and conservation of soils. While the SDG framework and the Global Biodiversity Framework operate on a broader scale (not focused on soil), NETSOB and GLOSOLAN, both initiated by FAO, aim to provide the means to globally promote the sustainable use and conservation of soil biodiversity, and to establish a global network of laboratories to analyse soil properties in a harmonised manner, respectively. The pilot project can contribute to these initiatives by providing the data and indicators needed to monitor and evaluate local soil biodiversity and by testing harmonised protocols.

According to a recent study, soils are home to the vast majority (59 % (± 15)) of life on earth (Anthony et al., 2023), which is twice as much as the previous estimate (25 % by Decaens et al., 2006), and many more, particularly from the microbial species pool, are still unknown. The importance of soil organisms for ecosystem functioning is undisputed, but how soil organisms are affected by human intervention and global change, and how changes in community composition affect ecosystem processes, remains largely unexplored. To obtain a holistic view of local soil biodiversity, many different methods are needed to cover this enormous diversity of soil organisms (microbes, micro-, meso- and macrofauna, Potapov et al. 2022). Furthermore, until the advent of high-throughput sequencing (HTS), species identification has been difficult due to the wide range of taxa that make up soil communities, and taxa have mostly only been identified at the order, family (for invertebrates) or operational taxonomic unit

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[3] Biodiversa+ priorities for biodiversity monitoring: https://www.biodiversa.eu/biodiversity-monitoring/priorities/

(OTU, for microorganisms) level. The selection of appropriate methods will therefore be of paramount importance for a future transnational monitoring scheme.

To support and prepare for a transnational soil biodiversity monitoring scheme, the Biodiversa+ partners agreed to launch a pilot in January 2023. During its second year, the pilot involved ten countries: Italy - Autonomous Province of Bolzano, Belgium - Flanders, Denmark, France, Germany, Israel, Slovakia, Sweden, Portugal - Autonomous Region of the Azores, and Turkey. Additionally, Catalonia, financed by the Departament d'Acció Climàtica, Alimentació i Agenda Rural (DACC) of the Catalonia Government (a key partner in the Biodiversa+ project), contributes with a single site.

This year 2 report focuses on methodological challenges of the soil biodiversity monitoring pilot, which need to be considered when planning a transnational monitoring programme, and describes suggestions for common protocols for field and laboratory work. By this, it builds up on the year 1 report published in February 2024[4].

2. Experimental design

2.1. Site selection

The coordinators chose to sample forest types from the different biogeographical regions of Europe to complement existing initiatives such as LUCAS (focus on agricultural sites) and SoilBON (paired approach with only few sites in Europe) as well as national initiatives such as RMQS Biodiversity (France), SISEBIO (Catalonia, Spain), and MBAG (Flanders, Belgium), which monitor various habitat types. The categorisation of the forest types followed the classification provided by the European Environment Agency[5]. The sites for each country were selected in bilateral online meetings between coordinators and each partner to ensure a good representation of the main European forest types. However, some forest types were under-represented due to lack of coverage by the participating countries. Additional criteria for selecting a site included a protection status (as far as possible) and that it had a high degree of naturalness.

2.2. Field and lab work

The SoilBON protocol was used as the starting point for the sampling in the field and the sample preparation in the laboratory. For DNA extraction and sequencing, this protocol also corresponds to the LUCAS protocol (see below). For the vegetation survey, a minimal protocol to create a list of plant species present in the plots was developed by the coordinators. All work steps were summarised in a step-by-step protocol and shared with the participants along with a list of materials. For the second sampling year, the step-by-step protocol was updated, based on discussions during the first workshop in Bolzano in November 2023. Please refer to the first mid-term report for more detailed information on protocols and field work[2].

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[4] First report of the Biodiversa+ soil pilot: https://www.biodiversa.eu/2024/02/01/pilot-on-soil-biodiversity-monitoring-first-year-report/

[5] EEA. European Forest types. EEA technical report. N°9/2006: https://www.eea.europa.eu/publications/technical_report_2006_9

Soil properties are analysed by the coordinator, who also pre-sorts pitfall traps and soil core samples. Two external companies were contracted to carry out morphological species identification (ÖKOTEAM, Austria) and eDNA metabarcoding analysis (biome-ID, Germany), the latter in accordance with the specifications published in the LUCAS protocol[6]. In brief, DNA from three 0.2 g aliquots of each sample is extracted using the Qiagen DNeasy PowerSoil HTP 96 Kit and amplified by PCR. Primers used to amplify DNA from archaea, bacteria and eukaryotes (fungi and other eukaryotes) are shown in Table 1. All amplicon libraries were sequenced on Illumina or PacBio platforms. The raw sequencing data (FASTQ files) was further bioinformatically processed by the contracted company. Briefly, all reads were subjected to preprocessing and quality control, and sequences that did not meet basic quality criteria (e.g. minimum length, maximum expected errors, chimeric sequences) were discarded. The resulting data was then clustered into Amplicon Sequence Variants (ASVs) or Operational Taxonomic Units (OTUs) depending on the primers used, which represent species-level proxies. OTU- or ASV-representative sequences were then compared to public reference databases (e.g. PR2 for 18S, UNITE for ITS2) for taxonomic classification.

Table 1: Primers used in the pilot

Taxon	Primers
Archaea 16S (SSU)	SSU1ArF (TCCGGTTGATCCYGCBRG) and SSU1000ArR (GGCCATGCAMYWCCTCTC)
Bacteria 16S (SSU)	515F (GTGYCAGCMGCCGCGGTAA) and 926R (GGCCGYCAATTYMTTTRAGTTT)
Eukaryote ITS2	ITS9mun (GTACACACCGCCCGTCG) and ITS4ngsUni (CGCCTSCSCTTANTDATATGC)
Eukaryote 18S (SSU)	Euk575F (ASCYGYGGTAAYWCCAGC) and Euk895R (TCHNHGNATTTCACCNCT)

Additionally, biomass of carabid beetles will be measured by the University of Aarhus using an automatic image-based technology (BIODISCOVER[7]).

3. Methodological challenges

General remark:

The implementation of a harmonised protocol raises a number of methodological questions. This is particularly true for a large-scale study such as the soil pilot and for a future transnational monitoring programme. Despite a detailed step-by-step protocol, each partner sets up the protocol depending on their own experience and equipment at hand. Minor variations in carrying-out the work must be accepted.

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[6] Orgiazzi et al., (2022) LUCAS Soil Biodiversity and LUCAS Soil Pesticides, new tools for research and policy development. *European Journal of Soil Science*. https://doi.org/10.1111/ejss.13299

[7] Ärje et al., (2020) Automatic image-based identification and biomass estimation of invertebrates. *Methods in Ecology and Evolution*. https://doi.org/10.1111/2041-210X.13428

One aim of the Biodiversa+ soil pilot is to compare the results of traditional and molecular methods, with a view to making recommendations on the methodology of large-scale monitoring in the final report. Here we discuss advantages and limitations of each of the methods employed in the pilot.

3.1. Traditional methods (pitfall traps and hand-sorting of soil cores)

The use of pitfall traps to collect soil-dwelling invertebrates and the manual sorting of soil cores to collect soil-dwelling invertebrates are long-established and standard methods in soil ecology (Potapov et al., 2022). Both methods are used to collect macrofauna only (i.e. all invertebrates larger than 2 mm). The advantages and disadvantages of these methods are generally well known but need to be reviewed with a view to large-scale monitoring, which will include many partners and a wide variety of habitats with different site and soil conditions.

3.1.1. Pitfall traps

Fig. 1: Pitfall trap at Montiggl (Province of Bolzano, Italy) and Kastamonu Yenice (Turkey)

General remarks

Pitfall traps provide a measure of activity density rather than abundance per surface area. This aspect has to be taken into account when analysing and interpreting the data. Target taxa of pitfall traps are mainly highly mobile organisms (e.g. spiders, ground and rove beetles, millipedes), therefore the data are not representative for the entire macrofauna.

Advantages:

The traps are cheap and easy to install and there is flexibility in the use of collection fluids (in the pilot salt water is used, but also ethylene glycol, propylene glycol, or ethanol mixtures are common). Covered by a roof, they can be installed regardless of the weather and in almost any type of habitat, as long as a deep enough hole can be dug. Also, there is no observer bias, which is an important advantage for large-scale studies. Pitfall traps can be used throughout the season and, emptied regularly, can provide important data on seasonality of invertebrates. In heterogeneous habitats, a higher number of replicates can easily be installed to account for a high variability in the occurrence of invertebrates.

Disadvantages:

Traps must be collected after a fixed number of days (in the pilot 14 days), which might result in an additional effort, in particular for remote or far away sites. The traps are susceptible to damage by wild animals or even removal by humans, therefore a minimum number of traps needs to be installed to avoid losing data. Snails and slugs can also contaminate samples with their mucus, making sample processing difficult. In addition, small vertebrates such as shrews and lizards can be trapped and have no means of escape.

Results from the pilot

Taxon diversity of ground-dwelling invertebrates on family level (Fig. 2), based on two sampling dates in 2023, is significantly different between forest types ($F_{9,237} = 10.54$, $p < 0.001$). Interestingly, the highest taxon diversity was found in alpine larch forests, but due to a low replicate number, this result has to be taken with caution (FCL, only sampled in the Province of Bolzano, n = 2 forests). High taxon diversity of ground-dwelling invertebrates was also found in deciduous oak forests (FDE, n = 11 forests). The lowest diversity was found in evergreen forests of the Macaronesian region (FEL, only sampled on the Azores, n = 4 forests). However, these results for the Azores are inconsistent with data from Borges et al. (2005) and Cardoso et al. (2007), who used identical methodology (pitfalls) and found a much higher diversity. This discrepancy is likely due to specific abiotic factors in the selected sampling areas (steep slopes on volcanic cones), as well as unusually high rainfall during the 2023 campaign. These factors were considered in the methodological adjustments for the 2024 campaign, which resulted in a significantly higher number of specimens captured by the same traps. Patterns are already well established at this taxonomic resolution, but will be compared to patterns at species level for selected taxa (spiders, ground and rove beetles) as soon as the data are available for the full year 2023.

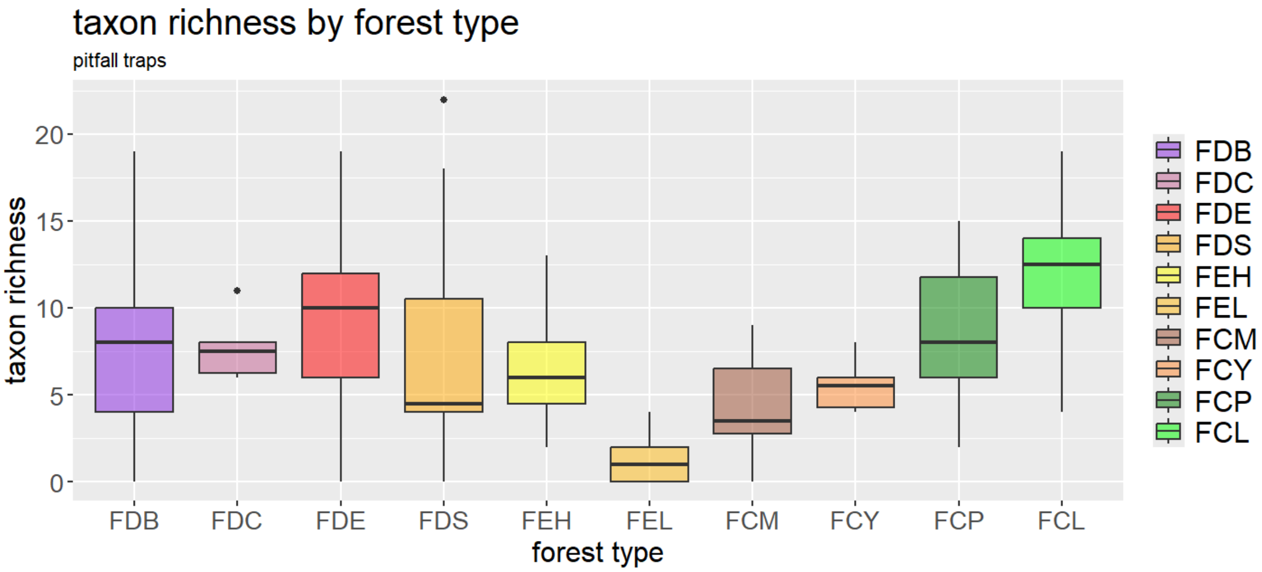

Fig. 2: Taxon diversity (family level) of ground-dwelling invertebrates in different forest types, collected by pitfall traps during two sampling campaigns (spring and autumn 2023). For abbreviations of forest types please see Table of abbreviations.

3.1.2. Hand-sorting of soil cores

General remarks

Hand-sorting of soil cores is the standard method to collect soil-dwelling invertebrates, especially since the alternative method, heat-extraction, needs lab equipment (Kempson or Berlese extractor), which is not readily available. It is also the only standardised method to collect earthworms. It provides abundance data (individuals per unit of area). Hand-sorting is usually carried out for a fixed period of time (e.g. 30 minutes for one person) and can be reduced if several people work on the same sample.

Fig. 3: Hand-sorting of soil cores at sites in the Province of Bolzano, in Israel and in France (clockwise from left to right)

Advantages:

Cheap and easy method, which needs almost no equipment and does not require soil to be carried to a laboratory (especially from remote sites). It also leaves the soil on site, reducing the general destructiveness of soil sampling.

Disadvantages:

The two main limitations of hand-sorting are that it is time-consuming (30 minutes for one replicate, less, if more people work on one sample) and the observer bias is very high. It should also be noted that, depending on the type of soil, extraction of the soil block can be quite demanding. If the soil is stony, it is more difficult to get the block out in one go, and the vibrations cause certain organisms such as earthworms to flee. It might also be very difficult, especially in grasslands, to tear up the turf, find the invertebrates living between the roots and extract them without damaging them. Due to the high spatial variability in invertebrate distribution within a site (e.g. due to aggregated occurrence of dipteran larvae), the number of replicates must be well chosen. Statistically, at least 5 samples should be taken, but this is again very time-consuming (therefore, only two replicates were taken in the pilot).

Results from the pilot

Also, taxon diversity of soil-dwelling invertebrates on family level (Fig. 4), based on two sampling dates in 2023, is significantly different between forest types ($F_{8,178}$ = 10.97, p < 0.001). The highest taxon diversity was found in deciduous oak forests (FDE, n = 7 forests), followed by coniferous pine (FCP, n = 4 forests) and larch forests (FCL, n = 2 forests). The lowest diversity was again found in evergreen forests of the Macaronesian region (FEL, only sampled on the Azores, n = 4 forests).

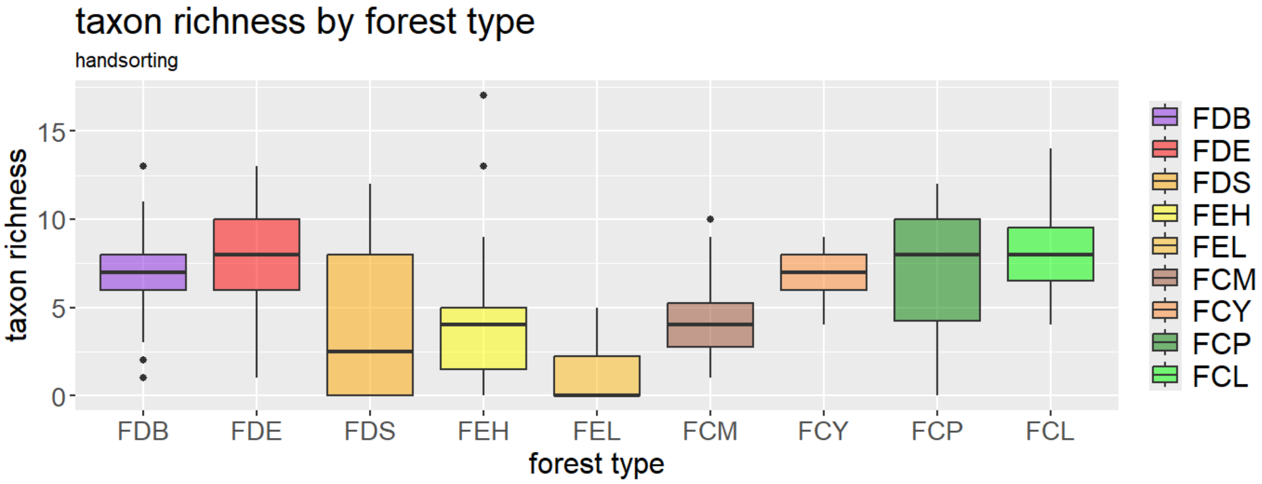

Fig. 4: Taxon diversity (family level) of soil-dwelling invertebrates in different forest types obtained by hand-sorting during two sampling campaigns (spring and autumn 2023). For abbreviations of forest types please see Table of abbreviations.

3.1.3. Taxonomic resolution

A general remark on taxonomic resolution: The pilot will identify spiders and harvestmen (Araneae and Opiliones), ground beetles (Carabidae) and rove beetles (Staphylinidae) to species level. The selection is based on relevance to the soil macrofauna and on the taxonomic expertise of the contracted external company. In general, species identification of soil organisms is hampered by the lack of specialists and by costs. For transnational monitoring it will be important to decide on the taxonomic resolution required (description of local biodiversity vs. patterns across the European Union).

3.2. Molecular methods (eDNA)

General remarks

eDNA metabarcoding has been demonstrated as a powerful technique to survey aquatic biodiversity (Deiner et al., 2017; Keck et al., 2022; Ruppert et al., 2019; Serrana et al., 2019), soil microbial biodiversity (Heyde et al., 2022; Romero et al., 2024), and soil invertebrate biodiversity (Arribas et al., 2021; Calderón-Sanou et al., 2022; Hermans et al., 2022; Leclerc et al., 2023; Lilja et al., 2023; Llanos et al., 2023; Porter et al., 2019; Remmel et al., 2024). The quality of the data as a measure of soil biodiversity highly depends on primer choice, the depth of the soil layer sampled, the amount of starting material, the quality of the reference databases used, and to a lesser extent, other factors such as the DNA-extraction method, and the processing of the eDNA sequence data (Blackman et al., 2024; Dopheide et al., 2019; Jurburg et al., 2021; Kirse et al., 2021; Taberlet et al., 2012).

Advantages:

The main advantage of the eDNA method is that the entire soil community, from microorganisms to micro-, meso- and macrofauna, can be sequenced from a single bulk soil sample. The sampling of the soil is fast, easy and less invasive than any traditional method. DNA extraction and sequencing procedures can be harmonized and centralised in a single laboratory, limiting handling bias. Also, it can detect a wider range of taxa, including cryptic or rare ones, juveniles, etc, that are often missed by traditional methods.

Disadvantages:

The method requires measures to avoid contamination during sampling, processing and storing, and a minimum of laboratory equipment is necessary. For soil invertebrates, the method is less developed compared to applications in aquatic biodiversity monitoring or soil microbial biodiversity monitoring. The primers used by LUCAS and SoilBON to target Eukaryotes are very general, but have limited taxonomic resolution, and do not recover all taxa equally, thereby creating amplification bias (Fig. 5, see 3.3 for more details). Reference sequences are not available for many species, leaving the taxonomic identifications of many Operational Taxonomic Units (OTUs) unclassified. In addition, the current protocol uses a very small amount of soil for DNA extraction and is therefore likely to miss DNA fragments from larger animals.

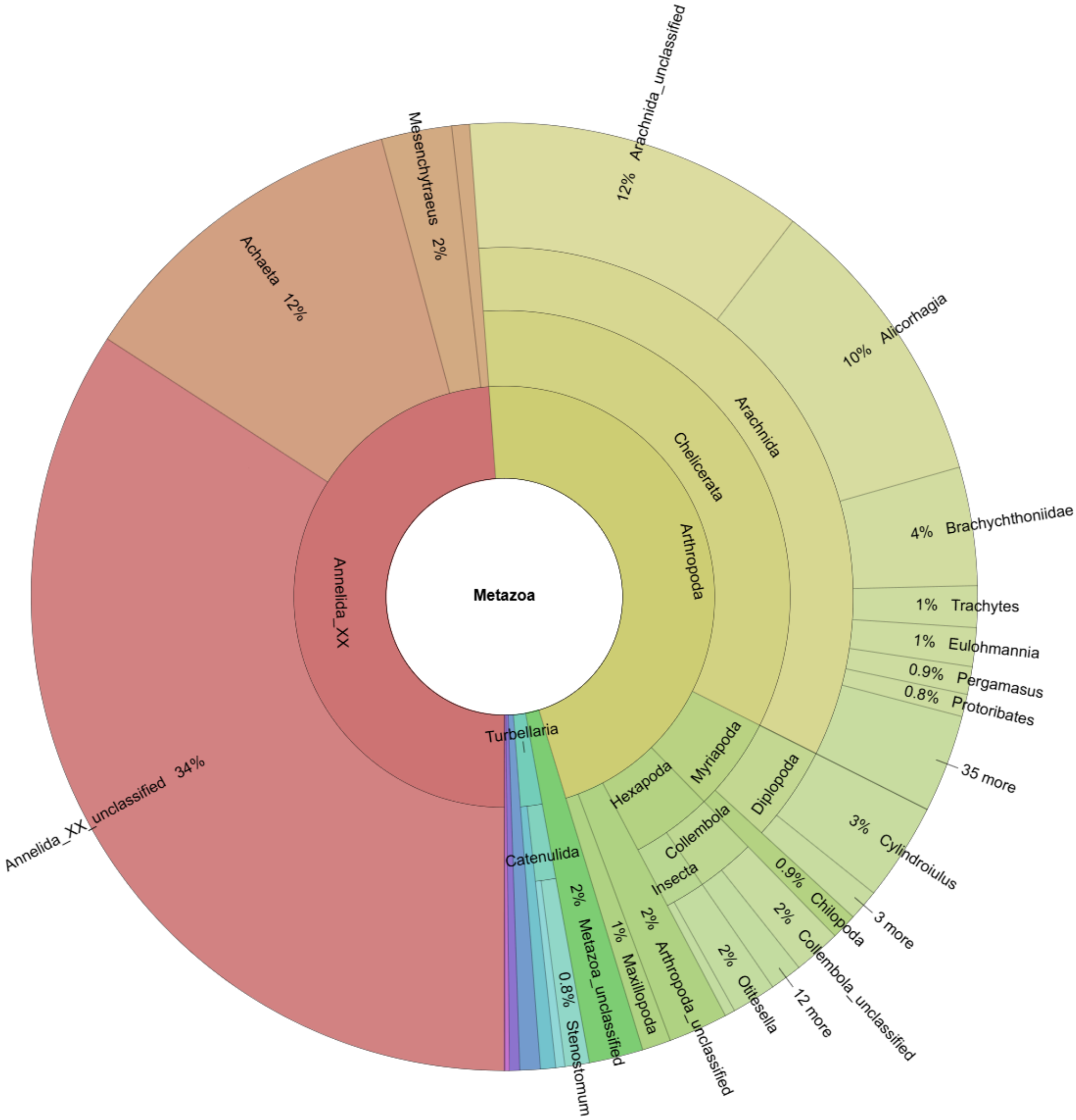

Fig. 5: Overview of invertebrate taxa identified with molecular methods.

3.3. Methodological issues tested in the pilot

Here we focus on comparing the results for soil macrofauna, in particular for representatives of the phylum Arthropoda, considering them to be the most representative taxa in soil samples. Arthropods from hand-sorted soil samples were identified to family level, while sequences were translated using the PR2 reference database.

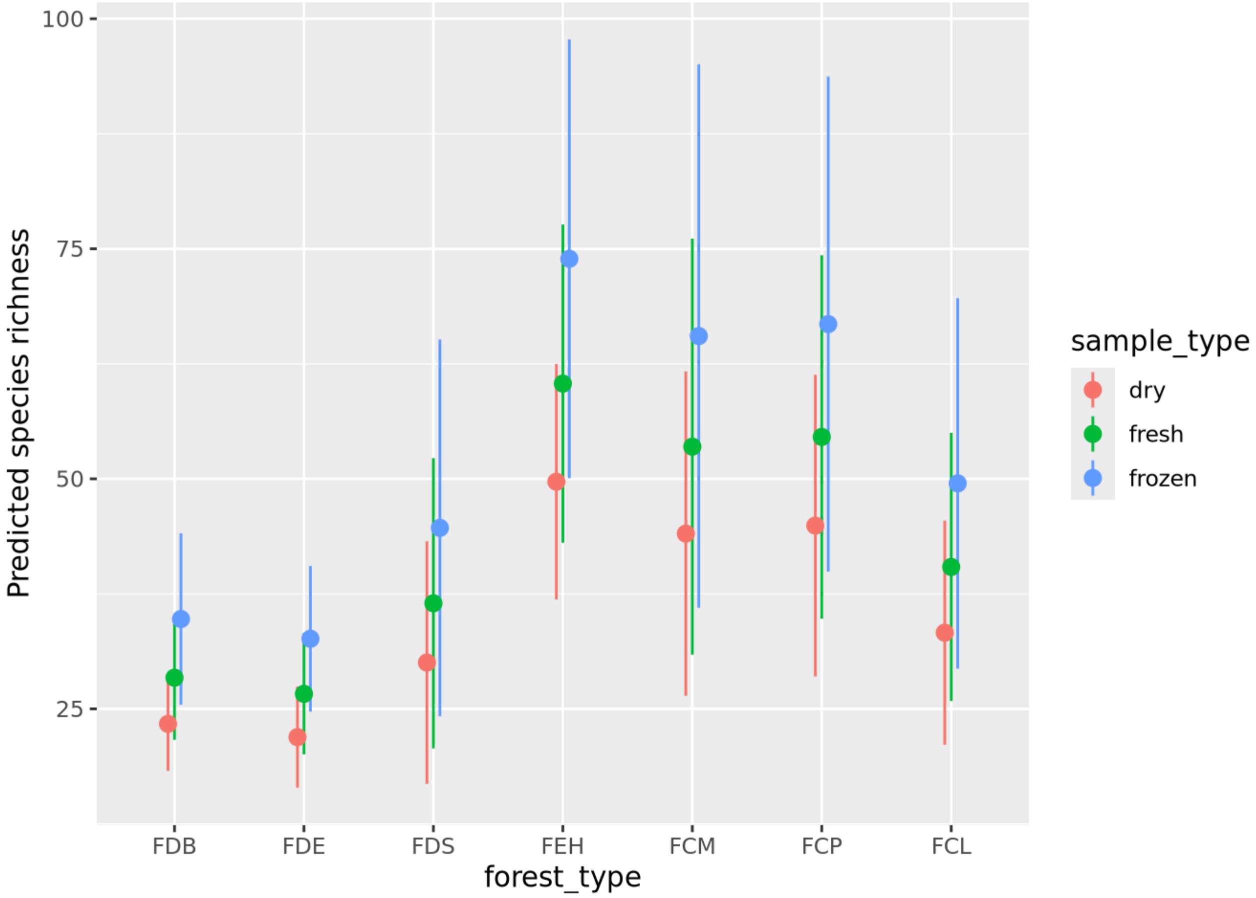

Fig. 6: Predicted species richness for arthropods (ASVs) across different forest- and sample- (dried, fresh and frozen) types. Fresh samples were frozen in the laboratory, frozen samples were put on ice in the field.

For logistical reasons, partners were asked to send dried soil samples, but two partners (Province of Bolzano and Belgium) also provided fresh and frozen samples to allow us to analyse the effect of the drying process on the soil community. Due to the small number of replicates, the results are not yet statistically meaningful, but it is already clear that drying and even freezing soil samples in the lab rather than in the field reduces the alpha diversity of soil organisms. More samples will be analysed in the pilot to look at sample handling in more detail. When analysing the effect of drying on the soil community, it must be taken into account that the duration of the drying process differs between forest types and climatic regions.

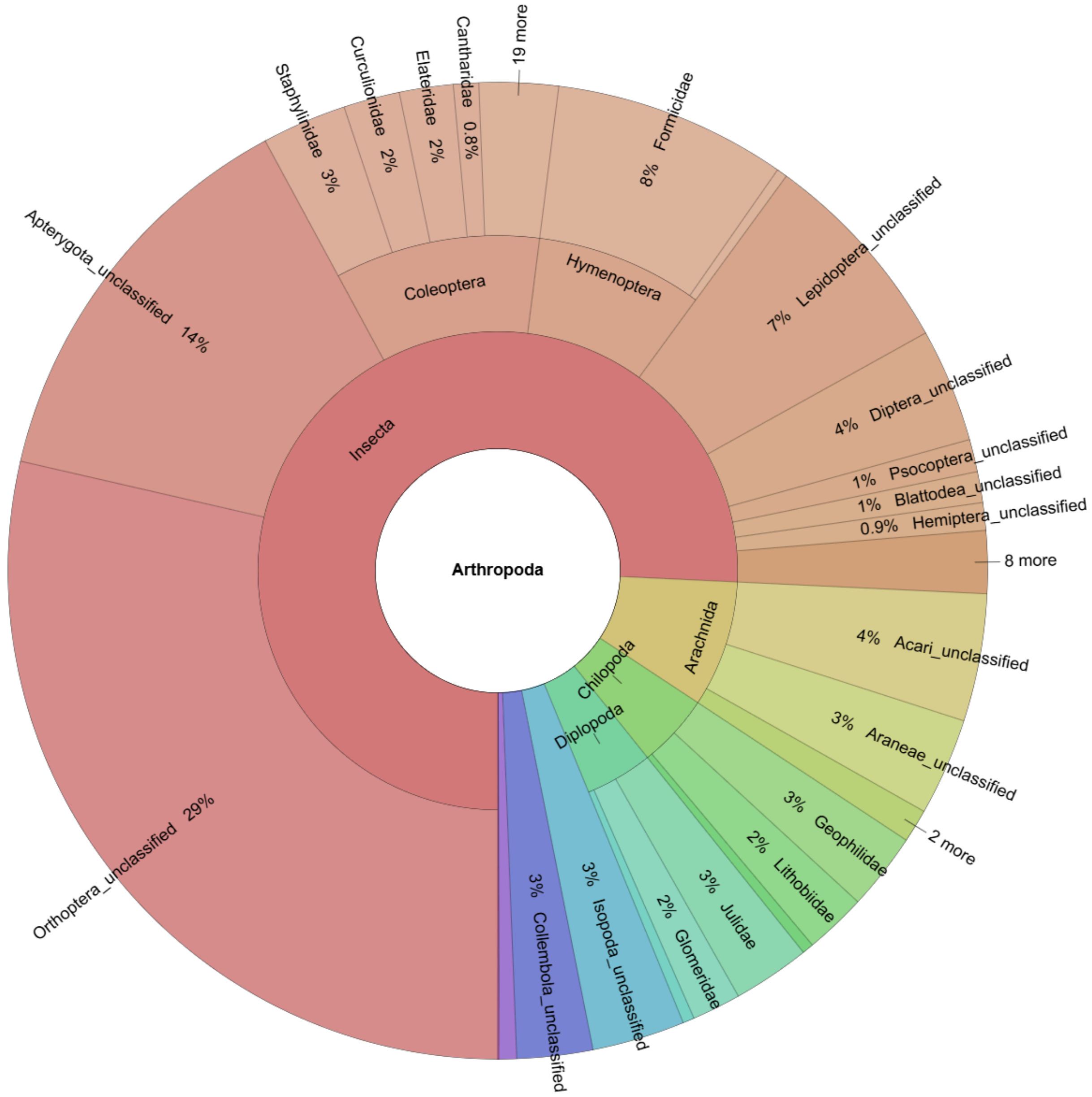

Fig. 7: Proportions of taxa identified from hand-sorted samples.

This comparison mainly shows that what we find as individuals in our samples is not the same as what we find as sequences in the bulk soil (Fig. 7). When we compare the three methods for surveying soil biodiversity—universal 18S primer-based eDNA metabarcoding, handsorting, and pitfall trapping—distinct differences in taxonomic resolution and group-specific performance were observed. Overall, the universal 18S primers used for the eDNA method identified taxa with high resolution for some specific groups, particularly mites (Acari), while handsorting and pitfall trapping identified taxa with much broader taxonomic coverage but lower taxonomic resolution. For mites, the universal 18S primers provided the highest resolution, identifying 34 specific families, whereas the traditional methods tested here recorded them only as "Acari" without family-level identification. In contrast, for beetles (Coleoptera), traditional methods detected 23 families through handsorting and 37 families through pitfall trapping, including ecologically important groups such as Carabidae and Staphylinidae, compared to only six families identified by the universal 18S primers (Elateridae, Aphodiidae, Scirtidae, Scraptiidae, Ptiliidae, Tenebrionidae), of which three families (Elateridae, Scraptiidae, and Tenebrionidae) were shared across all methods. In addition, the universal 18S primers did not recover any spiders (Aranea), demonstrating the limitations of these primers. Both traditional and eDNA methods detected pseudoscorpions and harvestmen. For myriapods, both methods performed comparably, with the universal 18S primers identifying six families and traditional methods identifying five families. Four myriapod families were detected by all methods (Geophilidae, Julidae, Lithobiidae, Polydesmidae), while traditional methods uniquely detected one family (Glomeridae) and eDNA uniquely detected two families (Polyxenidae, Cryptopidae). For springtails (Collembola), the universal 18S primers identified four specific families (Entomobryidae, Isotomidae, Hypogastruridae, Sminthuridae), whereas traditional methods recorded them only as "Collembola" without family-level resolution. These findings provide a glimpse into the strengths and limitations of each method, with the universal 18S primers excelling in taxonomic resolution for certain groups (Acari), but exhibiting biases that limit their ability to detect others.

As future transnational monitoring programmes will likely rely mostly on molecular methods due to the huge effort and cost of traditional methods, the use of eDNA for invertebrates needs to be refined. The following problems were identified and need to be addressed:

Primer development: The universal 18S primers used by LUCAS and SoilBON to target Eukaryotes lack sufficient taxonomic resolution and predominantly amplify protists, with limited recovery of animals such as annelids and arthropods. Also, the proportion of reads attributed to these taxa is typically too small to reliably use their richness as a response variable for monitoring ecological change. Using more targeted primers that enhance amplification of key soil taxa, such as annelids and arthropods, is essential to improve the utility of eDNA for monitoring soil biodiversity (Ficetola & Taberlet., 2022; Giebner et al., 2020; Jurburg et al., 2021; Kirse et al., 2021). Even at the family level, the comparison between traditional and molecular methods shows discrepancies. A possible solution to the primer problem is the use of multiple group-specific primers (Leclerc et al., 2023), bearing in mind that costs increase with each library. For the pilot, it was decided to stick to the primers used for the first season to ensure comparability of data, but depending on the budget, other primers and pipelines (e.g. Olig01 for annelids, Bienert et al., 2012; Coll01 for collembolans, Janssen et al., 2018; Terr_EPTDr2n for annelids and arthropods, Perrelet et al., unpublished) will be tested.

Another issue is the quantity of soil used for DNA extraction. Following the LUCAS protocol for DNA extraction, 0.25 g of soil is used, which is relevant for microorganisms, but not for animals, where at least 15 g is needed (Dopheide et al., 2019; Taberlet et al., 2012).

Reference databases: Incomplete taxonomic reference libraries currently limit the potential of eDNA metabarcoding, specifically for assessing community composition and bioindicator taxa (Blackman et al., 2024, Taberlet et al., 2012). Increased investment in standardized barcoding initiatives to build comprehensive reference libraries is critical to unlocking its full capability for soil biodiversity monitoring. However, it should be noted that with major initiatives such as the International Barcode of Life or the Earth BioGenome underway, the development and expansion of such reference databases is very likely (Blackman et al. 2024).

The decision on how to store soil samples after collection (dried soil, fresh soil, frozen soil, etc.) is important as this will affect the results. Previous studies suggest that freezing the samples in the field is the best way to preserve DNA (van der Heyde et al., 2022), but this may be a challenge, especially in very remote areas. In the pilot, tests were carried out on frozen, fresh and dried soil samples to address this issue and to understand whether storage methods affect diversity, the detection of genera or species, or the observed community structure. The effects may even be different for bacteria, fungi and other eukaryotes. As an additional method, placing the soil in ethanol to preserve DNA should be discussed.

Behaviour of DNA in the environment: Soil eDNA transport remains understudied; however, it is thought to occur primarily in a vertical direction, likely influenced by rainfall (Lyet et al., 2021; Macher et al., 2023; Valentin et al., 2021).

Data interpretation: eDNA metabarcoding currently primarily provides relative abundance data, reflecting the proportional representation of taxa across samples. Abundances may not be absolute due to PCR amplification bias between taxa. Recent advances have explored methods to move towards quantitative metabarcoding, aiming to derive true biomass or abundance of organisms from sequencing data. Several approaches have already shown promise in reducing bias and increasing the reliability of quantitative inferences (e.g. Luo et al., 2022; Shelton et al., 2022; Serrana et al., 2019).

Another discussion point identified which is not related to molecular methods is the depth of the soil layer sampled: the diversity of taxa and eDNA in the 10–30 cm soil layer is insufficient for annelids and arthropods to serve as indicators of ecological changes, making it less suitable for monitoring soil biodiversity (Lambrechts et al., unpublished). Moreover, it is hypothesized that deeper soil layers contain more relic DNA and dead organisms (necromass), inherited from former times, obscuring diversity estimates (Köninger et al., 2023; Lambrechts et al., unpublished).Therefore, efforts to monitor soil biodiversity should focus on the 0–10 cm soil layer (as has been done in the pilot). In addition, the litter layer has shown significant promise for monitoring soil biodiversity through metabarcoding (Ruppert et al., 2023; Zinger et al., 2019).

Table 2: Summary of pros and cons of methods tested in the pilot.

Method	Pros	Cons
pitfall traps	+ cheap + easy to install + suitable for all kinds of habitats + weather-proof + no observer bias	- must be emptied more often under warm weather conditions - time-consuming for remote areas - susceptible to damage by wild animals - contamination by snails and slugs possible - vertebrates might be trapped - for species identification experts are needed

hand-sorting of soil cores	+ cheap + easy method under ideal conditions (few stones and roots) + reduces destructiveness of soil methods by leaving soil in the field	- time-consuming - difficult in sites with dense roots and stony soils - observer bias - for species identification experts are needed
eDNA	+ entire community can be sequenced from a single bulk sample + sampling is easy + less invasive than traditional methods + higher detection rate of rare species and juveniles + analyses can be centralized, limiting handling bias	- Infrastructure is needed to store and process samples - contamination must be avoided - for invertebrates, DNA extraction protocol is not yet optimized - no suitable primer for invertebrates available, increasing costs by the need to use group-specific primers - reference databases not yet fully available

3.4. Questions still to be answered

Administrative, logistic, and legal issues have been identified in the Year 1 report. With the identification of methodological challenges and limitations discussed in this report, we are one step further in developing a transnational monitoring scheme to monitor soil biodiversity. Once the full data is available, the following questions can be addressed:

- Frequency of sampling to assess changes in soil biodiversity (e.g. sampling every 2 years)
- Is seasonal sampling needed to account for within-year variability in species distribution (e.g. spring and autumn sampling)?
- Do all functional groups need to be included (Bacteria, Archaea, Fungi, protists, micro-, meso-, and macro-invertebrates)?
- Is species-level resolution necessary? If not, which taxonomic level is sufficient?
- Which additional measurements would be needed for a more comprehensive list of EBVs? This could include, but is not limited to, the analysis of soil respiration, soil enzymes, soil carbon stocks, and litter decomposition.

4. Conclusions

In this report, we compared the results obtained by **traditional methods** (pitfall traps and hand-sorting of soil cores, both standard methods in soil ecology) and **molecular methods** (eDNA) in order to understand methodological possibilities and limitations for a transnational monitoring scheme. As the traditional methods target only macro-invertebrates (all invertebrates > 2 mm), the comparison is limited to this size group of soil animals. We used data obtained during the first year of the pilot study (spring and autumn 2023 for traditional methods, spring 2023 for molecular methods) for the comparison.

We found traditional methods (pitfall traps and hand-sorting of soil cores) to be cheap, simple and good at providing data suitable for evaluating and monitoring soil invertebrates (activity density or abundance data at family level across all taxa). They can be used to describe the status-quo of local soil biodiversity and to assess changes in soil biodiversity over seasons and years. However, they are time consuming, destructive and require expert knowledge if species level is required.

Molecular methods have great potential for monitoring schemes in general and are already established in aquatic sciences and soil microbiology. The big advantage is that the entire soil community can be analysed from a single sample. However, for the study of soil invertebrates, the method is rather new. We identified several limitations when analysing the data obtained during the first sampling season of the pilot, which need to be solved before using eDNA as standard method in soil biodiversity monitoring:

- Primers: The universal 18S primers used by LUCAS and SoilBON to target Eukaryotes lack sufficient taxonomic resolution and more targeted primers that enhance amplification of key soil taxa, such as annelids and arthropods, is essential to improve the utility of eDNA for monitoring soil biodiversity
- Quantity of soil used for DNA extraction. Following the LUCAS protocol for DNA extraction, 0.25 g of soil is used, which is relevant for microorganisms, but not for animals.
- Reference databases: Incomplete taxonomic reference libraries currently limit the potential of eDNA metabarcoding, specifically for assessing community composition and bioindicator taxa.
- Sample storage: In the pilot, tests were carried out on frozen, fresh and dried soil samples and we found large differences in alpha diversity between samples stored in different ways (not yet statistically significant due to low replicate numbers).
- Data interpretation: eDNA metabarcoding currently primarily provides relative abundance data, reflecting the proportional representation of taxa across samples. Abundances may not be absolute due to PCR amplification bias between taxa. Recent advances have explored methods to move towards quantitative metabarcoding, aiming to derive true biomass or abundance of organisms from sequencing data.

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EUROPEAN PARTNERSHIP

The Automated Biodiversity Monitoring Stations (ABMS) Pilot draft report

A Transnational Sensor Network for Birds, Bats and Insects

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What is Biodiversa+

The European Biodiversity Partnership, Biodiversa+, supports excellent research on biodiversity with an impact for policy and society. Connecting science, policy and practice for transformative change, Biodiversa+ is part of the European Biodiversity Strategy for 2030 that aims to put Europe's biodiversity on a path to recovery by 2030. Co-funded by the European Commission, Biodiversa+ gathers partners from research funding, programming and environmental policy actors in European and associated countries to work on 5 main objectives:

16. Plan and support research and innovation on biodiversity through a shared strategy, annual joint calls for research projects and capacity building activities
17. Set up a network of harmonised schemes to improve monitoring of biodiversity and ecosystem services across Europe
18. Contribute to high-end knowledge for deploying Nature-based Solutions and valuation of biodiversity in the private sector
19. Ensure efficient science-based support for policy-making and implementation in Europe
20. Strengthen the relevance and impact of pan-European research on biodiversity in a global context.

More information at: https://www.biodiversa.eu/

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List of acronyms

ABMS	Automated Biodiversity Monitoring Stations
AI	Artificial Intelligence
AMI	Automated Monitoring of Insects (refers to insect cameras)
BON	Biodiversity Observation Network
BTO	British Trust for Ornithology
EBV	Essential Biodiversity Variable
ENV	Genus aggregate for bats (*Eptesicus, Nyctalus, Vespertilio*)
ERDA	Electronic Research Data Archive (at Aarhus University)
EUNIS	European Nature Information System
FAIR	Findable, Accessible, Interoperable, and Reusable (data principles)
GAM	Generalized Additive Model
GBIF	Global Biodiversity Information Facility
GEO BON	Group on Earth Observations Biodiversity Observation Network
ISO	International Organization for Standardization
LUCAS	Land Use/Cover Area frame Survey
SD	Secure Digital (referring to memory cards)
SFTP	Secure File Transfer Protocol
SSD	Solid State Drive
UKCEH	UK Centre for Ecology & Hydrology
YOLO	You Only Look Once (referring to the YOLOv8 insect segmentation model)

Executive Summary

Addressing biodiversity change means filling data gaps in space and time, building understanding of patterns, trends and drivers of species' spread and decline. Automated methods, including sensors and artificial intelligence (AI), promise to generate affordable and standardized data with extensive spatial, temporal and taxonomic coverage. However, their deployment has rarely been coordinated at transnational scales. The Automated Biodiversity Monitoring Stations (ABMS) pilot implements a transnational sensor network for bats, birds and night-flying insects, evaluating the potential of automation for scalable biodiversity monitoring across Europe and elsewhere.

Running throughout 2024 and 2025, the pilot deployed ~200 sensors at 70 sampling locations across 12 EU member states. Sensors comprised acoustic sensors for birds and bats, camera systems for night-flying insects, and loggers for temperature and moisture. Huge volumes of data were generated; 3 million audible acoustic files, adding up to 5.43 recording-years; 5 million ultrasonic acoustic files, adding up to 1.58 recording-years; over 200,000 time-lapse images, with millions more motion-triggered images, covering more than 8,000 recording-nights. Raw data were transferred to Aarhus University's Electronic Research Data Archive for centralized processing.

To enable centralized processing of images and sounds, we developed three novel open-source AI processing pipelines. We deployed BirdNet for bird detection and classification, BatDetect2 for bat detection and classification, flatbug for insect detection and several custom models for insect classification. These AI models generated over 1 million preliminary species records. However, recognizing the need to understand AI uncertainty, we also undertook an extensive verification programme. Experts from five countries checked 8,690 AI bird detections, while experts from seven countries checked 3,048 AI bat detections. Verifications authenticated records of 127 bird and 24 bat species, and helped to interpret AI outputs. For bats, they allowed us to generate bat activity metrics at appropriate taxonomic resolutions. For birds, they enabled confidence calibration curves, allowing summaries of AI-reliability for 86 European species.

Opportunities for analysis are vast, so we showcase the utility of the data to generate transnational Essential Biodiversity Variable (EBV) indicators. Ecosystem phenology indicators depict the annual rise and fall of bird, bat and insect activity across countries and habitats. Community abundance and taxonomic diversity indicators highlight dominant taxa, and estimate the species richness of each sampling location. Finally, we summarize the lessons learned during the pilot, aided by a partner questionnaire. We capture limitations of sensors, especially when technological readiness level is low, and the need for expert verification and local data processing options. Crucially, 100% of our partners said they could integrate ABMS approaches into their national monitoring; we conclude that sensor networks are a viable tool for transnational monitoring of birds, bats and insects, but that coordination and central data processing are fundamental to success.

5. Introduction

There is widespread concern over the state of biodiversity globally, supported by accumulating evidence of declines in the abundance and diversity of many taxonomic groups. However, patterns vary across time, space, and taxa, while there are significant gaps in the available data. Automated methods for biodiversity monitoring, such as insect camera trapping and passive acoustic monitoring of birds and bats, could help to fill data gaps and better understand trends in biodiversity. Specifically, automated methods may offer more extensive spatial, temporal and taxonomic coverage, with repeatable and standardised data to fill coverage gaps left by intensive traditional monitoring methods.

However, automated methods have rarely been rolled out on international scales - especially for cryptic and difficult to observe taxa such as insects, bats or nocturnal birds. For example, a variety of bat monitoring schemes deploying acoustics devices, but these usually operate at regional or national scales, and efforts are still under way to align protocols (López-Baucells *et al.*, 2025). In short, the feasibility and scalability of novel methods needs further evaluation. This Biodiversa+ pilot aimed to perform such an evaluation, implementing coordinated sampling across biogeographical regions to assess the potential of sensors and AI for European biodiversity monitoring. The taxonomic scope was nocturnal insects, birds and bats, including cryptic and nocturnal taxa, for which automated monitoring methods have been developed but need to be tested at scale. Specific objectives of the ABMS pilot were to:

1. Enable each active contributing partner to operate three multi-taxa sensor stations for at least three months during the 2024 and 2025 growing seasons
2. Develop and make publicly available user-friendly, online databases hosting audio and image data and associated metadata
3. Establish an operational pipeline for recognition of nocturnal insects from images and birds and bats from sound
4. Prepare tools to visualise the locations, identity and time of observation of insect, bird and bat species recognised from image and sound

In building centralized and scalable data infrastructure and analysis pipelines, the pilot attempts to measure the transnational potential of sensor systems. Similarly, coordinated testing and protocol refinement is a proof of principle for more joined-up transnational monitoring, including sharing of digital resources and expertise. The pilot produces recommendations for realistic yet ambitious sensor-based biodiversity monitoring across Europe.

6. Implementation

6.1. Equipment

Acoustic recorders were selected based on their battery life, sound quality, and previous user experiences. We specifically examined products from Wildlife Acoustics, including the Song Meter Mini 2 AA and Song Meter Mini Bat 2 AA, and compared them with the AudioMoth recorder and other devices (Mennill, 2024). Key points are captured below, while broad recommendations related to the equipment used in the ABMS pilot are captured in Table 1.

Song Meter devices:

- Quality: The frequency response is superior to cheaper alternatives.
- Battery life: Powered by 8 AA batteries, offering reasonable longevity for field use.
- Storage capacity: Support for up to a 2 TB SD card, so storage is not a limiting factor.
- Durability: Designed to be robust and well-suited for long-term installations.
- User friendly interface and outputs.

AudioMoth devices:

- Affordability: Priced lower than many competitors, but requires purchase of additional weather-resistant casing.
- Fragility: Based on previous experiences, it is more prone to damage or failure.
- Sensitivity: The AudioMoth is less able to capture faint sounds than Song Meter devices.

We also explored alternatives from Titley Scientific; however, their products were not accessible to all participating partners. In contrast, Wildlife Acoustics products are widely available and commonly used in research projects worldwide.

For automated monitoring of night flying insects, the primary option was Automated Monitoring of Insects (AMI) devices, which had begun to be batch produced by the UK-based companies Rototherm and UKCEH. These had been successfully purchased for the Invasive Alien Species pilot, though there had been delays and challenges - particularly related to a global shortage of Raspberry Pi devices. The only alternative produced and supplied internationally was the DIOPSIS device, which is not specialized for night-flying insects and did not have open-source data processing solutions.

Left: A Song Meter Mini 2 deployed in Denmark. Right: An AMI trap deployed in Belgium. Photo credit Jamie Alison (left) and Lucia Manzanares (right).

Table 1. Recommendations related to equipment used in the ABMS pilot.

Device	Topic	Recommendations
	General	Song Meter devices were found to be accessible and reliable.
Song Meter Mini 2 & Song Meter Mini Bat 2	Placement	● Height: Post or tree (~1m), or tree (4-5m) if there is flood/wildlife/livestock disturbance risk ● Securing: Duct tape or self-locking plastic nylon ties, with a lock where additional security is needed
	Mic Direction	● With prevailing wind: For recording quality and repeatability ● Open spaces, pond, or streams: Maximize bat activity ● Into target habitat: Maximize occurrence of birds or bats
	For bats	● Sample frequency > 250 kHz ● Microphone capable of recording high-frequency sounds
	Batteries	● Disposable batteries are recommended for remote sites, for example ENERGIZER Ultimate Lithium AA FR6/4 1,5 V, 2950 mAh. These often last 2 months for audible and even ultrasound, unless bat activity is extremely high ● Rechargeable batteries can be used for very accessible sites, for example VARTA Recharge Accu Power AA 2100 mAh. These last 2-4 weeks for audible and ultrasound, depending on temperature and bat activity
	Storage	● 1TB means almost an entire season fits on one card, but 512GB is sufficient if emptied during the season. For example, SanDisk Micro SDXC Extreme Pro, read 200 MB/s, write max. 140 MB/s, U3, V30, A2 + SD adapter
AMI devices	General	AMI devices were difficult to obtain and sometimes faulty. If they have no internet connectivity upgrade, visit them once per month
	Placement	● A pedestal may be required in wet areas with flood risk (e.g. steel frame platform, wooden pallet)
	Batteries	● At least one rechargeable deep cycle battery, for example AGM or GEL Sealed Lead Acid batteries ● One 175-watt, or 2 100-watt, solar panel(s) with mounts, facing south, elevated to 20-40 degrees depending on latitude
	Storage	● A 500GB Samsung Portable SSD is large enough to hold an entire year of images, if the jpegs are compressed

6.2. Site selection

To showcase and evaluate novel technologies in diverse ecological contexts, each partner selected three sites representing each of three broad classes of habitats: forest, grassland and wetland. These were defined based on European Nature Information System habitat types (EUNIS; https://eunis.eea.europa.eu/habitats.jsp; Table 2). Forest sites were deciduous broadleaved forest (T1) unless this wasn't possible, in which case partners were advised to select a coniferous forest site (T3) instead. Partners were also instructed to prioritize sites inside Natura 2000 areas. Sites needed to contain large areas of the relevant habitat to establish up to two sampling locations separated by >200m (Fig. 1). Accessibility and long-term viability was also an important consideration during site selection. The map of sites sampled at the end of 2025 is shown in Figure 2, while the distribution across biogeographical regions is shown in Table 3.

Table 2. EUNIS habitat definitions used to define woodland, grassland and wetland habitats in the ABMS pilot. Names and codes are based on the EUNIS 2021 habitat types.

Level	Code	EUNIS name	ABMS habitat
2	T1	Deciduous broadleaved forest	Forest
2	T3	Coniferous forest	Forest
1	R	Grasslands and lands dominated by forbs, mosses or lichens	Grassland
1	Q	Wetlands	Wetland

Top-left: Grassland site in Czechia. Bottom-left: Forest site in the Netherlands. Right: Forest site in the Province of Bolzano. Photo credit Jonas Gaigr (top-left), Rotem Zilber (bottom-left) and Jarek Scanferla (right).

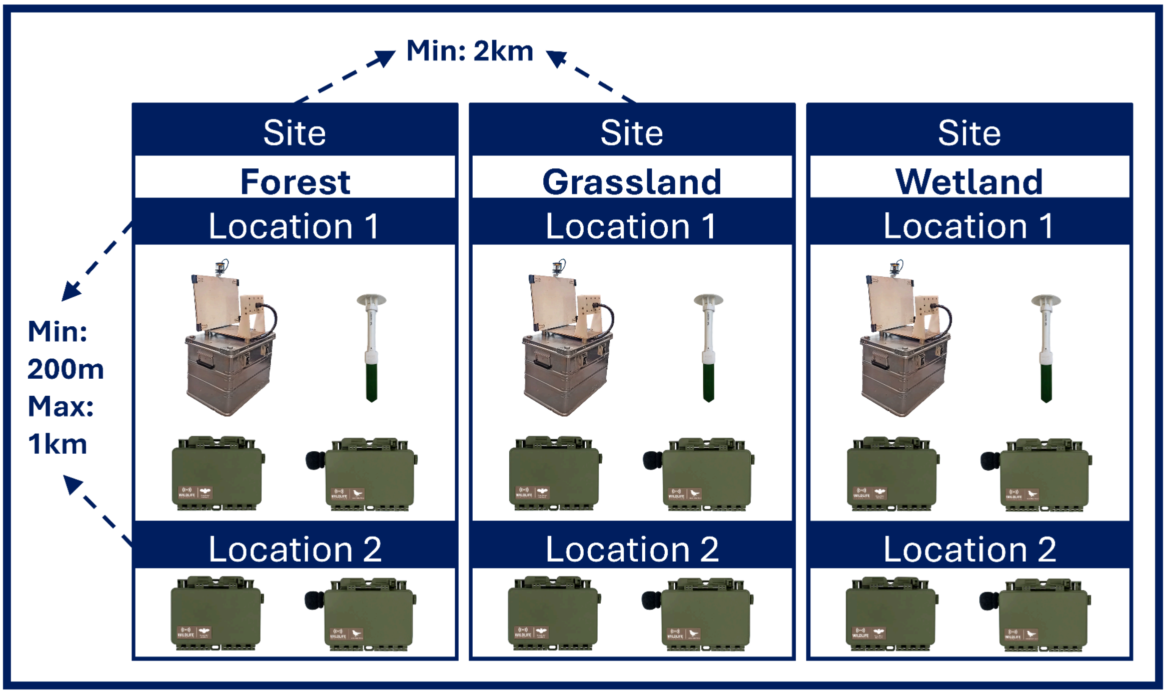


Figure 1. Overall design of ABMS sampling with AMI devices, Song Meter devices and TMS-4 climate loggers. Up to two locations were sampled at sites associated with three broad habitat types: forest, grassland and wetland.

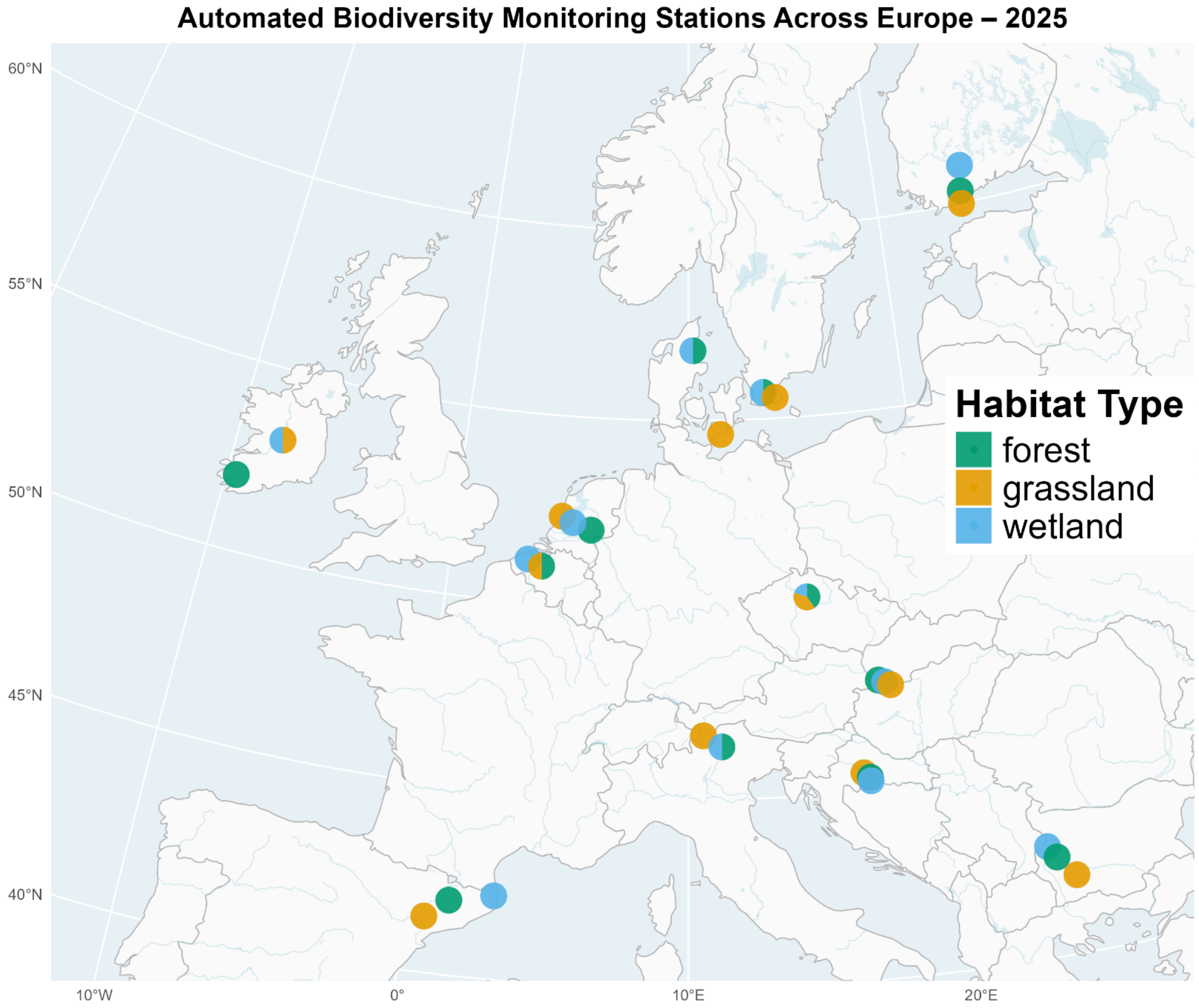


Figure 2. Map of ABMS sampling sites distributed across Europe, selected to represent forest (green), grassland (amber) and wetland (blue) habitats. Up to two locations were monitored at each site. Where two or three sites are highly clustered, points are segmented based on the habitats of the underlying sampling locations - for example five locations in Czechia were very close to one another - two forest, two grassland and one wetland.

Table 3. Distribution of the ABMS sampling locations across biogeographical regions of Europe.

Biogeographical Region	N locations	N grassland	N forest	N wetland
Continental	26	8	10	8
Atlantic	18	6	6	6
Alpine	8	4	2	2
Boreal	6	2	2	2
Mediterranean	6	2	2	2
Pannonian	6	2	2	2

6.3. Device deployment and maintenance

At each site, up to two sampling locations with similar characteristics, representing “replicates” for the site, were selected. One location would be sampled with an AMI trap, Song Meter Mini 2, Song Meter Mini Bat 2, and a TMS-4 logger, while the other would be sampled with only Song Meter devices. Locations were separated by at least 200m, following good practice guidelines for ecoacoustic monitoring (Metcalf *et al.*, 2022), ensuring the relevant habitat type was dominant within 100m of each location. To minimize placement bias, partners were asked to place locations at the closest intersection of the 100×100m EuroStat grid (EPSG:3035, ETRS89-extended / LAEA Europe). Furthermore, to enable a fair comparison of bat activity between locations with/without AMI traps, partners were asked to decide randomly which of the two locations would include the AMI trap and TMS-4 logger.

Pictured: Deploying an AMI trap in the field in Bulgaria. Photo credit Radoslav Stanchev.

Devices were placed in clusters at sampling locations (Fig. 3). The Song Meter Mini 2 and Song Meter Mini Bat 2 were placed on a post or tree (sometimes the same post or tree), 1m from the ground, facing the same direction, ideally with the prevailing wind. The exception was in Croatia, where Song Meter devices were placed higher in the canopy to prevent damage by animals.

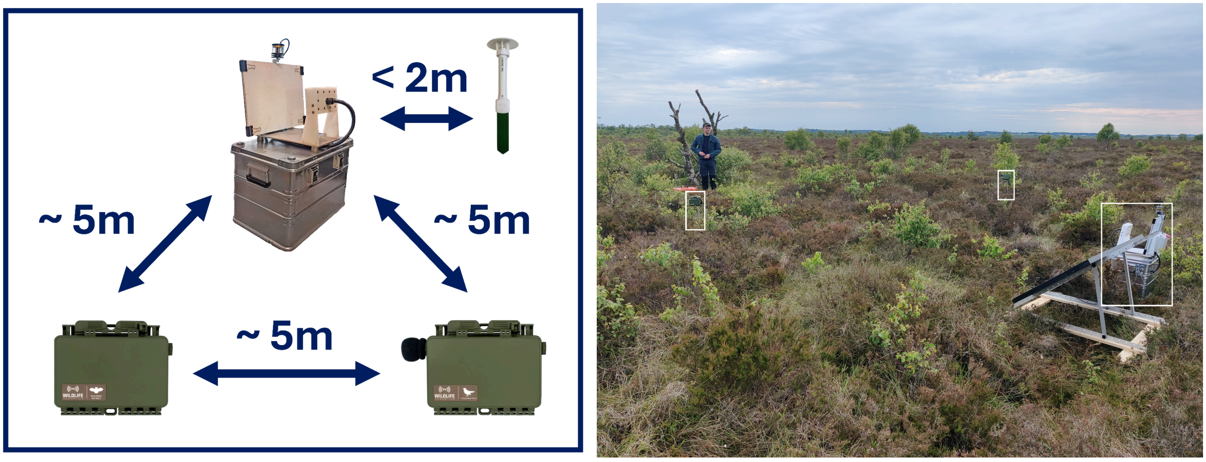


Figure 3. Device deployment in the ABMS. At sites with AMI devices, Song Meter devices were placed around 5m away, while TMS-4 loggers were placed <2m away. Right: Layout of Song Meter devices and an AMI trap (white boxes) at the wetland site in Denmark (photo credit Jamie Alison).

The pilot aimed to keep devices active every day from the beginning of May to the end of October in both 2024 and 2025. As such, we chose recording schedules and duty cycles that enabled acoustic devices to record for weeks, and AMI devices for months, without servicing battery or storage. Recording parameters for acoustic devices are presented in Table 4. AMI devices operated from 11pm to 3am local time, taking a “snapshot” image every 10 minutes (2 minutes in Sweden during 2025). Furthermore, an image was recorded every 2 seconds while motion was detected in the frame.

Table 4. Key parameters used for acoustic monitoring in the ABMS. Minimum frequency to trigger ultrasound recording was lowered from 16kHz in 2024 to 10kHz in 2025 (9 kHz in Croatia), to increase potential to detect Tadarida spp. To further align with parameters used in other bat monitoring schemes (López-Baucells et al., 2025), Croatia adopted a max recording length of 5s. Audible monitoring parameters draw on advice from Metcalf et al. (2022).

Parameter	Song Meter Mini 2	Song Meter Mini Bat 2
Schedule	24 hour	Dusk -1h to dawn +1h
Trigger	None	Above 10kHz (3 second trigger window)
Duty cycle	Recording 1 minute in 5	Always (triggered)
Max recording length	1 minute	15 seconds (min 3 seconds)
Sample rate	48kHz	256kHz (Full-spectrum)

6.4. Processing pipelines

The pilot aimed to design and deploy low-cost, replicable, open-source pipelines to extract ecological data from images and sounds. Importantly, these pipelines should be deployable without any further training. Silva del Pozo *et al.* (2023) highlighted several approaches to harmonized biodiversity monitoring, differing in whether raw data are processed at national or transnational scales. Our pipeline achieves centralized, transnational processing of raw data (see section 3. Data Management), providing the easiest comparison of results. However, considering the need to boost local knowledge, motivation and ownership, we only considered pipelines that partners could feasibly run free-of-charge with local computing resources. While paid or subscription-based processing services were not used for central processing in the pilot, they could minimize technical barriers to local data processing in future. We created a pipeline for acoustics data, with BirdNet (Kahl *et al.*, 2021) and Batdetect2 (Aodha *et al.*, 2022) models for audible and ultrasound respectively, and a pipeline for AMI image data, with custom insect detection models (Svenning *et al.*, 2025) and classifiers (Bjerge, Karstoft & Høye, 2024; Jain *et al.*, 2025).

6.4.1. Acoustics pipeline

Automated processing is crucial to make effective use of acoustic monitoring data. Many software tools are available to efficiently sort and label sounds, facilitating biodiversity analyses. While several indices exist to quantify biodiversity and ecosystem health - for example the Acoustic Complexity Index (ACI), the Acoustic Diversity Index (ADI), and the Bioacoustic Index (BI) - we focus on tools that produce species-level information. Similarly, while commercial software, such as Kaleidoscope Pro from Wildlife Acoustics, offers advanced features for professional labelling of bird songs, frog calls, and bat vocalizations, we focus on tools that are freely available and open-source, at least in terms of model weights.

Birds

Code related to the AI pipeline for birds can be accessed here.

Data management for acoustics was the same for audible and ultrasound data, but AI models and downstream processing differed (Figure 4). For audible acoustic data, BirdNet was the main available open-source solution to detect and classify bird species across Europe (Kahl *et al.*, 2021). Alternatives discussed during the pilot included the BTO Acoustic Pipeline, which requires payment for large scale processing, and AvesEcho, an extension of BirdNet utilizing a wider range of training data (Ghani *et al.*, 2025). We adopted BirdNet, as a published, tried and tested model that was easy to set up. Developed by the Cornell Lab of Ornithology and Chemnitz University of Technology, BirdNet uses machine learning to locate bird sounds in recordings and identify the species. Before analysis, you can adjust various settings, such as the minimum confidence level (affecting the sensitivity of the algorithm), or the candidate species list. The latter is particularly important to prevent the algorithm from searching for all bird species in training data at any given location (over 6000). BirdNET gives the option to generate a reasonable species list, based on eBird, from coordinates provided by the user.

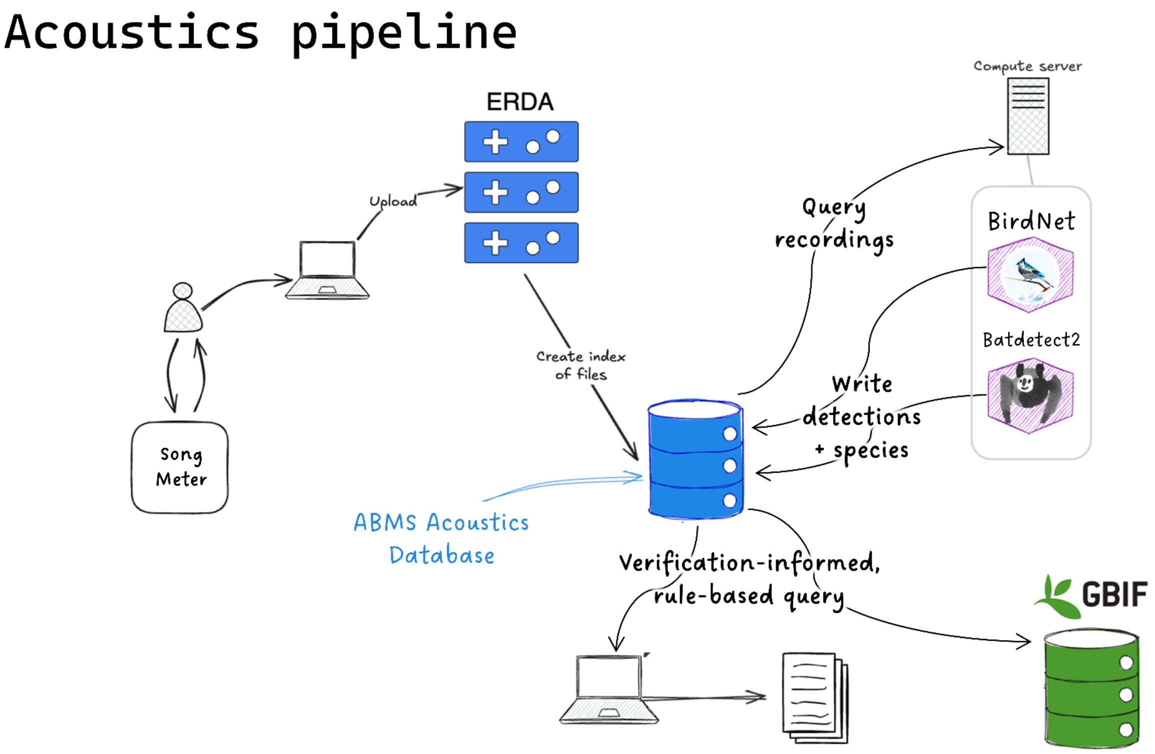


Figure 4. The acoustics data processing pipeline in the ABMS.

We ran BirdNet v2.2 using cloud computing resources at Aarhus University. Raw .wav files were passed to the BirdNet model, along with the location of the recording device, to classify based on a bespoke list of possible species for each site. We set a minimum confidence threshold of 0.1 for BirdNet, opting to produce a full list of predictions for later confidence-based subsetting. We used the default parameters for *Overlap* = 0 and *Sensitivity* = 1, although these could be varied in future iterations to improve performance (Pérez-Granados *et al.*, 2025). BirdNet provides text-based table outputs, where each row is a predicted bird detection within a 3-second snippet of the input .wav file. Each prediction has an associated confidence, which was used to subset data used for downstream analysis. Specifically, for 86 species receiving expert verification from two partner regions during our evaluation of BirdNet (see 2.5. Model evaluation), we used species-specific confidence thresholds to achieve a precision of 0.90, but enforced minimum and maximum thresholds of 0.5 and 0.9. For the remaining species we used a confidence threshold of 0.7, based on previous verifications of the BirdNet model (Wood & Kahl, 2024; Scanferla *et al.*, 2025; Pérez-Granados *et al.*, 2025).

Bats

The current AI pipeline for bats can be accessed here.

For ultrasound data, processing options without payment or further training were even more limited than for birds. BatDetect2 was the main option (Aodha *et al.*, 2022), as we excluded paid services such as Kaleidoscope or the BTO Acoustic Pipeline which are widely deployed in other bat monitoring schemes (López-Baucells *et al.*, 2025). We also excluded alternatives such as ANIMAL-SPOT (Bergler *et al.*, 2022), which does not come pretrained. We opted for BatDetect2, although the most relevant

BatDetect2 model is trained to detect and classify just 17 species of bats occurring in the UK, while upwards of 30 bat species can be found in ABMS partner regions (Battersby, 2010). It uses a machine learning algorithm for joint detection and classification of bats, and provides confidence scores for detection (corresponding to the presence or absence of a bat call) and classification (corresponding to the species for that bat call).

We ran BatDetect2 with the python package, run from the command line (with bash) using cloud computing resources at Aarhus University. Raw .wav files were passed to BatDetect2, which output text based tables corresponding to detections of bats within each file. As with BirdNet, we set a minimum confidence threshold of 0.1, opting to produce a full list of bat call predictions for later confidence-based subsetting. BatDetect2 output tables comprise one row per detected call, of which there were often hundreds for each file, each associated with a bounding box (lower and upper frequency limits, as well as start and end times), a detection confidence and a classification confidence score. These outputs were not immediately biologically meaningful, with many calls from many species in each file.

A rule-base was used to generate file-level detections and classifications from hundreds of calls, lasting for fractions of a second. This rule-base was informed by manual verifications across 7 countries (see 2.5. Model evaluation). This involved iterating over 3,048 verified files, varying the threshold detection and classification confidence, as well as the minimum number of calls above that confidence. Detection was optimized by assuming bats were present where there were 2 or more detected calls above a threshold detection confidence of 0.495. For classification, we accepted the species identity with the highest summed class confidence in calls above the detection threshold, and considered the file to contain multiple species if there were at least 6 calls from each of two species above a threshold classification confidence score of 0.65.

6.4.2. AMI pipeline

Code related to the AI pipeline for insects can be found here, here and here.

Processing of AMI data built on the pipeline developed for AMI devices in the Invasive Alien Species pilot (Høye *et al.*, 2024). First, images were passed through a detection algorithm known as flatbug (Svenning *et al.*, 2025). Flatbug is a YOLOv8 instance segmentation model, pre-trained on images from several other automatic insect localization projects, including >150 AMI trap images. Instance segmentation presents a major advantage compared to bounding boxes, in that when two or more insects are close to each other, bounding boxes can contain several insects, while polygons extract individual insects more precisely. This facilitates the classification process, which is carried out in two stages: Order-level classification of insects and spiders, and species-level classification of Lepidoptera (moths). The order-level classifier is trained on annotations of a wide variety of arthropods seen in AMI trap images from Denmark, and classifies Araneae, Coleoptera, Diptera, Ephemeroptera, Hemiptera, Hymenoptera, Lepidoptera, Neuroptera, Opiliones and Trichoptera (Bjerge *et al.*, 2024). Lepidoptera are further classified as moths that belong to Macroheterocera (i.e. macro-moths) and those that do not (micro-moths). The species-level classifier was trained on a dataset derived from GBIF, covering 2,530 species distributed across the UK and Denmark (Jain *et al.*, 2025). Classifiers trained on larger subsets of European Lepidoptera were trained as a part of the ABMS, but these models were not sufficiently refined to use for processing for this report (see 2.5. Insect classifiers).

2.5. Insect classifiers).

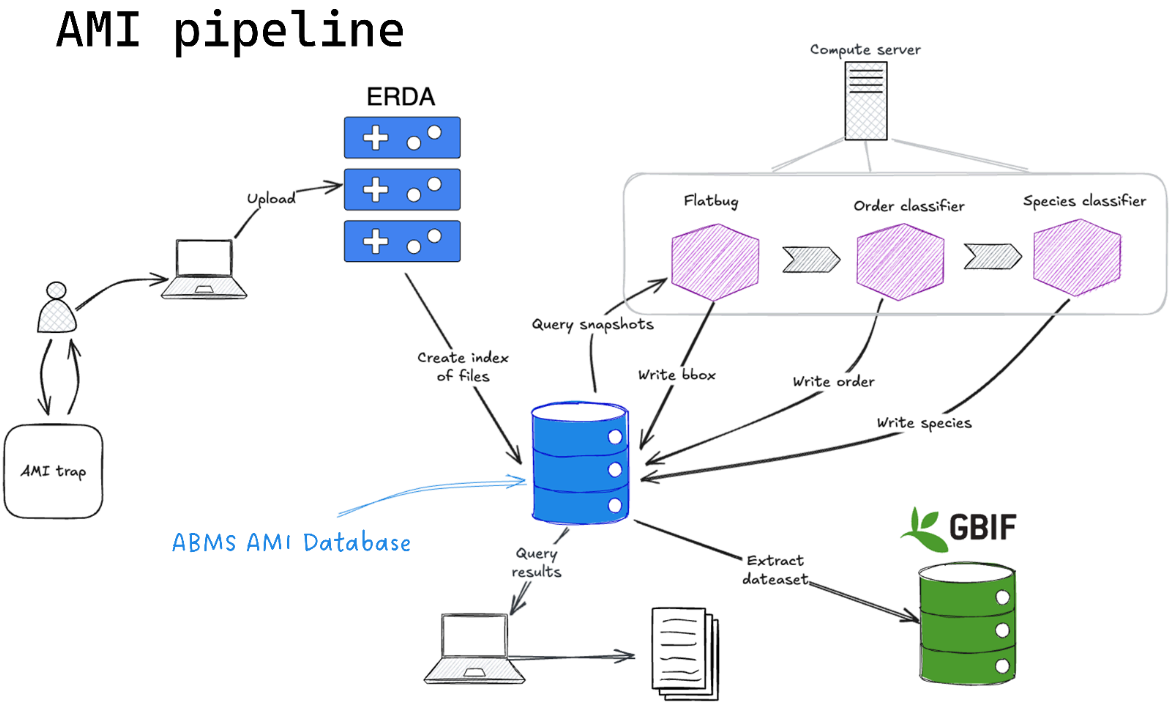


Figure 4. The AMI data processing pipeline in the ABMS pilot.

6.4.3. Model evaluation

When deploying AI models in the pilot, it was considered vital to verify a subset of AI outputs, and quantify model performance in the context of the pilot. For birds and bats, we sent a strategic subset of data from 2024 for expert verification. For moths, we used a dataset from AMI traps in Denmark to evaluate the species classifier. We also developed an interactive tool to visualize and label insects in images (see 5.2. Data visualization and smart annotation with AnnFlux).

BirdNet

When verifying outputs of BirdNet, we aimed to quantify uncertainty, but also build confidence calibration curves (Wood & Kahl, 2024) to improve interpretation of BirdNet outputs for Europe-wide monitoring. Six partners were able to make experts available to verify AI predictions from 2024, of which five were available for this report. We selected species for verification based on the presence of at least three detections in each of nine confidence bands, ranging from 0.1-0.2, to 0.9-1.0. We then took a random sample of 27 3-second recordings of those species: three recordings from each of the nine confidence bands (note, for many species, verifiers expressed that they would have preferred significantly longer recordings to be sure about their IDs; see 5.2. Working with sensor data). The number of species sent for verification ranged from 29 for Ireland, to 133 for Denmark, and depended on the amount of recordings taken in 2024 as well as local diversity.

The verification process was made as efficient as possible, with a focus on identification of false positive detections. Given a single page of guidance on bird verification, the verifier simply answered the question: *Can the AI-suggested species be identified in the recording?* A yes or no answer was provided by entering a “1” or “0” in a provided table, as well as the initials of the verifier and some notes where applicable. Not all species sent to each partner were able to be verified in the time available, and partners prioritized species that were most common or most interesting for local monitoring needs.

Experts from Belgium, the Province of Bolzano, Denmark, Ireland and Slovakia verified 8,690 files with bird species predictions, of which 4,909 were deemed correct. Of 142 species proposed by BirdNet and verified by at least one partner, 127 were considered correct in at least one recording. Only six species were fully verified by all five partners (of which only four were confirmed in all regions): *Ardea cinerea, Athene noctua, Erithacus rubecula, Strix aluco, Troglodytes troglodytes* and *Turdus iliacus*. Given 27 verifications per species per country, it was possible to produce provisional confidence calibration curves for each species in each country (e.g. Fig. 5). This process hinted at distinct curves between countries, which could relate to variation in calls and call types, background noise, confusion species, and observer effects.

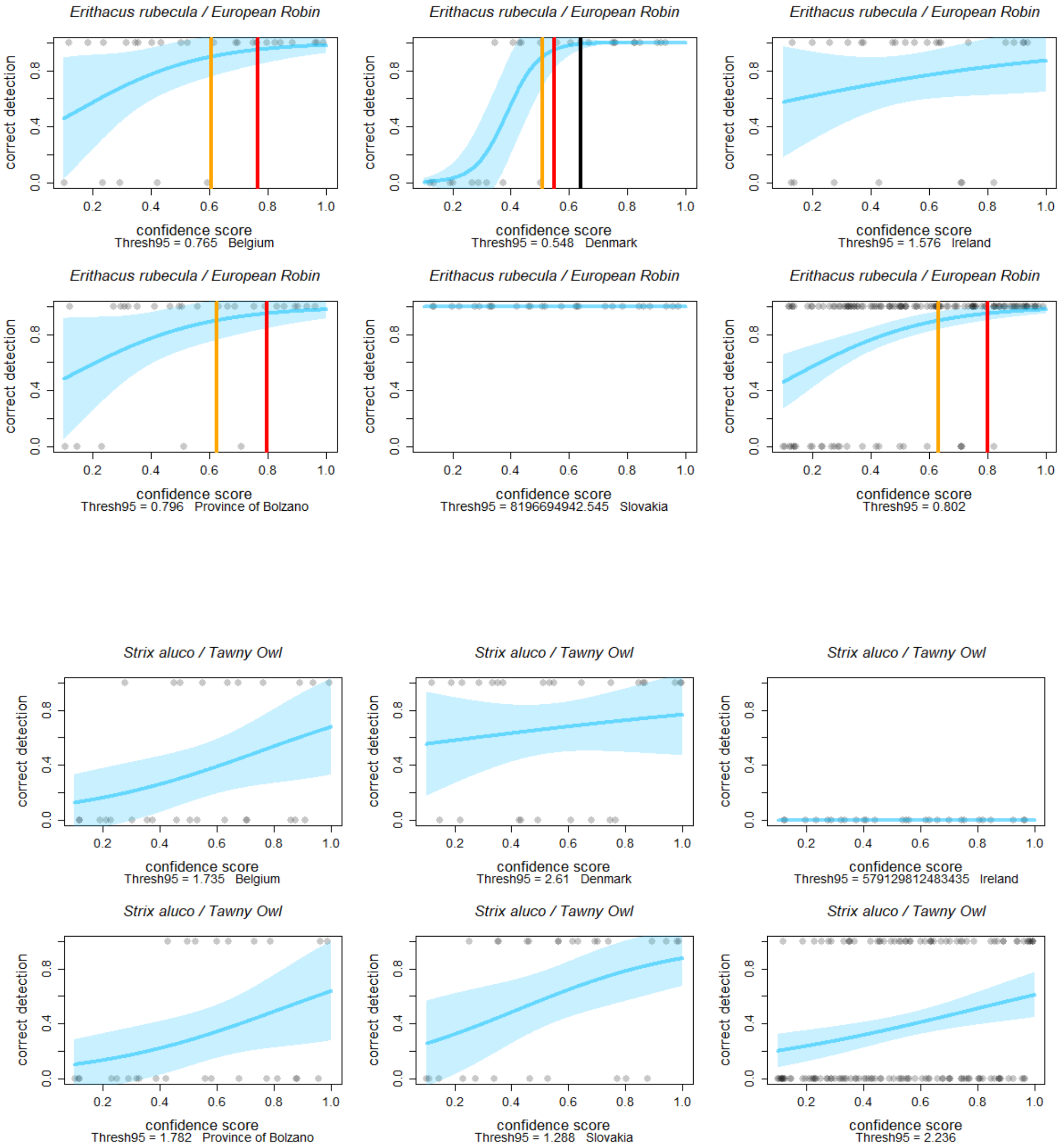


Figure 5. Confidence calibration curves for Erithacus rubecula (top six) and Strix aluco (bottom six) across Belgium, Denmark, Ireland, the Province of Bolzano, Slovakia, and all five countries combined. The graphs show precision, or the proportion of BirdNet detections that are correct, across confidence scores from 0.1-1. For Erithacus rubecula in Slovakia, all calls were confirmed, regardless of confidence, while Strix aluco was never confirmed in Ireland. For Erithacus rubecula, it is possible to set confidence thresholds to achieve precision of 0.90 (yellow line) and 0.95 (red line) across the five countries, while in Denmark it was even possible to set a threshold for 0.99 precision (black line).

A total of 86 species had at least 54 verifications across two or more partner regions for a more reliable confidence calibration. This allowed the assignment of species to traffic light groupings (Table 5) based on precision, which represents the proportion of classifications of a species that are correct. For example, precision didn’t reach 0.9 at any confidence in any region for *Strix aluco* (Fig. 5, bottom). However, we can achieve 50% precision with a threshold of 0.778, thus *Strix aluco* is considered an amber species by the ABMS. Clearly detections of this species should be interpreted with caution. On the other hand, *Erithacus rubecula* is a green species, as 90% precision can be ensured by setting a confidence threshold of 0.633 (Fig. 5, top). Finally, *Athene noctua* is an example of a red species, as even 50% precision cannot be achieved; this species was commonly mistaken for dogs, cats and foxes according to the verifier from Slovakia.

Transnational confidence curves were further explored and used to improve data processing. Specifically, for 86 species with verification data across two or more regions (Table 5) we applied a custom confidence threshold to achieve a precision of 90%, but enforced minimum and maximum thresholds of 0.5 and 0.9. Recent work suggests that confidence thresholds above 0.5 can remove false-positives, but increase false-negatives (Pérez-Granados *et al.*, 2025). While we favoured precision, we used the 90% over the 95% precision threshold, because the latter would lead to a disproportionate increase in false-negative bird detections.

Table 5. Results of confidence calibration for species identification with BirdNet. Confidence calibration used 8,690 expert verifications from five regions: Belgium, Province of Bolzano, Denmark, Ireland and Slovakia. Species shown here had at least 54 3-second snippets verified across a minimum of two partner regions. Threshold confidence scores to achieve 50%, 90% and 95% precision are shown, and species are assigned to traffic light (green, amber and red) groupings based on this. Coloeus monedula is referred to as Corvus monedula, in keeping with BirdNet naming.

Species	**N snippets**	**N regions**	**0.50 prec. threshold**	**0.90 prec. threshold**	**0.95 prec. threshold**
Merops apiaster	54	2	0.000	0.000	0.000
Certhia familiaris	108	4	0.000	0.208	0.000
Sitta europaea	108	4	0.097	0.126	0.135
Phylloscopus collybita	108	4	0.057	0.214	0.267
Alauda arvensis	54	2	0.107	0.292	0.355
Cyanistes caeruleus	117	4	0.013	0.363	0.482
Cuculus canorus	81	3	0.029	0.412	0.542
Corvus monedula	81	3	0.189	0.464	0.558
Dendrocopos major	108	4	0.159	0.467	0.572
Corvus corax	108	4	0.135	0.477	0.593
Prunella modularis	54	2	0.023	0.449	0.593
Linaria cannabina	54	2	0.000	0.420	0.623
Turdus merula	108	4	0.000	0.451	0.633
Fringilla coelebs	108	4	0.000	0.437	0.674
Troglodytes troglodytes	135	5	0.000	0.432	0.702
Phasianus colchicus	81	3	0.000	0.518	0.718
Garrulus glandarius	108	4	0.000	0.530	0.725
Cettia cetti	54	2	0.313	0.636	0.746

Gallinago gallinago	81	3	0.115	0.589	0.750
Parus major	96	4	0.000	0.498	0.785
Erithacus rubecula	135	5	0.135	0.633	0.802
Motacilla alba	81	3	0.352	0.688	0.803
Pica pica	81	3	0.123	0.640	0.815
Certhia brachydactyla	108	4	0.288	0.686	0.822
Regulus regulus	108	4	0.142	0.660	0.837
Dryocopus martius	81	3	0.234	0.703	0.862
Phylloscopus trochilus	54	2	0.295	0.719	0.863
Curruca communis	54	2	0.202	0.727	0.905
Columba palumbus	81	3	0.071	0.701	0.915
Sylvia atricapilla	108	4	0.000	0.608	0.916
Apus apus	54	2	0.603	0.855	0.941
Emberiza schoeniclus	81	3	0.165	0.771	0.977
Carduelis carduelis	108	4	0.000	0.709	0.987
Anthus pratensis	108	4	0.000	0.543	NA
Delichon urbicum	81	3	0.000	0.639	NA
Hirundo rustica	108	4	0.000	0.723	NA
Turdus viscivorus	54	2	0.000	0.747	NA
Aegithalos caudatus	108	4	0.055	0.789	NA
Anser anser	81	3	0.330	0.835	NA
Poecile palustris	81	3	0.000	0.846	NA
Spinus spinus	54	2	0.448	0.869	NA
Turdus philomelos	81	3	0.271	0.965	NA
Pernis apivorus	54	2	0.293	0.980	NA
Tringa nebularia	54	2	0.497	0.987	NA
Picus viridis	108	4	0.155	NA	NA
Buteo buteo	108	4	0.242	NA	NA
Muscicapa striata	108	4	0.257	NA	NA
Alcedo atthis	54	2	0.318	NA	NA
Anas platyrhynchos	108	4	0.475	NA	NA
Corvus frugilegus	108	4	0.489	NA	NA
Ficedula hypoleuca	81	3	0.495	NA	NA
Nucifraga caryocatactes	54	2	0.548	NA	NA
Rallus aquaticus	108	4	0.607	NA	NA
Dendrocoptes medius	54	2	0.620	NA	NA
Fringilla montifringilla	54	2	0.648	NA	NA
Anas crecca	54	2	0.678	NA	NA
Ardea cinerea	135	5	0.705	NA	NA
Tringa ochropus	81	3	0.707	NA	NA
Anthus trivialis	108	4	0.769	NA	NA
Strix aluco	135	5	0.778	NA	NA
Dryobates minor	81	3	0.783	NA	NA

Fulica atra	54	2	0.846	NA	NA
Motacilla cinerea	81	3	0.847	NA	NA
Columba oenas	54	2	0.872	NA	NA
Numenius arquata	54	2	0.879	NA	NA
Mareca strepera	54	2	0.922	NA	NA
Phoenicurus phoenicurus	81	3	NA	NA	NA
Botaurus stellaris	81	3	NA	NA	NA
Caprimulgus europaeus	54	2	NA	NA	NA
Asio otus	54	2	NA	NA	NA
Bubo bubo	54	2	NA	NA	NA
Tyto alba	54	2	NA	NA	NA
Athene noctua	135	5	NA	NA	NA
Coturnix coturnix	54	2	NA	NA	NA
Scolopax rusticola	108	4	NA	NA	NA
Ixobrychus minutus	108	4	NA	NA	NA
Coccothraustes coccothraustes	108	4	NA	NA	NA
Calidris alpina	54	2	NA	NA	NA
Pyrrhula pyrrhula	54	2	NA	NA	NA
Turdus iliacus	135	5	NA	NA	NA
Phoenicurus ochruros	54	2	NA	NA	NA
Nycticorax nycticorax	108	4	NA	NA	NA
Cygnus cygnus	54	2	NA	NA	NA
Grus grus	81	3	NA	NA	NA
Locustella naevia	54	2	NA	NA	NA
Ficedula parva	54	2	NA	NA	NA

BatDetect2

When verifying outputs of BatDetect2, we aimed to quantify uncertainty, but also to refine a rule-base to translate BatDetect2 outputs, with hundreds of detected calls, to species- or genus-level occurrences at the file-level. We also aimed to determine the taxonomic level at which it is sensible to interpret AI outputs. Experts from Belgium, Bulgaria, Denmark, Finland, Ireland, Slovakia and Sweden were able to make experts available to verify AI predictions from 2024. As only 17 species can be predicted by BatDetect2, we sent examples of all species to each expert to be verified. For each species, files were selected by randomly selecting up to four predicted calls in each of nine confidence bands, ranging from 0.1-0.2, to 0.9-1.0. The file corresponding to each call was sent for verification. Given there were very few calls in the highest confidence band of 0.9-1.0, this generally resulted in a maximum of 32 files, of a maximum of 15 seconds, per species.

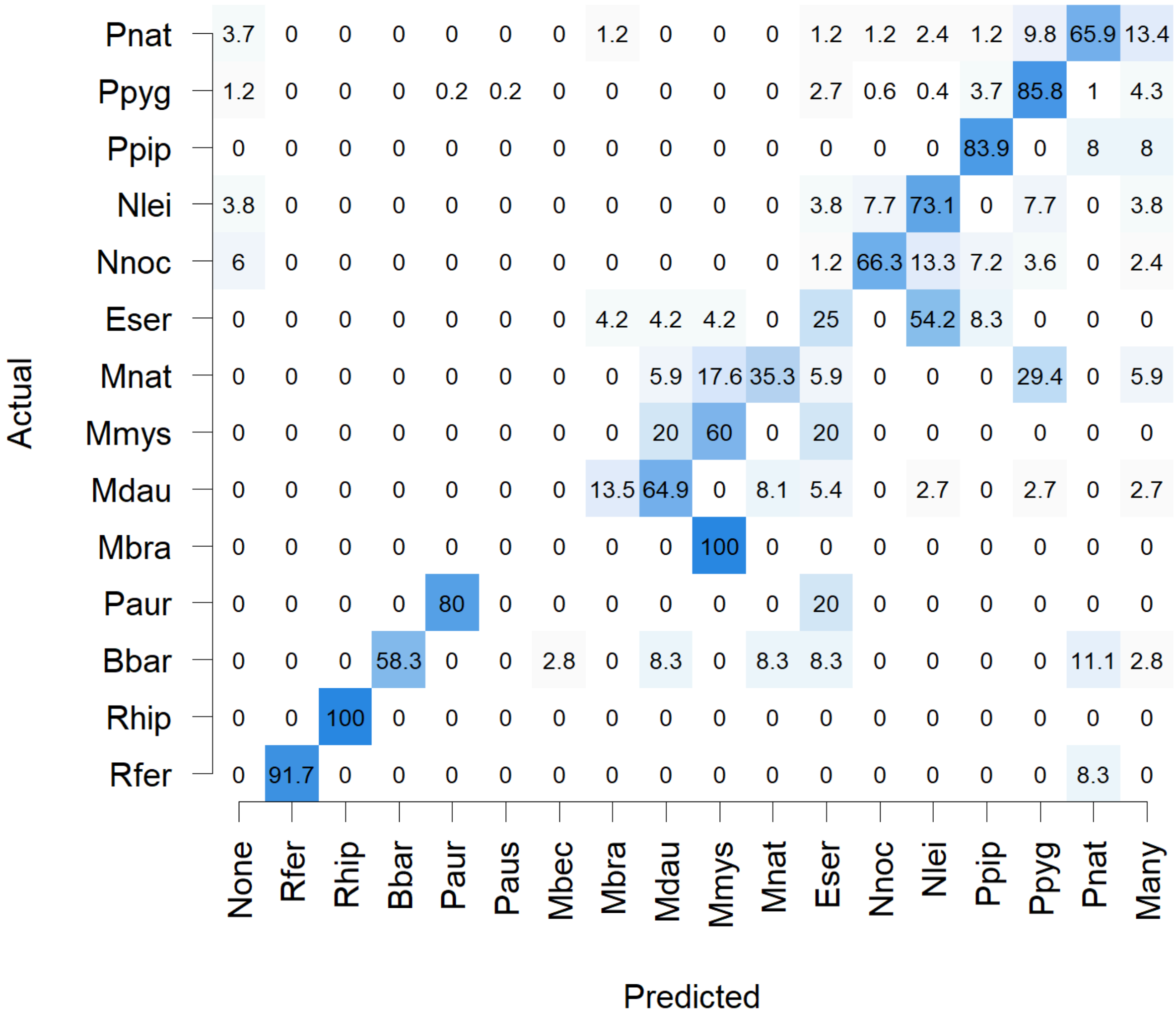
For bat verification, we focused heavily on detection as well as classification, aiming to capture not only false-positive detections, but also quantify misclassification. Given a single page of guidance on bat verification, the verifier answered three questions: *Does the window contain a call from the suggested species? If not, what would you identify the call in the window as? Does the file contain multiple bats (of any species)?* The answers to the first two questions were used to evaluate BatDetect2. Verifications ultimately corresponded to the entire file - not just the small time window in which the call was detected.

Verifiers provided bat identifications (or absences) for all 3,048 files according to their own taxonomies, which were aligned and unified in order to ensure interoperability of the seven datasets (Tables 6 & 7).

Table 6. Bat verifications across 3,048 files, focussing on species-level IDs. While 1762 files had no species ID, most of these contained bats that were not identified to species resolution (see Table 7). Verifiers confirmed 24 species in total, including one individual of Vespertilio murinus in Sweden, included here under "Many bat species" (it occurred in the same file as another Pipistrellus pygmaeus). Species codes, corresponding grouping under a Genus/ENV aggregate, and number of verified files are also shown. Seven species not featured in the BatDetect2 training set are in bold.

Code	Species name	Genus/ENV aggregate	Verified
Many	Many bat species	-	208
Pkuh	***Pipistrellus kuhlii***	***Pipistrellus***	**1**
Pnat	*Pipistrellus nathusii*	*Pipistrellus*	82
Ppip	*Pipistrellus pipistrellus*	*Pipistrellus*	174
Ppyg	*Pipistrellus pygmaeus*	*Pipistrellus*	513
Nlas	***Nyctalus lasiopterus***	**ENV**	**1**
Nlei	*Nyctalus leisleri*	ENV	26
Nnoc	*Nyctalus noctula*	ENV	83
Enil	***Eptesicus nilssonii***	**ENV**	**34**
Eser	*Eptesicus serotinus*	ENV	24
Hsav	***Hypsugo savii***	***Hypsugo***	**15**
Malc	*Myotis alcathoe*	*Myotis*	0
Mbec	*Myotis bechsteinii*	*Myotis*	0
Mbra	*Myotis brandtii*	*Myotis*	1
Mdas	***Myotis dasycneme***	***Myotis***	**2**
Mdau	*Myotis daubentonii*	*Myotis*	37
Mema	***Myotis emarginatus***	***Myotis***	**7**
Mmys	*Myotis mystacinus*	*Myotis*	5
Mnat	*Myotis nattereri*	*Myotis*	17
Paur	*Plecotus auritus*	*Plecotus*	5
Paus	*Plecotus austriacus*	*Plecotus*	1
Bbar	*Barbastella barbastellus*	*Barbastella*	36
Tten	***Tadarida teniotis***	***Tadarida***	**1**
Rfer	*Rhinolophus ferrumequinum*	*Rhinolophus*	12
Rhip	*Rhinolophus hipposideros*	*Rhinolophus*	2
None	No species ID	-	1762

The rule-base to convert call detections into file-level verifications was determined based on the verification data (See 2.4.1. Acoustics pipeline). With a detection rule of two or more calls above 0.495 detection confidence, we achieved a detection macro-F1 score of 0.924. Of files confirmed to contain bats, 97.4% were also predicted to contain bats. However, there were still a number of false positives, as 13.9% of files confirmed to contain no bats were still predicted to contain bats. For files where the verifier confirmed one of the 17 BatDetect2 species, classification performance was reasonable for e.g. *Pipistrellus* but poor for e.g. *Myotis* (Fig. 6). Poor performance for *Myotis* was expected; experts often cannot separate species in this genus, for example *M. brandtii* and *M. mystacinus*. Of 61 files with bats identified as species not in the BatDetect2 training data, 59 were successfully detected, but classified as other bat species (Fig A1).

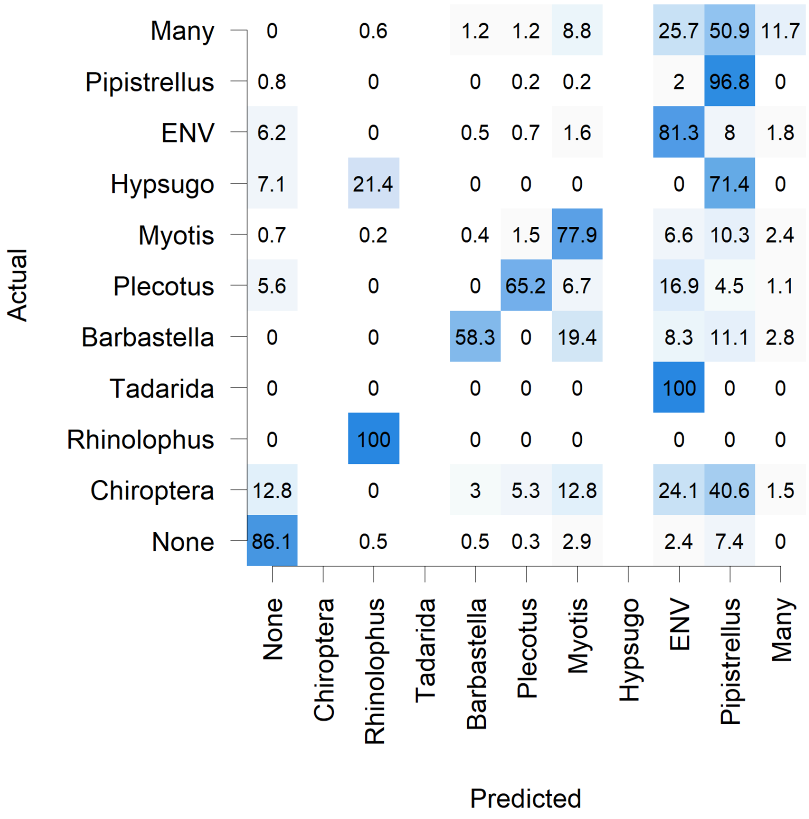


	None	Rfer	Rhip	Bbar	Paur	Paus	Mbec	Mbra	Mdau	Mmys	Mnat	Eser	Nnoc	Nlei	Ppip	Ppyg	Pnat	Many
Pnat	3.7	0	0	0	0	0	0	1.2	0	0	0	1.2	1.2	2.4	1.2	9.8	65.9	13.4
Ppyg	1.2	0	0	0	0.2	0.2	0	0	0	0	0	2.7	0.6	0.4	3.7	85.8	1	4.3
Ppip	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.9	0	8	8
Nlei	3.8	0	0	0	0	0	0	0	0	0	0	3.8	7.7	73.1	0	7.7	0	3.8
Nnoc	6	0	0	0	0	0	0	0	0	0	0	1.2	66.3	13.3	7.2	3.6	0	2.4
Eser	0	0	0	0	0	0	0	4.2	4.2	4.2	0	25	0	54.2	8.3	0	0	0
Mnat	0	0	0	0	0	0	0	0	5.9	17.6	35.3	5.9	0	0	0	29.4	0	5.9
Mmys	0	0	0	0	0	0	0	0	20	60	0	20	0	0	0	0	0	0
Mdau	0	0	0	0	0	0	0	13.5	64.9	0	8.1	5.4	0	2.7	0	2.7	0	2.7
Mbra	0	0	0	0	0	0	0	0	0	100	0	0	0	0	0	0	0	0
Paur	0	0	0	0	80	0	0	0	0	0	0	20	0	0	0	0	0	0
Bbar	0	0	0	58.3	0	0	2.8	0	8.3	0	8.3	8.3	0	0	0	0	11.1	2.8
Rhip	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rfer	0	91.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8.3	0

Figure 6. Species-level confusion matrix for BatDetect2, for files where verifiers provided a single species-level ID (see Table 6 for numbers of files per species). Paus and Mbec were not recorded in any files, so the diagónal of the confusion matrix is shifted. A large proportion of errors occur within Myotis, and within the ENV Genus aggregate. “Many” indicates where several bat species were detected in a given file.

Given the mixed performance of BatDetect2 at species-level, as well as the fact that some species cannot be reliably distinguished by experts, we opted to interpret BatDetect2 outputs at Genus level.

However, we further lumped easily-mistaken genera *Eptesicus, Nyctalus* and *Vespertilio* into the ENV aggregate, giving a class that could be classified with an F1 of 81.3% (Fig. 7). The overall performance of our BatDetect2 classification pipeline at the level of genus/ENV aggregate was 82% (Macro-F1; Fig. 7). While 100% of *Rhinolophus* and 96.8% of *Pipistrellus* were identified correctly by the pipeline, this was only true for 58.3% of *Barbastella* and 65.2% of *Plecotus*. During further analysis, to retain detail within *Pipistrellus*, which was both abundant and relatively well classified by BatDetect2 (Fig. 6), we treated *Pipistrellus pipistrellus/pygmaeus* and *P. nathusii* separately.



	None	Chiroptera	Rhinolophus	Tadarida	Barbastella	Plecotus	Myotis	Hypsugo	ENV	Pipistrellus	Many
Many	0		0.6		1.2	1.2	8.8		25.7	50.9	11.7
Pipistrellus	0.8		0		0	0.2	0.2		2	96.8	0
ENV	6.2		0		0.5	0.7	1.6		81.3	8	1.8
Hypsugo	7.1		21.4		0	0	0		0	71.4	0
Myotis	0.7		0.2		0.4	1.5	77.9		6.6	10.3	2.4
Plecotus	5.6		0		0	65.2	6.7		16.9	4.5	1.1
Barbastella	0		0		58.3	0	19.4		8.3	11.1	2.8
Tadarida	0		0		0	0	0		100	0	0
Rhinolophus	0		100		0	0	0		0	0	0
Chiroptera	12.8		0		3	5.3	12.8		24.1	40.6	1.5
None	86.1		0.5		0.5	0.3	2.9		2.4	7.4	0

Figure 7. Genus/ENV aggregate-level confusion matrix for BatDetect2 across all verified files. While Hypsugo, Tadarida and Chiroptera cannot be identified correctly by BatDetect2, they were at least detected by the model.

Table 7. Number of Genus/ENV level bat verifications across 3048 files

Genus/ENV aggregate	**Verified records**
Many genera	171
Pipistrellus	1063
ENV	439
Hypsugo	14
Myotis	457
Plecotus	89
Barbastella	36
Tadarida	1
Rhinolophus	14
Chiroptera (bat)	133
None (no bat)	631

Insect classifiers

We used a published classifier trained to identify 2,530 species occurring in the UK and Denmark for this first iteration of ABMS processing (UK Denmark Classifier; Jain *et al.*, 2025). This model achieved an accuracy of 86.45% on a test set of GBIF data. However, when tested on a dataset that more fairly represented the ABMS use case, with images of 244 species at AMI traps in the UK and Denmark, accuracy fell to 79.39% (with a per-class accuracy of 72.84%). This performance is probably still inflated, as the evaluation only included examples where a verifier could confidently produce a species ID; in reality, for most moths, experts could not provide a species ID (Jain *et al.*, 2025). While the scope of the UK Denmark classifier is limited, we are not aware of any existing open-source moth species classifiers for the whole of Europe. The species coverage of the UK Denmark classifier, as well as our “in progress” European classifier, is shown in Table 8 for 13 ABMS partner countries.

Table 8. Moth species coverage per ABMS country for each model. Species coverage is calculated as the proportion of a country’s listed moth species (including micromoths) that are included in the model training data. The European classifier has improved species coverage across all countries, but did not yet achieve adequate performance for deployment in the ABMS. The moth species list per country is maintained by Jurrien van Deijk at the De Vlinderstichting (“The Butterfly Foundation”) in the Netherlands.

Country	**UK Denmark classifier (deployed in ABMS)**	**European classifier (in progress)**
Belgium	85.81%	**95.73%**
Bulgaria	53.07%	**83.95%**
Czech Republic	72.37%	**93.25%**
Germany	69.87%	**91.96%**
Denmark	90.04%	**94.70%**
Spain	46.13%	**87.51%**
Finland	80.70%	**91.03%**
Croatia	60.02%	**90.27%**
Ireland	92.75%	**96.37%**
Italy	48.71%	**86.74%**
Netherlands	88.66%	**95.88%**
Sweden	83.25%	**91.88%**
Slovakia	67.02%	**91.49%**

During this project, we have trained European classifiers to better reflect the species pool of countries such as Croatia, which have a richer moth fauna. To do so, we downloaded all Lepidoptera images from GBIF flagged with European country codes. After some quality filtering, removing non-adults images, background images and blurry images, we trained models on this dataset. The resulting data had a high number of species and an extremely long-tailed distribution: Of 7121 species in total, 351 had 500 or more images and 2030 had 5 or less images. As such, the European classifier has not yet achieved adequate performance for deployment in the ABMS.

Models perform well on GBIF data, but we have found results that can differ in the context of AMI traps. As such, we carried out further evaluation of UK Denmark and European classifiers using perhaps the largest expert-annotated AMI dataset in Europe. It includes 58,640 images with 522 moth species detected across a network of AMI traps in Denmark. Performances of both the UK Denmark model and the European and Global classifiers are represented in Table 9. Among the two currently integrated models, the UK Denmark model was the most performant one on AMI data. Furthermore, the model performs particularly well for the most common species in the Danish AMI dataset (Table 10). Furthermore, some of the species in the Danish AMI dataset were also highly abundant in forest, grassland or wetland habitats in the ABMS pilot. Four of these had reasonable model performance, but predictions of *Eilema complana* across Europe should be interpreted with caution (F1=0.406, Table 8).

Table 9. Performance of the UK Denmark classifier deployed in the ABMS pilot, and the in progress European classifier, for an expert annotated AMI dataset in Denmark.

Classifier	Macro F1	Macro Precision	Macro Recall	Micro F1	Micro Precision	Micro Recall
UK Denmark	**61.14%**	**64.24%**	**67.10%**	**74.29%**	72.08%	**72.08%**
European	46.43%	53.22%	52.06%	60.67%	**76.89%**	53.08%

Table 10. Performance of the UK Denmark classifier for the 30 most abundant species in the expert-annotated AMI dataset, making up just over half of the verification data. While per-species F1 is 61.14%, performance is high for 26 of these 30 common species. Three of the species for which the model performed poorly were not present in the training data for the UK Denmark classifier (<u>underlined</u>). Species in bold are among the top 10 species in at least one habitat type across the ABMS dataset in 2025 (Fig. 18). The specific habitats are in parentheses (F = Forest, G = Grassland, W = Wetland).

Species	**Count**	**F1 score**
***Deltote pygarga* (F, W)**	**3441**	**0.970**
***Pelosia muscerda* (F, G, W)**	**2843**	**0.962**
Spilosoma lubricipeda	2074	0.982
Chrysoteuchia culmella	2067	0.861
***Eilema complana* (F, G, W)**	**1901**	**0.406**
Calliteara pudibunda	1335	0.959
***Eilema lutarella* (G)**	**1232**	**0.876**
Hypena proboscidalis	1146	0.937
Pheosia tremula	1068	0.952
Eupithecia nanata	953	0.976
<u>*Ectropis crepuscularia*</u>	<u>905</u>	<u>0.000</u>
<u>*Collita griseola*</u>	<u>878</u>	<u>0.000</u>
Colocasia coryli	837	0.917
Parapoynx stratiotata	728	0.925
Stauropus fagi	712	0.954
Ecliptopera silaceata	698	0.964
<u>*Nyea lurideola*</u>	<u>694</u>	<u>0.000</u>
Biston betularia	688	0.945
Sphinx pinastri	682	0.925
Epirrhoe alternata	678	0.987

Acronicta megacephala	639	0.955
Pleuroptya ruralis	617	0.936
Rivula sericealis	607	0.958
Thera obeliscata	570	0.824
Pheosia gnoma	567	0.930
Arctia caja	518	0.964
Apoda limacodes	486	0.889
Ochropacha duplaris	483	0.871
***Euproctis similis* (F)**	**476**	**0.843**
Cybosia mesomella	460	0.926

7. Data management

The project generated many types of data, primarily images and recordings collected by insect camera systems and acoustics systems for birds and bats. Beyond images and audio files, we collected data about the locations and deployments during implementation of the pilot. The structure of the metadata tables created during the project are highlighted in Fig. 8. Centralized data management was coordinated by Jamie Alison and Lars Dalby at Aarhus University, with local data management by national or regional data controllers named in the data management plan. Relevant information for data generation is contained in the site selection protocol, the device deployment protocol and the data transfer protocol. In particular, the data transfer protocol captures how partners remotely transfer media files to ERDA (electronic research data archive) at Aarhus University, using a Secure File Transfer Protocol (SFTP), according to standard naming conventions. Other metadata for locations and deployments were collated using online forms, and standardized using quality control scripts written in R.

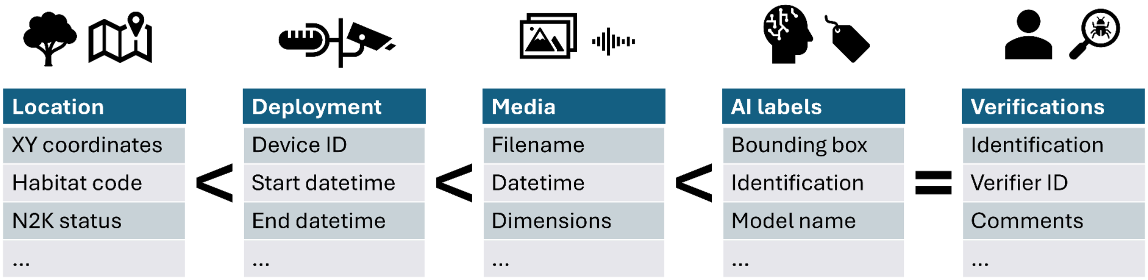


Figure 8. Linkages between data and metadata tables within the ABMS. Tables are generated for locations, deployments, and media, with a variety of fields. Following data processing, tables of AI labels and human-generated verifications are produced. The “<” symbol indicates a one-to-many relationship between tables, while “=” indicates a one-to-one relationship.

7.1. Description of data & metadata

Data summaries represent only data available in the ABMS databases as of October 2025; upload of some data from Ireland was delayed.

Image data: AMI traps collected 45,476 snapshot images (4096 x 2160 pixels in jpg format) in 2024 and 169,523 in 2025, representing more than 8,000 trapping nights in total. The date and time of recording is stored as part of the filename of each image. Significantly more images were captured due to the motion trigger, but these were not processed in order to make efficient use of computing resources, and because motion triggering failed for several devices.

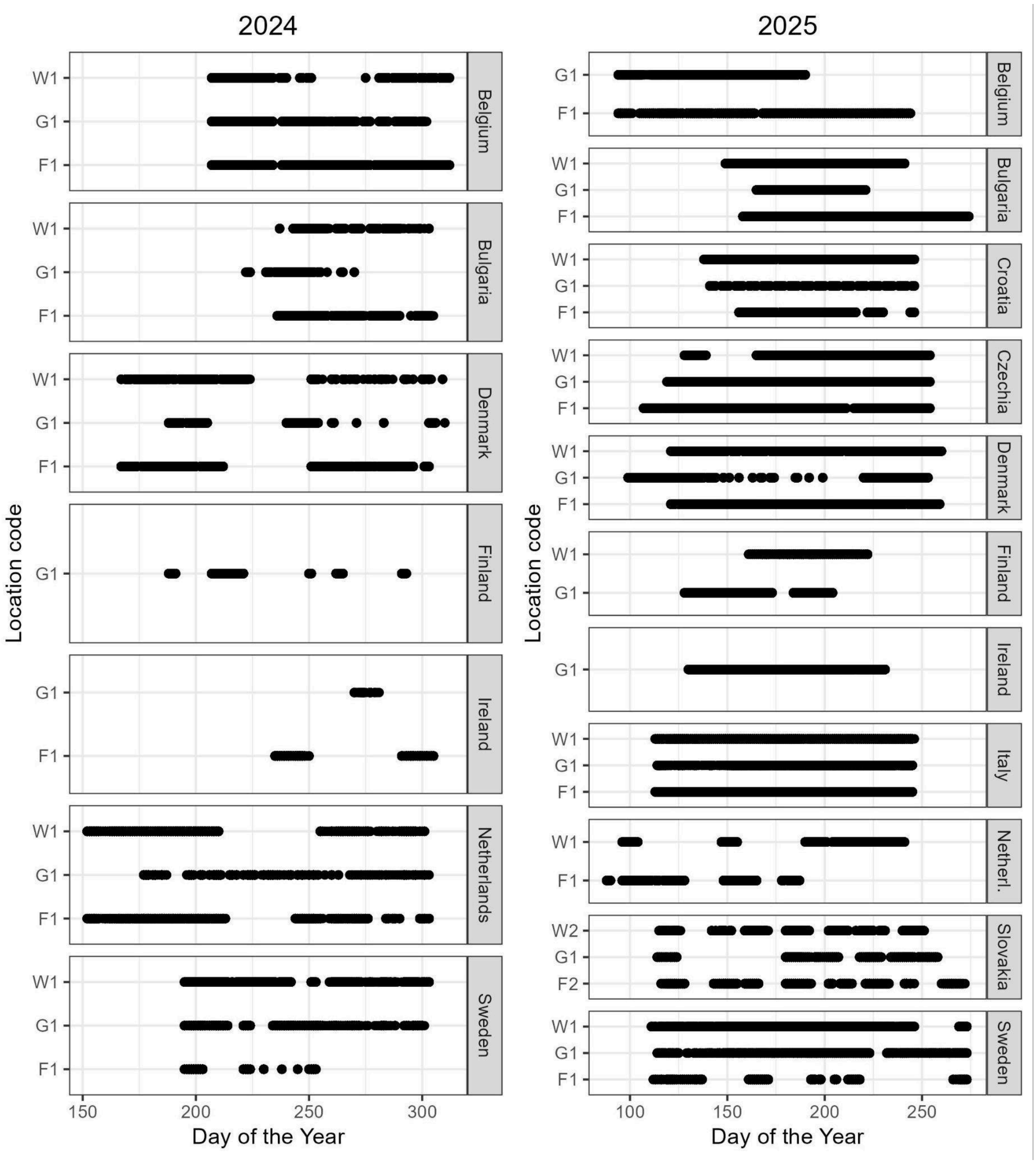


Figure 9. Timeline of image data across all partner countries with active AMI devices in 2024 (left) and 2025 (right). Represents the data submitted to the ABMS AMI database as of October 2025; upload of some data from Ireland was delayed. Gaps correspond to device maintenance constraints.

Sound data: Song Meter Mini 2 systems recorded 2,818,453 audible acoustic files (1 minute long, 48kHz sample rate, in wav format) adding up to 5.43 recording-years, and equating to 26.81 deployment years. Each file is also referenced in a summary text file containing details such as location and temperature.

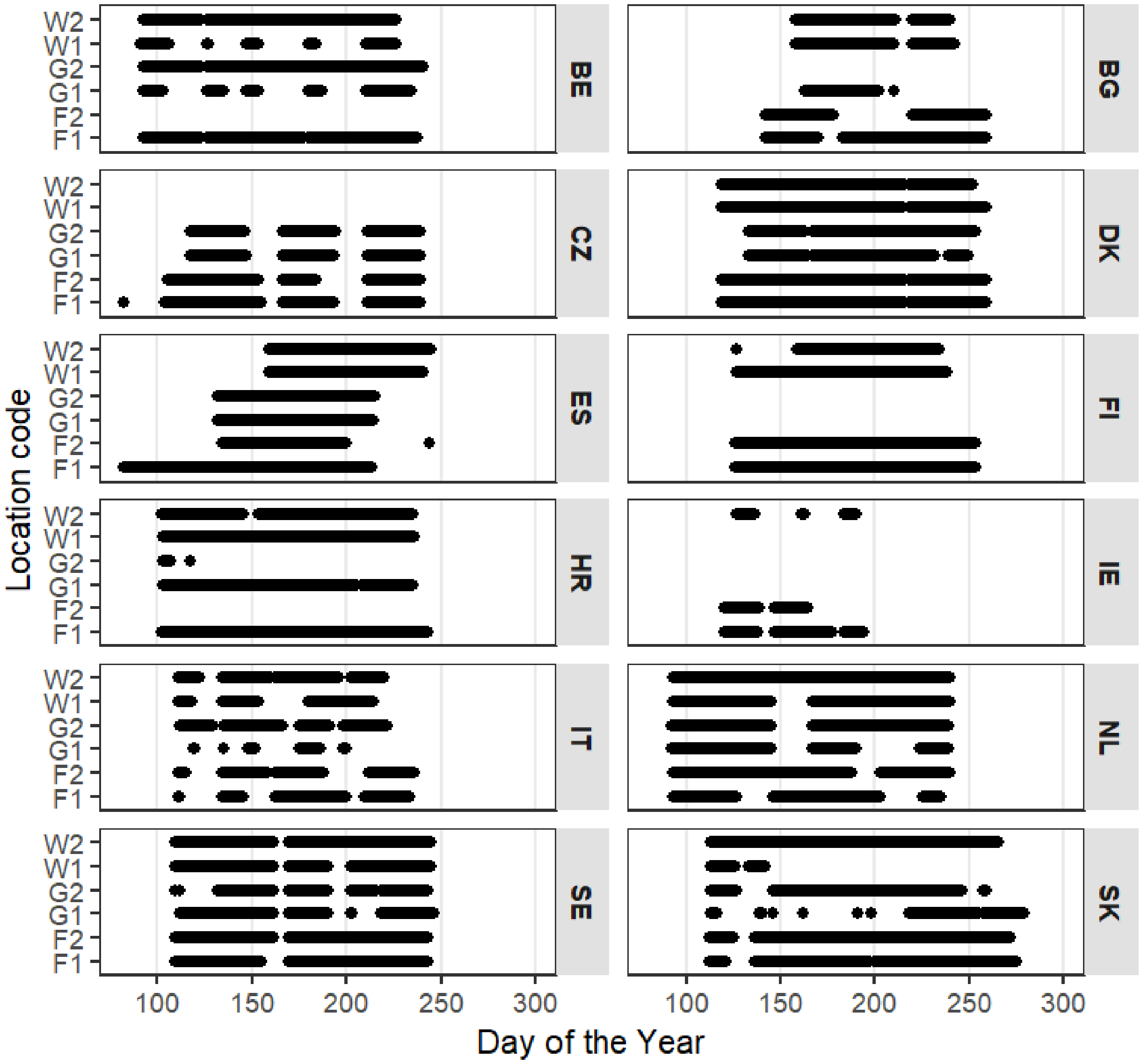


Figure 10. Timeline of audible acoustic data collection for 2025. Represents the data available in the ABMS acoustics database as of October 2025; upload of some data from Ireland was delayed. Gaps correspond to device maintenance constraints. Countries denoted using ISO 3166-1 alpha-2 abbreviations.

Song Meter Mini Bat 2 systems recorded 4,924,603 ultrasonic acoustic files (up to 15 seconds long, 256kHz sample rate, in wav format) adding up to 1.58 recording-years. Each file is also referenced in a summary text file containing details such as location and temperature.

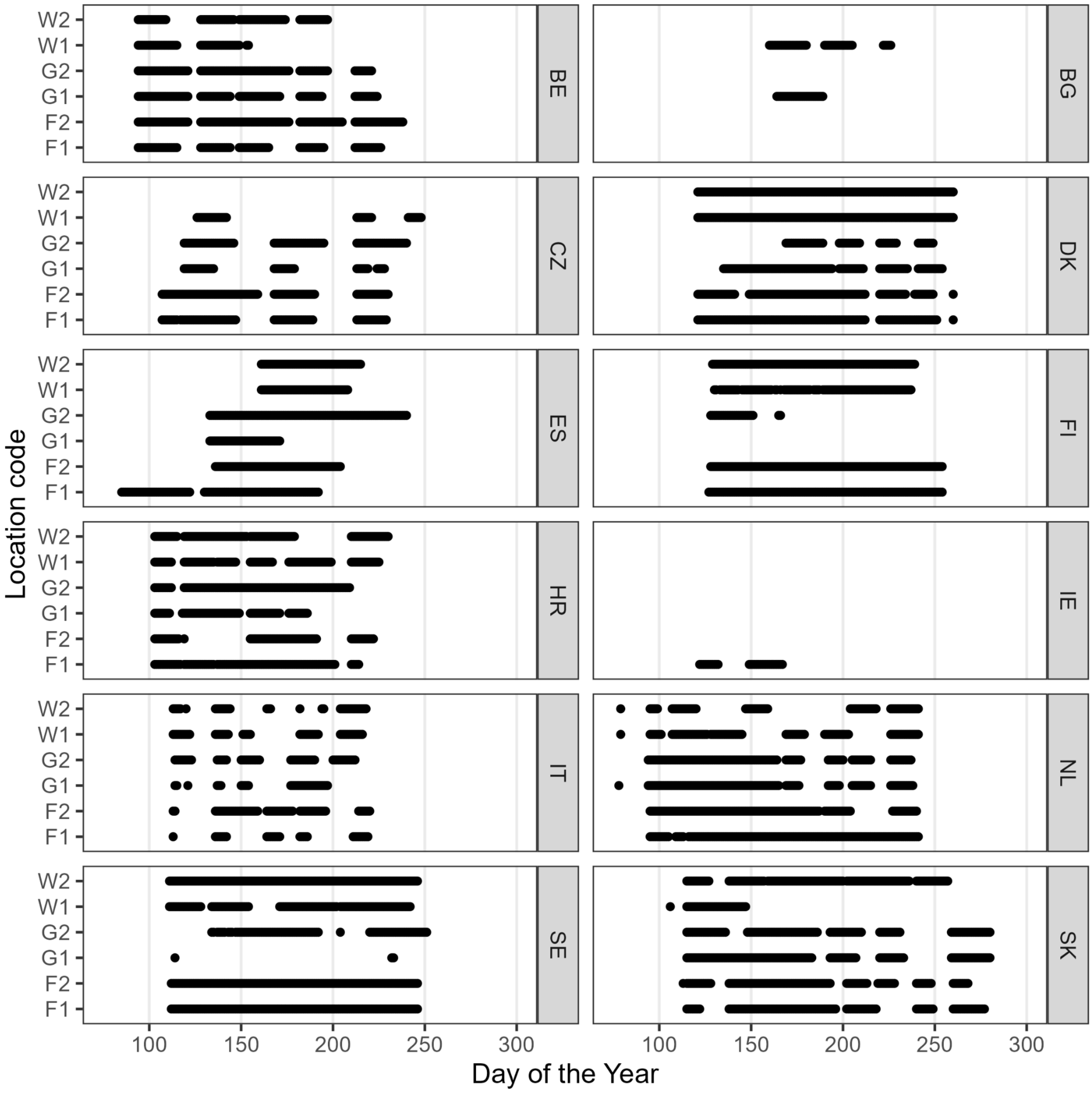


Figure 11. Timeline of ultrasound acoustic data collection for 2025. Represents the data available in the ABMS acoustics database as of October 2025; upload of some data from Ireland was delayed. Gaps correspond to device maintenance constraints. Countries denoted using ISO 3166-1 alpha-2 abbreviations.

Location data: Coordinates, associated descriptors and notes about 51 locations in 2024 and 70 locations in 2025 are tracked in an online spreadsheet, quality checked and written to a central database during indexing of image and sound data.

Deployment data: Partners provide details of devices, locations and time periods that comprise 326 individual ABMS deployments in an online spreadsheet. These data are useful to capture sampling effort and contextual information.

AI model predictions: Images and sounds in the central AMI and acoustics databases are processed using AI models (see 2.4. Processing pipelines). AI predictions are stored in a bespoke database, and output as csv files for analysis and EBV generation. These files refer to source images or sounds, and provide identifications related to regions of the media where species occurred.

Verification data from experts: A subset of 8690 audible and 3048 ultrasound acoustics files were presented to taxonomic experts for review. Outputs were formatted according to the verification protocols, and unified into a single csv file of image names and bat or bird species verifications.

Climate logger data: TMS-4 climate loggers provide data on temperature, moisture and other variables in a single table for each deployment. Data are downloaded from the device as a csv with predefined columns described in the device manual. These are uploaded to the project's cloud storage, to be unified and analysed at a later stage.

7.2. Ensuring the FAIR data principle

All image and sound data collected as part of the ABMS pilot is stored in the Electronic Research Data Archive (ERDA) at Aarhus University, Denmark. All generated data will be made publicly available at the end of the pilot through a Danish implementation of the dataverse. AI labels will be made available with clear acknowledgement of model uncertainty, as quantified in 2.5. Model evaluation.

Expert verifications for acoustic data will be given special attention, with the creation of an annotated dataset of bird and bat taxa on xeno-canto and an associated publication. Following this, confirmed occurrences will be submitted to the Global Biodiversity Information Facility (GBIF).

8. Deriving EBV Indicators from Sensor Data

The analytical possibilities of ABMS data are vast. To showcase the potential of sensor-derived data to produce high-level indicators across Europe, we centred our approach on Essential Biodiversity Variables (EBVs). Specifically, we identified and produced indicators relevant to several EBV categories defined by the Group on Earth Observations Biodiversity Observation Network (GEO BON; https://geobon.org/ebvs/what-are-ebvs/). Across insects, birds, and bats, we derived three indicators to efficiently capture ecosystem function and community composition (Table 11). These indicators also relate to a wide range of indicators described by EuropaBON for Europe (Quoss, Junker & Wendt, 2024).

Table 11. Summary of three EBVs defined by GEO BON and their implementation in the ABMS. GEO BON descriptions retrieved from https://geobon.org/ebvs/what-are-ebvs/ on 04/12/2025.

GEO BON EBV	GEO BON Description	ABMS Description
Ecosystem Phenology	Duration and magnitude of cyclic processes observed at the ecosystem level, such as in vegetation activity, phytoplankton blooms, etc.	Duration, fluctuation and magnitude of bat, bird and insect activity throughout the year.
Community Abundance	The abundance of organisms in ecological assemblages.	The abundance of insect orders, bat genera, and moth and bird species, where activity is a proxy for abundance.
Taxonomic diversity	The diversity of species identities, and/or phylogenetic positions, of organisms in ecological assemblages.	The diversity of moth and bird species identities, as estimated with species accumulation curves.

Beyond EBVs, it is important to note the impressive depth and temporal resolution of the data collected in the ABMS. Exciting questions could be addressed about day-night cycles in activity of bats, birds and insects, impacts of temperature and moisture, and species interactions - especially between insectivorous birds, bats and nocturnal insects. These could include sophisticated methods of imputation for missing data, as well as estimating density from activity data. The analysis presented in this report only scratches the surface of the underlying data, and further work should delve deeper into such questions.

8.1. Ecosystem phenology indices

Regular observations collected throughout the season enable statistical modelling techniques designed to estimate complex non-linear patterns in time. Species activity periods typically exhibit non-linear, hump shaped curves, and Generalised Additive Models (GAM) are suitable to distinguish the seasonal trend from day-to-day “noise”. Furthermore, by modelling many species (or other taxonomic groupings), habitats and countries together, traps with sparse data due to technical difficulties can “borrow” statistical strength from more data-rich traps. Resulting phenology curves can be drawn for most country and habitat combinations, allowing precise predictions of metrics such as peak activity and magnitude, activity onset, activity end and seasonal duration, both at species and community levels. All of these metrics are thought to be sensitive to climate change and intensive management, and multi-year tracking will provide critical information about species and community responses to stressors.

While phenology curves from order-level to species level are also possible, we applied GAMs to all arthropod detections from AMI traps in 2025, modelling total arthropod activity. The resulting curves (Fig. 12) show how arthropod activity increases or decreases over time, after controlling for sampling effort and other confounding factors. These curves have the potential to provide important insights into the timing of activity across habitats within and between countries, even at the community level. For example, in Bulgaria, the timing of peak activity is relatively conserved across habitats but the magnitude of the peaks varies greatly. Conversely, in Denmark, the forest and grassland habitats have long activity periods with multiple peaks, whereas the wetland habitat appears to have a short activity season. Further research into the drivers of these and other patterns, such as vegetation patterns, weather conditions and background species pools could enhance ecological understanding (Gillespie *et al.*, 2025), particularly if patterns can be monitored over long time periods. If produced at species-level, phenology curves could also identify indicator species sensitive to climate changes at levels of precision that exceed traditional monitoring methods.

As for arthropod activity, we also produced indicators of bird and bat activity over time (Fig. 13 & 14).

Importantly, these phenology curves show not only the timing, but the magnitude of activity across countries and habitats (but not axis scales vary between countries). Interestingly, the curves for birds do not always show an expected spring and early summer distribution, highlighting that BirdNet is bird calls, and not just bird songs. For bats, activity is generally higher in forest than in grassland and wetland sites (Fig. 14). Especially in the case of the nocturnal taxa, comparisons between prey and predator species' activity patterns could reveal important intra-species interactions within habitats. Although there are gaps in the raw data (Fig. 10 & 11; large confidence intervals for bat activity in Fig.14), several overlaps in peak activity can be observed between bats and arthropods such as for the Netherlands or the Province of Bolzano. Such multi-taxon analysis of phenology could be used to generate cumulative impact assessments in future.

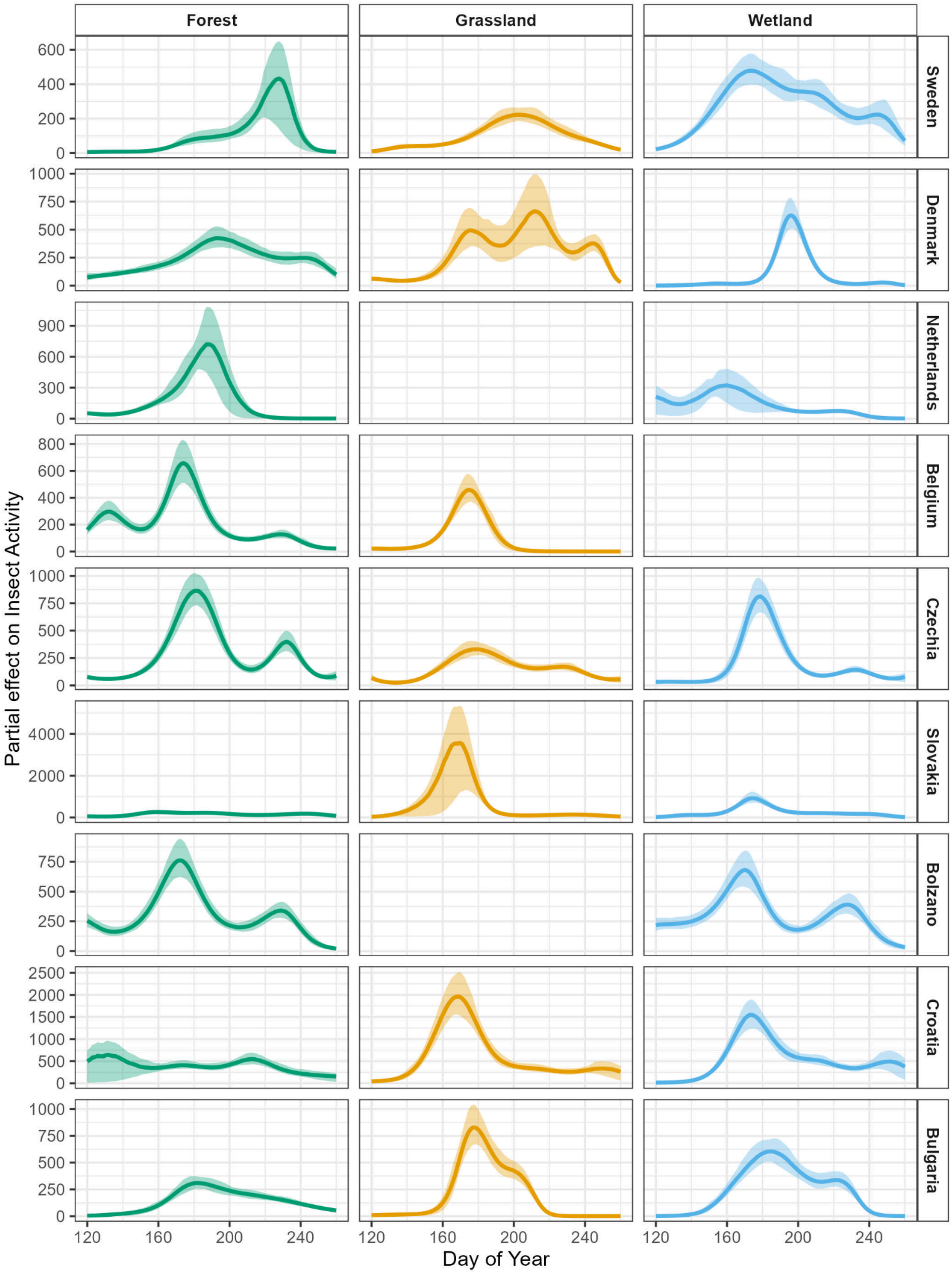


Figure 12. Ecosystem phenology index for activity of night-active arthropods at forest (green), grassland (amber) and wetland (blue) sites across seven ABMS partner regions in 2025. Solid lines represent average activity over time and shaded areas are 95% credible intervals. Sufficient data were not available to construct the indicator for all region and habitat combinations (blank panels) and in some cases, activity was relatively low resulting in "flat" curves that lack detail at this plotting scale.

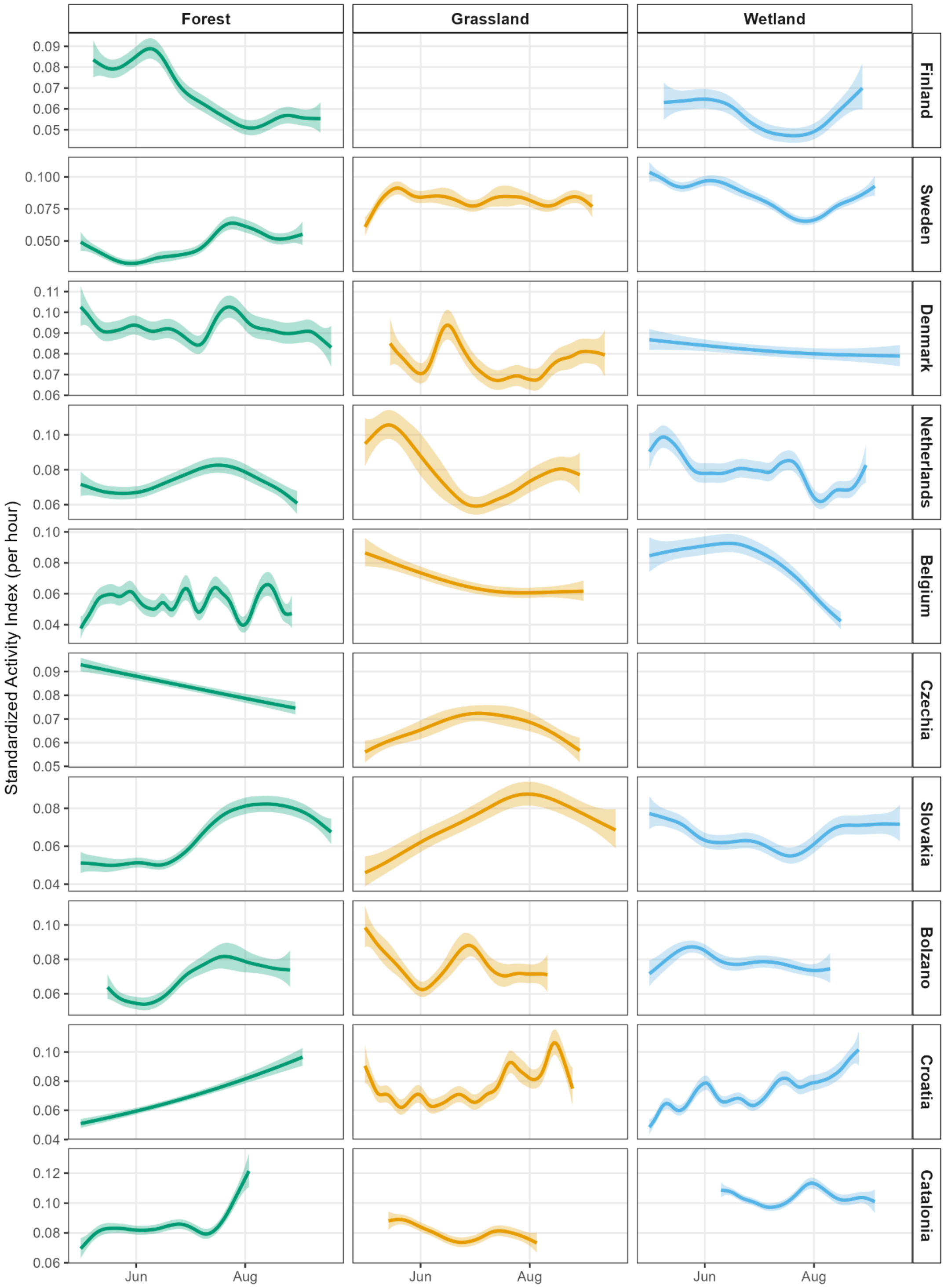


Figure 13. Ecosystem phenology index for activity of birds at forest (green), grassland (amber) and wetland (blue) sites across seven ABMS partner regions in 2025. Solid lines represent average activity over time and shaded areas are 95% credible intervals. Sufficient data were not available to construct the indicator for all region and habitat combinations (blank panels).

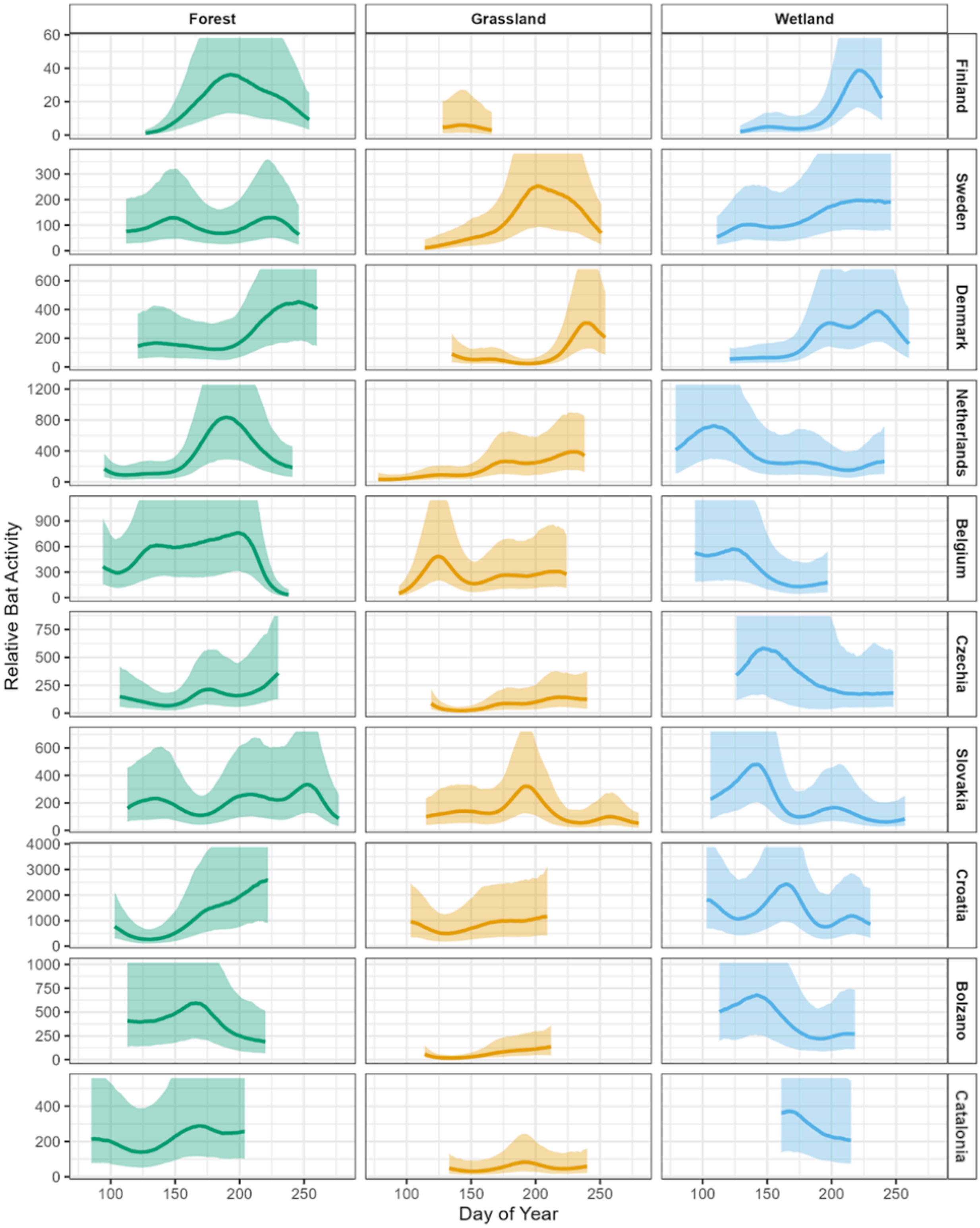


Figure 14. Ecosystem phenology index for activity of bats at forest (green), grassland (amber) and wetland (blue) sites across 10 ABMS partner regions in 2025. Solid lines represent average activity over time and shaded areas are 95% credible intervals (upper intervals are often cut off by the y-axis limits, to better

visualize trends). Sufficient data were not available to construct the indicator for all region and habitat combinations.

8.2. Community abundance indices

The community composition class of EBVs includes “community abundance”, which can be interpreted in several ways. At its most basic, an index of the relative activity of different taxa detected by sensors, across habitat and country combinations, provides an informative overview of communities that can also be compared across time and space. This can sometimes be done at species-level, but the simplest presentation of this is shown in Fig. 15 for bats and Fig. 16 for arthropods. For bats, the dominance of *Pipistrellus* species is evident in many habitats and countries, with notable exceptions close to the northern range edge. Long-term monitoring of these relative activity patterns will provide important insights for managers aiming to improve diversity or track dispersal across spatial gradients. Further work might take steps to better convert relative activity metrics into relative abundance, by better accounting for the possibility of double-counting. For bats, this might include developing coefficients of detectability, that relate acoustic activity to the actual number of individuals (Roemer *et al.*, 2025).

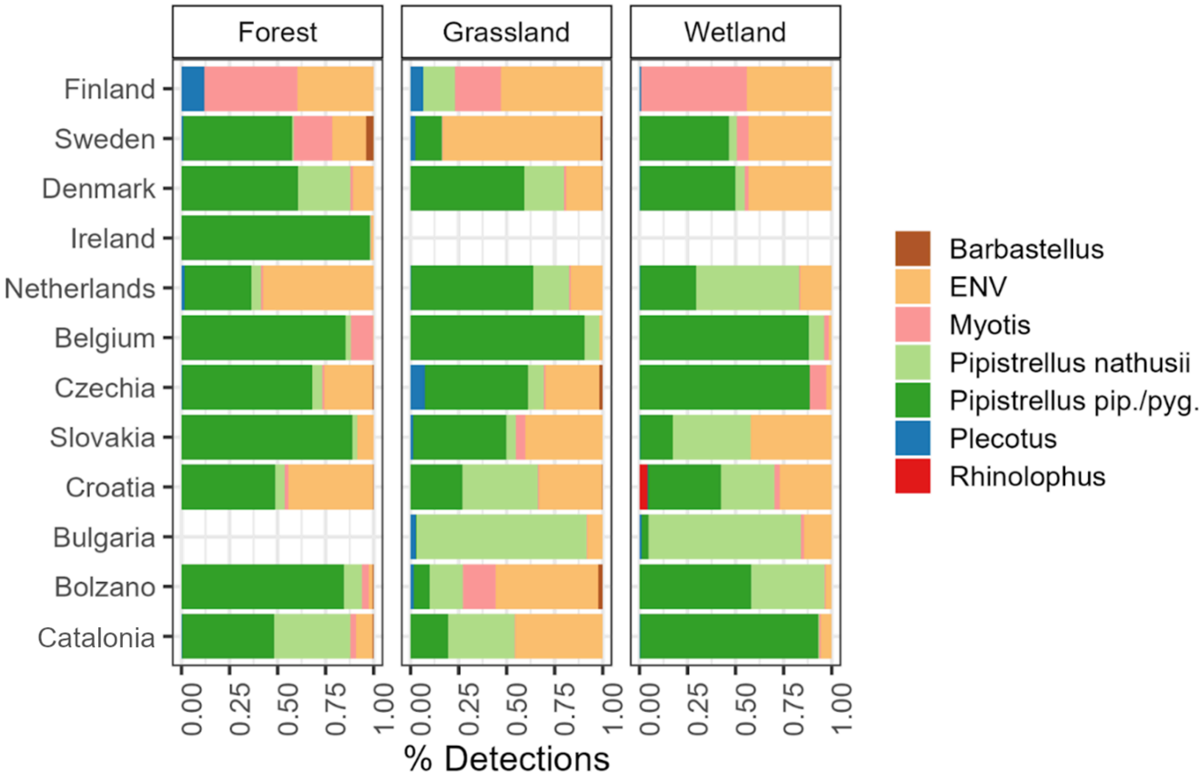


Figure 15. Relative abundance of seven bat taxa across three habitats and 11 ABMS partner regions in 2025. Fractions of bars represent the proportion of acoustic files identified to species in a given taxon by the BatDetect2 model. ENV represents a genus aggregate for three genera that are easily mistaken for one another: Eptesicus, Nyctalus and Vespertilio. The separation between Pipistrellus pipistrellus/pygmaeus and Pipistrellus nathusii is retained, to show variation within Pipistrellus which was relatively well classified (Fig. 6). Species outside the listed taxa cannot be classified by BatDetect2, and are often subsumed into ENV

(Fig. A1). Data were not available to construct the indicator for all region and habitat combinations; upload of some data from Ireland was delayed, for example.

For night active arthropods in 2025 (Fig. 16), relative activity levels of different orders vary greatly across habitats and countries, with some northern grasslands and wetlands dominated by Diptera, and diversity increasing further south. The interpretation of these patterns are subject to an understanding of the location of the traps, but with replication across multiple sites and environmental data about vegetation, management and weather, researchers and managers could explore the drivers of community abundance patterns across ecological gradients.

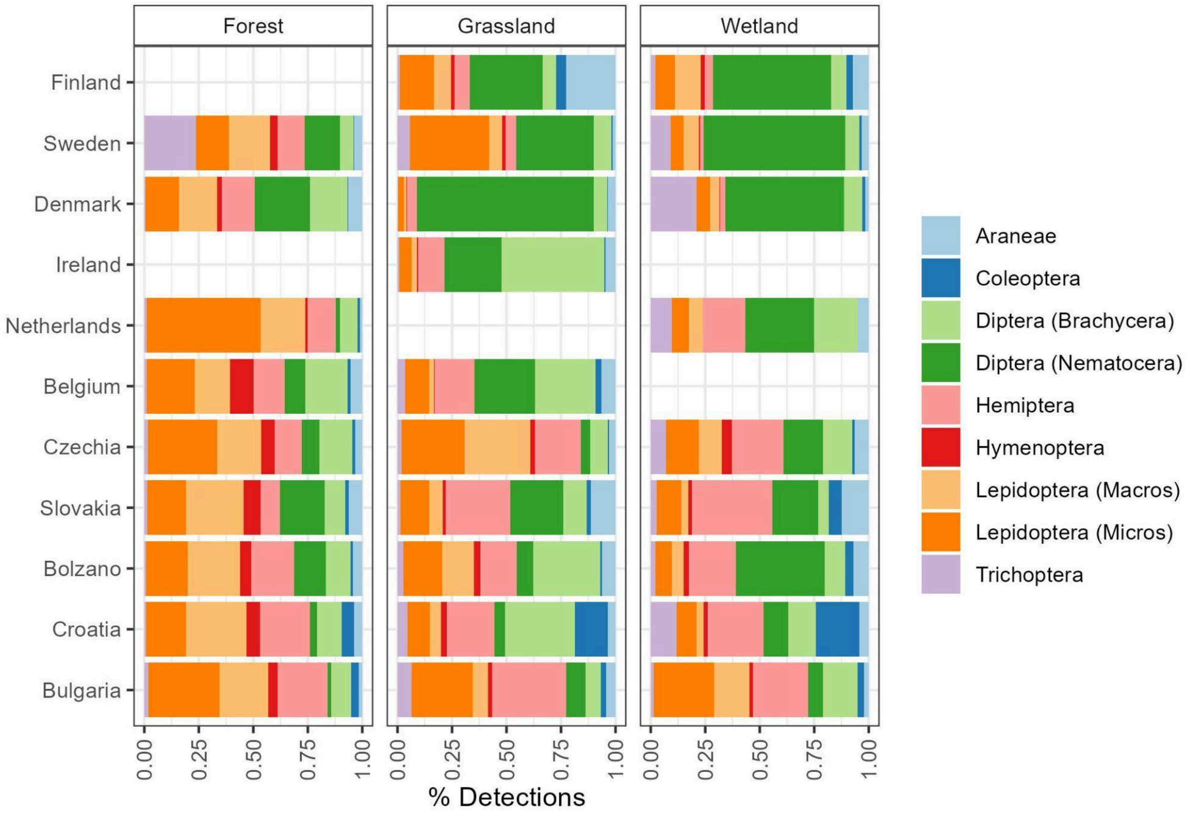


Figure 16. Relative abundance of nine arthropod taxa across three habitats and 11 ABMS partner regions in 2025. Fractions of bars represent the proportion of recorded instances of arthropods belonging to each taxon. Images were recorded every ten minutes between 2300 and 0300 local time. Data were not available to construct the indicator for all region and habitat combinations; upload of some data from Ireland was delayed, for example.

Community abundance can be further broken down to lower taxonomic levels, subject to classification confidence. For example, the top 10 bird species detected with high confidence across countries in the three habitats (Fig. 17) reveal insights into the species that dominate European bird communities, which could be tracked over time and further broken down by spatial units. *Phylloscopus collybita* emerges as the most abundant species in both forest and wetland locations. This pattern reflects how this species mainly occupies different types of forests during the breeding season, while it can be found in abundance in wetlands with reed beds during migration and wintering periods. On the other hand, *Alauda arvensis* is the most frequently detected species in grasslands. This finding is consistent with the ecology of the species, as it specializes in grassland habitats throughout the year. Still, some results would benefit from further investigation. For example, *Anthus trivialis* appears as the second most detected species in grasslands, and the third in wetlands. However, this is typically considered a forest species, and it was an “amber” species in our verification (Table 5; not possible to reach 90% precision). Thanks to our verification, we might suspect that other *Anthus* species are being mistaken for *Anthus trivialis* in this case.

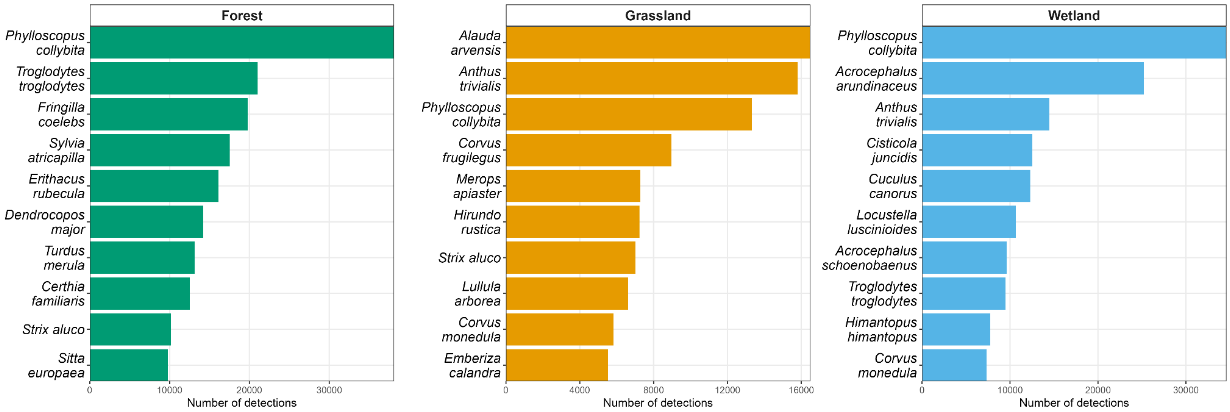


Figure 17. The number of AI (BirdNet) detections of the top 10 bird species in each habitat type summed across all countries..

A summary of the most abundant moth species across Europe (Fig. 18), shows some ever-present species such as *Pelosia muscerda* (the dotted footman), known for an association with mild climates, wet woodlands and wetlands. However, the habitat types also have distinct species, for example *Chiasmia clathrata* (the latticed heath) which is found in open habitats and was highly abundant at grassland locations. While monitoring the relative abundance of common species will reveal much about community abundance changes over time, biodiversity sensors will also provide vital information about rare and threatened species. Still, as for birds, species-level detections from AI should be interpreted with caution; *Eilema complana* (the scarce footman) is commonly detected in all three habitats, being widespread across Europe and found in a range of habitats. However, our verification in Denmark suggested the results for this species should be interpreted with caution, while those for *Deltote pygarga* and *Pelosia muscerda* are probably much more reliable (Table 10).

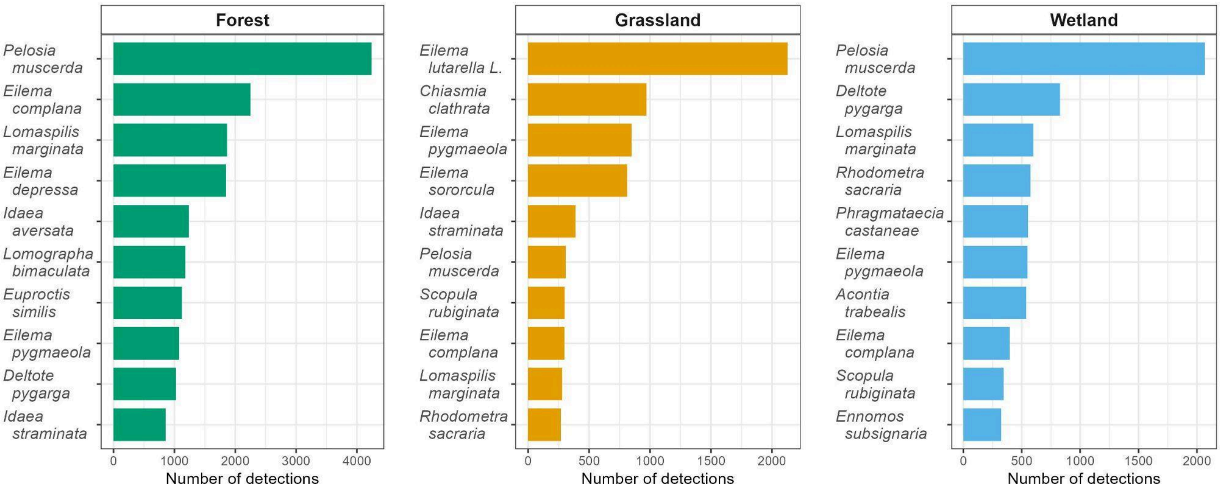


Figure 18. The number of AI detections of the top 10 night-flying macro moth species in each habitat type summed across all countries.

Exploring further than the focal EBV, relative abundance of species in a community can be viewed collectively in terms of their associations with each other and their habitats. A common way to do so is with ordination techniques, where community composition is plotted by measures of “dissimilarity”. Sampling locations that are close together on the ordination graph tend to exhibit bird or insect communities that are more similar, while those that are far apart are made up of very different species. This is important for monitoring, especially to determine whether communities are becoming more alike (i.e. “homogenizing”) over time - perhaps becoming increasingly dominated by a few common species.

Interestingly, for the 2025 data, species community ordinations for moths and birds (Fig. 19) reveal that across Europe, forest communities tend to be more similar from country to country, while grasslands and wetlands vary widely in their community makeup. Further study can help to identify why this might be the case, for example by comparing the context of each site, or by identifying ecological gradients associated with these patterns.

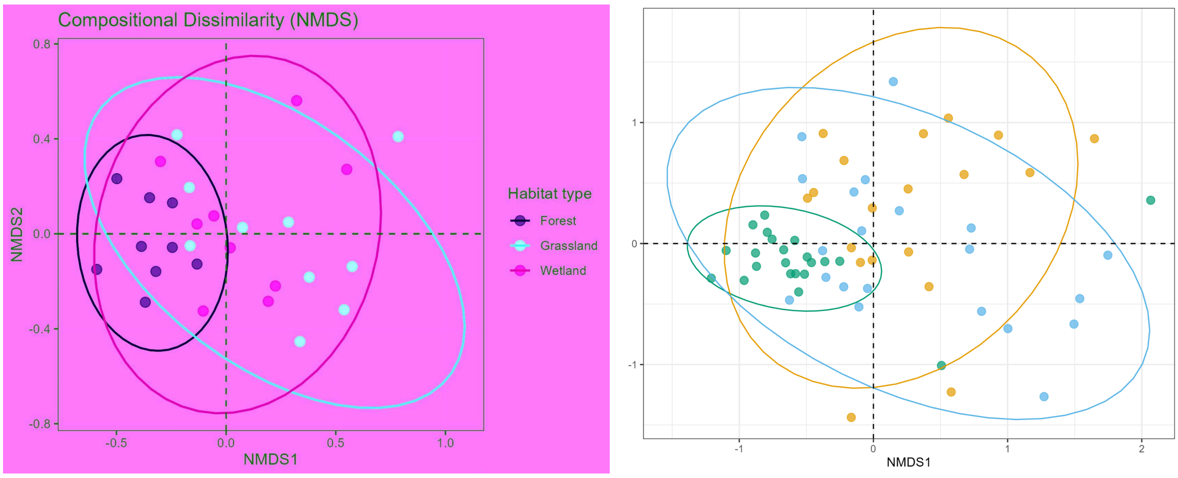


Figure 19. Compositional dissimilarity of the macro moth (left) and bird (right) species communities across Europe, separated by habitat. Each point represents a sampling location in the given habitat, while ellipses represent the 95% confidence interval around the group's centroid. For both taxa, communities in forest habitats are much more homogenous than those in wetland or grassland habitats.

8.3. Taxonomic diversity indices

A third EBV derived rapidly from sensor-based data represents taxonomic diversity, the simplest measure of which is species richness. This can be a simple count of the number of species detected, subject to classification confidence, but techniques are available to account for differences in sampling effort. For example, sampling effort can be measured as the number of nights that an AMI trap is active over 2025, which ranges from 55 days in Finland to 150 days in Sweden, such that total species richness is incomparable. However, using a method known as rarefaction, we can draw species accumulation curves for each country and habitat combination. These derive the rate of new species detection with increasing sampling effort, up to the observed level (the solid line in Fig 20). Beyond the observed level of species richness, the technique can extrapolate the rate of new species detection if the device continued to operate. We can then more easily compare the Finnish grasslands and wetlands to the Swedish sites, at different levels of sampling effort.

Within each country it is also informative to explore the relative species richness between habitat types. In most countries, particularly in northern Europe, forest sites are the most species rich, while in southern Europe the sites chosen for monitoring are more closely matched. Following these patterns over longer time scales will provide critical insights into the impact of factors such as land management on diversity. These metrics can also be adjusted to account for the relative abundance of each species (e.g. Shannon or Simpson diversity indices) to study diversity patterns in conjunction with the community composition methods above. While comparisons between habitats are robust, comparisons between countries should be made with caution until a European classifier is available; the best available AI moth classifier is currently trained with images from the UK and Denmark (See 2.5. Model evaluation), so that species numbers in southern European countries are probably underestimated.

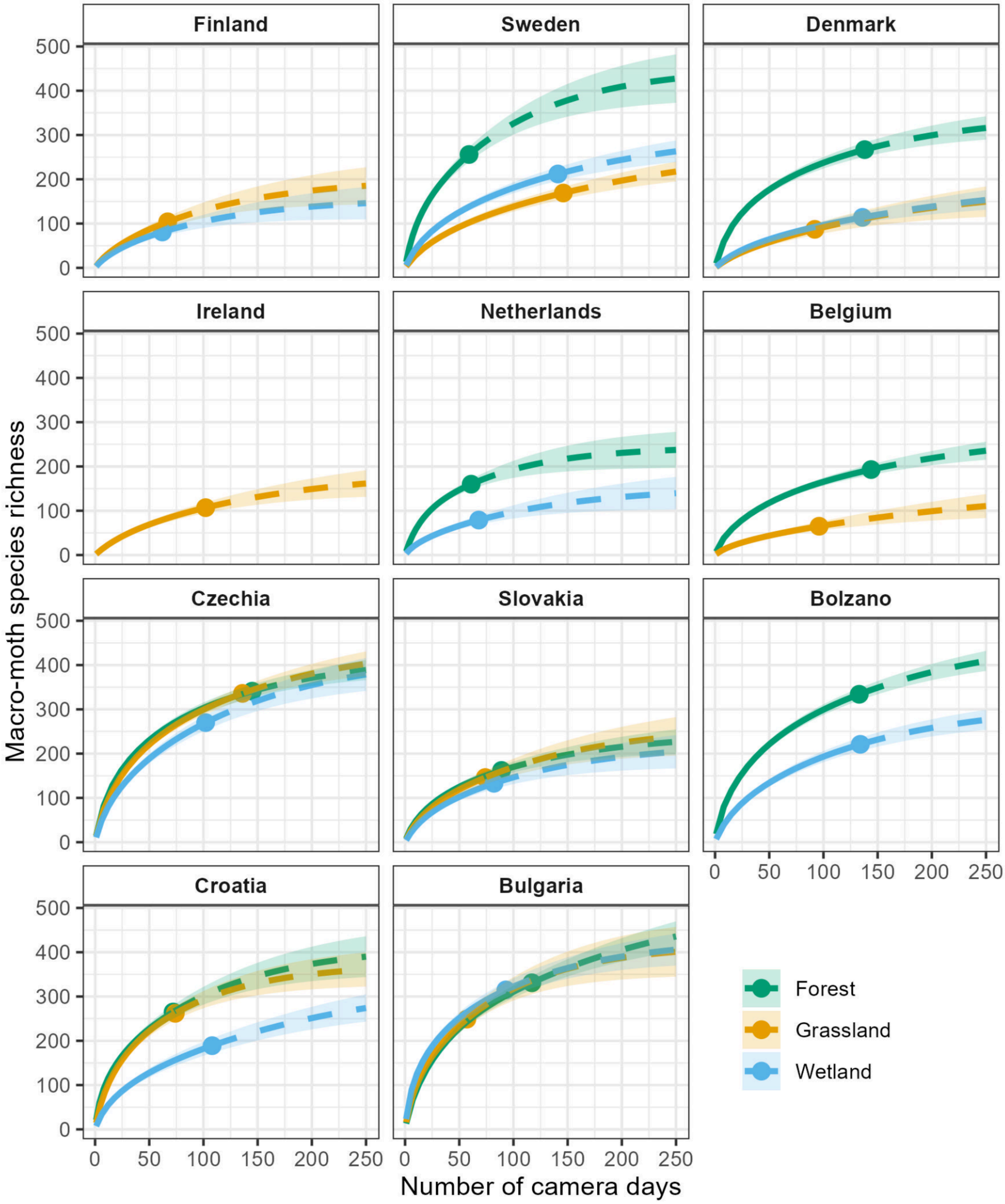


Figure 20. Species accumulation curves for macro moths at forest (green), grassland (amber) and wetland (blue) sites across 11 partner countries. Species were classified using an AI model. The point symbol depicts the observed number of species detected, the solid line depicts the interpolated number of species likely to be detected with reduced sampling effort (active camera days), and the dashed line shows the extrapolated number of species likely under increased effort. The shaded error shows uncertainty in the extrapolation - uncertainty increases when fewer observations are available.

9. Towards a European Biodiversity Sensor Network: Lessons learned from the ABMS pilot

Beyond a rich dataset and suite of transnational monitoring sites, the ABMS pilot has yielded an active community of practice, with strong ties to national biodiversity monitoring networks, and clear lessons learned. To capture these, a survey was completed by all 13 ABMS partners. Answers to the most pertinent questions are presented below, under headings related to six key lessons learned, with answers from 15 respondents representing 13 regions and partner organizations.

9.1. Sensors are viable for transnational biodiversity monitoring

Our dataset highlights the efficiency and scalability of sensors for biodiversity monitoring across borders, and this was also reflected in our survey. When asked “Could ABMS-like monitoring be integrated with existing monitoring schemes in your country?” every respondent replied “yes”. For acoustics sensors, 13 of 14 respondents agreed that “working with sensors and sensor-derived biodiversity data has been a positive experience” (10 of 14 for AMI data). Furthermore, 11, 10 and 8 respondents (69%) agreed that biodiversity data derived from bat recorders, bird recorders and AMI devices were more cost-effective than traditional alternatives.

9.2. Costs related to sensors can exceed expectations

While offering good return on investment, we experienced unpredictable costs when using sensors for biodiversity monitoring. Half of our respondents found that equipment for the pilot exceeded the budgeted amount, as the cost of devices differed between countries. Furthermore, we experienced major problems with the purchasing of AMI devices, a “bleeding edge” and thus risky technology which turned out to have a very poor chain of distribution; the devices are not yet marketed by retailers in the European Union. Almost half (7 of 15) of our respondents rated the ease of purchasing of AMI devices as 1 or 2 out of 5. Rototherm was the UK supplier, chosen on behalf of UKCEH, and many partners experienced issues related to significant delays in delivery, tax, customs clearance and condition of the devices. Many arrived with damage, needing to be repaired before deployment; respondents reported that 16 of 36 AMI devices had to be repaired over the course of the pilot, while 3 devices failed completely. Some other devices also failed: 2 bird recorders, 3 bat recorders and 4 climate loggers failed completely, while 1 bird recorder and 1 climate logger were stolen. Clearly, replacement costs must be budgeted throughout any sensor-based monitoring programme.

Investment in sensors goes much further than replacing and repairing them; we found that human resources to understand, deploy and maintain devices can also exceed expectations. Again, these costs were increased for AMI devices; 9 of 14 respondents (64%) rated the ease of deployment of AMI traps as 1 or 2 out of 5. Furthermore, half of our partners found that more than 35% of the time spent working with the AMI devices, including transport, was spent on troubleshooting the device (usually 10% or less for other sensors). This represents a considerable human resource investment in the use of these sensors. When using pioneering technologies, it is necessary to budget extra time to deploy them, but also to recruit or train technicians who specialize in their maintenance. In order to be safe and sure that custom sensors are functional, field technicians may need training in basic electronics, including use of a multimeter, soldering, and identifying short circuits.

9.3. Sensors constrain sampling and site selection

When selecting sites for the ABMS, we kept our criteria broad, but tried to introduce some rules to increase consistency across partners (see 2.2. Site selection). However, when selecting sites and sampling locations, ABMS partners faced a variety of constraints (Fig. 21). The most important related to permission, accessibility, and habitat quality, which are common constraints to ecological monitoring. However, in the context of sensors, constraints such as security from people, local perceptions and privacy were particularly important. Partners were generally concerned about the theft of their equipment, or that land users would not perceive the monitoring positively (Fig. 21). Some partners were also concerned about terrain, distance, and security from wildlife and livestock, but others less so. Thankfully, light pollution from equipment was not a prevalent concern, as sites were often remote, and power provision was not an issue when using battery powered devices.

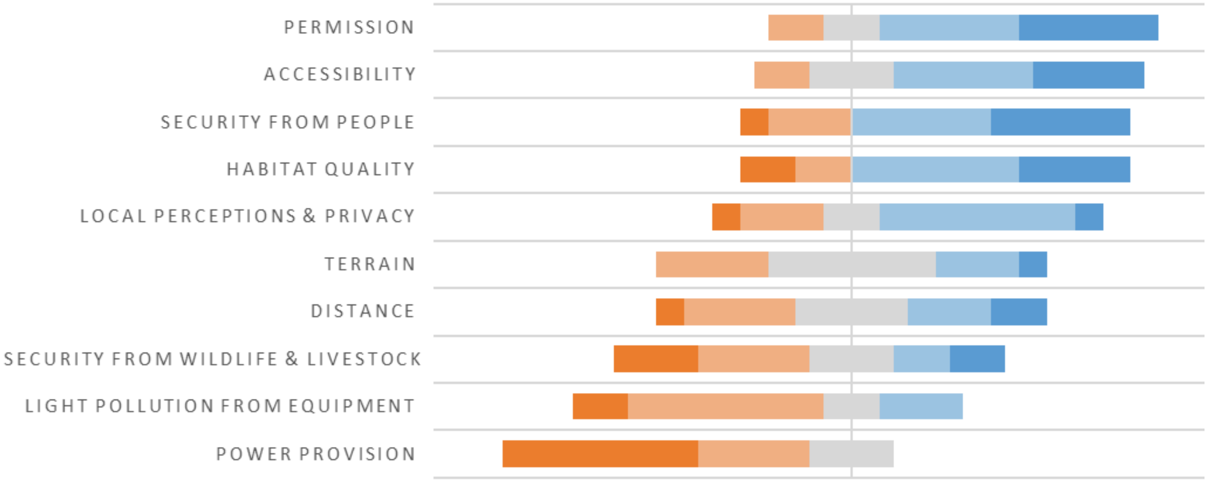


Figure 21. Constraints on selection of sites and locations for sensor-based monitoring, ranked from most to least important. Ratings from 1-5 were provided for each constraint by 14 partners, with a rating of 1 (red) being least important and 5 (blue) being most important.

These constraints made it difficult to meet strict sampling criteria over short timescales. In 2024, Finland could not access a wetland site, and sampled another available site that did not meet habitat criteria. Furthermore, for practical reasons, 10% of locations needed to be moved between 2024 and 2025, showing the importance of keeping location metadata for analysis and interpretation. Just over 75% of locations were able to be placed within Natura 2000 sites. Given site selection constraints, it makes sense that almost two thirds of locations were based on sites where monitoring or research partnerships already existed. This highlights synergies with existing research and monitoring across partner regions. However, it also highlights the importance of existing networks and partnerships for access and continuity of sensor data.

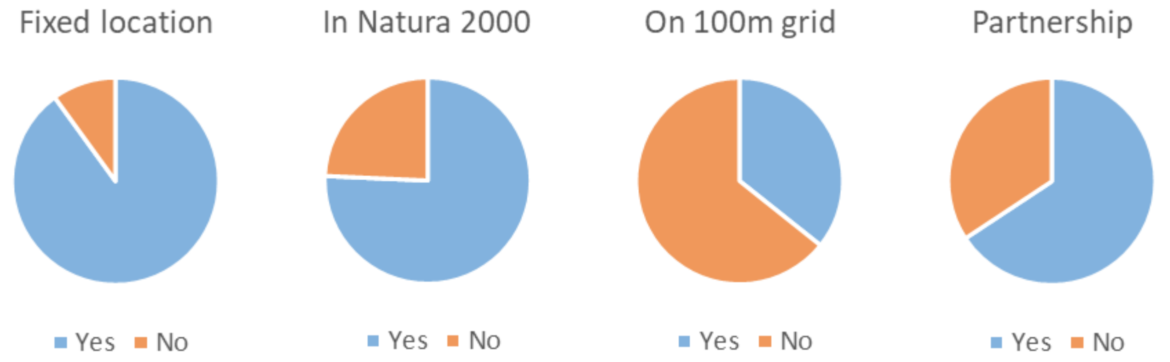


Figure 22. Characteristics of 70 ABMS sampling locations for 2025. Each of 12 partners reported the number of locations that (1) did not need to be moved 20m or more between 2024 and 2025, (2) were inside Natura 2000 areas, (3) were successfully placed on the 100m EuroStat grid, and (4) were placed on sites where there was an existing partnership in place.

Finally, initiative was taken in the pilot to test the possibility of sampling predetermined points using sensors, much like the LUCAS soil survey (Fernandez-Ugalde *et al.*, 2022). To that end, partners were asked to sample points at the closest intersection of the 100×100m EuroStat grid (EPSG:3035, ETRS89-extended / LAEA Europe). However, almost two thirds of locations failed to meet this criterion, highlighting the difficulty of probability sampling with sensors that are heavy, costly, or require attachment to stakes or trees. This is a shame, as probability samples are very useful for statistical inference. However, nonprobability samples are common in biodiversity monitoring, and methods exist to make best use of them (Boyd, Powney & Pescott, 2023).

9.4. Continuity of sensors is high - but expect gaps in the data

A major strength of sensor-based approaches, confirmed during this pilot, is the continuity of data collection. Collecting data every few minutes ensures that most passing organisms can be counted, and allows intricate study of trends over short or long timescales (see 4.1. Ecosystem phenology indices). For this reason, among others, on average 13 of 14 respondents agreed that data from AMI, bird, and bat sensors offer added value compared to traditional alternatives. Beyond this, sensors offer consistent sampling and data structures, enabling robust comparisons of sites and habitats (see 4.2. Community abundance indices).

However, this pilot highlights that while sensor data are continuous in nature, gaps are difficult to avoid (See Figures 9-11). For continued operation, 10 of 12 partners agreed that acoustic sensors needed at least monthly maintenance; in the Province of Bolzano in 2025, battery life even dropped below two weeks for acoustics devices. Biweekly visits cannot always be upheld in a busy field season. Even for the AMI traps, which usually had solar panels, most ABMS partners agreed that one visit every two months is prudent. However, even with frequent visits, equipment can fail unexpectedly. As well as mentioned AMI trap failures, respondents reported that 5 bird recorders, 5 bat recorders and 3 climate loggers failed temporarily during the pilot.

Of course, some data gaps are preventable. Acoustic sensors supported 1tb SD cards, so storage was not an issue, but gaps in acoustics data could be minimized by investing more in batteries. Most partners opted for rechargeable alkaline batteries, partly on the grounds of environmental impact. However, in reality, these batteries increased the frequency of site visits, and were probably a false economy - both in terms of finance and environmental footprint. We would recommend high capacity lithium batteries in future. For AMI devices, gaps could be minimized through the installation of internet-of-things infrastructures, allowing real-time browsing of data via an internet connection. These have been well-received in the Invasive Alien Species pilot, helping prioritize field visits to times when sensors really need maintenance. However, some data gaps are difficult to quantify, let alone prevent. For example, heavy wind, rain and other interference can severely impact the ability of recorders to detect birds and bats. Methods are needed to quantify and control for the effects of weather.

However, this pilot clearly highlights how processing and analysis pipelines must be able to deal with gaps in the data. An important element of this is retaining information on sensor downtime and failures, so that sampling effort can be properly controlled for. The presence of media files is an initial indicator of the status of sensors, but some failures result in invalid media - for example, a dysfunctional microphone or a spider web or a blurry camera. Once these phenomena are documented, statistical tools exist to recognise and cope with gaps in the data. For example, when constructing ecosystem phenology indicators, our models interpolate gaps by borrowing information from other sites in the same country or habitat. The result is continuous indicators with increased uncertainty during data gaps (Fig. 12).

9.5. Strategic expert verification helps deal with AI uncertainty

We selected AI models that we considered the most available, reputable and suitable for running on cloud computing resources. However, we anticipated from an early stage that models would make identification errors, especially in regions for which they had not been trained. The clearest example of this was for the BatDetect2 model, which was only trained to identify 17 species. Partners in Croatia provided a list of 18 species that they would expect to pick up in bat recordings, of which only 8 are captured in the BatDetect2 list; *Hypsugo savii, Miniopterus schreibersii, Myotis capaccinii, Myotis emarginatus, Nyctalus lasiopterus, Pipistrellus kuhlii, Rhinolophus blasii, Rhinolophus euryale, Tadarida teniotis* and *Vespertilio murinus* are possible species at the Croatian sites which cannot be detected by BatDetect2. Furthermore, even experts cannot always distinguish species that form phonic groups, such as *Eptesicus/Nyctalus/Vespertilio*, *Myotis* spp., or *Hypsugo savii/Pipistrellus kuhlii/nathusii*. Given similar issues for birds and insects, it is not surprising that all respondents agreed that human verification is necessary to make use of AI outputs.

But how can verification help us make use of AI outputs, without negating the benefits of rapid AI processing? As we do not expect to verify all the data, it is important to strategically subset data for verification, and the best strategy may depend on the overall goal (Fig 23). In the ABMS, our verification was focussed on error quantification and confidence calibration. For moth species, we used existing verifications from Denmark to understand the performance of AI models. However, partners expressed interest in generating many more verification data for insects across Europe. This is especially important for the southern parts of the continent, where there are even more similar looking moth species that can not be reliably identified using AI models for northern Europe and the UK. For bats, we carried out a more comprehensive verification in which seven partners delivered verifications of bat records across 17 species. This helped us capture the variable performance of BatDetect2 at species level (Fig. 6), allowing us to select a more appropriate taxonomic level at which to interpret the data (Fig. 15). The verifications also allowed us to set thresholds to move from call-level to file-level identifications. Similarly, for birds, we used verifications from five countries to build confidence calibration curves for 86 species, converting BirdNet confidence scores into ABMS probabilities (Wood & Kahl, 2024). We identified some species that were identified very reliably, such as the European Robin *Erithacus rubecula*, and others that were not, such as the Tawny Owl *Strix aluco* (Fig. 5, Table 3). Crucially, we were able to use adjusted confidence thresholding for those 86 species to increase the accuracy of our EBV indicators. When published, ABMS verifications will also contribute to improving the performance of AI models across Europe.

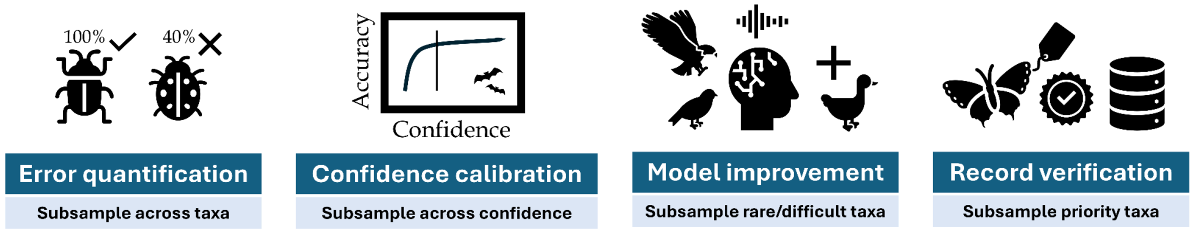


Figure 23. Different verification goals require different strategies for subsampling data. Experts can help to determine how and where a model tends to fail across a range of taxa, aiding interpretation of uncertain AI outputs. Furthermore, if verifications are made across a range of AI confidence levels, they can be used to calibrate confidence to true probabilities for a given context, making more accurate predictions using the same AI model. Alternatively, AI models can be improved using additional verified data capturing difficult taxa or contexts. Finally, experts can offer final verification of records of species of interest, such as invasives, pests or priority species, focussing expert time and attention to maximize impact.

Beyond interpreting and improving AI models, verification must be a requirement for a species-level biological record to be considered valid. A perspective from the Nature Conservation Agency of the Czech Republic emphasizes that occurrences of protected and red-listed species may have an impact on area development. When an observation is made by a human expert, the expert can be held accountable, and this is not yet the case for AI; a human expert still needs to validate red-listed and protected species and inform management. This is important when sensors generate records of rare or elusive species. For example, the black-crowned night heron (*Nycticorax nycticorax*) was detected at the grassland site in Ireland in 2024. This species is a rare visitor to Ireland with a few records every year, normally on coastal sites around the south or east of the country. Files with *N. nycticorax* detections were sent to two experts as a part of the verification process, and two detections, recorded between 1 and 3am on the same day, were deemed correct. Given there were only eight other records for *N. nycticorax* in the whole country in 2024, and none in the midlands of Ireland, verification was crucial to confirm that these records were not false-positive detections.

While verification was extremely valuable for the pilot, we also determined areas of improvement for the verification process. In particular, we found that verifiers benefit from having more information than the AI model in order to reach reliable identifications. That may include access to longer recordings, but also information on the location and ecological context. Previous studies with bird verification have used snippets of 5s (Scanferla *et al.*, 2025) or ⩾3s (Wood & Kahl, 2024); we opted for 3s to avoid the complexity of pooling confidence scores across snippets. However, verifiers found that for a considerable number of species, particularly *Sylvia borin* and *Anthus spinoletta* in Belgium, 3s was simply too short to identify with real certainty. Future efforts might provide longer snippets, or even entire 1 minute files (Pérez-Granados *et al.*, 2025), giving verifiers more information to work with. The downside is that annotation of longer files is much more intensive, as exact start and end times must be provided for bird calls. For bat verification we asked for identifications at file-level, but also call-level to match the BatDetect2 predictions. The 15 second snippets were apparently sufficient for file-level verification, but call-level identifications were not feasible or useful for most of our verifiers, highlighting the importance of longer time windows for species identification. Finally, we found it was advantageous to have verifications across as many taxa and regions as possible, but that larger sample sizes for each species were also highly desirable. In general, development of consistent and robust verification or annotation protocols is a priority for comparable sensor-based monitoring.

9.6. Local processing fosters engagement and understanding

Centralized processing has been a huge draw for partners of the ABMS (see recommendation 7). At the same time, partners have shown a collective interest in AI processing solutions. Throughout the pilot, it became clear that there is significant interest in capacity building across partner regions in terms of data processing, analysis and verification. This could include training in how to install, use, filter, and analyze outputs from BirdNet, BatDetect2 or insect classifiers. It could also include workshops and provision of user-friendly code to generate EBV indicators from sensor data. Experience from the ABMS supports the principle laid out by Silva del Pozo *et al.* (2023); Specifically, there is a role for both centralized and localized data processing in transnational monitoring, and localized processing is crucial to build an equitable network in which all partners are empowered and motivated.

While the pilot will make resources available for AI data processing, a main objective was to make tools available to visualise the locations, identity, and time of observation of species recognized by sensors. We focussed on images with insect species, aiming to facilitate creation of annotated datasets of insects across all partner regions. We explored efficient ways of doing so, including software tools such as MothBot, Antenna, and AnnFlux. AnnFlux in particular is a research tool for exploring and annotating large datasets with Active Learning, developed by Laurens Hogeweg at Naturalis. It uses a few annotations from a human expert to infer labels across the rest of the dataset, aiming to target annotations to maximize model improvements.

For the ABMS pilot, an instance of the AnnFlux application was created for each partner country. Clustering of detected animals can be visualised in a 2D scatterplot based on features derived from an AI model (Fig. 24). The distance between samples in this so-called “embedding space” is used to label clusters of points that are visually similar, and likely to belong to the same taxon. Users are actively prompted for annotations where uncertainty is highest, and the internal model is periodically fine-tuned, updating the clustering. Our other ideas for AnnFlux or similar tools include streamlining verification and adjustment of AI outputs, loading them in as preliminary annotations for the user to explore and correct. Further development and evaluation is needed to integrate such tools, but early testing indicates that they are crucial to maximize engagement and access to AI-generated data, as well as to generate annotations in regions with poor coverage.

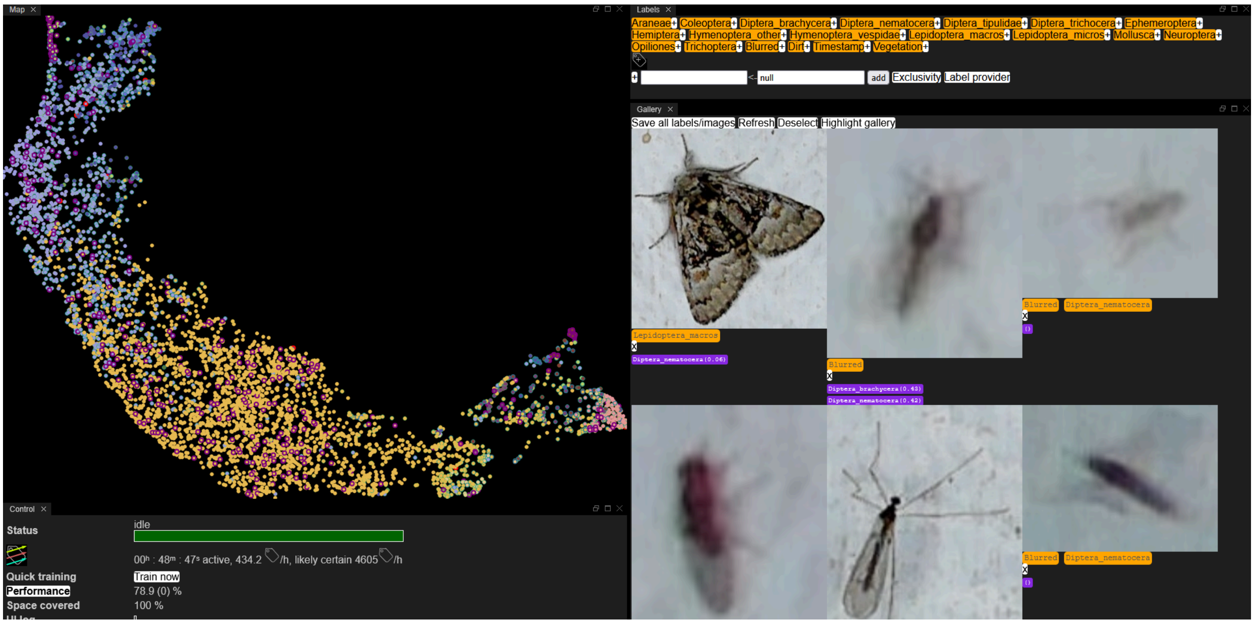


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Figure 24. Screen capture of the AnnFlux-application's user interface for a random selection of 5000 detections from data collected from AMI-traps in Denmark in 2025. The left panel shows clustering of detected insects, while the right panel allows a user to provide annotations. So far, the user has provided 432 annotations, allowing the model to infer provisional labels for all 5000 samples.

9.7. Coordination and centralized processing enable sensor networks

In their guide on harmonizing biodiversity monitoring across scales, Silva del Pozo *et al.* (2023) highlighted potential roles for both centralized and localized data processing in transnational monitoring. Local data processing options are desirable for pilot partners (see recommendation 6). However, the ABMS has trialled centralized AI processing for sensor-based monitoring, successfully generating a huge number of provisional species records, as well as spatially and temporally replicable EBV indicators. Furthermore, when survey respondents were asked about minimum requirements to continue sensor-based monitoring, the most frequent response was the provision of AI processing and outputs (Fig. 25). Remarkably, this response was more popular than three which related directly to funding for monitoring, whether for existing locations, new locations or equipment. Clearly a centralized data management and processing solution is highly desirable and motivating for partners to continue sensor-based monitoring, and should receive investment in future. This means communication and collaboration with an ever-growing number of projects and initiatives in image and sound processing, ensuring that the community converges on solutions that are most accurate, but also most repeatable.

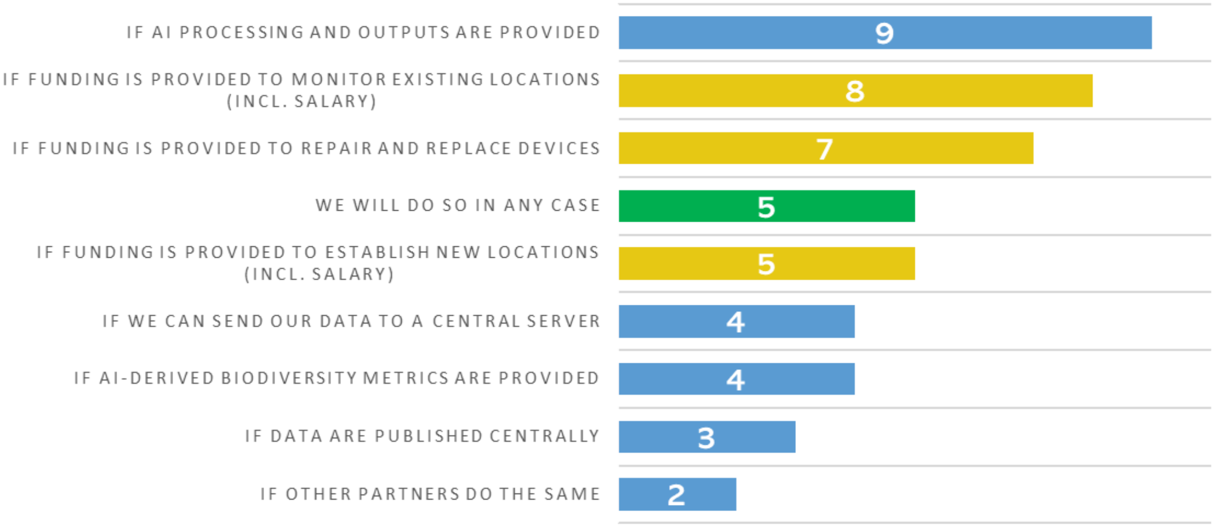

Figure 25. Conditions that facilitate sensor-based monitoring at ABMS locations. Respondents were asked to select a set of minimum requirements to continue ABMS monitoring at their locations. Of the 14 respondents, none selected two other options: “We will not do so” or “If data rights are more clearly defined”.

However, the benefits of coordination go beyond centralized data management and processing. Silva del Pozo *et al.* (2023) highlight the relative roles of strict vs. general protocols, in that the former can lack flexibility, but generate data that are easy to process and compare. In the ABMS pilot we tried to develop relatively strict protocols - specifically protocols for site selection, device deployment and data transfer. Strict protocols for device deployment and data transfer were relatively easy to uphold; exceptions involved the recording frequency of AMI devices, for which Sweden preferred a 2 minute interval, and deployment of acoustic devices in Croatia, where recording parameters were adjusted and devices placed further from the ground. While relatively strict protocols for device deployment and data transfer provided consistent data flows from partners across Europe, a strict protocol for site selection was difficult to adhere to (see 3. Sensors constrain sampling and site selection). Collaboration and coordination to develop protocols was crucial in the pilot, and continue to be necessary going forwards.

From the perspective of the pilot, sensor-based monitoring should provide opportunities to coordinate efforts across Europe. Further work is needed to finalize protocols and produce automated monitoring handbooks, and funding is needed to maintain, repair, upgrade or replace devices being used to collect baseline data. Initiatives and tools are needed to strategically annotate sensor data, whether for model evaluation or to efficiently generate biological records (Fig. 23). Importantly, general AI and EBV pipelines need further development, including new classifiers for insects and amphibians in acoustic data. In particular, options should be made available for centralized data management and processing (Fig. 25). Furthermore, pipelines need to be replicable and well-disseminated, ensuring that localized processing is also an option (Silva del Pozo *et al.*, 2023). In general, there are opportunities to better exploit both new and existing streams of sensor data for ecological and policy insights. Meanwhile, continuity of biodiversity trends is best ensured by deploying novel and traditional monitoring methods in tandem.

Thanks to connections with existing and emerging automated monitoring initiatives, the ABMS pilot has built a strong foundation for a transnational biodiversity sensor network. While the pilot officially ends in 2025, five respondents stated that they will continue monitoring the same locations regardless of any further support (Fig. 25). While centralized funding has not been made available, further alignment of regional and national monitoring goals is the primary avenue to maintain joined-up transnational sensor networks. We hope that support for capacity building and networking around sensing of bats, birds and night-flying insects will provide both economic and collaborative incentives to continue monitoring at as many locations as possible, building on the strong foundation of the pilot.

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