

## VIEWPOINT

Advances in Insect Biomonitoring for Agriculture and Forestry

# Bugs and bytes: Entomological biomonitoring through the integration of deep learning and molecular analysis for merged community and network analysis

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## Abstract

1. Insects play a vital role in ecosystem functioning, but in some parts of the world, their populations have declined significantly in recent decades due to environmental change, agricultural intensification and other anthropogenic drivers. Monitoring insect populations is crucial for understanding and mitigating biodiversity loss, especially in agro-ecosystems where a focus on pests and beneficial insects is gaining momentum in the context of sustainable food systems.
2. Biomonitoring has long played an important role in providing early warnings of insect pests and their vectored pathogens and for assessing agro-ecosystem management. However, identification of invertebrates by taxonomists is time-consuming and fraught with numerous other challenges, particularly when it comes to real-time monitoring.
3. Recent technological advances in both computational image recognition and molecular ecology have enhanced biomonitoring efficiency and accuracy, reducing labour efforts, but leading to unprecedented volumes of data generated.
4. This perspective article examines the significance and further potential of deep learning with image-based recognition, aided by complementary technologies, in advancing entomological biomonitoring. Using entomological sticky traps as an example, we discuss each step of the workflow required to create ecological networks using image-based recognition, multimodal data and deep learning, and we identify the challenges inherent to this method and other insect survey techniques.
5. In order to become mainstream for global biomonitoring, access to long-term, standardised multimodal data is required for comprehending ecosystem dynamics, structure and function and for mitigating insect population declines.

## KEYWORDS

biodiversity conservation, ecological networks, entomology, insects, integrated pest management, metabarcoding

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## INTRODUCTION

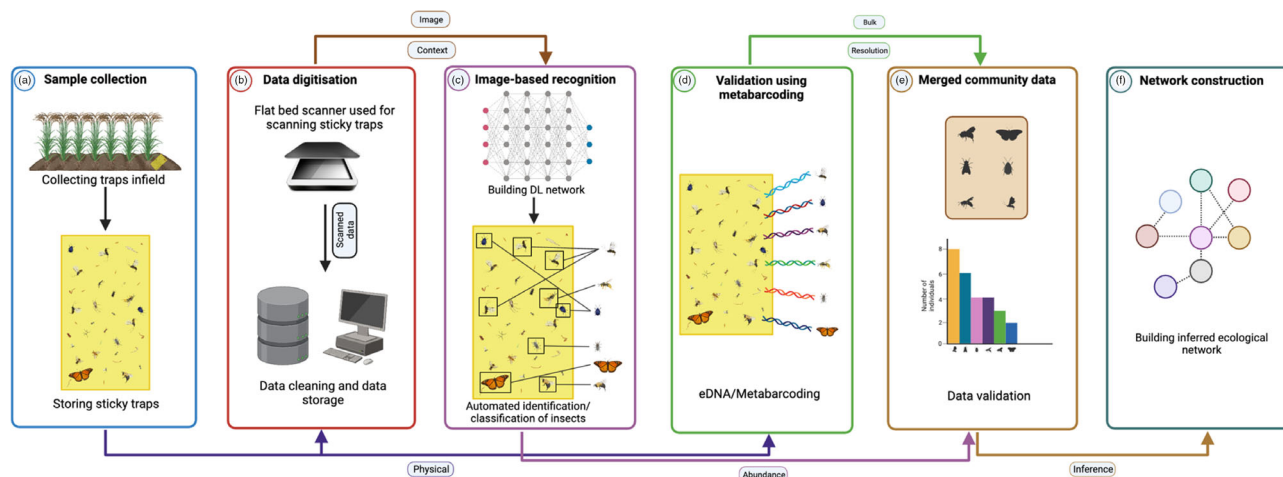
Insects play a crucial role in ecosystems, providing important ecological processes such as pollination and nutrient cycling as well as being embedded in complex food webs (Leather, 2005). Recent research suggests serious declines in insect populations in many parts of the world due to a range of factors including agricultural intensification, climate change, increases in urban spaces and light pollution (Ärje et al., 2020; Blair et al., 2022; Boyes et al., 2021; Coulibaly et al., 2022; Høye et al., 2021; Ramalingam et al., 2020; Zapico et al., 2021). Fewer than 1% of the 1.4 million described invertebrate species have been assessed by the International Union for Conservation of Nature (IUCN), but of those that have ~40% are considered threatened, with terrestrial insect abundances in particular undergoing significant declines in recent years (Dirzo et al., 2014; van Klink et al., 2023). There is an urgent call to better understand and mitigate insect population declines through effective monitoring (Blair et al., 2020; Gerovichev et al., 2021).

Whilst insect biodiversity and abundance have generally declined globally, agricultural and forest insect pests as well as vectored pathogens are increasing in many parts of the world (e.g., Shortall et al., 2024) and their ranges have expanded due to climate change (Skendžić et al., 2021). Thus, a greater understanding of the functional roles of insects within these ecosystems is important for sustainable pest management. Agricultural pests varyingly impact nearly half of the world's crops, costing the global economy around \$200 billion USD every year (Karar et al., 2021). Outbreaks of insect pests therefore pose a serious threat to food production. The increase in pests is due to a combination of factors including climate change (air-temperature, relative humidity, etc.), extreme weather conditions and seasonal variability (Marković et al., 2021). Invasive alien species are also of considerable concern to agriculture and forestry. The Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services' (IPBES) *Thematic Assessment of Invasive Alien Species and their Control* asserts the importance of early detection of the spread of invasive alien species through effective biomonitoring, as this is vital to policymakers for intervention and decision making (Roy et al., 2023). Biomonitoring strategies are therefore key for early detection and effective control of insect pests in agriculture and forestry (Coulibaly et al., 2022; de Cesaro Júnior et al., 2022; Saradopoulos et al., 2022).

There are a number of well-established entomological trapping techniques that are used to collect specific invertebrate samples in the field for biomonitoring purposes, including pan, pitfall, aerial suction and sticky traps (see Strickland, (1961) and Hawthorne et al., (2024) for reviews of methods used in agriculture and (Leather, 2005) for a comprehensive overview in forest ecosystems). Such entomological trapping methods are used in different scenarios to trap specific types of insects for a range of purposes, but each trapping technique has its own advantages and disadvantages (Cuff, Deivarajan Suresh, et al., 2023; Cuff, Tercel, et al., 2024; Hawthorne et al., 2024). In agricultural and forestry settings, these methods are predominantly used for detecting pests (including disease vectors). The identification and

classification of caught target insects is typically done manually by highly trained taxonomists; however, taxonomic skills are in decline (Engel et al., 2021). Furthermore, the process of manual taxonomic identification is time-consuming, costly and does not scale (Besson et al., 2022), making real-time monitoring of pest species is more challenging (Bjerge et al., 2022; Wang et al., 2020; Wang, Zeng, et al., 2023; Wang, Zhang, et al., 2023; Wang, Zhao, et al., 2023). Recent advances in both computational image-based recognition technology and molecular ecology are helping improve, automate and computerise this process thereby potentially making biomonitoring extremely efficient, accurate and ultimately easier to scale up with less manual labour (van Klink et al., 2022). Long-term monitoring samples obtained through various biomonitoring schemes can enable streamlining and the integration of various techniques, thereby enabling researchers to construct advanced ecological networks through inference methods to assess ecological changes (Cuff, Deivarajan Suresh, et al., 2023). With multiple data types and contexts (location, time, temperature, behaviour, functional traits, etc.) available from a diverse range of biomonitoring techniques, it is beneficial to combine them to form multimodal datasets. Ultimately, this can help in the progression towards large-scale automation of multimodal biomonitoring data using deep learning (DL; Cuff, Deivarajan Suresh, et al., 2023).

In order to respond to anthropogenic impacts such as environmental change, agricultural intensification and land-use change, a better spatio-temporal and real-time understanding of global biodiversity is required. Distributions, ecological functions and species interactions are good indicators of the state and/or condition of ecosystems (Chua et al., 2023), but for invertebrates, much work is needed to improve taxonomic databases at relevant scales for effective biomonitoring (McGee et al., 2019; van Klink et al., 2022). Currently, large numbers of taxa and diverse geographic locations make it hard to standardise monitoring of global insect biodiversity and at least 80% of the insect population still remains undescribed (McGee et al., 2019; Saradopoulos et al., 2022; van Klink et al., 2022). New methods for biomonitoring insects at appropriate spatio-temporal scales are urgently needed for crop and forest protection, which can also help in understanding ecosystem processes and restoration, and ultimately human health. This perspective article examines the development and application of DL with image-based recognition and other technologies in advancing entomological biomonitoring. Taking sticky traps as an example of a common entomological research method primarily to trap aerial insects, we discuss how DL with image-based recognition can be applied to provide a better understanding of species richness, abundance, trait and interaction data and how such data should be handled—from bugs to bytes. By describing each step of a workflow, we aim to (i) provide a brief overview of the state-of-the-art; (ii) identify the benefits and limitations of the existing approaches; (iii) discuss the potential applications, whilst acknowledging the knowledge gaps and lack of well-established frameworks for ecosystem insights; and (iv) explore how multimodal data can be used to construct ecological networks that provide a framework for understanding biodiversity, ecological functioning and ecosystem resilience.



**FIGURE 1** Methodological workflow depicting the combination of complementary data types from image-based recognition and validation using metabarcoding to produce inferred ecological networks from sticky traps. Starting with (a) sample collection from the field; sticky traps are then (b) digitised before DL is used to automatically identify/classify insects (c), providing contextual data. Species identification can be (d) validated using DNA/RNA metabarcoding (providing additional information, such as host–parasitoid detections), providing resolution to taxonomical identities. (e) Information on species identification, abundance, traits and other data is merged and then used to (f) construct ecological networks using inference (Image created using BioRender).

Our overall aim is to provide an introduction to a rapidly developing technical topic of interest to agricultural and forest entomologists, sign-posting researchers to in-depth papers and reviews on particular aspects of our perspective. We provide a glossary of the technical terms used throughout the article as a [supplementary document](#).

## FROM BUGS TO BYTES: STEPS TO CREATE ECOLOGICAL NETWORKS USING IMAGE-BASED RECOGNITION, MULTIMODAL DATA AND DL

We provide a unifying framework that combines molecular and image-based monitoring for automated identification/classification of insects from sticky traps (Figure 1). Specifically, the workflow enables the construction and analysis of ecological networks (here, interspecific species–interaction networks), moving beyond simple species lists currently obtained from most biomonitoring schemes to new metrics for assessing both biodiversity and ecosystem function (see Cuff, Deivarajan Suresh, et al., 2023; Cuff, Tercel, et al., 2024). We examine the state-of-the-art of each step separately (Figure 1a–f), identifying some of the outstanding challenges, and then discuss the merits of this integrative approach.

### Insect sample collection for biomonitoring

Many government agencies, organisations and researchers use entomological surveys for early detection and mitigation of insect pests, invasive species and/or assessing insect populations. But there is a geographical skew in entomological surveys and specificity in

monitoring of certain insects. The UK, however, has a long history of well-established insect surveillance and monitoring programmes. For example, biomonitoring schemes such as the Rothamsted Insect Survey (RIS), Butterfly Monitoring Scheme (UKBMS), UK Environmental Change Network (ECN) and Fera Yellow Water Pan trap network (YWP) are trusted and respected for a range of purposes. For these and other similar schemes across the world, some of the entomological data are archived in physical form whilst others are stored digitally after taxonomic classification is completed (Høye et al., 2021; Petsopoulos et al., 2024). However, most non-target insect catches are often discarded due to lack of resource for identification meaning valuable biodiversity data are lost (but for RIS, see Petsopoulos et al., 2024).

Classical biomonitoring methods are manual and shown to be inefficient (Høye et al., 2021). Typically, the workflow includes trapping, manual inspection, morphological identification and counting of insects that are time- and labour-intensive tasks requiring highly trained personnel (Albanese et al., 2021; Årje et al., 2020; De Cesaro Júnior et al., 2022; Høye et al., 2021; Høye et al., 2022; Lins et al., 2020; Roosjen et al., 2020; Sütő, 2021; Zhao, Zhou, et al., 2022). The morphological identification and counting of insects in high-density samples are prone to a range of human errors including observer biases and fatigue as well as factors such as inadequate magnification and similarity between insects (Albanese et al., 2021; Barbedo, 2014; Butterworth et al., 2022; Lins et al., 2020; Thenmozhi & Srinivasulu Reddy, 2019; Zhao, Liu, et al., 2022). Small insects and debris present in traps also reduce the identification efficiency (Barbedo et al., 2020), thus making accurate counting and detection of insects difficult, especially on sticky traps (Diller et al., 2022; Rustia et al., 2021). Furthermore, spatiotemporal replication of monitoring traps in the field is difficult due to the labour involved in setting,

maintaining and collecting a large number of traps and the area that must be covered by the field scientists (Roosjen et al., 2020). In-field biomonitoring is mostly used for identifying economically significant flying insects (such as aphid pests) using manual identification, with non-target catches mostly discarded. However, other trap types such as pitfall traps, delta traps and sticky traps can also be deployed depending on the question being asked (Chua et al., 2023). Sticky traps often capture non-target insects, termed 'bycatch', which can compound biomonitoring problems. This is especially true in the case of pest biomonitoring schemes that are deployed to monitor certain insects, but also result in a significant amount of non-target bycatch. However, a more holistic understanding of insect populations within ecosystems could identify impacts of land management (e.g. farm tillage practices and implementation of agri-environment schemes) on ecosystem functioning across scales. Such relationships can ultimately be analysed using ecological networks, but this first requires better resolved and more complete data that could be obtained by identifying bycatch using methods such as DL and/or DNA/RNA metabarcoding (Chua et al., 2023; Petsopoulos et al., 2021; discussed further in section F).

## Data digitisation

In the past decades, there has been a steady rise in the development of sensor-based automated insect biomonitoring systems involving cameras, radars and microphones that produce vast amounts of data (Big Data). Such systems reduce the need for continuous and expensive biomonitoring that accompanies traditional methods (Li et al., 2021; Nanni et al., 2020) and reduce the bias of observers and sample handling time, whilst increasing the amount of samples collected and reproducibility, thereby giving a more holistic spatio-temporal resolution of communities for ecological assessments (Ärje et al., 2020; Beermann et al., 2021; Høye et al., 2022).

Image acquisition from sticky traps (and other types of traps), by scanning and digitising the insect images under controlled lab environments, provides better image quality than in-field photographs (Ärje et al., 2020; Lins et al., 2020; Zhao, Zhou, et al., 2022) and also importantly provides a consistent image quality, collected from a static viewpoint (Roosjen et al., 2020); in-field automated detection of insects on plants, whilst now available, has technical limitations due to the detection of insects in complex differing backgrounds and insect population densities (Albanese et al., 2021; Li et al., 2022; Lins et al., 2020). This is an important consideration for image-based recognition training (see section C). Digitisation of traps in lab settings is done manually using flatbed scanners or for other types of samples through automated imaging systems, such as the BIODISCOVER robot-enabled image-based identification machine (Ärje et al., 2020; Wührl et al., 2022).

Data cleaning, such as removing irrelevant or blurred images, and alterations such as augmentation and data annotation are done during this step of preparing data that will later be used for model training. The cleaned data with appropriate annotation are then stored locally

or on cloud-based servers for ease of access. However, standardised, well annotated insect image-based and multimodal datasets and pipelines are currently lacking for the different trapping methods, including sticky traps. The lack of such datasets causes severe issues, which are further explained in the sections below.

Image preprocessing (image resizing and data augmentation) is vital for dataset preparation, especially for digitised sticky trap scans (Figure 1b). This tackles problems such as occlusion, object overlapping, insufficient number of images for rare insect species, morphologically damaged insects, varying image sizes and overall improvement of detection accuracy (Albanese et al., 2021; Ärje et al., 2020; Diller et al., 2022; Li et al., 2021). Given the random fixed positions of insects on sticky traps, image data collected from sticky traps are likely to be particularly susceptible to these problems.

## Image-based recognition

### Deep learning and machine learning for image-based recognition

Image-based approaches for studying invertebrates have recently been gaining attention (Høye et al., 2022; Lürig et al., 2021) and advancements in computer vision (CV) have given rise to identification of insects using automatic image-based technologies (Ärje et al., 2020; Li et al., 2021). These new systems can be utilised to their maximum efficiency by employing DL as a tool for counting and identifying insects (Besson et al., 2022). Machine learning (ML) is a field of artificial intelligence that enables systems to learn patterns from data and make predictions or decisions through interconnected artificial neurons (neural networks). DL is a subset of ML that comprises types of neural networks that are large in size with multiple hidden layers, which can extract higher level features (individual measurable properties) from data fed into them.

Due to ease of accessibility of big data, application of ML and DL has risen sharply in recent years, especially in ecology and evolution, but their relationship with classical data analysis tools is still debated (Pichler & Hartig, 2023). Overall, DL performs better in classification/identification than ML methods in terms of accuracy, but is slower in image-based tasks (Karar et al., 2021). For automated biomonitoring, time taken to taxonomically identify specimens will be an important consideration for selecting these methods rather than traditional biomonitoring with morphological identification (Ärje et al., 2020).

The main advantage of DL is that it can help computers build complex descriptions using only simple concepts and deeper algorithms, unlike ML. DL has a greater capacity than ML to identify the intrinsic image characteristics from any presented image dataset (Li et al., 2021). Data are typically split into 70%–80% for training, 10%–15% for testing and 10%–15% for validation of DL algorithms (Karar et al., 2021). Another distinction is that ML requires hand-crafted features whilst DL automatically extracts features through the neural networks. ML techniques were widely used in entomological identification before the development of DL methodologies (Høye

et al., 2021; Kirkeby et al., 2021), but DL is now often preferred due to its greater performance. However, all the limitations (like insect densities, lack of rare insect samples) and alternative model enhancement techniques (such as data augmentation) used to tackle case-specific entomological classification/identification issues should be considered when building DL models for automated insect biomonitoring. Limitations prevalent in developing databases for automated entomological biomonitoring include the inability to identify insects that are not present in the reference database (Årje et al., 2020) and poor generalisation issues between the model trained and the data being input for analysis, particularly due to differences in image quality (Hansen et al., 2020; Li et al., 2021; Popkov et al., 2022).

Other limitations in DL methods are collecting, standardising and annotating reliable data, which itself can be expensive, labour-intensive and time-consuming (Barbedo et al., 2020; Høye et al., 2021; Rustia et al., 2021), at least in the short-term set-up of such data. For multimodal data, it is challenging to fuse the data from different modalities during the training. The amount of training data required for image-based DL classification is also a limiting factor, as large, high-quality datasets with many classes are required (Årje et al., 2020; Gerovichev et al., 2021; Høye et al., 2022; Sütő, 2021), which will increase the time taken for training (Barbedo et al., 2020). But once sufficiently large, quality databases are built, the future iterations of DL training and implementations can be much faster and efficient. In the case of sticky traps, this brings other complications as some insects may be damaged during the trapping process or get trapped in positions where important distinguishing features are obscured, making morphological identification difficult (Butterwort et al., 2022). Decay, lighting glare and movement of the trap are also some of the other challenges that make image-based detection and classification of insects from sticky traps much harder.

Convolutional neural networks (CNNs), a type of multi-layered DL model, have a convolutional layer, in addition to the usual input layer, rectified linear unit layer, pooling layer, fully connected layer and classification layer, which are also present in other DL models (Chodey & Noorullah Shariff, 2022). CNNs automatically extract features from raw pixels of images (Karar et al., 2021) and have been widely implemented in insect identification and classification tasks with varied amounts of successes and limitations, depending on image data source (Alves et al., 2020; Cheng et al., 2017; Nanni et al., 2020). Usually, for training of such automated CNN models, with data such as sticky trap images, the specimens (insects) are annotated by drawing bounding boxes around them and manually identifying them. DL methodologies such as Inception v3, Deep CNN, Residual Neural Network (ResNet-50), VGG-16/19 and many others have been used in several studies for entomological identification and classification (Karar et al., 2021). Generally, two-stage algorithms (Faster-R CNN and Mask-R CNN) are more accurate, whilst one-stage algorithms are faster (Li et al., 2022). However, combining different CNN architectures can help boost the generalisation of methods, rather than building a single large CNN (Li et al., 2021).

Python is commonly used for training of DL models, which are for object detection and classification tasks. TensorFlow and PyTorch

libraries are particularly used for training DL models in Python (Lins et al., 2020). Commonly used object detection benchmarks are ImageNet, Pascal VOC and MS COCO, which can be used for model pre-training (Li et al., 2022; Wang et al., 2020). Presently, running DL networks requires high parallel computing power for processing and training data, usually by utilising powerful Graphical Processing Units (GPUs) (Karar et al., 2021; Rustia et al., 2021).

## Supervision, imaging techniques and data sources

Supervision in the context of supervised learning involves human annotators providing labelled examples, which the DL model uses to learn and generalise patterns for accurate predictions on unseen data. This is an important determinant of accuracy. Automated insect identification using DL, under the fully supervised learning setting, is more reliable with tasks such as counting, size and weight estimation, compared to unsupervised learning. Supervised learning implemented to identify specimens, such as aphids (Li et al., 2022), show high reliability and accuracy, on par with humans. Fully supervised, standardised species level classification DL algorithms like this can potentially aid in building a reliable, interoperable generalistic automated insect classification system of the future.

Species level identification is currently hard to classify using DL and ML, whilst genera is comparatively easier in terms of accuracy, depending on the taxonomic group (Årje et al., 2020; Hansen et al., 2020; Høye et al., 2022; Johnson & Khoshgoftaar, 2019; Kirkeby et al., 2021; Lima et al., 2020; Popkov et al., 2022). Morphologically demanding species ('classes' in DL) require more training data and demanding tests to establish how error rates can vary depending on the number of closely related species (Årje et al., 2020; Høye et al., 2022). Adding more classes reduces the performance of the classifier in identification of the targeted classes (Rustia et al., 2021). Low availability of training data of certain classes can lead to poor multi-class classifications, and hence, it is important to balance, increase the dataset and have images of specimens from different imaging conditions, angles and presentations (Albanese et al., 2021; Blair et al., 2022; Høye et al., 2022; Li et al., 2022; Lins et al., 2020).

Taxonomic identification of insects depends on the quality of images and the quantity of training data used for training DL algorithms (Årje et al., 2020; Høye et al., 2022). The primary images acquired for DL are from internet searches, public data sets (IP102, DO, etc), mobile cameras and stationary cameras. Image datasets built on images from the internet alone have limitations such as varying image quality, inconsistent resolution of images, images with texts, incorrect identification/labelling and lack of required images, all of which reduces training data availability and increases development time of DL. Internet-sourced images must be cleaned before using it for DL algorithms. Whilst public images are used for training of DL algorithms for general insect identification, they are not yet used in the specific case of identifying insects on sticky traps. This may be due to the above-mentioned issues arising from images collected from the internet. Additionally, models trained on insects will not generalise



to the specific nature of sticky trap images due to size variations of insects, occlusion, etc. Hence, bespoke datasets specific to sticky traps are required.

Current automated biomonitoring systems often use cameras alongside DL methods to capture and analyse images of insects from traps, or in the environment (e.g. on crops to detect pests). Microprocessors and Internet of Things (IoT) are used to send the collected data to the cloud for further processing (Ayaz et al., 2019). Fully autonomous biomonitoring systems for insect scanning, identification and classification are currently being developed (Ärje et al., 2020; Høye et al., 2021; Li et al., 2021). By integrating various in-field biomonitoring techniques with wider data collection methods, large multimodal datasets with valuable contextual data (e.g. location, time, temperature) can be obtained (Besson et al., 2022). This big data enables the building of well-defined DL systems and will broaden the scope of analyses of biomonitoring data using other data sources. In order to do this, cleaning, annotating and storage of standardised image data are required (Figure 1b). By successfully implementing this step, a sufficient amount of high-quality multimodal training data is available to build and train efficient DL systems. Training of such DL systems using appropriate resources (such as robust algorithms, high quality data) can create a positive feedback loop by which future automated biomonitoring DL systems can be easily created with significantly less hassle. However, the initial annotation and digitisation of data require a considerable amount of time, money and effort (Barbedo et al., 2020; Høye et al., 2021; Rustia et al., 2021) but pay dividends in the long-term.

Automated and semi-automated identification of insects has potential applications not just for biodiversity monitoring but also for museum collections and wider ecological studies (Hansen et al., 2020). Museum collections paired with image-based monitoring can substantially increase occurrence data and will be helpful to analyse long-term ecological responses to environmental changes, but cannot help with the generalisation of the DL models applied to ongoing monitoring, because of the difference between training data and the data fed into the model for analysis (Hansen et al., 2020; Popkov et al., 2022). The EU-funded DISSCo project and the UK's NHM Digital Collection Programme are some examples of museum specimen digitisation efforts that will help in developing better DL models, through the valuable image databases they provide (Høye et al., 2021; Popkov et al., 2022).

There have been attempts to implement automated morphological classification models for similar insect species in museum specimens (Hansen et al., 2020; Popkov et al., 2022). Dead specimens are useful as lighting and background can be kept uniform in order for the DL models to learn better, which will greatly help in the validation process (van Klink et al., 2022), but CNN models should be trained with diverse mixed datasets, so that the models avoid failure in real-world conditions. Models trained with high-quality images pose a problem in recognising poorer quality images, but the reverse is not true (Barbedo et al., 2020; Sütő, 2021). Hence, variability of image quality through different sources should be assessed further, as this will open up a huge potential to utilise the digitised images from

museums to pre-train DL algorithms that can be used in automated biomonitoring.

## Additional classification, annotation and data processing methods

The dataset size currently available is relatively small for annotated sticky trap images (Li et al., 2021; Rustia et al., 2021). Lack of open-source code and public datasets is a common problem in ecology and evolution, especially in research focused on developing AI for biomonitoring purposes. Only a few research papers have open source code (i.e. Blair et al., 2020, 2022; Diller et al., 2022; Gerovichev et al., 2021; Gomes & Borges, 2022; Li et al., 2021; Popkov et al., 2022; Saradopoulos et al., 2022) and even less have datasets publicly available (these tend to be unique groups of invertebrates) (Ärje et al., 2020; Blair et al., 2020; Chodey & Noorullah Shariff, 2022; Hansen et al., 2020). In many instances of insect biomonitoring, the training dataset required is rarely available and ecological data of different scales are harder to combine. To tackle this in the short term, few shot learning and transfer learning (TL) can be used in DL (Pichler & Hartig, 2023). Few-shot learning (FSL) can specifically be helpful in focusing on one species for a particular context (eg. one crop) (Gomes & Borges, 2022).

Most research commonly uses various CNN models for insect identification/classification tasks. Recently, vision transformers (ViT) such as Swin transformers are being developed in tandem with CNNs for automatic insect biomonitoring purposes. ViT require substantially lower computational resources than their CNN counterparts and perform equally or better. ViTs are used alone or in combination with CNNs for increasing efficiency in insect identification/classification tasks (An et al., 2023; Batz et al., 2023; Guo et al., 2023; Hechen et al., 2024; Lee et al., 2023; Peng & Wang, 2022; Venkatasachandranthand & Iyapparaja, 2023; Wang, Zeng, et al., 2023; Wang, Zhao, et al., 2023; Xia et al., 2022).

Learning strategies can be used to tackle the limitations of CNNs in automated insect classification/identification. These include TL (Pichler & Hartig, 2023), FSL (Gomes & Borges, 2022), attention mechanisms (Zhao, Liu, et al., 2022), density map estimation (Bereciartua-Pérez et al., 2023), weakly supervised learning (WSL) (Coulibaly et al., 2022), cascading classification (Rustia et al., 2021), fused pest context detection (Wang et al., 2020), network pruning (Albanese et al., 2021), mutual information scoring (Coulibaly et al., 2022), coarse-to-fine network (CFN) (Li et al., 2021) and adding contextual information such as location, time and temperature (Blair et al., 2022). These methods are implemented on a case-by-case basis depending on the quantity and the quality of the data.

Fine-grained classification is particularly useful for detailed classification processes when differences between classes are subtle, for example, to classify closely related species or smaller insects that are hard to identify correctly because they are represented by fewer pixels, but it requires a very large amount of data to be trained on. A large balanced training dataset helps with accurate classification, but

most biological samples have class imbalances (i.e. some species are more abundant than others). This is hard for invertebrate classification when datasets often do not have enough specimens for training, which is currently the case for many rare insect species. Classification accuracy is consequently better achieved at the genus-level rather than the species-level (Årje et al., 2020; Hansen et al., 2020; Høye et al., 2022; Johnson & Khoshgoftaar, 2019; Lima et al., 2020). Attention mechanisms are another method that is capable of extracting global features and discriminative features in regions of interest. Attention mechanisms can improve multi-scale feature extraction of insects, without increasing the number of model parameters (Zhao, Liu, et al., 2022). They help in much more efficiently extracting features of small insects much more efficiently (Li et al., 2021).

The manual drawing of bounding boxes is a key obstacle for building datasets and can be addressed by density map estimation. Density map estimation is robust and scalable and can enhance the specimen annotation process by making it simpler and faster than drawing bounding boxes on specimens; instead, this method just involves placing a dot on each specimen (Bereciartua-Pérez et al., 2023). WSL, on the other hand, can help identify certain specimens without the need for bounding boxes or other forms of complex labelling (Coulibaly et al., 2022).

Fused pest context detection can help increase the accuracy of pest detection and recognition in complex environments by adding contextual information as prior information from the images (geographic location, time, temperature, etc), and mutual information scoring can further help with increasing accuracy of insect detection and recognition (Coulibaly et al., 2022; Wang et al., 2020). Neural network pruning, the removal of unnecessary neurons or weights from a trained model, can help to make the DL algorithm more lightweight, without losing its functionality and can enable remote deployment of advanced identification/classification algorithms in the field on edge devices (Albanese et al., 2021).

## Validation of image-based monitoring using molecular techniques (eDNA and metabarcoding)

Validation of biomonitoring data by independent verification of detections is a critical challenge in DL to conclusively identify insects from images. In the case of our proposed workflow (Figure 1), validation of image data (identified insects) is compared with a list of insects identified from the independently generated metabarcoding. We contend that a combination of taxonomic expertise, complemented by metabarcoding, is optimal for data validation (ground truthing). Indeed, DNA/RNA metabarcoding and traditional barcoding, when implemented alongside image-based DL techniques, will become invaluable for highly resolved insect identification and classification to validate and enhance taxonomic resolution (Høye et al., 2021). In our sticky trap example, the image-derived insect data (identified insects) are compared with the complementary list of insects identified by metabarcoding to validate those identifications and subsequently form a comprehensive multimodal species list (whilst also providing

additional detections that could yield interaction data, such as parasitism, which cannot be detected using images alone).

DNA/RNA metabarcoding of bulk and environmental invertebrate samples (eDNA) is gaining considerable traction as a biomonitoring tool in its own right, not least as it can distinguish morphologically similar insects (Derocles et al., 2016). This can help standardise biomonitoring and provide highly resolved data for wider ecosystem assessment (McGee et al., 2019). Of particular interest is the identification of bycatch typically ignored in morphological identification, which can be identified in parallel with target taxa using metabarcoding, and this process can be scaled-up by using automated techniques (Petsopoulos et al., 2021). Specifically, DNA-based techniques such as high throughput sequencing (HTS) have enabled researchers to simultaneously identify multiple target species and have reduced the time needed for identification of bulk insect samples (Chua et al., 2023).

This is important when moving on to the next step of merging community data (Figure 1e). However, before discussing this, it is important to consider the limitations of molecular ecological methods, particularly in the context of validation. Insect specimens caught on sticky traps are exposed to different temperatures, UV radiation and humidity, leading to reduction in DNA integrity and recovery that affects DNA-based techniques. Currently, metabarcoding for sticky trap bulk sample processing is not commonplace, likely due to inherent problems such as manually removing the insects from the sticky traps. The effect of glue and clearing agents can further degrade DNA and inhibit PCR (Butterwort et al., 2022; Maxwell et al., 2011). Some decay and genetic degradation of insects on traps can be prevented by collecting traps more frequently (Rustia et al., 2021) and processing the traps as soon as possible after collection. The latter is particularly important for image-based DL systems, as morphologically degraded insects are likely to make it harder for DL to generalise from the data it is trained on. The ability of molecular data to determine species abundances for quantitative network construction and analyses from bulk samples is currently problematic, but species richness can be determined (Evans & Kitson, 2020); however, the lack of abundance from molecular data mitigated by incorporation of functional, contextual and trait data determined through DL, which can introduce context such as the roles that different species play towards ecosystem function (Chua et al., 2023; Høye et al., 2021). As an example for functional traits, CV can provide measurements of morphological features linked with interactions (e.g. tongue length in pollinators), whilst DNA metabarcoding can provide detection of species not visible to CV (e.g. endoparasites), highly resolved species identities and genetic diversity (Chua et al., 2023; Høye et al., 2021). Indeed, quantitative community data can still be generated based on this experimental design by merging these datasets.

Metabarcoding, particularly for smaller sample sizes, can be more expensive than traditional morphological identification because sample collection still requires manual labour (Årje et al., 2020; Besson et al., 2022). However, metabarcoding is scalable and cost/time efficient on a large-scale (van Klink et al., 2022) and varying depths and breadths in terms of analysis are required for different environmental sample types (McGee et al., 2019). Some specimens may not be

identified from bulk samples via metabarcoding, and it may not always be possible to relate data to morphology afterwards (Chua et al., 2023; Høye et al., 2021). Further misclassifications can occur because of sequencing errors and reference database inaccuracies. These limitations related to barcode database completeness are now being tackled by national and international taxon-specific initiatives (van Klink et al., 2022). Also, collaborative efforts such as International Barcode of Life (iBOL) and GenBank help in standardising workflows and promoting best practices in building these genetic databases (Chua et al., 2023; McGee et al., 2019). Different clustering (grouping similar sequences together) and filtering (removing erroneous sequences) thresholds can also lead to misclassification of taxa (McGee et al., 2019). Misclassifications and poor quantitative measurements from the metabarcoding process could cause potential problems for the validation of DL in our workflow. The validation process of comparing the data between DL (relative frequency) and metabarcoding (binary detections or inaccurate quantities) data might affect the accuracy and, in turn, impair the decision making surrounding the accuracy of DL. More research in this area is needed.

Rapidly developing DNA sequencing technologies help in highly resolved identification of communities and help towards building plant-insect ecological networks, including insect pollination, host-parasitoid interactions and wider food-web studies (Evans & Kitson, 2020). Molecular data containing species interaction information can then be incorporated into ecological networks (Popkov et al., 2022).

## Merged community data

Towards better understanding of ecosystem functioning, there is growing interest in combining biodiversity data from different trapping methods, especially the inclusion of interactions, which in turn has promoted the development of new biomonitoring frameworks (Cuff, Deivarajan Suresh, et al., 2023; Cuff, Tercel, et al., 2024). The ability to collect and combine community data made possible through new technologies has given researchers potential to construct complex merged ecological networks in a range of biomes (Windsor, 2023). Although challenges remain (Cuff, Deivarajan Suresh, et al., 2023; Cuff, Tercel, et al., 2024), the successful combination of community data from different methods has been shown to provide a more complete understanding of complex ecosystem dynamics (Quintero et al., 2022).

Image-based recognition and metabarcoding of sticky trap samples can separately provide information on species identity, abundance, biomass, traits and some interactions (Figure 1e), all of which can be merged to create context-rich community data and, downstream from that, ecological networks.

In Figure 1d, metabarcoding is suggested as a way of confirming the identity of species from image-based recognition in the previous step (1c). Whilst this is shown for validation purposes, metabarcoding data will also provide a range of species interactions not detected by image-recognition, through remnant DNA either in or on the insects

(Cuff, Deivarajan Suresh, et al., 2023; Cuff, Tercel, et al., 2024; Høye et al., 2021). Metabarcoding therefore also help towards building interspecific (e.g. plant-insect, insect-pathogen, dietary and endosymbiont interactions) ecological networks, including insect pollination, host-parasitoid interactions and wider food webs by detecting these interactions (Evans & Kitson, 2020; Popkov et al., 2022). However, creating networks from entomological community data such as those generated from sticky traps alone presents a particular challenge, even when using a combination of methods, as most species interactions necessary to build them need to be inferred.

## Network construction

We have already shown that new technologies for biomonitoring can yield vast amounts of data, especially when including other data from metabarcoding (e.g. parasitoids; Miller et al., 2021). Finding ways of moving beyond long species inventories generated from biomonitoring schemes to new metrics that better describe ecosystem 'health' and resilience is a priority (Cuff, Deivarajan Suresh, et al., 2023; Cuff, Tercel, et al., 2024).

Ecological networks describe the interactions between species, the underlying structure of communities and the function and stability of ecosystems (Montoya et al., 2006). They have been shown to quantify the effects of human activities on a wide range of complex ecological interactions (Memmott et al., 2007; Tylianakis et al., 2008) and have the potential to guide ecological restoration, particularly when integrated with high-resolution methods such as metabarcoding (Raimundo et al., 2018). There is increased interest in studying plant-herbivore, plant-pollinator and host-parasitoid networks using molecular methods to answer previously intractable questions in ecology and evolution (Evans et al., 2016), as well as helping to detect cryptic interactions (e.g. host-parasitoid interaction; Derocles et al., 2016; Yang et al., 2023). Unravelling cryptic interactions can be vastly improved by utilising the advantages of molecular methods as a validation method in tandem with DL techniques, as described previously. With regard to biomonitoring, a recent review by Cuff, Deivarajan Suresh, et al. (2023), Cuff, Tercel, et al. (2024) provided a detailed discussion of how combining technologies to create ecological networks can lead to new metrics for assessing biodiversity and ecosystem functioning. The metrics, based on the structure and complexity of the networks, are important because these are more informative for studying ecological resilience compared to traditional richness measures.

A key challenge for biomonitoring is how to convert basic species community data into ecological networks, particularly when most species-interaction data are absent (Dubart et al., 2021). Here, both mathematical and computational network inference methods have roles to play. To date, co-occurrence analysis tends to be the default method for researchers grappling with similar issues where context is lacking (e.g., eDNA data; Djurhuus et al., 2020; Seymour et al., 2020). However, Blanchet et al. (2020) showed that spatial associations poorly relate to ecological interactions. Morales-Castilla et al. (2015)



propose predictions of ecological interactions from the type of data generated in our workflow, in particular functional traits, phylogenies and geography, as well as relying on a priori expectations that are often available in well-studied agro-ecosystems. Theoretically, Max-Ent network inference methods (Volkov et al., 2009) and matrix auto-regression (MAR), with either single (Hampton et al., 2013) or multiple delays (Barraquand et al., 2021), show particular promise but are yet to be widely tested empirically. Of the few studies that have, Ovaskainen et al. (2017) used MAR to investigate community-level drivers of network properties and successfully predicted community dynamics with empirical data.

Networks are usually represented as a graph, where nodes denote insect species. The data for each node can be structured in a tabular format or other database schema, including the species taxonomic identification along with additional data modalities such as visual representations, acoustic signatures and other relevant information. The edges in the graph represent interactions occurring between the nodes. Network analysis metrics, including connectance, centrality, nestedness and modularity, can be computed to characterise the topology and attributes of the graph network, and these can then be compared, for example, to null models.

ML is rapidly developing as a method to automate network inference and elucidate novel ecological interactions with even limited data (Bohan et al., 2017; Strydom et al., 2021). This can more accurately predict ecological interactions than conventional regression models (Pichler et al., 2020) but still requires high-quality training data. According to Cuff, Deivarajan Suresh, et al. (2023), Cuff, Tercel, et al. (2024), such datasets must be purposefully collected to represent specific contexts (e.g. study systems, taxa, seasonality, traits) and computational tasks (e.g. translating presence-absence, trait-based or count data into networks), for which as-yet-non-existent network-based databases could form an invaluable source of standardised data (Strydom et al., 2021). Looking ahead, the creation of multilayer networks for understanding the individual and synergetic effects caused by multiple environmental stressors on invertebrates are gaining traction (Beermann et al., 2021; Evans & Kitson, 2020). Graph neural networks (GNNs) could also become an important embedding/predictive technique in the future for building interaction networks (Strydom et al., 2023).

## FUTURE OF AUTOMATED BIOMONITORING

Development is underway for the integration of deep neural network with cutting-edge, automated biomonitoring tools for identification and classification of insects, currently including Edge devices (Albanese et al., 2021; Saradopoulos et al., 2022), mobile ID-DL devices (van Klink et al., 2022), automated imaging systems for example BIODISCOVER (Årje et al., 2020), networks of time-lapse cameras with swarm intelligence (Besson et al., 2022; Høye et al., 2021) and unmanned aerial vehicle-based trap monitoring and robotics (Besson et al., 2022). Automated monitoring equipment is currently much more expensive than traditional methods, but these costs might

reduce in future (Roosjen et al., 2020). A combination of eDNA technologies and sensor data could help in scaling up automated data gathering and creation of robust datasets (Pichler & Hartig, 2023; Zapico et al., 2021), as damage to morphological features of insects can reduce of taxonomic resolution in DL models if used alone (Chua et al., 2023). Large-scale multimodal data sets are likely required for DL algorithms to work on par with humans. Lack of sufficient properly annotated datasets is a major challenge especially regarding sticky traps, as are issues of accessibility (open source) and standardisation of reliable data sets (Li et al., 2021). For datasets containing classes (e.g. species/taxonomic groups) with very few specimens, alternative DL methods such as ViT can help considerably.

Substantial investment in interdisciplinary research is required to bring the full potential of DL in entomology to fruition. This will also provide a unique opportunity for cross-fertilisation of both the fields of computing and biological sciences (Høye et al., 2021). Such interdisciplinary ventures can help establish biological laws as constraints for ML/DL models, which in turn can help development of better Explainable AI (xAI) models for ecology research (Pichler & Hartig, 2023), as current DL models are opaque in how they work and what they have learnt. Next-generation biomonitoring techniques can produce larger datasets on species interactions, which in turn have potential for GNNs to become an applicable embedding/predictive technique in the future for building interaction networks (Strydom et al., 2023), although testing and validation of these approaches are going to be key to their success. Real-time analysis of massive datasets has the potential to improve over time with the development of Quantum computing and can therefore significantly help towards the development of complete automation of biomonitoring (Woolnough et al., 2023).

## DISCUSSION AND CONCLUSION

DL has great potential to tackle future challenges and improve the field of automated biomonitoring for both biodiversity assessment and pest management. This potential can be further enhanced when it is used in tandem with other technologies such as metabarcoding, as demonstrated for the example of sticky traps throughout this article. Here, the bottlenecks and opportunities for each step of our workflow are summarised in Table 1.

Whilst DL models can help to determine the insects present in agricultural ecosystems, image data alone cannot, as yet holistically identify communities as some cryptically interacting insects are overlooked, or morphologically similar species are difficult to delineate (Miller et al., 2021). For example, insects that are parasitised and similar looking insects on a sticky trap could be detected using DL methodologies, but their parasitoids would be overlooked. Holistic species lists and the interactions between species are hard to obtain through a single biomonitoring method (van Klink et al., 2022). Complementing DL on image data with the addition of eDNA/metabarcoding (or indeed other technologies, such as acoustic monitoring; Mankin et al., 2011) will greatly enhance the detection and identification of

**TABLE 1** The bottlenecks and opportunities of the sticky trap methodological workflow that combines complementary data types from image-based recognition and validation using metabarcoding to produce ecological networks.

Pipeline stages	Bottlenecks	Opportunities
Sample collection	<ul style="list-style-type: none"> <li>Manual collection of traps and long-term storage</li> <li>Different type of traps and types of insects captured</li> <li>Ethics of insect trapping, especially rare species</li> </ul>	<ul style="list-style-type: none"> <li>Unified methods for long-term data collection</li> <li>Standardisation for trapping methodology</li> <li>Establish insect ethics for insect collection</li> </ul>
Data digitisation	<ul style="list-style-type: none"> <li>Cost of digitisation equipment</li> <li>Manual labour and time involved in digitisation initially</li> <li>Requirement of taxonomic knowledge—differentiation between similar looking species</li> <li>Curation and data storage</li> <li>Complexity of directly collecting digital data in field</li> </ul>	<ul style="list-style-type: none"> <li>Open databases curated through collaboration</li> <li>Interdisciplinary ventures for automated digitisation of traps</li> <li>Transition to semi-supervised learning for auto-annotation</li> <li>Semi-hybrid edge systems</li> </ul>
Image-based recognition	<ul style="list-style-type: none"> <li>Lack of publicly available, standardised spatio-temporal data for algorithm training</li> <li>Off-the-shelf algorithms with poor direct performance</li> <li>Manual labour involved in fully supervised learning</li> <li>Undiscovered species of insects and limited data</li> <li>Current processing power requirements and technical limitations</li> </ul>	<ul style="list-style-type: none"> <li>Building publicly available, standardised spatio-temporal data available in the UK, using bycatch</li> <li>Implementing advanced learning strategies</li> <li>Customised DL algorithms</li> <li>Advancement of semi-supervised learning in parallel to supervised learning methods</li> <li>Utilising edge systems, IoT and other technical advancements</li> </ul>
Validation using metabarcoding	<ul style="list-style-type: none"> <li>DNA degradation on sticky traps</li> <li>Insect removal from sticky traps involves manual labour and cost</li> </ul>	<ul style="list-style-type: none"> <li>Highly replicated bulk samples reduce overall cost</li> <li>Complementing data through computer vision</li> </ul>
Merged community data	<ul style="list-style-type: none"> <li>Incomplete multimodal datasets encompassing large spatio-temporal biodiversity</li> <li>Ground truthing with useful metrics as output</li> </ul>	<ul style="list-style-type: none"> <li>Enhanced efforts from national and international taxon-specific initiatives and museum collection digitisation</li> <li>Combining various methodologies and interdisciplinary efforts</li> </ul>
Network construction	<ul style="list-style-type: none"> <li>Accurate and efficient network inference for informed decision making</li> </ul>	<ul style="list-style-type: none"> <li>Rapid interpretations when combined data are used</li> <li>Assisting policy through useful metrics and ground-truthing</li> </ul>

pest and beneficial insects and could give us deeper insight into insects in various ecosystems.

The complementary use of eDNA/metabarcoding may also fill gaps in data that arise in DL methodologies caused by insects being under- or over-represented. This representation problem has causal factors ranging from inability to capture certain types of insects because of the nature of traps to the insects being seasonal in nature (Alvarado-Robledo et al., 2024). Ground-truthing using eDNA/metabarcoding can be done periodically to enhance the results obtained through DL. DL in turn will complement the missing barcodes of rare species of insects, taxonomic and sampling biases present in eDNA/metabarcoding databases.

Currently, almost all ML/DL models used for insect identification and classification tasks are trained through purely supervised learning. This methodology is hard to scale up due to human limitations such as manual annotation, limited availability of samples, unidentified insects and taxonomical classification complexity. In order to overcome this bottleneck, a transition towards semi-supervised learning is required. This transition can be done using methodologies like generalised category discovery combined with few shot learning. These methodologies can help in identifying and categorising new and unidentified species of insects using very few annotated samples, thereby aiding researchers in better describing the vast biodiversity of insects. Off-the-shelf algorithms (e.g. YOLO, ResNet) trained on image data perform less than optimal on unknown testing data. Hence, in the initial

stages of developing a custom semi-supervised learning model, a fully supervised learning model should be built in parallel, with the help of taxonomists in order to compare the models' performance and for error correction. This approach can pave the way for the future of entomological biomonitoring in a rapidly changing world. Automated biomonitoring with its multidimensional data can help create ecological networks to analyse community structure, complexity and vulnerability; such spatiotemporal data are otherwise prohibitively laborious to obtain using conventional manual methods (Besson et al., 2022). Trophic networks involving invertebrate predators and prey can also reap the benefits of Big Data obtained through combinations of sampling methodologies. Molecular methods can determine the prey that predators are eating, which is influenced by the abundance of those prey or sometimes the preferences of the predator. To explore this, molecular methods are poorly positioned to establish prey availability because they lack reliable quantitative data, whereas automated image-based methods could overcome these data shortfalls without the time-intensive process of sorting and identifying hundreds of individual arthropods, thus tackling the scalability issue (Cuff, Tercel, et al., 2024).

Integrated pest management (IPM), which is a critical tool for sustainable crop protection, and farm ecosystem management requires rapid detection, identification, classification and counting of insects to prevent the spread of pests, pathogens and/or invasive species in a timely manner (Barbedo et al., 2020; Butterworth et al., 2022; Diller

et al., 2022; Li et al., 2021; Martinez et al., 2020; Roosjen et al., 2020; Rustia et al., 2021). Implementation of advancements in AI, miniaturisation of efficient microprocessors, IoT and cloud computing have improved traditional IPM systems giving rise to a new method known as smart pest monitoring (SPM). SPM can help improve automatic collection of data on crop pest abundance and aid in accurate decision making. It is currently implemented on an experimental basis only (Ayaz et al., 2019; Karar et al., 2021; Li et al., 2021; Lima et al., 2020) but has the potential to be further advanced using the methodological pipeline suggested in this article.

For next-generation biomonitoring to come of age, Cuff, Deivarajan Suresh, et al. (2023) highlights three distinct challenge areas in need of urgent progress: (1) unified methods for data collection, (2) reproducible and robust big data and (3) accurately inferring and analysing networks. We exemplified each of these challenges using the single example of sticky traps. Moving forward, a combination of methods and technologies will be needed for surveillance and biomonitoring in agro-ecosystems, bringing complementary data sources together. Sticky traps combined with pan traps and plant-insect survey transects are currently being used to create species interaction networks as part of the EU Horizon 2020 'EcoStack' project (<https://ecostack-h2020.eu/>) to better understand invertebrate ecosystem service provisioning in crop and non-crop habitats across the UK. Here, there is a need to establish a versatile tailor-made DL algorithm and build a UK-based (and beyond) standardised multi-class open-source benchmark insect dataset for automated biomonitoring as there are presently no large-scale annotated datasets for agricultural landscapes. Building a large-scale standardised annotated dataset is a priority, and this will pave the way to advance automated biomonitoring technology. A UK/EU specific DL algorithm and a standardised dataset are the primary focus of this methodological initiative. An open access approach towards building such a dataset will foster transparency, enhance research utility and empower evidence-based policy making to address UN SDG Goals (Barlow & O'Neill, 2020; Cuff et al., 2024; Li et al., 2022).

## AUTHOR CONTRIBUTIONS

**Mukilan Deivarajan Suresh:** Conceptualisation; visualisation; writing – original draft; writing – review and editing. **Tong Xin:** Conceptualisation; supervision; writing – original draft; writing – review and editing. **Samantha M. Cook:** Supervision; writing – review and editing. **Darren M. Evans:** Conceptualisation; supervision; writing – original draft; writing – review and editing.

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## CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

## DATA AVAILABILITY STATEMENT

No data were used in this manuscript.

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## SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

**Data S1.** Supporting Information.

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