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PlanktoShare: A large (50k+) and FAIR learning set for the Plankton Imager (Pi-10) for the Greater North Sea and NE Atlantic, based on a new flexible classification protocol

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Abstract. The use of imaging techniques for the study of particles and plankton is a rapidly advancing field in marine sciences. The data the tools produce require automated classification solutions that are trained on learning sets of manually labelled images. In this study we present PlanktoShare, a comprehensive (50k+ images) database with manually labelled images captured by the vessel-mounted Plankton Imager (Pi-10), in the 200 – 2,000 µm size range and including phytoplankton, holoplankton, meroplankton and various gelatinous taxa. The Pi-10 images particles continuously in a flow-through mode and can operate alongside research operations and during transits making it a popular choice for plankton monitoring. PlanktoShare provides a robust resource for training classifiers as an open resource. A key challenge in developing classifiers such as these is that commonly arises when merging learning sets from different sources, because images are often organized in a folder-like structure with incompatible or inconsistent nomenclature. To address this, we propose a database approach which separates the taxonomic information from descriptive attributes. Each image is assigned to one of the classes 'Organism' (whole organism), 'Taxo_particle' (particle with taxonomic information, such as exuvia) and 'Non_taxo_particle' (particle without taxonomic information, such as marine snow aggregates). Taxonomic information is standardised using the aphiaID system from the WOrld Register of Marine Species while additional descriptive information (e.g. Life_stage) is stored as attributes. This database approach ensures full interoperability across learning sets from research groups allowing rapid expansion of geographical coverage and improved classification performance. Finally, we provide open-source code to apply pre-trained classifiers for users and outline future directions for collaborative plankton imaging.

1 Introduction

Zooplankton are a highly diverse group of organisms that plays a key role in ecosystem functioning. These organisms form an important trophic link in the pelagic food web (Steinberg and Landry, 2017), with many (commercial) fish species being reliant on zooplankton for their dietary requirements (Heath, 2005). Zooplankton also contribute to the biological pump through various mechanisms, including the production of sinking faecal pellets (Brun et al., 2016; Luo et al., 2020), exoskeletons and mucous feeding nets (Jaspers et al., 2023) and by the so-called lipid-pump (Jónasdóttir et al., 2015). Finally, many benthic organisms have a temporary planktonic life stage, the meroplankton, which can be numerically dominant in coastal seas (Kirby et al., 2007, 2008) and represent a bottleneck for the settling and spatial distribution of benthic fauna. Zooplankton biomass and diversity is recognised as an Essential Ocean Variable (EOV) in the Global Ocean Observing System (GOOS) and is used in several quality indicators in the latest OSPAR's quality status report (Holland et al., 2023a; Louchart et al., 2023).

To quantify the importance of these ecosystem services and support these quality indicators, zooplankton monitoring is essential. In this light, the decades long-term time series collected over large areas using the Continuous Plankton Recorder (CPR, Richardson et al., 2006) provides a rich and invaluable data source but also comes with caveats. The CPR can often not be used by vessels engaged in water quality and fisheries monitoring, because its deployment would interfere with other ship operations. Instead, it is commonly used on ships of opportunity such as ferries and container ships, and consequently there is a spatial bias to its coverage, with coastal regions and some ocean basins poorly covered. Furthermore, sample processing is time-consuming, reliant on taxonomic experts, and most gelatinous taxa are missed because of the damage incurred (Richardson et al., 2006). Imaging techniques, combined with automated classification, may be an effective complementary method which would alleviate some of these problems (Irisson et al., 2022; Lombard et al., 2019). Giering et al. (2022) present a roadmap outlining how imaging instruments combined with Artificial Intelligence (AI) approaches can play a complementary role in the future of zooplankton monitoring and research. They conducted a survey among zooplankton researchers and found community consensus that images are a valuable addition in plankton monitoring, especially to increase temporal and spatial coverage. However, respondents were less favourable towards AI-based classification. An important reason for the low confidence in AI-based classification was that training datasets are produced by single (sometimes non-specialist) researchers for a specific study site using a categorisation that is difficult to generalise. In essence, this result can be interpreted as a call from the zooplankton research community for high-quality, cross-verified and standardised training datasets, which would also greatly facilitate cooperation amongst research teams working with images and lower the learning curve for novice users.

The Plankton Imager (Pi-10) is a relatively new imaging tool and holds a unique use-case (Scott et al., 2025; Scott, 2023). Rather than being used in the water column (e.g. the Video Plankton Recorder [VPR] or Underwater Video Profiler [UVP]), or in the laboratory for analysis of net samples (e.g. Zooscan or FlowCam-Macro), the Pi-10 continuously images particles with an onboard line scanner from a continuous supply of pumped surface water. The built-in automated segmentation ensures

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that users deal with comparable regions-of-interest (ROIs). This Pi-10 setup implies that its operation doesn't interfere with other activities on the vessel and can therefore be integrated widely, including on research vessels and vessels that are used for water quality and fish stock monitoring.

The Pi-10 was developed by Cefas (Centre for Environment Fisheries and Aquaculture Science) and Plankton Analytics Ltd. in the UK (https://www.planktonanalytics.com/) and first installed on R/V Endeavour (Pitois et al. 2018). Subsequently, Pitois et al. (2021) collected a set of Pi-10 images from the Celtic Sea and inferred an ecological indicator based on copepod size and abundance (Copepod Mean Size and Total Abundance [CMSTA]) and related this to both lower and higher trophic levels. Scott et al. (2021) presented another application for the Celtic Sea, where they showed the importance of summer stratification in the annual zooplankton dynamics.

In 2023 a Pi-10 was installed on the Dutch fisheries research vessel R/V Tridens II where a first survey in May/June 2023 showed that the Pi-10 could reliably detect densities and variation therein of a wide range of plankton groups along the Dutch coast (Van Walraven et al., 2025). In 2024 a Pi-10 was operated on the British research icebreaker Sir David Attenborough on a transect from the UK to Antarctica. In 2025 tests by NIOZ showed that operation of a Pi-10 in a shore-based container is feasible, allowing for continuous monitoring of zooplankton dynamics in coastal systems. Finally, a buoy-mounted Pi-10 is being developed and tested by Plymouth Marine Laboratory for deployment at the L4 station (Clark et al 2025).

As the number of Pi-10 instruments in operation continues to grow, so too does the need for a common, standardised, easily shareable, and extendible training library of Pi-10 images validated by experts. This paper, arising from a series of Pi-10 user group meetings, presents: (1) a flexible, standardised annotation scheme for living and non-living Pi-10 ROIs; (2) an open-source, quality-controlled training set comprising more than 50,000 ROIs; and (3) a description of the version-controlled framework that will support the long-term maintenance and development of the training set.

2 Plankton Imager (Pi-10) and data collection

An extensive description of the Pi-10 is given in Scott et al. (2025). In short, the Pi-10 is installed in a metal frame (width x height x depth, 75 x 100 x 30 cm, Fig. 1). Ambient water is lit by a LED light source and imaged by a downward facing Basler 2048-70kc line scan camera, with a scanning rate of 70,000 lines per second, capturing 2048 10-µm pixels per line, appropriate for imaging identifiable organisms with a lower size limit of 200 µm. Flow-through needs to be stable at 34 L min^{-1} (equivalent to 2 m^3 h^{-1}) and is therefore monitored with a flowmeter. A pump supplies water from several meters below sea level throughout the survey. High-capacity centrifugal pumps are used on the R/V Endeavour and R/V Tridens II which are run at low speed to minimise severe damage to fragile zooplankton species.

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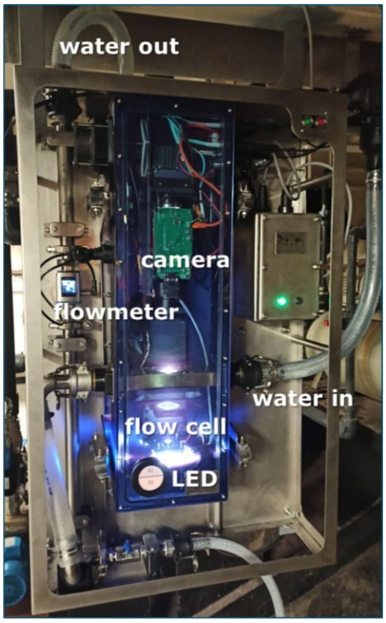

Figure 1: The Pi-10 installed on the Dutch fish monitoring vessel R/V Tridens II with indication of water inflow point, LED source, flow cell, camera, flow meter and water outflow point.

Data are transmitted by fibre optic cable to an onboard PC for immediate segmentation and storage. The system has been shown to be able to reliably save up to 100,000 regions-of-interest (ROIs) per minute, which is sufficient for clearer offshore water, but in turbid waters not all ROIs are saved. However, a count of the total ROIs is kept, so one can posteriorly correct densities for the proportion of ROIs that was counted but not saved. The Pi-10 can run continuously during surveys. A selection of zooplankton ROIs from the Pi-10 is presented in figure 2 to illustrate the quality of the collected images.

Figure 2: Examples of plankton images with taxonomic information taken from the North Sea with the Pi-10.

3 Standardised classification scheme

Most learning sets are structured in a folder-like fashion, such that an image falls into a single folder or category, e.g. 'copepod' or 'appendicularian_with_house'. This rigid organization makes it challenging and cumbersome to merge learning sets from different research institutes. To facilitate learning set sharing, we realised that a more flexible classification is needed. Below, we first describe the principles of this classification scheme and then apply these principles in a case study on a small set of images.

Our classification scheme consists of classes and attributes, but before introducing these, it is useful to explain two primary choices. Firstly, rather than organising images in a single folder, information is assigned to each image in a database. In this database, we explicitly separate between ‘taxonomic’ and descriptive ‘attribute’ information. Although seemingly trivial, this separation generates a lot of flexibility to group or ungroup images from the database in a later stage without compromising the initial taxonomic labelling. Secondly, when collecting the descriptive attribute information, we explicitly distinguish between 'NULL = not looked for', 'ZERO = looked for, but not found' and 'non-NULL / non-ZERO = looked for, found'. This has two advantages 1) one can easily check which images in the learning set have been checked for an attribute and which not and 2) a new column with descriptive attribute can be added to a new version of the learning set with NULL as default value. The main advantage of storing taxonomic and attribute information in a database, is that a specific? bespoke? learning set instance can be generated by querying the database.

3.1 Taxonomic classification

We first apply a taxonomic classification from one of three main groups, after which various descriptive attributes can be added to the taxonomic classification. The three main groups are:

1) Organism – A whole organism to which taxonomic information can be assigned, e.g. 'Copepoda',
2) Taxo_particle – a non-living particle to which taxonomic information can be assigned, e.g. exuviae of a cirriped larvae, tentacle of a jellyfish or mucous house of Appendicularia, and
3) Non_taxo_particle – a non-living particle to which no taxonomic information can be assigned, e.g. marine snow or plastic fibre. Artefacts, such as bubbles, are also included in this class.

Taxonomical information, relevant for the groups ‘Organism’ and ‘Taxo_particle’, is added to each image following the AphiaID from WoRMS (www.marinespecies.org) thus allowing for assigning low (e.g. Copepoda, AphiaID = 1080) or high (e.g. *Temora longicornis*, AphiaID = 104878) taxonomic resolution to an image. This ensures that taxonomic information can be kept up to date, because WoRMS can be queried through APIs for R or Python. The group ‘Non_taxo_particles’ is often dominated by marine snow aggregates. In general, we would advise to not artificially create sub-groups (e.g. ‘fluffy’, ‘solid’ or ‘elongated’) for marine snow aggregates, as these are very difficult to define objectively. Rather, we advise to posteriorly cluster aggregates with automated clustering methods based on morphological properties (Trudnowska et al. 2021, Van Oevelen et al. Subm).

3.2 Descriptive attributes

Attributes are used to add descriptive information to the taxonomic classification to the database. These attributes are flexible and can be extended or refined in a later phase without incurrence on the taxonomic classification. In the current database, we have ‘Life_stage’ and ‘Body_part’ as descriptive attributes. In the future, we foresee additional attributes like ‘Egg_sac’ or ‘Antennae_posture’. We realise that the nomenclature and use of these descriptive attributes is ambiguous and therefore curation of the database is needed to avoid confusion. We will actively maintain the database using a version control system (see Section 4.4 Availability and version control) to avoid this ambiguity.

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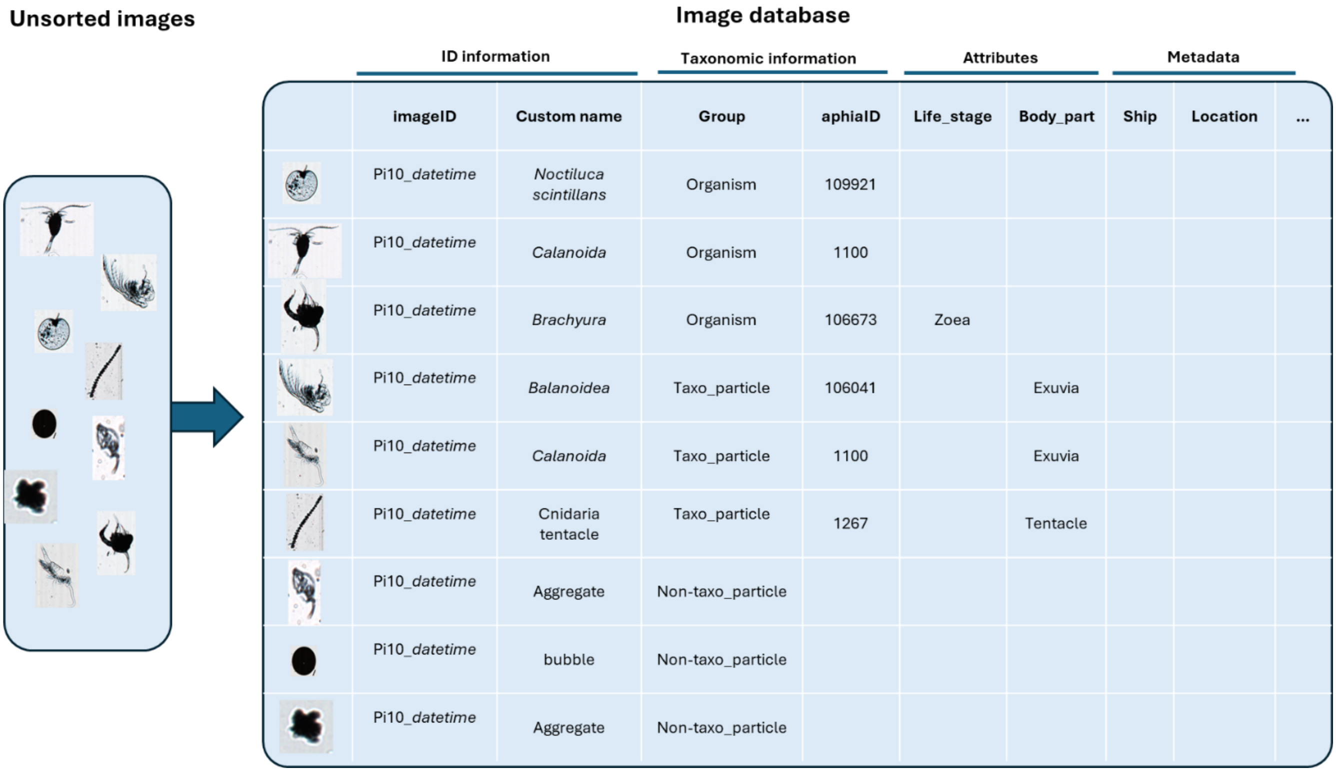
3.3 Classification example

To exemplify the workflow, we show a classification scheme for 9 unsorted Pi-10 images into the PlanktoShare database (Fig. 3).



	ID information		Taxonomic information		Attributes		Metadata		
	imageID	**Custom name**	**Group**	**aphiaID**	**Life_stage**	**Body_part**	**Ship**	**Location**	**...**
	Pi10_*datetime*	*Noctiluca scintillans*	Organism	109921					
	Pi10_*datetime*	*Calanoida*	Organism	1100					
	Pi10_*datetime*	*Brachyura*	Organism	106673	Zoea				
	Pi10_*datetime*	*Balanoidea*	Taxo_particle	106041		Exuvia			
	Pi10_*datetime*	*Calanoida*	Taxo_particle	1100		Exuvia			
	Pi10_*datetime*	Cnidaria tentacle	Taxo_particle	1267		Tentacle			
	Pi10_*datetime*	Aggregate	Non-taxo_particle						
	Pi10_*datetime*	bubble	Non-taxo_particle						
	Pi10_*datetime*	Aggregate	Non-taxo_particle						

Figure 3: Classification scheme for several unsorted Pi-10 images (left). Images are assigned to groups "Organism", "Taxo_particle" and "Non-taxo_particle". The imageID is provided by the Pi-10 instrument, Custom name is a name provided by the researcher. An empty cell indicates *NULL*.

3.4 Generating a training set instance

The PlanktoShare database that we share with this publication is composed of a single folder with the images and the associated database with information on ID, taxonomy, attribute and metadata (see Fig. 3). Note how flexibly PlanktoShare can be used. Each user can generate a specific learning set 'instance' from the database. For example, an instance can be generated with all Group 1 and 2 (i.e. organisms and particles with taxonomic information) images separated at taxonomic level 'Class', which would have all Copepoda in one group. Alternatively, one can select only images from a specific geographical region or time stamp. Again differently, one can choose to create a learning set instance in which only copepods are included that have been identified at genus level. Providing the exact database query and the version of the queried learning set will suffice for a fully transparent workflow. The generality of PlanktoShare also ensures that images from other users, provided they follow the same database structure, can be directly appended to the present database (see also section 4.4 Availability and version control of the training set below), in which case the attributes that have not been checked will be set to ‘NULL’.

4 Learning set development

4.1 Data collection cruises

The raw set of images from which the present learning set is derived were collected during fish surveys with the R/V Tridens II and the R/V Cefas Endeavour. Most images (43,160) were collected on an acoustic survey for small pelagic fish in the Dutch coastal zone from May 30 to June 16, 2023 (Van Walraven et al., 2025). Additional images (5,884), especially of classes that were missing or scarce in the initial dataset, such as radiolaria and doliolids, were collected with the R/V Tridens II during subsequent fisheries surveys such as the ICES International Bottom Trawl Survey (IBTS), Downs Recruitment Survey (DRS), International Blue Whiting Stock Survey (IBWSS), Beam Trawl Survey (BTS) and Herring Acoustic Survey (HERAS) and International Herring Larvae Surveys (IHLS). The Plankton Imager on R/V Tridens II takes in water at a depth of approximately 4.5 m, depending on ship draft. It was set to store a maximum of 10,000 images per minute with a size threshold set between 200 and 20,000 µm.

The other set of images (3,838) were collected across several cruises in 2023 and 2024 on R/V Cefas Endeavour on the Mackerel Egg Survey (MEGS) and *Nephrops* survey off the east coast of the UK, and the Pelagic Ecosystem Survey of the Celtic Sea and Western Channel (Peltic) in the Celtic Sea.

4.2 Creating the PlanktoShare database

When creating PlanktoShare, we had to overcome several challenges. Below, we describe how we dealt with these challenges.

4.2.1 Dominance of non-living particles

In most marine systems, non-living particles such as marine snow and aggregates are often numerically dominant (>90%) compared to planktonic organisms (Forest et al., 2012; Trudnowska et al., 2021). However, marine snow particles seem to be less abundant in Pi-10 imagery compared to instruments that are towed through the water column. This discrepancy may be due to the shear stress created by the pump which can fragment marine snow into particles below the retention threshold of 200 µm. Consequently, a 'simple' random subsample of the ROIs will be biased towards dominant particles (e.g. non-living particles), making it very time-consuming to collect sufficient ROIs of rarer particles/organisms.

Several, not mutually exclusive, strategies are available to tackle this issue. One approach is to apply a very simple start classifier with just a few categories 'plankton', 'detritus', and, if needed, 'bubble' to the whole dataset (Hovenkamp et al. In revision). Because the task is simple, the accuracy is typically high (> 90%) and separates a lot of 'plankton' ROIs from the dataset that can be inspected for further manual labelling. Alternatively, unsupervised learning methods can cluster particles based on various features and use this as a pre-classification (Schröder et al., 2020). Existing training sets such as those from EcoTaxa (https://ecotaxa.obs-vlfr.fr/),or ISIIS (Schmid et al., 2021) could also be leveraged for a coarse pre-classification of the dataset to separate 'plankton' from 'detritus' particles. For the development of our learning set we used the following iterative approach:

1. Inspect a subset of unlabelled images from the survey and define initial classes based on taxonomy, life stage and other attributes, as described above,
2. Add images to these classes, aiming to have a heterogeneous selection of at least 100 images within each class where a range of image size, degree of damage, focus and organism orientation is included,
3. Train an initial ResNet-50 convolutional neural network (CNN) on this initial learning set (here we worked with 57 classes, 9,818 images),
4. Evaluate performance of classes by manually validating 100 images per class after applying the trained classifier on all images. Identify missing and poorly performing classes,
5. Add missing classes to the learning set, and add manually validated images,
6. Retrain the ResNet-50 CNN (49 classes, 14,697 images),
7. Repeat steps 4-6 two times, manually validating 300 images per class each time, adding these to the learning set together with images from scarce classes from later surveys,
8. For the final learning set, additional images of classes that were not present in the initial coastal survey, but encountered in later research surveys, were added.

4.2.2 Size class spectrum

A well-known feature of marine particles is the negative log-log relation between abundance and size (Dugenne et al., 2024; Lombard et al., 2019, Van Oevelen et al. In revision), or, in other words, smaller particles are (much) more abundant than larger particles. Hence, a random subset of the ROIs will be heavily skewed towards smaller particles. This issue can be relatively simply tackled by subsampling randomly from different ROI size (e.g. pixels, kb or equivalent circular diameter) intervals. Image sizes of our training set were therefore plotted on a log-log scale to check whether the training set covered a realistic size range.

4.3 Overview of the training set

The full training set consists of 52,882 images distributed across 3 main groups: ‘Organism’ (39,291 images) in Class, ‘Taxo_particle’ (3,451 images) and ‘Non_taxo_particle’ (10,140 images). In addition three descriptive attributes: Life_stage, Body_part and Shape (e.g. to distinguish diatoms on morphology) were applied to selected images. Figure 4 shows the spatial distribution of the ROIs over the Dutch coastal North Sea, Greater North Sea and NE Atlantic Ocean. The size spectrum shows the expected $\log_{10}$-$\log_{10}$ relationship between size and abundance (Fig. 5), indicating that our training set represents an appropriate subset of the full data set.

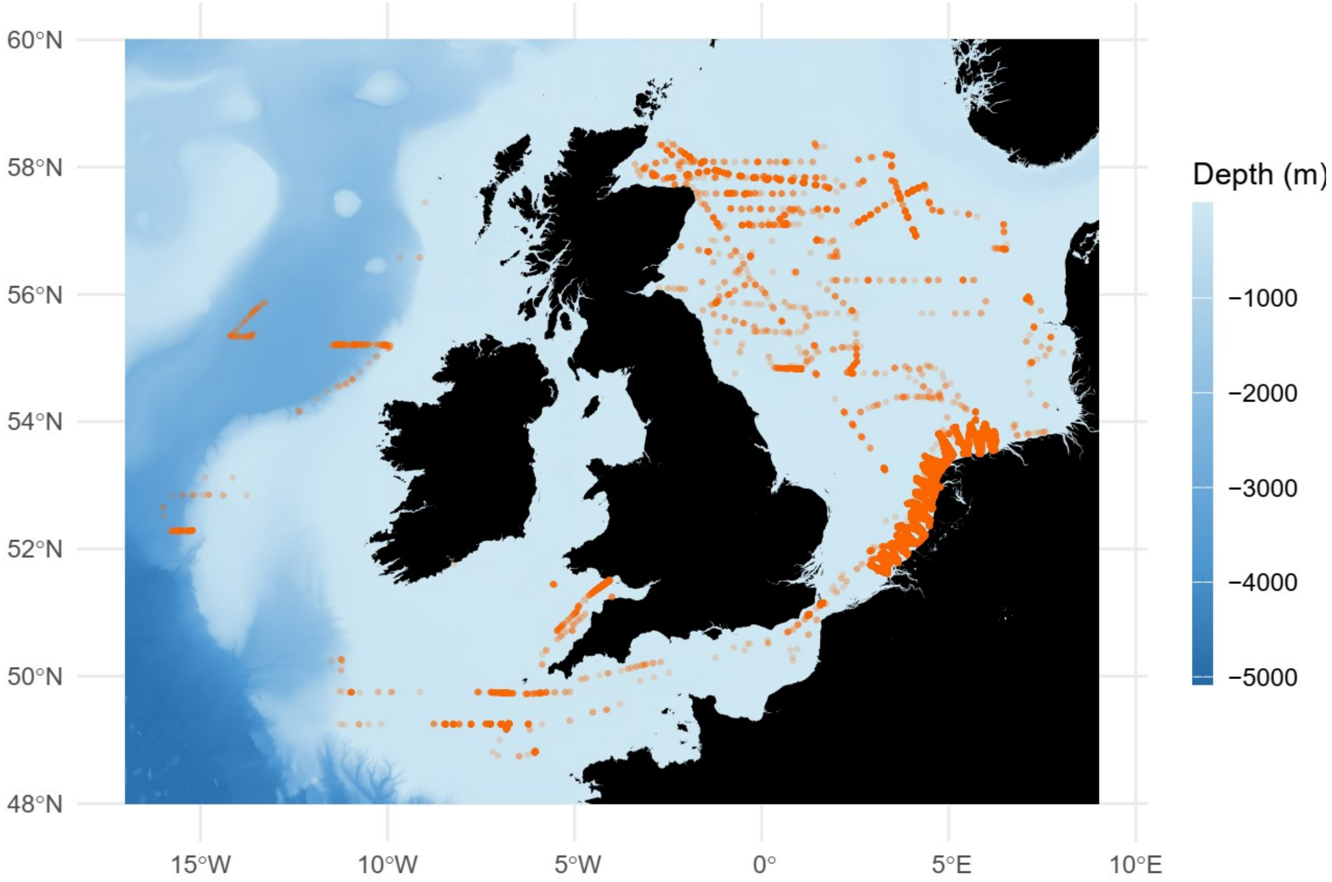


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Figure 4: Location of all the images in PlanktoShare learning set. The black line indicates the Dutch Continental Shelf.

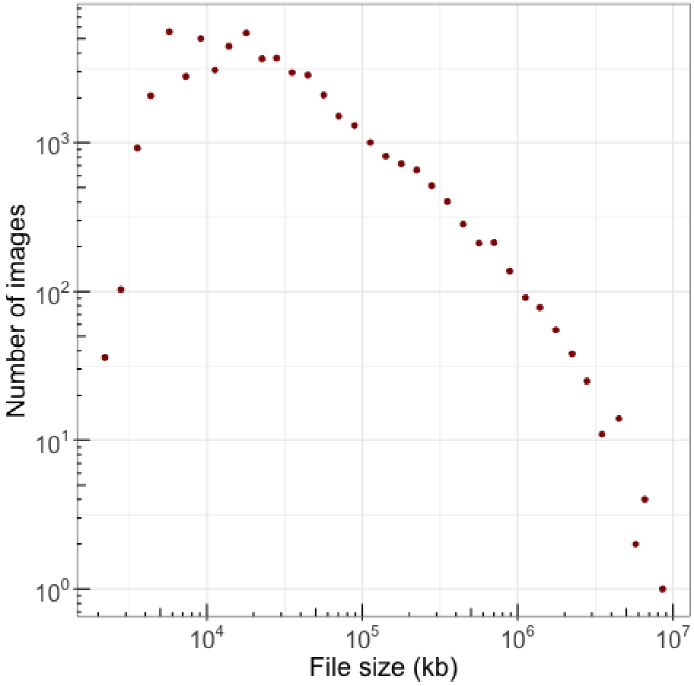

Figure 5: The spectrum of image sizes from the PlanktoShare learning set.

The learning set encompasses a high taxonomic diversity, with 20 different phyla of holo- and meroplankton distinguished, and several of these phyla being resolved to a higher taxonomical resolution, as shown in the Krona plot for the classes with taxonomical information (Fig. 6). Several taxa could be identified to the genus level from images, e.g. the Larvacean genera *Oikopleura* and *Fritillaria*, the Cladocera *Evadne* and *Penilia* and several polychaete larval taxa such as *Magelona* and *Poecilochaetus*. Copepod images from Cefas Endeavour were identified to genus level if possible; the genera *Acartia*, *Calanus, Centropages, Temora* and *Oithona* could be recognised from the images, although the taxonomic resolution attainable for copepod images depended on whether body parts with identifyig characteristics such as antenulles and caudal rami were clearly visible in the images. It should be noted that, even though the Plankton Imager is aimed at mesozoöplankton, some larger groups commonly considered phytoplankton are also imaged, such as *Tripos* and *Noctiluca* dinoflagellates, chain-forming diatoms and colonies of *Phaeocystis*. The smallest recognisable organisms on the images were copepod nauplii, mollusc veliger larvae and diatoms. The largest organisms imaged were chaetognaths, fish larvae, euphausids and gelatinous organisms such as siphonophores, hydromedusae and ctenophores and the branchiolaria larval stage of sea stars from the genus *Luidia*.

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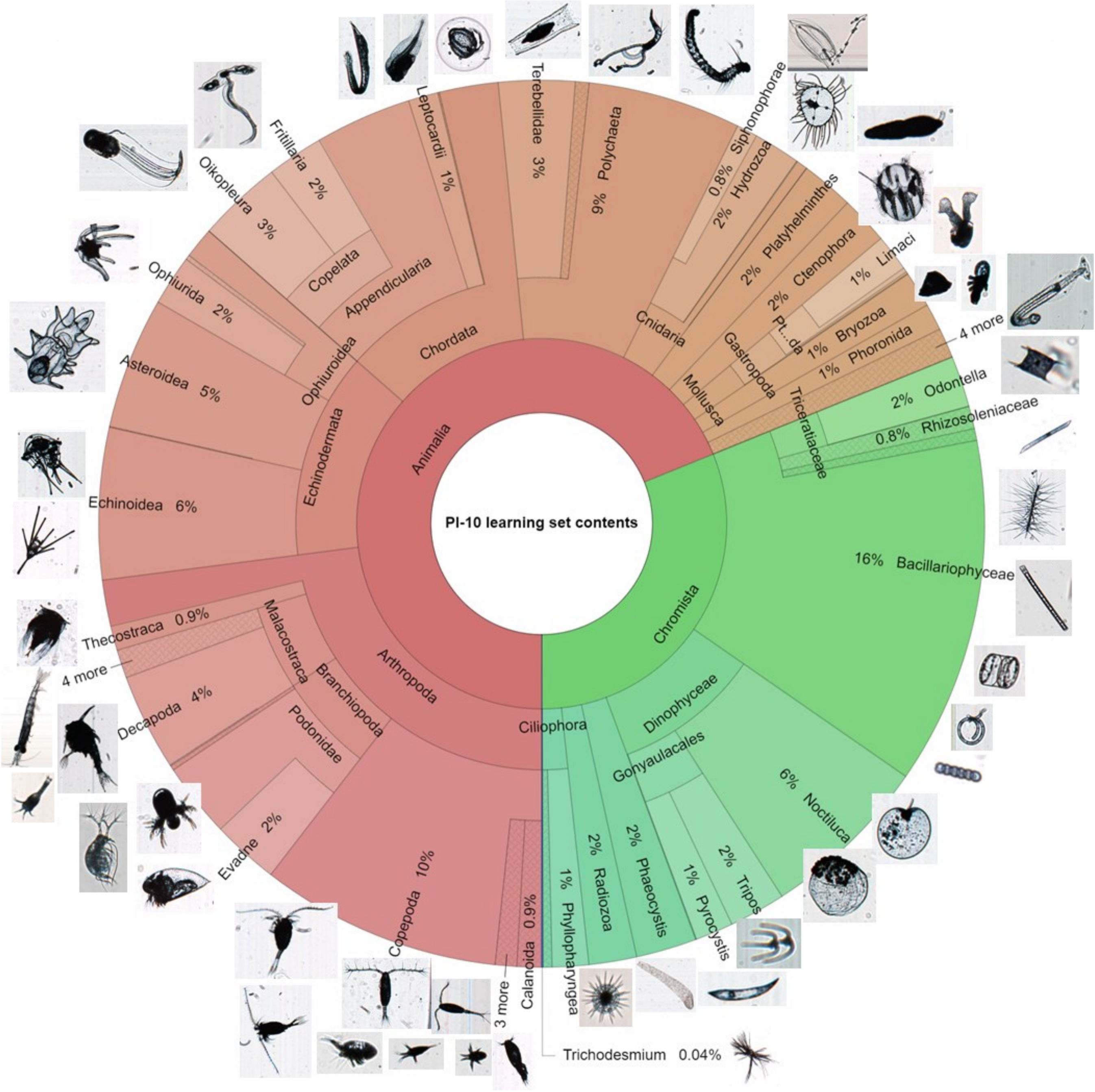

Figure 6: Krona plot of all group 1 images (i.e. Organism) in the PlanktoShare learning set (n = 42742), with percentages based on the number of images for that taxon. Example ROIs of shown taxa are indicated for illustrative purposes. 255

4.4 Data availability and version control of the PlanktoShare learning set

The PlanktoShare database, including the labels and raw images, is available in the public repository Zenodo under doi: https://doi.org/10.5281/zenodo.19119233. We have considered how the learning set needs to be maintained. To ensure proper curation, we will adopt a 'version control' approach. The present training set is released as 'PlanktoShare_v1', but new versions of the learning set will be released when sufficient data or new attributes have been added. The older versions will remain available online so that classifications based on an earlier version of the learning set can still be reproduced.

5 Applying PlanktoShare

Using the PlanktoShare database, we trained two ResNet50 (pretrained on ImageNet; He et al., 2016) models using the FastAI framework, with input images resized to 300px and augmented using standard techniques. Training was performed in two stages: frozen training of the final layer(s) to identify optimal initial learning rates, followed by full fine-tuning of the model. The best model was selected based on the validation loss. Further details, including hyperparameters and augmentation settings, are provided in the Appendix.

For the first classifier, classes were defined with the aim of achieving a high taxonomic resolution (‘detailed classifier’). The classes of the second classifier were defined based on the OSPAR lifeforms (see e.g., Holland et al., 2023b) (‘OSPAR classifier’). The OSPAR plankton lifeforms are: Diatoms, Dinoflagellates, Large copepods, Small copepods, Gelatinous zooplankton, Fish larvae, Holoplankton and Meroplankton. Based on these classes we defined the classes Diatoms, Dinoflagellates, Copepods, Gelatinous zooplankton, Fish larvae, Holoplankton and Meroplankton, whereby the classes “Holoplankton” and “Meroplankton” consisted of holoplankton and meroplankton that did not fit in the other classes. Both instances of the training set were complemented with the group Non_taxo particles. Both models have high classification accuracy, with F1-scores of 91.3 % for the detailed classifier and 95.4 % for the OSPAR lifeforms-based classifier. This shows that PlanktoShare can be used to achieve high performance with database instances of varying taxonomic complexity.

5.1 Code availability

The code for training and inference on new unseen images is publicly available at: https://github.com/geoJoost/planktoshare, to allow iterative model development by other researchers.

5.2 PlanktoShare-based classifier with high taxonomic resolution

The detailed classifier is trained on the dataset with 47,731 images distributed accross 49 classes, see Figure A1. The dataset has notable class imbalance, with some classes (e.g., Detritus, Heterokontophyta Bacillariophyceae) containing substantially more labels, reflecting real-world variability. Despite this imbalance, the model demonstrates consistent performance across most classes, with a macro F1-score of 91.3%. The confusion matrix (see Figure 7) shows that the model performs robustly along the diagonal, indicating high accuracy for most classes. However, a recurring pattern of misclassification is observed for the ‘Detritus’ class in both false positives and false negatives, suggesting similar visual semantics with other classes.

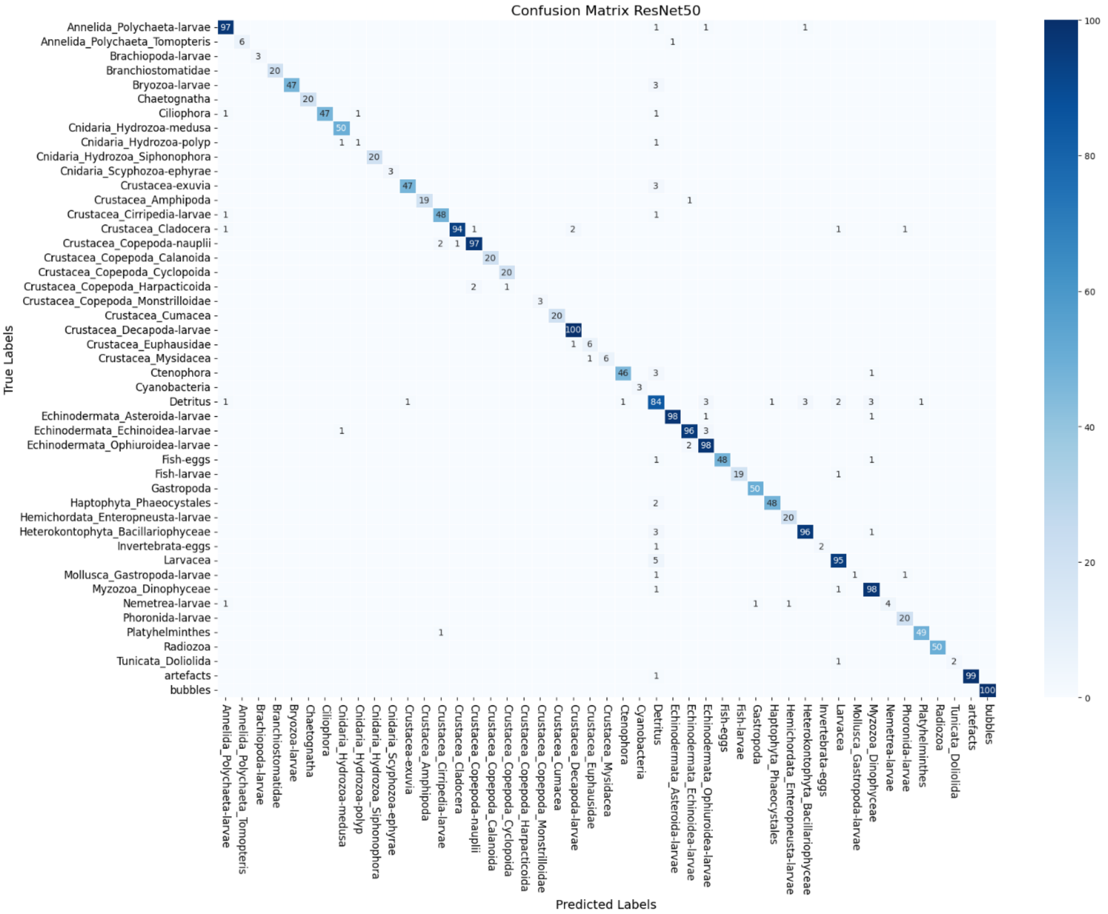

Figure 7: Confusion matrix for the detailed classifier.

5.3 PlanktoShare-based classifier for the OSPAR lifeforms

The second model, the OSPAR lifeform classifier, has a total of 53,538 images distributed in 12 different classes. The OSPAR classifier has a macro F1-score of 95.42%. Similar to the detailed classifier, incorrect classifications occur with the ‘Detritus’ class which is predicted as ‘Holoplankton’ and ‘Meroplankton’.
(Fig. A2).

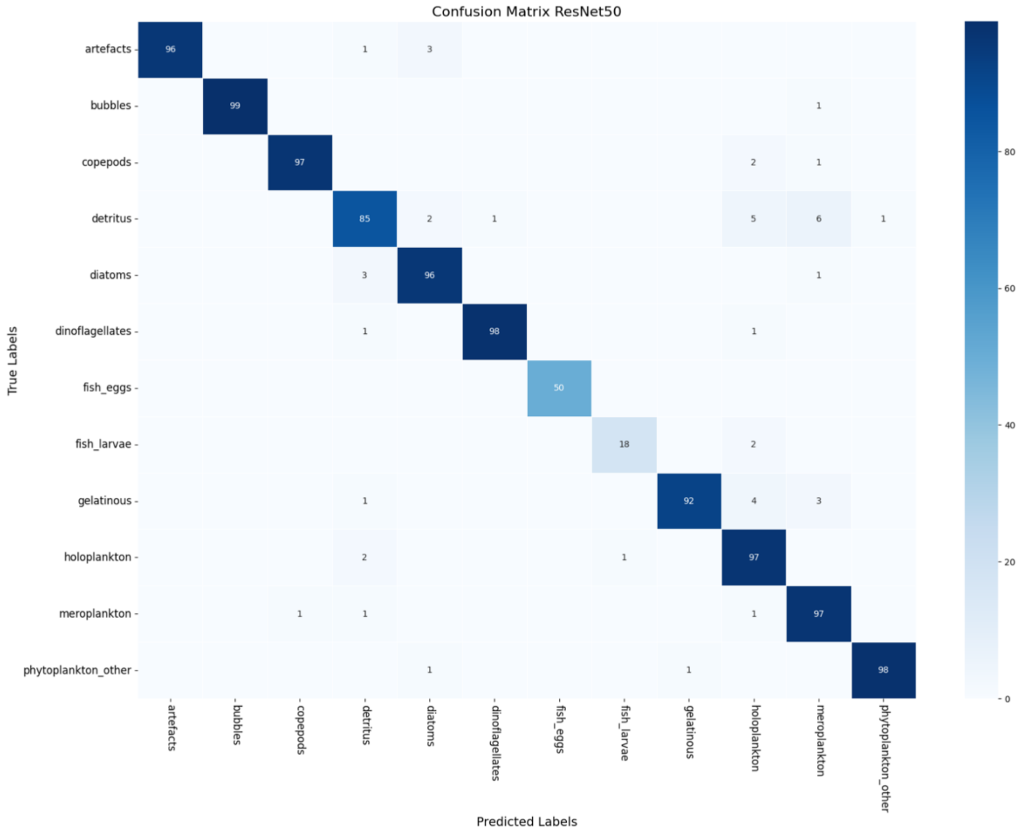

Figure 8: Confusion matrix for the OSPAR classifier.

6 Conclusion, outlook and challenges

We offer a general and flexible protocol for the cooperative development of learning sets for planktonic organisms. We believe that such an approach is missing from the present literature and can aid in a FAIR use of learning sets for planktonic particles. In addition, the flexibility of the protocol implies that it can be extended to other imaging systems, like the underwater vision profiler (UVP), Continuous Particle Imaging Classification System (CPICS) and *In Situ* Ichthyoplankton Imaging System (ISIIS) but also the laboratory-based Zooscan or FlowCam (Lombard et al. 2019).

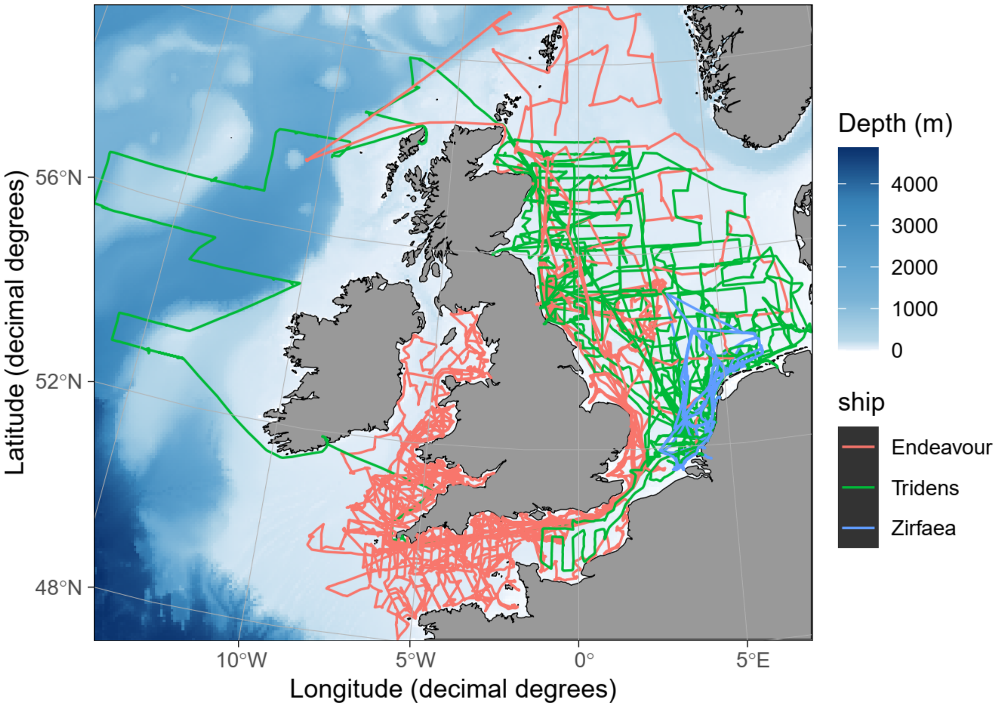

Figure 9: Yearly transects of R/Vs CEFAS Endeavour, Tridens II and Zirfaea in 2023 showing the potential spatial coverage possible with the Pi-10 on government survey vessels. Map based on AIS data from globalfishingwatch.org.

Fisheries and hydrographic surveys often sample large areas in a structured, regularly repeated way making them ideal platforms for the inclusion of continuous monitoring systems. As the Pi-10 does not interfere with ship operations such as steaming or fishing, it can run continuously during surveys or transits. The three Dutch and British vessels currently using or planning to use the Pi-10 already cover a large part of the Greater North Sea and Celtic Sea area (Fig. 7), highlighting the potential for widespread Plankton Imager monitoring in European waters. Our learning set approach can be part of a standardised pipeline for PI-10 data acquisition, processing and analysis, supporting the development of food-web indicators such as the Copepod Mean Size and Total Abundance (CMSTA, Pitois et al., 2021).

Several classes in the learning set could be refined to a higher taxonomic resolution. For example, copepods initially labelled only to (taxonomic level) Class could be identified to the order level and for some taxa to the genus level where clear morphological characteristics enable separation from other genera. A challenge is that such higher-level taxonomical classification will only be possible for a select number of images of the taxon, depending on image quality and organism orientation. Incorporating higher-level taxonomy into an automated classifier will require a hierarchical classifier, or the development of a dedicated classifier for specific groups such as copepods. The flexible structure of our learning set makes it possible to subset these images with different taxonomical resolutions for the training of such specialised classifiers.

Author contribution

LvW, JS, SP and RJ collected the data. LvW and JP performed taxonomical identification of taxa on the images. JH and JvD developed the machine learning pipeline. LvW and DvO analysed the data. All authors were involved in the conceptualisation of the study and the writing of the manuscript within the framework of the Plankton Imager User Group (PIUG).

Competing interests

The authors declare that they have no conflict of interest.

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Appendix A: Classes included in the two trained classifiers

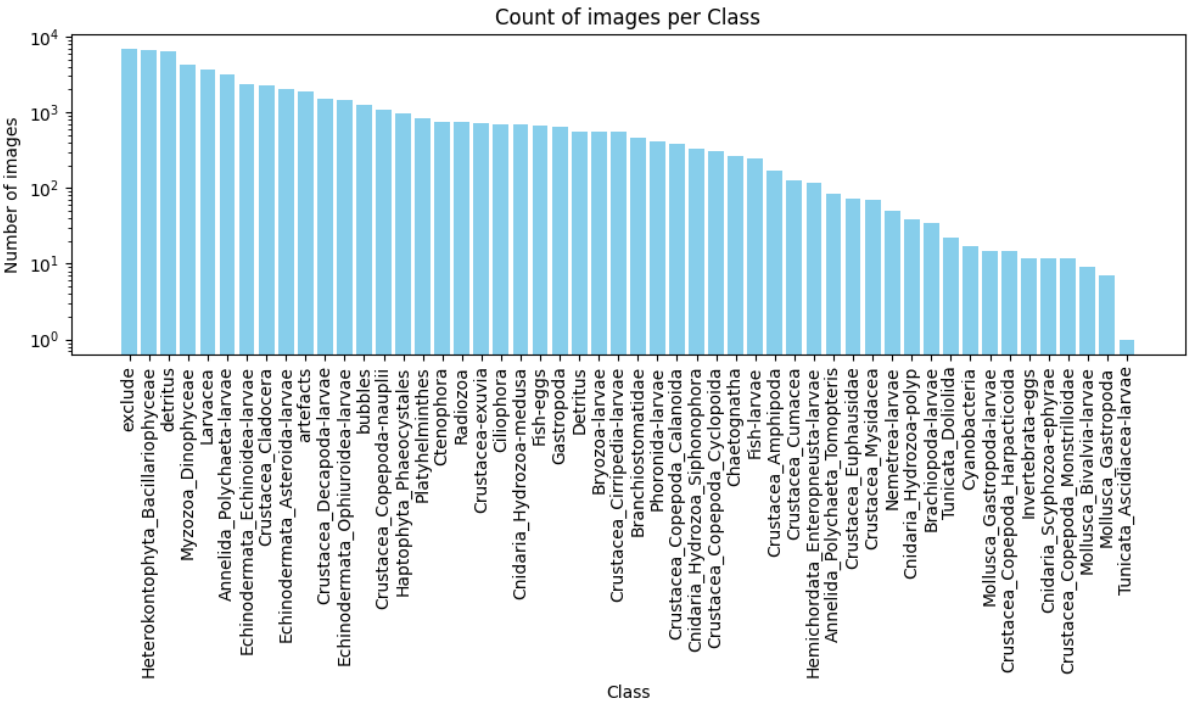

Figure A1: Classes and number of images included in the taxonomically detailed classifier.

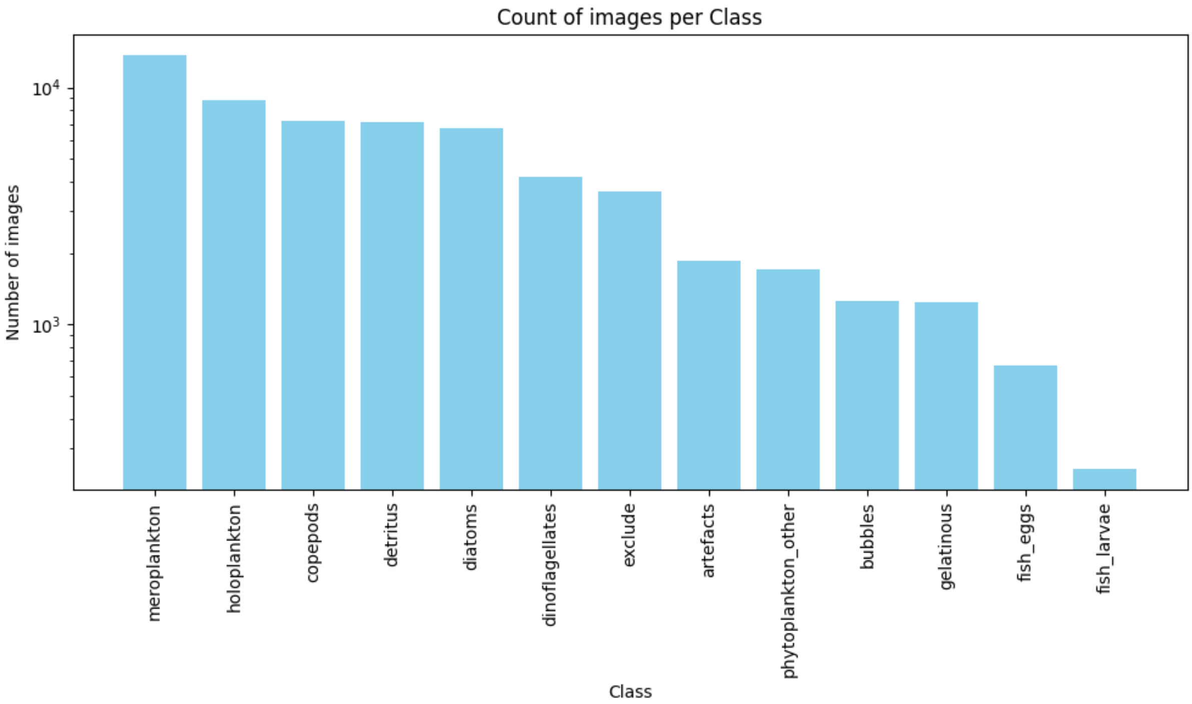

Figure A2: Classes and number of images included in the OSPAR lifeform classifier.

Appendix B: Model training

The model architecture is based on ResNet50 (He et al., 2016), pretrained on ImageNet (Deng et al., 2009), and implemented using the FastAI framework (v2.8.3; Howard & Gugger, 2020) with a PyTorch backend. For data preparation, the dataset was split into 80% training and 20% validation using a random split. Data augmentation included random horizontal and vertical flips, rotations of up to ±0.2 radians, zoom levels between 1.0 and 1.1×, lighting adjustments of ±0.3, and warping of ±0.1. Input images were normalized using ImageNet statistics with a mean of [0.485, 0.456, 0.406] and a standard deviation of [0.229, 0.224, 0.225].

Training was conducted in two stages. In stage 1, the model was trained with frozen weights, using learning rates ranging from 4e-4 to 9e-2 for either 20 or 50 epochs. The best model from this stage was selected based on validation loss and used in the second stage. In stage 2, the entire model was fine-tuned using decreased learning rates ranging from 3e-7 to 3e-3 and 1e-6 to 1e-4 over 10, 20, or 50 epochs. The optimizer used was stochastic gradient descent (SGD) with momentum, as per FastAI's default settings, and cross-entropy was used as the loss function. The batch size was set to 600, and the final model was selected based on the lowest validation loss.