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Coupling autonomous underwater vehicles (AUVs) and AI to enhance biodiversity assessment

Georgina Vickery

Autonomous underwater vehicles (AUVs) are increasingly used to survey marine ecosystems, offering opportunities to collect data on a broad range of taxa beyond the target species. However, extraction of this additional data depends on the availability of trained taxonomists or reliable AI models capable of detecting the full range of species present. This talk presents a robust AI modelling approach developed to classify the dominant taxa observed during an AUV survey in the fjords of Northern Norway, with additional automated size determination for king crab. The approach circumvents the need for time-consuming manual annotation and is a flexible, transferable pipeline which is adaptable across survey designs.

The Megalodon object detector from Hugging Face was applied to extract image crops, followed by clustering to species level. These clustered crops were used as the basis for training multiple classification models and for creating bounding box annotations for single shot or combined

object detection and classification models. This method achieved an average classification accuracy of 95% across all species, including jellyfish, corals, sponges, skates, shrimp and crabs, demonstrating an efficient, reliable method to easily expand the number of taxa detected using AI.

The AUV deployment was integrated into the routine trawl and trap survey design, enabling the comparison of abundance estimates and length distributions between gear types. In addition to facilitating gear calibration and timeseries integration, this demonstrated both the higher diversity captured by visual surveys as well as the effectiveness of AI to quantify the resulting data. Coupling AUVs with AI creates a highly efficient monitoring tool with the potential to greatly enhance the spatial extent and resolution of data available for marine biodiversity assessment.

From Net Tows to Soundscapes: Integrative Approaches to Sustained Ecosystem Monitoring in the Gulf of Maine

Cameron Thompson

Coastal and ocean observation systems like NERACOOS sustain monitoring efforts to understand how ecosystems are changing. Historically focused on met-ocean variables, NERACOOS has expanded its marine life program to integrate biological essential ocean variables, including plankton biomass and diversity and ocean sound.

Through the US Marine Biodiversity Observation Network (MBON), NERACOOS maintains two time series stations with over two decades of observations. These stations serve as sentinels of ecosystem change, tracking the abundance and phenology of the sub-arctic copepod *Calanus finmarchicus*, the lipid-rich foundational species of the Gulf of Maine and primary prey of the critically endangered North Atlantic right whale (NARW). Following a major oceanographic shift around 2010, the time series and broadscale ecosystem surveys have documented a pronounced decline in *C. finmarchicus* abundance, linked to a subsequent decline in the NARW population. These findings underscore the value of sustained monitoring, but understanding the drivers of such variability demands integrative approaches. To that end, these stations also serve as a testbed for trialing novel methods in a well-characterized environment. In the current phase, we are incorporating complementary methods including eDNA metabarcoding, lipid analysis, and in situ imaging to increase taxonomic resolution and functional characterization across multiple trophic levels.

Enabled by improved technology and motivated by the need to monitor NARW habitat use and assess the impact of offshore wind development, passive acoustic monitoring (PAM) data collection has also greatly expanded across the region. Beyond detecting whale presence, ocean sound observations present an opportunity to track ecosystem changes, but only if petabytes of data can be curated, standardized, and disseminated. To meet that need, NERACOOS has begun integrating PAM data into the observing system through PAM Hub, a cloud-based cyber infrastructure. Datasets are processed into hybrid millidecade spectral summaries, a standardized acoustic metric enabling sustained characterization of the regional soundscape across time and space.

Central to any observation effort is the commitment to making data accessible and building partnerships that put it to use. NERACOOS collaborations span universities, federal agencies, and state partners across disciplines from physical oceanography to bio-acoustics. Sustained sampling cruises and derived data products provide opportunities for education and public engagement, while open access through OBIS, ERDDAP, and PAM Hub ensures data are discoverable by the wider community. This investment in accessibility, collaboration, and

methodological integration transforms what might otherwise remain an isolated monitoring program into a platform for discovery and cross-disciplinary synthesis.

Mesozooplankton-protist interactions inferred by co-occurrence analyses of eDNA data across French coastal ecosystems.

Elisa Blanchetiere de Torres

Coastal and estuarine areas represent vital transition zones between land and sea where planktonic organisms, including zooplankton, protists, bacteria, archaea, and viruses, perform essential ecological functions such as nutrient recycling and energy transfer. These services depend on complex biotic interactions, with parasitism playing a central but often underappreciated role in shaping community composition and ecosystem functioning. Because environmental factors like temperature and nutrient availability influence host susceptibility and parasite strategies, parasitic pressure varies significantly across spatial and temporal gradients. Understanding these spatio-temporal dynamics is crucial for anticipating how estuarine ecosystems will respond to anthropogenic pressures and climate change.

The primary aim of this study is to characterize regional patterns of associations between zooplankton and protists, focusing specifically on copepod-dinoflagellate parasitic interactions, inferred from DNA metabarcoding datasets and co-occurrence networks. To evaluate the robustness of this approach, results will be validated using already documented parasitic models between crustaceans and protists. Additionally, the study investigates whether co-occurrence networks generated with the 18S V4 marker provide results consistent with those obtained with the COI gene.

This research was conducted as part of the ROME project (Réseau d'Observatoires de Microbiologie Environnementale intégrée). Seawater samples were collected bi-monthly between 2020 and 2023 at four ecologically distinct sites: the Bay of Veys in Normandy, the Bay of Brest in Brittany, Marennes-Oléron in Nouvelle-Aquitaine, and the Thau Lagoon in Occitania. Planktonic communities were surveyed by DNA metabarcoding. Zooplankton communities were characterized using both the cytochrome-c oxidase 1 (COI) gene and the V4 region of the 18S rDNA, while phytoplankton was analysed using the 18S-V4 region only. Raw sequences were processed through the SAMBA bioinformatic pipeline, which performed inference of amplicon sequence variants (ASVs) using DADA2, taxonomic assignment was conducted by BLAST against the MIDORI2 COI database, followed by ecological analyses using R packages such as phyloseq and NetCoMi.

Overall, this study seeks to determine if the molecular approaches can monitor complex marine interactions across different scales, providing a more efficient framework for future multi-trophic ecological studies.

Functional biodiversity of tiny plankton for UK Marine Strategy- what can they tell us about marine health

Rowena Stern-Kluckner

Bacteria and microbial eukaryotes under 20 micrometers (termed here as “tiny plankton”), are diverse communities and dominate plankton abundance, but are poorly represented in marine pelagic health assessments. These challenging plankton species are traditionally difficult to monitor routinely due to their small size. To improve biodiversity assessments, we evaluated five, aggregated groups of plankton measured by flow cytometry for their inclusion as indicators for biodiversity and foodwebs using time series at the Western Channel Observatory L4 (WCO-L4) and the Scottish Coastal Observatory at Stonehaven (North Sea) over 9 and 14 years,

respectively. Their utility as an indicator of biodiversity would require tiny plankton groups to show an association with human environmental pressures, such as anthropogenic induced elevated ocean temperature and nutrients changes. Likewise, as indicators for foodwebs requires a sustainable balance of diversity and abundance of foodweb elements and reproductive capacity. Tiny plankton groups identified by flow cytometry used in this analysis were photosynthetic nanoeukaryotes, photosynthetic picoeukaryotes, *Synechococcus* cyanobacteria, High Nucleic Acid bacteria and Low Nucleic Acid bacteria. Flow cytometry can measure abundance accurately but could only resolve groups by size, presence of a pigment and DNA quantity for the two heterotrophic bacterial groups. We used a functional trait approach to designate size and abundance traits to tiny plankton groups. Corresponding 18S-V4 genetically derived taxonomic data from the same or similar samples, were used to derive or infer trophic traits into four trophic categories. Abundance trends showed long-term declines in photosynthetic nanoeukaryotes and increased abundance of heterotrophic bacterial groups, with WCO-L4. At the same time, human pressure variables: sea surface temperature and nutrients, indicated WCO-L4 was under temperature and nutrient stress whilst Stonehaven experienced nutrient stress. Principal Component Analysis and Plankton Index analysis approaches showed contrasting responses between tiny plankton, nitrate and sea surface temperature between these sites. All tiny plankton groups showed greater correlation between each other at Stonehaven than at WCO-L4, except two groups showing greater interactions between groups. Assessing potential foodwebs, tiny plankton were associated with a different suite of larger plankton lifeforms at WCO-L4 than Stonehaven. Overall, these results show tiny plankton respond to human-associated environmental pressures, with responses related to their fundamental physiological traits. We observe that different foodweb dynamics at different at these sites, which are associated with different human pressures. This approach has allowed us to demonstrate that poorly resolved “tiny plankton” are suitable for marine health assessments.

Decapod gut DNA metabarcoding for biodiversity sampling in deep-sea Adriatic ecosystem

Lorenzo Zacchetti

No abstract

Unlocking the potential of environmental DNA for marine benthic monitoring: A case study from marine protected areas of the southern Baltic Sea

Judith Piontek

Monitoring biodiversity is a key tool for evidence-based ecosystem management, as it documents the current status of ecosystem components and enables the evaluation of anthropogenic pressures and the effectiveness of conservation measures. With regard to protected features in sensitive ecosystems, such as macrofaunal communities in marine protected areas (MPAs), their high conservation value must be carefully considered, and the extent of extractive sampling using heavy gear should be minimized. Non-invasive approaches, such as environmental DNA (eDNA) analysis, offer promising alternatives; however, their systematic integration into existing monitoring frameworks remains a challenge. We will present a comprehensive evaluation of eDNA and metabarcoding approaches for the analysis of macrozoobenthic and demersal fish communities in MPAs of the southern Baltic Sea. This evaluation includes ground-truthing against data derived from conventional survey methods, such as dredges and grabs, combined with morphological species identification. In addition, we provide a detailed analysis of sampling effort requirements and examine the underlying causes

of imperfect species detection. Our results highlight the strong potential of taxonomic marker gene sequences for biodiversity assessments in marine seafloor communities. Notably, for demersal fish communities, the eDNA approach yielded species inventories comparable to those obtained through extractive beam trawling. At the same time, our study identified distinct challenges in the analysis of fish and macrozoobenthic communities, underscoring the need for target group-specific strategies tailored to the ecosystem. Based on our findings, we propose recommendations for integrating eDNA analyses into monitoring frameworks in a manner that preserves the continuity of long-term time series while fully harnessing the potential of eDNA-based methods.

Leveraging AI imagery data reuse for ecosystem biodiversity assessments: A case study from the *Nephrops norvegicus* LANGOLF-TV survey

Robin Faillettaz

Annual *Nephrops norvegicus* stock assessment surveys are conducted by several European countries in Atlantic and Mediterranean waters. In the Bay of Biscay, the LANGOLF-TV survey samples >180 stations per year, yielding >25 km² of seafloor recording through >30 hours of high-resolution imagery data using a towed vehicle. The stock assessment is conducted using *Nephrops* burrow counts, but given the difficulty to identify *Nephrops* burrows, the images are manually screened by trained scientists. Attempts to automate burrow counts are taking ground with the advent of AI for image analysis, yet remain challenging due to changing seafloor structure, burrow orientation and complexity, etc. While AI may underperform at counting burrows, it could be a fast and robust approach to extract information on a number of other species that may be used for benthic ecosystem-level description and monitoring. We here annotated 17 taxa, including mobile and sessile invertebrates as well as fish, observed in 35 stations from the 2019 LANGOLF-TV dataset to train a YOLOv9-c model coupled with a tracker to count individuals, and evaluated it on an independent dataset. The model was then used to infer the abundance of these species in the remaining stations of 2019 as well as all stations from surveys in 2020-2025. The time series obtained will enable quantification of spatial (by depth, area, etc.) and temporal (interannual) variability in biodiversity indicators (species richness, Simpson index, etc.), which may be key to understand the variability in benthic communities. The AI-derived biodiversity patterns were then compared with human-validated data over 90 stations from 2019 and 138 stations from 2020, showing an overall good match in spatial and temporal trends. Still, taxa-specific mismatches were yielded due to the lower taxonomic resolution achieved by AI identification compared to expert. By focusing on species for which AI demonstrates robust identification, our study highlights that, in specific cases, AI may enable collection of key biodiversity data at minimal additional costs, which may have otherwise been overlooked. However, AI will never reach the complexity achieved through human knowledge, limiting the range of its ecological applications.

Assessment of benthic biodiversity: Do we know our species?

Eivind Oug

Many of the most common and well-known invertebrate taxa in North Atlantic waters were described by early scientists in the 18th and 19th centuries. Original descriptions were generally little specific, presented in the scientist's mother language and with diagnoses in Latin. The species were reported from wide geographic areas. In recent decades it has been acknowledged that many so-called "well-known and widely distributed species" essentially encompass complexes of confused similar-looking species. This notion has been clearly

demonstrated through modern integrative taxonomy, especially with use of DNA barcoding as a tool for species discrimination. For the group Polychaeta, recent studies in Norwegian waters have documented species complexes in practically all present families. Based on extensive sampling, more than 4000 DNA barcodes (CO1, 16S, 28S) representing more than 500 species level taxa have been obtained. Barcodes of well documented 'species' (e.g. *Scalibregma inflatum*, *Amphicteis gunneri*) cluster into 3-10 separate groups (clades or barcode 'bins' = putative species). Consequently, polychaete species numbers in Nordic waters are estimated to be 30-40% higher than presently known. Further, different clades show different geographical distributions, suggesting that clades represent species with different environmental requirements. A recently established project ('PolyType'), funded by the Norwegian Biodiversity Information Centre, aims at resolving species complexes and discover further 'hidden' diversity among polychaetes. Well-known early described 'species' are delineated and redescribed combining genetic characterisation with advanced morphological techniques. To anchor original species name with 'correct' genetic clade, original sampling localities (type localities) are revisited to collect type-specific specimens for DNA and morphology. The presently acquired knowledge of hitherto unknown diversity and restricted distribution of species is highly relevant for management and environmental monitoring. The potential of eDNA and metabarcoding techniques for biodiversity assessments will rely heavily on the development of quality-assured sequence libraries, that only can be obtained through critical taxonomic work combined with best sequencing techniques. Similarly, initiatives in Europe and globally to obtain genomes of species rely on sequencing the 'correct' genetic clade to establish a reference genome to a species name. Provision of updated species descriptions for traditional monitoring is presently constricted by limited taxonomic expertise (the 'taxonomic impediment') yet may foster a discussion about alternative methods for species characterisation. It is recommended for monitoring and long-term trend series addressing spatial or temporal gradients to collect and store reference material for future analyses, taking advantage of the rapidly developing availability and precision of molecular genetic methods.

Investigating multi-contaminant profiles across the European coastline and its impact on benthic biodiversity

Lilian Greau

Man-made chemicals have enhanced our quality of life, however the pollution they generate has the potential to negatively impact both the environment and human health. The chemical exposome associated with human activities includes a wide array of substances, which can be grouped into two main categories, organic and inorganic chemicals both containing legacy pollutants and contaminants of emerging concern (CEC). The Traversing European Coastlines (TREC) expedition is a pan-European survey that aims to extensively study coastal ecosystems and their responses to environmental changes and pollution pressures. Sediment sampled in TREC are used within CONTRAST and BIOcean5D, as one case study to characterize chemical contamination and its effect on microbial communities.

This study investigates how contamination gradients shape benthic microbial biodiversity and functional potential across European coastal sediments. Sixty-one sites along the North-east Atlantic and Mediterranean coasts were surveyed. An extensive list of contaminants has been monitored and analysed, including i) both legacy organic contaminants and CECs (Polycyclic Aromatic Hydrocarbons (PAHs), Polychlorinated biphenyls (PCBs), Polybrominated Diphenyl Ethers (PBDEs), Per- and Polyfluoroalkyls Substances (PFAS), Organophosphate Esters (OPE)), ii) trace metals and rare-earth elements (REEs), as well as iii) 64 unregulated CEC recently prioritized by Yulikayani et al., (2025). Microbial biodiversity and predicted functions were

characterized using 16S and 18S rRNA metabarcoding, and linked with sediment contamination which was comprehensively assessed to describe site-specific chemical profiles.

Sites were classified according to their contamination levels and types, reflecting surrounding anthropogenic pressures (e.g., estuaries, industrial areas, ports, mining activities). Some sites show a profile dominated by PAH contamination due to their proximity to refineries and ports while others indicate a profile dominated by PFAS probably due to their proximity to industrial sites. There are also some hotspots of metal contamination found in sediments likely due to nearby mining or industrial activities. We hypothesized that benthic microbial diversity and functional structure would vary along these contamination gradients. Multivariate analyses revealed that the presence and relative abundance of specific taxa and functional pathways were associated with site-specific contamination profiles.

This continent-wide assessment provides a unique baseline to understand how complex contamination gradients structure benthic microbial communities and offer a framework for integrating chemical and biodiversity monitoring in European coastal ecosystems.

Are monitoring programs fit for global change? Evaluating and optimizing the representativity of coastal benthic monitoring networks supporting the French WFD and MSFD

Nathan Chauvel

Biodiversity monitoring programs must track ecological responses to rapid and spatially heterogeneous environmental change while operating under strong financial and logistical constraints. Their relevance depends on how well existing networks represent the diversity of ecosystems, environmental conditions, and anthropogenic pressures. Are observations biased toward low-impact or heavily impacted systems? Are long-term time series located in climate refugia or high-risk zones? Without such assessments, monitoring networks risk providing a biased view of biodiversity change and its drivers. Beyond diagnosing biases, it is essential to develop quantitative tools to optimize monitoring design, enabling efficient allocation of limited resources to maximize spatial representativity, coverage of key natural and human pressure gradients, and anticipation of emerging conditions under climate change.

We propose an integrative framework combining univariate and multivariate representativity analyses with spatial extrapolation diagnostics to (1) quantify biases in spatial and environmental coverage of existing networks, including future climate conditions, and (2) support optimization by identifying priority locations to increase coverage. We demonstrate the framework using French coastal benthic monitoring as a case study, focusing on coastal infralittoral and circalittoral habitats and evaluating whether networks implemented under the Water Framework Directive (WFD) can support the Marine Strategy Framework Directive (MSFD) objectives. We combine a data synthesis of natural and anthropogenic drivers structuring benthic habitats with the spatial distribution of monitoring stations, enabling computation of representativity metrics and model extrapolation assessment. Outputs are integrated with stakeholder-defined prioritization scenarios into optimization algorithms to derive recommendations for targeted sampling.

Results reveal substantial gaps in representation of environmental and anthropogenic gradients, with variability among habitat types and regions. Across habitats, areas adequately represented by the WFD network rarely exceed one third of total habitat extent. Extrapolation analyses disentangle causes of poor representativity, distinguishing regions with unobserved variable ranges (most frequent) from regions with novel driver combinations. By mapping extrapolation levels and identifying drivers limiting extrapolability, our framework enables prioritization of future monitoring according to objectives, such as improving coverage of pressure gradients, minimally impacted areas, or regions undergoing rapid climate change.

Integrated with scientific and stakeholder priorities, this approach provides a transparent, scalable pathway to redesign coastal monitoring networks robust to current limitations and future global change.

Comparison of image and molecular-based hard-bottom survey methods for early detection of non-indigenous species

Everthon Xavier

Early detection of non-indigenous species (NIS) is critical for early warning and effective biosecurity, and remains methodologically challenging. In this context, bryozoans can be considered good species-models to evaluate detection methods, due to their ability to settle on almost any substrate and their high tolerance to environmental variations. Here, we compared two survey methods for detecting non-indigenous bryozoans: (i) an approach using Autonomous Reef Monitoring Structures (ARMS) combining DNA metabarcoding and photo quadrats of settlement plates and (ii) a field-based approach combining *in situ* rapid assessment surveys (RAS) with video observations and photo quadrats, based on morphological taxonomy. Sampling was conducted during spring tides in October 2024 in the Port of Brest (France), within a recently built polder designed to support the marine renewable energy sector. The site is bounded by a ~900 m-long dyke that hosts eco-engineering structures, consisting of concrete artificial rock pools embedded in the dyke revetment at three intertidal elevations (high, mid, and low). Presence data derived from both approaches were then compared to quantify detection performance. Fourteen bryozoan species were recorded in total, of which four were non-indigenous. The ARMS-based protocol detected 11 species, including two NIS (*Juxtacribrilina mutabilis* and *Watersipora subatra*). In contrast, traditional RAS surveys detected only three species, including two NIS (*Bugula neritina* and *W. subatra*). Only one abundant NIS (*W. subatra*) was common to both survey methods. After, we quantified species richness of bryozoans and NIS, evaluated the complementarity between the protocols, and modelled the probability of detecting at least one NIS per replicate. Our results indicate that ARMS could enhance detection of recruitment-stage or small-bodied taxa settling on standardized substrates. In contrast, traditional surveys offer two advantages: (1) direct assessment of established and spatially dominant species on natural or artificial substrata, increasing the detection of conspicuous invaders; and (2) rapid evaluation over larger spatial extents, enabling immediate management-relevant detection during routine inspections. Our results show a complementarity of the two methods at operational scales. ARMS provide greater taxonomic coverage and detection of small organisms, while traditional surveys may be more effective at detecting established invaders allowing a greater number of replicates to be sampled over space and time. For coastal monitoring and biosecurity, no single strategy seems to be more effective. Instead, adopting a multidimensional evaluation framework – combining standardized recruitment-based tools, DNA analysis and targeted visual surveys – may enhance early detection across invasion stages and optimizing NIS surveillance.

Increasing accuracy and biodiversity captured from acoustic surveys using in-trawl stereo cameras and open cod end towing

Georgina Vickery

With increasing innovation in underwater observation technologies, the range of data sources available for fish stock assessment are expanding. Whilst standardised trawl and acoustic survey time series remain essential, these methods are known to contain systematic biases. Trawl gears exhibit species- and size- selective catchability, and biomass estimates from

acoustic surveys can vary depending on how the individual analysts interpret and scrutinize the signals. In-trawl camera systems combined with automated image processing and machine learning approaches, offer a complementary, non-invasive means to validate abundance indices and increase data reliability of both benthic and pelagic ecosystems.

Biomass estimates from acoustic surveys are typically based on allocating acoustic backscatter to individual species, using ecosystem knowledge, species-specific behaviour and supporting trawl samples. The trawl tows are used to verify species composition and obtain size distributions of large or uncertain acoustic targets. By placing a stereo camera inside the trawl and towing with an open cod end, individual fish could be directly linked to their corresponding acoustic backscatter, allowing detailed validation of species and size assignments. This approach facilitated the development of an area-specific, cross-validated database to inform future backscatter allocation and to serve as a training dataset for AI-based classification models. Furthermore, obtaining size and identity data for individuals across an entire acoustic transect reduced the risk of bias associated with sampling only the largest aggregations. This project demonstrates how integrating in-trawl camera systems with AI can improve the accuracy, taxonomic resolution and biodiversity captured by acoustic surveys, whilst remaining operationally accessible and preserving time-series continuity.

Crabs on camera: from underwater video to automated coastal monitoring using object detection

Gina Brøten

Despite the growing interest in machine learning for marine sciences, most object detection models remain at proof-of-concept stage, leaving questions around their practical application in fisheries science largely unanswered. Simultaneously, surveys with non-invasive Baited Remote Underwater Systems (BRUV) continue to generate large volumes of observational data that remain underutilized due to the bottleneck of recourse-demanding manual annotation. For data-limited stocks, such as brown crab (*Cancer pagurus*), where more abundance and habitat information is needed these two challenges present a clear opportunity. We investigated if the application of machine learning and BRUV can deliver a practical and scalable approach to monitoring the brown crab along the Norwegian coast.

We developed and applied an object detection model to identify and quantify brown crabs (*Cancer pagurus*) on BRUV videos in Norway. The object detection model achieved a mean average precision (mAP50) of 0.75, precision and recall of 0.83 and 0.65, respectively, and produced few false positives. Crab abundance was estimated using the maximum number of crabs visible within a single frame per station (MaxN), which showed positive correlation with catches from nearby crab pots.

A key contribution of this work is an ecology-informed filtering approach applied to the object detection model's predictions. Rather than relying solely on confidence thresholds, predictions are retained based on known crab behavior and habitat associations. This yielded more accurate MaxN estimates than the unfiltered predictions alone. Our results demonstrate that combining optical survey methods, machine learning, and ecological expertise can bridge the gap between model output and operational monitoring.

Five Years of Baited Video in the North Sea: Fishery Exclusion Effects and Method Comparisons to eDNA Metabarcoding and Bottom Trawling

Nicolas Bill

Marine Protected Areas (MPAs) are designated to conserve vulnerable habitats and biodiversity. However, in the North Sea, these areas have been in parts heavily impacted by anthropogenic pressures, in particular by bottom trawling—a fishing method known to cause substantial damage to benthic habitats and associated fauna. To strengthen protection measures, bottom trawling exclusion zones were established in 2023 within the German Bight, covering large parts of the MPAs Sylt Outer Reef and Borkum Reef Ground. With the restrictions also traditional scientific bottom trawling surveys were banned.

To test and to provide a minimal invasive alternative for biodiversity monitoring, Baited Remote Underwater Video Stations (BRUVS) have been deployed in these areas since 2020. They provide information on taxonomic richness, relative abundance, size and biomass of benthic and pelagic fish and invertebrate communities. Method comparison studies were conducted to evaluate whether BRUVS can replace traditional trawl surveys, and to assess their complementarity with another emerging non-invasive monitoring approach, the eDNA metabarcoding from water samples.

A five-year BRUVS time series was established, comprising 376 deployments conducted before and after the trawling restriction, inside and outside the MPAs. A substantial proportion of this data set was used to evaluate the effects of bottom-trawling and the early effects of the trawling exclusion. Furthermore, environmental and methodical influences on BRUV performance were evaluated.

The results provide an overview of advantages and disadvantages between minimal-invasive methods and the traditional bottom-trawling surveys, highlighting differences in ecological metrics, taxonomic resolution and spatial resolution. Method-specific environmental influences, such as visibility or currents, were evaluated and correction models developed. Methods showed both complementary strengths and inherent limitations.

This comprehensive and integrated study provides one of the first insights into the effects of trawling restrictions on fish and invertebrates in the MPAs of the German Bight, covering up to 2.6 years after fishery exclusion. However, longer-term monitoring will be necessary to detect more robust ecological responses.

eDNAcheck: An online plausibility assessment tool for integrative marine biodiversity monitoring

Kingsly Chuo Beng

The increasing adoption of molecular approaches such as environmental DNA (eDNA) metabarcoding has transformed marine biodiversity monitoring and assessment. However, molecular surveys frequently yield unexpected, erroneous, or biogeographically implausible species detections, raising challenges for data interpretation, integration with traditional methods, and transfer into operational monitoring frameworks. Ensuring ecological plausibility and transparency in species detections is therefore critical for the uptake of eDNA in long-term biodiversity monitoring and marine conservation. Here we present eDNAcheck, an open-access online tool designed to assess the plausibility of species detections in molecular biodiversity datasets. The tool integrates molecular occurrence records with global biodiversity repositories on species physical occurrences, including OBIS, WoRMS, and GBIF. By placing detections in context with previous species recordings within a spatial and temporal buffer, the tool provides ecologically informed validation of detected taxa. eDNAcheck standardizes taxonomic data, queries reference databases via Application Programming Interface access, aggregates matching occurrence records, and produces summary tables alongside interactive geospatial visualizations. By contextualizing molecular detections against independent occurrence data, eDNAcheck supports the identification of potential range expansions, novel records, misassignments, or contamination. The tool thereby enhances data quality control, facilitates

cross-method comparison with morphological and observational datasets, and contributes to methodological calibration across monitoring programs. eDNAcheck requires no installation and accepts standard biodiversity data formats (.csv, .xlsx, .tab), lowering the barrier for authorities, research institutions, and industry stakeholders to implement reproducible plausibility screening workflows. A custom-database validation module is currently under development to enable integration with regional monitoring datasets and time-series programs. By strengthening confidence in molecular detections and promoting transparent, reproducible interpretation, eDNAcheck contributes to integrative marine biodiversity assessment and supports the operationalization of eDNA-based monitoring in the context of accelerating environmental change.

Autonomous Imaging of Pelagic Predators for Integrated Biodiversity Assessment

Ciara Willis

Understanding marine biodiversity in pelagic ecosystems is constrained by the difficulty of observing highly mobile predators within dynamic habitats. Traditional surveys provide limited spatial and temporal coverage, and many methods (e.g., vessels, nets, submersibles) unintentionally repel target species. Here we present Piscivore, an autonomous visual observation system designed to enable persistent, minimally intrusive biodiversity sampling in the open ocean through an integrated observing approach. Piscivore combines imaging systems and environmental sensors on long-range autonomous underwater vehicles (LRAUVs), enabling multi-week surveys across broad spatial scales. A trailing attractor (hookless fishing lure) promotes investigative behavior, while forward- and rear-facing cameras (custom optimized for high resolution, low-light sensitivity, and rapid aperture response) record predator and prey encounters alongside concurrent system measurements of oceanographic conditions, directly linking biological observations to their environmental context. The extensive video datasets from these deployments are then processed using machine-learning-assisted detection pipelines to describe the distributions of predators and prey as they relate to measured habitat parameters and behavior. Initial applications, shared here as case studies, demonstrate the system's capacity to document diverse predator assemblages (> 60 species observed to date, including fishes, sharks, invertebrates, marine mammals, and seabirds) and relate encounter patterns to fine-scale habitat variability. Beyond research applications, Piscivore enables operational monitoring in areas inaccessible to ships (e.g., offshore wind farms and oil platforms) and supports year-round sampling of species of commercial and conservation concern beyond periodic research vessel surveys. Piscivore demonstrates how autonomous imaging can bridge oceanographic monitoring and biodiversity assessment, advancing ecosystem-scale understanding of pelagic ecosystems by observing predators, prey, and environment simultaneously.

Can an innovative multi technology approach revolutionize how we monitor the environment in offshore wind farms? The SeaMe Project – already in full swing

Petra Ringeltaube

The monitoring programs implemented to control the environmental impacts of offshore wind farms are traditionally focused on four broad receptor groups—mammals, birds, fish, and benthos—which are usually analysed independently. However, in line with the ecosystem-based approach and recent environmental legislation, monitoring should shift from a species-centric focus towards an integrated and holistic view of the marine environment. The SeaMe (Sustainable Ecosystem Approach in Monitoring the Marine Environment) project employs a

variety of new technologies to adopt this comprehensive ecosystem approach within offshore wind farms, utilizing sustainable and technologically advanced methods for simultaneous data collection and integrated data analysis.

Methodologies:

Stationary underwater cameras and AI-supported image analysis replace invasive monitoring techniques (such as trawling and grab sampling) for fish and epibenthos.

Environmental DNA (eDNA) sampling is used to assess local and regional biodiversity, documenting the presence of many more species (including plankton) than the few sentinel ones currently considered.

Drones are used to monitor marine birds and mammals, replacing scientists on planes or ships. Image analysis is conducted using AI.

Stationary cameras installed at foundations observe migrating birds continuously, day and night, for extended periods, with AI used for image analysis, instead of scientists conducting limited observations from platforms and ships.

An autonomous underwater vehicle (AUV), equipped with sensors for measuring oceanographic and biological parameters and cameras for monitoring fish and benthos. AI is used for navigation and image analysis—enabling multidirectional measurements.

The technologies described above will be deployed concurrently in monthly sampling campaigns, with certain systems permanently installed.

In addition, a dedicated data management team will interpret and integrate all collected data, making it publicly accessible via a specialized portal developed for SeaMe.

By working closely with the Operations and Maintenance (O&M) team, SeaMe integrates its activities into asset monitoring by utilizing the same ships that the O&M team uses daily. This approach further reduces the overall CO₂ footprint.

SeaMe's approach is non-invasive and sustainable, offering valuable insights into biodiversity, behavioral patterns, and seasonal changes. This innovative monitoring system is cost-effective, surpasses the German government's monitoring requirements, and supports adaptive management through the ecosystem approach. All collected data will be compared with results from traditional monitoring methods. Methods, initial results and specific lessons learnt will be presented.

eDNA Metabarcoding for Comprehensive Community Analysis and Assessment of Seasonal Dynamics of Marine Metazoa in a North Sea Offshore Wind Farm

Marrit Jacob

Environmental DNA (eDNA) metabarcoding is a non-invasive and sustainable method for biodiversity and community analysis, which can complement and enhance established monitoring methods for marine metazoan biodiversity. Offshore wind farms (OWFs) represent a unique environment combining the introduction of hard substrate infrastructure with a restriction of fishing. Thus, OWFs may serve as artificial reefs and refuges to create stepping stone habitats between natural populations particularly of hard-substrate dwelling marine taxa. In a transdisciplinary collaboration with the industry partner RWE Offshore Wind GmbH, we employed eDNA metabarcoding to assess seasonal shifts in marine metazoan communities in the OWF Kaskasi in the North Sea. Using two genetic markers (COI and 12S), we were able to detect a broad range of typical North Sea vertebrate and invertebrate taxa. The results yield a

comprehensive insight into the faunal richness and seasonal dynamics and investigate the differential effect on hard-substrate vs. soft-bottom and pelagic species within the OWF. The findings support the suitability of eDNA metabarcoding for the identification of North Sea fauna with regard to the general occurrence of species in the German Bight and corroborate its use as a valuable resource-aware and sustainable monitoring approach in expanding OWF sites.

Transdisciplinary research in offshore wind farms: The use of eDNA metabarcoding to assess spatial patterns of marine metazoan biodiversity

Alica Ohnesorge

The North Sea experiences high anthropogenic impacts. Among them are the rapid development of offshore wind farms (OWFs) to ensure a growing supply of sustainable energy in the future. For science, long-term data on the establishment and development of faunal communities in OWFs are not publicly available, which makes holistic biodiversity assessments for the German Exclusive Economic Zone challenging. This is specifically important as OWFs related changes such as the development of artificial reefs and the exclusion of fishing are likely to alter the species composition of the benthic, sessile and mobile communities compared to surrounding areas. In the North Sea, this is especially important, as OWFs introduce hard substrata into sandy bottom-dominated habitats.

In order to identify spatial differences in marine metazoan biodiversity and assess community dynamics, we applied an environmental DNA (eDNA) metabarcoding protocol as a non-invasive method at six fixed stations and at different depths in the OWF Kaskasi (German Bight, North Sea) as part of the transdisciplinary projects CREATE (German Research Alliance, sustainMare research mission) and SeaMe led by RWE Offshore Wind GmbH. In a standardized way, we applied a multi-marker approach (COI and 12S) to capture a broad taxonomic spectrum of the invertebrate and vertebrate fauna in the pelagic and benthic realms.

This evaluation will enable us to better understand general patterns in the applicability of eDNA metabarcoding in local and regional contexts. Furthermore, we evaluate the transfer of this non-invasive method in protocols for monitoring requirements mandated to industry and other stakeholders.

The forecast horizon of marine biodiversity predictions for effective conservation planning and protection

Martin Lindegren

Tackling the biodiversity crisis calls for immediate conservation actions to safeguard “areas of particular importance for biodiversity”. However, identifying suitable protected areas relevant for conservation requires methods capable of monitoring and estimating multiple aspects of biodiversity in both time and space, while ensuring robust forecasts of future “hotspots” and responses to climate variability and change. Here we show that joint species distribution models (JSDMs) trained on high-resolution monitoring data across the North-East Atlantic can provide reliable forecasts of several species- and community-level properties of marine demersal fish biodiversity at a decadal timeframe fitting the marine spatial planning process, with functional (trait-based) indicators performing considerably better than taxonomic indicators. Our first large-scale assessment of the forecast horizon of JSDMs provides a generally applicable framework to evaluate the robustness of biodiversity predictions across areas and organism groups which can serve to guide the identification and prioritization of protected areas safeguarding current and future hotspots of biodiversity.

SurveySync: Harmonizing Fishery-Independent Survey Data into a National Database

Emily Markowitz

Fishery-independent surveys are vital for sustainable management, yet data often remain siloed in regional formats and repositories, hindering cross-regional analysis. This presentation introduces the proposal of SurveySync, a National Survey Database System, designed to unify these data into a cloud-native architecture. Building on efforts like the surveyjoin R package, SurveySync establishes national standards for survey data and metadata.

SurveySync features an event-driven ingress pipeline that standardizes regional data under the guidance of a National Survey Data Standards Task Team. By offering data egress via a secure API and web GUI, SurveySync will deliver downstream-ready data for tools like the Fisheries Integrated Modeling System (FIMS). This modernization enhances efficiency and accessibility while ensuring FAIR compliance.

While the initial phase focuses on NOAA Fisheries bottom-trawl data, the architecture aims to be scalable for all fishery-independent survey data streams. Critically, SurveySync adds to the value of survey data through traceability from 'deck to decisions' by serving standardized, assessment-ready data products. SurveySync establishes a robust foundation for integrating diverse surveys to provide synoptic information on large marine ecosystems.

Does eDNA Dispersal Influence Its Applicability for Management and Conservation? Insights from Lagrangian Particle Tracking Modelling

Mohamed Yosri Zanni

Environmental DNA (eDNA) has emerged as a novel tool for fisheries management and biodiversity monitoring, offering novel insights into marine ecosystems. However, linking eDNA concentrations to species abundance remains challenging because the biotic and abiotic drivers of eDNA production, decay, and transport in the ocean are still imperfectly understood. Lagrangian particle tracking has emerged as a powerful approach to study marine eDNA dispersal, as it tracks individual particles through space and time, links detected eDNA to its likely source locations and can apply particle-specific characteristics. Here, we present applications of Lagrangian simulations using the Connectivity Modeling System (CMS) in the Bay of Biscay to address two key questions: (i) How do the decay rate value and decay processes shape eDNA dispersal? (ii) Does the size of the eDNA footprint (area of origin) impact observed biodiversity patterns? We show that decay rate value strongly controls eDNA transport distance and persistence, with its influence being modulated by local hydrodynamic variability, and that the shape of the decay process has important consequences on predicted eDNA concentrations (up to a factor of 4). Furthermore, in a field study we find evidence for a positive relationship between the size of the estimated eDNA footprint and species richness, indicating that the use of eDNA for monitoring should pay attention to hydrological conditions which shape the eDNA footprint to avoid detection of spurious patterns or changes. Together, these applications advance our understanding of how eDNA moves and persists, tightening the link between transport pathways and source locations.

A glimpse of a Digital Twin of Ocean for long-term marine ecological observatories

Morane Clavel-Henry

Long-term ecological monitoring provides essential information on patterns and variability in marine ecosystems, including continental margins fishery depleted areas. This information is

also crucially relevant for following the track of ecosystem function and biodiversity recovery after restoration interventions. While deployed mobile and fixed platforms have increasingly targeted biodiversity, particularly megafauna, monitoring efforts often remain fragmented and lack fully integrated, interdisciplinary approaches. The emerging Digital Twin of the Ocean (DTO) framework offers new opportunities to combine complementary biological and environmental monitoring and modelling methodologies to generate near-real-time, spatially upscaled ecological indicators. Within the EU-funded project DIGI4ECO, we are developing a prototype DTO tailored to marine biodiversity observatories that are expanding in 4D their data collection thanks to the addition of remotely controlled mobile robotics.

We will show how a DTO framework can enhance the value of observatories and their network of platforms by connecting in-situ observations, modelling tools, and decision-support interfaces within a coherent digital framework. Our work focuses on monitoring efforts in the project along six main axes: (i) automated organism classification using image analysis, supported by remote mission supervision and multi-parameter sensor control; (ii) computationally assisted environmental DNA (eDNA) approaches; (iii) end-to-end analytical workflow frameworks spanning ecological indicator calculation through modelling of “what-if” scenarios, enabling local to regional ecosystem representations; (iv) socio-ecological analyses linking indicators with fisheries behaviour, economic drivers, and management measures; (v) integration of cross-site, multi-sectors data streams that ensures interoperability within the Digital Twin framework; and (vi) data transmission between assets (fixed platforms and mobile robots), for example through docking systems that enable both data and power transfer.

The services provided by this DTO can be progressively expanded with new datasets, installation of new marine observatories, and evolving monitoring objectives fed with DIGI4ECO blueprint. This approach supports the development of an integrated monitoring strategy while bringing diverse stakeholders together around a common decision-support platform.

Refining expert annotation for the deep learning based classification of echotraces and fish acoustic biomass estimation in Atlantic and Mediterranean coastal seas

Calin Arnaud

No abstract

Development of an Automated Stomach Content Analysis System for Deep-Sea Demersal Fishes

Akira Eto

Despite the global trend toward deeper fisheries, ecological knowledge of deep-sea ecosystems remains limited. Species interactions, such as predator–prey relationships, are one important component of these ecosystems. However, the visual analysis of stomach content, commonly used in dietary analysis, requires substantial time and labor. In particular, the most labor-intensive steps in this workflow are the identification and counting of prey items.

Therefore, this study aimed to improve the efficiency of stomach content visual analysis by automating these processes, thereby reducing overall time and labor costs.

In our previous work, we demonstrated that deep learning–based object detection models can automatically detect prey items in fish stomach contents. Based on this model, this study aimed to achieve full automation of prey identification and counting by developing an integrated system covering the entire workflow, from image acquisition to detection.

To automate prey identification and counting, the workflow was divided into four stages: automated imaging, image processing, object detection, and output integration. First, an

automated imaging device was developed to provide stomach content images to the prey-detection model. In this system, a Petri dish containing stomach contents was mounted on an acrylic stage controlled by a two-axis actuator and a microcontroller (ESP32). This configuration enabled full-coverage imaging of stomach contents using a conventional stereomicroscope. The captured images were processed to prepare them for model input: a panorama image was first generated, followed by re-tiling. Prey detection was performed using a YOLOv11-based object detection model. Detection outputs were subsequently converted into statistical information on prey composition using an output integration program.

For performance evaluation, stomach contents of fish collected by bottom trawling in Suruga Bay, located in central Japan, were used. System performance was evaluated using manually identified and counted prey items as ground truth data. Processing speed was also measured, and efficiency was evaluated by comparison with manual analysis.

The frequency-based percent agreement between the developed system and the ground-truth data was 80%. The average processing time was about 1.6 times shorter than that of manual analysis. Because manual analysis time varied substantially across samples, the system achieved a maximum speedup of more than 5 times. This system is expected to serve as a foundational technology for efficient large-scale food-web analysis and species-interaction monitoring, which would otherwise require substantial manual labor. In addition to evaluating the system, this presentation will report novel ecological insights obtained with it.

The Genetic Diversity Risk Indicator (GDRI) at FishBase

Natalia Petit-Marty

Maintaining genetic diversity in fish populations is not merely a scientific or conservation goal but a fundamental requirement for resilient, productive aquatic resources and effective stewardship of the future. The Genetic Diversity Risk Indicator (GDRI) presented in FishBase aims to accelerate the genetic monitoring of fish species, offering a practical step forward by combining curated global datasets with modern molecular tools in an accessible, actionable format. GDRI is built on COI- π , a measure of genetic diversity that represents the average number of nucleotide differences per site in the COI sequence between pairs of individuals in a population. This metric has proven useful for detecting population declines in animal species, particularly in harvested fish populations (Petit-Marty et al. 2021, 2022; Ferragut-Perelló et al. 2023).

The GDRI tool in FishBase categorises populations into risk levels—High, Medium, or Low—by comparing COI- π values against threshold ranges established from a global synthesis of empirical data collected for nearly 1,700 fish species. These thresholds vary by region and taxonomic class (i.e., Actinopterygii and Elasmobranchii), reflecting differences in ecological conditions and evolutionary histories. For Actinopterygii, the underlying datasets encompass 1,426 species globally, including specific subsets for East Asia (118 species) and the Mediterranean (47 species). For Elasmobranchii, the dataset compiles COI- π estimates for 256 species worldwide. Ideal for preliminary screening, this tool supports conservation and fisheries management by highlighting populations that may warrant closer genetic monitoring to ensure their long-term sustainability.

The GDRI tool is further complemented by the GENDIVERSITY Table at FishBase, which compiles over 2,000 COI- π estimates for different populations of 953 fish species, obtained using standardised methods across more than 220 peer-reviewed studies. This table enables straightforward comparisons across species and regions, helping to identify potential stressors and providing essential insights for assessing population health, adaptability, and resilience. It also offers a scientific basis for conservation and fisheries management strategies.

Applications of the GDRI based on COI- π include: (1) prioritising ecological and genomic studies of fish species with a high risk of genetic diversity loss; (2) designing Marine Protected Areas with emphasis on genetic diversity hotspots; and (3) monitoring Vulnerable Marine Ecosystems under fishing pressure. Case studies for each application are presented and discussed.

From coastal coverage gaps to species-level insight: integrating split-beam, multibeam echosounders and eDNA to monitor pelagic fish in shallow waters

Julie Salvetat

Coastal areas constitute both productive fishing grounds and ecosystems of paramount ecological significance due to the indispensable functions they provide throughout the life cycle of numerous marine species. They sustain local fisheries while providing critical habitats, such as nurseries and spawning grounds, fundamental to the renewal of exploited stocks. However, these ecosystems face intensifying anthropogenic pressures (urbanization, pollution, physical habitat degradation, and climate change) that compromise ecological integrity. In this context, robust monitoring systems tailored to shallow coastal waters are crucial for assessing Good Environmental Status (GES) under the European Marine Strategy Framework Directive (MSFD). The shallow coastal zone (0–40 m) has long remained under-sampled by conventional surveys. The ACaPELA project, embedded within the MSFD framework, addresses this gap through a portable acoustic system deployed on small vessels (~15 m). The platform integrates three split-beam echosounders (Simrad EK80 at 70/120/200 kHz) and a multibeam sonar (Simrad M3) mounted on a pole, enabling standardized repeatable transects across three pilot sites in Brittany (Saint-Malo/Rance, Roscoff, Brest/Douarnenez) since 2020.

Methodologically, the EK80 operated in narrow-band continuous wave (CW) mode from 2020 to 2023 and in broadband frequency-modulated (FM) mode during 2024–2025, preserving continuity in CW-derived school metrics while revealing wideband frequency-response features that enhance target discrimination. The M3 provides three-dimensional descriptors capturing school morphology, complementing EK80-derived metrics. Feature fusion between split-beam and multibeam descriptors improves shoal discrimination and supports data-driven clustering and preliminary species inference. Each cruise is paired with thermosalinometer, CTD, or sound-speed profiling to contextualize environmental variability affecting detectability and aggregation patterns.

In 2025, along-track environmental DNA (eDNA) filtration was conducted concurrently with acoustic acquisition to provide non-extractive taxonomic information. Rather than acting as strict ground truth, eDNA constrains species hypotheses derived from acoustic school properties. Metabarcoding characterizes the local species pool, reducing the set of plausible taxa responsible for observed shoals and strengthening probabilistic species attribution. This framework advances community-level indicators toward cautiously derived species-level assessment.

ACaPELA demonstrates a deployable, minimally invasive coastal monitoring solution: the pole-mounted EK80–M3/eDNA configuration is modular, rapidly transferable between vessels, and scalable across sites. This combined acoustic–eDNA approach strengthens operational observation of mid- to high-trophic dynamics and supports the development of coastal indicators for MSFD population descriptor D4 and biodiversity descriptor D1.

Developing an integrative, trait-based indicator of species and ecosystem sensitivity to exploitation for monitoring purposes

Marianne Robert

Functional traits are responsible for how organisms respond to environmental factors and affect ecosystem functioning. This presentation aims to illustrate how trait-based approaches can be used to assess functional diversity response to anthropogenic pressures, particularly through the development of an integrated sensitivity index that can be used for diagnostic and monitoring purposes.

We calculated an integrated fishing sensitivity score based on biological traits known to response to trawling for 101 taxa from six classes (Actinopterygii, Bivalvia, Cephalopoda, Elasmobranchii, Holocephali and Malacostraca) sampled during scientific campaigns in the Celtic sea. We then correlated this score with: i) temporal changes in biomass; ii) intensity of fishing pressure in space; and iii) ecosystem functioning metrics. This work enabled us to draw the following diagnostics and conclusions: First, the biomass of at least four fairly sensitive species (mainly elasmobranchs) has increased in areas where bottom trawling has decreased significantly over the last two decades. This demonstrates the positive influence on the whole ecosystem of the spatial and temporal closure of the 'Trevose Box', which was initially implemented in 2005 to protect the reproduction of gadids. Then, by plotting sensitivity against exposure we can monitor species vulnerability. In the Celtic Sea there are no species that are both highly sensitive and highly exposed to fishing. Finally, plotting the sensitivity indicator against the trophic network stability index provides insight into food-web robustness by assessing its capacity to withstand cascading effects triggered by species removal. Eigenvalue centrality, which accounts for both direct and indirect trophic links, helps evaluate a species' role in mediating the propagation of perturbations across the food web. Our analysis indicates that no species are simultaneously highly sensitive and highly central. Notably, the main commercial species occupy relatively central positions within the network. Consequently, the current level of exploitation in the area does not appear to substantially compromise food-web robustness, although this ecosystem has been subjected to intense fishing pressure for the least decades.

We demonstrated that trait-based indicators provide valuable diagnostics of specific systems and, more importantly, facilitate comparisons over time and across ecosystems, thereby supporting monitoring efforts and informing species conservation priorities.

Environmental DNA approaches for bycatch assessment in pelagic fisheries

Nina Strand

Reliable estimation of bycatch is essential for sustainable fisheries management and effective biodiversity conservation. However, current monitoring approaches—including fishermen's logbooks, third-party observer programs, and manual subsampling of landings using the "bucket method"—are constrained by small sample sizes, high operational costs, and reliance on visual species identification by observers with variable expertise. In large pelagic fisheries, where landings often exceed several thousand tonnes, even a small percentage of bycatch can represent substantial and ecologically important biomass that remains poorly resolved using traditional methods.

To overcome these limitations, we developed an integrated environmental DNA (eDNA) workflow combining digital PCR (dPCR) and metabarcoding to quantify catch composition in the blue whiting (*Micromesistius poutassou*) fishery. Controlled experiments using known mixtures of blue whiting and the primary bycatch species, atlantic mackerel (*Scomber scombrus*), were first conducted to evaluate DNA-to-biomass conversion. This framework was subsequently applied to industrial-scale landings through water sampling from onboard holding tanks.

Across landings, eDNA-based methods provided markedly higher taxonomic resolution and reproducibility than the bucket method and reliably detected bycatch at levels below 1%. Metabarcoding revealed a diverse assemblage of mesopelagic taxa—far exceeding the coarse categories (e.g., “lanternfish”) employed by third-party observers—thereby uncovering biodiversity that remains effectively invisible to visual subsampling. The workflow also detected rare and low-abundance species of ecological concern that were entirely absent from traditional monitoring records. Notably, dPCR-derived abundance estimates showed strong congruence with fishermen’s logbook information and outperformed the third-party subsampling method in both consistency and quantitative agreement. By capturing both small, rare taxa and large, low-abundance individuals, eDNA offers a more sensitive and representative assessment of biodiversity within commercial catches. These findings demonstrate the potential of integrated molecular tools to enhance bycatch estimation, improve the ecological resolution of fisheries monitoring, and support the transition toward more comprehensive ecosystem-based management frameworks.