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B-USEFUL

User-oriented Solutions for Improved Monitoring and Management of Biodiversity and Ecosystem services in vulnerable European Seas

Deliverable 2.4 Report on data standardisation methods and applications

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Executive summary

Standardisation and harmonization of data are key requirements for making spatio-temporal data sets of biodiversity and their pressures interoperational and information exchangeable. Standardisation generates consistency at measurement level including consistency checks within a data set. Harmonization means standardisation across data sets at attribute information level and of meta-data associated with the observations. As an example,. classifications like taxonomic hierarchical systems belong here. In this report principles of standardisation and harmonization of spatio-temporal data sets under European policies (INSPIRE) are reviewed. For the purpose of application within B-USEFUL, standardising haul-by-haul fish survey data, standardising abundance data, length composition data and diversity data are discussed, as well as harmonization of taxonomic information is covered in principle and applications are shown with regards to harmonization of meta-data and standardisation of Atlantic and Mediterranean bottom trawl survey data. Furthermore, data checking and standardization methods for three large-scale data sets are presented, including a benthic infauna data set newly published within B-USEFUL, the ICES DATRAS bottom trawl data and the Mediterranean bottom trawl data MEDITS.

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1. The role of this deliverable

This report covers the outcome of activities under Task 2.3 aiming at developing and presenting methods and procedures for correcting and standardising raw monitoring data, such that its format and units enable robust and unbiased data input to WP3 where estimates of the selected set of biodiversity and ecosystem services indicators (co-developed under T.1.3) will be provided in space and time. The methods and procedures for data preparation includes developing and harmonizing a set of transparent scripts and R packages for each of the monitoring data sets to flag and correct potentially erroneous or duplicate records, correct outdated or erroneous taxonomy, as well as ensure comparable units, etc. Among others, we will employ a stepwise process to standardise abundance estimates stemming from various scientific bottom-trawl survey (i.e., including data preparation, explorative analysis, modelling and time series analysis) based on Generalized Additive Models (GAMs). Models based only on minimal geo-positional variables (latitude, longitude, depth, month and year) can be the starting point of the analysis. If more elaborate data standardisations are needed further complexity can be added with additional covariates (e.g., gear, vessel etc), or by applying more advanced statistical methods for data standardisations (e.g., INLA-SPDE or VAST).

Contributors

For this report, contributions from the following colleagues are gratefully acknowledged:

Table 1. Names and roles of authors and contributors to B-USEFUL WP2.3 Deliverable D2.4.

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Acronyms and abbreviations

COM	European Commission
DATRAS	Database of Trawl Surveys, see ICES
DCF	Data Collection Framework of the Common Fisheries Policy
EMODnet	European Marine Observation and Data Network
ERMS	European Register of Marine Species
GAM	Generalized Additive Models
GFCM	General Fisheries Commission for the Mediterranean
GLM	Generalized Linear Model
GOV	Grande Ouverture Verticale survey trawl
IBTS	ICES International Bottom Trawl Survey
ICES	International Council for the Exploration of the Sea
INSPIRE	Infrastructure for Spatial Information in the European Community
ITIS	Integrated Taxonomic Information system
MEDITS	Mediterranean International Trawl Survey
MSFD	EU Marine Strategy Framework Directive
OT	Otter board trawl
WORMS	World Register of Marine Species

2. Introduction

Data standardisation and harmonization and data analysis are processes that depend on each other. This in particular becomes evident when the focus switches to long-term datasets that provide an added value in terms of the potency of the insights that can be obtained from their analysis (Gal and Rubinfeld 2019). Advancements in data science such as machine learning and deep learning have increased the ability of algorithms to reveal interesting relationships between attributes and to mine valuable knowledge for descriptive, as well as predictive functions as a prerequisite for decision-making (Gal and Rubinfeld 2019). As such, "big data" have become a standard in large-scale ecological (Cooper and Barry 2017; Kissling et al. 2018) and climate change research (Sebestyén et al. 2021). Nevertheless, foundations of standardisation procedures in marine science were laid decades ago, when for instance Beverton & Holt (1957) urged for the need of standardisation of commercial statistics of fishing effort for the analysis of dynamics of exploited fish stock.

The European dimension: INSPIRE and EMODnet

At the European level the development of an European Spatial Data Infrastructure (SDI) by means of the INSPIRE directive (2007/2/EC) has set standards regarding data harmonization and accessibility. With regards to fisheries management, the Council Regulation (EC) No 199/2008 of 25 February 2008 concerning the establishment of a Community framework for the collection, management and use of data in the fisheries sector and support for scientific advice regarding the Common Fisheries Policy initiated the modern Data Collection Framework (DCF), after first efforts to collect fisheries data commenced in 2000. The intention of the INSPIRE Directive was to promote as much as possible the sharing of environmental data to support the development and implementation of environmental and related legislation at all levels of administration. This principle is more relevant than ever in view of the common European ambition for a transition to a more sustainable society.

In the context of INSPIRE, spatial data are categorised by themes which each are described by data specifications detailing the different spatial object types (see INSPIRE document series D2.8[1]). The spatial data will be provided by different producers, from different Member States, and with different levels of detail. The value of INSPIRE is not only to define an architecture and the services to provide spatial data sets, but also to ensure the coherence between these data sets. Data are supposed to be provided only once in order to avoid duplicates probably with slight differences.

In order to maintain accessibility, the interoperationability of data is a key requisite. This in particular applies to data repositories that predate INSPIRE with specific thematic lots, for instance the European Marine Observation and Data Network (EMODnet) and the Marine Strategy Framework Directive (MSFD) (Abrami et al. 2015). However, as a directive, INSPIRE bears a higher rank and EMODnet standards need to match with INSPIRE standards (COM (2010) 461). EMODnet was announced as part of the Integrated Maritime Policy for the European Union (COM (2007)575 final). It was acknowledged that using data from single marine data sources would not help policies to effectively govern measures at scales relevant to processes in the marine realm. It was concluded that "applying marine data inevitably requires assembling data collected from a variety of sources into a seamless picture", and activities related to this task were identified as "setting up catalogues, defining standards and developing algorithms and software necessary to assemble data" (COM (2010) 461).

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[1] https://inspire.ec.europa.eu/theme/hb

In the implementation phase, a mid-term evaluation based on five key features of INSPIRE, i.e.

- document spatial data and services,
- establish more internet based services,
- facilitate access to spatial data by improving interoperability,
- arrange for public authorities to have better access to spatial data and services, and
- improve the structures and mechanisms for the coordination of spatial information,

concluded that despite some progress, improvements regarding interoperability of data sets are still much needed stating that "there is room for further improvement to reach higher levels of conformity" (European Environmental Agency 2014; European Commission 2022). The interoperability of spatial data sets comprises inter alia to specify common data models, code lists, map layers and additional metadata (for evaluation and use) to be used when exchanging spatial data sets. These implementing rules provide the semantic interoperability layer and ensure that users of data can unambiguously interpret the data they are accessing through the network services (European Environmental Agency 2014).

The interoperability aspect has been taken into account when defining the relationship between INSPIRE and other environmental data repositories. Here, the non-duplication of information has been considered explicitly (INSPIRE 2014) such that:

- Data models in either reporting framework should be compatible and cooperation between both be fostered
- INSPIRE data models should not duplicate information from other sources
- With alternative data models available, INSPIRE models should focus on the SDI context.

Principles of standardisation and harmonization

A robust definition for data standardisation and harmonization comes from HARMONY Inc. (Harmony Inc. 2024) stating that: "Standardisation is about uniformity in data formats and protocols, while harmonization is about ensuring data from different standards can be used together effectively. Harmonization is crucial when dealing with multiple data sets with varied origins and standards, whereas standardisation is about setting and following a single standard." However, both processes are not always separable from each other. Hence, Gal & Rubinfeld (2019) defined data standardisation as "key to facilitating and improving the use of data increasing data portability and interoperability", clearly also addressing harmonization with the latter two aspects.

Both the **data level** and the **data model** level need to be considered. To distinguish between the two processes, standardisation can be understood to be associated with physical units and their mathematical operations, while harmonization is linked to coding of attributes assigned to the data. As such, standardisation is often conducted using common measurement units, of which the *International System of Units* or SI-metric system consisting of seven base units is the one applied as the world's most widely used system of measurement. Derived standardised properties can be obtained by simple mathematical operations, for instance by dividing travelled distance by unit time leading to the definition of speed.
Data harmonization requires a stringent coding regime for the organization and formatting of meta-data, which again is often referred to as following standards as well, and might require re-categorization of observations (Baaré et al. 2017). Only variables that measure the same concept and set of dimensions can be harmonized, otherwise, harmonization is impossible. A second

aspect of harmonization lies in the way the measured dimensions are presented, i.e. on a binary (yes/no), ordinal (ordered groups) or ratio scale (quantitative measurement such as temperature). The re-categorization of ordinal (for instance: less than 1 pair of birds breeding in a certain place) and ratio scale measurements (10 breeding pairs per acre) to binary coded variables (breeding birds present yes/no) inevitably leads to loss of information (Baaré et al. 2017).

The smoking example firstly shows, that the original information stemming from different sources is re-categorized based on new meta-data, i.e. each observation transformed into categories of the smoking classification table. Secondly, it provides a simple data model, defining how the original observation can be made interoperational based of the associated feature attribute information as part of the meta-information domain. The close relationship between attribute information and meta-data is noticed in INSPIRE (2008, section 6.4.7).

The development of data models can ideally be followed using the INSPIRE process. The implementation rule on interoperability of data sets and services was in the first place defined by specifications referred to the themes of the annexes of the INSPIRE Directive (Reis and Barrot 2009). For maritime observations, Annex III defined the themes of 'sea regions', 'habitats' and 'species distributions', amongst others. The specification framework considers a conceptual framework, subsequently complemented by specific data specifications for each theme.

In INSPIRE (2008), six steps of the data specification model were detailed (Figure 1). The 'case study development' defines what the expected actors or 'case users' might need in consideration of the expected outputs. At the 'requirements of spatial objects' stage, theme-specific requirements are extracted from the use cases defined before, which are applied to the data set in its raw format in an 'as-is analysis'. The 'gap analysis' in turn identifies user requirements that cannot be met by the data in the raw format. For each gap, a data interoperability approach needs to be defined. Data gaps are solved by amending and developing the raw format data into a more complex data model while assigning classification/categorizations in terms of meta-data. In the testing phase, the usefulness of the chosen data model for enduser needs is reviewed.

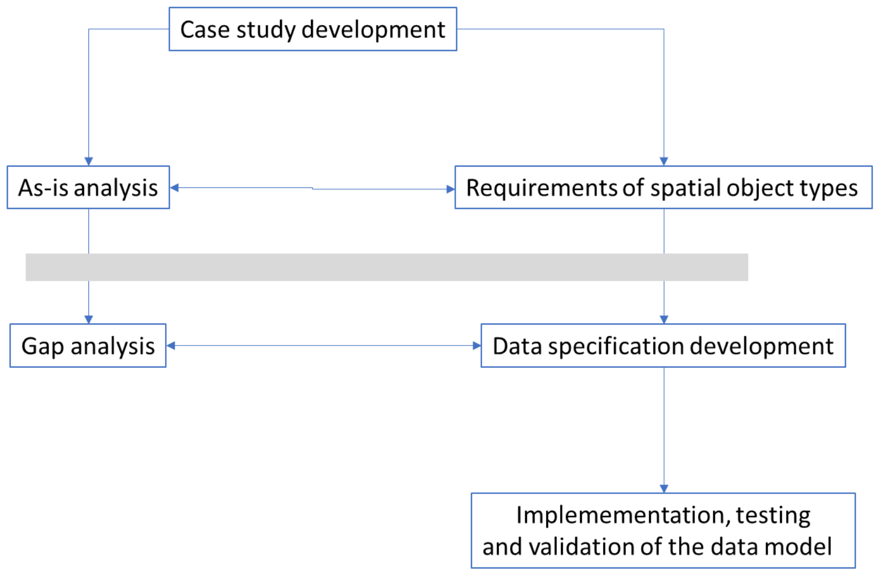


Figure 1 : Methodology for developing INSPIRE data specifications (source: D2.6 v2.0). Detailed in INSPIRE (2008).

Consistency and the level-of-detail problem

Consistency checks within a data set belong to standardisation and are typical quality control measures, such as search for outliers, misspellings, mistakes in dates and localities, etc. Problems arise with data sets where certain variables cannot be harmonized due to missing transformations of the feature attributes considered. These non-hamonized data generate undesired inconsistency in the information network (DG ENV 2021). In turn, harmonization leads to consistency (INSPIRE 2014).
Four different types of consistencies can be distinguished in INSPIRE:

- Consistency within a data set
- Consistency between spatial objects of different themes at the same level-of-detail (LoD)
- Consistency of spatial objects of a theme at two different levels of detail
- Consistency of spatial objects along a boundary

The level-of-detail (LoD) simply represents the quantity of information that portrays the real world. Previously described by scale for maps, the notion has been extended and adapted for geographic data bases (Ruas and Bianchin 2002) or taxonomy. Basically, in maps the loD is linked to the resolution, e.g. park benches cannot be resolved at country scale. In this case, the information is either generalized (aggregated, simplified, abstracted) or deduced by computation from sample data (like geostatistical modelling, see next section). Of course these complex processes of generalisation and computation make hard the consistency between data having different resolutions.

The definitions applied in this report are

- Standardisation – standardisation at measurement level including consistency checks within a data set
- Harmonization – standardisation across data sets at attribute information level and of meta-data associated with the observations. Classifications like in INSPIRE and taxonomic hierarchical systems belong here. INSPIRE (2008) shows the sequence from a data product specification that specifies a data product to its implementation as a data set described by metadata (their Fig. 6). This includes consistency checks between data sets.

Consistency checks often follow a structured approach (e.g. Schaap et al. 2011) and can be supported by software (e.g. ROME, see Zupa et al. 2024).

3. Components of the standardisation and harmonization procedure

In the following section we refer to protocols of data standardization and harmonization that were relevant for B-USEFUL given the data sets at hand (see D2.2 for more information and meta data).

Harmonizing species names

Assigning names to species, i.e. taxonomy, is among the oldest human activities (Costello et al. 2013). In a systematic way, Carl von Linné started to harmonize taxonomic information in the 18th

century. In the aftermath of this development, a manifold of local and regional inventories were established ("Tierwelt der Nord- und Ostsee", e.g. Remane 1940). However, these were often compromised by limited expertise of contributors, misuse of names, for instance assigning the same name to species in different kingdoms of life or dissimilar species in different locations and vice versa, or by using differing names for the same species in different locations, and by combinations of these problems (Costello et al. 2013). To overcome these shortcomings, comprehensive revisions were prepared, starting with the US NODC Taxonomic Code in 1972 which blended into the Integrated Taxonomic Information system (ITIS) in 1996[2]. In 2001, a register of European Marine Species was presented (ERMS) (Costello et al. 2001), which soon after was expanded into a World Register of Marine Species, i.e. WORMS.

The WORMS registry proves to be a helpful tool in the quality control processes of survey data (ICES 2020). As an example, the ICES beam trawl survey group WG_BEAM tabulated survey species records and discovered inconsistencies between species names, reported species ID number and WORMS (aphia ID), which was back reported to the data center. A helpful library is the R package *'worrms'* (Chamberlain and Vanhoorne 2023).

Another useful application of the WORMS registry applicable within B-USEFUL is the detection of new species, which appear in a certain area for the first time. Some working groups developed specific code to detect suchspecies[3]. However, it should be understood if new occurrences are derived from improvements in species identification, or reflecting true new occurrences. For example, WKABSENS noted that a number of species are not reliably determined to species level or are identified only to the genus or family level (ICES 2021). One possibility to overconme such issues would be to identify cases and analyse recordsat higher taxonomic levels.

Standardising haul-by-haul information

Within-survey standardisation

In multi-vessel surveys, standardisation between vessels is essential, as well as some level of calibration when different types of gear and equipment are deployed (Bagley et al. 2015). As Beverton and Holt pointed out (1957, p. 172 ff), "an accurate knowledge of fishing intensity is obviously important in studying the dynamics of fishery. .. For example, data containing statistics of actual fishing time would satisfy this criterion only if all vessels had the same fishing power." Calibration is required when alterations to trawl survey components may change catchability of the gear. Minor changes to the trawl gear may be expected to have little influence on catchability but, when major changes, or many minor changes are made simulatenously, inter calibration experiments may be needed. Calibration of bottom trawl surveys requires the estimation of a conversion factor that allows the catch per unit effort found by one survey vessel and gear combination to be related to another, usually on a species specific basis (Bagley et al. 2015, see also next section 'Between surveys').
Attention has been both attributed to fishing technology (vessel, trawl winches, electronic equipment), gear setup and net geometry in the water. Net geometry in the water depends on fishing depth (Berg et al. 2019). Sensors are required to measure the spread and height of different net components, typically expressed as door spread (guiding plates connected to net

[2] http://www.nodc.noaa.gov/General/CDR-detdesc/taxonomic- v8.html

[3] https://github.com/ices-eg/wg_WGBEAM/blob/master/New_Species_consistency.R

wings via bridles) or wing spread (actual horizontal opening of the net). Wing spread and net height are interdependent, and the drag of doors forcing the net wings open increases with depth. Electronic sensors attached to wings and doors measirung the distance between either allow for measuring all relevant horizontal net parameters.
For the calculations for a given survey dataset, the choice of effort metric can be evaluated by fitting two models to the haul-by-haul data including all factors that can explain changes in catch rates as explanatory variables (as. e.g. in (Berg et al. 2014). The two models should only differ in the choice of the effort metric, and the model that best explains the variation in data (best model likelihood) is the preferred option. Other effort metric could be be tow duration, fishing days etc.

Between surveys

Effects of gear selectivity (retainment as a function of cod-end mesh size, mesh shape, cod-end extension and diameter (Piet et al. 2009)) need to be omitted from CPUE time series by means of standardisation procedures (Maunder et al. 2006). Standardising haul-by-haul information between surveys can basically be achieved by modelling or assigning conversion factors. The latter is appropriate in most cases where historical trawling information is considered. Fock et al. (2014) assessed several factors that influence catchability of bottom trawls. Net selectivity is affected by, gear rigging (type of footrope, positioning of doors, net height in relation vertical habitat utilisation (Fock et al. 2002)) as well asspatial coverage and amount of catch affecting net clogging. Catchability of similar nets with similar rigging can be analysed by – amongst others – the catch ratio method (Fraser et al. 2007). Fock et al. (2014) compared two historical otter board trawls of 90 (OT90) and 115 meshes net mouth opening (OT115). The observed catch rate increase for the OT115 was attributed to the increased trawl size. To analyse changes in gear rigging and mesh size, results from comparative fishing experiments need to be acquired. Variability in conversion

Table 2: Catchability parameters and conversion coefficients to calculate IBTS unit CPUEs from historical data (Fock et al. 2014)

	Catchability parameters	Fish ecotype	GOV otter board trawl (IBTS standard gear)	Historical single codend otter board trawls (OT90SC, OT115SC)	Historical double codend otter board trawls (OT90DC, OT115DC)
(a)	Herding by doors	Roundfish, sharks	1	0.5-0.8	0.5-0.8
(b)		Flatfish, rays and skates	1	0.8	0.8
(c)	Swept area (speed and horizontal net opening	All	1	0.5	0.5
(d)	Retainment (Selectivity and inverse escapement)	Roundfish	1	0.9	1
(e)		Flatfish, rays and skates	1	1-1.1x	1.15 -1.5x
Conversion coefficients	Historic into IBTS GOV	Roundfish 1/(a x c x d)	1x	2.7-4.5x	2.5-4x
		Flatfish 1/(b x c x e)	1x	2.3-2.5x	1.7-2.2x

parameter estimates from different studies can be used to determine parameter ranges and to analyse the sensitivity of the mean CPUE estimate in relation to these ranges. Gear standardisations in order to combine different data series have been carried out for gear specific swept areas (Rijnsdorp et al. 1996; Rogers and Ellis 2000; ter Hofstede and Rijnsdorp 2011) or with regard to catchability parameters considered separately for different fish ecotypes and size classes (Greenstreet et al. 2007; Piet et al. 2009), thus referring to traits-based approaches in fisheries catch harmonization (Pecuchet et al. 2017; Maureaud et al. 2020). Combining both approaches (conversion factors and traits), catchability parameters for historical otter board trawls OT90 and OT115 can be determined in relation to the IBTS GOV trawl for two fish types, i.e. demersal roundfish and flatfish (Table 2). The example shows how herding through doors, bottom contact of footrope as a factor affecting catchability of benthic fish species like flatfish (Fock et al. 2002) and selectivity, as well as swept area as determined through towing speed and horizontal net opening, can be considered. Overall, the comparison of historical trawls with the modern ICES IBTS GOV trawls shows that the GOV is assessed to be more efficient mainly due its size and towing speed (Table 2).

With regards to modelling approaches, Gislason et al. (2020) showed how a Generalized Additive Model (GAM) can be used to identify the significance, functional form, and error structure of the relationship between the independent variables and species richness. The number of species recorded, $\mu_{i,j}$, in survey i, maximum length group, j, was assumed to follow a Negative Binomial distribution. It was furthermore assumed that $\mu_{i,j}$ could depend on a number of different variables. Hence:

$$\log(\mu_{i,j}) = \alpha + \sum_{1}^{k} s_k(E_k) + s_4(depth_i) + s_5(size_j) + s_6(asampl_i) + s_7(asurv) + s_8(density_{i,j}) + s_9(vertop_i) + s_{10,j}(mesh_i)$$

where α is a constant; E_k are environmental factors with respective parameter terms; $depth$ is depth (m); $size$ is midpoint of log maximum species size interval (cm); $asampl$ is area swept (km^2); $asurv$ is the total survey area (km^2), $density$ is the density of fish in survey i, maximum length group j; $vertop$ is the vertical opening of the trawl (m); and $mesh$ is mesh size (mm). The $s_1, \dots, s_9$ are general spline smoothers, while $s_{10,j}$ denotes that for each log maximum length group, j, a separate spline smoother was applied to describe the effect of mesh size on log richness.

This approach is similar to GLM approaches where certain factors (vessels, gear type) are accounted for (see next section).

Berg et al. (2014) applied a similar model to fish abundance, i.e.

$$g(\mu_i) = U(i)_{ship} + f_1(lon_i, lat_i) + f_2(depth_i) + f_3(time_i)$$

where U(i) accounts for the vessel factor, f1-f3 are regression splines to model environmental effects and g is the link function of abundance value µ of haul i. Replacing the lon-lat factor by a straum effect and including a further year effect leads to models to estimate survey abundance (see next setion). It should be also considered that, as reported in within-survey standardisation, catchability can also differ due to the different gears in use, with significan differences. To consider these differences among gears, WKABSENS classified gears reported in DATRAS in main categories to be further included in standardization models (ICES, 2021).

Standardising abundance data

Where (fisheries) management depends on time series of abundance, reliable indices based on catch and effort data are necessary to make informed decisions about sustainable fishing (Orio et al. 2017). After standardising haul information within- and between surveys (see previous chapter), aspects of survey coverage, i.e. spatio-temporal variability in sampling effort are to be considered in this section.

Core methods for abundance standardisation

GLMs and GAMs

Generalized Linear Models (GLMs) provide a fundamental tool for standardising catch-effort data. They help model the relationship between catch rates and various explanatory variables such as location, year, and environmental conditions (Maunder and Punt 2004; Venables and Dichmont 2004). GLMs assume a linear relationship between the explanatory and transformed response variables (for example, using log transformations). However, this assumption can be a limitation since real-world data often exhibit non-linear patterns that do not fit to a specific distribution function (for instance with excess zero's, although the Tweedie distribution family can handle zero-inflated data, other methods can also be applied, see section on delta methods). As a further method when linear assumptions do not apply, Generalized Additive Models (GAMs) provide another and more flexible alternative (Maunder and Punt 2004; Venables and Dichmont 2004). This because GAMs can capture non-linear relationships by incorporating smoothing functions like splines or loess smoothers. GAMs are particularly valuable because they do not require pre-assumptions about the shape of the relationship, making them useful for predicting spatial distributions of species based on environmental factors such as sediment type, temperature, or primary productivity. They can also model size-related factors like maximum length, which is critical for fisheries management (Maunder and Punt 2004; Grüss et al. 2014). One challenge with GAMs is that they require large datasets to avoid the risk of overfitting (Grüss et al. 2014). Because these models are commonly used for stock assessments, Potts and Rose (2018) compared three GLMs and three GAMs to see how well each model estimated population indices from fishery-independent surveys. They evaluated factors such as species occurrence, density, and abundance (Fig. 2). Their findings showed that GAMs, particularly those incorporating spatial data with smoothing splines, performed better at higher population densities. However, they also emphasized the importance of considering sample size when choosing the best model (Potts & Rose, 2018). In turn, robust results of (delta)GLM methods can be obtained if the interaction of spatial stratum and year is treated as random effect – this accounts for high spatial variability and low densities (Thorson 2019).

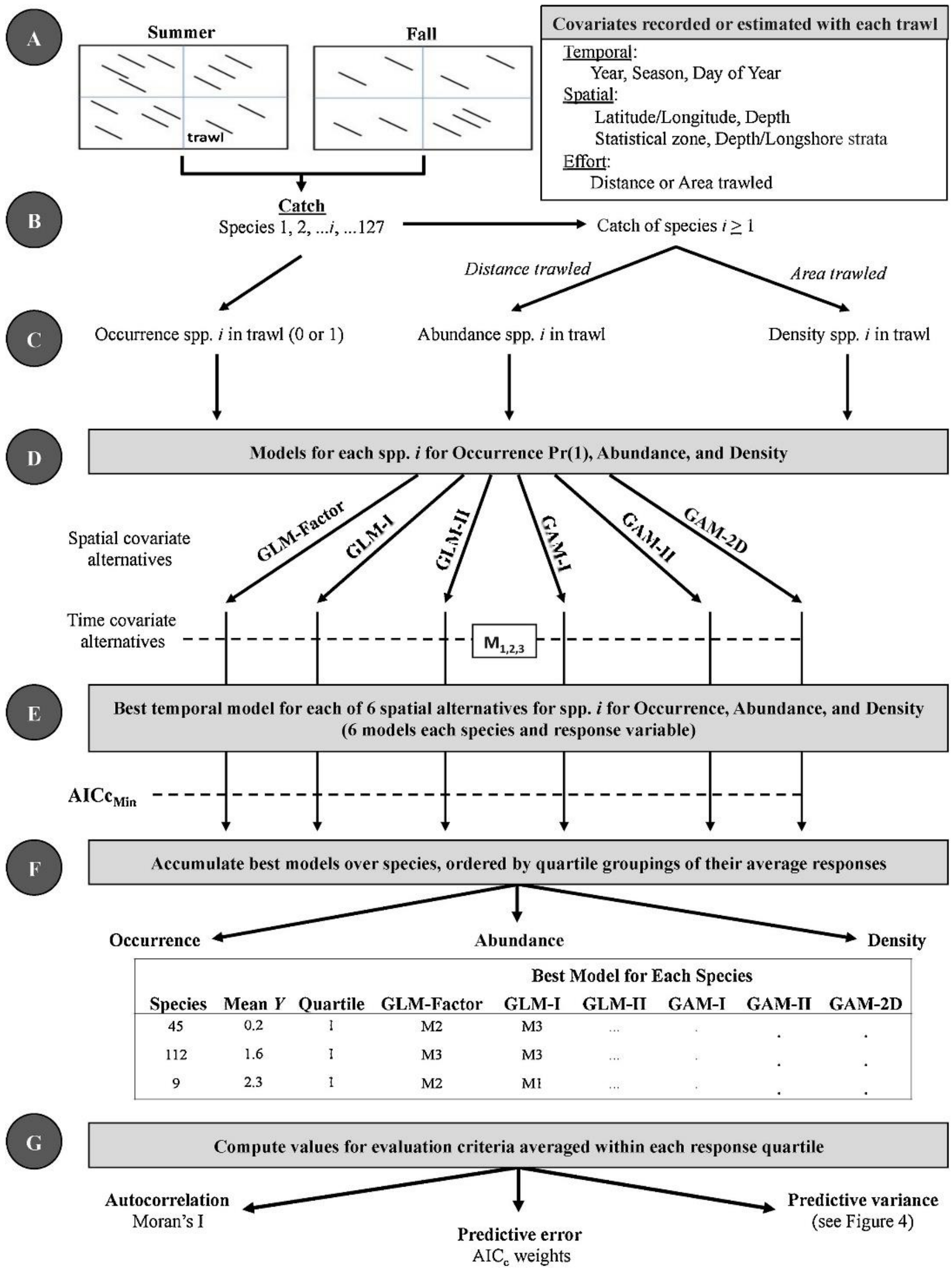
Delta approach

One of the most common challenges in catch data analysis is dealing with zero-inflated data sets. A useful method to address this, building on GAMs or GLMs, is the Delta approach. This two-step method was specifically designed to handle zero-inflated data and recognizes that the factors influencing whether a fish species is present might differ from those affecting its abundance when present (Maunder and Punt 2004; Grüss et al. 2014). The Delta approach fits two independent models: a binomial model based on presence/absence and a distribution model of non-zero values. The binomial model estimates the probability of encountering the target species using presence/absence data, typically with a logit link function (Grüss et al., 2014). When using trawl data, an offset is often added to account for variable sampling effort, which is common during research cruises or when combining data from multiple surveys. The distribution model of abundance, often quasi-Poisson, determines the abundance or biomass using only non-zero catch data and applies a log link function. The final abundance estimates are determined by combining the predictions from these two models using the delta method. Specifically, the product of the predicted probability of presence from the binomial GAM and the predicted abundance from the quasi-Poisson GAM yields the final abundance estimate. Depending on the study, factors like season or region can also be included, making this method highly adaptable (Grüss et al 2014). The two fitted GAMs are then combined using,

$$predicted\ (y) = p * u,$$

where y is the estimated abundance, p is the probability of species presence, and u is the predicted abundance. Grüss et al. (2014) developed this method to produce spatial distribution maps for ecosystem models like OSMOSE, testing it on pink shrimp in the Gulf of Mexico during

Figure 2: Overview of methods for selecting the best GAM and GLM models according to Potts & Rose (2018): A) representation of SEAMAP survey data; B) splitting trawls with zero and non-zero catch for each species; C) estimating the three response variables for each species in each trawl; D) three GAM and three GLM models with different representations of spatial and temporal covariates; E) selecting the best model for the 3 GAMs and 3 GLMs; F) ordering species by quartile average response; and G) presentation of median autocorrelation, prediction error, and prediction variances across quartiles for each of the six models.



summer. It has also been used to model the abundance and size of species like cod and flounder in the Baltic Sea using both historical and recent trawl data (Orio et al., 2017). This approach is easily applied when standardising catch data or CPUE (catch per unit effort), as seen in ICES DATRAS reports (ICES DATRAS report 2006). The Delta method offers several advantages. Ecologically, it provides a robust framework by separating the factors influencing species presence from those affecting abundance. Computationally, GAMs are more efficient than GLMs since they avoid iterative parameter estimation required by negative binomial models. Importantly, Delta methods handle overdispersion which is a common issue with count data where variance exceeds the mean (Grüss et al. 2014).

To address uncertainty in abundance estimates using the Delta approach, bootstrapping is a widely used and effective method. It helps estimate variability in abundance predictions and allows for the use of Spearman's correlation coefficient (ρ) to test for significant differences from zero (Grüss et al., 2014). Bootstrapping is particularly valuable when the distribution of an estimator is unknown or complex, or when traditional variance methods aren't suitable—for instance, when data aren't normally distributed since bootstrapping is a non-parametric test (Grüss et al., 2014). The bootstrapping process involves creating multiple datasets by resampling from the original dataset. In this process, some data points may be selected multiple times, while others may not be selected at all. For each resampled dataset, the Delta GAM approach (or other statistical procedures) is applied, generating multiple estimates of the abundance index. These sets of estimates represent an approximation of the sampling distribution, and uncertainty can be quantified by measuring the variability of these distribution estimates, such as calculating the standard deviation or confidence intervals (Grüss et al., 2014).Bootstrapping offers several advantages. Because it is non-parametric, it can provide robust estimates of covariance and works well with complex statistical models and asymmetric distributions. Furthermore, it avoids assumptions about data distribution and is relatively easy to implement, even for non-statisticians (Grüss et al., 2014).

Stochastic models

Instead of resampling the original data set, stochastic methods resample from a predefined parameter space. Thus, stochastic spatial models can be derived from the GLM framework applying Bayesian parameter estimation. Extending a generalized linear model (GLM) framework, a link function is defined that maps the mean of the response to the linear predictor (Cosandey-Godin et al. 2014). The stochastic component can be either realized through Monte Carlo Markov Chain (MCMC) resampling methods, or through integrated nested Laplace approximations (INLA). The sampling distribution of the parameters accounts for random effects not parameterized in the model. Given that random effects can be formulated either as process or observation error, a hierarchical design is obtained. INLA techniques appear superior to MCMC given that INLA uses an approximation for inference and hence avoids the intense computational demands, convergence, and mixing problems sometimes encountered by MCMC algorithms (Cosandey-Godin et al. 2014).

Autoregressive methods: VAST

The ' Vector Autoregressive Spatio- Temporal'-method (VAST) can be seen as a regression approach where point estimates are obtained via terms accounting for covariance among variables and spatial factors to account for spatial (or spatio-temporal variability) and environmental variables. It seeks to estimate variables occurring over a pre-defined spatial domain or stratum. VAST predicts population density for all locations sampled within this spatial domain, and then predicts derived quantities (e.g., total abundance, spatial concentration, or the centroid of spatial distribution) by aggregating population density across the spatial domain while weighting density estimates by the area associated with each estimate. A reference to geostatistical methods (next section) is the installation of an "extrapolation grid" after defining a spatial structure. The extrapolation grid accounts for all survey stations that have been previously analyzed and reaches beyond the realized current sampling scheme so that known environmental and habitat relationships can be included. A smoothing term resembling the gradient of the geostatistical variogram can be applied. VAST builds on the relationships between covariates, i.e.

fish species as well as environmental variables, and the spatial structure of fish populations. Interaction terms can be specified. Altogether, 15 modelling specifications can be selected (Thorson 2019).

Geostatistical data standardisation

In the previous chapters spatial structure was referred to by assigning strata or by inferring from environmental relationships. These strata as spatial units apply well mostly to one species only and its specific habitat requirements, but perform less well for others. Petitgas (1999) pointed at the pronounced similarities in maths between gridded sampling (Cochran 1977) and geostatistical methods in that both expand sampling to a grid covering the entire sampling domain in order to obtain an unbiased mean and variance. Spatial structure of the target assemblage and the geometry of the domain are not seprated. These methods are insensitive to sampling distribution and can deal with zero values in the sampling, given that the sampling is able to estimate the structure of the target assemblage. These methods assume stationarity, i.e. there is no trend towards the borders etc. This assumption is critical in light of the often applied stratified sampling acknowledging spatially different means (nonstationarity) and thus gradients in assemblage structure. Models with a drift component have been applied to solve for nonstationarity (Rivoirard et al. 2000), and it then depends on the drift function how well the spatial structure can be captured. Linear and polynomial functions have been considered (Rivoirard et al. 2000). Petitgas and colleagues (1999) developed two linear geostatistical models, EVA and EVA2, to estimate the global mean and its variance for differing sampling designs, most recently also as the package *RGeostats* (Petitgas et al. 2017). Because of the stationarity dilemma, geostatistical methods are preferably carried out in conjunction with a stratified sampling design to estimate straum means etc. A regular grid is recommended for within-strata design of sampling.

Standardising compositional data

Several methods exist to arrive at standardized length- and age-compositional data of populations.

Design-based methods

Design-based methods take into account the structure of the sampling scheme, i.e. different habitats, sexes, sampling vehicles, seasons etc. Design-based methods can be used in order to estimate the proportion at age for a population or the accuracy of abundance indices. But the approach that is used to determine this can differ, such as through simulation (Thorson 2014) or through implementation across multiple surveys (ICES 2012). In order to estimate the proportion at age from compositional data, the West Coast expansion method has been frequently applied (Thorson 2014). There are several steps to correct for differing sampling intensity to make sure that the data represents the composition of the entire population (Thorson 2014). These steps are taken within the data collection where compositional data (D_i) are collected for each trip, represented by *i*. This data generally includes age or length composition. The next step is weighting the sampling intensity in order to correct for differences in the proportion of the catch (that is sampled for age or length). This is done by multiplying the compositional data for each trip by the inverse of the sampling intensity for that trip (C_i/c_i). Strata weighting then takes place by multiplying this with the ratio of the total landings (L_s/l_s) to landing *s* in sampled trips within each stratum *s*. Finally, the expanded compositional dataset (D_a) represents the total expanded composition, which is determined by summing the expanded composition across all trips and strata as seen below and described in Thorson (2014), $\overline{D}$

$$\overline{D}_a = \sum_{i=l}^{n_i} \left(\sum_{s=1}^{n_s} I(S_i = s) \frac{L_s}{l_s} \right) \left(\frac{C_i}{c_i} \right) D_{a,i,}$$

which as seen is not a simple addition of raw data, but instead a carefully weighted aggregation that corrects for biases that can be due to uneven sampling, which realistically is often the case.

Normal approximation method & Dirichlet-Multinomial (D-M) Model

The Normal-Approximation method was proposed by Thorson (2014) in order to standardise compositional data and in particular to address variable sampling intensity and overdispersion. It is very useful because it provides unbiased estimates of the proportion at age and a model-based estimate of the effective sampling size. The Dirichlet-multinomial (D-M) model is another method that can be used for standardising compositional data and it is especially useful when there is overdispersion and different correlation structure (Hrafnkelsson and Stefánsson 2004; Thorson 2014). It is a hierarchical model that is better at dealing with complex covariance in a data set and estimates the true distribution of ages in a stratum and the variablility within sampling trips (Hrafnkelsson and Stefansson 2004, Thorson 2014).

Bootstrapping procedures

Bootstrapping as mentioned in the previous chapter on standardising abundance data, refers to the general bootstrapping procedure where resampling with replacement takes place from original data as well as test statistics and estimation of variability of the statistic (ICES 2012). Bootstrapping with regards to compositional data is to aggregate the data in order to represent the characteristics of a stock (eg. length at age), while taking to account different factors such as differing sampling intensities or other covariates (ICES 2012; Schwamborn et al. 2023). There are multiple assessments that can be used such as Length-at-Age Analysis (bootAA), Length-Frequency Analysis (bootLFA), Age Distribution by Length Class (ALK), general bootstrapping for Design-Based Estimators, and confidence interval calculation which will be discussed further here in terms of the current literature (ICES 2012; Thorson 2014; Schwamborn et al. 2023). Both bootAA and bootLFA estimate body growth, with bootLFA using age readings from otoliths and the latter using length-frequency data (Schwamborn et al. 2023). It has been shown that using otolith readings was over twice as precise when determining the van Bertalanffy growth coefficient ‘K’ and the corresponding asymptotic length ‘L∞’ than when using length (Schwamborn et al. 2023). Unfortunately, otolith readings are not very realistic in most cases because they are time consuming, are more easily available for some species than others, and growth rings on otoliths can differ between regions, especially when there is no strong seasonality (Schwamborn et al. 2023). The Fishboot R package can be used for data from both otolith readings and length frequencies. The function growth_length_age_boot estimates growth from otolith readings and the function ELEFAN_GA_boot estimates growth from length frequency (ie. to determine the best combinations of the growth parameters and to determine the confidence intervals (Schwamborn et al. 2023)).
Bootstrapping age distribution by length class (Age-Length-Key; ALK) is often implemented, especially with DATRAS ICES data (ICES 2012). For surveys, a large number of fish is measured and

a subset of this is aged through otolith readings. The ALK is then made from this data to relate the length to age (ICES 2013). The bootstrapping procedure is consequently used to create the ALK multiple times, so for each length class in a given area, the ages of the fish are resampled with replacement. For example, if there are 10 aged fish in a length group, 10 fish would be randomly selected from that group to yield a new age distribution, which is repeated 1000 times (Lehtonen and Pakhinen 2004; ICES 2012) and results in a distribution of Age-Length-Keys. The benefits of this method is that it is non-parametric, it can quantify uncertainty, and it deals well with complex processes (ICES 2013).

A general bootstrapping procedure can also be used for design-based methods, in order to estimate effective sample size (Thorson 2014). Data needed for this is compositional data that are collected across different regions, depths, etc. Resampling can take place in three different ways; within tows, tows within strata, and heierarchical bootstrapping which is a combination of the two aforementioned methods (Thorson 2014). The effective sample size can then be estimated by bootstrapping the original compositional data (Sterwart and Hamel, unpublished data within Thorson 2014) and the bootstrapped estimates can be used in order to determine the confidence intervals.

Standardising for diversity analysis

The description and the analysis of dynamcis of biodiversity for management purposes are among the major tasks of B-USEFUL. Diversity indicators useful for management purposes have been elucidated in B-USEFUL WP1 (see Table 3).Diversity measures are designed in order to describe the quality of a community, as either `complex' and `rich' or `simple'. Taxonomic species diversity measures depend on either on species numbers or on the relative abundances of species, while functional diversity depends on the combination of taxonomic diversity and biological traits (see section 'Harmonization of benthic traits').In B-USEFUL WP3, **taxonomic diversity in terms of species numbers** is applied as probability of occurrence (for concept of probability of occurrence also see section 'Delta approach') and species richness.**Taxonomic diversity in terms of relative species abundances** is either applied as index value, for instance the Hill numbers including Shannon diversity (Hill 1973) (see WP3) or in terms of species–abundance relationships (SNR) or species–area relationships (SAR). The latter was conducted in B-USEFUL deliverable D2.2 (footnote 4) in the meta-data section as standardised information of fisheries data by area and time period (see Figure 3)

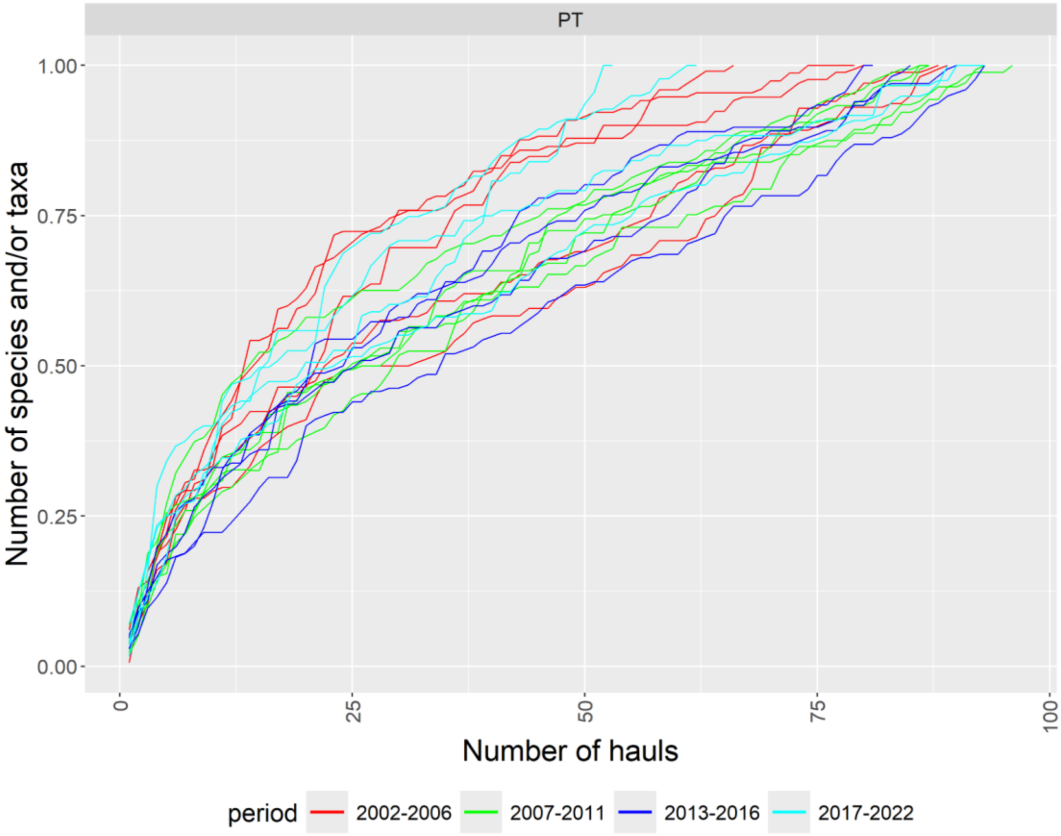


Figure 3 Species-sample accumulation curve as example of species-area relationship, here PT-IBTS Q4 survey, source: B-USEFUL deliverable D2.2.

Diversity is scale dependent (Hubbell 2001) so that local, regional and continental scale need to be considered, and metrics such as species numbers depend sample size.

Species numbers

If the samples are of different size (numbers of specimens collected), comparisons between samples can be achieved by relating species numbers to the smallest sample size by rarefaction (in Postel et al. 2000). Hurlbert (1971) applied the **rarefaction method** to a formula in which rarefied values are calculated for every species and summed:

$$R(n) = \sum_{1\ to\ i} \left\{ 1 - \left[\binom{N - N_i}{n} / \binom{N}{n} \right] \right\}$$

where R(n) is the number of species in the standardised (rarefied) sample, n is the size of the standardised sample, N is the total number of individuals in the original sample, and N_i is the number of individuals of species i. Though the formula seems complicated, the idea behind it is easy to understand. For each species the probability of not being in the sample after it is reduced to size n is subtracted from the probability of being in the original sample (which is 1). The difference represents the probability of being in the sub-sample.

For instance a thresholds T can be implemented to estimate R(n), i.e. in the rarefaction context the probability term

$$\left\{ 1 - \left[\binom{N - N_i}{n} / \binom{N}{n} \right] \right\}$$

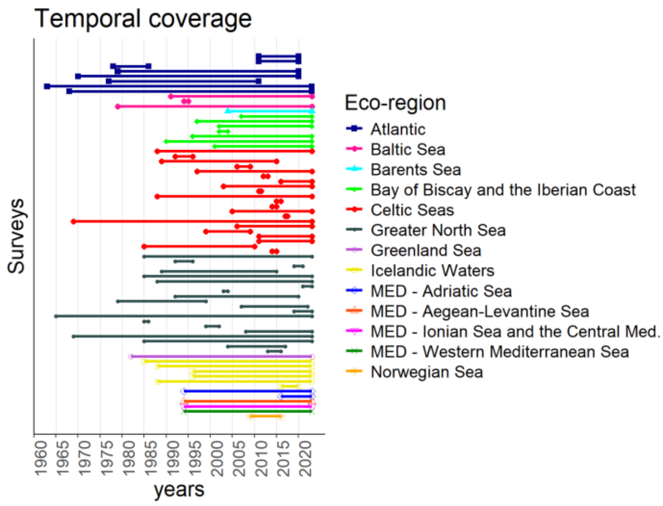


Figure 4 Example of analysing standardised meta-data of fisheries data series. Source: B-USEFUL deliverable D2.2.

must either exceed 0.5 (T>0.5, only counting abundant species) or is set to zero (T=0, counting all species). Instead of the rarefaction term, also frequency of occurrence can be applied to calculate probability, in this case scaled by sample number.

Rarefaction leads to a loss of information for the larger sample, i.e. total number of species etc. Problems arise when a number of sub-samples with different species dominance patterns are pooled and the species numbers for the sub-samples are recalculated from the pooled total. Rarefaction then can overestimate the rarefied species number for the sub-samples considerably

Table 3 Selection of B-USEFUL diversity indicators, excerpt from B-USEFUL milestone "M.1.3 Indicators of biodiversity and ecosystem services defined and delivered to WP3"

INDICATOR NAME	BRIEF DESCRIPTION	TYPE
Species distributions	The presence or absence of a species at a given space and time combination	Taxonomic
Species abundances	The abundance/biomass of a species at a given space and time combination	Taxonomic
Species traits	Within-species variation in trait measurements (e.g., in terms of morphology, physiology, phenology)	Functional
Community abundance/biomass	The total abundance of organisms in ecological assemblages (or functional groups)	Functional
Community weighted mean traits	The mean trait value of a community weighted by the relative abundances of species in an ecological community, landscape or region	Functional
Species richness	Number of different species represented in an ecological community, landscape or region	Taxonomic
Species evenness	Similarity of abundances of each species in an ecological community, landscape or region	Taxonomic
….		

(in Postel et al. 2000). In turn, rarefaction can be used to calculate a su•cient sample size (in Postel et al. 2000).

Metrics related to relative abundances of species

Indices as unidimensional features condensating diversity into one single value have often been critized (Hurlbert 1971; Green and Chapman 2011). The different indices can be ranked according to their capabilities of emphasizing rather abundant or rather rare species, i.e. the Hill family of diversity indices (Hill 1973). With regards to sample size, some indices cannot be calculated with non-integer numbers (e.g. Gamito 2010). Thus, chosing the appropriate sample scale is critical. Species-abundance relationships(SAD), as opposed to community assembly patterns based on rules for permitted overlap and un-allowed (niche) overlaps, provide a two-diemnsional metric of diversity. or with respect to power law relationships and fractal dimensions. So far, SADs in terms of Coleman curves can be analyzed in terms of a semi-log model (Gleason model). The semi-log model refers to the log-series distribution of species and is related to the Margalef index of diversity (Bandeira et al. 2013), which in turn is often applied to indicate environmental pressure effects. It resembles patterns predicted by the zero-sum multinomial distribution model in the neutral theory of biodiversity (Hubbell 2001), thus allowing to link SADs both to theory and practical application. The semi-log curves described by their inclination and offset can be arranged along a linear gradient ranging from oligotrophic deep-sea conditions to mesotrophic communities in shallow oceanic waters. Departures from the general figure can be explained as increases in disturbance and trophic status of the system. These coherent cross-system assembly patterns allow to define rules of change of diversity in a 2-dimensional figure.

4. Applications

Harmonizing meta-data and trait information in B-USEFUL deliverable D2.2[4]

For the trawl surveys compiled in D2.2, a two-step approach of quality checks took place.

Firstly, at the level of DATRAS and MEDITS survey data bases, quality check routine were applied before uploading data to the main repository.

Secondly, in order to achieve a consistent description of the data sets involved, a catalogue with 24 different categories was developed which permitted the comprehensive analysis of data sets (Figure 4). This activity was carried out as consistency checks between spatial objects of different themes with same level of detail (see section 'Consistency and the level-of-detail problem'). With regards to biological traits, in the Mediterranean Sea a comprehensive effort was made within the framework of the B-USEFUL project to compile a new set of ecological traits for marine species relevant for the basin, based on an existing trait framework expanding for Atlantic faunas. This initiative aimed to create a robust database, starting from the extensive list of species and taxa recorded in the MEDITS trawl survey, spanning the period from 1999 to 2021. The species list compiled from the survey includes nearly 1000 species. Among these, approximately 300 are teleostean fish, while the remaining species include significant macroinvertebrates such as cephalopods and crustaceans.For cephalopods, a total of approximately 60 species were included in the database, with all species recorded in the MEDITS survey retained. In contrast, for crustaceans, a more selective approach was taken. Only those species that appeared in more than 1% of the total samples were included, resulting in a selection of around 70 species (further details are in the D2.2).

Atlantic bottom trawl surveys

For comparisons across different bottom trawl surveys in B-USEFUL, tailor-made standardisations were applied to available bottom trawl data from the North Atlantic shelf region, as well as the Northeast Pacific to satisfy the specific needs of data input into the modelling analysis performed in WP3 using joint species distribution models (JSDMs). Below we briefly describe the standardization performed and presented in van Denderen et al.(2023).

To ensure a broad spatial coverage within and beyond European shelf seas publicly available bottom trawl data from the Northeast Pacific and North Atlantic shelf regions were collected (see Deliverable 2.2 for meta-data regarding European surveys). We selected all scientific surveys that sampled the fish community with otter trawls (Appendix , Table S1). For each tow in each survey, we selected all teleost and elasmobranch species. For the European and Norwegian surveys, we used length-based information per species and haul to estimate fish weight per tow. To estimate weight, we obtained relationships between length and weight for each fish species in each large marine ecosystem (LME) from FishBase (Froese and Pauly 2018). For missing information at the species or LME level, we used FishBase to infer the relationship between length and weight based on higher taxonomic groupings (genus/family) and wider geographic regions (FAO region, world). For all tows where weight estimates were also provided, we verified that the estimated weight based on length is a good proxy for measured weight. For the North American survey data, we used the provided weight per species per tow (note that length-based information can be

[4] https://b-useful.eu/library/deliverables/

obtained from the different data providers, but it was not necessary for the purpose of this project).

Correcting fish weights for differences in sampling area

We updated available processing scripts (Maureaud et al. 2019; Stuart et al. 2022) by standardizing all surveys per unit area to correct for differences in sampling area. For some North American surveys, species weight was already standardized per unit area to correct for differences in sampling area. For all other surveys, we estimated sampling area (in km^2) using information on wingspread, speed of vessel and tow duration. In many surveys, there was missing information on wingspread. For most trawl surveys in the Northeast Atlantic, we inferred the missing wingspread information per survey based on relationships between observed wingspread and doorspread, sweep length, depth, vessel and/or country. For most other surveys, we used a fixed reported wingspread (Appendix , Table S1). Differences in the quality of wingspread information per region can amplify differences in estimated fish biomass. Therefore, we verified that the biomass obtained from the trawl surveys compares favorably with biomass estimates from >100 stock assessments. This comparison indicates that despite the obvious uncertainties, the cross-regional differences in biomass are upheld.

Correcting fish weights for gear catchability

In addition to correcting for sampling area, we also updated available processing scripts (Maureaud et al. 2019) to account for potential differences in catchability. Species-based correction factors (hereafter termed catchabilities) were available for 80 species in the Northwest Atlantic (Link et al. 2008) and length- and species-based catchabilities were available in the North Sea for 128 species and 7 functional groups (Walker et al. 2017). The estimated catchabilities from the two data sources are generally in agreement with each other when compared at the functional group level (correlation coefficient is 0.76, Figure 5).

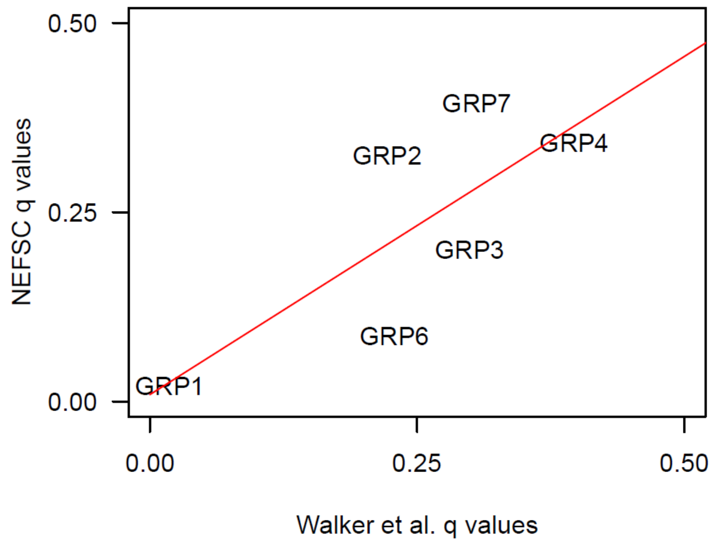


Figure 5. Estimated q-values per functional group based on data from the northeastern Atlantic and the North Sea for the GOV (Grande Ouverture Verticale) trawl type. Correlation coefficient is 0.76. Red line in the bivariate plot is fit using linear regression. GRP1 = Predominantly buried in sediment, GRP2 = On or near the seabed - anguilliform or fusiform, GRP3 = Predominantly on the seabed - flat, GRP4 = Predominantly close to the seabed, but not on it, GRP6 = Pelagic, GRP7 = Predominantly on the seabed - lumpiform. No species were classified as GRP5 (Midwater species with some seabed association) in the Northwest Atlantic dataset and this group was therefore not included in the comparison. Biomass estimates of all pelagic species (GRP6) were excluded in the main analysis.

We therefore assumed that the catchabilities can be used in the other regions to correct for catchability. For all species for which catchabilities were available at species or genus level, we corrected their biomass in the eastern North Atlantic with the length- and species-based catchabilities and in the western North Atlantic and Pacific with the species-based catchabilities. All other species were classified into one of seven functional groups, following Walker et al. (2017), and biomass was corrected using the functional group estimate.

Validation of biomass estimates

To validate the range and distribution of biomass estimates, we compared the observed trawl survey biomass with fisheries stock assessment biomass in the period 2000-2005. To this end, we created a spatial grid of equal area (6000 km^2) which was overlayed with the coordinates of the trawl surveys. We then calculated spatial overlap between the gridded surveyed area and the bounding region of all fisheries assessment areas from the RAM Legacy database (Ricard et al. 2012) (Figure 6). The bounding region polygons were taken from (Rising and Heal 2019). For each fisheries assessment area that overlapped at least 50% with the surveyed area, we obtained total biomass estimates of the assessed stocks (or spawning stock biomass when total biomass was unavailable) from the RAM database (2018). The biomass was then averaged for the period 2000-2005 and compared with the observed trawl survey biomass for the corresponding set of species during the same time period.

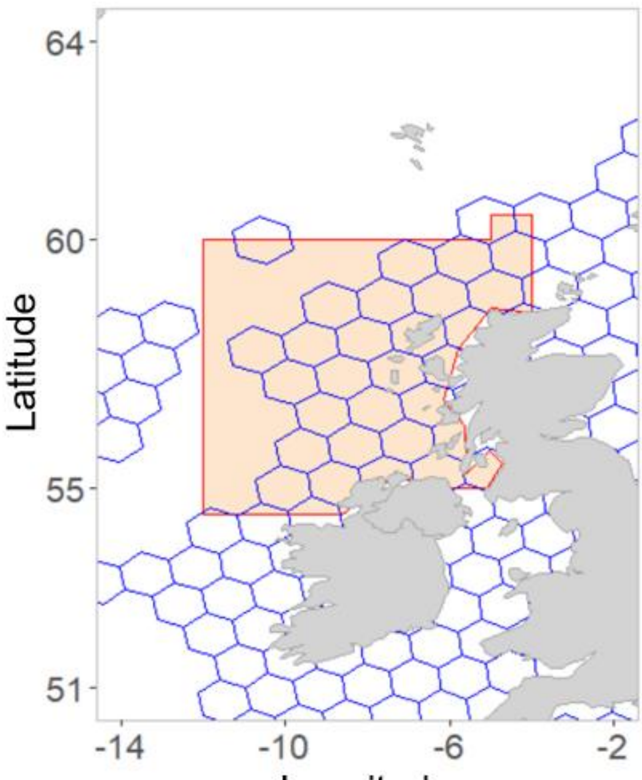


Figure 6 Example of overlap between surveyed grid and a fisheries assessment area in the Celtic Seas. The fisheries assessment area has assessment information for two stocks: Atlantic cod (West of Scotland) and Whiting ICES VIa. The percentage overlap is 68%.

We found that the uncorrected survey biomass estimates are generally lower than the stock assessment biomass, whereas the gear-corrected biomass has a reasonable match, and no bias, for most of the 120 stocks (Figure 7). The largest outliers in the latter are some reef/rock associated fish with a small stock size. However, these fish are of limited importance for total community biomass in most regions. The reasonable match between gear-corrected biomass and assessment biomass is upheld when separately analyzed for 1) the Northeast Pacific and the two North Atlantic shelf regions, 2) pelagic (mainly herring) and demersal fish stocks, and 3) for stocks where the fisheries assessment area overlaps at least 80% with the surveyed area (Figure 8). Taken together our finding provides confidence that the gear-corrected trawl survey estimates across the North Atlantic are comparable across areas and surveys and can be used to evaluate cross-regional patterns as part of WP3..

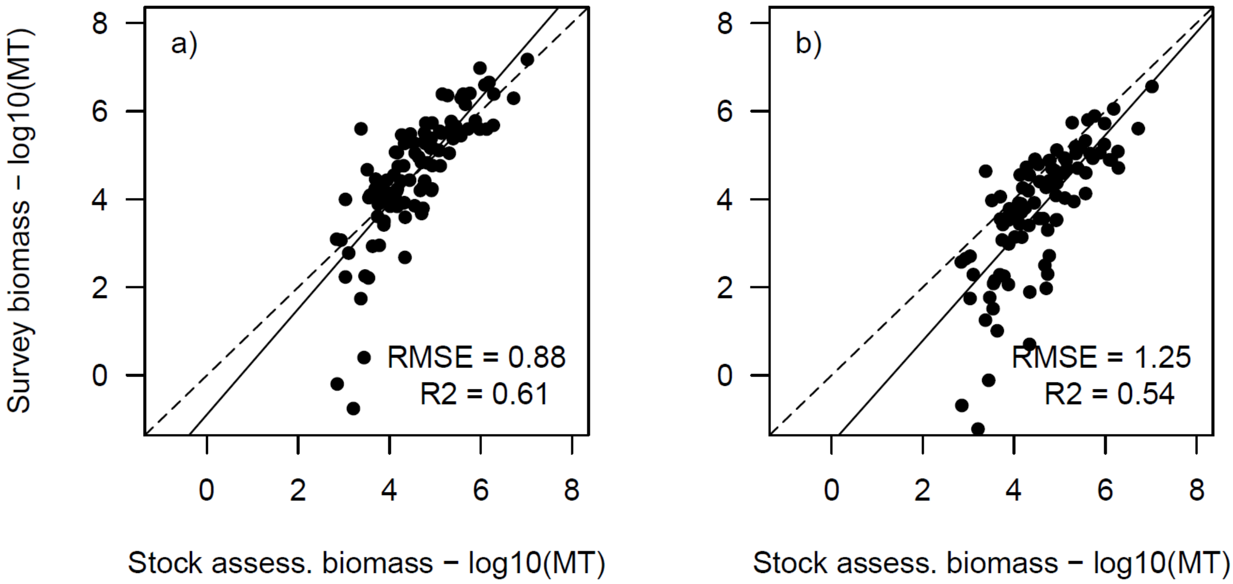


Figure 7 Comparison of fish stock biomass based on stock assessment data from the RAM legacy database with survey biomass with (a) and without (b) gear-corrected catchabilities. The dashed lines are the 1:1 line, and the solid lines are a linear fit. Biomass is mean biomass in metric tonnes (MT) between 2000-2005. R^2 is the coefficient of determination, RMSE the Root Mean Square Error.

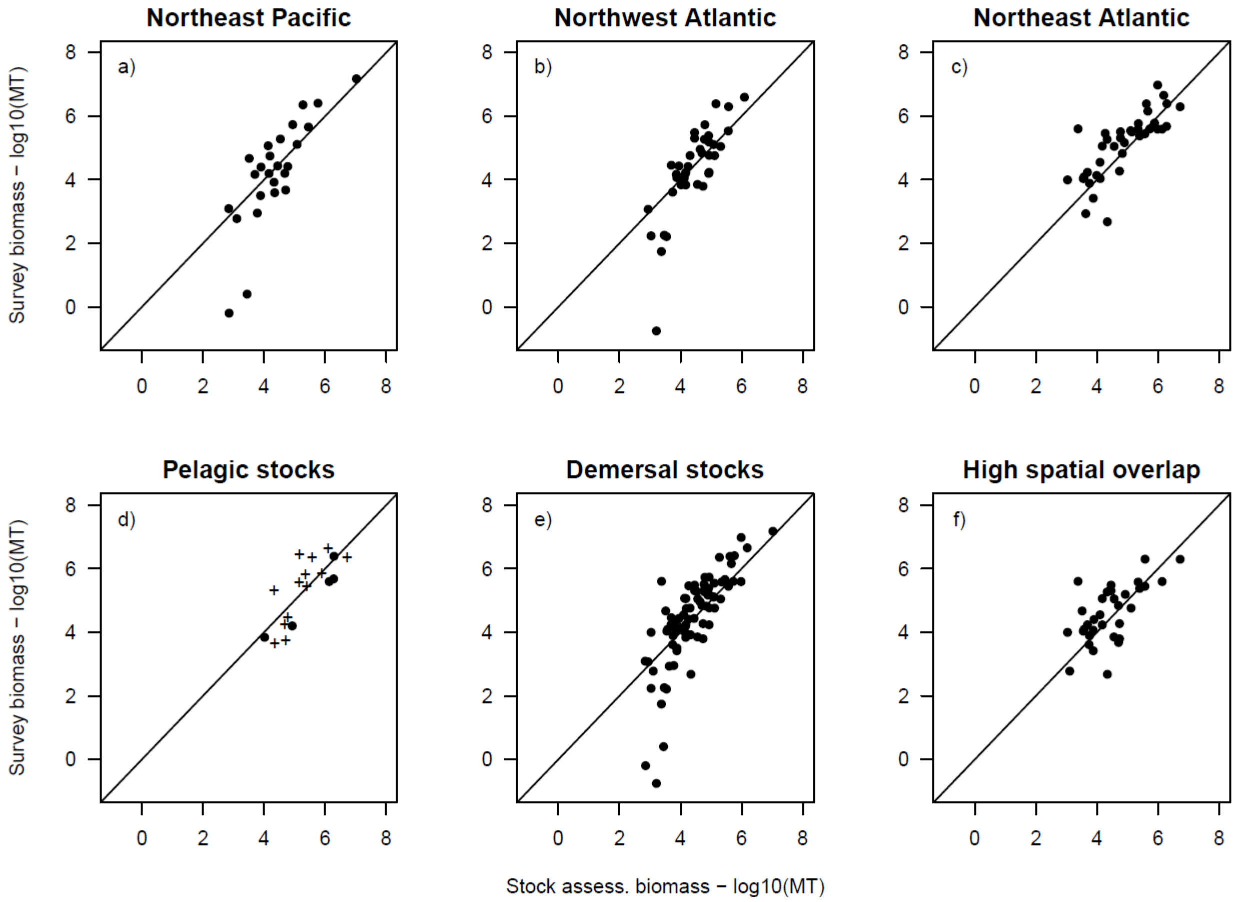


Figure 8 Stock assessment comparison with gear-corrected trawl survey biomass when separately analyzed for 1) the northeastern Pacific (a), the northwestern Atlantic (b) and northeastern Atlantic (c), 2) pelagic, mainly herring (marked with +) (d) and demersal fish stocks (e), and 3) for stocks where the fisheries assessment area overlaps at least 80% with the surveyed area (f).

Data model of new benthos data of the German Bight and Wadden Sea/North Sea (Wadden Sea data set)

B-USEFUL in the first place focusses on existing benthic data from the Greater North Sea already implemented in the EMODnet framework including a habitat classification map(e.g. Vasquez et al. 2021) and from the Mediterranean. This is complemented by another data set compiling benthic infauna data from the shallow part of the German Bight and Wadden Sea/North Sea hitherto not covered by the EMODnet NSBS, North Sea Benthos Survey data[5].

Data model

The data set comprises observations of 471 benthic infauna sampled in the German Wadden Sea, 2019 to 2021, at stations, organized in 3 data tables. All samples were sampled with the same gear, which is specified in the 'ENDOFAUNA' table. The 'STATION' table contains also date and time. 'STATION', 'SEDIMENT' and 'ENDOFAUNA'-tables are indexed via the station ID, *STATID*. To filter the stations in the 'STATION' table, a *purpose* has to be selected.

[5] https://emodnet.ec.europa.eu/geonetwork/static/api/records/6d617269-6e65-696e-666f-000000000067

Consistency checks

Within-data set checks were carried out with regards to taxonomy (misspellings), data checks (outlier detection etc) and location data (outlier detection).To provide consistency between data sets, three different consistency checks were undertaken, i.e. taxonomy harmonization in relation to WORMS (see section 'Harmonizing species names'), European Nature Information System habitat classification (EUNIS) and biological traits (see next section).
The **taxonomic consistency** check included checking for synonyms and for cryptic species groups. With regards to synonym checks, some differences appeared between the annotated checklists available for the region (Zettler et al. 2018) and the respective red lists (Rachor et al. 2013). For instance, the bivalve *Macoma balthica* (L., 1758) (AphiaID: 141579), which is the accepted name by WORMS, is synonym to *Limecola balthica* (AphiaID: 880017). For each synonym, the respective AphiaIDs were presented.

With regards to cryptic species groups, these are indicated by the name qualifier 'agg.' (Sigovini et al. 2016). This refers to a group of related species characterized by unclear boundaries, typically due to phenotypical similarities. Three major aggregate species groups appeared in the Wadden Sea data set:

- *Tubificoides pseudogaster* agg. (Annelida, Clitellata): In monitoring ring test studies, this aggregate has been established for practical reasons, since an exact determination in this aggregate can be mostly achieved with mature specimens. Therefore, *Tubificoides* spp. that lack papillations and have only bifid chaetae are recorded as *Tubificoides pseudogaster* agg. (Tim Worsfold 2003).

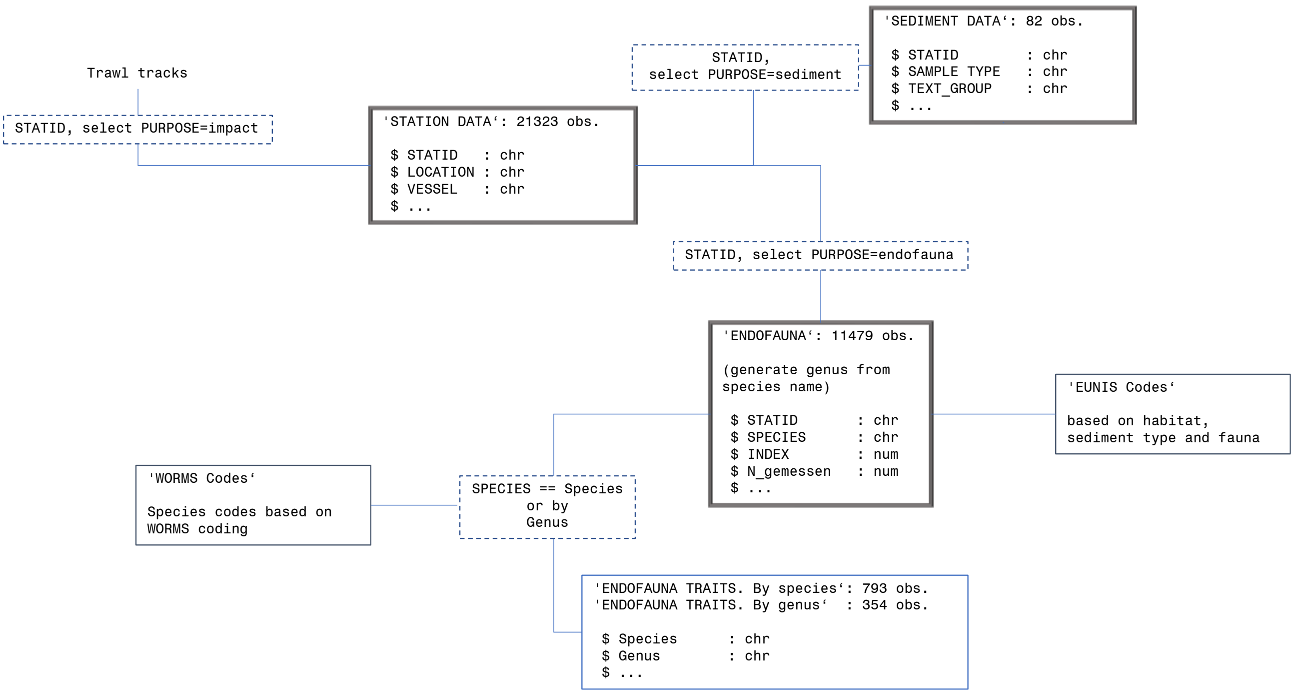


Figure 9 Data model for the endonbenthic fauna contained in the Wadden Sea data set. Indexing variables are indicated in boxes with broken lines, data tables have bold lines and attribute tables are indicated by thin lines.

- *Scoloplos armiger* agg. (Annelida, Polychaeta): The common polychaete worm *Scoloplos* cf. *armiger* is a cryptic species complex comprising entirely different developmental modes: holobenthic and pelago-benthic development (Luttikhuizen et al. 2011). In the northeast Atlantic, three putative species have been described on the basis of molecular data and a breeding study. The three putative species have been identified with respect to habitat preferences, i.e. the intertidal clade with holobenthic development, the type clade and the subtidal clade with a pelago-benthic ontogentic development. However, the overlap in habitat utilization is high in particular between inter- and subtidal clades (Luttikhuizen et al. 2011).
- *Capitella capitata* agg. (Annelida, Polychaeta): As for *Scoloplos armiger* agg., the *Capitella capitata* sibling species are found to occur in the same habitat (Gamenick et al. 1998). Three different morphotypes can be distinguished by means of body size, i.e. types, S, M and L. Whereas S lives close to the surface, type L dwells deeper in the subtstrate. In normal grab samples for monitoring purposes, this distinction cannot be made.

It is clear, that aggregate species cause problems in defining biodiversity indicators such as species numbers correctly.

Habitat classification was carried out based on the most recent revision of the EUNIS system from 2022[6]. According to the INPSIRE framework, spatial data model have to provide characterisation of geographical areas being functional for living organisms in two different categories: biotopes being the spatial environment of a biotic community; habitats being the spatial environment of specific species. The link to INSPIRE is defined as such, that in order to achieve harmonization on local, national and international level, habitat types should refer to the the European Nature Information System habitat classification in the first place, but could also use Habitats Directive 92/43/EEC and Marine Strategy Framework Directive 2008/56/EC as a reference.[7] This makes sure that habitat classification in all reference systems are compatible.
Biotopes were defined at EUNIS level 5 (MXxxxx, M=marine, X inter- and subtidal classification, x = biotope digits) referring to three types, i.e. MB5233 ("Nephtys cirrosa and Bathyporeia spp. in Atlantic infralittoral sand"), MB3237 ("Dense Lanice conchilega and other polychaetes in Atlantic tide-swept infralittoral sand and mixed gravelly sand "), and MB5235 ('Echinocardium cordatum and Ensis spp. in Atlantic infralittoral slightly muddy fine sand"). Only EUNIS level 4 and 5 classification is considered precise enough to meet conservation targets of the Habitats Directive and MSFD (OSPAR Commission 2012).

Harmonization of benthic traits

Biological traits were compiled for the Wadden Sea data set, providing new information for 49 species.

Next to classical community analysis, the analysis of functional diversity and ecosystem functions within a community has turned into the focus of ecosystem ecology and has become the central topic of ***'biological traits analysis'*** (BTA) (Bremner et al. 2006; Frid et al. 2008; Bolam et al. 2014). Traits as characteristic quantifiable features of species or of higher taxonomic classification levels allow to aggregate these functional characteristics across communities and ecosystems. The quality of BTA depends on the level of expertise while evaluating traits and linking them to the

[6] https://www.eea.europa.eu/data-and-maps/data/eunis-habitat-classification-1/eunis-marine-habitat-classification-review-2022/eunis-marine-habitat-classification-2022
[7] https://inspire.ec.europa.eu/theme/hb

desired taxonomic level, which grossly depends on expert knowledge (de Juan et al. 2022). Hence it is recommendable to work on existing inventories and modify/standardise them accordingly.

The aim of BTA is to replace the abundance matrix by a corresponding trait matrix, also known as *'trait by species'*-matrix or *'trait-based approach'*. This allows to trace changes in community functioning in either way, i.e. from species→trait and from trait→species.
BTA comprises characteristics such as feeding, body sizes, longevity, reproduction mode and many more, depending on the scope of the analysis. As such, multiple classification schemes for the same species assemblage are possible.
The quantification of traits is conducted in terms of *'fuzzy-coding'* (Chevenet et al. 1994). For each trait, the performance is indicated by a rank on ordinal scale, representing the response strength or performance category (='modality' *sensu* Beauchard et al. (2023)). Values normally range between 0 (no evidence) to 4 (complete, always) or are assigned to categories (e.g. "burrowing depth 5 cm"). For instance, the decapod *Carcinus maenas* mainly moves by crawling but may also swim over short distances, thus for adult movement it receives "swimming" = 1; "crawling" = 3; "burrowing" = 0; "attached" = 0 (in Neumann et al. 2016). These scores are normalized to 1 within a category group (=proportions) and then multiplied with the abundance or biomass value (Chevenet et al. 1994).

Three different data sets are acquired. The first compilation is from Shojaei et al. (2015) for benthic fauna of the German Bight. Data were available upon request from the originator from PANGAEA [8]. More than 330 species are contained in this data set. However, for the purpose of this analysis the data set was not complete with regards to species coverage and thus was complemented by a data set on genus level, i.e. the CEFAS *'traits'*-data set (Clare et al. 2021). For B-USEFUL purposes, a third data set with about 812 species was used (Beauchard et al. 2023), focussing at ecosystem-engineering functions altering seafloor and creating habitat structure.

Overlap between the three trait classifications is limited (**Fehler! Verweisquelle konnte nicht gefunden werden.**). Even in cases where the same category type is addressed (e.g. 'maximum size'), different numbers of modalitities (4 in Shojaei et al. (2015) and 6 in Clare et al. (2021)) make is necessary to harmonize modality sets. The R software package *Btrait* (Soetaert and Beauchard 2023) can be applied to manage the Beauchard et al. (2023) data set.

Missing trait information was collated from literature data (size, habitat features), was assumed from congeners or at level of same family (Oligochaeta, Naididae). Traits were completed for 49 endofauna species with a frequency of occurrency > 0.03 in the Wadden Sea data set.

[8] http://doi.pangaea.de/10.1594/PANGAEA.813419

Table 4 Trait classifications of three different trait concepts for North Sea benthic fauna.

Category	Number of modalities by category in Shojaei et al. (2015)	Number of modalities by category in Clare et al. (2021)	Number of modalities by category in Beauchard et al. (2023)
Feeding habit	8	6	
Environmental position	3	4	
Adult movement	4	4	
Diet type	3		
Larval devlopment	3	3	
Sexual differentiation	3		
Adult longevity	4	4	5
Age at maturity	4		
Fecundity	6		
Maximum size	4	6	6
Body mass			6
Morphology		6	
Egg development		4	
Living habit		6	
Bioturbation mode		5	
Substrate depth			5
Biodiffusion			3
Downward conveying			3
Upward conveying			3
Regeneration			3
Bioerosion			4
Biodeposition			3
Biostabilisation			3
Ventilation/Pumping			3
Burrow width			4
Endo-bioconstruction type			8
Endo-bioconstruction depth			5
Epi-biocontruction type			8
Epi-bioconstruction extension			6
Epi-bioconstruction extension size			7

Data access

Trait data are uploaded to ZENODO (Fock 2025).

Endofauna data upload to PANGAEA, DOI assignment pending (**PDI-40483**).

Data model of the ICES – DATRAS database

DATRAS is an online database of trawl surveys with access to standard data products (see online : ICES 2001).DATRAS (the Database of Trawl Surveys) has been developed to collate and document the survey data, assure data quality, standardise data formats and calculations, and ease data handling and availability (Daan et al. 2001). With the possibility for instant remote access, the data from DATRAS are used for stock assessments and fish community studies by the ICES community and public users. DATRAS stores data collected primarily from bottom trawl fish surveys coordinated by ICES expert groups. The survey data are covering the Baltic Sea, Skagerrak, Kattegat, North Sea, English Channel, Celtic Sea, Irish Sea, Bay of Biscay and the eastern Atlantic from the Shetlands to Gibraltar. At present, there are more than 45 years of continuous time series data in DATRAS, and survey data are continuously updated by national institutions. Data products (such as CPUE per area or indices) and raw data, can be freely downloaded according to the ICES Data policy (see online : ICES 2001).

Data model

The data model consists of four tables (Figure 10), i.e.

HH record type

There are more than 65 available fields in this record type. These represent the haul characteristics, such as date, time, coordinates, gear specifications, haul duration and distance, and environmental conditions.

HL record type

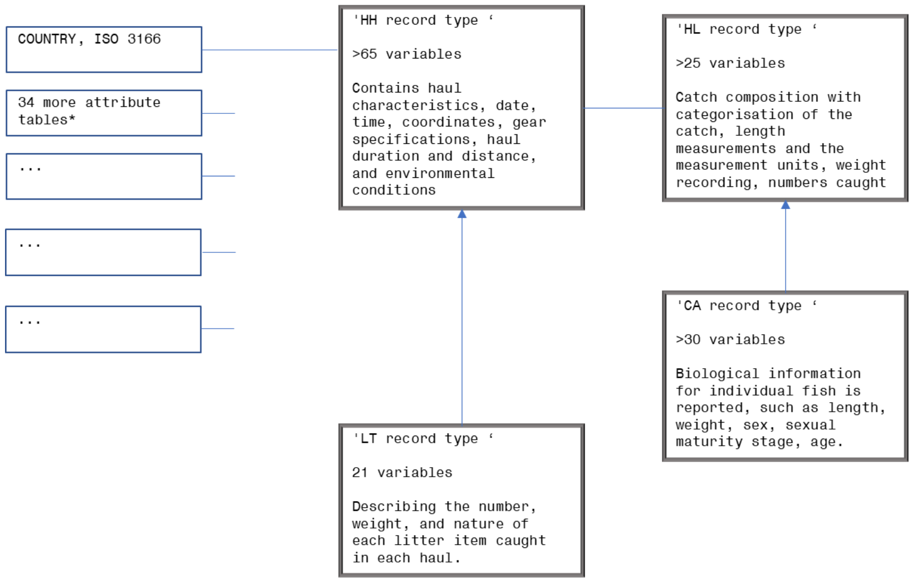
There are more than 25 available fields in this record type that allow among others for recording subsampling and categorisation of the catch, length measurements and the measurement units, weight recording, numbers caught.

CA record type

In the CA record type, there are more than 30 available fields. This record type is linked with HL records by species and length class. In the CA record type, biological information for individual fish is reported, such as length, weight, sex, sexual maturity stage, age. When a species is reported in CA, also a record in HL should be available for that species, even if all information is marked as '-9' (missing information).

LT record type

Litter data records are submitted in separate files and consists of 21 fields describing the number, weight, and nature of each litter item caught in each haul. For the submission to be successful the corresponding HH records must already exist in the database.



*https://vocab.ices.dk/?CodeTypeRelID=98&CodeID=33966

Figure 10 Data model for the ICES DATRAS data base. Data tables have bold lines and attribute tables are indicated by thin lines.

Consistency checks

DATRAS has an integrated quality check utility. All data, before entering the database, have to pass an extensive quality check (Figure 11). Unit specifications and their attribute tables are defined and provided (ICES Data Centre 2021).

Data submitters have to comply with submission standards. Each submission consists of data from a single survey, country, year, quarter, ship and gear.Submissions require a single file with the three record types one after the other, each one preceded by a row of headers. The three record types (HH, HL and CA) are linked by a few common fields, including those identifying the submission plus the haul and station IDs.

A spreadsheet provides the descriptions of all the available fields in the DATRAS format including a template file with all headers (ICES 2001). Before uploading a file, data is checked by a screening utility called DATSU. The list of DATSU checks differs between surveys. Results are displayed to the user and can be errors which are non-compliances with the survey type standards which must be corrected, or warnings that are non-critical errors accepted by submitter and can uploaded as-is into DATRAS database with or without later resubmission or correction.

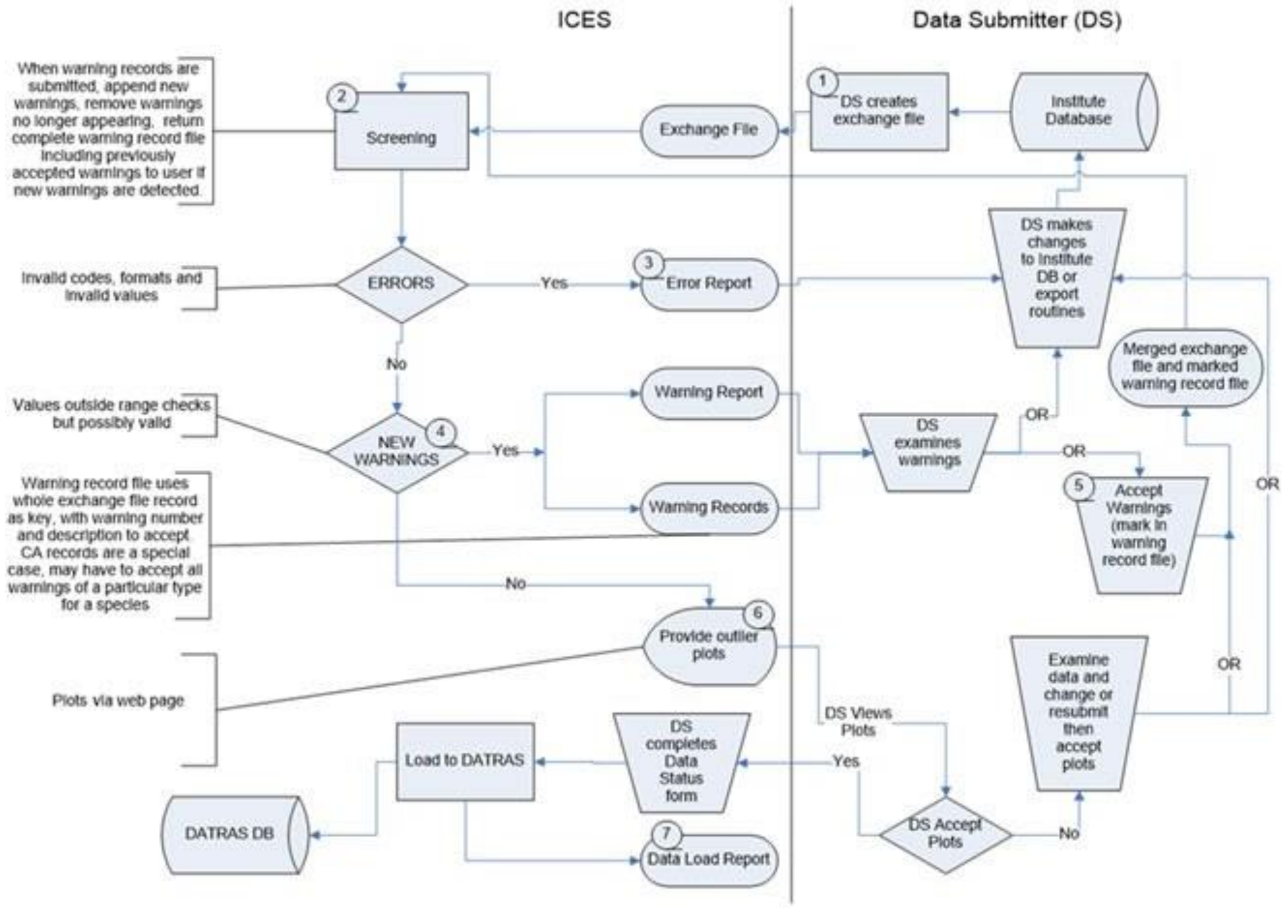


Figure 11 Pre-submission consistency checks in the DATRAS data base.

Data users can apply a library, the R package *icesDATRAS* (Millar et al. 2023). This package provides three different optional consistency checks before data can be retrieved, i.e. *checkSurveyOK*, *checkSurveyYearOK*, *checkSurveyYearQuarterOK*. These functions check a quarter and/or year and/or survey name against a list of all survey-year-quarter combinations in the DATRAS database before data queries can executed. If the combination is not matched it puts up a message showing the available options.

Data access

The data repository DATRAS is publicly available under a CC BY[9] license, see host website of the International Council for the Exploration of the Sea (ICES) (https://datras.ices.dk) and related meta-data records[10].

Data model of Mediterranean trawl surveys MEDITS

The MEDITS survey (Mediterranean International Trawl Survey) is a long-term scientific monitoring program established in 1994 to assess demersal fish stocks and ecosystems in the Mediterranean Sea (Bertrand et al. 2002; Spedicato et al. 2019). It is conducted annually across several Mediterranean countries, according to a standardised and well defined sampling protocol. In most areas, commercial bottom trawl vessels are used, all using the same gear type and doors. The surveys collect data on species abundance, biomass, and biometric data at individual level (length,

[9] https://creativecommons.org/licenses/by/4.0
[10] https://gis.ices.dk/geonetwork/srv/eng/catalog.search#/search?any=datras

sex, sexual maturity stage), providing the basis to assess population demography and crucial information for stock assessment.The MEDITS survey, established in 1994, originated as a collaborative programme among Mediterranean countries, initially involving France, Spain, Italy, and Greece (Bertrand et al., 2002). Over time, it expanded to include a total of 8 countries (Slovenia, Croatia, Malta, and Cyprus joined), ensuring a more comprehensive spatial coverage of the Mediterranean basin covered by EU countries (Spedicato et al., 2019). The survey spans the depth range 10 to 800 meters, from coastal waters to deep-sea environments. With over 30 years of data collection since its inception in 1994, the MEDITS dataset covers an extensive time series, allowing for the long-term analysis of species distribution and population structure of main fish, crustacean and cephalopod species.

Data model

The MEDITS data model is a structured system designed to manage the complex data collected during the surveys. It ensures uniformity in data collection, storage, and analysis across different research institutions and Geographical Sub-Areas (GSAs, as defined by the General Fisheries Commission for the Mediterranean (GFCM). The data model is built upon a relational database structure, enabling seamless exchange of fishery-independent data (MEDITS working group, 2017)[11]. It is designed to accommodate biological and technical data, ensuring that all aspects of the survey are well-documented and accessible for analysis.The MEDITS data exchange format is organized into multiple interconnected tables, each with a specific role in structuring and storing survey information. The TA table serves as the core of the database, containing metadata for each haul, including vessel specifications, gear configurations, and environmental conditions, which form the basis for all subsequent data entries. The TB table documents all captured species per haul, providing information on total weight and number of individuals caught. The TC table expands on this data, but focuses mainly on target species, detailing their size distribution, aggregating data by sex, maturity stages, and length classes, while also documenting any sub-sampling applied to the catches. Since the TC table is derived from the TB table, it cannot include species not already recorded in the TB table.

Building on this structure, the TE table captures even more granular biological details, recording individual-level characteristics such as age, weight, and additional biological metrics. However, it remains strictly dependent on the TC table, meaning it only provides additional insights into species already listed in the TC table, which, in turn, must be present in the TB table. This hierarchical dependency ensures that all individual fish records are directly linked to higher-level aggregated species information, preserving consistency. Lastly, the TL table provides an environmental perspective by documenting marine litter encountered during hauls, directly associating debris records with the respective haul data (TA table).

[11] https://www.sibm.it/MEDITS%202011/docs/Medits_Handbook_2017_version_9_5-60417r.pdf

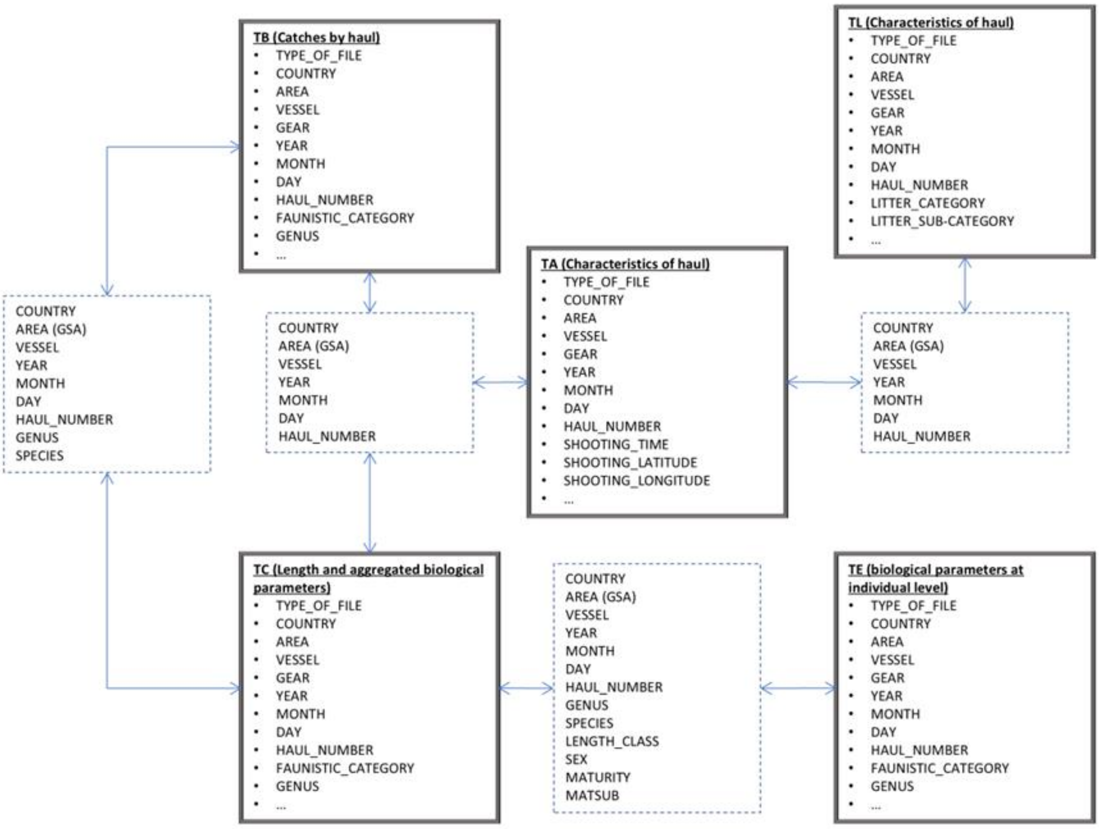


Figure 12 Data model for the MEDITS data base. Indexing variables are indicated in boxes with broken lines and data tables have bold lines. Attribute tables not shown.

Consistency checks

- To ensure data quality across the MEDITS database, before using them in the B-USEFUL project, a standardised validation framework for data consistency has been implemented specifically to be implemented on the TA, TB and TC tables received following a dedicated cata call for MED & BS data submitted to DGMARE.
- A fundamental tool in the MEDITS data validation process is the R-package *RoME* (Zupa et al. 2024)[12] which automates data consistency checks and error identification. This package, developed in agreement with the MEDITS survey handbook (MEDITS working group, 2017), is now embedded in the RDBFIS regional database for the Mediterranean, ensuring a standardised approach to data validation and harmonization. RoME applies a series of data consistency checks across multiple variables, cross-referencing species composition data, verifying measurement units, and detecting inconsistencies in haul positions. Additionally, the validation process assesses data coherence within and between tables, implementing automated checks, error flagging, and structured correction procedures to mitigate inaccuracies that may arise from data entry errors or inconsistencies also in numbers and weight of catches, ensuring that all recorded species follow expected distributions and align with reference taxonomies.
- To ensure comparable data quality standards in B-USEFUL, common methods and procedures were applied to MEDITS data to automatically flag and correct errors. The validation process involves

[12] https://github.com/COISPA/RoME

verifying haul positions and distances by cross-checking them with haul duration, identifying any inconsistencies in recorded values, and making corrections when discrepancies are detected. Species taxonomic classifications are validated against the reference list of species for the MEDITS survey (TM list of species). Length classes are also validated by comparing them against expected species distributions, adjusting any values that fall outside plausible ranges.

- Further quality checks ensure consistency between the number of individuals and their corresponding weight in the TB table. Any discrepancies between reported numbers and weights are resolved by recalculating totals using species-specific length-weight relationships. Because the TC table is dependent on the TB table, a cross-verification process ensures that all species listed in TC are also present in TB. If a species appears in TC but not in TB, potential misclassifications are reviewed and addressed, when necessary. Validation also extends to subsampling in the TB and TC tables. The number of individuals raised in TC must match the total count in TB, and any inconsistencies caused by rounding errors or incorrect weight measurements are first corrected at the weight level to maintain alignment. The verification process also checks hauls depth data to ensure that start and end depth values remain consistent within the same stratum.
- Consistency checks of categories applied in the MEDITS and ICES frameworks for marine litter and stock assessment standards have been applied (Spedicato et al. 2019, 2020).
- This common protocol was applied by the partners involved in B-USEFUL.This validation process ensures that all MEDITS survey data meet the highest quality standards before integration into the analytical workflow, enhancing the accuracy and consistency of species composition, abundance and biomass estimates improving the reliability of modeling and biodiversity analyses conducted within B-USEFUL project.

Data access

Joint Research Centre Data Catalogue - EU Mediterranean and Black Sea Fisheries Independe... - European Commission under an open access license (European Commission Joint Research Centre (JRC) 2025).

https://data.jrc.ec.europa.eu/dataset/f25092c4-3f0f-449f-ba60-5fbfe385defc

5. Conclusions

The objectives of the current deliverable were fulfilled as detailed below:

- Provide an overview of main standardisation and harmonization techniques applied in biological oceanography and fisheries science.
- Provide an overview of standardisation and harmonization principles in line with EU policies on infrastructure for spatial information and environmental data (INSPIRE, EMODnet).
- Provide detailed information how this was achieved in B-USEFUL deliverables and WP products.
- Provide information on data models for speficic data sets necessary to conduct standardisation and harmonization. This includes information on study specific designs, standard operating procedures, data collection methods, and metadata on variables, e.g. variable names, variable description, data type, data format, etc.

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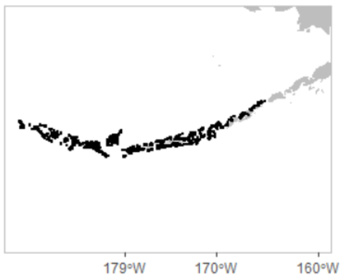
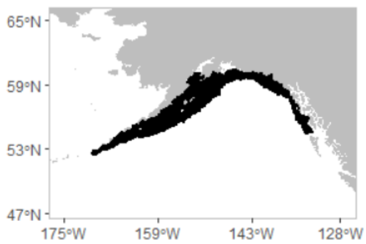
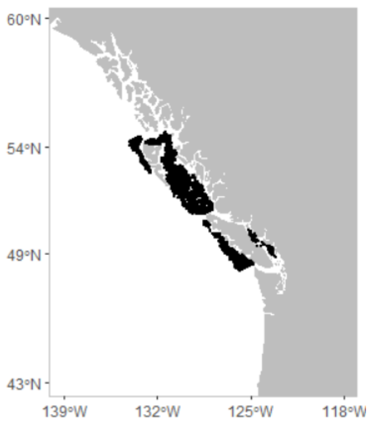
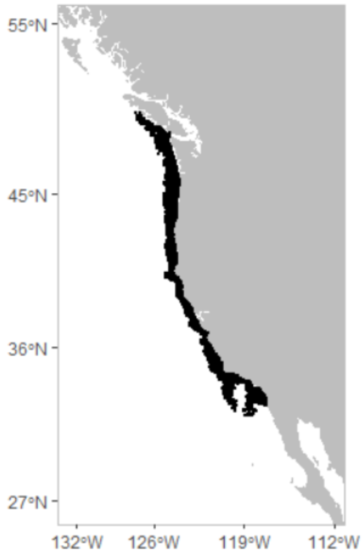
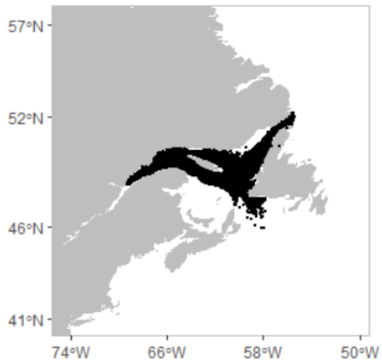
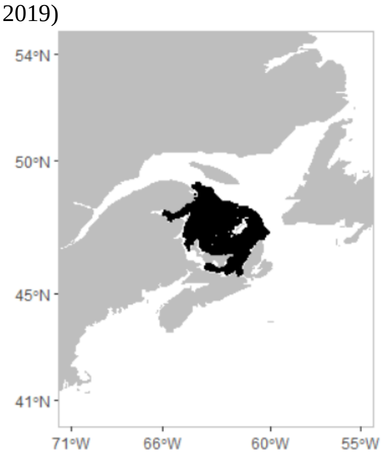
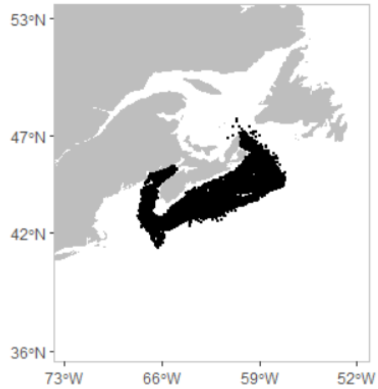
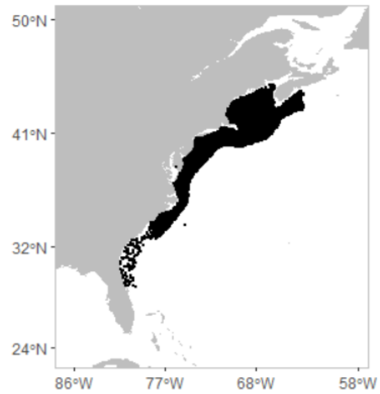
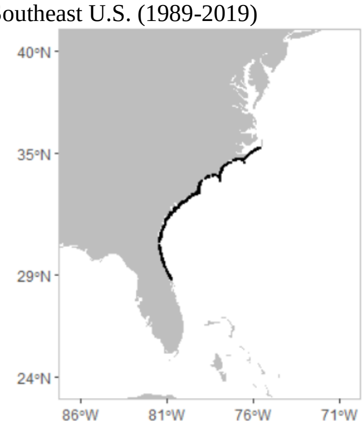
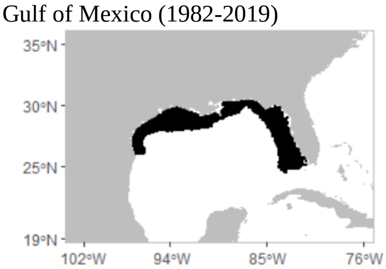
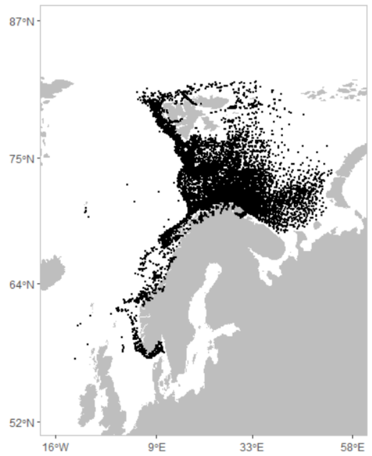
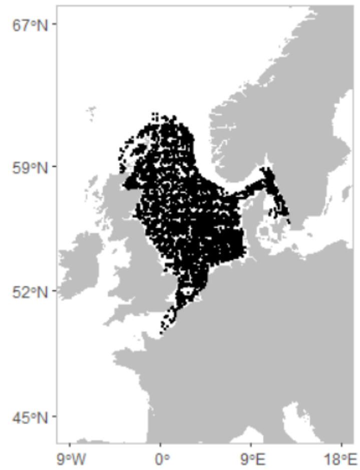
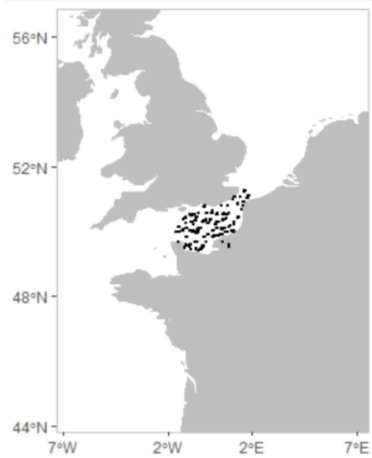
Appendix

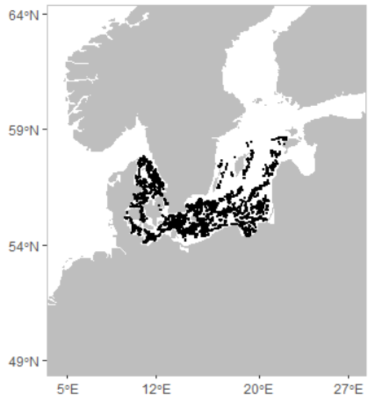
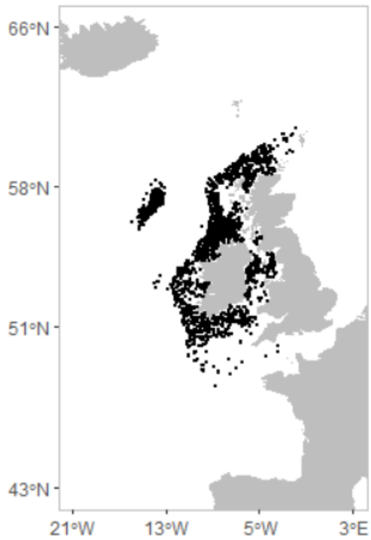
Table S1. *Map of surveyed regions with information on swept area and common gear type* (van Denderen et al. 2023) .

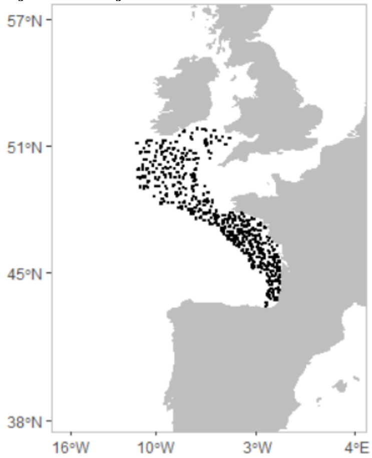
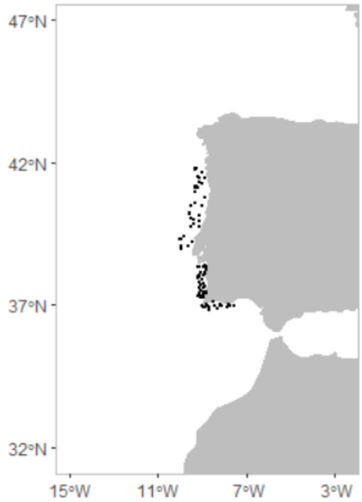
Region	Swept area	Common gear type
Northwest Pacific		
Aleutian Islands (1983-2018) 	File downloaded contains catch weight per area swept	Standard Nor'Eastern otter trawl
Eastern Bering Sea (1982-2019) 	File downloaded contains catch weight per area swept	Standard Nor'Eastern otter trawl
Gulf of Alaska (1984-2019) 	File downloaded contains catch weight per area swept	Standard Nor'Eastern otter trawl
Canadian Pacific (2003-2019) 	All swept areas are estimated from data on distance fished and door spread, converting door spread to wing spread by assuming wing spread = 0.3 · door spread. Queen Charlotte Sound average area swept is 0.040 km^2 (sd = 0.005) West Coast Vancouver average area swept is 0.035 km^2 (sd = 0.004) Hecate Strait average area swept is 0.032 km^2 (sd = 0.007) West Coast Haida Gwaii average area swept is 0.043 km^2 (sd = 0.011) Strait of Georgia average area swept is 0.034 km^2 (sd = 0.006)	Atlantic Western IIa box trawl

West Coast U.S. (1977-2019) 	West Coast Triennial (WCT): Swept area estimated from data on net width and distance fished. Average area swept is 0.037 km^2 (sd = 0.006). West Coast Annual (WCA): area swept is provided. Average area swept is 0.018 km^2 (sd = 0.004).	WCT: Poly Nor'Eastern trawl WCA: Aberdeen trawl
Northeast Atlantic		
Gulf of St. Lawrence North (1983-2019) 	All swept areas are estimated from data on distance fished and fixed wing spread information (value is depending on vessel). MV Lady Hammond: wing spread is 10.7 m[A]. Average area swept is 0.038 km^2 (sd = 0.014). MV Gadus Atlantica: wing spread is 14 m[A]. Average area swept is 0.049 km^2 (sd = 0.014). CCGS Alfred Needler: wing spread is 13.4 m[B]. Average area swept is 0.029 km^2 (sd = 0.006). CCGS Teleost: wing spread is 17.5 m[C]. Average area swept is 0.024 km^2 (sd = 0.005). DFO Mobile gear sentinel fisheries program: wing spread is 15.8 m[D]. Average area swept is 0.037 km^2 (sd = 0.014).	MV Lady Hammond: Western IIA trawl MV Gadus Atlantica: Engel 145 Otter trawl CCGS Alfred Needler: URI shrimp trawl (81'/114') CCGS Teleost: Four-sided Campelen 1800 shrimp trawl equipped with a Rockhopper footgear DFO Mobile gear sentinel program: 300 Star Balloon trawl mounted on a Rock Hopper footgear
Gulf of St. Lawrence South (1970-2019) 	All swept areas are estimated from distance fished (fixed at 3200 m) and wing spread information (fixed, see value below), both taken from Hurlbut and Clay (1990)[E]. Western IIA trawl wing spread is 12.5 m, all swept areas are 0.041 km^2 (sd = NA) Yankee 36 otter trawl wing spread is 10.7 m, all swept areas are 0.035 km^2 (sd = NA).	Western IIA trawl Yankee 36 otter trawl

Maritimes (1970-2020) 	All swept areas are estimated from data on distance fished and fixed wing spread information taken from Hurlbut and Clay (1990)[E]. Western IIA trawl wing spread is 12.5 m, average area swept is 0.040 km^2 (sd = 0.004); Yankee 36 otter trawl wing spread is 10.7 m, average area swept is 0.036 km^2 (sd = 0.006).	Western IIA trawl Yankee 36 otter trawl
Northeast U.S. (1963-2019) 	NEUS Fall survey: Swept area estimated from gear width (fixed value of 13 m)[F] and distance fished calculated from start and end position (no positional data before 1996). Average area swept is 0.036 km^2 (sd = 0.011). NEUS Spring survey: Swept area estimated from gear width (fixed value of 13 m)[F] and distance fished calculated from start and end position (no positional data before 1996, except for 1971). Average area swept is 0.036 km^2 (sd = 0.012). Biomass conversion factors were used to calibrate between vessels[G]	Yankee 36 otter trawl Standardized 3-bridle, 4-seam survey bottom trawl rigged with a rockhopper sweep
Southeast U.S. (1989-2019) 	Swept area estimated from gear width (fixed value of 15 m)[H] and distance fished calculated from start and end position. Average area swept per haul (paired trawl) is 0.042 km^2 (sd = 0.004).	Paired 75-ft (22.9-m) mongoose-type Falcon trawl nets
Gulf of Mexico (1982-2019) 	Summer SEAMAP Groundfish Survey: Swept area estimated from gear width (fixed value in data is 12.2 m), fishing time and vessel speed (fixed value in data is 4.6 km/h). Average area swept is 0.033 km^2 (sd = 0.014).	40 ft. shrimp trawl

Northwest Atlantic		
Barents Sea and Norwegian waters  	Swept area estimated from wing spread and distance fished. Wing spread is assumed to be 0.3 · door spread. Door spread is measured. Average area swept is 0.058 km^2 (sd = 0.047)	Norwegian Campell Trawl 1800
North Sea  	Swept area estimated from wing spread and distance fished. Wing spread is partly measured and partly estimated with a statistical model with door spread, log$_{10}$(depth), country and sweep length as predictor variables. Average area swept is 0.074 km^2 (sd = 0.020)	GOV (Grande Ouverture Verticale) trawl
East English Channel  	FR-CGFS: Swept area estimated from wing spread and distance fished. Wing spread is partly measured and partly estimated with a statistical model with door spread, where door spread is partly estimated with a statistical model with log(depth). Average area swept is 0.046 km^2 (sd = 0.009)	GOV (Grande Ouverture Verticale) trawl

Baltic Sea  	Swept area estimated from wing spread and distance fished. Wing spread is partly measured and partly estimated with a statistical model with door spread, where door spread is partly estimated with a statistical model from log(depth), country and gear type. Average area swept of GOV is 0.123 km^2 (sd = 0.032) Average area swept of TVL is 0.015 km^2 (sd = 0.081) Average area swept of TVS is 0.012 km^2 (sd = 0.073)	GOV (Grande Ouverture Verticale) trawl TV-3 trawl large (TVL) TV-3 trawl small (TVS)
Celtic Seas  	IE-IGFS - Swept area estimated from wing spread and distance fished. Wing spread is partly measured and partly estimated with a statistical model with door spread, sweep length, where door spread is partly estimated with a statistical model with log(depth) and sweep length. Average area swept is 0.076 km^2 (sd = 0.010) NIGFS: Swept area estimated from wing spread and distance fished. Wing spread is partly measured and partly estimated with a statistical model with door spread, where door spread is partly estimated with a statistical model with log(depth). Average area swept is 0.051 km^2 (sd = 0.028) SWC-IBTS - Swept area estimated from wing spread and distance fished. Wing spread is partly measured and partly estimated with a statistical model with door spread, log(depth), where door spread is partly estimated with a statistical model from log(depth) and sweep length. Average area swept in km^2 is 0.091 (sd = 0.042) ROCKALL - Swept area estimated from wing spread and distance fished. Wing spread is partly measured and partly estimated with a statistical model with door spread and sweep length, where door spread is partly estimated with a statistical model from log(depth) and sweep length. Average area swept is 0.069 km^2 (sd = 0.008)	GOV (Grande Ouverture Verticale) trawl (IE-IGFS, SWC-IBTS, ROCKALL) Rock-hopper otter trawl (NIGFS)

Bay of Biscay 	EVHOE. Swept area estimated from wing spread and distance fished. Wing spread is partly measured and partly estimated with a statistical model with door spread and sweep length as predictor variables. Average area swept in km^2 is 0.071 (sd = 0.007).	GOV (Grande Ouverture Verticale) trawl
Iberian Coast 	PT-IBTS - Swept area estimated from wing spread and distance fished. Wing spread is fixed at 15.1 m[I]. Average area swept is 0.047 km^2 (sd = 0.007)	Norwegian Campell Trawl 1800

A ‑ Carrothers PJG 1988. Scotia-Fundy groundfish survey trawls Canadian Technical Report of Fisheries and Aquatic Sciences 1609

B ‑ Bourdages H, Savard L, Archambault D, Valois S 2007. Results from the August 2004 and 2005 comparative fishing experiments in the northern Gulf of St. Lawrence between the CCGS Alfred Needler and the CCGS Teleost Canadian Technical Report of Fisheries and Aquatic Sciences 2750

C ‑ McCallum BR and SJ Walsh 2002. An update on the performance of the Campelen 1800 during bottom trawl surveys in NAFO subareas 2 and 3 in 2001 NAFO SCR Doc. 02/32 Serial No. N4643

D ‑ Brattey J, NG Cadigan, K Dwyer, BP Healey, MJ Morgan, EF Murphy, D Maddock Parsons and D Power 2008. Assessments of the cod (Gadus morhua) stock in NAFO Divisions 2J3KL (April 2007 and April 2008) Research Document 2008/086

E ‑ See Table 1.1 in Hurlbut T, and D Clay (eds) 1990. Protocols for Research Vessel Cruises within the Gulf Region (Demersal Fish) (1970-1987). Can. MS Rep. Fish. Aquat. Sci. No. 2082: 143 p.

F ‑ See Table 2 in Brown RW, Fogarty M, Legault C, Miller T, Nordahl V, Politis P and Rago P 2007 Survey Transition and Calibration of Bottom Trawl Surveys along the Northeastern Continental Shelf of the United States ICEM CM2007/Q:20

G ‑ Miller TJ, Das C, Politis PJ, Miller AS, Lucey SM, Legault CM, Brown RW, Rago PJ (eds). 2010. Estimation of Albatross IV to Henry B. Bigelow calibration factors. North-east Fish Sci Cent Ref Doc. 10-05; 233 p. Available from: National Marine Fisheries Service, 166 Water Street, Woods Hole, MA 02543-1026, or online at http://www.nefsc.noaa.gov/nefsc/publications/

H - See Appendix Table 7 in Watson Jr JW, Workman IK, Taylor CW, Serra AF 1984 Configurations and relative efficiencies of shrimp trawls employed in southeastern United States waters NOAA Technical Report NMFS 3 – horizontal spread is approx. 15 m (49 ft.) with a bridle length 300 ft, door size 9 ft x 40 in and head rope 86 ft

I - https://datras.ices.dk/Home/Descriptions.aspx#POR

Version History

HISTORY OF CHANGES		
Version	**Publication date**	**Changes**
1	13/03/2025	Complied version from corresponding author
2	19/03/2025	Edited version by coordinator
3	25/03/2025	Final edits and approval by coordinator (Martin Lindegren)