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Predicting optimal combinations of bycatch reduction devices in trawl gears: a meta-analytical approach

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Running title:

Towards a new generation of trawls

Abstract

Global efforts to reduce unwanted catches have led to the development of a vast array of bycatch reduction devices (BRDs), in particular for mixed trawl fisheries. Some of these BRDs could likely benefit from being combined. However, the number of possible combinations would be prohibitive to be tested experimentally. Therefore, in this study we propose a meta-analytical approach that combines the data available on BRDs tested independently in a fishery and predict the theoretical selectivity of all possible combinations of those devices. This allows to identify promising BRD combinations, worth experimental investigation and flexible trawl configurations, where the selectivity can be substantially modified by adding or removing one BRD, thus aiding fishermen in adapting to high variability in catch composition and quota availability. To illustrate the approach, we used BRDs developed for the well-studied *Nephrops* (*Nephrops norvegicus,* Nephropidae) directed mixed trawl fishery in the Skagerrak and Kattegat seas. We predicted the selectivity of 100 BRD combinations for *Nephrops*, cod (*Gadus morhua,* Gadidae) and haddock (*Melanogrammus aeglefinus,* Gadidae), compared them in terms of absolute selectivity and performance under realistic catch scenarios, from both single- and multi-species perspectives, and identified 15 BRD combinations that could be worth future experimental investigation. The meta-analytical approach makes best use of existing knowledge and leads to new insights about the potential for improvement and flexibility in trawl selectivity. This could benefit a variety of mixed trawl fisheries and help developing a new generation of more flexible gears, with multiple BRDs integrated in their structure.

Keywords

Combined selectivity, flexible trawl design, gear modifications, mixed trawl fisheries, optimal gear design, trawl selectivity

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1. Introduction

Addressing the issue of unwanted catches is one of the major challenges of fisheries science and management (Pérez Roda et al., 2019; Karp et al, 2019). For decades, efforts to reduce the capture of non-target species and/or undersized individuals have involved the development of fishing gear modifications, herein termed Bycatch Reduction Devices (BRDs; Kennelly and Broadhurst, 2002). These BRDs modify the selectivity of the gear, i.e. its ability to retain the individuals encountered (Wileman et al., 1996), and exploit differences in shape, size and behaviour among species to select out unwanted individuals (e.g. Robertson, 1986; Isaksen et al*.,* 1992; Fujimori et al., 2005; Graham and Fryer, 2006; Broadhurst et al., 2012; Herrmann et al., 2015; Brinkhof et al., 2017; Lomeli et al., 2018; Melli et al., 2018a). Together with ecosystem-based management approaches, BRDs have contributed to successfully reducing global discards of unwanted catches (Worm et al., 2009; Hall and Mainprize, 2005; Zeller et al., 2017). Nevertheless, continuous gear development is required for the industry to be able to cope with the variability in catch composition and management objectives (Kennelly and Broadhurst, 2002; O'Neill et al., 2019).

In trawl fisheries, where proportions of unwanted catches are often high (Kelleher, 2005), substantial effort has been devoted to developing and testing numerous BRDs and alternative gear designs (reviewed by: Broadhurst, 2000; Catchpole and Revill, 2008; Graham, 2010). Moreover, the process is expected to accelerate in coming years, with multiple projects now directly involving the industry in the development and testing of gear modifications (Armstrong et al., 2013; Mangi et al., 2016; Eliasen et al., 2019, Feekings et al., 2019). To help promote awareness of the BRDs available and build future designs on the existing information, the scientific community has dedicated effort towards sharing the summarized results and/or data of the experimental trials through open-access databases (e.g. http://www.discardless.eu/selectivity_manual; http://www.seafish.org/geardb/; https://tool.gearingup.eu/; O'Neill and Mutch, 2017; O'Neill et al., 2019). Moreover, results from different studies have been combined through meta-analyses to extrapolate common patterns useful in designing future gear modifications (e.g. ICES, 2007; Madsen, 2007; Fryer et al., 2015; Fryer et al., 2017). Ideally, both scientists and fishermen could use this information to choose the most appropriate gear design with respect to their specific catch goals (O'Neill et al., 2019). However, for most mixed trawl fisheries, the optimal gear design is not constant; it varies, within and between years, according to management objectives (e.g. quota availability and discard bans), market values, as well as environmental and biological fluctuations (Catchpole et al., 2005; Rochet and Trenkel, 2005; Feekings et al., 2012). Historically, fishermen have coped with such variability by adopting different gears throughout the year or by changing fishing dynamics (i.e. fishing grounds and period), more than relying on multiple and often complex BRDs (Broadhurst, 2000). Nonetheless, achieving a more flexible trawl design, where selectivity could be temporarily changed without having to change gear or fishing ground, could be ultimately beneficial to fishermen's incomes, while improving their capacity to align to the management and environmental objectives for sustainable fisheries.

To push the boundaries of trawl selectivity, recent studies have begun to combine sequential BRDs (e.g. Stepputtis et al., 2016; Brinkhof et al., 2018; Larsen et al., 2018a). Indeed, a combination of BRDs could be more effective in reducing unwanted catches of multiple species (Larsen et al., 2018a) or even achieving alternative selective profiles for the target ones (Stepputtis et al., 2016). Despite these few studies, the potential benefit of combining existing BRDs remains still widely unexplored. For example, some BRDs which were designed to be easily added and removed from the anterior part of the trawl (e.g. McHugh et al., 2015; Melli et al., 2018a) could be combined with posterior BRDs to obtain flexible and convertible trawl selectivity. However, the combination of BRDs would need to be proven significantly more efficient in reducing unwanted catches than the single BRDs to be of interest to the industry. Given the number of BRDs, testing all possible combinations experimentally would be extremely expensive and time-consuming (Veiga-Malta et al., 2019). A cost-efficient alternative would be to identify the most promising combinations before testing them experimentally. Therefore, in this study we aimed at presenting a meta-analytical approach to (i) predict the selectivity of a gear with multiple BRDs, and (ii) compare the predicted combined selectivity to identify the most promising combinations. The meta-analytical approach presented here combines data available on BRDs that have been individually tested within a specific fishery to predict the selectivity of the potential BRD combinations. The theoretical performance and potential applicability of BRD combinations for the fishery is then investigated in terms of differences in size selectivity, catch profile and potential consequences on fishermen’s incomes (Sala et al., 2015; Larsen et al., 2017; Veiga-Malta et al., 2019) to identify the most promising options.

The meta-analytical approach presented is applicable to any well-studied fishery worldwide, where multiple BRDs have been developed and documented. To illustrate it, we chose BRDs developed for the *Nephrops* (*Nephrops norvegicus*, Nephropidae) directed mixed trawl fishery in the Skagerrak and Kattegat (North-east Atlantic; between Denmark, Norway and Sweden). This fishery, one of the most economically-important in Europe (Graham and

Ferro, 2004; Krag et al., 2008), catches a wide range of species, including roundfish and flatfish (Kelleher, 2005; Krag et al., 2008). The diversity of unwanted species and sizes caught in this fishery has led to the development of a vast array of BRDs (see for review Graham and Ferro, 2004; Catchpole and Revill, 2008). Many of these BRDs could potentially be combined to obtain different catch profiles, both in terms of species and sizes, and flexible trawl configurations.

2. Materials and Methods

2.1 Criteria for the selection of BRDs

To predict the species-specific selectivity of a combination of BRDs it is first necessary to know the species-specific, population-independent, selectivity of each BRD included. This is described by a species-specific selection curve that expresses the probability of retaining an individual of length *l* given that it was available to the gear (Wileman et al., 1996). Population-independent size-selectivity, also known as absolute selectivity, can be estimated using data-collection methods such as the covered-codend method and paired gear methods where a non-selective codend is used as a control (Wileman et al., 1996; Millar, 2009). Therefore, we selected studies where these methods were used. Moreover, since the efficiency of BRDs is often species dependent (e.g. Melli et al., 2018a), and their applicability further influenced by a number of factors (Feekings et al., 2012), we included multiple species in the analysis. Subsequently, we selected studies that provided size selectivity for the main target species as well as several bycatch species. Homogeneity in length-range, within species, among the studies included was also essential, as the dataset with the most restrictive range will affect the predictive power for the relative combinations. Finally, we selected BRDs that were strongly effective on at least one of the species of interest, and could be assumed to function independently in the trawl, i.e. applied to different sections of the trawl, without interfering with each other. In particular, this last criteria for the selection of BRDs aimed at preventing the risk for unpredictable synergies or contrasts deriving from applying multiple BRDs to the same trawl section, e.g. a device that counters the herding response (e.g. Melli et al., 2018a) with one that prevents the herding stimulus (e.g. Sistiaga et al., 2015; 2016). However, this assumption does not imply that impairment in the efficiency of the BRDs due to, for example, an increased state of fatigue in the individuals interacting with sequential BRDs, was excluded. Such risk can only be acknowledged and investigated experimentally after the most promising BRD combinations have been identified.

2.2 Estimation of bootstrap set for individual BRDs

Once the BRDs were selected, the original data for each independently-tested BRD were re-analysed, according to the model used in the original study (see Appendix 1), while applying a double-bootstrap method with 1000 repetitions to consider both within- and between-hauls variation in size selectivity (Millar, 1993). The purpose of this step was to obtain a bootstrap set for each BRD and each species. Besides being used to estimate Efron 95% confidence intervals (CIs; Efron, 1982) for the population-independent selectivity curve of each individual BRD, the resulting bootstrap set was necessary to estimate the uncertainties for the population-independent combined selectivity, as described in the following section. These and all the following steps were conducted using the software SELNET (Herrmann et al., 2012).

2.3 Prediction of combined selectivity

For a standard trawl gear (i.e. without BRDs), size-selectivity is mostly determined by the characteristics of the codend, in particular mesh size and shape (Glass, 2000; Herrmann et al., 2009). However, for an individual to end up being retained in the codend it has to be retained during the previous steps of the capture process. Therefore, the size selectivity of a trawl gear can be considered as a sequence of selective processes. Indeed, if we divide the trawl in four main sections *s*, the likelihood for an individual of length *l* being retained in the codend requires that it is herded into the trawl, and passed through the body and extension sections without escaping (Fig. 1). Assuming the retention probability $r(l)_s$ of each section to be independent, we modelled the overall retention probability $r_{Combined}(l)$ as the product of the population-independent, size selection processes in each section of the trawl:

$$r_{Combined}(l) = \prod_{s=1}^{4} r(l)_s = r_{Herding}(l) \times r_{Body}(l) \times r_{Extension}(l) \times r_{Codend}(l) \qquad \textbf{(1)}$$

where $r_{\text{Herding}}(l)$, $r_{\text{Body}}(l)$, $r_{\text{Extension}}(l)$ and $r_{\text{Codend}}(l)$ are the population-independent size selectivity in the respective sections of the trawl, conditioned entering the section.

To estimate 95% Efron CIs for each $r_{\text{Combined}}(l)$, we used the bootstrap sets obtained in section 2.2 for each original design. Because these bootstrap sets were obtained independently, a new bootstrap set of results for $r_{\text{Combined}}(l)$ could be created using:

$$r_{Combined}(l)_i = r_{Herding}(l)_i \times r_{Body}(l)_i \times r_{Extension}(l)_i \times r_{Codend}(l)_i \; i \in [1 \ldots 1000] \qquad \textbf{(2)}$$

where *i* denotes the bootstrap repetition index (Herrmann et al., 2018). In Eq. (2) the 1000 bootstrap sets generated from the original datasets were multiplied to obtain the new bootstrap set for the combined configuration. Based on this final bootstrap set, 95% Efron Percentile CIs for $r_{\mathrm{Combined}}(l)$ were estimated.

2.4 Comparison of BRD combinations

To investigate if and how a combination of BRDs was significantly better with respect to the single BRDs or other BRD combinations, we quantified changes in (i) absolute selectivity, by using the delta selectivity (Larsen et al., 2018b); (ii) catch profile, by estimating the cumulative catch curve (Veiga-Malta et al., 2019); and (iii) potential consequences for the fishery, using performance indicators (Sala et al., 2015).

2.4.1 Delta selectivity

The delta selectivity consists of subtracting the predicted, species-specific, absolute selectivity of two BRD combinations to identify size-ranges where there was a significant change in selectivity (Larsen et al., 2018b). If $r\mathrm{B}(l)$ is the size selectivity of a trawl used as a baseline, for example one having a simple codend or a single BRD, and $r\mathrm{C}(l)$ the size selectivity of the combination of interest, then the difference in selectivity, $\Delta r(l)$ is:

$$\Delta r(l) = r\mathrm{C}(l) \; - \; r\mathrm{B}(l) \qquad \textbf{(3)}$$

Uncertainties for $\Delta r(l)$ were estimated using the approach described in (section 2.3) while subtracting the two independently generated bootstrap sets. In general, $\Delta r(l)$ spans between -1.0 and 1.0, where values above 0.0 imply that the combination has a higher retention probability for individuals of length l than the baseline, while values below 0.0 imply a lower retention probability. The difference in retention probability is significant when the Efron 95% CIs do not overlap the 0.0 baseline for equality.

2.4.2 Cumulative catch curve

The cumulative catch curve expresses what would be the catch profile under a specific scenario of population encountered by the gear (Veiga-Malta et al., 2019). To estimate cumulative catch curves for the BRD combinations we applied the predicted combined selectivity to realistic, species-specific population scenarios. These scenarios were estimated from the datasets of the BRDs included in the case-study, using the catch of the non-selective control gears (see Appendix 2). For each species, we selected three scenarios with different size-structures and modes (i.e. most frequent length class represented) in the population. For each scenario $nPop_l$, uncertainties (95% Efron CIs) were obtained based on a double bootstrap method to include both between- and within-hauls variability in the structure of the population (see Appendix 2).

Using the size-selection curves predicted in section 2.3 for each BRD combination, and applying them to $nPop_l$, we obtained simulated catches, $nCatch(l)$. We then expressed these catches as a cumulative distribution function for the catch:

$$CDF\_nCatch(L) = \frac{\sum_{l=0}^{L}\{r_{combined}(l)\times nPop_l\}}{\sum_{l}\{r_{combined}(l)\times nPop_l\}} \qquad \textbf{(4)}$$

For each $CDF\_nCatch(L)$ we calculated 95% CIs based on the bootstrap sets for $r_{combined}(l)$ and $nPop_l$ using the approach previously described for $r_{combined}(l)$.

The cumulative catch curve provides insights about how the efficiency of the single BRDs or BRD combinations may be impaired by the structure of the population encountered. BRD combinations whose efficiency is significantly affected by the population structure have non-overlapping CIs for the different $CDF\_nCatch(L)$. Moreover, the cumulative catch curves show the proportion of the catch of a species that would be below the Minimum Conservation

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Reference Size (MCRS; i.e. minimum size at which the individual can be sold for human consumption) under that population scenario.

2.4.3 Performance indicators

The population scenarios estimated in the previous section were also used to quantify the performance of the BRD combinations, from the fishermen's perspective. While the size of an individual typically defines whether it is commercially saleable or not, quotas and catches are typically expressed in weight. Thus, for a fisherman, the performance of a gear is determined by the proportion of weight retained with respect to that of other designs (Sala et al., 2015). Therefore, we converted the number of individuals per length-class into weights and used them to calculate, for each species and each population scenario, the percentage (in weight) of undersized and commercial-sized individuals retained. This conversion was conducted by using a length-weight relationship, $w(l) = a \times l^b$ where *w* is the weight (in g) *l* the length (in cm) and *a* and *b* are the coefficients for the specific species, season and study-area.

To estimate these performance indicators, we first applied the size-selection curves predicted in section 2.3 for each BRD combination to the population scenarios expressed in weight, $w(l) \times nPop_l$, and obtained simulated catches in weight, $w(l) \times r_{combined}(l) \times nPop_l$. We then calculated the percentage of weight retained for individuals below (wP^-) and above (wP^+) the species-specific MRCS, respectively, for a specific combination of BRDs. The indicators were calculated by:

$$wP^- = 100 \times \frac{\sum_{l<MCRS}\{a \times l^b \times r_{combined}(l) \times nPop_l\}}{\sum_{l<MCRS}\{a \times l^b \times nPop_l\}}$$

$$wP^+ = 100 \times \frac{\sum_{l>\mathrm{MCRS}}\{a \times l^b \times r_{combined}(l) \times nPop_l\}}{\sum_{l>MCRS}\{a \times l^b \times nPop_l\}} \qquad \textbf{(5)}$$

Both indicators (wP^{-}, wP^{+}) were estimated with uncertainties for each species and population scenario, using the bootstrap set for $r_{combined}(l)$ and $nPop_l$. Specifically, by first calculating the values for the indicators based on the result of each bootstrap repetition for $r_{combined}(l)$ and $nPop_l$ synchronous in (5) to obtain a bootstrap set for the indicator values. Efron 95% CIs were estimated for each of the indicators based on the resulting bootstrap set.

Because uncertainties are typically wider at the tails of the length range represented in the data, and since the conversion into weights accentuates the influence of the larger and less represented length classes when estimating the indicators, we restricted the length range for each of the species analysed according to the data included. In particular, we set the minimum length of the range as the smallest length class including at least five individuals in all the single BRD datasets. Similarly, we determine the maximum length as the largest length class with at least five individuals in all the datasets. This approach prevented the less-represented length classes from compromising the information contained in the main bulk of data.

Finally, to investigate the proportion of weight retained of bycatch species with respect to the main target species, and compare the performance of different BRD combinations, we used a multispecies population scenario (see Appendix 2). The performance indicators calculated for this scenario were used to discuss the most promising BRD combinations for the case-study fishery, depending on hypothetical catch goals (e.g. maximum quota saving or maximum economic output).

3. Application to a case-study fishery

The *Nephrops*-directed mixed trawl fishery in the Skagerrak-Kattegat (ICES sub-division IIIa) typically uses Combi trawls (i.e. wide-body trawl model for mixed bottom fisheries; Cosmos Trawl A/S) to target both *Nephrops* and valuable fish species (ICES, 2014). Most of these species are quota-regulated at the vessel level (Individual Transferable Quota system; Squires et al., 1998) and are subjected to the EU landing obligation (i.e. discard ban; EU, 2013). Among the legal gear options, most of the fleet adopts a 90 mm diamond mesh codend with a 3 m long escape panel of larger meshes (140, 180 or 270 mm depending on fishing area and mesh shape; ICES, 2014) inserted in the upper netting of the codend, 4 m ahead of the codline (see Krag et al., 2016). The escape panel was designed to reduce the catch of undersized fish, in particular gadoids (Frandsen et al., 2009; Briggs et al., 2010). However, under the landing obligation, quota for fish species can be exhausted prior to that of the main target species, *Nephrops*, potentially chocking the fishery (Catchpole et al., 2017).

To investigate the multispecies performance of BRD combinations for this fishery we chose three species: the main target species, *Nephrops*; cod (*Gadus morhua*, Gadidae), recognized as the main potential choke species for the area; and haddock (*Melanogrammus aeglefinus*, Gadidae), a species with low risk of chocking the fishery (North Sea Advisory Council, 2018).

3.1 BRDs selected

We identified seven datasets to be included in the meta-analytical approach: a total of five independently tested BRDs, selected due to their effect on the species of interest, and two simple codends of 90 and 120 mm diamond mesh size, common mesh sizes used within the fishery (Table 1). All the datasets were collected with similar trawl designs, fishing dynamics (e.g. towing speed) and fishing area. Figure 2 illustrates the BRDs designs: a counter-herding device (Melli et al., 2018a), a modification of the upper netting panel in the trawl body (Krag et al., 2014), a horizontally-divided trawl codend (Melli et al., 2018b; Melli et al., 2019b); a 90 mm diamond mesh codend with a 120 mm Square Mesh Panel (SMP; Krag et al., 2013), and a 120 mm diamond mesh codend with a 180 mm SMP (Krag et al., 2015). Each of these BRDs was effective on at least one of the bycatch species analysed, without completely excluding all commercial fish from the catch (like for example a grid would; Frandsen et al., 2009). This choice was made to respect the multispecies feature of the *Nephrops*-directed mixed trawl fishery in the Skagerrak-Kattegat.

The selectivity of the two simple codends (i.e. 90 and 120 mm diamond mesh size) were included as options to be combined with the BRDs in the herding zone, trawl body and/or upper and lower codend after the separation inserted in the trawl extension. The specifics of each codend and eventual SMP are summarized in Table 2. In addition, we included the option of leaving the codend open by considering zero retention for those individuals entering that codend.

The model used for each BRD and codend selectivity, its parameters and fit statistics are summarised in Appendix 1.

3.1.1 Nomenclature system

To generate an ID for each of the BRD combinations we adopted a nomenclature system where the letter define the section of the trawl (H=herding zone; B=trawl body; E=trawl extension; C=codend). For the first three sections (H, B and E), where only one BRD option was included in the study, we used a binary number system to identify the absence (0) or presence (1) of the BRD. In the codend section (C), the five codend options were numbered from 0 to 4, with C0 being the baseline codend (90 mm diamond mesh), C1 the 120 mm diamond mesh codend, C2 the 90 mm diamond mesh with a 120 mm SMP, C3 the 120 mm diamond mesh with a 180 mm SMP, and C4 the open codend. As a result, the ID for a combination of the counter-herding device and a codend of 90 mm diamond mesh with a 120 mm SMP (C2), with no modification on the body and extension sections, was named H1B0E0C2. When the horizontal separation in the trawl extension was present (E1) the two codends, lower and upper respectively, were specified in the ID. For example, a BRD combination with the modification of the upper netting panel in the trawl body, the vertical separation in the trawl extension leading to a 90 mm diamond lower codend and an open upper codend was identified as H0B1E1C0C4.

3.2 Predicted combined selectivity

Due to the BRDs selected, and because the modification introduced in the Extension section was a separation into two compartments, Eq. (1) becomes:

$$r_{Combined}(l) = r_{Herding}(l) \times r_{Body}(l) \times [r_{Extension}(l) \times r_{CodendL}(l) + (1.0 - r_{Extension}(l)) \times r_{CodendU}(l)] \qquad \textbf{(6)}$$

where $r_{\text{Extension}}(l)$ expresses the probability of an individual of length l to enter the lower compartment, $r_{\text{CodendL}}(l)$ is the size selectivity of the lower codend and $r_{\text{CodendU}}(l)$ of the upper one. When no separation is included in the trawl (E0), $r_{\text{Extension}}(l)$ equals one, meaning that all individuals enter one codend. When no BRD is inserted in the Herding zone (H0) and Body section (B0), $r_{\text{Herding}}(l)$ and $r_{\text{Body}}(l)$ are assumed to equal one, meaning that the individuals entering that section are retained as they would in a standard trawl.

We predicted the selectivity of all possible combinations, obtaining a total of 100 predictions for *Nephrops* and cod. Since data for haddock were unavailable for C2, the number of possible combinations for haddock was 64. For all the species, four combinations had $r_{Combined}(l)$ equal to 0.0, relative to the theoretical option of fishing with an open codend (C4) when no separation in the extension was included (E0). Thus, the final number of species-specific, combined selectivity curves was 96 for *Nephrops* and cod, and 60 for haddock (see the Supplementary Material for representation of all predicted selectivity curves).

Figure 3 illustrates examples of the predicted selectivity of different combinations of BRDs for the three species considered. The first two rows show the selectivity of a trawl with one BRD; for example H0B0E1C0C1 introduced a second codend with larger meshes (C1) by modifying the trawl extension with a vertical separation. The third and fourth rows show examples of two BRDs combined, such as a large mesh panel in the trawl body and a codend with a SMP inserted (H0B1E0C3). The fifth and sixth rows show examples of three and four BRDs combined, respectively.

For each predicted selectivity curve, the 95% Efron CIs reflected the strength of the data and the consistency (between-hauls variation) of the effect in the original datasets. Thus, combinations of BRDs with high binomial noise in one or more of the original datasets resulted in wide CIs. In particular, this is the case for the tails of the length-range of each species, where the dataset with the most restricted length-range limited the inferential power for that combination. This result prevented predictions that were not supported by the original experimental data. Examples can be observed in Fig. 3, where the combined selectivity curves of H1 and H1B1 for *Nephrops* resembled a bell-shaped curve (Dickson et al., 1995; Lövgren et al., 2016) with a high retention of the central length classes and a low retention of the smaller and larger classes. However, as expressed by the wide CIs, the effect on the larger classes is inconclusive and should not be interpreted.

Moreover, combined selectivity curves for *Nephrops* involving the counter-herding device (H1) exceeded retention rates of 1.0 (Fig. 3). This was caused by the use of the catch ratio (see Appendix 1) to describe the effect of the counter-herding device, which in some cases increased the number of individuals entering the trawl, although not significantly (Melli et al., 2018a).

3.3 Comparison of BRD combinations

3.3.1 Delta selectivity

To understand if and how the addition of BRDs could significantly affect the species-specific absolute selectivity of a BRD combination, we subtracted their predicted selectivity (Delta selectivity, Fig. 4). Three examples, with increasing complexity (i.e. No. of BRDs), are provided with respect to the relative simpler version of trawl (Fig. 4). In particular, the addition of a counter-herding device to a trawl with a 90 mm diamond codend was predicted to significantly reduce the retention rate of cod (24–72 cm; green curve) and haddock (15–60 cm; blue curve), without affecting that of *Nephrops* (red curve; Fig. 4a). The further addition of the BRD in the trawl extension (i.e. separation into two codends) in the trawl extension did not change the retention of haddock but significantly reduced that of cod (19–73 cm; Fig. 4b). However, the retention of *Nephrops* was also significantly affected (22–70 mm; Fig. 4b). Finally, the addition of a large-mesh panel in the upper netting of the trawl body did not further reduce the retention of either *Nephrops* or haddock, but it significantly reduced that of cod (11–70 cm; Fig. 4c). Thus, if one single BRD can be effective in substantially reducing the retention of haddock, the addition of more BRDs can be useful to reduce that of cod.

However, additional BRDs can significantly affect the retention of the main target species, *Nephrops*.

3.3.2 Cumulative catch curves

In terms of catch profile for each species, the cumulative catch curves indicated that the proportion of catch composed of undersized individuals (i.e. < MCRS), can vary significantly when using the BRD combinations under different population scenarios (Fig. 5). For example, the proportion of undersized *Nephrops* predicted to be caught under the population scenarios P2 and P3 with the combination H1B0E1C0C1 was less than 10%, whereas under the population scenario P1 it reached approximately 45% (Fig. 5). The efficiency of most BRD combinations in selecting out undersized individuals was found to be significantly affected by the structure of the population encountered, as represented by the non-overlapping CIs of the cumulative catch curves (Fig. 5). The highest proportion of undersized individuals was always caught when the mode of the population structure was close to the MCRS. For example, in the third population scenario for cod (P3), where the mode in the population is at 25 cm (MCRS for cod in the Skagerrak/Kattegat is 30 cm), approximately 80% of the catch with the combination H1B0E1C0C1 consisted of undersized individuals (Fig. 5). Similarly, under the second population scenario, the proportion of undersized haddock in the catch was approximately 60% (Fig. 5). If on one hand this is the result of the higher density of undersized individuals in the population scenario, on the other it can highlight that the BRDs included in the combination were less effective in improving the selectivity in proximity of the MCRS. For example, with the combination H1B0E1C0C1, cod below 30 cm are not counter-herded and enter more frequently the lower compartment, thus they are less likely to encounter the 120 mm mesh size of the upper codend (Melli et al., 2018a; Melli et al., 2018b). However, a high proportion of undersized individuals can also imply that the combination of BRDs has a length-dependent efficiency, i.e. it is more effective in reducing the catch of larger individuals (e.g. haddock; Melli et al., 2018a). Consequently, the proportion of undersized individuals in the catch is high because the commercial-sized ones have been selected out. To distinguish between these two cases, the cumulative catch curve should be complemented by the performance indicators, which provide the proportion of undersized and commercial-sized retained with respect to the population encountered.

3.3.3 Performance indicators

To estimate the performance indicators from a fisherman's perspective, the number of individuals per length class in each population scenario was converted to weight per length class. For cod and haddock, we used length-weight relationships available on fishbase.org (Froese and Pauly, 2014) for ICES Division IIIa (cod: a = 0.00587 and b = 3.140; haddock: a = 0.0065 and b = 3.1083). For *Nephrops* we used the data from the Data Collection Framework (DCF) and International Bottom Trawl Survey (IBTS) programs in Skagerrak and Kattegat (a = 0.000765 and b = 2.98025). Prior to conversion, the length ranges were restricted (see section 2.4.3) as follow: 20.5–59.5 mm for *Nephrops*, 20.5–76.5 cm for cod and 18.5–43.5 cm for haddock. Moreover, to estimate the proportion of weight retained of individuals below and above the MCRS, we used the MRCS for the ICES division IIIa: 32 mm carapace length for *Nephrops*, and 30 cm and 27 cm total length for cod and haddock, respectively.

The performance indicators were estimated for all the possible combinations of the BRDs considered and for each of the population scenarios, i.e. P1-P3 per species and a multispecies scenario (Supplementary Material). A subset of BRD combinations, with decreasing retention of cod, is presented in Table 3. The results showed that, from the fishermen's perspective, most BRDs combinations were predicted to have a consistent effect across population scenarios, with very few combinations having non-overlapping CIs between scenarios (Table 3). Moreover, the number of BRDs combined was found to not necessarily significantly reduce the proportion of weight retained. For example, the addition of one (e.g. H1B0E0C0) or even two BRDs (e.g. H0B0E1C2C0) did not significantly reduce the proportion of undersized cod retained, with respect to a simple trawl with no BRDs (H0B0E0C0; Table 3). Similarly, combinations consisting of three BRDs (e.g. H1B0E1C2C1) did not significantly reduce the weight retained of neither undersized nor commercial-sized cod with respect to combinations consisting of two BRDs (e.g. H1B0E0C2 or H1B1E0C0; Table 3). In contrast, an almost complete elimination of cod catches was achieved only from combinations of four BRDs (e.g. H1B1E1C2C4), the maximum level of complexity considered in this study.

3.3.4 Most promising combinations

The performance indicators proved to be the fastest measure to determine if the BRD combination could represent a viable option for the case-study fishery. Indeed, we excluded any BRD combinations that would cause a loss of commercial-sized *Nephrops*, across population scenarios, greater than 15% with respect to a trawl with no BRDs and a 90 mm diamond mesh codend. Fifteen combinations were subsequently identified which could be suitable for the case-study fishery (Table 4). Of these 15 combinations, only 10 included predictions for haddock, due to the lack of data for the 90 mm diamond mesh size codend with a 120 mm SMP (C2). Most of these combinations had a lower codend of 90 mm diamond mesh size, whenever the horizontal separation was introduced. Only one of the selected BRD combinations had a different lower codend, C2, in combination with a 90 mm diamond codend as upper codend (Table 4). Furthermore, out of the 15 BRD combinations identified, 10 included the counter-herding device (Melli et al., 2018a) and six the large mesh size in the upper netting of the trawl body (Krag et al., 2014). Only three of the identified combinations included the maximum level of complexity (i.e. No. of BRDs) possible in this study. This was mainly caused by the potential loss of commercial-sized *Nephrops* associated with each additional BRD introduced in the trawl.

When comparing the performance of the BRD combinations identified under a multispecies catch scenario (see Appendix 2), the results highlighted potential strategies for the fishing vessels operating in the Skagerrak and Kattegat (Fig. 6). In Figure 6, the #0 indicates a simple trawl with no BRDs and a 90 mm diamond mesh codend. Under the catch scenario considered, all the selected combinations had similar predicted retention rates for the main target catches, i.e. commercial-sized *Nephrops*, which did not differ significantly from the one of a simple trawl with a 90 mm diamond mesh codend. This baseline design retained 75.3% (66.2–84.0) undersized cod and a highly variable percentage of undersized haddock (10.7–67.7%). Moreover, catches of commercial-sized bycatch were 97.4% (96.4–98.2) and 62.0% (26.0–92.0) for cod and haddock, respectively. With respect to this baseline, most of the identified BRD combinations had desirable catch profiles: they caught less than 50% of the weight of undersized bycatch of both cod and haddock (highlighted sections in Fig. 6). One exception, the combination #6 (H1B0E0C0), was predicted to retain on average 60.6% (48.3–73.0) of the weight of undersized cod in this population scenario (see Appendix 2 for description of the scenario).

In terms of commercial-sized individuals, all the BRD combinations identified as most promising minimized the percentage of commercial-sized haddock retained, with the exception of combination #1 (H0B0E1C0C1). These results show that, with the BRDs included in this study, which are among the most effective for the case-study fishery, it is impossible to substantially reduce catches of cod, without affecting those of commercial-sized haddock (Fig. 6). Nonetheless, since cod is a potential choke species for the case-study fishery under the EU landing obligation (North Sea Advisory Council, 2018), a reduction of cod, and thus haddock, may be necessary to continue fishing for *Nephrops* when the cod quota is approaching exhaustion. We could identify several combinations of BRDs that could potentially help the fishery to significantly reduce catches of this species. The results showed that an almost complete avoidance of cod could be achieved by combing up to four BRDs (#15; Fig. 6). In particular, by including a BRD in each of the four sections of the trawl considered in this study, this combination achieved overall retention below 25% and 1% of the weight of cod and haddock, respectively, a result that until now has only been achieved by introducing a grid in the trawl codend at the cost of all commercial catches of fish (Frandsen et al., 2009; Drewery et al., 2010). In contrast, even though the BRD combinations identified here would reduce commercial catches of some species (e.g. haddock) they are likely to allow the retention of others, such as monkfish (*Lophius piscatorius*) and flatfish species, less affected by these types of BRDs (Krag et al., 2008; Fryer et al., 2017; Melli et al., 2018a).

If fishermen were to minimize the bycatch of undersized roundfish, while maintaining the majority of the income deriving from commercial-sized cod, for example when cod quota is available, the BRD combinations #2 (H0B0E1C0C2) and #7 (H1B0E1C0C1) could represent the best options (Fig. 6). Although many other BRD combinations achieved similar results, these two had the advantage of retaining on average the same percentage of undersized *Nephrops* as the baseline design (see Supplementary Material for all Performance Indicators). In particular, #2 retained 83.0 % (78.3–87.6) of commercial cod catches and although data for haddock were not available for this BRD combination, haddock catches can be expected to be low due to its high escape rate through 120 mm SMPs (Krag et al., 2008; Fryer et al., 2015).

Finally, the meta-analytical approach allowed to identify three convertible BRD combinations that could lead to a flexible trawl configuration. In particular, the BRD combination #2 retained most of the commercial-sized cod while reducing the catch of undersized fish (Fig. 6), a catch profile useful at maximizing catch value when cod quota is available. However, when the quota comes close to exhaustion, combination #2 can be converted into combination #8 by simply adding the counter-herding device and to #10 by leaving the upper codend open. This substantially modifies the trawl selectivity without requiring a trip to the harbour.

4. Discussion

The meta-analytical approach described in this study makes best use of the existing knowledge on BRDs and leads to new insights about the potential for improvement in trawl selectivity. By using the data already available we were able to predict the combined selectivity of multiple BRDs and quickly inspect a great number of potential BRD combinations, without the time and cost outlay associated with experimental investigation. The use of this approach could ultimately speed up the identification of promising gear designs, thus aiding the industry in pursuing individual catch goals (O'Neill et al., 2019).

Moreover, the meta-analytical approach allows to determine if an increase in complexity in the gear design, i.e. no. of BRDs combined, would result in a significant reduction of unwanted catches. Indeed, because simplicity is often key when considering the uptake of a gear design by fishermen (Broadhurst, 2000; Kennelly and Broadhurst, 2002), and because each additional selection process can lead to a loss of target catch, the number of BRDs should be kept to a minimum. To do so, the approach proposed in this study starts from a simple gear design and adds levels of complexity (i.e. BRDs) until there is no significant improvement in selectivity, for each species, with the addition of further BRDs. Finally, by combining BRDs, we can expand the boundaries of trawl selectivity, moving away from the standard S-shaped selectivity curve (Wileman et al., 1996) and achieving alternative selective profiles more in line with the most recent management objectives (e.g. balanced harvesting; Law et al., 2015; Stepputtis et al., 2016).

The case-study presented herein, led to the identification of 15 potentially applicable combinations that could help the fishery to cope with the requirements of the European landing obligation (ICES, 2013) and, thus, are worth experimental validation. This result was achieved by only including five BRDs into the meta-analysis out of those available for the *Nephrops*-directed mixed trawl fishery. Other strongly effective BRDs, such as grids in the trawl extension (Graham and Fryer, 2006; Frandsen et al., 2009), could be considered in future analyses, especially when including more fish species to better investigate the overall effect on fishermen's income. The designs identified as most promising, here and in future applications of the meta-analytical approach, are relative to the case-study considered; nonetheless, there are several well-studied fisheries in the world where multiple BRDs have been developed due to high temporal and spatial variability in bycatch rates (Catchpole et al., 2005; Rochet and Trenkel, 2005) that could benefit from the application of the meta-analytical approach described. This is the case, for example, for trawl fisheries such as the Australian penaeid-trawl fishery (Broadhurst, 2000; Broadhurst et al., 2012), the US West coast groundfish bottom trawl fishery (Lomeli et al., 2017; 2018; 2019), the Gulf of Maine pink shrimp trawl fishery (He and Balzano, 2007; He and Balzano, 2012), and the Irish Sea *Nephrops* fishery (Briggs, 1992; Cosgrove et al., 2019). To maximize the advantage of predicting the combination of multiple sequential BRDs, the choice of BRDs should be limited to highly efficient designs, targeting different species and size-groups.

It is important to highlight that the scope of the approach presented is the identification of promising combinations and that experimental validation of the predictions is essential. Indeed, the predicted combined selectivity curves are based on the assumption of independence among the BRDs, meaning that when combined the BRDs would perform as they do when applied individually. However, a certain level of impairment in performance should be expected, depending on the type of modifications introduced. For example, anterior BRDs (e.g. Melli et al., 2018a) can potentially increase the resuspension of sediment and, thus, affect the visibility inside the trawl (O'Neill and Ivanović, 2015). This might have consequences on the vision-dependent behaviours of the individuals in the trawl, thus affecting their response to the posterior BRDs (e.g. mesh penetration; Glass et al., 1993). Moreover, individuals that are stimulated or enter in contact with multiple sequential BRDs may be subjected to increased states of fatigue and/or stress, with potential implications on their ability to contact the BRDs and escape (Winger et al., 2010). The introduction of each BRD may also alter or divert the water flow in the trawl, with consequences on the hydrodynamic performance and selective properties of the gear and

BRDs (e.g. Riedel and DeAlteris, 1995). Finally, when testing the combination of BRDs experimentally, a certain degree of divergence from the prediction should be expected due to the potentially necessary scaling in size of the trawl and BRDs, with respect to the experimental trawl used for data collection. Nonetheless, the meta-analytical approach substantially reduces the amount of experimental work by narrowing the list of BRD combinations to be tested.

Finally, a major outcome of the meta-analytical approach was to identify flexible gear configurations that could be quickly converted from one to the other, with substantial changes in selectivity. A flexible trawl configuration would allow fishermen to adjust their selectivity on a day-to-day or even haul-to-haul level, creating a multi-purpose trawl where selectivity could be adjusted to match the variability in management objectives, market values, and temporal and spatial variability in catch composition (Catchpole et al., 2005; Rochet and Trenkel, 2005; Feekings et al., 2012). The advantage deriving from such flexibility, especially under strong economic drivers such as discard bans (Karp et al., 2019), could offset the additional complexity in gear design and number of BRDs. The entire trawl design could even be re-thought with potential BRDs already integrated in its structure. This would likely reduce the risk for loss of target catch or impairment of the gear geometry deriving from applying the BRDs to the trawl as a second thought. With this meta-analytical approach, we hope to facilitate the identification of compatible gear configurations and initiate further discussion about multi-purpose trawl designs.

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6. Data availability statement

The data that support the findings of this study are either published or available from the corresponding author upon reasonable request.

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List of Tables

Table 1 Summary of the datasets included in the meta-analysis.

Reference	Trawl section	ID	Type of data	Description
Melli et al., 2018a	Herding	H0/H1	Paired gears	Counter-herding device
Krag et al., 2014	Body	B0/B1	Paired gears	Trawl with 800 mm diamond meshes in the upper netting of trawl body
Melli et al., 2018b and Melli et al., 2019b	Extension	E0/E1	Covered-Codend	Horizontally divided trawl codend
Krag et al., 2013	Codend	C0	Covered-Codend	90 mm diamond mesh codend; cod and *Nephrops*
Krag et al., 2016	Codend	C0	Covered-Codend	90 mm diamond mesh codend; haddock
Krag et al., 2015	Codend	C1	Covered-Codend	120 mm diamond mesh codend
Krag et al., 2013	Codend	C2	Covered-Codend	90 mm diamond mesh codend with 120 mm square mesh panel
Krag et al., 2015	Codend	C3	Covered-Codend	120 mm diamond mesh codend with 180 mm square mesh panel

Table 2 Summary of codend specifications. Circum. = circumference in the codend; Twine thickness = twine thickness of the netting; SMP = square mesh panel; m = metre, mm = millimetre.

Codend	Length (m)	Circum. (No. meshes)	Codend mesh size (mm)	Twine thickness	SMP mesh size (mm)	SMP Length (m)	Cover mesh size (mm)
C0	7	100	95	4 mm, Double	-	-	40
C1	6	92	127	5 mm, Double	-	-	40
C2	7	100	95	4 mm, Double	126	3	40
C3	6	92	127	5 mm, Double	180	3	40

Table 3 Performance indicators of a simple trawl design with no BRDs (H0B0E0C0) and six examples of BRD combinations for cod, under three population scenarios (P1, P2 and P3). 95 % Efron CIs are shown within parenthesis. wP^- = Percentage (in weight) of undersized cod retained; wP^+ = Percentage (in weight) of commercial-sized cod retained. The examples are ordered according to their mean wP^-, colours are used to highlight the efficiency of the BRD combination in reducing catches of cod: red = low effect; yellow = medium effect; green = high effect.

		***w* P− (%)**	***w* P+ (%)**	***w* DiscardRatio (%)**
H0B0E0C0	P1	66.6 (53.9 – 77.6)	98.7 (98.0 – 99.3)	2.8 (1.6 – 4.9)
	P2	78.2 (70.5 – 86.1)	96.0 (94.3 – 97.2)	8.1 (5.4 – 11.1)
	P3	69.0 (57.0 – 78.5)	94.0 (91.7 – 96.4)	59.9 (48.3 – 66.8)
H0B0E1C2C0	P1	52.7 (41.4 – 63.0)	95.5 (93.7 – 97.1)	2.3 (1.3 – 4.0)
	P2	63.6 (56.2 – 71.2)	90.7 (88.0 – 93.2)	7.0 (4.7 – 9.8)
	P3	54.7 (44.4 – 63.2)	86.7 (83.0 – 91.7)	56.2 (43.2 – 63.7)
H1B0E0C0	P1	55.8 (41.7 – 67.5)	63.4 (50.0 – 81.4)	3.6 (1.8 – 6.3)
	P2	61.7 (50.1 – 73.8)	63.2 (51.3 – 79.0)	9.5 (6.0 – 13.3)
	P3	57.6 (43.4 – 68.6)	62.9 (52.2 – 77.8)	65.0 (52.4 – 71.7)
H1B1E0C0	P1	33.6 (23.4 – 42.7)	38.8 (28.3 – 51.9)	3.6 (1.7 – 6.8)
	P2	33.0 (24.7 – 42.4)	35.9 (27.8 – 48.1)	9.0 (5.4 – 13.6)
	P3	34.2 (24.0 – 43.6)	33.3 (26.4 – 44.9)	67.6 (51.8 – 76.0)
H1B0E1C2C1	P1	12.4 (7.6 – 16.6)	55.0 (41.9 – 71.3)	1.0 (0.5 – 1.8)
	P2	15.8 (10.9 – 20.5)	47.4 (36.3 – 61.3)	3.5 (2.0 – 5.4)
	P3	12.6 (7.8 – 16.5)	40.9 (32.2 – 55.5)	38.6 (22.9 – 49.7)
H0B1E0C2	P1	6.1 (3.2 – 10.9)	52.9 (43.4 – 64.6)	0.5 (0.2 – 1.0)
	P2	9.4 (5.8 – 15.6)	43.1 (35.9 – 55.1)	2.3 (1.2 – 3.9)
	P3	6.2 (3.0 – 10.6)	34.6 (25.3 – 49.6)	26.9 (11.5 – 40.9)
H1B1E1C2C4	P1	1.2 (0.6 – 2.4)	8.3 (5.1 – 11.5)	0.6 (0.3 – 1.5)
	P2	1.8 (1.0 – 3.1)	6.8 (4.4 – 9.7)	2.8 (1.3 – 5.2)
	P3	1.3 (0.6 – 2.3)	5.4 (3.3 – 8.6)	32.1 (14.9 – 49.3)

This is the authors' version of a paper with reference: Valentina Melli , Bent Herrmann, Junita Diana Karlsen, Jordan Paul Feekings, , Ludvig Ahm Krag (2019) Predicting optimal combinations of by-catch reduction devices in trawl gears: A meta-analytical approach. Fish and Fisheries, Published by Wiley Online Library, December 2019, The version of record is available at: https://doi.org/10.1111/faf.12428

Table 4 Summary of the BRD combinations identified as most promising for the case-study fishery. H = Herding zone; B = Trawl body; E = Trawl extension.

Combination	**ID**	**BRDs included**				
		H	**B**	**E**	**Lower codend**	**Upper codend**
H0B0E1C0C1	1	-	-	x	90 mm diamond	120 mm diamond
H0B0E1C0C2	2	-	-	x	90 mm diamond	90 mm + 120 mm SMP
H0B0E1C0C3	3	-	-	x	90 mm diamond	120 mm + 180 mm SMP
H0B1E0C0	4	-	x	-	90 mm diamond	-
H0B1E1C0C2	5	-	x	-	90 mm diamond	90 mm + 120 mm SMP
H1B0E0C0	6	x	-	-	90 mm diamond	-
H1B0E1C0C1	7	x	-	x	90 mm diamond	120 mm diamond
H1B0E1C0C2	8	x	-	x	90 mm diamond	90 mm + 120 mm SMP
H1B0E1C0C3	9	x	-	x	90 mm diamond	120 mm + 180 mm SMP
H1B0E1C0C4	10	x	-	x	90 mm diamond	open
H1B0E1C2C0	11	x	-	x	90 mm + 120 mm SMP	90 mm diamond
H1B1E0C0	12	x	x	-	90 mm diamond	-
H1B1E1C0C1	13	x	x	x	90 mm diamond	120 mm diamond
H1B1E1C0C2	14	x	x	x	90 mm diamond	90 mm + 120 mm SMP
H1B1E1C0C3	15	x	x	x	90 mm diamond	120 mm + 180 mm SMP

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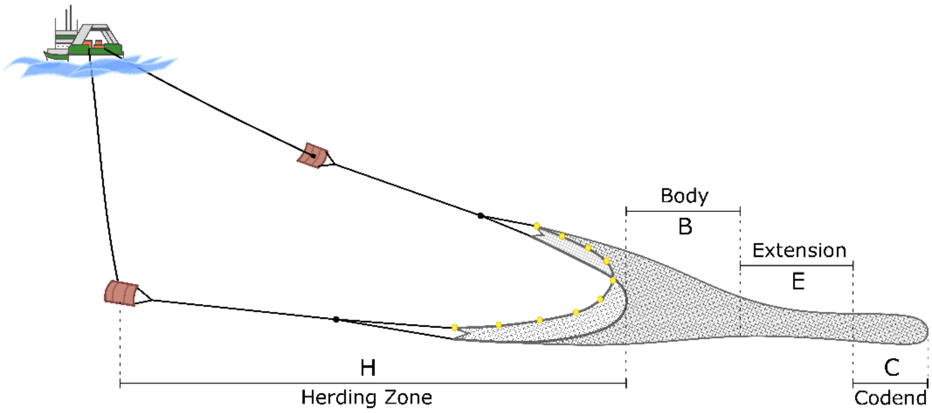

Figure 1 Schematic drawing of the four independent trawl sections considered in this study.

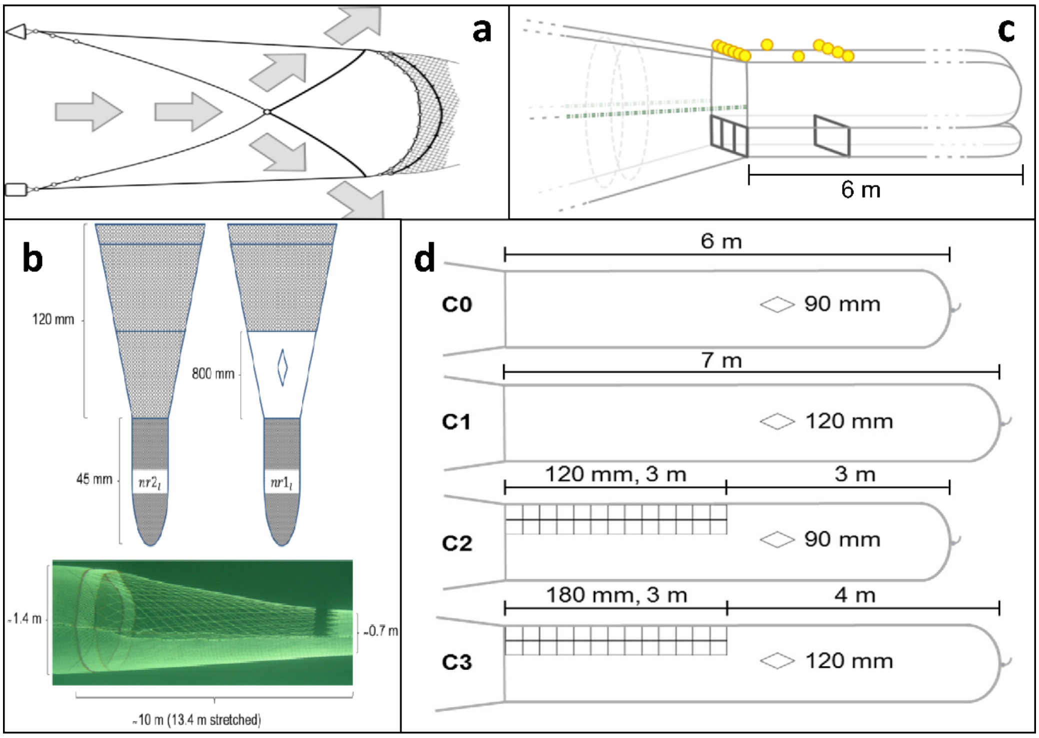

Figure 2 Schematic drawings of the BRDs included in the study. **a)** Counter-herding device from Melli et al., 2018a; **b)** Large meshes in the upper netting of the trawl body from Krag et al., 2014; **c)** Horizontally divided trawl codend from Melli et al., 2018b; **d)** C0: 90 mm diamond codend from Krag et al., 2013; C1: 120 mm diamond codend from Krag et al., 2014; C2: 90 mm diamond codend with

892 120 mm SMP from Krag et al., 2013; C3:120 mm diamond codend with 180 mm SMP from Krag et
893 al., 2014.

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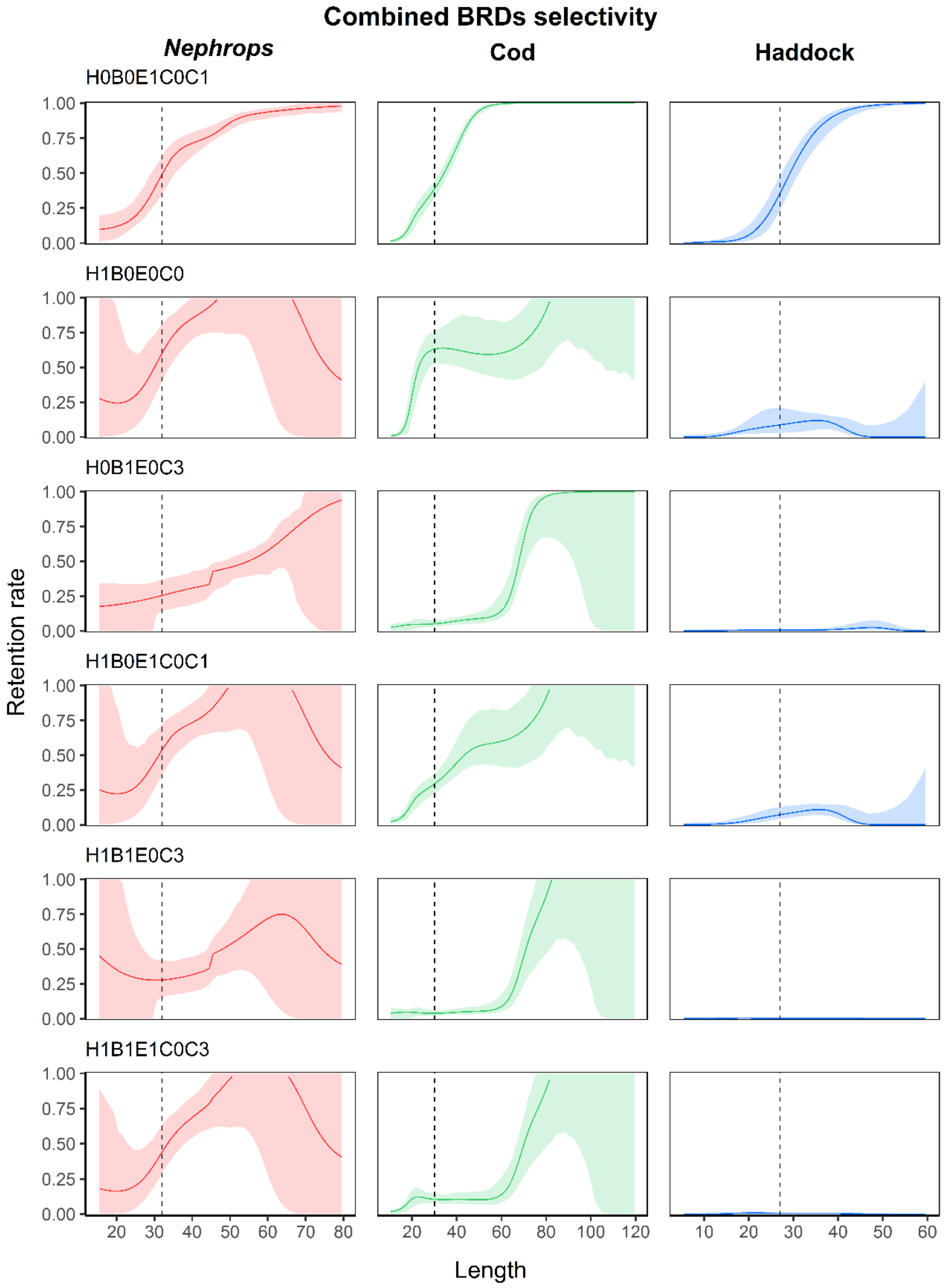

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Figure 3 Predicted selectivity curves (full lines) with 95% Efron CIs (ribbons) of six BRD combinations for the three species of interest. Lengths are in centimetres (total length) for fish species and millimetres (carapace length) for *Nephrops*.

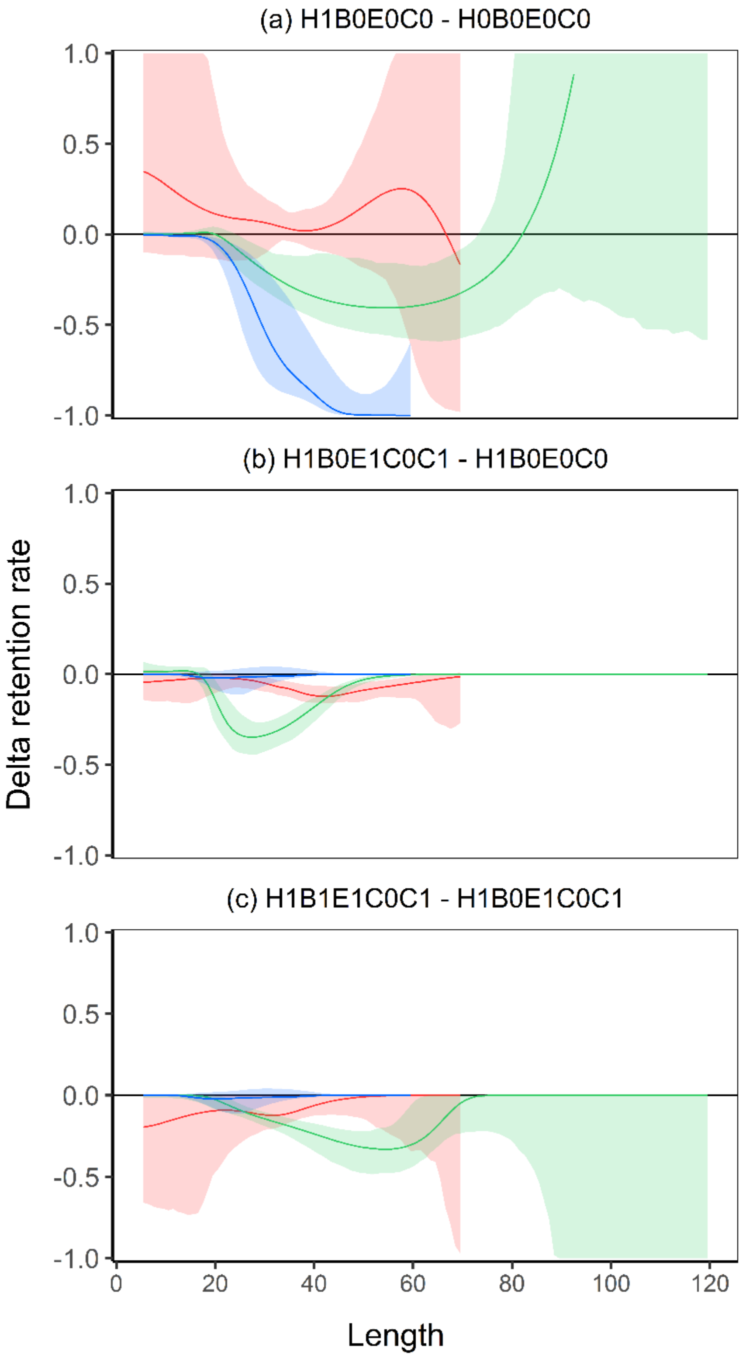

Figure 4 Delta selectivity with 95% Efron CIs (solid lines with ribbons) of increasing numbers of BRDs combined, for *Nephrops* (red), cod (green) and haddock (blue). (a) Counter-herding device+90 mm diamond codend (1 BRD) with respect to a trawl with a simple 90 mm diamond codend; (b) Addition of a second codend (2 BRDs) with respect to the 1-BRD selectivity; (c) Addition of a large

mesh size in the trawl body (3 BRDs) with respect to the previous 2-BRDs combination. Lengths are in centimetres (total length) for fish species and millimetres (carapace length) for *Nephrops*.

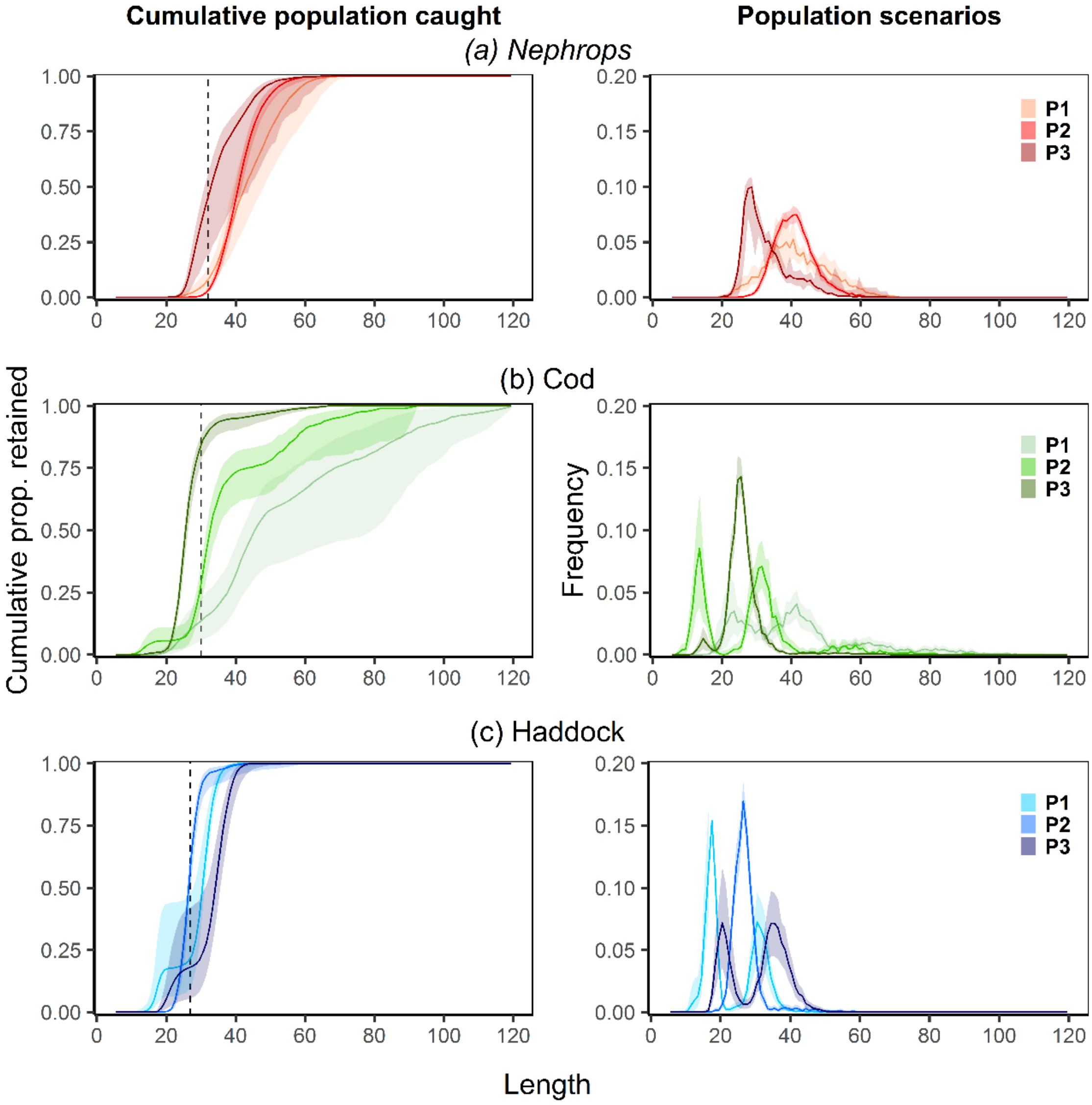

Figure 5 On the left column, cumulative catch curves with 95% Efron CIs (solid lines with ribbons) for the combination H1B0E1C0C1 under three population scenarios for (a) *Nephrops*, (b) cod and (c) haddock. The vertical dashed line indicates the MCRS for the species. On the right column, structure of the three population scenarios with 95% Efron CIs (solid lines with ribbons). Lengths are in centimetres (total length) for fish species and millimetres (carapace length) for *Nephrops*.

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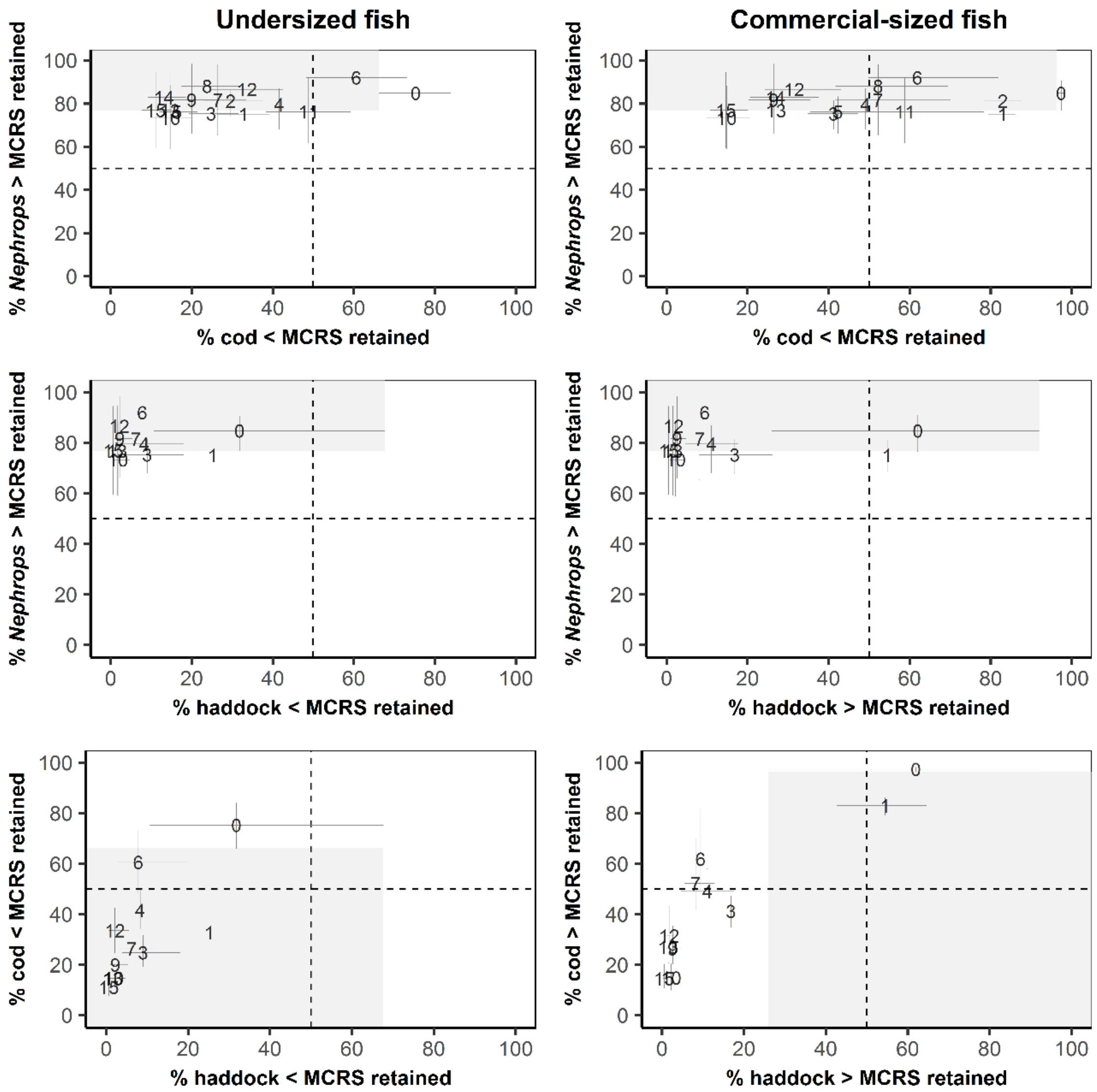

Figure 6 Two species comparisons of the performance of the most promising BRD combinations (15 for *Nephrops* and cod, and 10 for haddock) under the multispecies catch scenario. The numbers represents the ID of the combination as expressed in Table 4. On the left column, percentage (in weight) of undersized fish retained (wP^-). On the right column, percentage (in weight) of commercial-sized fish retained (wP^+). The first two rows show the percentage (in weight) of fish retained with respect to the percentage (in weight) of target catches (i.e. commercial-sized *Nephrops*). Dashed lines (vertical and horizontal) delineate 50% retention. Highlighted sections indicate desirable performances. MCRS = Minimum Conservation Reference Size.

APPENDIX 1

In this appendix we describe the models used for the size-selectivity in each of the original datasets and species included in the meta-analyses. Moreover, we report the fit statistics for each model fit.

In case of poor fit statistics (p-value <0.05; deviance >>DoF), the model curve plots and the residuals were examined to determine whether there were structural problems in describing the experimental data with the model or if it could be a case of data overdispersion (Wileman et al., 1996). When no systematic structure was detected, we considered the low *p*-values to be a consequence of overdispersion in the data. Such cases are frequent, especially when subsampling occured, and have been reported before in all the original studies included in this meta-analysis (Krag et al., 2013; Krag et al., 2014; Krag et al., 2015; Krag et al., 2016; Melli et al., 2018a; Melli et al., 2018b; Melli et al., 2019).

1. Paired gears datasets

1.1 Herding zone and trawl body

Data for these two Bycatch Reduction Devices (BRDs) were collected using paired gears, i.e. a modified test trawl towed in parallel with a control trawl. For each species, length-dependent count data for each gear were used to estimate the size-dependent catch comparison rate *cc(l)* with 95% Efron confidence intervals (Efron, 1982). The catch comparison rate *cc(l)* expresses the probability of a catching an individual of length *l* with the test trawl given that it was available to either trawl.

To model *cc(l)* we used a highly flexible model, often applied to this type of experiments (Krag et al., 2014; Melli et al., 2018a):

$$cc(l,\boldsymbol{v}) = \frac{\exp\left(f(l,\boldsymbol{v})\right)}{1.0+\exp\left(f(l,\boldsymbol{v})\right)} \qquad \textbf{(1)}$$

where *f* is a polynomial of the fourth order with coefficients $v_0,\ldots,v_4$ so $\boldsymbol{v} = (v_0,\ldots,v_4)$. We used *f* (*l*,***v***) in the following form:

$$f(l,\boldsymbol{v}) = \sum_{i=0}^{4} v_i \times \left(\frac{l}{100}\right)^i = v_0 + v_1 \times \frac{l}{100} + v_2 \times \frac{l^2}{100^2} + \cdots + v_4 \times \frac{l^4}{100^4} \qquad \textbf{(2)}$$

where the length *l* is divided by 100 to improve the numerical stability of the model fitting by preventing numerical overflow due to lengths being raised to powers in the polynomials. Leaving out one or more of the parameters $v_0\ldots v_4$ in equation (4) provided 31 additional models that were considered as potential models to describe *cc*(*l*,***v***). We then applied model averaging to describe *cc*(*l*,***v***), ranking the models according to how likely they were compared to each other (Burnham and Anderson, 2002). The individual models were ranked and weighted according to their Akaike's Information Criterion (AIC) values (Akaike, 1974; Burnham and Anderson, 2002; Herrmann et al., 2017) and models with AIC values within +10 the value of the model with the lowest AIC, were considered to contribute to *cc*(*l*,***v***) (Katsanevakis, 2006; Herrmann et al., 2017).

Fit statistics highlighted overdispertion in the data for both cod and haddock in the dataset used for the Herding zone (Melli et al., 2018a) and for cod in the trawl body dataset (Table 1).

Tabel 1. Fit statistics for the modelled catch comparisons.

	Cod	***Nephrops***	**Haddock**

	***p*-value**	**Deviance**	**DoF**	***p*-value**	**Deviance**	**DoF**	***p*-value**	**Deviance**	**DoF**
Herding zone	0.03*	100.75	76	0.06	53.49	39	0.01*	61.50	39
Trawl Body	0.01*	109.94	76	0.55	45.03	47	0.62	35.75	39

2. Covered-codend datasets

2.1 Trawl Extension

The BRD introduced in the trawl extension was a horizontal separation into two compartments; all individuals that entered the trawl were assumed to be caught in either the upper or lower compartment because of the mesh size used (40 mm T90) that is non-selective for the species considered. We were interested in estimating the length-dependent probability for an individual to enter the upper compartment, $c_{UPPER}(l)$. According to Krag et al. (2014), we used a length-dependent model containing four parameters (c_1, c_2, $L50_C$, and SR_C):

$$c_{\text{UPPER}}(l) = c_1 + (c_2 - c_1) \times \frac{\exp\left[\left(\frac{\ln(9)}{SR_C} \times (l - L50_C)\right)\right]}{1.0 + \exp\left[\left(\frac{\ln(9)}{SR_C} \times (l - L50_C)\right)\right]} \qquad (3)$$

In a Eq. (3) the probability for an individual to enter the upper compartment, $c_{UPPER}(l)$, follows a logistic curve within two asymptoms, c_1 and c_2. The constants c_1 and c_2 are constrained to the interval [0.0; 1.0] and represent the asymptotic probabilty of entering the upper compartment for the largest and smallest individuals, respectively. $L50_C$ is the length at which $c_{UPPER}(l)$ is the mean of c_1 and c_2. SR_C defines how quickly $c_{UPPER}(l)$ shifts from a value close to c_1 to a value close to c_2 with increasing length in the vicinity of $L50_C$. Thus, if SR_C is close to 0.0, the change in $c_{UPPER}(l)$ will appear over a small length range, whereas if SR_C has a value far from 0.0 the change in $c_{UPPER}(l)$ will cover a wider length span.

Model fits statistics (*p*-value, deviance, DoF) and parameters for $c_{UPPER}(l)$ of each species are summarized in Table 2.

Tabel 2. Fit statistic for the modelled $c_{UPPER}(l)$

Parameters	**Cod**	***Nephrops***	**Haddock**
$L50_C$	16.29	35.97	12.92
SR_C	4.91	5.11	2.38
c_1	0.76	0.22	0.77
c_2	0.30	0.11	0.00
p-value	0.31	0.34	0.03*
Deviance	79.59	47.21	57.96
DoF	74	44	39

2.2 Codends

For each species and each codend separately, we tested different parametric models to estimate the retention rate at length, $r(l, \boldsymbol{v})$, where $\boldsymbol{v}$ is a vector consisting of the parameters of the model. We chose the model with the lowest individual Akaike information criterion (AIC) value (Akaike, 1974).

2.2.2 *Nephrops*

The triple logistic model (Eq. 4) was found to describe best the size selectivity of *Nephrops* in the codends C0, C1 and C3 with the retention probability described by:

$$r(l, c_1, L50_1, SR_1, c_2, L50_2, SR_2, L50_3, SR_3) = c_1 \times Logit(l, L50_1, SR_1) + c_2 \times Logit(l, L50_2, SR_2) + (1.0 - c_1 - c_2) \times Logit(l, L50_3, SR_3) \quad \textbf{(4)}$$

The triple logistic model is constructed by assuming that there are three different selective processes which contribute to the overall selectivity, i.e. it is the sum of three logit models in which the weights of the contributions add up to 1.0 (Noack et al., 2017). These processes are determined by the multiple possible contacts modes of *Nephrops* with the codend meshes (Frandsen et al., 2010). In the triple logistic model, a fraction of individuals, c_1, will be subjected to one logistic size selection process with parameters $L50_1$ and SR_1; another fraction c_2 will be subjected to a second logistic size selection process with parameters $L50_2$ and SR_2; the remaining fraction ($1.0–c_1–c_2$) will be subjected to a third logistic curve with parameters $L50_3$ and SR_3. The contact ratio parameters c_1 and c_2 indicate the probability for an individual to have its selectivity determined by the first and second process, respectively (Herrmann et al., 2013). Thus, they are numbers between 0.0 and 1.0.

In contrast, the selectivity of *Nephrops* in the codend C2 was found to be described best by a Dual sequential selection curve (Eq. 5) with the first process modelled by a logistic curve and the second by the size selection model “Gompertz” (Wileman, 1996). This model implies that the selectivity of the codend is the result of two sequential selective processes. The first process is described by a logistic selection curve with parameters $L50_1$ (i.e. length of fish with a 50% retention probability) and SR_1 (i.e. difference in length between fish with 75% and 25% retention probabilities) while the second process is described by a “Gompertz” selection curve, with parameters $L50_2$ and SR_2. Because the two processes are sequential, the proportion of individuals that are exposed to the second process is assumed to consist of those that did not attempt to escape in the first process and additionally those that attempted to, but were retained. Therefore, c_1 represents the assumed length-independent probability that the size selection of the individual will be defined by both selection processes (double escape attempt), while 1.0 – c_1 represents the probability of the individual encountering only the second process. Thus, c_1 is a number between 0.0 and 1.0.

$$r(l, c_1, L50_1, SR_1, L50_2, SR_2) = (1.0 - c_1) \times Gompertz(l, L50_2, SR_2) + c_1 \times Logit(l, L50_1, SR_1) \times Gompertz(l, L50_2, SR_2) \quad \textbf{(5)}$$

Model fits statistics (*p*-value, deviance, DoF) and parameters for the size selectivity of *Nephrops* are summarized in Table 3.

Tabel 3. Fit statistics of the modelled size-selectivity for *Nephrops* in the four codends C0, C1, C2 and C3.

Parameters	**C0**	**C1**	**C2**	**C3**
L50	31.14	47.91	34.98	54.70
SR	10.20	17.13	19.21	65.97
1/δ	-	-	-	-
$L50_1$	48.72	52.37	28.80	66.10
SR_1	4.03	22.53	5.11	13.60
$L50_2$	30.97	47.33	33.79	44.63
SR_2	7.10	5.00	25.54	0.10
$L50_3$	0.10	33.75	-	0.58

SR_3	76.31	1.12	-	0.09
c_1	0.09	0.63	0.73	1.78
c_2	0.75	0.27	-	0.10
Model	4	4	5	4
p-value	0.96	0.42	0.06	0.93
Deviance	30.44	43.10	64.83	29.39
DoF	46	42	49	42

2.2.1 Cod

A Dual sequential size selection curve was found to describe best the selectivity of cod in the 90 mm diamond mesh size codend (C0) and in the 120 mm diamond codend with a 180 mm Square Mesh Panel (SMP; C3). For both codends the two selective processes were modelled using a logistic curve and a “Probit” curve, respectively (Eq. 6).

$$r(l, c_1, L50_1, SR_1, L50_2, SR_2) = (1.0 - c_1) \times Probit(l, L50_2, SR_2) + c_1 \times Logit(l, L50_1, SR_1) \times Probit(l, L50_2, SR_2) \quad \textbf{(6)}$$

Although a dual sequential size selection model is often expected when the codend include a SMP (e.g. C3), a second selective process can occur also in simple codends (e.g. C0) for example during haul-back of the gear (Madsen et al., 2012).

Similarly, the selectivity of cod in a 90 mm diamond mesh size codend with a 120 mm SMP (C2) was found to be described best by a Dual sequential size selection curve, but with both processes modelled by a logistic curve (Eq. 7).

$$r(l, c_1, L50_1, SR_1, L50_2, SR_2) = (1.0 - c_1) \times Logit(l, L50_2, SR_2) + c_1 \times Logit(l, L50_1, SR_1) \times Logit(l, L50_2, SR_2) \quad \textbf{(7)}$$

Finally, the selectivity of cod in a 120 mm diamond mesh size codend (C1) was described best by the classical size selection model “Richard” (Wileman, 1996). This is described not only by the parameters L50 and SR, but also by an additional parameter (1/δ) that describes the asymmetry of the curve.

Model fits statistics (*p*-value, deviance, DoF) and parameters for the size selectivity of cod are summarized in Table 4.

Tabel 4. Fit statistics of the modelled size-selectivity for cod in the four codends C0, C1, C2 and C3.

Parameters	C0	C1	C2	C3
L50	22.21	37.67	39.27	66.27
SR	7.57	13.35	14.14	13.84
1/δ	-	0.39	-	-
$L50_1$	19.63	-	44.01	68.08
SR_1	3.68	-	4.86	7.31
$L50_2$	19.29	-	29.83	36.63
SR_2	14.96	-	6.67	27.01
$L50_3$	-	-	-	-
SR_3	-	-	-	-
c_1	0.98	-	0.53	0.73
c_2	-	-	-	-
Model	6	Richard	7	6
p-value	0.90	1.00	0.98	0.79
Deviance	56.90	49.59	43.04	73.40
DoF	72	88	64	84

2.2.3 Haddock

The dataset used to estimate haddock size selectivity in a 90 mm diamond mesh size codend included a 270 mm SMP (Krag et al., 2016). Therefore, data for haddock in this codend were considered to have a binomial distribution, because individuals escaping from both the SMP and the codend were collected in the same cover. Following Krag et al. (2016), we estimated the selectivity of the codend indirectly based on the length-dependent retention data for the combined selection of SMP and codend. Indeed, the overall selectivity of a codend with a SMP is generally modelled as Dual selection model with two logistic curves (Eq. 7), where the first selection process is described by $L50_{SMP}$ and SR_{SMP} and the second by $L50_{codend}$ and SR_{codend}. Therefore, in the meta-analysis we considered only the parameters estimated for the logistic curve describing the selectivity of the 90 mm diamond mesh size codend.

Finally, the selectivity of haddock in the codend C1 and C3 was found to be described best by the size selection model “Richard” (*l*, L50, SR, 1/δ) and “Gompertz” (*l*, L50, SR), respectively (Wileman, 1996).

Model fits statistics (*p*-value, deviance, DoF) and parameters for the size selectivity of haddock are summarized in Table 5.

Tabel 5. Fit statistics of the modelled size-selectivity for haddock in codends C0, C1 and C3.

Parameters	C0	C1	C3
L50	52.96	29.61	111.39

SR	21.10	8.69	78.50
$1/\delta$	-	2.94	-
$L50_1$	53.01	-	-
SR_1	0.10	-	-
$L50_2$	28.01	-	-
SR_2	7.98	-	-
$L50_3$	-	-	-
SR_3	-	-	-
c_1	0.67	-	-
c_2	-	-	-
Model	7	Richard	Gompertz
p-value	<0.01*	0.98	0.89
Deviance	71.87	24.49	23.41
DoF	38	41	33

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APPENDIX 2

In this appendix we describe the populations used when investigating the performance of each combination under realistic catch scenarios for each of the species considered. The populations were generated using the original datasets included in this study, by pooling data over hauls for hauls with more than 20 individuals (Table 1).

Table 1. Summary of the data used to generate each population the three population scenarios for each of the species analysed.

Species	Population	Original dataset	No. of hauls	No. of individuals
Nephrops	P1	Krag et al., 2016	8	6438
	P2	Krag et al., 2014	22	12172
	P3	Melli et al., 2019	4	7014
Cod	P1	Krag et al., 2015	25	3018
	P2	Melli et al., 2018a	12	2333
	P3	Melli et al., 2019	6	3835
Haddock	P1	Melli et al., 2018b; 2019	14	5753
	P2	Krag et al., 2014	22	4793
	P3	Krag et al., 2015	15	4550

For the multispecies scenario, hauls from the dataset by Krag et al. (2014) containing more than 20 individuals for all the species considered were included (Table 2).

Table 2. Summary of the data used to generate the multispecies scenario.

Species	Original dataset	No. of hauls	No. of individuals
Nephrops	Krag et al., 2014	22	12172
Cod	Krag et al., 2014	22	4803
Haddock	Krag et al., 2014	22	4793

This is the authors' version of a paper with reference: Valentina Melli , Bent Herrmann, Junita Diana Karlsen, Jordan Paul Feekings, , Ludvig Ahm Krag (2019) Predicting optimal combinations of by-catch reduction devices in trawl gears: A meta-analytical approach. Fish and Fisheries, Published by Wiley Online Library, December 2019, The version of record is available at: https://doi.org/10.1111/faf.12428

Fig. 1 illustrates the structure of the resulting populations (P1-P3 for each species and the Multispecies scenario), as well as the 95% Efron (Efron, 1972) Confidence Intervals obtained by the bootstrapping procedure.

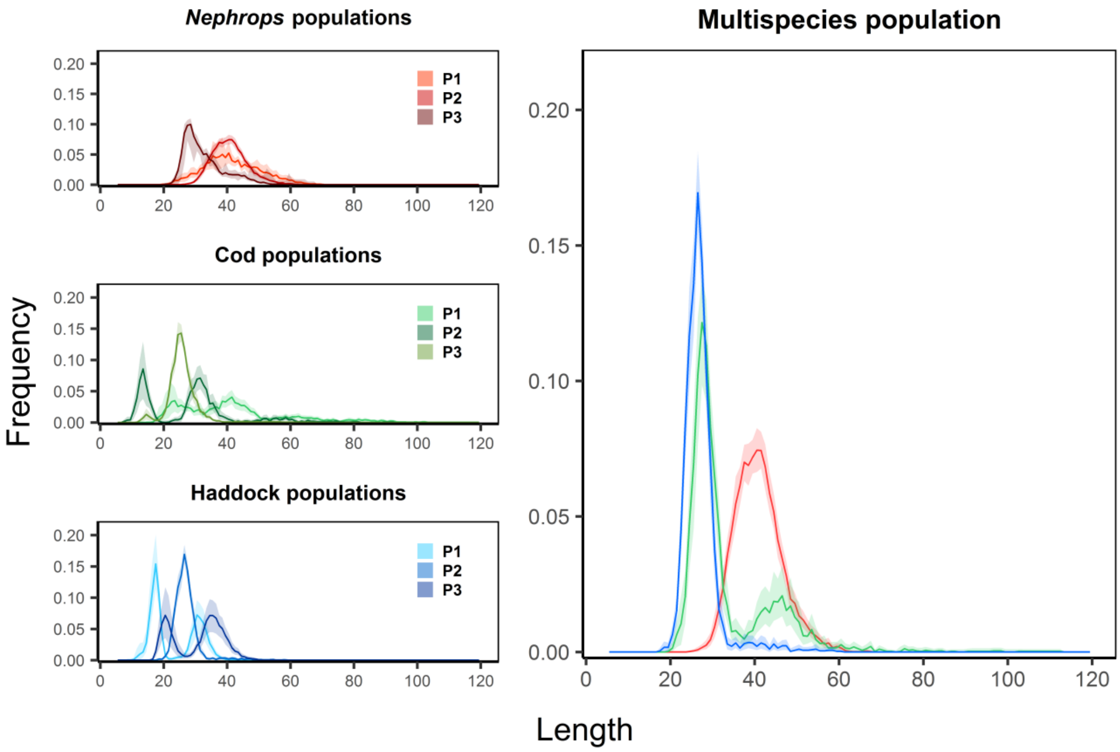

Figure 1. Frequencies of the length classes represented in each single-species and multispecies population scenario. Lengths are carapace length (mm) for *Nephrops* and total length (cm) for cod and haddock.

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