

Adapting the sampling design of research surveys to
improve the biomass estimation of non-target species -
the case study of *Raja clavata*

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Abstract

Research surveys are important to evaluate the spatial distribution of fishery resources and to monitor their abundance. However, the underlying sampling is usually conceived with the focus on specific species and an efficient design may reconcile this objective with the collection of non-target species data. This study evaluates the adequacy of different sampling designs for the IPMA bottom trawl survey conducted along the Portuguese continental coast. It aims to obtain the maximisation of accuracy estimates for the non-target thornback ray *Raja clavata*, while maintaining the estimates quality for the European hake, *Merluccius merluccius*, one of the target species. A geostatistical model-based approach was developed considering the semi-continuous nature of the data and the excess of zero values for *R. clavata*. The proposal of new sampling designs relied on eight optimisation weights and the resulting prediction exactness. Eight survey designs were then evaluated, each adding 11 sampling locations to the survey locations from the original survey design. Three designs resulted in higher accuracy for both *R. clavata* and *M. merluccius* estimates than those obtained from the random design. The sampling design that maximised the accuracy of *R. clavata* estimates showed an acceptable trade-off between bias and variance of *M. merluccius* estimates.

Keywords: Spatial sampling design; Species distribution models; Two-part models; Research Surveys; *Raja clavata*

1 Introduction

The fishery-independent quantitative species data collected during research surveys are important for monitoring the abundance of fishery resources, are commonly used as input for stock assessment models, and provide a basis for scientific advice on stock conservation status and fishing opportunities. Survey georeferenced data is also used to investigate the spatial and temporal distribution of species.

Although during the 1960s and 1970s stock trend analysis from stock assessments performed with virtual population analysis (VPA) were matched to fishery-dependent data (commercial catch per unit effort, CPUE), issues with the underlying assumption of a proportional relationship between CPUE and abundance emphasised the importance of

11 using fishery-independent information. The research survey programmes that began in
12 the 1960s were originally conceived as sources of biological information. Examples of these
13 are the Woods Hole bottom trawl resource survey, which started in 1963 (Smith, 2002),
14 and the International Bottom Trawl Survey in the North Sea, which started in 1965,
15 initially aimed at juvenile herring in the central and southern North Sea (ICES, 2020).
16 It was mainly in the 1980s that the data collected from research vessel surveys became
17 important to estimate fish abundance for use in stock assessments, at the same time
18 that survey design and estimation methodology were being developed (e.g., Pennington
19 (1983, 1986); Pennington and Volstad (1994); Smith (1999)). To improve cost efficiency,
20 the majority of research vessel surveys in the Northeast Atlantic area aim to collect data
21 for several species and stocks. In 2021, for example, 18 countries conducted bottom
22 trawl surveys in the North Sea and northeastern Atlantic areas on board several research
23 vessels, collecting data on the distribution and relative abundance as well as biological
24 information for a large number (over 50) of demersal species and stocks (ICES, 2021).
25 One of these surveys is the Portuguese International Bottom Trawl Survey (PT-IBTS-
26 Q4), conducted in Portuguese continental waters during Autumn. This survey started in
27 1979 and was initially designed to monitor the distribution and abundance of the most
28 important commercial species in the Portuguese trawl fishery (Cardador et al., 1997)),
29 although with a focus on estimating abundance indices of recruits of European hake
30 *Merluccius merluccius* and horse mackerel *Trachurus trachurus* (Borges, 1984; ICES,
31 1989).

32 The design of the PT-IBTS-Q4 survey has changed to that of a multi-species survey,
33 collecting data to estimate abundance and biomass indices in addition to biological pa-
34 rameters for other commercially important species, including fish (e.g., blue whiting *Mi-*
35 *cromesistius poutassou*, mackerel *Scomber scombrus* and chub mackerel *Scomber colias*),
36 crustaceans (e.g., *Nephrops norvegicus* and *Parapenaeus longirostris*) and cephalopods
37 (Chaves, 2018).

38 The design of multi-species or multi-purpose surveys requires attention to accuracy
39 for both target and non-target species, therefore requiring more complex and on-demand
40 sampling schemes. Classical sampling theory and geostatistics address similar questions
41 and result in unbiased estimates, but they are different. The former is related to design-
42 based inference and the latter relies on model-based inference (Hoef, 2002). According to
43 a comparison study presented in Hoef (2002), geostatistical methods can be more efficient
44 since they perform estimates closer to the true values. In particular, a Bayesian model-
45 based approach may easily account for the particularities of the species under study and
46 their habitat, as well as dealing with the different sources of variability usually present
47 in complex data. This flexibility entails some additional computational cost.

48 In this study, we develop a framework and propose methodologies to investigate
49 whether the Portuguese bottom trawl survey can be more efficient by adopting an al-

50 ternative spatial sampling design. The aim is to maximise the accuracy of abundance
51 estimates for non-target species of the survey while maintaining the precision of the sur-
52 vey target species abundance estimates. The species considered are the European hake,
53 which is a target species of the surveys, and the thornback ray, a non-target species, for
54 which PT-IBTS-Q4 data has been used to estimate biomass indices.

55 European hake is one of the most important species in western demersal surveys, given
56 its high abundance, wide distribution, and importance in the trophic chain (Casey and
57 Pereiro, 1995). This species is distributed from the coast of Mauritania to the western
58 coasts of Norway and Iceland; it is also found in the North Sea, Skagerrak, Kattegat, and
59 Mediterranean waters (Stehmann and Bürkel, 1984). It inhabits depths ranging from
60 30m to more than 500m, over mud/sand and rocky substrata (Casey and Pereiro, 1995).
61 Moreover, Portugal is one of the largest European markets for hake products (Sylvia,
62 1995).

63 The thornback ray is caught by Portuguese fisheries along the coast and is one of the
64 most common elasmobranch and skate species found in European waters (Walker and
65 Hislop, 1998; Machado et al., 2004) [Figueiredo et al, 2010](#). It is distributed along the
66 eastern Atlantic from Norway and Iceland to South Africa, including the Mediterranean
67 and Black Seas (Stehmann and Bürkel, 1984). The species is mainly found on hard seabed
68 (e.g., gravel and pebble), in areas of intermediate to strong tidal currents (Ellis et al.,
69 2005), from near shore to 300m deep, with extreme records around 1000m (Ebert and
70 Dando, 2021). From 1956, studies observed a decline in the occurrence of thornback ray
71 in the North Sea (Walker and Heessen, 1996; Dulvy et al., 2000), but in recent years its
72 stock has recovered in that area and throughout European waters (ICES, 2021).

73 This study evaluates survey efficiencies in estimating species biomass or abundance
74 by comparing estimates derived from a random survey (under this design fishing hauls
75 are randomly selected) to others obtained with alternative spatial sampling designs. To
76 achieve this, a common methodology is applied to the two selected species: one target
77 and one non-target. The procedure proposed is structured under a hierarchical Bayesian
78 framework, which includes the adjustment of a model-based approach that accounts for
79 the semi-continuous nature of the data and the excess of zero values for thornback ray.
80 We also consider the environmental variables that might impact on the distribution and
81 occurrence of the species under study. Finally, we compare the species model-based
82 abundance estimates obtained under eight alternative non-random survey designs with
83 those obtained from a random design. The eight different designs resulted from eight
84 different ways of selecting the fishing hauls, depending on the specific priorities of each
85 survey design. Comparison of the survey designs takes into account a balance between
86 maximising the accuracy of estimates and minimising the uncertainty, and a balance
87 between the objectives defined for both target and non-target species.

2 Material and Methods

2.1 Description of survey design

The PT-IBTS-Q4 survey, carried out by the Portuguese Institute for the Sea and Atmosphere (IPMA) using a bottom trawl (type Norwegian Campbell Trawl 1800/96 NCT) with a 20 mm codend mesh size and ground rope with bobbins, adopted a stratified random sampling design during the period 1979-1989. Initially (1979-1980), the surveyed area along the Portuguese continental coast (from latitude 41°20'N to 36°30'N and from 20 to 750 m bottom depth) was divided in 15 strata (Cardador et al., 1997). The boundaries of each stratum were based on five geographic areas and three bathymetric levels, each stratum being divided into units of around 25 square nautical miles. In 1981, with the aim of decreasing the total variance of mean abundance indices by species, the fishing hauls (sampling units) were spread at random over 36 strata (combination of twelve geographic areas and three bottom depth intervals: [20-100m]; [100-200m]; [200-500m]). Following analysis of the trade-off between biased estimates of species abundance with low variance and unbiased estimates with large variance, the survey design was changed to a predefined fishing hauls scheme in 1989 (ICES, 2002, 2017). The reduced variance of the abundance estimates obtained with the predefined sampling scheme was the dominant objective for the assessment of the southern stock of hake, at the time carried out with VPA tuning (ICES, 1990).

In 2005, the survey design changed to a sampling with partial replacement scheme (Cochran, 1977), recognising that the precision of the estimates for fish abundance trends over time could be improved by combining predefined and random fishing hauls, with a subset of hauls being matched from one survey to the next (ICES, 2004). A maximum of 96 fishing hauls, along the 36 survey strata, were sampled. These include 66 predefined hauls, distributed according to a regular grid of 5 x 5 nautical miles and taking into account that at least two fishing hauls should be made by stratum, with 30 hauls selected at random, carried out if ship time is available (ICES, 2002). Fishing hauls are carried out during daylight at a towing mean speed of 3.5 knots with a haul duration of 30 minutes (Chaves, 2018).

2.2 Species studied and environmental data

The exploitable biomass index of thornback ray, referring to the population encompassing fish with length over 50 cm, was calculated by haul and the unit used is kg/hour. The index of hake abundance is the number of fish caught per hour (nb/hour), which was also determined by fishing haul. The centroid position of each fishing haul (longitude, latitude) was calculated using the geographic coordinates of the start and final position of each fishing haul.

124 The studied area covers the western coast of Portugal (36°30'N to 41°20'N) (Figure
125 6). We adopted this restriction because the geomorphology of the Portuguese coast de-
126 termines different directions of the southern coast and its bathymetry, which is associated
127 with distinct oceanographic features and environmental conditions (Relvas et al., 2007)
128 as well as community assemblages (Moura et al., 2020). Figure 6 shows the nine geo-
129 graphic areas considered in our study, from CAM in the north to ARR in the south. The
130 type of substratum and bathymetry are the environmental variables considered as both
131 are known to be related with the thornback ray habitat (Santos et al., 2021). Bathy-
132 metric and type of substratum sediment data were collected from the EMODnet central
133 portal, accessible from <http://www.emodnet.eu/>. Bathymetric data was represented in
134 meters. The type of substratum was classified into five categories (sand; rock and boul-
135 ders; mud to muddy sand; mixed sediment and coarse-grained sediment) (Figure 7). We
136 excluded non-trawlable zones, characterised by the rock and boulders substratum, from
137 our prediction area (black zones represented in Figure 7).

138 **2.3 The proposed methodology**

139 Our methodology focuses on proposing alternative survey designs that enhance the most
140 accurate estimation of species abundance possible. Moreover, the proposed methodology
141 is flexible: it allows application to other species groups or even more than two species, the
142 introduction of different objectives, like minimising the cost of performing a survey, and
143 the incorporation of other survey constraints. For each survey design, 65 fishing hauls
144 were considered, of which 54 were predefined by the Portuguese bottom trawl survey and
145 11 were selected according to a particular objective. The specific constraints governing
146 this methodology were: do not consider non-trawlable zones, the study region is restricted
147 up to a depth of 200m, at least two fishing hauls must be sampled in each stratum, and
148 there is a minimum distance between survey locations. In our study, this distance is given
149 by the minimum distance between two observed locations.

150 The methodology proposed in this study includes the following steps (Figure 1:

- 151 1. Selection of the *best* species distribution model (SDM) under a Bayesian framework
152 and estimation of the predicted surface on a fine grid for each species using the
153 available observed survey data. The selection of the *best* SDM, was based on good-
154 ness of fit and predictive quality criteria, using deviance information criterion values
155 (Spiegelhalter et al., 2002) and log-conditional predictive ordinate values (Roos and
156 Held, 2011).
- 157 2. Selection of 11 new fishing hauls, according to weight (Table 1), to be added to the
158 predefined fishing hauls and establish alternative sampling survey designs 1-8. For
159 reasons of terminological simplicity, hereafter these designs will be referred to as
160 non-random conditional to the SDM used for weight construction.

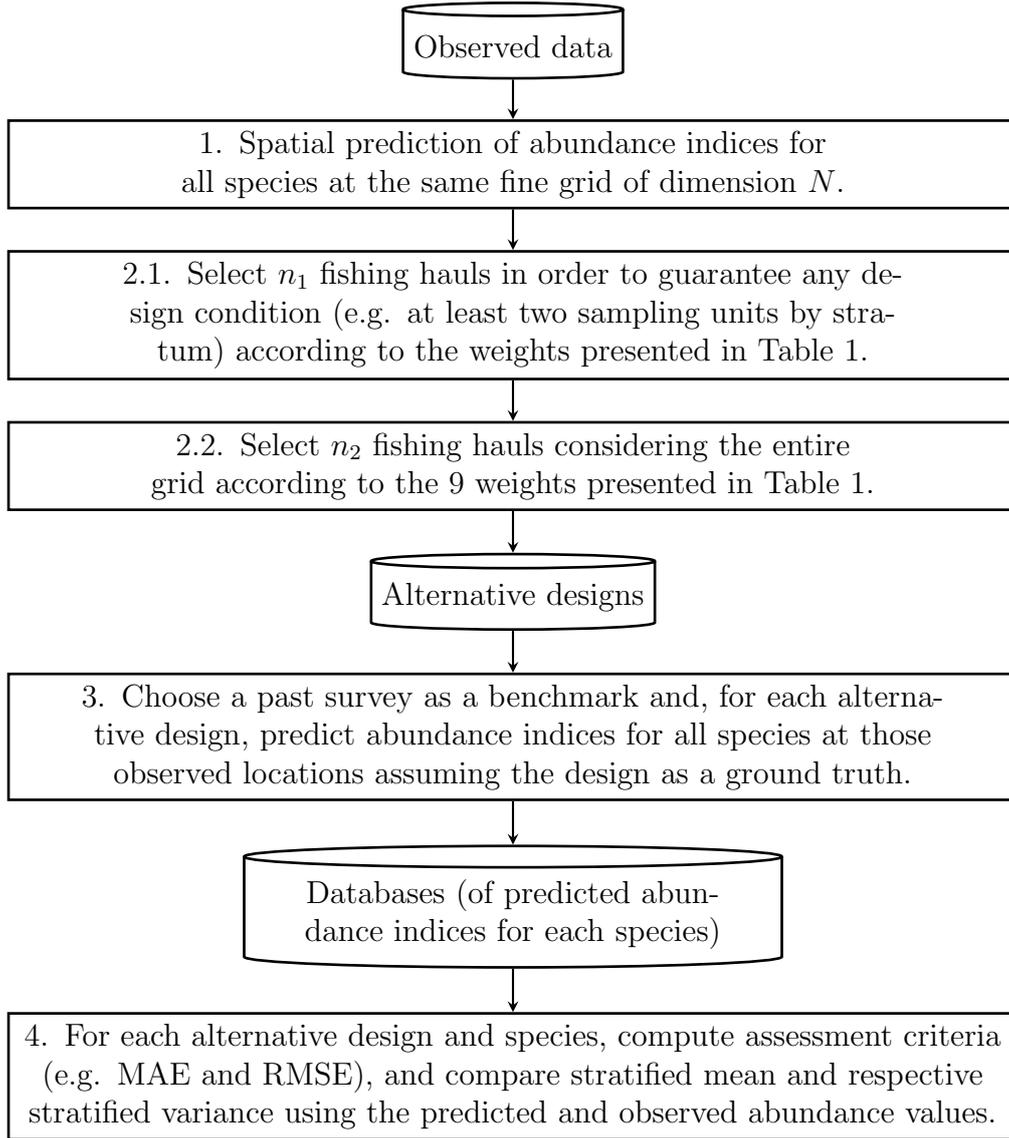


Figure 1: Methodology flowchart for the proposal and assessment of alternative survey designs.

161 3. Prediction of abundance indices for all species at the observed locations of the
 162 benchmark survey, assuming the design as the ground truth. This prediction pro-
 163 cedure considers the *best* SDM from step 1, for each of the species.

164 4. Comparison of the predicted and the observed values using the mean absolute or
 165 root mean square errors, the stratified mean and respective variance.

166 2.4 Species Distribution Model

167 The SDM of each species was constructed by assuming that, for the variables under study,
 168 no major differences occur between surveys as they take place at the same time of the

169 year. It is thus considered that the observations from the different surveys complemented
 170 each other and they are therefore treated as a single collection in time.

171 According to the SDM adopted, $Y(\mathbf{s})$ is a spatial process for the biomass index *Raja*
 172 *clavata* or the abundance index of *Merluccius merluccius* indices at location \mathbf{s} , and $Z(\mathbf{s})$
 173 is a presence/absence process that takes the value 0 if the species was not observed at
 174 location \mathbf{s} and 1 otherwise. Consequently, given that $Z(\mathbf{s}) = 1$, $Y(\mathbf{s})$ takes the positive
 175 value of biomass or abundance index observed at location \mathbf{s} . Under this SDM it is assumed
 176 that $Z(\mathbf{s})$ comes from a Bernoulli distribution with a probability of success, $p(\mathbf{s})$, and that
 177 $Y(\mathbf{s})$, given that $Z(\mathbf{s}) = 1$, follows a Gamma distribution with the shape parameter, $a(\mathbf{s})$,
 178 and scale parameter, $b(\mathbf{s})$. This two-part SDM is fitted under the Bayesian framework
 179 and can be defined as:

$$\text{logit}(p(\mathbf{s})) = \alpha_1 + \sum_{j=1}^{p_1} \beta_{i,j} f(X_{1,j}(\mathbf{s})) + W(\mathbf{s}) \quad (1)$$

180 and

$$\log(a(\mathbf{s})/b(\mathbf{s})) = \alpha_2 + \sum_{j=1}^{p_2} \beta_{i,j} f(X_{2,j}(\mathbf{s})) + kW(\mathbf{s}) \quad (2)$$

181 The probability of occurrence, $p(\mathbf{s})$, is modelled through the logit link function $\log\left(\frac{p(\mathbf{s})}{1-p(\mathbf{s})}\right)$,
 182 and the expected abundance or biomass index, $\mu(\mathbf{s}) = a(\mathbf{s})/b(\mathbf{s})$, through its logarithm.
 183 The $f(\cdot)$ denotes possible transformation functions, such as linear splines (Zuur et al.,
 184 2017) or a logarithm of environmental covariates, $X_{1,j}(\mathbf{s})$. The terms α_1 and α_2 represent
 185 the intercepts, and $\beta_{i,j}$, $i = \{1, 2\}$ are the regression coefficients (representing the impact
 186 of environmental conditions on the response variable). In this study, the environmental
 187 conditions considered were the bathymetry and the substratum sediment type. The *pri-*
 188 *ori* distributions for parameters α_i , $\beta_{i,j}$ and k were defined as Gaussian with mean zero
 189 and variance 1000, so that they are less informative since there is no a *priori* knowledge
 190 about these parameters.

191 $W(\mathbf{s})$ represents a spatial random effect modelled as a Gaussian Markov random field
 192 (GMRF), and it is further assumed to be an intrinsically stationarity process of mean
 193 zero. $W(\mathbf{s})$ resulted from an approximation of a latent Gaussian field (GF), using a
 194 method based on stochastic partial differential equations (SPDE), as proposed by Lind-
 195 gren et al. (2011). The SPDE approach allows approximation of a spatial continuous
 196 field, represented by a Matérn covariance function, by a Markov field. This approxi-
 197 mation was adopted due to its computational advantages. Parameterisation was carried
 198 out in terms of the marginal variance of the data, σ^2 , the radius of influence, ϕ , whose
 199 prior distributions were specified under PC prior framework (Simpson et al., 2017). The

200 two-part probability model can be represented as the product:

$$[Y(\mathbf{s})] = [Z(\mathbf{s})][Y(\mathbf{s})|(Z(\mathbf{s}) = 1)] \quad (3)$$

201 where $[\cdot]$ means “distribution of” and $\cdot|\cdot$ means “conditional to”.

202 **2.5 Alternative survey sampling designs**

203 Bearing in mind that the predefined fishing hauls could not guarantee at least two sam-
 204 pling units by stratum (combination of nine geographic areas and two bottom depth
 205 intervals: [0-100m]; [100-200m]), the second step considers a sampling procedure capable
 206 of selecting 7 (n_1) fishing hauls under this condition, and another 4 (n_2) spread over the
 207 entire prediction region.

208 The criteria for selecting the new fishing hauls varied according to two main specific
 209 objectives: minimisation of the uncertainty resulting from the modelling process, or max-
 210 imisation of the abundance index of both or either species, or even prioritising a specific
 211 region of the study area. Table 1 summarises the difference that corresponds to 8 weights,
 212 which are computed for each location of the prediction surface and condition the selection
 213 probability of those locations. These weights are based on the two components:

$$u_{\mathbf{s}}^i = \frac{\hat{y}_{\mathbf{s}}^i}{\max\{\hat{y}_{\mathbf{s}}^i\}} \quad (4)$$

214 and

$$v_{\mathbf{s}}^i = \frac{\hat{\sigma}_{\mathbf{s}}^i}{\max\{\hat{\sigma}_{\mathbf{s}}^i\}} \quad (5)$$

215 where $\hat{y}_{\mathbf{s}}^i$ refers to the median prediction estimate of biomass or abundance index and
 216 $\hat{\sigma}_{\mathbf{s}}^i$ represents the standard deviation of spatial effects for location $\mathbf{s} = \{\mathbf{s}_1, \mathbf{s}_2, \dots, \mathbf{s}_N\}$
 217 and species $i = \{R, M\}$, such that R identifies thornback ray and M identifies hake. It
 218 is possible to interpret $\hat{\sigma}_{\mathbf{s}}^i$ as an uncertainty measure of what was not explained by the
 219 covariates, that is, it represents the remaining variance after considering the explanatory
 220 variables. Both $\hat{y}_{\mathbf{s}}^i$ and $\hat{\sigma}_{\mathbf{s}}^i$ are standardised by the corresponding maximum, since the
 221 ranges of abundance and standard deviations of spatial effects were different for the two
 222 species.

223 In Table 1, the weights defined for designs 4 and 7 take into account the geographic
 224 area, through the component $q_{\mathbf{s}}$, which takes integer values from 1 to 9 ranging from
 225 higher to lower priority. Thus, locations from the same area have the same value for
 226 $q_{\mathbf{s}}$. In particular, weight 8 (maximise the similarity between the distributions of the
 227 two species) was aligned with that suggested by Pennino et al. (2016) to evaluate the
 228 overlapping of predictions from two datasets.

229 The new additional fishing hauls of alternative design, m , were defined as locations

230 of the fishing hauls corresponding to those that minimise the weights w_s^m : (i) for each
 231 incomplete stratum, leading to the proposal of 7 new fishing hauls to accomplish the
 232 survey condition together with 54 predefined hauls (at least two fishing hauls by stratum);
 233 (ii) for the entire study area to select the remaining 4 locations. Steps (i) and (ii) were
 234 repeated for each weight m presented in Table 1. This allows us to move forward with the
 235 proposal of the alternative survey sampling designs, which need to be evaluated among
 236 themselves and compared with a benchmark.

Table 1: Weights used to select new fishing hauls and corresponding objectives.

Design m	Weight w_s^m	Objective
1	$v_s^R \times v_s^M$	Minimise the uncertainty of what was not explained by the models applied to <i>R. clavata</i> and <i>M. merluccius</i> .
2	$v_s^R (1 - u_s^R) \times v_s^M (1 - u_s^M)$	Same objective of measure 1 maximising, at same time, the biomass or abundance of both species.
3	$v_s^R (1 - u_s^R) \times v_s^M$	Same objective of measure 1 maximising the biomass of <i>R. clavata</i> .
4	$v_s^R \times v_s^M \times q_s$	Same objective of measure 1 giving importance to geographic strata of the study area throughout q_s .
5	$\hat{\sigma}_s^R$	Minimise the uncertainty of what was not explained by the model for <i>R. clavata</i> .
6	$\hat{\sigma}_s^R (1 - u_s^R)$	Same objective of measure 5 maximising, at same time, the biomass of <i>R. clavata</i> .
7	$\hat{\sigma}_s^R \times q_s$	Same objective of measure 5 giving importance to geographic strata of the study area throughout q_s .
8	$\sqrt{(\sqrt{u_s^R} - \sqrt{u_s^M})^2}$	Maximise the similarity between the distributions of the two species.
Random	$\frac{1}{N}$	Random selection giving the same importance to all locations.

237 2.5.1 Assessment methodology of the alternative survey designs

238 The third step includes a survey that took place in the past used as a benchmark (in
 239 our case study, we chose the 2015 survey). Then, for each proposed design, we predict
 240 abundance indices for all species at the observed locations, assuming the design as the
 241 ground truth. This prediction procedure considers the *best* SDMs selected in step 1 of

242 Figure 1. We end up with eight databases of predicted abundance indices for each species.
243 Each database holds the centroid position (longitude and latitude) of the fishing hauls, all
244 covariates (in our case, the corresponding bathymetry and the substratum type), and the
245 predictive posterior medians for the non-target and target species (in our case, thornback
246 ray biomass and hake abundance indices).

247 In the last step of the flowchart shown in Figure 1, the biomass or the abundance
248 index predicted values for each species are compared with the values observed in the
249 benchmark survey using classic assessment metrics, such as mean absolute error (MAE),
250 root mean square error (RMSE) (Chai and Draxler, 2014), stratified mean (\bar{y}_{str}) and
251 corresponding stratified variance (s_{str}^2) (Ghosh, 1958).

252 Furthermore, with the aim of further evaluating the first eight survey designs that
253 result from the respective weights proposed in Table 1, we suggest contrasting them with
254 a random design (the ninth design presented in Table 1), which has a random selection
255 of locations according to a homogeneous spatial Poisson process. Firstly, we simulated
256 200 sets of fishing hauls, allowing the random selection of new locations (in our case,
257 11) as long as they meet the predefined design constraints (in our case, having at least
258 two sampling units by stratum). Secondly, we computed four assessment metrics, MAE,
259 RMSE, \bar{y}_{str} and s_{str}^2 , by comparing the predicted values of biomass or abundance index
260 obtained from each of the 200 simulated sets with those observed in the benchmark
261 survey. Finally, we considered the empirical distribution of the 200 values obtained
262 for the assessment metrics as an approximation of their theoretical distribution function.
263 That way, the random design is used for evaluating the performance of the eight proposed
264 non-random sampling designs.

265 The R code corresponding to the survey design procedure and its assessment is
266 available on GitHub ([https://github.com/SilvaPDaniela/Evaluation-of-survey-
267 designs-for-species-distribution-estimation](https://github.com/SilvaPDaniela/Evaluation-of-survey-designs-for-species-distribution-estimation)).

268 **3 Results**

269 **3.1 Frequency of occurrence and observed biomass of 270 thornback, and abundance of hake**

271 During the period 2013-2016, the thornback ray biomass index was computed in 212
272 fishing hauls along the west coast of Portugal, with this information available for at least
273 49 different fishing hauls each year. The number of fishing hauls with a strictly positive
274 value for the catch of thornback ray varied between 6 (2014) and 15 (2015) (Table 2).
275 Between 2015 and 2016, the hake abundance index was computed for 101 fishing hauls.
276 The number of hauls with strictly positive values for the catch of hake was 50 and 44, in
277 2015 and 2016, respectively (Table 2).

Table 2: Number (nb) of recorded fishing hauls, number of fishing hauls with a strictly positive catch, and percentage of zero catches by species, during PT-IBTS-Q4 surveys conducted between 2013 and 2016.

Species	Fishing hauls/catch	2013	2014	2015	2016	Total
Thornback ray	nb of recorded fishing hauls	57	49	54	52	212
	nb of fishing hauls with presence	9	6	15	11	41
	% of zero catch	84	88	72	79	81
Hake	nb of recorded fishing hauls	-	-	53	48	101
	nb of fishing hauls with presence	-	-	50	44	94
	% of zero catch	-	-	6	8	7

278 The highest exploitable biomass index of thornback ray (fish total length over 50cm;
 279 kg/hour) was observed in the area near Lisbon in 2015 and 2016 (Figure 6). The annual
 280 percentage of zero catches of thornback ray was high, varying between 72% and 88%
 281 (Table 2). The empirical distribution of positive of thornback ray catches (kg/hour)
 282 during 2013-2016 was right skewed, with a biomass index range of 2.0-24.9 kg/hour and
 283 a mean value of 7.8 kg/hour (Figure 8). The abundance index of hake (nb/hour) was
 284 higher in 2015 than 2016, particularly in the northern part of the western Portuguese
 285 coast (Figure 6). The percentage of zero catches for this species was low, 6% in 2015 and
 286 8% in 2016 (Table 2). The empirical distribution of positive hake catches (nb/hour) was
 287 also right skewed, with a range between 2 to 3933 individuals and a mean value of 411
 288 fish per hour (Figure 8).

289 3.2 Species Distribution Model

290 To check the assumption that both species have a similar spatial distribution over surveys
 291 because they take place at the same time of the year (near October), we applied the
 292 Knox and Mantel statistical tests for space-time interaction (Meyer et al., 2016) to our
 293 datasets. Both statistical tests resulted in high p-values for both species, indicating that
 294 our assumption was not violated. In addition, the results of the Kolmogorov-Smirnov test
 295 (Frank and Massey, 1951) confirmed the adequacy of a Gamma distribution to model the
 296 strictly positive values, which indicated p-values of 0.808 and 0.603 for thornback ray
 297 biomass and hake abundance, respectively.

298 3.2.1 Thornback ray biomass

299 Table 3 presents a summary of the results obtained for the *best* SDM chosen for the
 300 thornback ray. The model was fitted to these data, considering the SPDE approach and
 301 taking into account the substratum sediment type and bottom depth covariates as fixed
 302 effects. The probability of species occurrence increases more than five times for fishing

Table 3: Main statistics of the posterior distributions for fixed effects for the thornback ray biomass index. S.D. is the standard deviation and ‘:’ refers to interaction between covariates. χ_q identifies the quantile of probability q .

Process	Covariate	Mean	S.D.	$\chi_{0.025}$	$\chi_{0.5}$	$\chi_{0.975}$	Mode
$Z(\mathbf{s})$	Intercept	-1.574	0.517	-2.705	-1.546	-0.610	-1.505
	Substratum (Mixed sediment)	10.104	6.002	-1.529	10.046	22.071	9.937
	log(Depth):Substratum (Mixed sediment)	-2.488	1.508	-5.498	-2.475	0.439	-2.449
$Y(\mathbf{s}) Z(\mathbf{s}) = 1$	Intercept	3.630	1.054	1.519	3.639	5.684	3.659
	log(Depth)	-0.443	0.220	-0.879	-0.442	-0.010	-0.441

303 locations with a mixed sediment substratum (mean and median around 10.1). Depth
304 exhibited a negative relationship with species occurrence in mixed substratum sediment
305 (mean and median around -2.5) and also with species biomass index (mean and median
306 around -0.44). The thornback ray occurrence results indicated some uncertainty associ-
307 ated with these regression coefficient estimates, but we kept the corresponding covariates
308 to achieve better predictive performance of the model. The posterior distributions of
309 spatial covariance parameters for the thornback ray biomass model showed that spatial
310 autocorrelation is almost null from approximately 66 km and the mode for the marginal
311 standard deviation of the spatial effects was 1.1 (second and third panels in the upper
312 row of Figure 2). The mean precision of the Gamma observations was estimated as 3.5
313 (Figure 2, first panel, upper row).

314 The left panel of Figure 3 represents the posterior median of the predictive distribu-
315 tion for the thornback ray biomass index, obtained according to the product defined in
316 equation (3). As an indicator of uncertainty resulting from the modelling procedure, the
317 right panel of Figure 3 represents the posterior standard deviations of the spatial effects,
318 $W(\mathbf{s})$, derived for the thornback ray model. Unsurprisingly, the standard deviation esti-
319 mates of spatial effects were lower near to sampled locations since the estimation in these
320 locations is more accurate.

321 3.2.2 Hake abundance

322 Table 4 presents a summary of the results for the fixed effects resulting from the *best*
323 SDM chosen for hake. The probability of occurrence and the abundance index of hake
324 increase with logarithm of depth. In areas with a bottom depth shallower than 90m, the
325 abundance index of hake increases by 15 fish per hour, which rises to 31 fish per hour
326 for each increment of approximately 2.7m in depth in areas where water is deeper than
327 90m. Regarding substratum sediment type, results indicated that hake is nearly twice as
328 abundant in mud and muddy sand locations than in other type of sediment substratum.

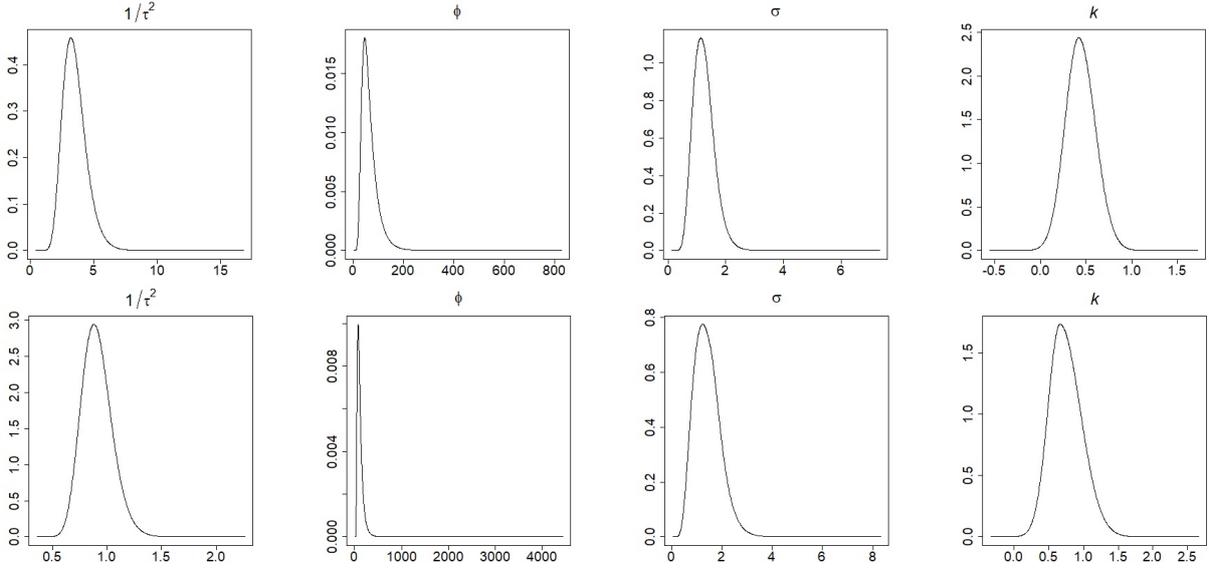


Figure 2: Posterior distributions of hyperparameters for thornback ray biomass (upper panel) and hake abundance (lower panel) indices. $1/\tau^2$ refers to the precision of the Gamma observations, ϕ to the spatial range, σ to the standard deviation of spatial effects, and k is the scale parameter between the two processes (occurrence and biomass or abundance given the occurrence).

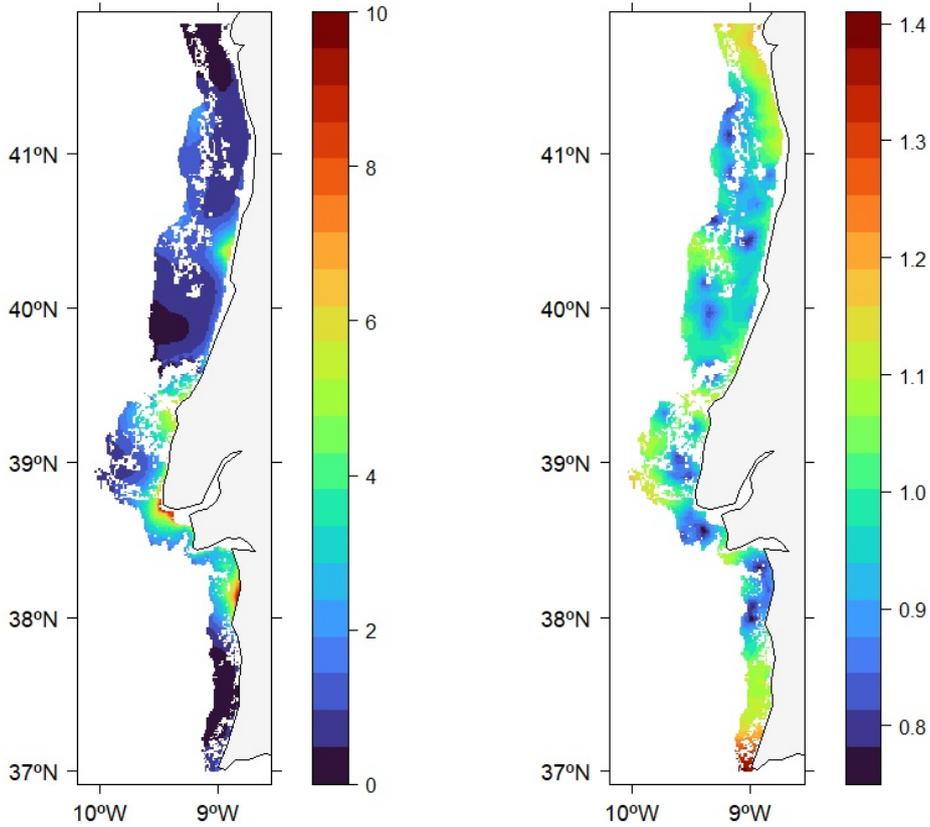


Figure 3: Map of the posterior median of the predictive distribution of biomass index (left panel) and posterior standard deviations (right panel) of spatial effects of thornback ray.

Table 4: Main statistics of posterior distributions for fixed effects for the hake abundance index. S.D. is the standard deviation and ‘:’ refers to interaction between covariates. χ_q identifies the quantile of probability q .

Process	Covariate	Mean	S.D.	$\chi_{0.025}$	$\chi_{0.5}$	$\chi_{0.975}$	Mode
$Z(\mathbf{s})$	Intercept	-12.963	5.596	-24.193	-12.910	-2.048	-12.816
	log(Depth)	3.768	1.368	1.134	3.746	6.538	3.708
$Y(\mathbf{s}) (Z(\mathbf{s}) = 1)$	Intercept	-9.834	3.260	-16.303	-9.816	-3.472	-9.781
	log(Depth)	15.039	3.361	8.445	15.032	21.665	15.020
	(log(Depth)- 4.521) ₊	15.902	3.260	9.577	15.872	22.397	15.814
	Substratum (Mud to muddy sand)	0.807	0.309	0.205	0.805	1.420	0.802

329 Regarding the spatial covariance parameters for the hake abundance model, no spatial
330 autocorrelation is expected for distances over 110 km and the mode for the marginal
331 standard deviation of the spatial effects was 1.2 (second and third panels in the lower
332 row of Figure 2). The precision mean for Gamma observations was estimated as 0.9 (first
333 lower row panel of Figure 2).

334 The left panel of Figure 4 represents the posterior median of the predictive distribu-
335 tion for the hake abundance index. The right panel of Figure 4 represents the posterior
336 standard deviations of the spatial effects, $W(\mathbf{s})$, derived for the hake model. In accor-
337 dance with what was also observed for the thornback ray biomass model, the uncertainty
338 indicators for hake estimates were lower near the sampled locations.

339 3.3 Evaluation of alternative survey designs

340 Table 5 presents, by species, the assessment criteria values (MAE, RMSE, the stratified
341 mean and its variance) used to evaluate each of the eight alternative non-random survey
342 designs. We also present the stratified mean and its variance for the thornback ray
343 biomass index and hake abundance index, as estimated for the 2015 survey. In the case
344 of the thornback ray, survey sampling designs with new fishing hauls selected according
345 to weights 4, 7 and 8 provided better results for MAE and RMSE criteria. In all sampling
346 designs, excluding 3 and 6, the stratified mean estimates of the thornback ray biomass
347 index were lower than the corresponding 2015 estimates. Regarding hake abundance,
348 survey designs 2, 5, 8 and 7 produced lower MAE and RMSE values than the other
349 designs. The stratified mean abundance estimate obtained with sampling designs 2, 8
350 and 7 were closer to the corresponding 2015 estimates (Table 5).

351 Weights 2, 3 and 6, which consider the standardised estimates of biomass/abundance
352 for one or both species, presented higher MAE and RMSE values for the thornback
353 ray. Indeed, maximising the biomass and/or abundance indices estimates provided a

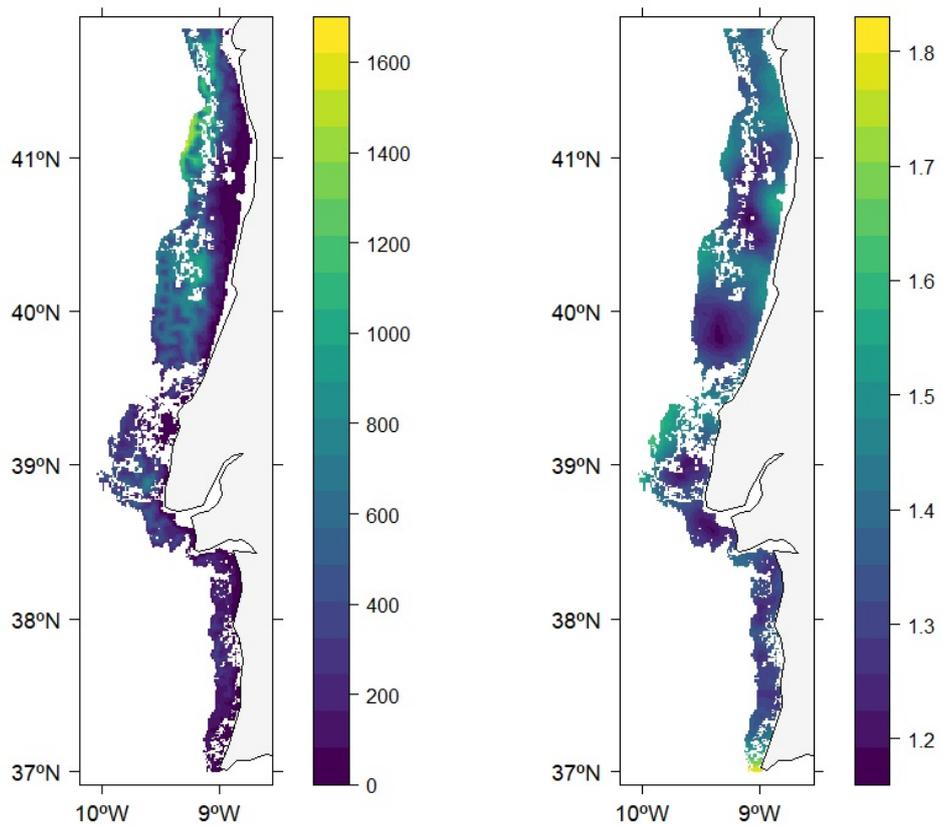


Figure 4: Map of the posterior median of the predictive distribution of the abundance index (left panel) and posterior standard deviation of spatial effects (right panel) for hake.

Table 5: Values of the assessment metrics computed for the thornback ray and hake for each proposed measure, to be used in performance evaluation of the eight alternative non-random survey designs. We also provide the values of the stratified mean and its variance, estimated from the benchmark survey (2015). Grey lines indicate the best alternative survey designs. MAE – mean absolute error; RMSE – root mean square error; \bar{y}_{str} – stratified mean; s_{str}^2 – stratified variance.

Alternative design	<i>Raja clavata</i>				<i>Merluccius merluccius</i>			
	MAE	RMSE	\bar{y}_{str}	s_{str}^2	MAE	RMSE	\bar{y}_{str}	s_{str}^2
1	2.714	5.186	1.199	0.023	362.817	679.665	361.103	514.626
2	3.131	5.613	1.302	0.039	351.124	651.092	398.689	649.951
3	2.907	5.326	1.442	0.021	359.350	675.524	380.254	473.513
4	2.551	4.866	1.083	0.015	353.809	670.369	379.395	578.688
5	2.862	5.191	1.163	0.029	344.788	660.462	371.376	586.391
6	3.005	5.394	1.464	0.048	360.094	677.111	381.132	480.876
7	2.533	4.848	1.205	0.023	350.664	664.200	381.839	597.662
8	2.690	5.186	0.953	0.012	349.950	659.390	388.539	602.207
Year 2015	-	-	1.401	0.208	-	-	460.246	3325.801

less accurate prediction process, highlighting the importance of minimising the standard deviation estimates of spatial effects, which can be seen as a measure of uncertainty in the estimation process. This feature was confirmed by the results for hake abundance index estimates, where designs 3 and 6 also presented two of the worst MAE and RMSE results.

Figure 5 presents the MAE and RMSE sampling distribution for the random design, in which the location of the 11 new fishing hauls were randomly selected from a homogeneous spatial Poisson process. Results confirmed that the survey sampling designs with new fishing hauls selected according to measures 4, 7 and 8 resulted in higher accuracy for thornback ray biomass than that obtained with a random selection of fishing hauls. Regarding estimation of the hake abundance index, all sampling designs outperformed the random design (Figure 5).

Survey design 7 presented the best results of the eight proposed non-random designs, since it provided the best balance between the accuracy of results for the target and the non-target species. This survey design was based on defining the location of the 11 new fishing hauls (western Portuguese coast) that minimise the uncertainty of what was not explained by the thornback ray biomass model and give importance to specific geographic areas in the study area (namely, those with higher values of ray biomass). Although it did not present the best results for estimation of the hake abundance index *per se* (design 8 may be preferable), it provided good commitment when analysing results together with the non-target species. Therefore, we believe that by adopting survey design number 7 for the PT-IBTS-Q4 survey, the accuracy of the thornback ray biomass index estimates will improve, without jeopardising estimation of the hake abundance index.

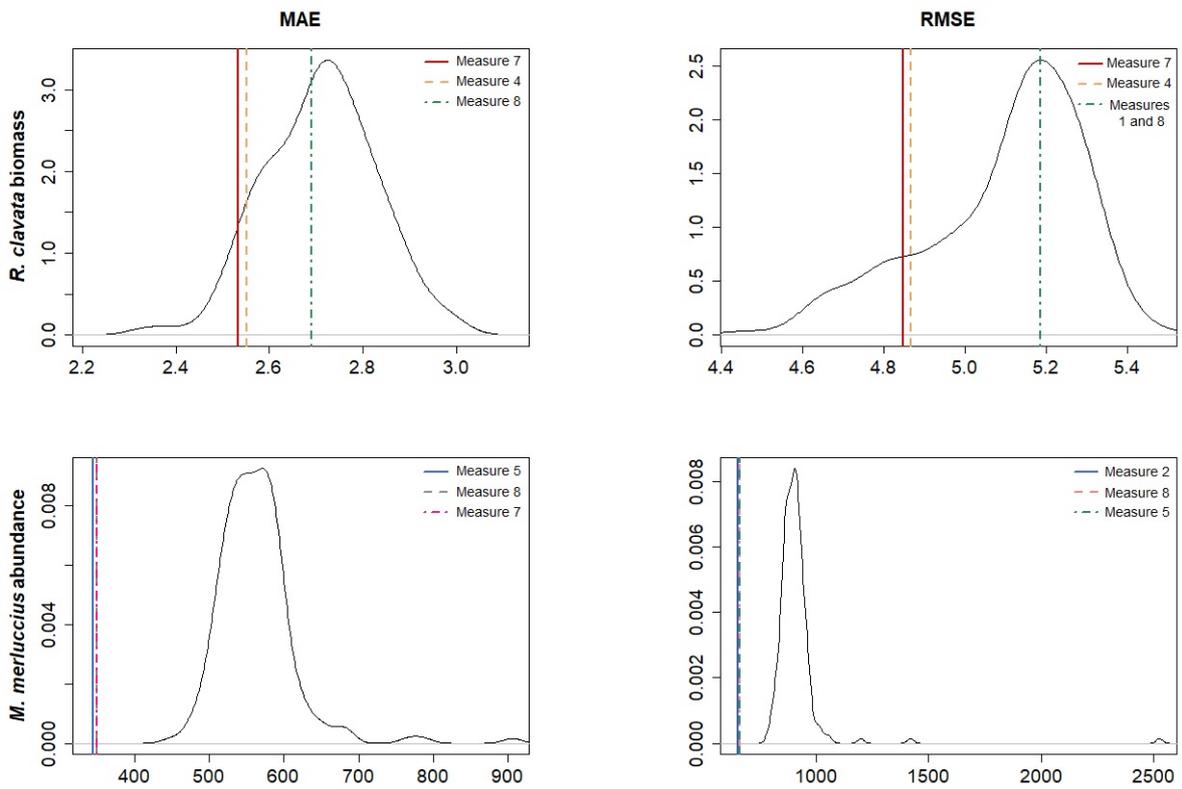


Figure 5: Distribution MAE (left panels) and RMSE (right panels) densities resulting from the estimation of thornback ray biomass (top panels) and hake abundance (bottom panels), indices based on 200 sets of 52, randomly selected fishing hauls. Vertical lines represent the three best alternative surveys for each species (with lowest values of MAE and RMSE). See Table 1 for the definition and objectives of each weight.

377 4 Discussion

378 Fisheries research vessel surveys should be efficient since marine survey programmes are
379 expensive and time-consuming, but few studies have been published investigating the
380 efficiency of multi-species sampling designs. Recently, Zhang et al. (2020) evaluated
381 multi-species fisheries surveys considering several sampling and estimation methods and
382 a wide range of sample sizes. The basis of their study was a simulation framework
383 considering the joint distribution of multiple species. In our study, we develop a four-
384 step framework to evaluate the accuracy of alternative sampling designs for a bottom
385 trawl research survey, focusing on improving the accuracy of abundance estimates for
386 one non-target species, while maintaining the precision of the abundance index estimates
387 of one target species. In the first step, we used the species spatial abundance index
388 observed in previous surveys coupled with spatial environmental data to model species
389 abundance. In the second step, and for a fixed number of fishing hauls, we defined
390 alternative sampling designs by selecting the extra fishing hauls while maintaining fishing
391 hauls from the adopted design (i.e., a combination of predefined and random fishing
392 hauls). In the third step, we took a previous survey as a benchmark, and predicted the
393 species abundance index for these locations. In the final step, we compared the predicted
394 values to those observed at the benchmark. The best alternative design was selected by
395 evaluating the trade-off between increasing the accuracy of abundance index estimates
396 for the non-target species and the precision of the abundance index estimates for the
397 target species. The trade-off was evaluated based on an analysis of the MAE, RMSE,
398 stratified mean and its variance obtained for each species, and an alternative survey
399 sampling design. The combination of MAE and RMSE metrics are often likewise used
400 to assess model performance (Chai and Draxler, 2014). The stratified mean abundance
401 estimate and its variance were selected from other possible abundance/biomass estimates
402 (e.g., the mean) so as to be in accordance with the survey’s stratified random sampling
403 design, an estimator commonly used in bottom trawl research surveys (ICES, 2017, 2020).
404 Indeed, the stratified sampling design provides higher accuracy for abundance/biomass
405 index estimates than simple random sampling, since it is based on strata that are more
406 homogenous within themselves than between them (Cochran, 1977; Lohr, 2009).

407 Species distribution models (SDMs) are increasingly popular (e.g., Coelho et al.
408 (2018); Thorson and Barnett (2017); Martínez-Minaya et al. (2018); Azevedo and Silva
409 (2020) as they allow the combination of species occurrence observations and/or abun-
410 dance with environmental information, incorporate both spatial and temporal variability,
411 and may have either a single or multi-species focus. In our study, we used a geostatistical
412 model-based approach instead of a design-based approach to define the sampling design of
413 research surveys. In a Bayesian framework, combining SDMs with geostatistical methods
414 has proven to be ideal for handling the different sources of variability underlying complex

415 data correlated in space (Izquierdo et al., 2022; Martínez-Minaya et al., 2018; Pennino
416 et al., 2019). Modelling was conducted assuming the SDM formulation for both species
417 and allowing for the particularities of the spatial distribution of each species. In this
418 sense, we performed a previous exploratory analysis of data to verify the reasonableness
419 of assuming the same SDM formulation. A common feature in abundance data is the
420 semi-continuous nature of the response variable and also a high number of zero values,
421 particularly for species with a patchy distribution (e.g., Paradinas et al. (2017)). Both
422 features were mainly observed for the thornback ray during the PT-IBTS-Q4 survey time-
423 series, but also for hake. Therefore, our SDM considered a two-part model for species
424 occurrence together with abundance or biomass. We incorporated ancillary information,
425 namely georeferenced data on substratum sediment type and bottom depth data, since
426 if there is a relationship between the covariates and the abundance of the species, it is
427 possible to predict species abundance for unsampled locations.

428 We proposed eight optimisation weights for selecting the extra locations of fishing
429 hauls and making it more likely to choose locations that better represent the spatial dis-
430 tribution of the non-target and/or target species (in our motivating example, the thorn-
431 back ray and hake species, respectively). We also assessed the performance of the eight
432 proposed designs by means of a simulation study. We believe that the adopted simula-
433 tion approach, aiming to derive the empirical distribution of MAE and RMSE assessment
434 metrics under a random design assumption, allows us to validate the importance of the
435 optimisation weights proposed in this work. The eight weights resulted in distinct survey
436 designs and, consequently, in different predicted surfaces for the benchmark survey. These
437 predicted surfaces were compared with the values observed in the benchmark survey. In
438 our motivating example, 2015 was chosen as the benchmark survey because it presented
439 a lower rate of zeros in the thornback ray biomass observed during the 2013-2016 period.

440 This work confirms the importance of including selected covariates in the spatial model
441 to make the stochastic component of the residuals irrelevant. The spatial distribution of
442 thornback ray biomass and hake abundance indices differed. The highest thornback ray
443 biomass index occurred close to the coast shelf and in the Lisbon area, while the abun-
444 dance index of hake was higher in the northern area and at locations more distant from
445 the coast. A particularly noteworthy observation was the negative effect of both depth
446 and type of substratum on the processes of thornback ray occurrence and biomass index.
447 In our study, occurrence was associated with mixed sediment substratum. However, the
448 impact of substratum type on the presence of thornback ray has been studied in other
449 marine areas with varying results. Greater occurrence was related to mixed sediment in
450 the North Sea (Sguotti et al., 2016), to coarse grain sediment in the British Isles (Elliott
451 et al., 2020), and to sandy mud sediment in Azorean waters (Santos et al., 2021). Informa-
452 tion provided by Portuguese fishermen further supports this substratum dependency, as
453 they report that thornback ray adults mainly occur in the substrata of rocks surrounded

454 by sand and between mud and fine sand (Serra-Pereira et al., 2014). The occurrence
455 and abundance index processes of hake show a positive correlation to depth. The hake
456 abundance index increases at depths lower than 90 m, a feature also observed off the Por-
457 tuguese continental coast and in the Thracian sea, where Maravelias et al. (2007); Korta
458 et al. (2015) reported higher abundance of hake between 100m and 200m, respectively.
459 In agreement with our study’s observations, Casey and Pereiro (1995); Papaconstantinou
460 and Stergiou (1995) also concluded that a mud to muddy sand substratum favours the
461 abundance of hake when compared with other substratum types in the northeast Atlantic
462 and eastern Mediterranean, respectively.

463 Analysis of the observed stratified mean for both the benchmark survey and the
464 predicted stratified mean suggested a preference for designs 2, 3 and 6 in case of the
465 thornback ray and for designs 2 and 8 in the case of hake observations. This result
466 was expected since these designs prioritise locations with higher estimates of biomass or
467 abundance indices for the respective species, thus resulting in higher mean values. Also as
468 expected, in all cases, the estimated stratified variance was lower than that determined for
469 the benchmark survey since, due to the modelling process, predicted values are smoother
470 than the observed values of biomass or abundance index. Finally, it is important to note
471 that the MAE, RMSE, stratified mean and stratified variance values did not vary greatly
472 between all the proposed designs, since they differ most in the location of 11 fishing hauls.

473 Given the importance of research surveys for marine conservation, improving survey
474 designs leads to higher precision and quality of the information collected, and conse-
475 quently to a more efficient management of fisheries resources. Our study emphasises the
476 use of spatial modelling techniques to inform about the spatial distribution of target and
477 non-target species caught in research vessel surveys to estimate the abundance and/or
478 biomass indices of these species. We investigated alternative survey sampling designs and
479 evaluated their performance. The analysis was applied to fish species occurring in Por-
480 tuguese waters but, more importantly, the framework and the methodology developed in
481 this study can be replicated for other bottom trawl research surveys and sets of species.
482 In addition, the measures investigated to propose alternative sampling designs are easily
483 adaptable to respond to other objectives. Although we showed that in the studied case,
484 survey sampling designs 7 and 8 complied with the objectives of maximising the accuracy
485 of abundance estimates for the non-target species without jeopardising the estimates for
486 the survey’s target species, survey sampling design 7 presented an acceptable trade-off
487 between bias and variance of the target species. We recommend that a decision on which
488 sampling design to adopt in future surveys should take into account a cost-efficiency
489 analysis. This analysis can easily be accomplished by comparing the costs related to the
490 duration of the survey and the displacement to fishing sites, among other survey costs
491 that may be considered relevant.

492 **Supplementary material**

493 Supplementary material is available at the ICESJMS online version of the manuscript.

494 **Data availability statement**

495 The sampling data will be shared on reasonable request to co-author B. Pereira (bpereira@ipma.pt).

496 **Author's contributions**

497 DS, RM, and IF developed the methodology. DS analysed the data and implemented the
498 method. All authors contributed to the interpretation of the results and discussed ideas.
499 DS led the writing of the manuscript, with contribution from RM, BP, MA and IF. All
500 authors approved the final version of the manuscript.

501 **Conflict of interest**

502 The authors have no conflicts of interest to declare.

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508

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510 **Complete**

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659 **Supplementary material**

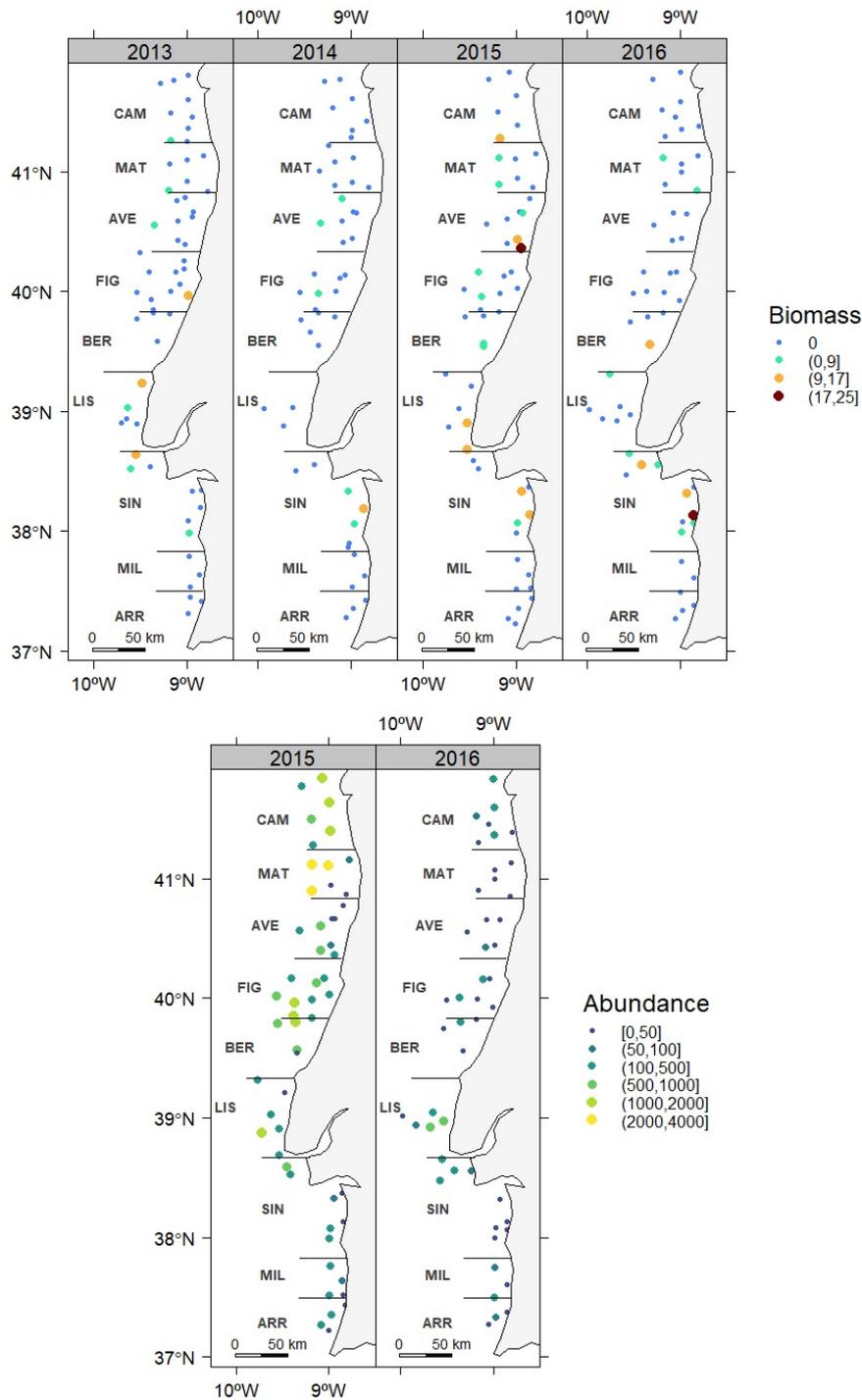


Figure 6: Exploitable biomass (fish larger than 50 cm; kg/hour) of thornback ray observed in the PT-IBTS-Q4 survey in the 2013-2016 period (upper panel) and abundance (number/hour) of hake during the PT-IBTS-Q4 survey carried out in 2015 and 2016 (lower panel). The geographic areas used in the study are (CAM: Caminha, MAT: Matosinhos, AVE: Aveiro, FIG: Figueira da Foz, BER: Berlengas, LIS: Lisboa, SIN: Sines, MIL: Vila Nova de Mil Fontes, ARR: Arrifana).

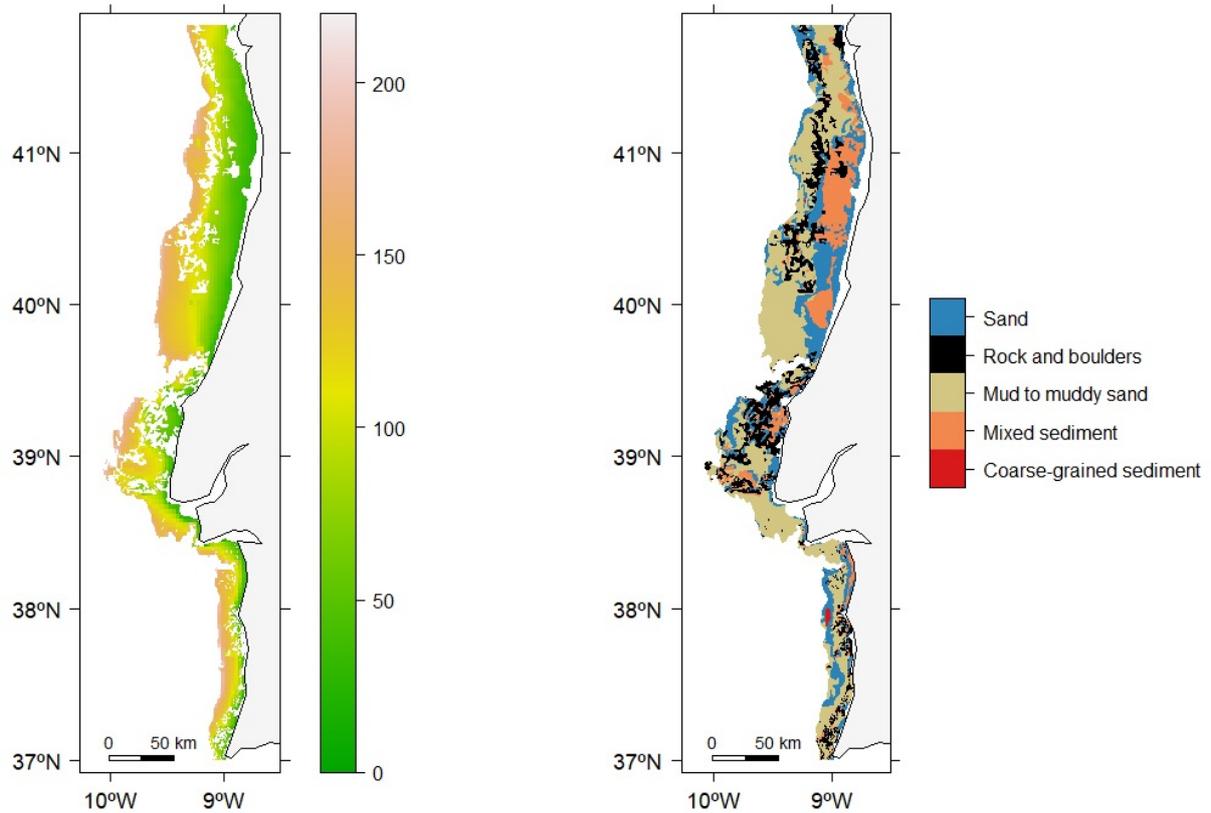


Figure 7: Bathymetry in metres (left panel) and type of substratum (right panel) of the study area. Two bottom depth intervals, [0-100m] and [100-200m], were used in our study.

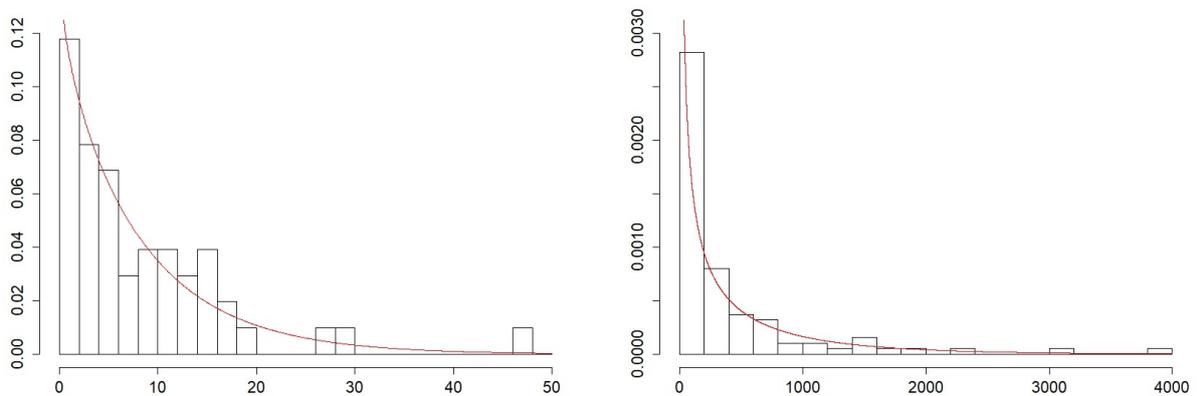


Figure 8: Histograms of strictly positive thornback ray biomass (left panel) and strictly positive hake abundance (right panel), with respective Gamma density curves (red lines).