Abundance of baleen whales in the European Atlantic

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ABSTRACT

The abundance of fin whales (*Balaenoptera physalus*), sei whales (*B. borealis)* and minke whales (*B. acutorostrata*) was estimated from data collected during shipboard sightings surveys conducted as part of CODA and TNASS (Faroese block) in July 2007 in offshore waters of the European Atlantic west of the UK, Ireland, France and Spain, combined with data collected from shipboard and aerial surveys of European Atlantic continental shelf waters conducted as part of SCANS-II in July 2005. Double platform methods employing the trial-configuration method (BT-method) were used in all shipboard surveys. Analysis used Mark-Recapture Distance Sampling to account for animals missed on the transect line. Density surface modelling was undertaken to generate model-based abundance estimates and maps of predicted density. Estimates are presented for the SCANS-II and CODA survey areas. Estimates for the Faroese block of TNASS have been presented elsewhere.

The abundance of fin whales in the CODA and SCANS-II areas was estimated as 19,354 (CV 0.24) for identified sightings and 29,512 (CV 0.26) when adjusted to include a proportion of unidentified large whale abundance (which included large baleen and sperm whales), prorated by number of sightings, because there were a large number of such sightings in one of the CODA survey blocks. The model-based estimate of identified fin whales was 19,751 (CV 0.17), more precise than the design-based estimate. Fin whales were mainly found in the southern part of the CODA survey area. Estimates based on identified sightings were comparable to those from the Spanish survey conducted as part of 1989 NASS but were larger if adjusted for a proportion of unidentified large whales. Sei whales were rare except in the southwest of the survey area; the estimate of abundance was 619 (CV 0.34) for identified sightings and 765 (CV 0.43) adjusted for a proportion of unidentified large whales. Minke whale abundance was estimated for shelf and offshore European Atlantic waters as 30,410 (CV 0.34). The model-based estimate was less precise and considerably larger.

FIN WHALE, MINKE WHALE, SEI WHALE, ABUNDANCE ESTIMATE, SHIP-BOARD SURVEYS, NORTHEAST ATLANTIC

INTRODUCTION

The abundance and distribution of cetaceans in offshore waters of the European Atlantic is not well known. The series of North Atlantic Sightings Surveys (NASS) in 1987-2001, T-NASS in 2007 and the Norwegian Independent Line Transect Surveys (NILS) in 1995-2007 have provided much information on abundance for the North Atlantic as a whole, including estimates of abundance for fin (*Balaenoptera physalus*) and minke whales (*B. acutorostrata*) (Sanpera & Jover 1989; Buckland et al. 1992; Schweder et al. 1997; Skaug et al. 2004; Pike et al. 2008, 2009, 2010; Bøthun et al. 2009; Vikingsson et al. 2009; Øien 2009). However, these surveys have focussed primarily on the northern and central North Atlantic; European waters have not received much coverage.

The Cetacean Offshore Distribution and Abundance in the European Atlantic (CODA) project conducted shipboard surveys in July 2007 to obtain data for the estimation of abundance of cetaceans in offshore waters of the UK, Ireland, France and Spain, outside continental shelf waters that had been surveyed in 2005 (SCANS-II 2008). In this paper, we analyse the data on baleen whales from the CODA surveys combined with data from SCANS-II and the Faroese block of T-NASS to generate the most comprehensive possible abundance estimates for the fin whale, sei whale and minke whale in European Atlantic waters. Estimates of abundance for the Faroese T-NASS block have been presented elsewhere (Pike et al. 2008; 2010). Here we present estimates for the CODA and SCANS-II regions.

This paper is a revision and extension of Macleod et al. (2009) presented to the Scientific Committee in Madeira.

METHODS

Data collection
The CODA survey area was divided into four strata (Figure 1) and surveyed by five ships[1] during July 2007 (CODA 2009). The Faroese block of TNASS had a common boundary with the CODA area. Survey methods replicated those used during the SCANS-II project (SCANS-II 2008), which had previously been updated from the SCANS 1994 survey (Hammond et al. 2002). T-NASS used the same survey methods (Pike et al. 2008).

Surveys were conducted using a 'trial configuration' or BT method (Laake & Borchers, 2004), with two teams of observers located on each survey vessel. The first team (referred to as Primary or observer 1) searched by naked eye close to the vessel (<500m). The second team (Tracker or observer 2) searched with bigeye or 7x50 binoculars, scanning a region sufficiently far ahead of the vessel that animals were unlikely to have reacted to the vessel's presence before being detected. This scanned region was also sufficiently wide that animals outside it at greater distances from the transect line would not be able to enter the region searched by Primary. A third observer, the Duplicate Identifier, was informed of all detections as they were made and was responsible for classifying duplicate sightings. A duplicate occurred when a sighting made by Tracker was subsequently recorded by Primary and was classified as either: D - definite (at least 90% likely); P - probable (more than 50% likely); or R: remote (less than 50% likely). In the analysis presented here, D and P duplicate categories were considered as duplicates. All sightings were tracked until abeam of the vessel or for 2-3 re-sightings after they had been declared a duplicate. Sightings were also classified with identification certainty levels: High, Medium, and Low.

Aerial survey methods used in SCANS-II are described in SCANS-II (2008).

In all analyses, only data collected under sea conditions of Beaufort 4 or less were used. Table 1 gives the areas and transect lengths surveyed in SCANS-II (ship and aerial), CODA and TNASS (Faroese block). All on effort transects were divided into segments with homogeneous sighting conditions. For the CODA, Faroese T-NASS and SCANS-II data (including aerial survey) combined, this gave a total of 8,169 segments ranging from 0.1 to 17.6 km (mean = 5.84 km, SD = 3.41 km), totalling 47,718 km on effort.

Analysis methods

Estimating detection probabilities
Detection probabilities for CODA, SCANS-II and Faroese T-NASS shipboard surveys (SCANS-II aerial survey data were not reanalysed) were estimated using Mark Recapture Distance Sampling (MRDS), which accounts for animals missed on the transect line ($g(0)<1$) and also potentially for any responsive movement (Borchers et al. 1998; 2006). In BT survey mode, the role of observer 2 (Tracker) is to generate detections of animals before they have responded to the vessel. Estimation of the detection function for observer 1 (Primary) is then conditioned on these detections, which serve as a set of binary trials in which success corresponds to a detection by observer 1. The probability that an animal is detected by observer 1 at a given perpendicular distance x and covariates z, $p_1(x,z)$ is modelled as a logistic function:

$$p_1(x,z) = \frac{e^{\left(\theta_{10}+\theta_{11}x+\sum_{r=1}^{R}\theta_{(r+1)}z_r\right)}}{1+e^{\left(\theta_{10}+\theta_{11}x+\sum_{r=1}^{R}\theta_{(r+1)}z_r\right)}}$$

where $\theta_i' = (\theta_{i0}, \ldots, \theta_{iQi})'$ represents the Qi parameters of the detection function of observer i ($i = 1,2$).

Several explanatory variables were explored in conjunction with perpendicular distance to fit the detection function models. These were: group size, vessel, primary platform height, Beaufort, swell, cue and sightability (Table 2).

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[1] The survey was planned with one ship per stratum but due to engine failure, two ships covered stratum 2.

Two MRDS models are available to estimate detection probability, one in which detections by each team are assumed to be independent from each other at all perpendicular distances (full independence) and one in which detections by each team are assumed to be independent from each other only on the transect line at zero perpendicular distance (point independence). Point independence estimators are more robust than estimators assuming independence at all perpendicular distances, which tend to underestimate abundance, and are thus preferable (Laake & Borchers 2004; Borchers *et al.* 2006). However, to account for responsive movement it must be assumed that all detections made by Primary are independent of detections made by Tracker and therefore the full independence model must be used (Laake & Borchers 2004).

Responsive movement of animals to survey ships before they are detected leads to bias in line transect estimates of abundance - negative if animals avoid ships and positive if animals are attracted to ships. The most severe bias is the positive bias caused by strong attraction, such as has been demonstrated for common dolphins (Cañadas et al. 2004).

We investigated evidence for responsive movement by examining plots of Tracker perpendicular distance vs Primary perpendicular distance for duplicate sightings and by using data on direction of movement of animals at first sighting as described by Palka & Hammond (2001). Although there was a tendency for Primary perpendicular distances to be closer than Tracker perpendicular distances, this is expected because if animals are moving randomly, more will be detected moving towards the ship than away from it (Hiby 1982) and because Primary observers searched closer to the ship. Data on direction of movement were equivocal but, if anything, suggestive of avoidance. There was thus no consistent evidence of responsive movement and we used the more robust point independence model to estimate detection probability.

In this model one detection function is fitted to the Primary sightings as in conventional distance sampling and another is fitted to those Primary sightings that were first seen by Tracker (the conditional mark-recapture probability function). The estimated probability of detection at zero perpendicular distance from the conditional mark-recapture probability function is an estimate of g(0) and is used to scale the Primary detection function.

Detection functions were fitted to a combined dataset comprising all large baleen whales, including fin, sei, fin/sei, blue and humpback whales and also including whales recorded as "unidentified large whale" (code W?), which were predominately seen as distant blows. The use of this code varied among vessels. In CODA blocks 3 and 4, only a small percentage of sightings of large whales were coded as unidentified large whale but in blocks 1 and 2, this was approximately 50%. It is possible that unidentified large whale sightings included some sperm whales but the number of sightings identified to species was heavily dominated by fin whales so we would expect the large majority of these sightings to have been fin whales. In any case, previous analysis has shown that the detection function for sperm whales was similar to large baleen whales (CODA 2009; Macleod et al 2009). In fitting the detection functions, data were truncated at an appropriate perpendicular distance.

Design-based abundance estimation
Abundance of groups was estimated using a Horvitz-Thompson-like estimator:

$$\hat{N}_1 = \sum_{j=1}^{n_1} \frac{1}{p_{1.}(\,z_j\,/\hat{\theta}\,)}$$

where n_1 is the number of detections made by observer 1 (Primary), some of which may also have been seen by observer 2 (Tracker), and $p_{1.}(z)$ represents the integration over the range of x.

Abundance of individuals was estimated by replacing the numerator in equation (1) with the group size, s_{j1}, the size of the jth detected group.

$$\hat{N}_{1_{indiv}} = \sum_{j=1}^{n_1} \frac{s_{j1}}{p_1(\,z_j\,/\hat{\theta}\,)}$$

Group sizes were corrected to take account of likely error recorded on the Primary observation platform; groups tracked from the Tracker observation platform are generally observed for a longer period and their estimates of group size should be more reliable. Therefore, a correction factor for group size made by Primary was estimated as:

$$\hat{c}_s = \frac{\sum s_j(2)}{\sum s_j(1)}$$

Where, for duplicate sightings, $s_j(1)$ is the group size estimated by the Primary observers and $s_j(2)$ is the group size estimated by the Tracker observers. Group size correction factors were calculated for the pooled data because of the lack of sufficient duplicates in some blocks. Calculated group size correction factors were 1.31 for fin whales, 1.11 for sei whales, 1.15 for unidentified large whales and 1 (no correction) for minke whales.

Estimates of mean group size were obtained as:

$$E[s_1] = \frac{\hat{N}_{1_{indiv}}}{\hat{N}_1}$$

Analyses were carried out in DISTANCE 6 Release 4 (Thomas *et al*., 2006). The estimated variance was based on the empirical variance in estimated density between samples (Innes *et al*. 2002), as implemented in program DISTANCE.

Abundance estimates were generated by survey block and for the entire CODA area for fin whales, sei whales, unidentified large whales and minke whales.

Adjusting estimates to account for sightings unidentified to species

Because the number of sightings of large whales identified to species was heavily dominated by fin whales but there were many sightings coded as unidentified large whales (especially in CODA block 2), estimates of abundance of unidentified large whales were apportioned to fin and sei whales in each CODA block and the relevant SCANS-II blocks to generate adjusted estimates:

$$N_{adj} = N_{id} + p_{id} N_{unid}$$

where N_{id} is the abundance estimate of fin or sei whales from sightings identified to species,

N_{unid} is the estimate of abundance of unidentified large whales, and

p_{id} , was estimated as the number of sightings of fin or sei whales divided by the total number of sightings of identified (fin, sei, humpback, sperm) whales in each block.

The variance of the adjusted estimate was estimated as:

$$var_{N_{adj}} = var_{N_{id}} + p_{id}{}^2 N_{unid}{}^2 \left(CV_{p_{id}}{}^2 + CV_{N_{unid}}{}^2 \right)$$

There was a 3.5% overlap in the CODA and SCANS-II survey areas so all estimates were divided by 1.035 to account for this.

Density Surface Modelling
A spatial grid of resolution 0.25 x 0.25 degrees was created covering all survey areas and populated with data on available environmental variables (Table 3). This resolution was chosen as it was the coarsest resolution in the available environmental covariates. This yielded a total of 6,830 grid cells within the study area. The grid is shown in Figure 2. Note that it does not include all of the TNASS survey area.

Each segment of effort was assigned to a grid cell based on the mid-point of the segment and values of environmental variables for each grid cell were associated with the segment.

Analysis was undertaken in two steps: modelling the abundance of groups; and modelling group size. Estimated abundance of animals was obtained by multiplying the results from the two steps. Modelling

was undertaken with statistical software R (R Development Core Team 2009) using the mgcv package (Wood 2006).

Abundance of groups

The response variable was estimated abundance of groups in each effort segment. This was obtained using the Horvitz-Thompson estimator:

$$\hat{N}_i = \sum_{j=1}^{n_i} \frac{1}{\hat{p}_{ij}}$$

where n_i is the number of detected groups in the ith segment, and $\hat{p}_{ij}$ is the estimated probability of detection of the jth group in segment i.

The probability of detection for each group encountered was obtained from the fitted detection function for the appropriate level or measurement of each covariate.

Abundance of groups was modelled in a Generalized Additive Modelling (GAM) framework. Due to over-dispersion in the data, a quasi-Poisson error distribution was assumed, with variance proportional to the mean. A log link was used. The searched area of each segment (length x twice the truncation distance) was used as an offset. The general structure of the model was:

$$\hat{N}_i = exp\left[ln(a_i) + \theta_0 + \sum_k f_k(z_{ik}) \right]$$

where the offset a_i is the search area for the ith segment (calculated as the length of the segment multiplied by twice the truncation distance), θ_0 is the intercept, f_k are smoothed functions of the explanatory covariates, and z_{ik} is the value of the kth explanatory covariate in the ith segment.

The maximum number of "knots" allowed in the fitted smooth function for each covariate (equivalent to degrees of freedom) was limited to avoid excessive and unrealistic "wiggliness". The maximum number of covariates per model was also limited. As a rule of thumb, the maximum total number of degrees of freedom allowed in a model was limited not to exceed 30-50% of the total number of non-zero observations to avoid over-fitting and to avoid problems when using bootstrap re-sampling of the data to estimate the CV of the estimates (see below).

Manual model selection used three criteria: (a) the GCV (Generalised Cross Validation) score; (b) the percentage of deviance explained; and (c) the probability that each variable was included in the model by chance. Plots of residuals were inspected to assess model fit.

Group size

Group size was also modelled using a GAM with a logarithmic link function. The response variable was the corrected number of whales counted in each group (s_j). A quasi-Poisson error distribution was again used, with variance proportional to the mean, because of over-dispersion in the data. The general structure of the model was:

$$E(s_j) = exp\left[\theta_0 + \sum_k f_k(z_{jk}) \right]$$

where θ_0 is the intercept, f_k are smoothed functions of the explanatory covariates, and z_{jk} is the value of the kth explanatory covariate in the jth group. Manual selection of the best models was done following the same criteria described for the models of abundance of groups.

If there was no appropriate model for group size, the mean group size was used.

Estimating model-based abundance and variance

Abundance of animals in each grid cell was obtained by multiplying the abundance of groups predicted by the best fitting model by the group size predicted by the best fitting model (or mean group size). Estimated abundance was summed over all grid cells in each area of interest.

The density surface modelling was replicated in 600 non-parametric bootstrap re-samples to obtain the coefficient of variation (CV) for this part of the analysis. The re-sampling unit used was the combination of day and transect (each line of the zig-zag survey track), so each day was considered a unit but was further divided if it encompassed segments of two or more transects.

The re-sampling process was stratified by survey region (SCANS-II, CODA, Faroese block of TNASS) as far as data allowed. For each resample, for each region, random re-sampling units were added until the total transect length was approximately the same as the total transect length surveyed in that region.

For each bootstrap resample, the models for abundance of groups and for group size were run (or mean group size calculated if no model was selected), and the degree of smoothing of each model term was chosen by the 'mgcv' package, within the maximum number of knots allowed for each covariate, thus incorporating some model uncertainty in the variance.

The Delta method was used to obtain the final CV by combining the bootstrap CV from modelling and the CV of detection probability. 95% confidence limits were calculated assuming the estimates of abundance were log-normally distributed.

RESULTS

Fin and sei whales
The dataset for all large baleen whales and unidentified large whales contained 540 detections, including 326 from Primary, 337 from Tracker and with 123 duplicates (D and P duplicate categories). The distributions of sightings of fin, sei and unidentified large whales are shown in Figure 1.

In fitting the detection function, a truncation distance of 4,000m was chosen. The final model included covariates Beaufort and swell in addition to perpendicular distance in the conventional detection function and Primary platform height and perpendicular distance in the conditional mark-recapture probability function (Figure 3). The average detection probability for Primary under this model was 0.337 (CV 0.061) and the estimated probability of detection on the transect line was 0.513 (CV 0.096).

Table 4 gives estimates of the number of groups, number of individuals and group size for identified fin and sei whales, for unidentified large whales and for all large baleen and unidentified large whales in the SCANS-II region and in each of the CODA blocks.

The abundance of identified fin whales was estimated as 19,277 (CV 0.24) in the CODA survey area and 77 (CV 1.04) in the SCANS-II survey area (block Q, SCANS-II 2008), giving a total of 19, 354 (CV 0.24) in both areas. Apportioning unidentified large whale abundance to species gave a total estimate in the SCANS-II and CODA survey areas combined of 29,512 (CV 0.26) fin whales (Table 5).

The abundance of identified sei whales was estimated as 590 (CV 0.36) in the CODA survey area and 29 (CV 1.00) in the SCANS-II survey area (block P, SCANS-II 2008), giving a total of 619 (CV 0.34) in both areas. Apportioning unidentified large whale abundance to species increased this to a total estimate in the SCANS-II and CODA survey areas combined of 765 (CV 0.43) sei whales (Table 3).

For comparison, the estimates of fin and sei whale abundance from identified sightings only using conventional line transect analysis combining Tracker and Primary sightings were 13,212 (CV 0.19) and 379 (CV 0.29), respectively, 68% and 61% of the equivalent MRDS double platform estimates.

Density surface modelling of fin whales
The best-fitting model for the abundance of fin whale groups retained three covariates: depth, the interaction of latitude and longitude, and contour index (Table 6). Fitted smooth functions are shown in Figure 4. No model fitted group sizes well so the average group size of 1.5 was used to estimate abundance. The estimate of abundance of fin whales was 18,826 (CV 0.18) in the CODA area and 925

(CV 0.39) in the SCANS-II area, giving a total of 19,751 (CV 0.17) (Table 7). A map of predicted abundance of animals is shown in Figure 5.

The model-based estimate of 19,751 (CV 0.17) fin whales in the CODA and SCANS-II areas was very similar but more precise than the equivalent design-based estimate of 19,354 (CV 0.24) for identified fin whales. On this basis, the model-based estimate is preferable. However, model-based estimates for unidentified large whales have not been generated, so an adjusted estimate to account for a proportion of unidentified large whales being fin whales cannot be made.

Minke whales
The dataset for all minke whales contained 131 detections, including 77 seen from Primary, 77 seen from Tracker and with 23 duplicates (D and P duplicate categories). The distribution of sightings is shown in Figure 2. A truncation distance of 1,000m was chosen. The final model included covariates Beaufort and swell in addition to perpendicular distance in the conventional detection function and Primary platform height and perpendicular distance in the conditional mark-recapture probability function (Figure 6). The average detection probability for Primary under this model was 0.195 (CV 0.25) and the estimated probability of detection on the transect line was 0.526 (CV 0.24).

Table 4 gives estimates of number of groups, number of individuals and group size for minke whales in the SCANS-II region and in each of the CODA blocks.

The abundance of minke whales was estimated as 11,535 (CV 0.74) in the CODA survey area and 13,557 (CV 0.28) in the SCANS-II area surveyed by ships. The estimate of minke whale abundance from the SCANS-II aerial survey was 5,318 (CV 0.55) (SCANS-II 2008), so the total estimate of minke whale abundance in the SCANS-II and CODA areas combined was 30,410 (CV 0.34).

For comparison, the estimates of minke whale abundance from identified sightings only using conventional line transect analysis combining Tracker and Primary sightings 22,902 (CV 0.23), 75% of the equivalent MRDS double platform estimate.

Density surface modelling of minke whales
The best-fitting model for the abundance of minke whale groups retained longitude and sea surface temperature (Table 6), and for group size the best-fitting model retained distance to the 2000m depth contour and longitude (Table 8). Fitted smooth functions are shown in Figures 7 and 8. The model-based estimate of abundance of minke whales was 14,850 (CV 0.57) in the CODA area and 23,529 (CV 0.44) in the SCANS-II area, giving a total estimate of minke whale abundance in both areas combined of 38,379 (CV 0.35) (Table 7). A map of predicted abundance of animals is shown in Figure 9.

DISCUSSION

Fin whales
There were few fin whale sightings in the north of the CODA survey (Figure 1), and low estimated abundance in block 1 (Table 4), the block adjacent to the Faroes T-NASS block. Previous surveys in this area (also in July) have shown the occurrence of fin whales to be variable, having been recorded in this region during some (Pollock et al. 2000; Weir et al., 2001; Macleod et al., 2006) and not in others (Joyce et al., 1990).

In contrast, there were a large number of fin whale sightings and predicted density was high in the southern part of the CODA survey area, especially in the southern part of block 2 and the northern part of block 3 particularly in the northeast off Galicia (Figure 5) and high estimated abundance in these blocks (Table 4).

This area was surveyed as the Spanish contribution to NASS-87 (Lens et al. 1989) and NASS-89 (Lens 1991) and the data used to estimate abundance of fin whales (Sanpera & Jover 1989; Buckland et al. 1992). Buckland et al. (1992) estimated fin whale abundance to be 17,355 (CV 0.266) in 1989, in an area with similar boundaries to CODA to the south and east, but extending further north than the predicted high density area found here, and much further to the west (25° W rather than 14° W) than CODA.

The 1989 survey was a single platform survey conducted in passing mode so there was no correction for animals missed on the transect line (and therefore no correction for Primary school size), and many sightings at large perpendicular distance were unidentified to species unless they were detected again at less than half a mile abeam, in which case they were closed on (Lens 1991).

If unidentified large whale abundance is prorated to fin whales in proportion to sample size, our estimate of fin whale abundance (Table 5) is considerably higher than the estimate for 1989. Buckland et al. (1992) also calculated an estimate that included unidentified large (baleen) whales (believed, as here, to have been mostly fin whales) but this estimate was only slightly higher despite there being more unidentified large whale sightings than fin whales. This was because most of the unidentified whales see in 1989 were made at large perpendicular distances, which was not the case in the CODA survey.

Although we cannot rule out changes in distribution and/or abundance of fin whales in the last two decades, the several differences in methodology used to obtain the estimates of abundance are more than sufficient to explain the difference between our estimate and that from 1989.

Notwithstanding comparisons with the 1989 estimate, there remains the question of whether our estimate that includes a proration of some unidentified large whales to fin whales is a better estimate than only using identified fin whale sightings. The difference in estimates was trivial in blocks 3 and 4 and small in block 1 but large in block 2 where there were more unidentified large whale sightings than identified fin whales and the estimate doubled (Table 5). In the other blocks, uncertainty in species identification was expressed mainly by using the code for identification certainty (High, Medium, Low). Exploratory analysis presented in Macleod et al. (2009) showed that removing Low certainty sightings from analysis had little effect on abundance estimates, but that removing Medium certainty sightings had a large effect.

There does not seem to be a good reason to exclude a proportion of the unidentified large whale sightings (although there might be better ways to do this calculation) and we believe that our adjusted estimate of 29,512 (CV 0.26) fin whales is the best estimate currently available. Extending the spatial modelling to unidentified large whales would allow the more precise model-based estimate for fin whales to be adjusted in the same way.

Sei whales
Sei whale sightings were confined to CODA block 3, and one in SCANS-II block P, (Figure 1) and the estimates of abundance were correspondingly low (Tables 4 and 5).

Minke whales
Minke whales occur both on and off the continental shelf of the European Atlantic. The small number of sightings in the CODA offshore survey did not allow a double-team MRDS analysis to be conducted so previously reported estimates were underestimated and imprecise (CODA 2009; Macleod et al. 2009). However, combining the CODA data with the continental shelf SCANS-II data (and Faroese T-NASS) data has allowed a more robust analysis. The estimates presented here are less biased because they are corrected for animals missed on the transect line and they are also much more precise. However, the SCANS-II aerial survey estimates are corrected only for availability bias, not perception bias (SCANS-II 2008). Combining the 2005 SCANS-II estimates with those from 2007 (CODA) means that the CV of the combined estimate should include some additional variance to include variation induced by any movement of whales between the survey areas. We have not attempted to incorporate such additional variance and our CV is therefore underestimated.

The model-based estimate of 38,379 (CV 0.35) minke whales in the CODA and SCANS-II areas was substantially larger and also slightly less precise than the equivalent design-based estimate. The best estimate is therefore the design-based estimate of 30,410 (CV 0.34). The modelled prediction of distribution does not reflect the sightings data around the coast of Ireland so, although it is important not to over-interpret the raw sightings distribution, additional hitherto unmodelled covariates may improve the model-based abundance estimate.

The central North Sea and waters to the west of Britain and Ireland are at the southern limit of the summer range of minke whales in the Northeast Atlantic (Reid, Evans & Northridge 2003). As such, one might expect distribution and abundance in these areas to vary from year to year, depending on prey

availability there and further north. This seems to be supported by the wide variation in the several estimates of abundance that have been made for the central/northern North Sea: 5,429 (CV= 0.34) for 1989; 7,250 (CV=0.21) for 1994; 20,294 (CV=0.26) for 1995; 11,713 (CV=0.29) for 1998; 6,246 (CV=0.48) for 2004; and 10,541 (CV=0.32) for 2005 (Schweder *et al.* 1997; Hammond *et al.* 2002; Skaug *et al.* 2004; Bøthun, Skaug & Øien 2009; SCANS-II 2008). There are no previous estimates for the offshore waters of the European Atlantic.

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Table 1. Areas and length of transect searched for each survey region used in analysis. Data are for Beaufort 0-4 for SCANS-II (ship), CODA and TNASS (Faroes), and for good and moderate conditions for SCANS-II (air) (equivalent to Beaufort 0-2).

Region	Area (km^2)	Transect (km)
SCANS-II (ship)	1,005,743	19,614
SCANS-II (air)	364,371	15,802
CODA	967,538	9,491
TNASS (Faroes)	685,628	2,318
Total	**3,023,280**	**47,225**

Table 2. Covariates available for fitting detection functions.

Name	Description	Type	Levels
sightability	Qualitative measure of the searching conditions for detecting dolphins (including sea state, glare, visibility, etc)	factor	0 – Excellent 1 – Good 2 – Moderate 3 – Poor
swell	Height and length of the swell	factor	0 – No swell 1 – Low <1m short/average 2 – Low <1m long 3 – Moderate <2m short/average 4 – Moderate <2m long 5 – Big <2-4m short/average 6 – Big <2-4m long 9 - Confused
swellf	Height of swell condensed in three levels	factor	0 – No swell 1 – Low <1m 2 – Moderate-Big >1m 3 – Confused
platfactor	Height of the Primary platform	factor	1 – < 6m 2 – > 6-8m 3 - > 8m
platheight	Height of the Primary platform (m)	continuous	
beaufort	Ad hoc scale of sea state	factor	0 - glassy mirror-like 0.5 - glassy & ripple patches 1 - scale ripples 2 - small wavelets 2.5 - rare whitecaps 3 - whitecaps, 1 - 5/sector 4 - frequent whitecaps
vessel	Vessel	factor	GO - Gorm IN - Investigador MC - Mars Chaser SK - Skagerak VH - Victor Hensen WF - West Freezer ZI - Zirfaea GE - Germinal RA - Rari CS - Cornide de Saavedra
size	Group size	continuous	
cue	Cue that caused the detection	factor	BL - Blow SP - Splash JU - Jump/Breach SL - Slick BY - Body FL - Flash AW - Associated wildlife SB - Seabirds SD - Sound
cue2	Cue that caused the detection, condensed into two levels	factor	UC – inconspicuous (BY + FL) C – conspicuous (rest of levels)

Table 3. Covariates used in the modelling analysis and to populate the spatial grid for prediction.

Name	Description	Source
depth	Average depth in the grid cell	2-Minute Gridded Global Relief Data (ETOPO2v2). National Geophysical Data Center (NGDC). NOAA Satellite and Information Service.
depthsd	Standard deviation of the depth data points within the grid cell	Derived from ETOPO2 bathymetric data
dist0	Distance to the 0 m depth contour (coast), in decimal degrees	Calculated with the Spatial Analyst extension of ArcGis 9.2, using GEBCO bathymetric data.
dist200	Distance to the 200 m depth contour, in decimal degrees	Calculated with the Spatial Analyst extension of ArcGis 9.2, using GEBCO bathymetric data.
dist2000	Distance to the 2000 m depth contour, in decimal degrees	Calculated with the Spatial Analyst extension of ArcGis 9.2, using GEBCO bathymetric data.
slope	Slope of the sea floor in m per km, calculated as follows: $$\frac{\left(\dfrac{depth_{max} - depth_{min}}{dis\tan ce\ in\ km_{(depth_{max} - depth_{min})}}\right)}{10}$$	Derived from ETOPO2 bathymetric data
ci	Contour index of the sea floor, calculated as follows: $$\frac{\left(depth_{max} - depth_{min}\right)}{depth_{max}} * 100$$	Derived from ETOPO2 bathymetric data
ssh	Average Sea Surface Height Anomaly for the months of June to August 2005 and 2007, calculated as the difference between measured SSH and the expected mean SSH.	Altimetry Sensors on multiple spacecraft (JASON-1, TOPEX/POSEIDON, ENVISAT, GFO, ERS 1/2, GEOSAT). Resolution: 0.25 degrees. NOAA CoastWatch Program
sst	Average Sea Surface Temperature for the months of June to August 2005 and 2007.	Sensor: Moderate Resolution Imaging Spectroradiometer (MODIS) on Aqua, Advanced Very High Resolution Radiometer (AVHRR) on POES, Imager on GOES, Advanced Microwave Scanning Radiometer (AMSR-E) on Aqua. Resolution: 0.1 degrees. NOAA CoastWatch Program
sst_sd	Standard deviation of Sea Surface Temperature for the months of June to August 2005 and 2007.	Derived from NOAA CoastWatch Program sea surface temperature data.
chla	Average Chlorophyll-a concentration for the months of June to August 2005 and 2007.	Sensor: Sea-viewing Wide Field-of-view Sensor (SeaWiFS). Resolution: 0.1 degrees. NOAA CoastWatch Program
chla_sd	Standard deviation of Chlorophyll-a concentration for the months of June to August 2005 and 2007.	Derived from NOAA CoastWatch Program Chlorophyll-a concentration data.
prpr	Average primary productivity for the months of June to August 2005 and 2007.	Measurement of primary productivity based on the following satellite measurements: Chlorophyll-a concentration and photosynthetically available radiation (PAR) measurements from the SeaWiFS sensor aboard the GeoEye spacecraft, SST measurements from the NOAA Pathfinder Project and from the Reynolds Optimally-Interpolated SST (OISST) v2 product from NOAA's National Climatic Data Center (NCDC). Resolution: 0.1 degrees. NOAA CoastWatch Program
prpr_sd	Standard deviation of primary productivity for the months of June to August 2005 and 2007.	Derived from NOAA CoastWatch Program primary productivity data.
lat	Latitude in decimal degrees	
lon	Longitude in decimal degrees	

Table 4. Number of primary sightings (n) and estimates of group and animal abundance for fin whale, sei whale, unidentified large whales and minke whale. SCANS-II aerial estimates for minke whales are from SCANS-II (2008).

	n	Number groups	CV	Lower 95% CL	Upper 95% CL	Number animals	CV	Lower 95% CL	Upper 95% CL
FIN WHALE									
CODA 1	6	945	0.52	364	2,456	1,238	0.52	477	3,217
CODA 2	61	6,764	0.38	3,289	13,910	10,561	0.39	5,035	22,151
CODA 3	105	4,116	0.23	2,647	6,400	6,102	0.25	3,740	9,956
CODA 4	24	977	0.85	231	4,133	1,376	0.82	337	5,616
CODA total	**196**	**12,802**	**0.23**	**8,252**	**19,860**	**19,277**	**0.24**	**12,148**	**30,589**
SCANS-II	1	59	1.04	11	315	77	1.04	14	413
Total	**197**	**12,860**	**0.23**	**8,305**	**19,914**	**19,354**	**0.24**	**12,217**	**30,659**
SEI WHALE									
CODA 1	0								
CODA 2	0								
CODA 3	12	462	0.36	233	914	590	0.36	299	1,164
CODA 4	0								
CODA total	**12**	**462**	**0.36**	**233**	**914**	**590**	**0.36**	**299**	**1,164**
SCANS-II	1	27	1.00	5	137	29	1.00	6	152
Total	**13**	**489**	**0.34**	**254**	**941**	**619**	**0.34**	**322**	**1,193**
UNIDENTIFIED LARGE WHALES									
CODA 1	6	926	0.44	407	2,107	1,256	0.46	531	2,970
CODA 2	84	10,156	0.46	4,336	23,792	12,084	0.45	5,216	27,994
CODA 3	6	257	0.28	152	437	337	0.26	206	551
CODA 4	1	50	0.90	11	229	58	0.90	13	263
CODA total	**97**	**11,390**	**0.41**	**5,280**	**24,573**	**13,734**	**0.40**	**6,484**	**29,093**
SCANS-II	5	158	0.66	49	511	232	0.51	90	600
Total	**102**	**11,548**	**0.40**	**5,404**	**24,676**	**13,967**	**0.39**	**6,670**	**29,248**
MINKE WHALE									
CODA 1	14	10,584	0.80	2,666	42,008	10,584	0.80	2,666	42,008
CODA 2	1	952	1.10	166	5,451	952	1.10	166	5,451
CODA 3	0	0	0.00	0	0	0	0.00	0	0
CODA 4	0	0	0.00	0	0	0	0.00	0	0
CODA total	**15**	**11,535**	**0.74**	**3,161**	**42,101**	**11,535**	**0.74**	**3,161**	**42,101**
SCANS-II ship	59	13,327	0.28	7,778	22,834	13,557	0.28	7,912	23,228
SCANS-II aerial	*15*	*3,919*	*0.48*	*1,431*	*10,734*	*5,318*	*0.55*	*1,942*	*14,566*
SCANS-II total	**74**	**17,246**	**0.30**	**9,718**	**30,603**	**18,875**	**0.30**	**10,636**	**33,494**
Total	**89**	**28,781**	**0.34**	**15,106**	**54,837**	**30,410**	**0.34**	**15,961**	**57,940**

Table 5. Estimates of abundance for fin and sei whales adjusted for the addition of a proportion of unidentified large whale abundance (p).

	p	CV	Number animals	CV	Lower 95% CL	Upper 95% CL
FIN WHALE						
CODA 1	0.43	0.31	1,776	0.43	798	3,953
CODA 2	0.76	0.06	19,775	0.38	9,678	40,404
CODA 3	0.75	0.05	6,355	0.24	3,963	10,190
CODA 4	0.65	0.12	1,413	0.80	356	5,605
CODA total			**29,319**	**0.26**	**17,633**	**48,750**
SCANS-II	0.50	0.71	193	0.73	53	699
Total			**29,512**	**0.26**	**17,805**	**48,918**
SEI WHALE						
CODA 1	0.00					
CODA 2	0.00					
CODA 3	0.09	0.28	619	0.34	323	1,187
CODA 4	0.00					
CODA total			**619**	**0.34**	**323**	**1,187**
SCANS-II	0.50	0.71	146	0.83	35	601
Total			**765**	**0.32**	**416**	**1,406**

Table 6. Covariates retained in the final models for abundance of groups for fin whale and minke whale, showing the estimated degrees of freedom, the probability of that covariate being included in the model by chance (p) and the deviance explained by the model. The symbol ":" means "interaction with".

	Covariate	Estimated degrees of freedom	p	Deviance explained
Fin whale	Depth	4.96	<<0.001	
	Latitude : Longitude	10.65	<<0.001	54.3%
	Contour index	4.95	<<0.001	
Minke whale	Longitude	8.84	<<0.001	14.3%
	Sea surface temperature 2007	5.85	<<0.001	

Table 7. Model-based estimates of abundance for fin and minke whales.

	Survey block	Abundance of animals	CV	Lower 95% CL	Upper 95% CL
Fin whale	CODA	18,826	0.18	15,825	22,397
	SCANS-II	925	0.39	634	1,348
	Total	**19,751**	**0.17**	**16,719**	**23,332**
Minke whale	CODA	14,850	0.57	8,723	25,281
	SCANS-II	23,529	0.44	15,449	35,834
	Total	**38,379**	**0.35**	**27,345**	**53,864**

Table 8. Covariates retained in the final model for group size for minke whale, showing the estimated degrees of freedom, the probability of that covariate being included in the model by chance (p) and the deviance explained by the model.

	Covariate	Estimated degrees of freedom	p	Deviance explained
Minke whale	Distance to the 2000m depth contour	3.31	0.015	16.1%
	Longitude	1	0.042	
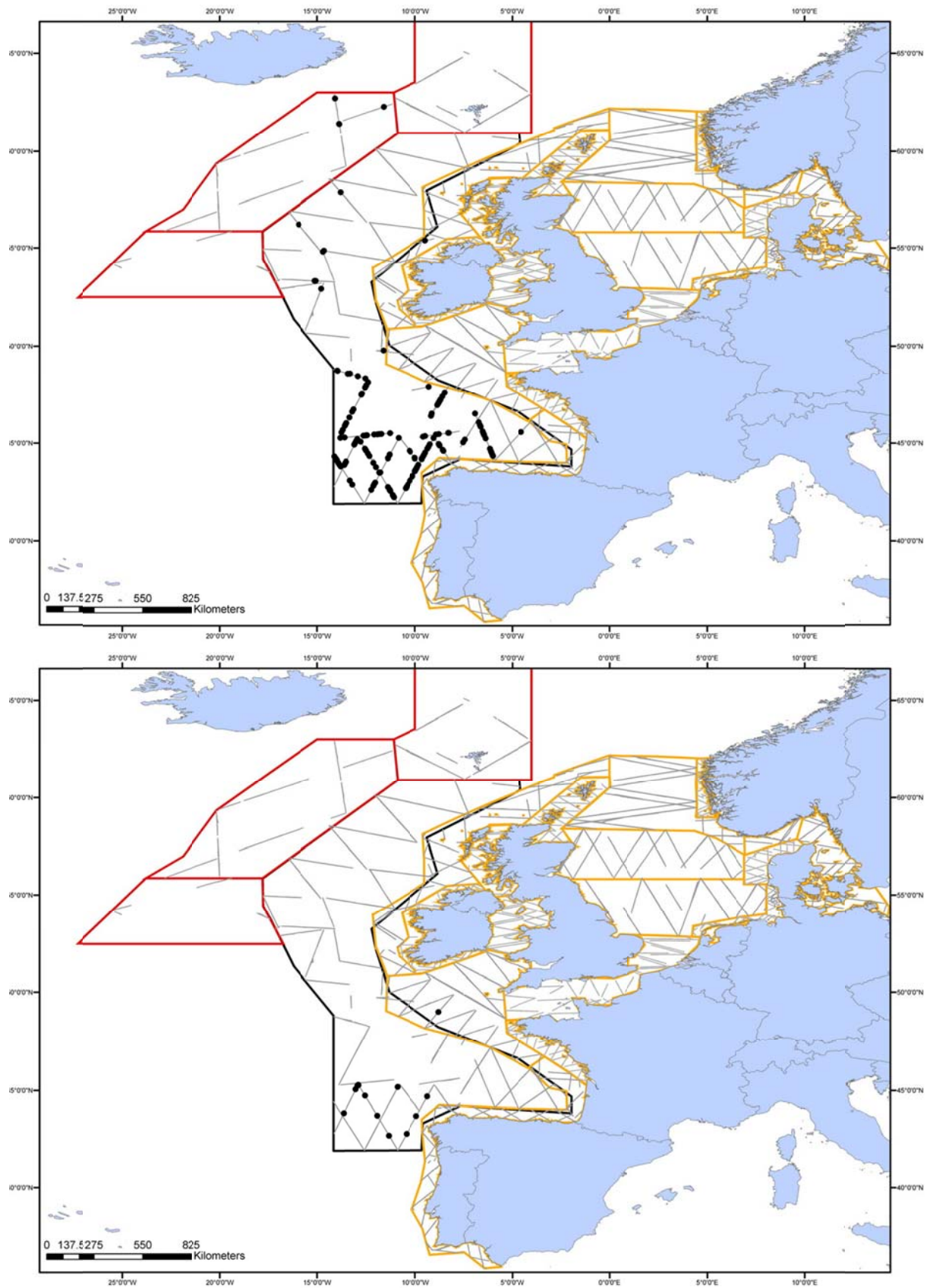
Figure 1. Survey blocks, realised survey effort and sightings of fin (top) and sei whales (bottom) during CODA, SCANS-II and Faroese T-NASS.
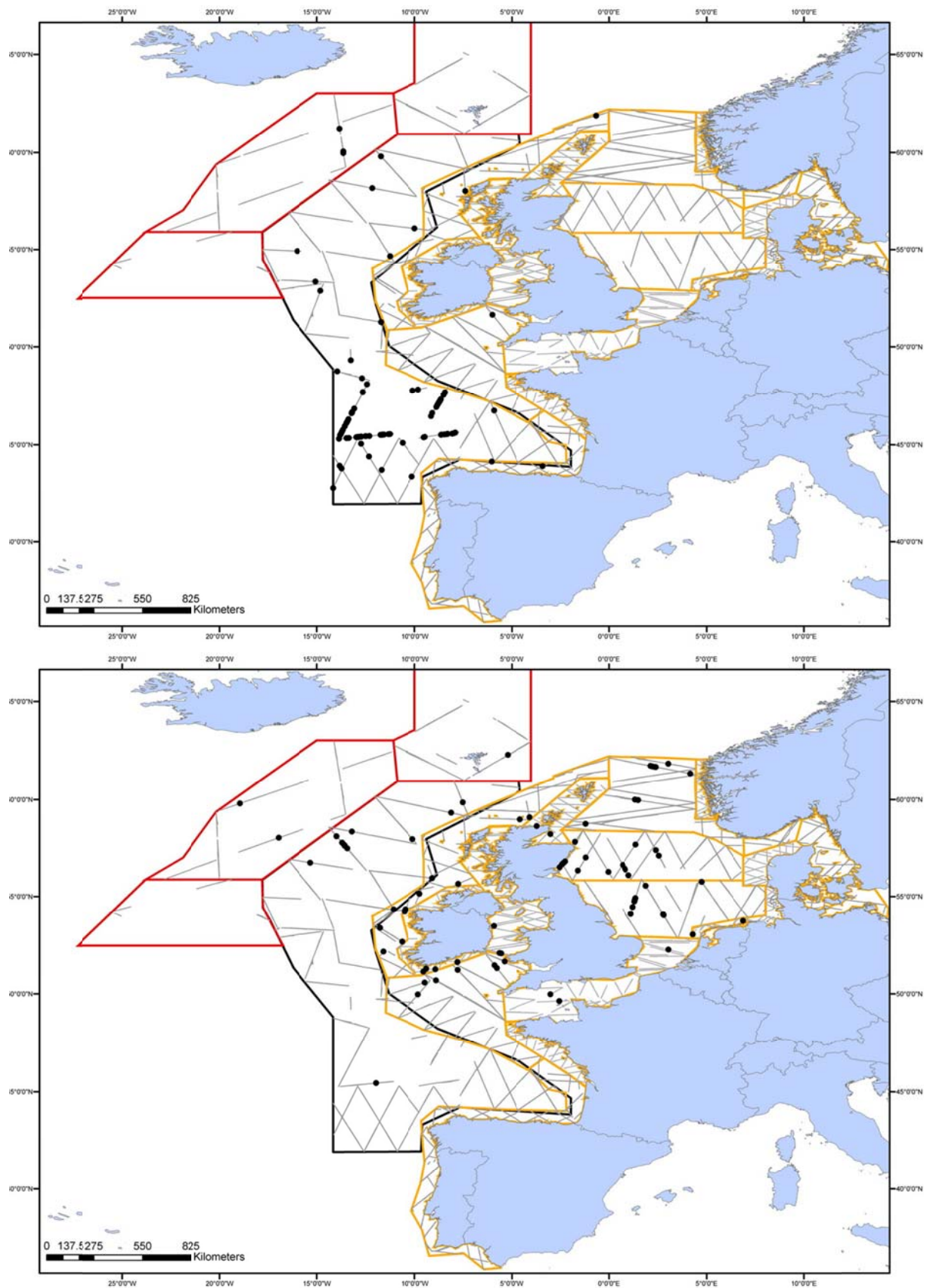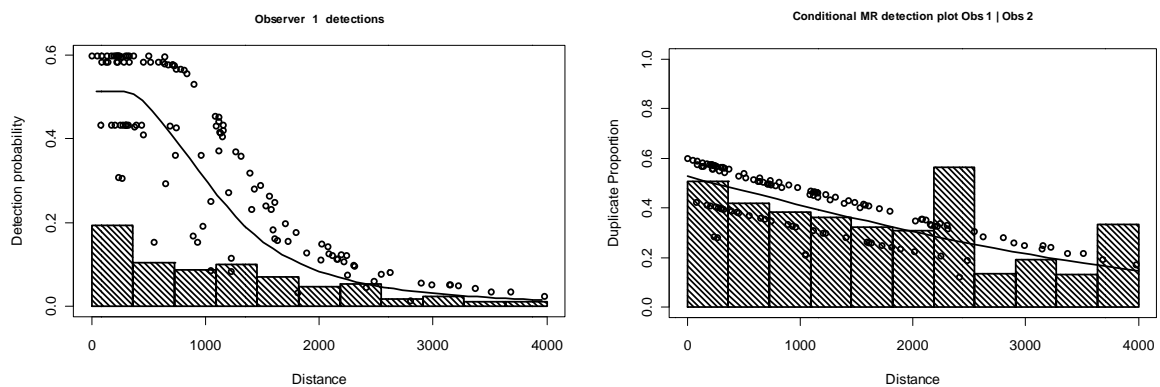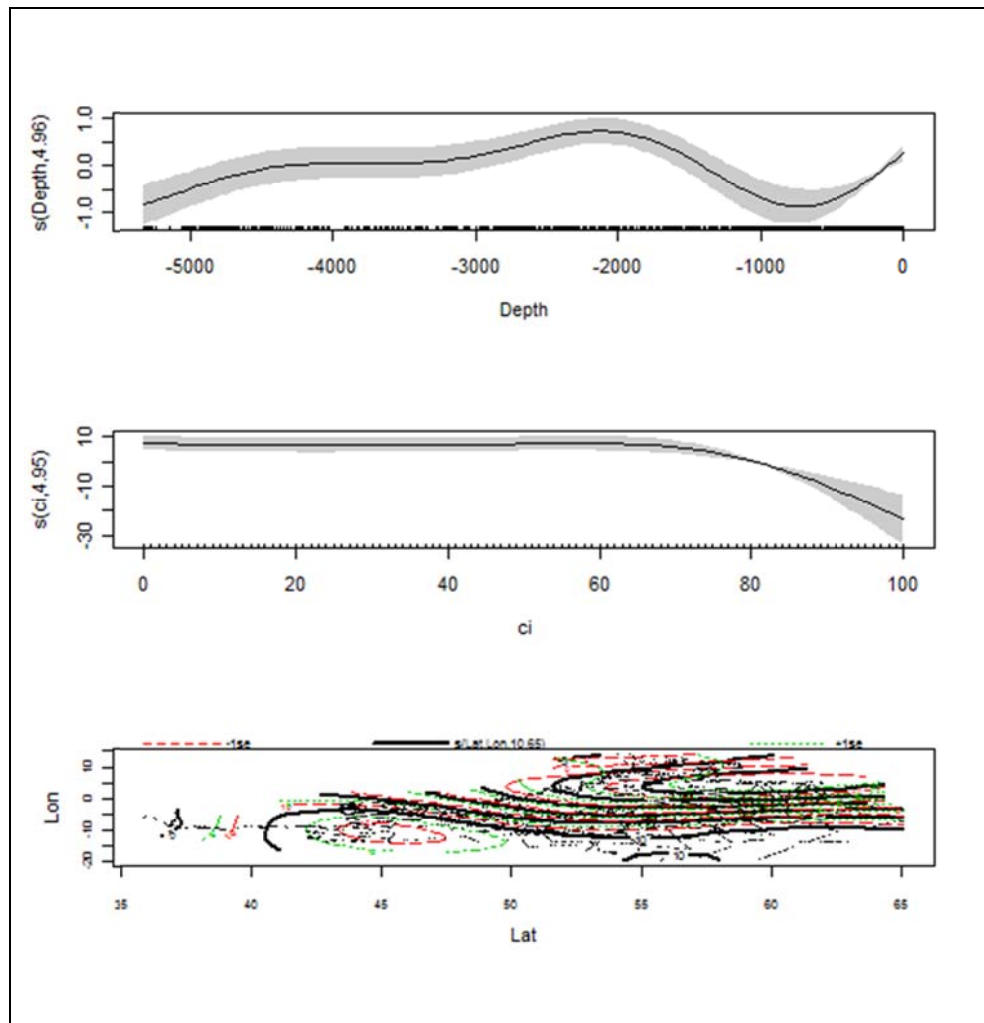
Figure 1 continued. Survey blocks, realised survey effort and sightings of unidentified large whales (top) and minke whales (bottom) during CODA, SCANS-II and Faroese T-NASS.
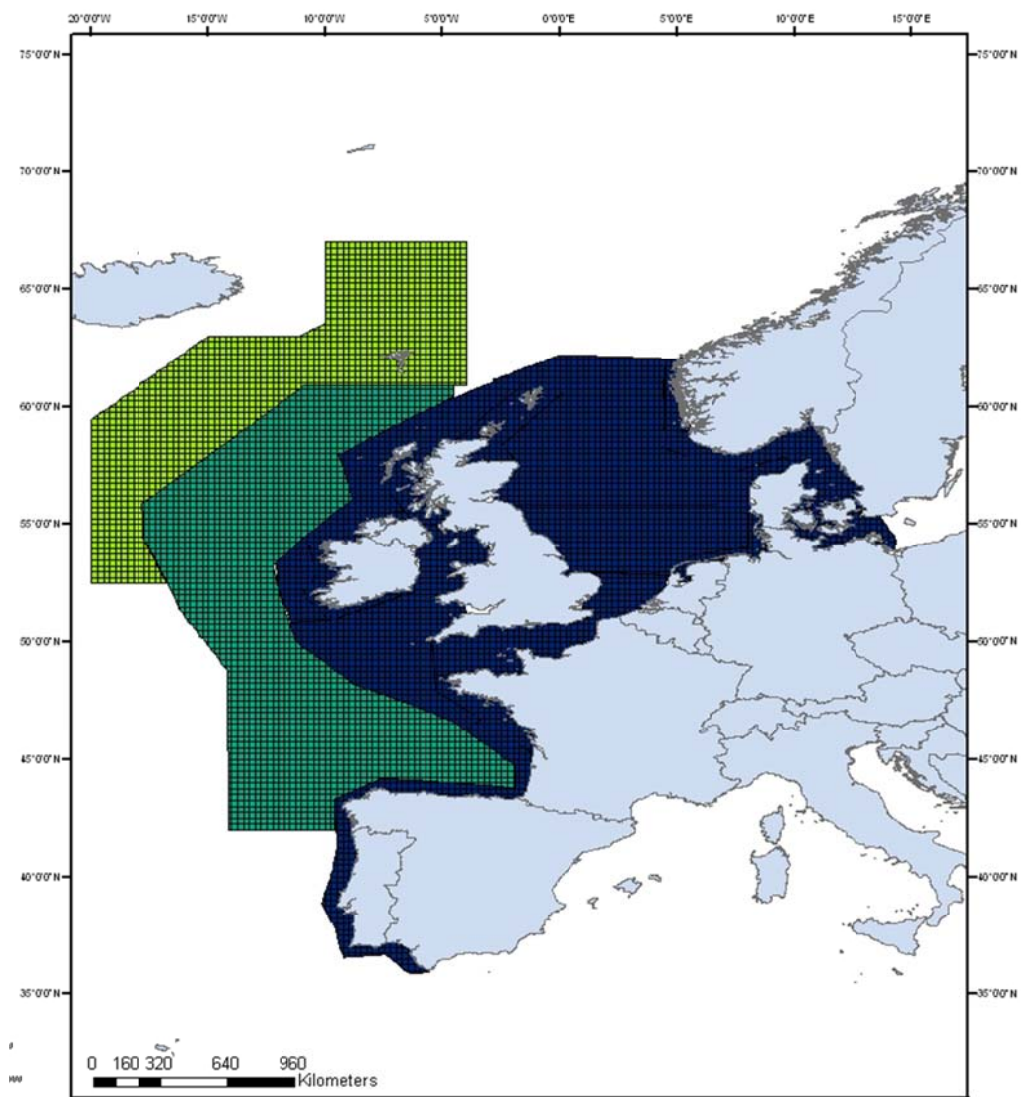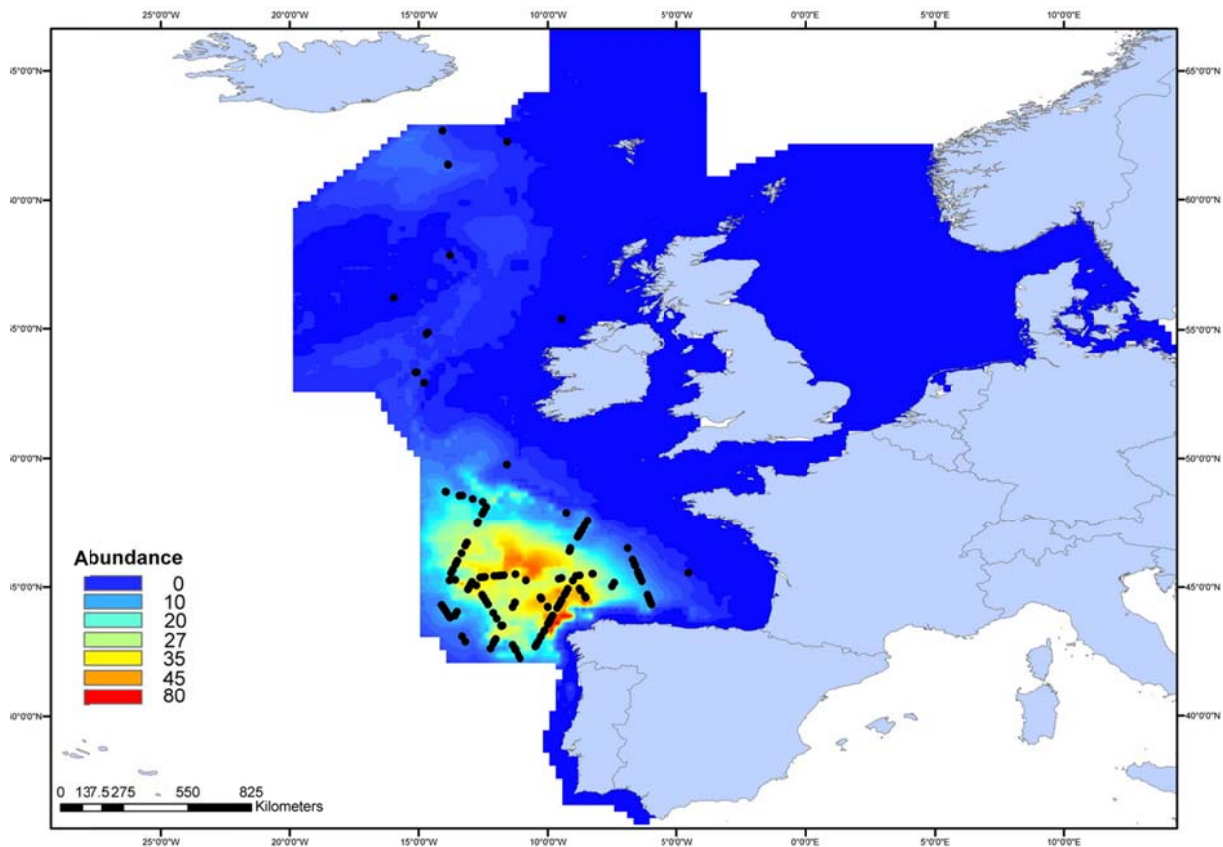
Figure 2. SCANS-II (dark blue), CODA (turquoise) and Faroes TNASS (green) survey areas.
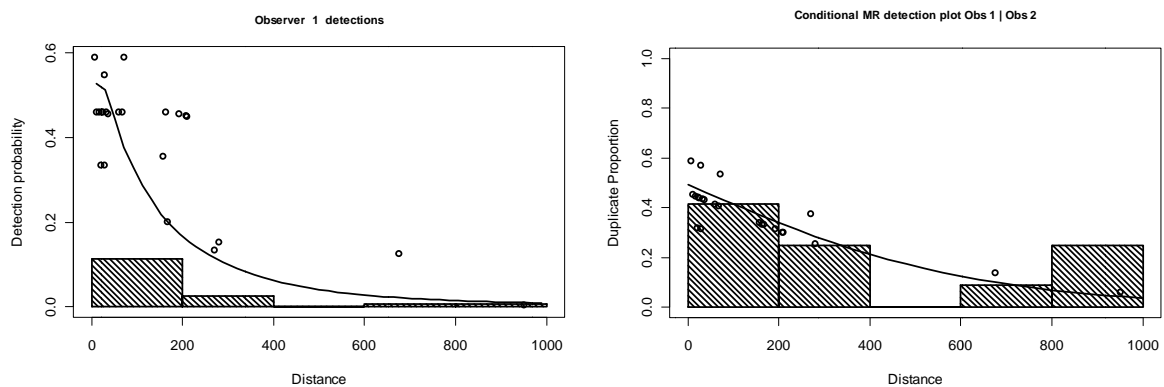

Figure 3. Detection functions for large baleen and unidentified large whales.
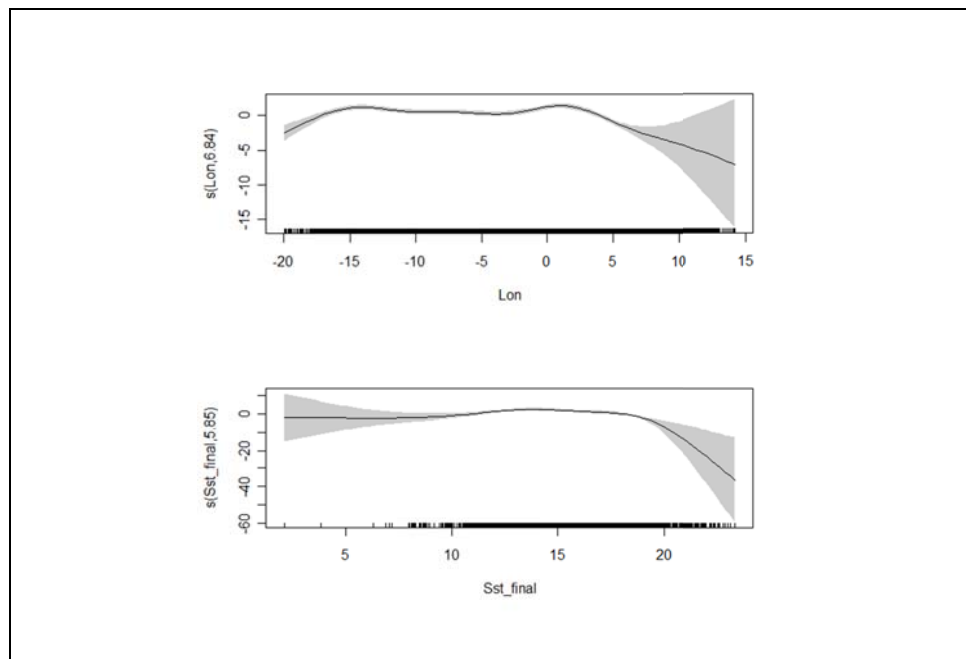
Figure 4. Smooth functions for the retained covariates (depth, contour index and the interaction of latitude and longitude) for the model of abundance of groups of fin whales.
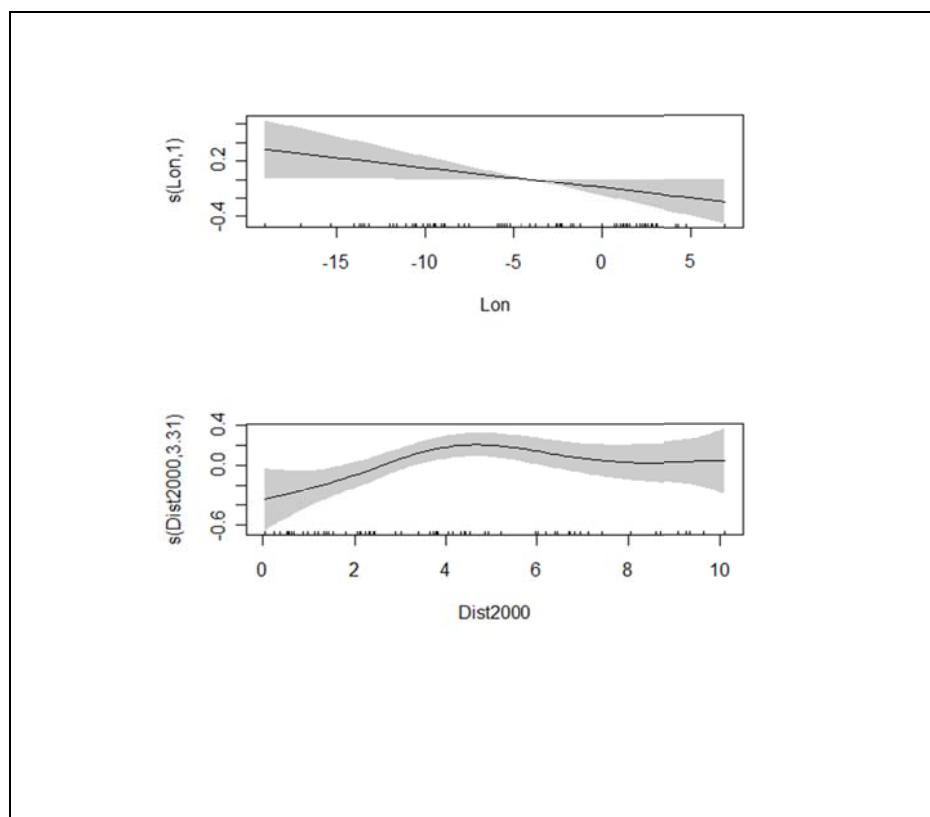
Figure 5. Model predicted map of abundance of fin whales

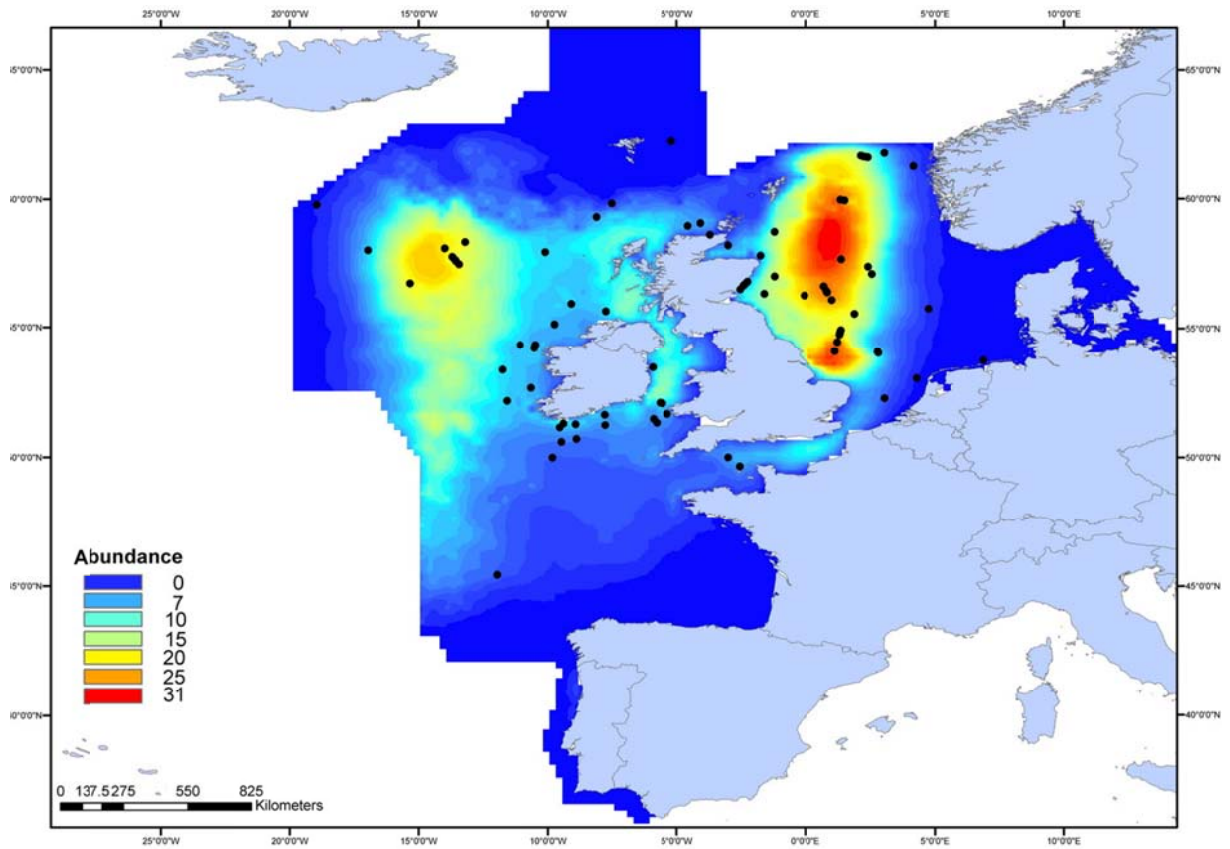**Figure 6.** Detection functions for minke whale.

Figure 7. Smooth functions for the retained covariates (longitude and sea surface temperature) for the model of abundance of groups for minke whales.

Figure 8. Smooth functions for the retained covariates (longitude and distance from the 2000m depth contour) for the model of group size for minke whales.

Figure 9. Model predicted map of abundance of minke whales.