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Abundance and distribution of common dolphins in the offshore NE Atlantic

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ABSTRACT
The objectives of the Cetacean Offshore Distribution and Abundance in the European Atlantic project (CODA) were to map summer distribution, generate unbiased abundance estimates, and investigate habitat preferences of common dolphin and other cetaceans in offshore waters of the European Atlantic. The study area was stratified into four blocks and surveyed by five ships during July 2007. Survey methods replicated those used during the SCANS-II project and the survey areas were adjacent. The survey was conducted using a 'trial configuration' ('BT mode'), with two teams of observers located on each survey vessel. This document gives results for common dolphins (*Delphinus delphis*). There were a total of 165 sightings of small odontocetes from the Primary platform including 104 of common dolphins, 33 of striped dolphins and 28 of common/striped dolphins (not identified to species) encountered during 9,494 km of searching effort. Abundance estimates were obtained for common and common/striped dolphins combined, both with design-based and with model-based methods, for each block. The total abundance estimates for the whole study area were: 118,264 common dolphins (%CV=37.8; 56,915-245,740) with the design-based method and 116,709 (%CV=33.7; 61,397–221,849) with the model-based method; and for common/striped dolphins combined 244,166 (%CV=48.0; 90,979-552,331) with the design-based method and 259,605 (%CV=36.9; 128,818-523,175) with the model-based method. The point estimates were very similar between the two methods for the two species groups. However, the estimated precision was much better for the model-based estimates, demonstrating the value of this approach in this case. The distribution patterns of common dolphins, with a clear preference for the Gulf of Biscay over other areas, are discussed. These results feed into a management framework developed under project SCANS-II, and further developed under CODA, to determine safe bycatch limits for small cetaceans, in particular common dolphins.

INTRODUCTION

European offshore waters have only been partially surveyed and the available abundance estimates suffer from several sources of bias. Offshore surveys are especially important to complement on-shelf surveys, such as SCANS (Hammond et al. 2002) and SCANS-II (SCANS-II 2008) for species that are distributed in both habitats such as the common dolphin. The objectives of the Cetacean Offshore Distribution and Abundance in the European Atlantic project (CODA) were to map summer distribution, generate unbiased abundance estimates, and investigate habitat preferences of common dolphin, bottlenose dolphin, fin whale, deep diving whales and other cetaceans in offshore waters of the European Atlantic. CODA also developed further the management framework developed under SCANS-II to determine safe bycatch limits for small cetaceans, in particular common dolphin. This paper presents preliminary abundance estimates obtained to date for common dolphins in the surveyed area.

SURVEY METHODS

The study area was stratified into four blocks (Figure 1) and was surveyed by five ships[1] during July 2007. Realised search effort is shown in Figure 2. Survey methods replicated those used during the SCANS-II

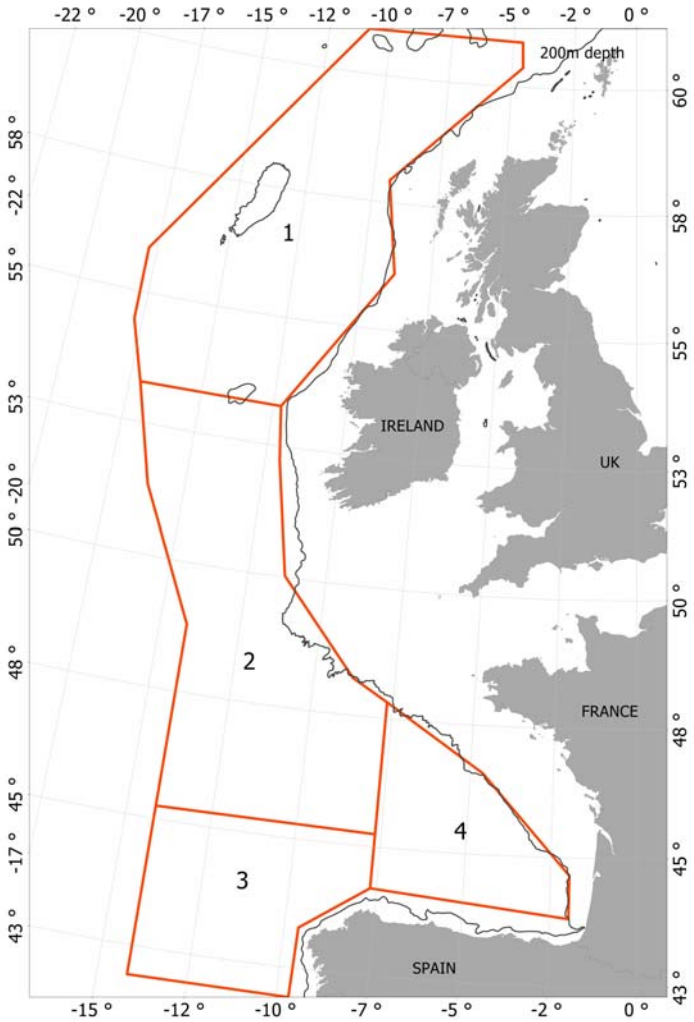
[1] The survey was planned with one ship per stratum but due to engine failure, two ships covered stratum 2.

project, which had previously been updated from the SCANS 1994 project (Hammond *et al.*, 2002) to incorporate new methods for data collection and analysis.

The shipboard survey was conducted using a 'trial configuration' (Laake & Borchers, 2004), also referred to as 'BT mode', with two teams of two observers located on each survey vessel. The first team (referred to as observer 1 or 'primary') searched with naked eye close to the vessel (<500m). The second team (observer 2 or 'tracker') 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 would not be able to enter the region searched by observer 1. A third observer (observer 3 or 'Duplicate Identifier') was informed of all detections as they were made and was responsible for classifying duplicates. A duplicate sighting occurred when a sighting made by observer 2, was subsequently recorded by observer 1. Duplicates were classified as either: D: definite (at least 90% likely), P: probable (more than 50% likely), R: remote (less than 50% likely).

All species were tracked until abeam of the vessel or for 2-3 re-sightings after they had been declared a duplicate. In the analysis that follows, classifications D (91.9%) and P (8.1%) are all considered to be duplicates to ensure adequate sample sizes for analysis (no R duplicates for common or striped dolphins).

Figure 1. Survey region divided into the survey blocks. The vessels that surveyed each block were: block 1 = Mars Chaser, block 2 = Rari and Germinal, block 3 = Cornide de Saavedra and block 4 = Investigador.



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AVAILABLE DATA

There were, in total, 165 primary sightings of common dolphins (CD), striped dolphins *Stenella coeruleoalba* (SD) and common/striped dolphins (not identified to species: CS), encountered during 9,494 km of searching effort in sea state ≤ Beaufort 4 (Figure 2). The distribution of the effort and sightings of species groups among blocks is given in Table 1.

	Effort	CD	SD	CS	CD-SD-CS
Block 1	3,408.8	4	1	0	5
Block 2	2,246.2	33	8	5	46
Block 3	2,178.1	8	8	6	22
Block 4	1,660.9	59	16	17	92
Total	**9,494.0**	**104**	**33**	**28**	**165**

Table 1. Effort (km) and primary sightings per block.

Figure 2. Realised search effort.

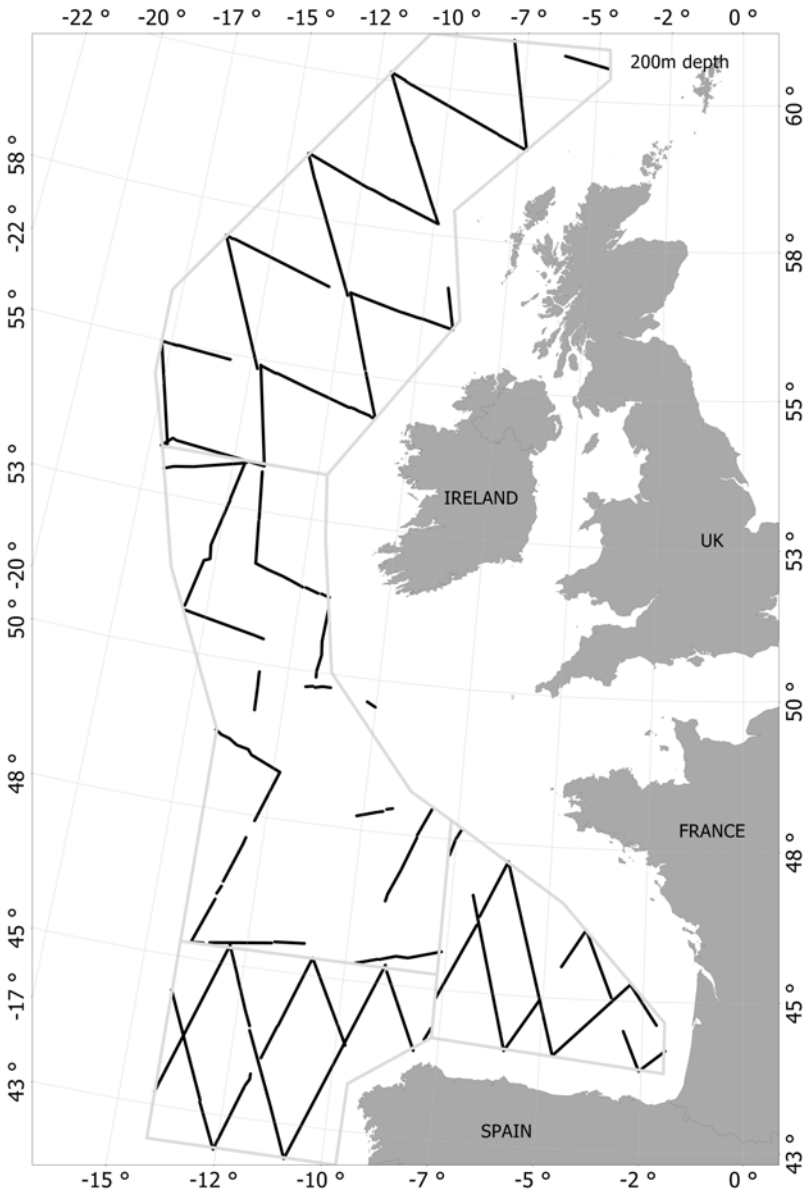

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Table 2 describes the environmental data available for the density surface modelling (DSM) of the data, which were organized in grid cells.

Name	Description	Source
depth_av	Average depth in the grid cell	2-Minute Gridded Global Relief Data (ETOPO2v2). National Geophysical Data Center (NGDC). NOAA Satellite and Information Service.
depth_sd	Standard deviation of the depth data points within the grid cell	Derived from ETOPO2 bathymetric data
depth_cv	Coefficient of variation of the depth data points within the grid cell	Derived from ETOPO2 bathymetric data
dist200_deg	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_deg	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_per	Slope of the sea floor as a percentage, calculated as follows: $\frac{\left(\frac{depth_{max} - depth_{min}}{distance\ in\ km_{(depth_{max},\ depth_{min})}}\right)}{10}$	Derived from ETOPO2 bathymetric data
slope_deg	Slope of the sea floor in degrees, calculated as follows: $degrees\left(\tan\left(\frac{slope_per}{100}\right)\right)$	Derived from ETOPO2 bathymetric data
ci	Contour index of the sea floor, calculated as follows: $\frac{(depth_{max} - depth_{min})}{depth_{max}} * 100$	Derived from ETOPO2 bathymetric data
ssh	Average Sea Surface Height Anomaly for the month of July 2007, calculated as the difference between measured SSH and the expected mean SSH.	Altimetry Sensors on multiple spacecrafts (JASON-1, TOPEX/POSEIDON, ENVISAT, GFO, ERS 1/2, GEOSAT). Resolution: 0.25 degrees. NOAA CoastWatch Program
sst	Average Sea Surface Temperature for the month of July 2007 for Blocks 1 and 2, for the first fortnight of July 2007 for Block 4 and for the second fortnight of July 2007 for Block 4.	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 month of July 2007 for Blocks 1 and 2, for the first fortnight of July 2007 for Block 4 and for the second fortnight of July 2007 for Block 4.	Derived from NOAA CoastWatch Program sea surface temperature data.
chla	Average Chlorophyll-a concentration for the month of July 2007 for Blocks 1 and 2, for the first fortnight of July 2007 for Block 4 and for the second fortnight of July 2007 for Block 4.	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 month of July 2007 for Blocks 1 and 2, for the first fortnight of July 2007 for Block 4 and for the second fortnight of July 2007 for Block 4.	Derived from NOAA CoastWatch Program Chlorophyll-a concentration data.
aspect	Orientation of the sea floor as a factor with 8 levels(N, NE, E, SE, S, SW, W, NW)	Calculated with the Spatial Analyst extension of ArcGis 9.2, using ETOPO2 bathymetric data.
aspectxyz	Orientation of the sea floor as a continuous variable (0 to 359)	Calculated with the Spatial Analyst extension of ArcGis 9.2, using ETOPO2 bathymetric data.
lat	Latitude in decimal degrees	
lon	Longitude in decimal degrees	

Table 2. Environmental covariates used in the density surface modelling.

ANALYSIS

Data organization

Effort

Effort data were divided into transects for the design-based analysis (Macleod *et al.* 2008) and further into segments for density surface modelling (DSM). One very long segment (31 km) was divided equally into two to make it more homogeneous with the remaining segments. This gave a total of 1,359 segments ranging from 0.1 to 17.6 km (mean= 6.96 km, sd=3.25 km), totalling 9,494 km on effort. A "search area" was calculated for each segment by multiplying the length of each segment by twice the truncation distance of 3,000m used for fitting the detection function.

Prediction grid of cells

A grid of cells of resolution 0.25 degrees covering the whole survey area was constructed in order to extrapolate the results of the DSM from the region covered during the survey to the whole study region. This resolution was chosen as it was the coarsest resolution in the available environmental covariates and yielded a total of 2,046 grid cells. Each grid cell was characterized by the values of environmental data used as potential predictive covariates in the DSM (see Table 2). The area of the sum of all grid cells was 987,037 km^2, slightly larger (2%) than the actual survey area (967,538 km^2) used to calculate design-based estimates, because some grid cells extended over the borders of the survey area. A correction factor was therefore applied to the DSM abundance estimate predicted over the grid (see later).

Detection function

To estimate the detection function, the three species groups (CD = common dolphin, SD = striped dolphin and CS = common or striped dolphin (unidentified to species level)) were pooled together because their size, group size and behaviour are very similar and therefore no differences in detectability were expected among them and because CS could be either CD or SD.

Sample size for estimating the detection function was:

Number of groups sighted	:	265
Number seen by Primary	:	165
Number seen by Tracker (trials)	:	173
Number seen by both (successful trials)	:	73

The full independence method of mark-recapture distance sampling was applied (Laake & Borchers 2004) because of the known strong responsive movement of, at least, common dolphins in the NE Atlantic. Therefore, only an MR model was defined. More details of the method are given in Macleod *et al.* (2008). All analyses were carried out in DISTANCE 6 Release 4 (Thomas et al., 2006).

Density surface modelling

Density surface modelling was undertaken in two steps: first modelling the abundance of groups and second modelling the group size; the estimated abundance of animals to be obtained by multiplying results from these two steps. This procedure is unavailable in program DISTANCE version 6; therefore program R (version 2.6.0), with the 'mgcv' package (version 1.1-4.1), was used.

Estimation of abundance of groups per segment

The probability of detection for each group encountered was obtained from program DISTANCE version 6, and with these, the estimated abundance of groups for each segment was calculated using the Horvitz-Thompson estimator:

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

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. This was done for the three groups of species analyzed: CD, SD and CD-SD-CS combined.

Modelling abundance of groups
The abundance of groups was modelled using a Generalized Additive Model (GAM) with a logarithmic link function. Due to over-dispersion in the data, a quasi-Poisson error distribution was used, with variance proportional to the mean, and using the searched area of each segment as an offset. The general structure of the model was:

$$\hat{N}_i = \exp\left[\ln(a_i) + \theta_0 + \sum_k f_k(z_{ik}) \right] \qquad (2)$$

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.

A maximum of 6 knots was allowed in modelling each covariate to avoid excessive, and probably unrealistic, "wiggliness" in the smooth function and therefore a potential problem of overfitting. An exception was in the model for common, striped and common/striped dolphins together where a maximum of 8 knots was allowed because of the larger sample size available and after visual inspection of the smooth functions, which did not show excessive wiggliness.

Automated model selection by a stepwise procedure was not yet implemented in the version of R used (2.6.0) (cran.r-project.org). Therefore, manual selection of the models was done using three criteria: (a) the GCV (General Cross Validation score); (b) the percentage of deviance explained; and (c) whether the variable was statistically significant.

Correcting group sizes
Group sizes are required for all groups detected by Primary to estimate mean group size and hence the abundance of individuals. In practice, group size cannot be estimated without error and may be biased. However, groups tracked by Tracker were observed for a longer period and their estimates of group size should be more reliable and a correction factor can be estimated from duplicate detections to correct bias in estimates of group size made by Primary as:

$$\hat{c}_s = \frac{\sum s_j(2)}{\sum s_j(1)} \qquad (3)$$

Where $s_j(1)$ is the group size estimated by the Primary observers in duplicate sightings, and $s_j(2)$ is the group size estimated by the Tracker observers in duplicate sightings.

Correction factors were pooled for Blocks 1 and 2, and for Blocks 3 and 4 to increase sample sizes. Correction factors for each block within each pooled group were similar. The correction factor estimated for Blocks 1 and 2 was 0.961. After visual inspection of the plots of Tracker *vs* Primary group size estimates, this correction factor was set to 1 (i.e. no correction factor was applied to Blocks 1 and 2). The correction factor estimated for Blocks 3 and 4 was 1.767.

These correction factors were applied to group sizes for all non-duplicate sightings. For duplicate sightings the Tracker group size estimate was used. The CV of the group size correction factor for Blocks 3 and 4 was estimated as 0.181.

Modelling group sizes
Group size was also modelled using a GAM with a logarithmic link function. The response variable was the number of dolphins counted in each group (s_j) and, given the large overdispersion due to the wide range of group sizes (1 – 228), a quasi-Poisson error distribution was used, with the variance proportional to the mean. The general structure of the model was:

$$E(s_j) = \exp\left[\theta_0 + \sum_k f_k(z_{jk})\right] \quad (4)$$

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 models was done following the same criteria described for the models of abundance of groups.

Estimating abundance of animals

Abundance of animals was obtained by multiplying the modelled abundance of groups by the modelled group sizes, and a prediction was made for all grid cells in the survey area.

Estimated abundance was summed over all grid cells in each block and corrected for the difference in surface area between the sum of grid cells and the actual survey area by multiplying the estimate by the respective correction factor: 0.969 for Block 1, 1.017 for Block 2, 0.920 for Block 3 and 0.997 for Block 4. Total abundance was estimated as the sum of the four blocks.

Estimating uncertainty

The whole analytical process was replicated in 600 non-parametric bootstrap re-samples to obtain CVs and 95% confidence intervals. The resampling unit used was a 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. Each re-sampling unit therefore corresponded to a transect or piece of transect surveyed over a single day.

The re-sampling process was stratified by block. For each resample, selections of re-sampling units for each block were performed simultaneously: within each block, random re-sampling units (allowing for repetition) were added until the total length was approximately the same as the total length actually surveyed in that block. Once each block had a new set of re-sampling units, these were all pooled together to construct the dataset for the whole survey area. This process conformed better with the survey design, which was stratified by blocks, than a re-sampling process for the whole survey area.

For each bootstrap resample, the models for abundance of groups and for group sizes were run, 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 selection uncertainty in the variance.
The Delta method was used to obtain the final CV for each block combining the CV obtained from the models in that block through the bootstrap, CV_{boot}, and the CV of the detection function, CV_{df}

$$CV_{block} = \sqrt{CV_{boot}^2 + CV_{df}^2} \quad (5)$$

The CV for the total abundance for the whole survey area, based on the stratified estimates, was obtained as:

$$CV_{total} = \sqrt{CV_{df}^2 + \frac{\sum var_{N_i}}{(\sum N_i)^2}} \quad (6)$$

where N_i is the abundance of animals in block i and var_{Ni} is the bootstrap variance of the abundance of animals in block i. 95% confidence intervals were obtained assuming the estimates of abundance were log-normally distributed. The CV and 95% CI were also obtained for each grid cell in order to be plotted as surface maps of uncertainty.

RESULTS

Design-based (MRDS) estimates of abundance

Detection function

The final model selected included the covariates: distance*size, sightabilitydolphins, cue2 and pplatheight, where size is the group size, sightabilitydolphins is a qualitative measure of the searching conditions for detecting dolphins (including sea state, glare, visibility, etc) organized in 4 factor levels, cue2 is the cue that caused the detection, condensed in two factor levels, and pplatheight is the height of the Primary platform in m. Distance and size were included as an interaction term.

This model had 8 parameters. The AIC of this model was 5.8 points higher than the best model according to AIC, which had the covariate "vessel" instead of "pplatheight". The second best model according to AIC was chosen for three reasons. First, it had only 8 parameters instead of the 11 included in the model with lowest AIC and was thus more parsimonious. Second, it gave an abundance estimate that was very similar to those from the next five models with a delta AIC up to 9.6 from the best model, while the best model had a much higher abundance estimate. Third, the CVs of the detection function and the final abundance estimate were much lower (0.24 and 0.48, respectively) than for the model with the lowest AIC (0.33 and 0.53, respectively). The estimates of probability of detection for the chosen model are shown in Table 3.

	Estimate	SE	CV
Average p	0.323	0.076	0.235
Average Primary p(0)	0.538	0.128	0.237
N in covered region	819.5	199.5	0.243

Table 3. Estimates of probability of detection for the primary platform

The detection function for the Primary is shown in Figure 3. The large peak in the first bin is probably a result of attraction to the vessel. The conditional detection probability is shown in Figure 4.

Figure 3. Detection function for primary observers

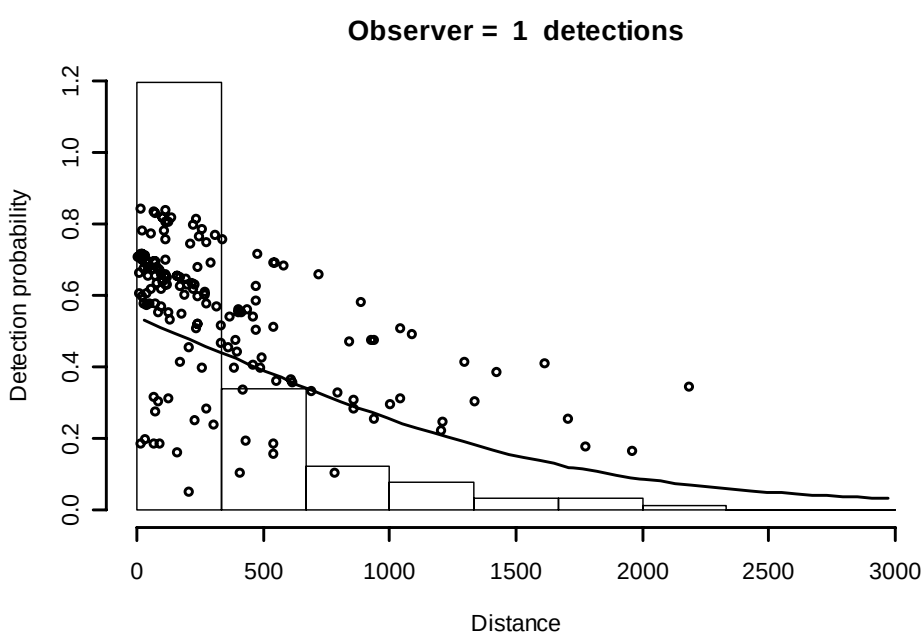
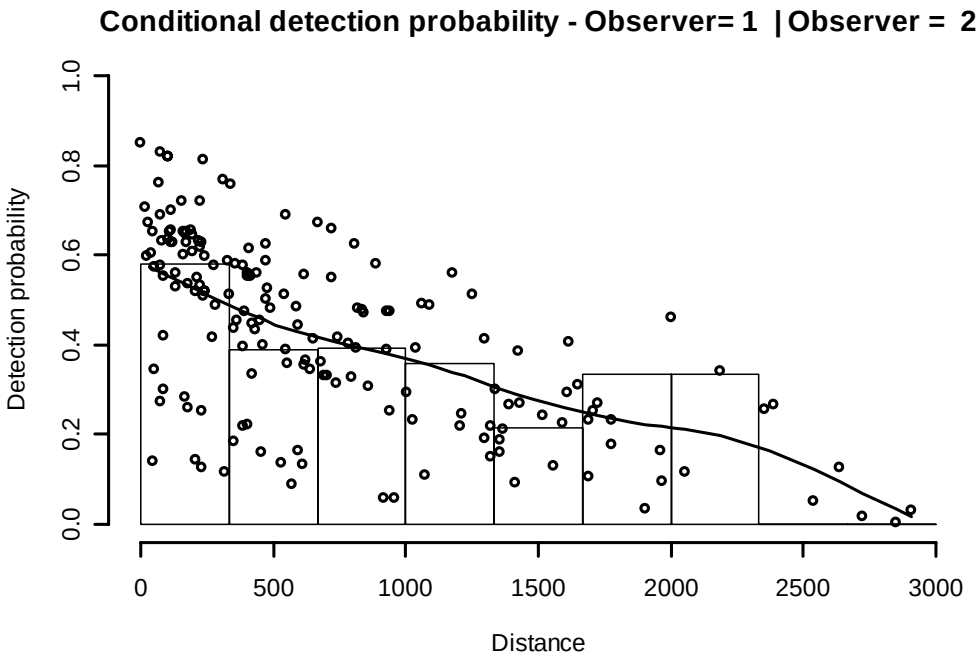


Figure 4. Conditional detection probability



Abundance estimates
Estimates of abundance, density and expected group size for common dolphins with their respective CV and 95%CI are given in Table 4 (middle column).

Model-based (DSM) estimates of abundance
Density surface modelling of abundance of groups
The covariates retained in the final model were: sea surface temperature, contour index, average depth and sea surface height anomaly, all with a p<<0.001. The deviance explained by the model was 49.4%. Figure 5 shows the smooth functions for the selected covariates. No autocorrelation was observed in the residuals

Density surface modelling of group sizes
The covariates retained in the final model were: an interaction term between sea surface temperature and contour index (p<<0.001). The deviance explained by the model was 52%. Figure 6 shows the smooth functions for the selected covariates. No autocorrelation was observed in the residuals.

Estimates of abundance and uncertainty
The total estimate of abundance of common dolphins (sum of the block estimates after correction for surface area) was 116,709. The surface map of smoothed predicted abundance of animals is shown in Figure 7.

Out of the 600 bootstraps, two yielded an extreme result (extremely high and unrealistic estimate). Therefore, 598 bootstraps were used for the analysis. The average estimate of abundance of animals for the bootstrap (uncorrected) was 130,546 (CV=0.285), very similar to the uncorrected point estimate (122,423). The CV estimated from the stratified abundance estimates and the CV of the detection function of 0.235 from equation 6 was 0.337, lower than the CV for the abundance estimate obtained with the MRDS analysis (0.378). The 95% CI for the total stratified estimate was 61,397 – 221,849.

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Figure 5. Smooth functions for the selected predictive covariates in the model of abundance of groups of common dolphins.

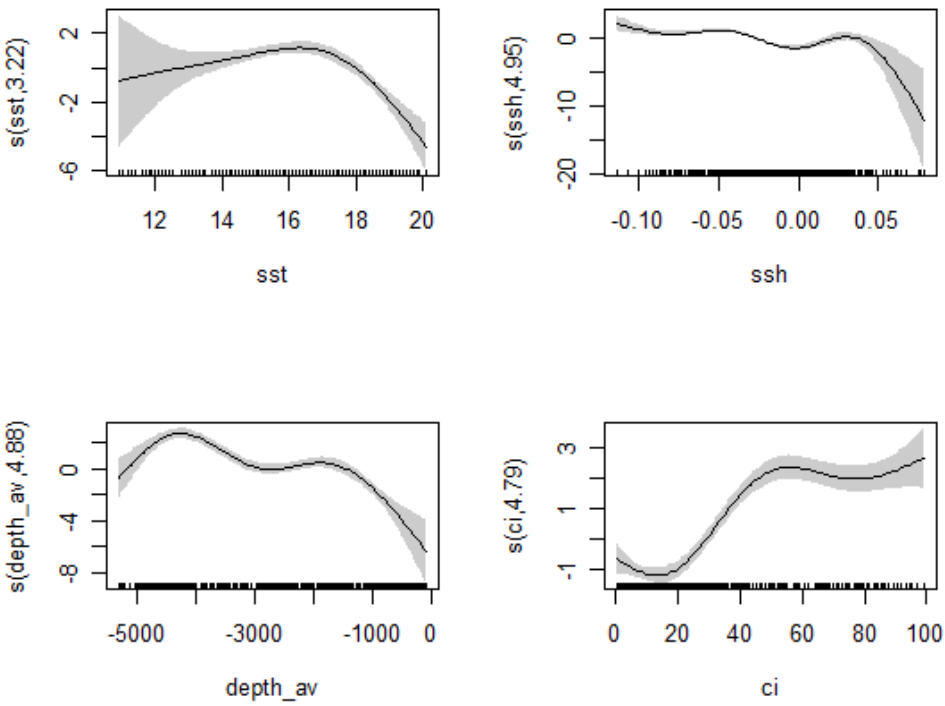

Figure 6. Smooth function for the selected predictive covariates in the model of group sizes of common dolphins.

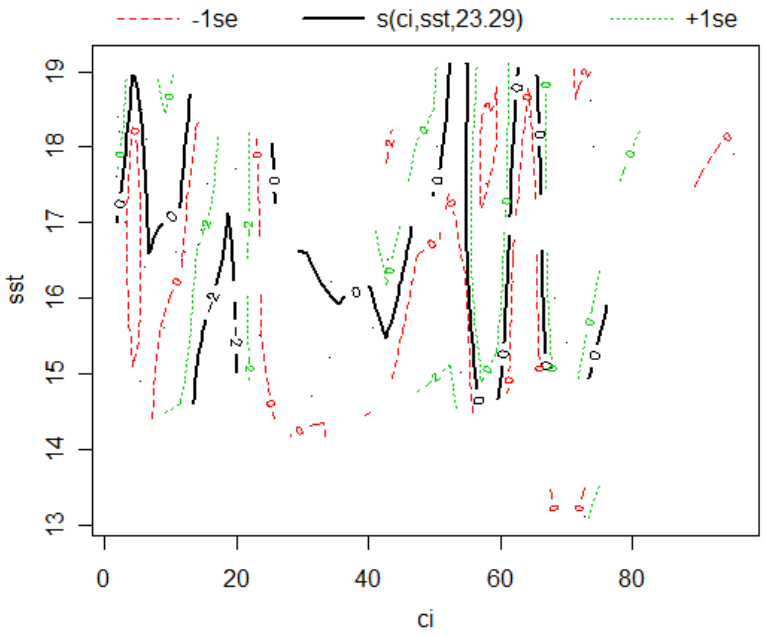

Figure 7. Surface map of smoothed predicted abundance of common dolphin

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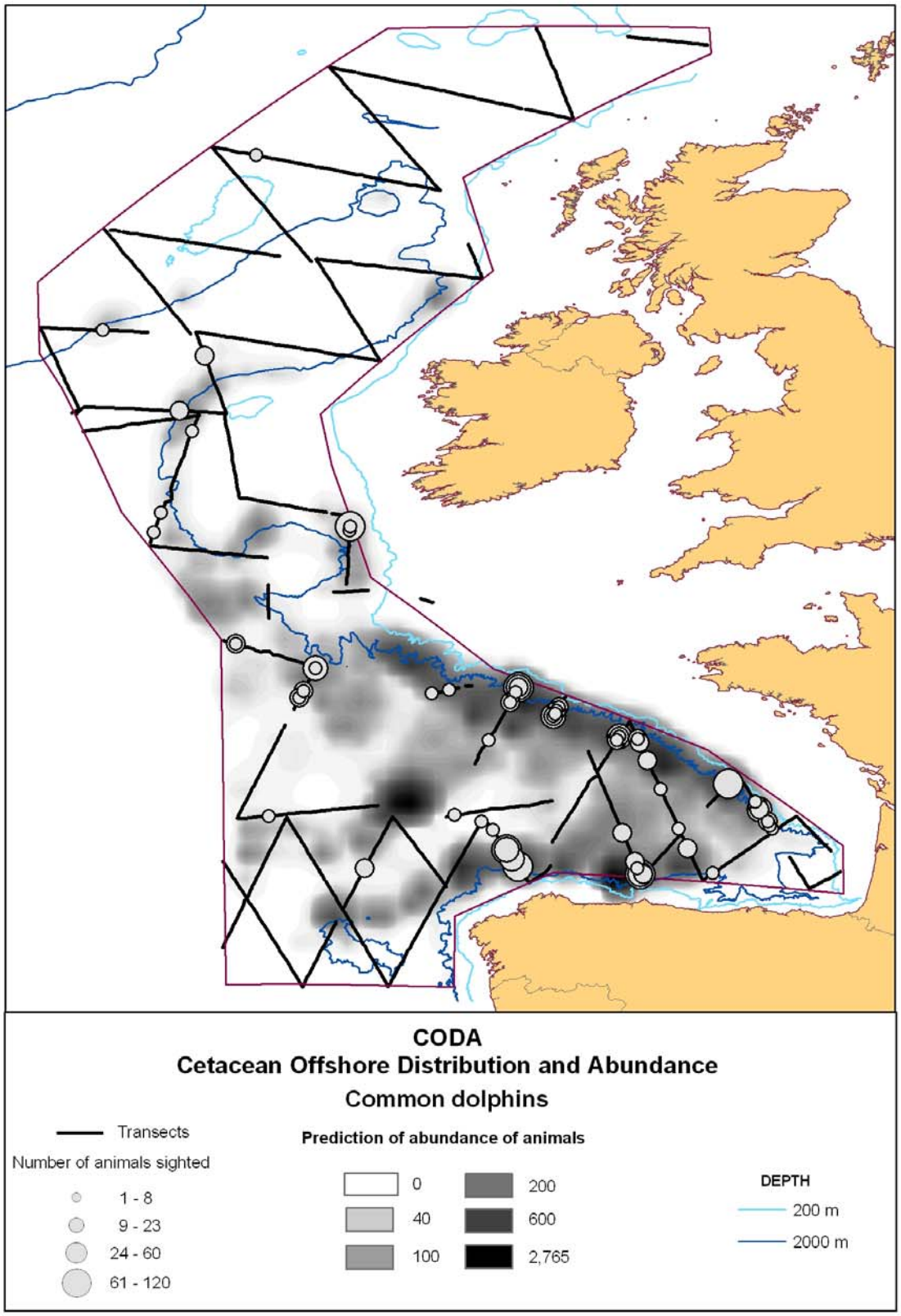

Details for the total survey area and each block are given in Table 4, as well as a comparison with the design-based estimates.

	Design-based (MRDS)			DSM (stratified and corrected)		
	Estimate	CV	95% CI	Estimate	CV	95% CI
Total area						
Number of groups	9,310	0.406		9.089	0.328	
Expected group size	12.7	0.236		12.8		
Detection function		0.235				
Number of animals	**118,264**	**0.378**	**56,915 245,740**	**116,709**	**0.337**	**61,397 221,849**
Density of animals	0.122	0.378	0.059 0.254	0.121	0.337	0.064 0.229
Block 1						
Number of groups	595	0.850		685	0.580	
Expected group size	6.0	0.192		6.2		
Detection function		0.235				
Number of animals	**3,547**	**0.758**	**900 13,971**	**4.216**	**0.575**	**1,478 12,027**
Density of animals	0.010	0.758	0.003 0.040	0.012	0.575	0.004 0.035
Block 2						
Number of groups	4,706	0.520		4,704	0.358	
Expected group size	11.4	0.361		11.2		
Detection function		0.235				
Number of animals	**53,638**	**0.537**	**18,900 152,220**	**52,749**	**0.394**	**25,054 111,059**
Density of animals	0.159	0.537	0.056 0.453	0.157	0.394	0.075 0.330
Block 3						
Number of groups	422	0.972		661	0.530	
Expected group size	29.3	0.300		31.9		
Detection function		0.235				
Number of animals	**12,378**	**1.226**	**1,346 113,836**	**21,071**	**0.506**	**8,270 53,689**
Density of animals	0.077	1.226	0.008 0.709	0.131	0.506	0.052 0.334
Block 4						
Number of groups	3,587	0.586		3,039	0.396	
Expected group size	12.7	0.187		12.7		
Detection function		0.235				
Number of animals	**48,701**	**0.514**	**17,211 137,807**	**38,673**	**0.457**	**16,464 90,839**
Density of animals	0.400	0.514	0.141 1.131	0.317	0.457	0.135 0.745

Table 4. Estimates of abundance and uncertainty for common dolphins.

DISCUSSION

Comparison of the design-based and model-based results

The point estimates of abundance of animals for the two methods are very similar. However, the estimates of uncertainty, i.e. coefficients of variation and 95% confidence intervals, are smaller and narrower, respectively, for the model-based than for the design based estimates (Table 4). This is because the density surface modelling accounts for more variability in the data through the modelled relationships between abundance and characteristics of the habitat. This demonstrates that, in this case, density surface modelling is a valuable technique to assess cetacean abundance and distribution and we consider the model-based estimates as the best estimates. This was also found for striped dolphins in the western Mediterranean (Gomez de Segura *et al*. 2007).

Differences in the modelled distributions of common and striped dolphins

For comparison with common dolphins, the map of predicted abundance of striped dolphins is shown in Figure 8. In general, there is considerable similarity in the modelled distribution patterns of common and striped dolphins, in that both species have higher densities in the southern half and very low densities in the northern half of the study area. Within the southern half, both species also have higher densities within the Gulf of Biscay, especially along the continental slope both on the northern and southern edges of the Gulf, and less towards the south, to the west of Galicia (Spain).

The main difference between the species is that striped dolphins show a concentration in density in the deep waters of the western part of the Gulf of Biscay and relatively less over the slope, compared to common dolphins.

There is one area that appears as high density for both species, around the centre of the Gulf of Biscay, in an area with no effort in the south of Block 2, and also, in the case of striped dolphins, to the north-west of there. This predicted high density area is characterised by steeper slope and shallower depth than the surrounding areas, corresponding to some seamounts. In addition, it is an area with the "best" sea surface temperature for both species according to the models. Therefore, this area seems to have the right environmental characteristics for holding high densities for both species. However, consideration of this area in a management context must wait until this prediction is supported by data.

Next steps

The model-based estimate of abundance of common dolphins from SCANS-II was 68,495 (CV = 0.672; 95% CI = 39,056 - 257,136) (SCANS-II 2008). Adding this estimate to the CODA estimate (116,709; CV = 0.337; 95% CI = 61,397 – 221,849) yields an estimate of abundance of common dolphins for the European Atlantic waters covered by SCANS-II and CODA combined of 185,204 common dolphins (CV = 0.327; 95% CI = 99,200 – 345,772).

The next step will be to combine the data from SCANS-II and CODA to obtain an overall model-based abundance estimate for the whole area. Both surveys were carried out during the month of July and with only two years between them, so it is not unreasonable to assume that any changes in abundance between the surveys would have been relatively minor. Importantly, the environmental covariates that are dynamic in nature (i.e. change with time, such as sea surface temperature, chlorophyll concentration or sea surface height anomalies) can be set according to the time in which the different areas were surveyed, accounting for any inter-annual changes that may have occurred in the patterns of these covariates. The rest of covariates used, such as depth, slope, etc. are fixed and do not change with time.

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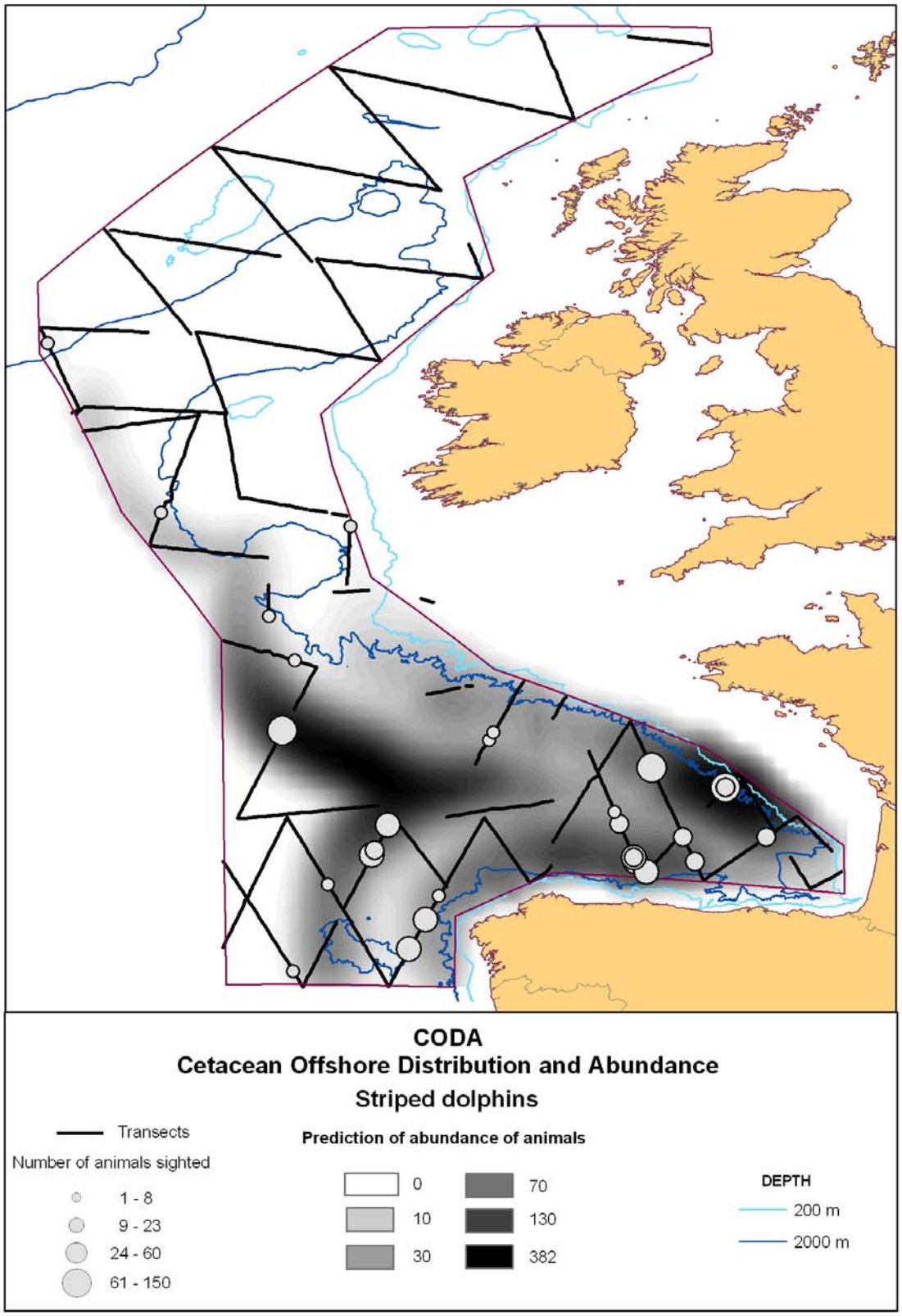
Figure 8. Surface map of smoothed predicted abundance of striped dolphin



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