

Appendix II

Model-based estimates of cetacean abundance in offshore European Atlantic waters

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INTRODUCTION

This paper presents abundance estimates obtained for the main species found in the surveyed area using density surfacing modelling (DSM), a model-based approach to abundance estimation. Design-based methods (Conventional Distance Sampling, CDS and Mark-Recapture Distance Sampling, MRDS) provide estimates of abundance for predetermined survey blocks with equal coverage probability but provide no information on density at a finer spatial resolution. In the DSM approach, animal density is modelled in a Generalised Additive Model (GAM) framework using geographical, physical and environmental covariates to generate abundance estimates.

Constructing a model in which variability in animal density is explained by covariates describing the environment provides information on distribution that is more useful than scatterplots of sightings or sightings per unit of effort. The resulting models and maps improve our understanding of which features of the environment influence density and where high use areas are. Care must be taken in interpreting these results because the method is predictive rather than explanatory. Nevertheless DSM is a useful technique to obtain additional information on distribution and abundance if suitable covariate data are available. Density surface modelling can generate estimates of abundance that have greater precision than design-based methods. It also allows abundance to be estimated for areas that are different to the survey blocks originally defined for the survey.

SURVEY METHODS

The study area was divided into four strata (Figure 1) and was surveyed by five ships¹ during July 2007. Realised search effort is shown in Figure 1. Survey methods replicated those used during the SCANS-II 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), with two teams of observers located on each survey vessel. The first team (referred to as observer 1 or ‘Primary’) searched by 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 chance (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. Definite and Probable duplicates were included in the MRDS analyses.

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

ANALYSIS

Data preparation

The response variable for the spatial modelling approach is the number of groups in each segment of effort. Each transect of survey effort was divided into segments of comparable lengths. Segments where seastate was greater than Beaufort 4 were excluded. 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 in length (mean= 6.96 km, sd=3.25 km), amounting to 9,494 km of on survey effort.

The spatial modelling requires the abundance of groups to be predicted throughout the survey area. The abundance of groups are estimated per unit area and requires that the survey area be divided into a grid. A grid of cells of resolution 0.25 degrees was constructed covering the whole survey area. This yielded a total of 2,046 grid cells. The width of a degree of longitude changes with latitude causing variation in the area of the grid cells as measured in km², ranging from 377.1 km² in the northernmost grid cells to 573.5 km² in the southernmost grid cells. Each grid cell was characterized by the values of a series of environmental data used as potential predictive covariates for the density surface modelling (DSM) (Table 1). The sum of all grid cells was 987,037 km², slightly larger (2%) than the actual survey area (967,538 km²) 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.

Analysis method

For model-based abundance estimation, five steps were followed, according to Cañadas & Hammond (2006): (1) a detection function was estimated from the line transect data and any covariates that could affect detection probability; (2) the number of groups in each segment was estimated through Horvitz-Thompson-like estimator (Borchers, Buckland & Zucchini, 2002); (3) abundance of groups was modelled as a function of geographical and environmental covariates; (4) group size was modelled as a function of covariates (for some species only); (5) abundance of animals was estimated in each grid cell as the product of model predictions from steps 3 and 4 or step 3 and a mean group size.

Estimation of detection function

Detection functions were used as estimated for the design-based abundance estimates previously presented (Appendix I, Figure 4).

Estimation of number of groups per segment

The response variable used to formulate a spatial model of abundance of groups was the estimated number of groups (\hat{N}_i) in each segment, estimated through the Horvitz-Thompson estimator:

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

where n_i is the number of detected groups in the i^{th} segment, and \hat{p}_{ij} is the estimated probability of detection of the j^{th} group in segment i . The probability of detection was obtained from the detection function fitted to the data.

Modelling abundance of groups and group size

The potential explanatory covariates used are listed in Table 1. Interactions between covariates were investigated.

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:

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

where the offset a_i is the search area for the i^{th} 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 k^{th} explanatory covariate in the i^{th} segment.

Models were fitted using package ‘mgcv’ version 1.0-5 for R (Wood 2001) either in R or in Distance 6, Release 4 (Thomas *et al.* 2006). In both, manual selection of the models was done using three indicators, as described in Cañadas & Hammond (2006): (a) the GCV (General Cross Validation score; Wood 2001); (b) the percentage of deviance explained; and (c) the probability that each variable is included in the model by chance. In all models, a visual inspection of the residuals was also made, especially to look for trends.

For species that occurred in larger groups and where group size may be related to environmental covariates, group size was also modelled using a GAM with a logarithmic link function. The response variable was the number of individuals counted in each group (s_j) (corrected for differences between observers for some species) and a quasi-Poisson error distribution was used, with the variance proportional to the mean. The general structure of the model was:

$$E(s_j) = \exp\left[\theta_0 + \sum_k f_k(z_{jk})\right] \quad (3)$$

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

Estimation of abundance

Abundance of groups and group size were predicted by the final models in all grid cells of the study area. The estimated abundance of animals for each grid cell was calculated as the product of its predicted abundance of groups and its predicted or mean group size. The point estimate of total abundance was obtained by summing the abundance estimates in all grid cells over the study area.

Estimation of variance

The variance of the abundance estimates was generated using bootstrap methods, in which the detection function and abundance was estimated from each bootstrap sample of data. The resampling unit corresponded to a transect or piece of transect surveyed over a single day. Between 499 and 600 bootstraps were run and the empirical variance calculated from the abundance estimates of the bootstrap samples. Approximate 95% confidence interval (CI) were obtained using the ‘percentile’ method.

The resampling process was stratified by block. For each resample, four selections of resampling units were performed simultaneously: for each block, random resampling 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 resampling units, these were pooled to construct the dataset for the whole survey area. This process conformed better with the survey design which was stratified by blocks, than a resampling 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 (eq. 4) 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}

$$CV_{block} = \sqrt{CV_{boot}^2 + CV_{df}^2} \quad (4)$$

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

$$CV_{total} = \sqrt{CV_{df}^2 + \frac{\sum var_{N_i}}{(\sum N_i)^2}} \quad (5)$$

where N_i is the abundance of animals in block i and var_{N_i} 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 obtained also for each grid cell so that surface maps of uncertainty could be plotted (see Annex 1).

RESULTS

Modelling abundance of groups

The abundance of groups was modelled for: common dolphin, striped dolphin, common and striped dolphins combined, fin whale, long-finned pilot whale, sperm whale, large baleen whales (fin, sei, fin/sei and blue) and beaked whales. The best models were chosen on the basis of the AIC and % deviance explained, and are given in Table 2.

Modelling group size

Group size was modelled for those species where group size is commonly greater than one. The best models were chosen on the basis of AIC and % deviance explained, and are given in Table 3. Group size for the large baleen whales was not modelled because they mainly occurred as single animals.

Abundance estimates

Common and striped dolphins

The total estimate of abundance of common dolphins was 116,709 (CV= 0.34; 95% CI = 61,397 – 221,849). Estimates for each block are given in Table 4. The surface map of smoothed predicted abundance of animals is shown in Figure 2.

The total estimate of abundance of striped dolphins was 67,414 (CV = 0.38; 95% CI = 32,543 – 139,653). Estimates for each block are given in Table 4. The surface map of smoothed predicted abundance of animals is shown in Figure 3.

The total estimate of abundance of striped and common dolphins together was: 259,605 (CV = 0.38; 95% CI = 128,818 – 523,175). Estimates for each block are given in Table 4. The surface map of smoothed predicted abundance of animals is shown in Figure 4.

Long-finned pilot whales

The total estimate of abundance of long-finned pilot whales was 25,338 (CV = 0.35; 95% CI = 12,912 – 49,725). Estimates for each block are given in Table 4. The surface map of smoothed predicted abundance of animals is shown in Figure 5.

Sperm whales

The total estimate of abundance of sperm whales was 2,077 (CV = 0.20; 95% CI = 1,404 – 3,073). Estimates for each block are given in Table 4. The surface map of smoothed predicted abundance of animals is shown in Figure 6.

Beaked whales

The total estimate of abundance of beaked whales was 7,332 (CV = 0.31; 95% CI = 4,067 – 13,220). Estimates for each block are given in Table 4. The surface map of smoothed predicted abundance of animals is shown in Figure 7.

Fin whales and large baleen whales

Group size was not modelled for large baleen whales because the majority of observations were of single animals. Modelled estimates of group abundance for each block were multiplied by mean group sizes. The total estimate of abundance of fin whales was: 9,019 (CV = 0.11; 95% CI = 7,265 – 11,197 259,605). Estimates for each block are given in Table 4. The surface map of smoothed predicted abundance of animals is shown in Figure 8.

The total estimate of abundance of large baleen whales (fin, sei, fin/sei, blue) was: 9,619 (CV = 0.11; 95% CI = 7,760 – 11,924). Estimates for each block are given in Table 4. The surface map of smoothed predicted abundance of animals is shown in Figure 9.

DISCUSSION

Common and striped dolphin

In general, there is considerable similarity in the modelled distribution patterns of common and striped dolphins, in that predicted densities of both species are higher in the southern half and lower in the northern half of the study area. Within the southern half, both species also have higher predicted densities within the Gulf of Biscay, especially along the continental slope both on the northern and southern edges of the Gulf, and less so towards the south, to the west of Galicia. The main difference between the species is that striped dolphins have a predicted high density area 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 is predicted as high density for both species, around the centre of the Gulf of Biscay in the southern part of Block 2 in an area with no effort. This predicted high density area has steeper slopes and shallower depths than the surrounding areas, corresponding to some seamounts. In addition, it is an area with the optimum 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 and would be interesting to investigate further.

Pooling together different species for modelling density is generally not a good idea because different species may be expected to have different relationships with their habitats and therefore be distributed differently. This may cause difficulties in model fitting and obscure the relationship between a species distribution and its environment. However, the model for common and striped dolphins combined worked well because of the relatively coarse similarities in their distribution over a large area, as described above. In addition, those groups in which the species could not be determined between striped or common dolphins could be included. This model thus provides a good picture of the distribution and high density areas of small dolphins in the study area.

Long-finned pilot whale

Long-finned pilot whales were predicted to occur mainly in the northern part of the survey area. The highest densities were predicted between 53° and 58°N, offshore from Ireland and Scotland. The model predicted that higher densities occurred in deep waters, seabed slopes with a south-easterly orientation, and warmer temperatures.

Fin whale

Predicted fin whale densities were highest in the southern part of the survey area. There were two areas in particular that had the highest densities: the southern part of Block 2 and the north-eastern part of Block 3 off the Galician coast.

Four covariates were found to be important in predicting fin whale density: sea surface temperature, average depth, longitude and distance to the 2000m contour. Density was predicted to be higher in areas of sea surface temperature 16-19°C and depths 1,000-3,500m. Peak density was predicted within 50m of the 2000m contour.

There were very few sightings of large baleen whales in the northern part (Block 1) of the survey area. Occurrence of fin whales in this area during July may be variable, having been recorded in this region during some previous surveys (Pollock *et al.*, 2000; Macleod *et al.*, 2006) but not in others (Joyce *et al.*, 1990).

Sperm whale

The spatial model predicted a clear pattern of higher densities of sperm whales towards the southern part of the study area: the Gulf of Biscay and north-western waters of the Iberian Peninsula. There was a second medium-density area in the northern part, west of the Hebrides. In the Gulf of Biscay, these results coincide with previous reports showing that the habitat of sperm whales in this area comprises the complex canyon

area of the lower northern Celtic-Biscay shelf edge, the edge of the Biscay abyssal plain and the Santander canyon, near Bilbao (Lewis *et al.* 2007).

Beaked whales

The spatial model predicted two high density areas for beaked whales in the study area: the most south-easterly section (the Gulf of Biscay), and the most north-westerly section. These widely segregated areas probably correspond to different species or groups of species. In the north-west, all sightings of beaked whales identified to species level were of Sowerby's beaked whale and Northern bottlenose whale, with only one sighting of Cuvier's beaked whale. In the Gulf of Biscay, all sightings identified to species level were of Cuvier's beaked whale; there was one sighting of Sowerby's beaked whales in Block 3.

The Gulf of Biscay, and particularly its south-eastern part, is known from previous surveys in more coastal waters of Spain and from the observations from the ferries crossing from the UK to Spain as an important habitat for beaked whales, especially Cuvier's beaked whales (SCANS-II, 2008; Williams *et al.*, 1999; Cresswell & Walker 2001, 2003; Walker *et al.*, 2004; Smith *et al.* 2007). However, two known important local areas, the Cap Breton and Torrelavega canyons (Vázquez *et al.*, 2004, 2007, 2008; Evans 2008) were not covered in this survey.

REFERENCES

- Borchers, DL, Buckland, ST & Zucchini, W. 2002. Estimating Animal Abundance: Closed Populations. Springer.
- Cañadas, A. & Hammond, P.S. 2008. Abundance and habitat preferences of the short-beaked common dolphin (*Delphinus delphis*) in the South-western Mediterranean: implications for conservation. *Endangered Species Research* 4: 309-331.
- Cresswell, G. and Walker, D. (Eds.) 2001. A report on the whales, dolphins and seabirds of the Bay of Biscay and English Channel. Organisation Cetacea, No. 1.
- Cresswell, G. and Walker, D. (Eds.) 2003. ORCA. The Annual Report of the Organisation Cetacea. Brunton Business Publications. 45pp.
- Evans, P.G.H., Smeenk, C., and Van Waerebeek, K. 2008. Cuvier's beaked whale *Ziphius cavirostris*. Pp. 690-692. In: *Mammals of the British Isles* (Eds. S. Harris & D.W. Yalden). Mammal Society, London.
- Hammond, P.S., Berggren, P., Benke, H., Borchers, D.L., Collet, A., Heide-Jørgensen, M.P., Heimlich, S., Hiby, A.R., Leopold, M.F. & Øien, N. 2002. Abundance of harbour porpoises and other cetaceans in the North Sea and adjacent waters. *Journal of Applied Ecology* 39: 361-376.
- Joyce, GG, Desportes, G & Bloch, D. 1990. The Faroese NASS-89 sightings cruise. Paper SC/42/O11 presented to the IWC Scientific Committee, June 1990.
- Laake, JL & Borchers, DL 2004. Methods for incomplete detection at distance zero. In: Buckland, ST, Anderson, DR, Burnham, KP, Laake, JL, Borchers, DL & Thomas, L (2004). *Advanced distance sampling: estimating abundance of biological populations*. Oxford University Press.
- Lewis, T, Gillespie, D, Lacey, C, Matthews, J, Danbolt, M, Leaper, R, McLanaghan, R & Moscrop, A. 2007. Sperm whale abundance estimates from acoustic surveys of the Ionian Sea and Straits of Sicily in 2003. *J. Mar. Biol. Ass. UK* 87: 353-357.
- Macleod, K, Simmonds, MP & Murray, E. 2006. Abundance of fin (*Balaenoptera physalus*) and sei whales (*B. borealis*) amid oil exploration and development off northwest Scotland. *J. Cetacean Res. Manage* 8(3): 247-254.
- Pollock, CM, Mavor, R, Weir, CR, Reid, A, White, RW, Tasker, ML, Webb, A & Reid, JB. 2000. The distribution of seabirds and marine mammals in the Atlantic frontier, north and west of Scotland. JNCC, Aberdeen, 92pp.
- Smith, J., Brereton, T., Macleod, C., Martin, C. & Tyler, P. 2007. Spatial and temporal distribution of Cuvier's beaked whale, *Ziphius cavirostris*, influenced by depth and sea surface temperature, in the bay of Biscay. 21st Annual Conference of the European Cetacean Society, San Sebastian, Spain.

Thomas, L., Laake, J.L., Rexstad, E., Strindberg, S., Marques, F.F.C., Buckland, S.T., Borchers, D.L., Anderson, D.R., Burnham, K.P., Burt, M.L., Hedley, S.L., Pollard, J.H., Bishop, J.R.B. and Marques, T.A. 2006. Distance 6.0. Release 4. Research Unit for Wildlife Population Assessment, University of St. Andrews, UK. <http://www.ruwpa.st-and.ac.uk/distance/>

Vázquez, J.A., Cermeño, P., Williams, A., Martin, C., Lazkano, O., Ruiz, L., Basáñez, A., and Guzman, I. 2004. Identifying areas of special interest for Cuvier's beaked whale (*Ziphius cavirostris*) in the southern part of the Bay of Biscay. Abstracts, 18th Annual Conference of the European Cetacean Society, Kolmårdon, Sweden.

Vázquez, J.A., Swift, R., and K. Macleod. 2007. Dive behaviour and photo id studies of beaked whales in Torrelavega canyon (northwest Spain) during diver project. 21st Annual Conference of the European Cetacean Society, San Sebastian, Spain.

Vázquez, J.A., Cobelo, P., Silva, P., Martínez-Cedeira, J., Guzmán, I., Solano, S. and A. López. 2008. Baseline information for the conservation and management of cetacean populations in offshore areas of Atlantic Spanish waters. 22th Annual Conference of the European Cetacean Society, Egmond aan Zee, The Netherlands.

Walker, D., Telfer, M., and Cresswell, G. 2004. The status and distribution of beaked whales (*Ziphiidae*) in the Bay of Biscay. Pp. 278-282. In: European Research on Cetaceans – 15 (Eds. P.G.H. Evans and E. O'Boyle). Proc. of the 15th Ann. Conf. of the European Cetacean Society, Rome, Italy, 6-10 May 2001. European Cetacean Society, Kiel, Germany. 478pp.

Williams, A.D., Breerton, T.M. and Williams, R. 1999. Seasonal variation in the occurrence of beaked whales in the southern Bay of Biscay. Pp. 275-280. In: European Research on Cetaceans – 13 (Eds. P.G.H. Evans, J. Cruz and J.A. Raga). Proc. of the 13th Ann. Conf. of the European Cetacean Society, Valencia, Spain, 5-8 April 1999. European Cetacean Society, Valencia, Spain. 484pp.

Wood SN 2001. mgcv: GAMs and generalized ridge regression for R. R News 1(2):20–25.

Table 1. Variables used in the models and associated with the grid cells.

Geographic	Abbreviation
Latitude	lat
Longitude	lon
Physiographic	
Average depth (m)	Depth_av
Standard deviation of depth (m)	depth_sd
Coefficient of deviation of depth	depth_cv
Distance from the 200 m isobath (degrees or km)	dist200
Distance from the 2000 m isobath (degrees or km)	dist2000
Aspect of the seabed (degrees)	Aspect
Slope (percentage)	slope_per
Contour index ((max depth - min depth)*100/max depth)	ci
Oceanographic	
Sea surface temperature	sst
Chlorophyll a concentration	chl
Sea surface height anomaly	ssh

Table 2. Best-fitting models predicting abundance of groups for each species. The term $s(\text{cov}, \text{df})$ represents a smooth function of the explanatory variable cov with df estimated degrees of freedom. The expression $k=n$ means that the function has been limited to fitting a smooth function with up to a maximum of n df . If k is not specified, then the maximum df allowed was 10 and 30 for a 1D and 2D smooth, respectively. The symbol “:” means “interaction with”.

Species	Best-fitting model	% deviance explained
Common dolphin	$s(\text{sst}, 3.22, k=6) + s(\text{ci}, 4.80, k=6) + s(\text{depth_av}, 4.88, k=6) + s(\text{ssh}, 4.95, k=6)$	49
Striped dolphin	$s(\text{sst}, \text{dist2000_deg}, 9.91, k=12)$	19
Common/striped dolphins	$s(\text{sst}, 6.83, k=8) + s(\text{ci}, 6.82, k=8) + s(\text{depth_av}, 6.52, k=8) + s(\text{dist200_deg}, 4.74, k=8)$	43
Large baleen whales	$s(\text{sst}, 6.82) + s(\text{depth_av}, 2.9) + s(\text{longitude}, 8.98) + s(\text{dist2000km}, 5.78, k=7) + s(\text{ci}, 7.98)$	47
Fin whale	$s(\text{sst}, 7.01) + s(\text{depth_av}, 8.56) + s(\text{longitude}, 8.92) + s(\text{dist2000km}, 5.72, k=7)$	40
Long-finned pilot whale	$s(\text{sst}, 2.84, k=4) + s(\text{depth_av}, 2.51, k=4) + s(\text{aspect_n}, 2.65, k=4)$	14
Sperm whale	$s(\text{sst}, 3.93, k=5) + s(\text{aspect}, 3.84, k=5) + s(\text{depth_av}, 3.97, k=5)$	17
Beaked whales	$s(\text{sst}:\text{lon}, 13.11, k=15) + s(\text{depth_av}, 3.94, k=5)$	23

Table 3: Best fitting model predicting group size for each species. The term $s(\text{cov}, \text{df})$ represents a smooth function of the explanatory variable cov with df estimated degrees of freedom. The expression $k=n$ means that the function has been limited to fitting a smooth function with up to a maximum of n df . If k is not specified, then the maximum df allowed was 10 and 30 for a 1D and 2D smooth, respectively. The symbol “:” means “interaction with”.

Species	Best-fitting model	% deviance explained
Common dolphin	$s(\text{sst}:\text{ci}, 23.29, k=30)$	52
Striped dolphin	$s(\text{lat}, 4.61, k=6)$	64
Common/striped dolphins	$s(\text{sst}:\text{dist2000_deg}, 19.68, k=30) + s(\text{ci}, 5, k=6)$	43
Long-finned pilot whale	$s(\text{sst}, 1, k=4) + s(\text{ssh}, 2.87, k=4)$	50
Sperm whale	$s(\text{lon}, 1.44, k=3) + s(\text{aspect}, 3.05, k=3) + s(\text{chla}, 1, k=5) + s(\text{dist200_deg}, 1, k=3)$	47
Beaked whales	$s(\text{lat}, 1.58, k=10) + s(\text{aspect}, 6.07, k=10)$	43

Table 4: Model based abundance estimates with 95% confidence intervals derived from bootstrapping.

Species	Block	Abundance of animals (CV)	95% Confidence Interval
Common dolphin	1	4,216 (0.57)	1,478 -12,027
	2	52,749 (0.39)	25,054 – 111,059
	3	21,071 (0.51)	8,270 – 53,689
	4	38,673 (0.46)	16,464 – 90,839
	Total	116,709 (0.34)	61,397 - 221,849
Striped dolphin	1	272 (0.80)	68 – 1,083
	2	39,534 (0.62)	12,863 – 121,504
	3	10,501 (0.42)	4,772 – 23,105
	4	17,108 (0.44)	7,543 – 38,800
	Total	67,414 (0.38)	32,543 – 139,653
Common and striped dolphin	1	2,317 (0.74)	637 – 8,428
	2	108,614 (0.35)	57,772 – 211,522
	3	26,010 (0.34)	13,627 – 49,647
	4	122,664 (0.49)	49,212 – 305,745
	Total	259,605 (0.37)	128,818 – 523,175
Long-finned pilot whale	1	18,255 (0.38)	12,912 – 49,725
	2	6,054 (0.43)	2,714-13,504
	3	429 (0.70)	126-1,465
	4	599 (0.46)	253-1,420
	Total	25,338 (0.35)	12,912- 49,725
Sperm whale	1	480 (0.33)	254-905
	2	509 (0.38)	249-1,042
	3	611 (0.34)	322 –1,159
	4	477 (0.33)	252 – 904
	Total	2,077 (0.20)	1,404-3,073
Beaked whales	1	3,889 (0.44)	1,694 –8,927
	2	642 (0.39)	306 – 1,346
	3	656 (0.34)	266 – 1,615
	4	2,156 (0.50)	860 – 5,409
	Total	7,343 (0.31)	4,075-13,230
Fin whale	1	204	163-255
	2	4,854	3855-6112
	3	3,206	2573-3996
	4	755	585-974
	Total	9,019 (0.11)	7,265 – 11,197
Large baleen whales	1	206	163-259
	2	5171	4072- 6566
	3	3487	2789-4358
	4	756	592- 965
	Total	9,619 (0.11)	7,760 – 11,924

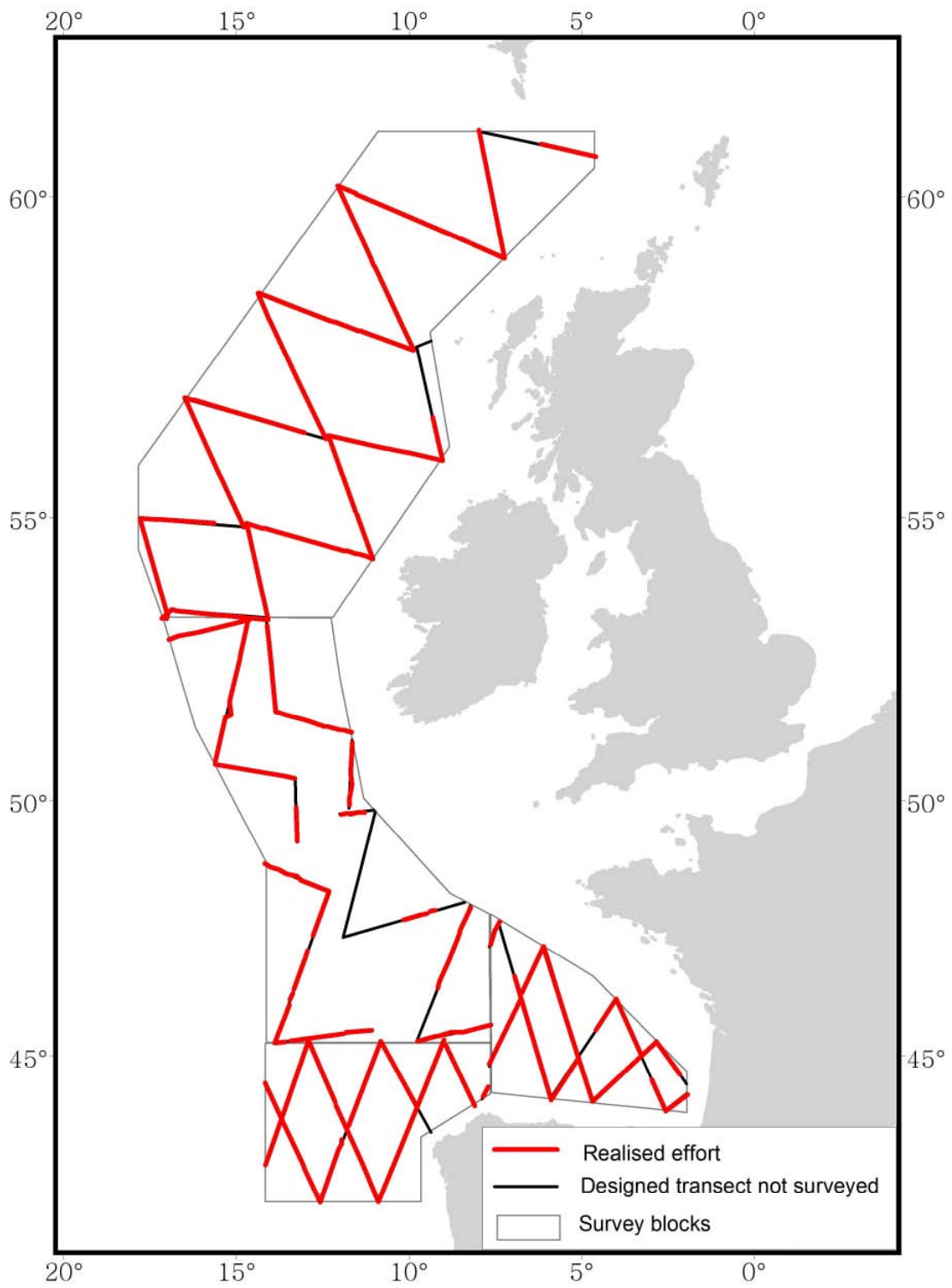


Figure 1: Survey blocks, designed effort and realised effort for the CODA surveys.

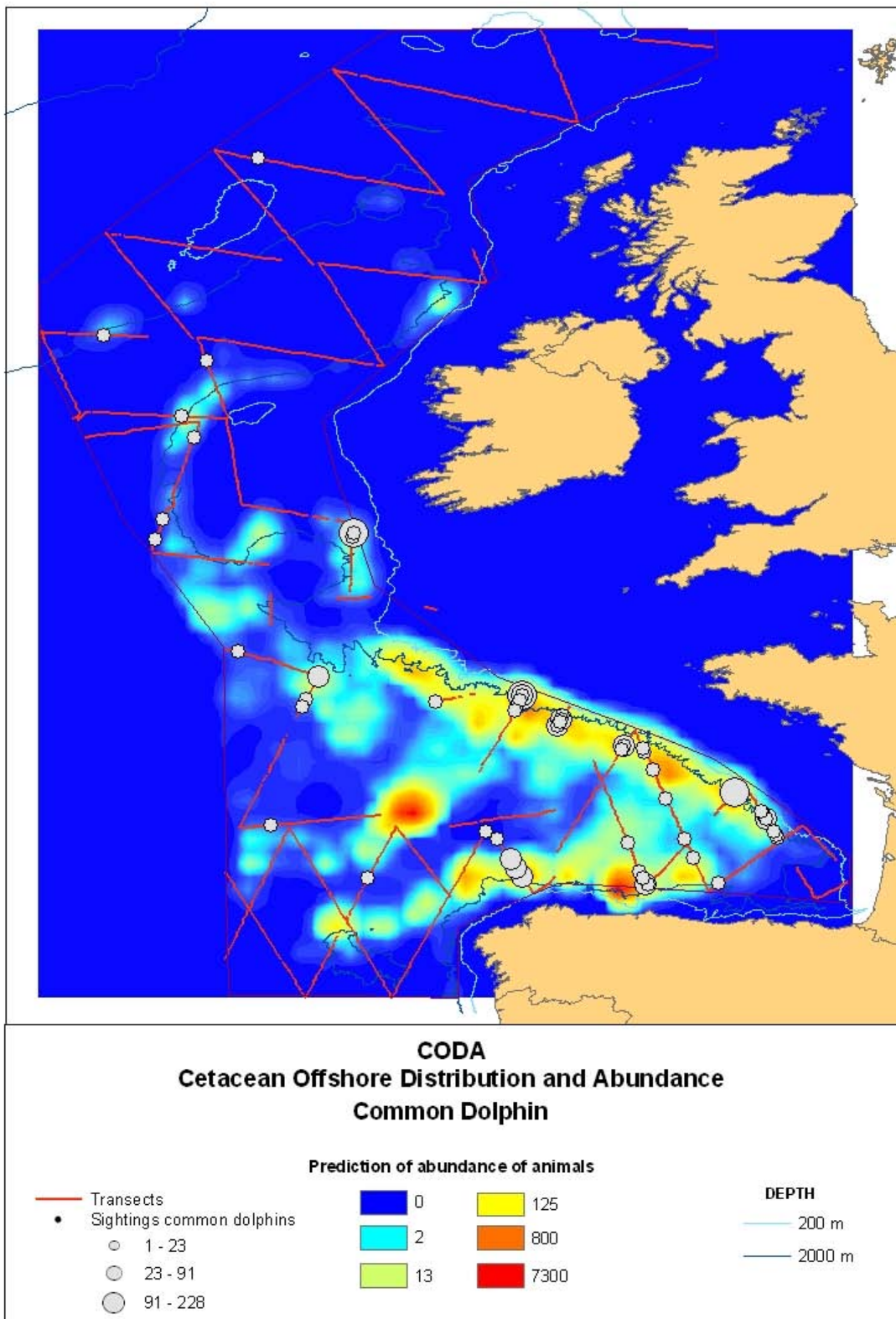


Figure 2: Surface map of smoothed predicted abundance of common dolphin.

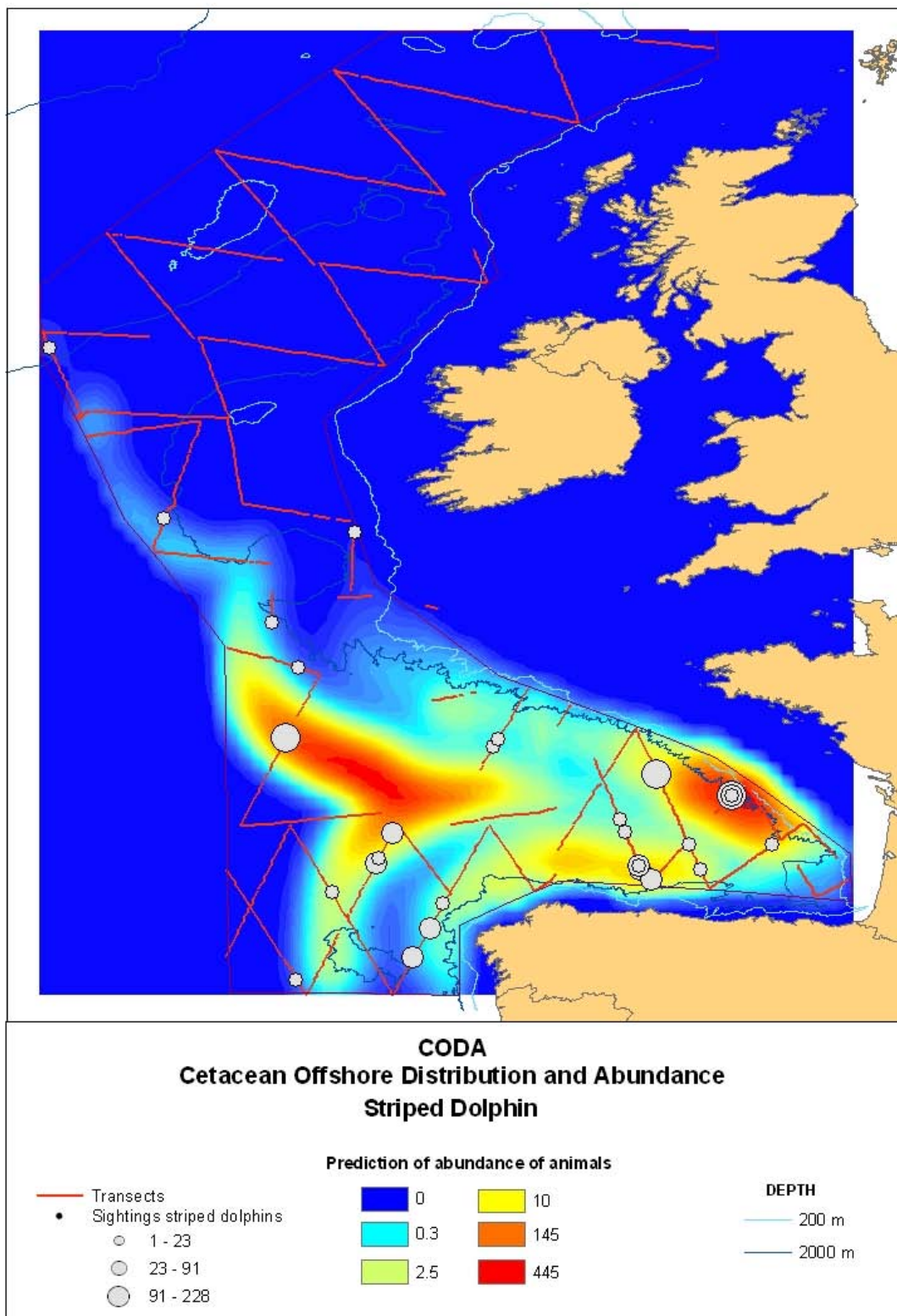


Figure 3: Surface map of smoothed predicted abundance of striped dolphin.

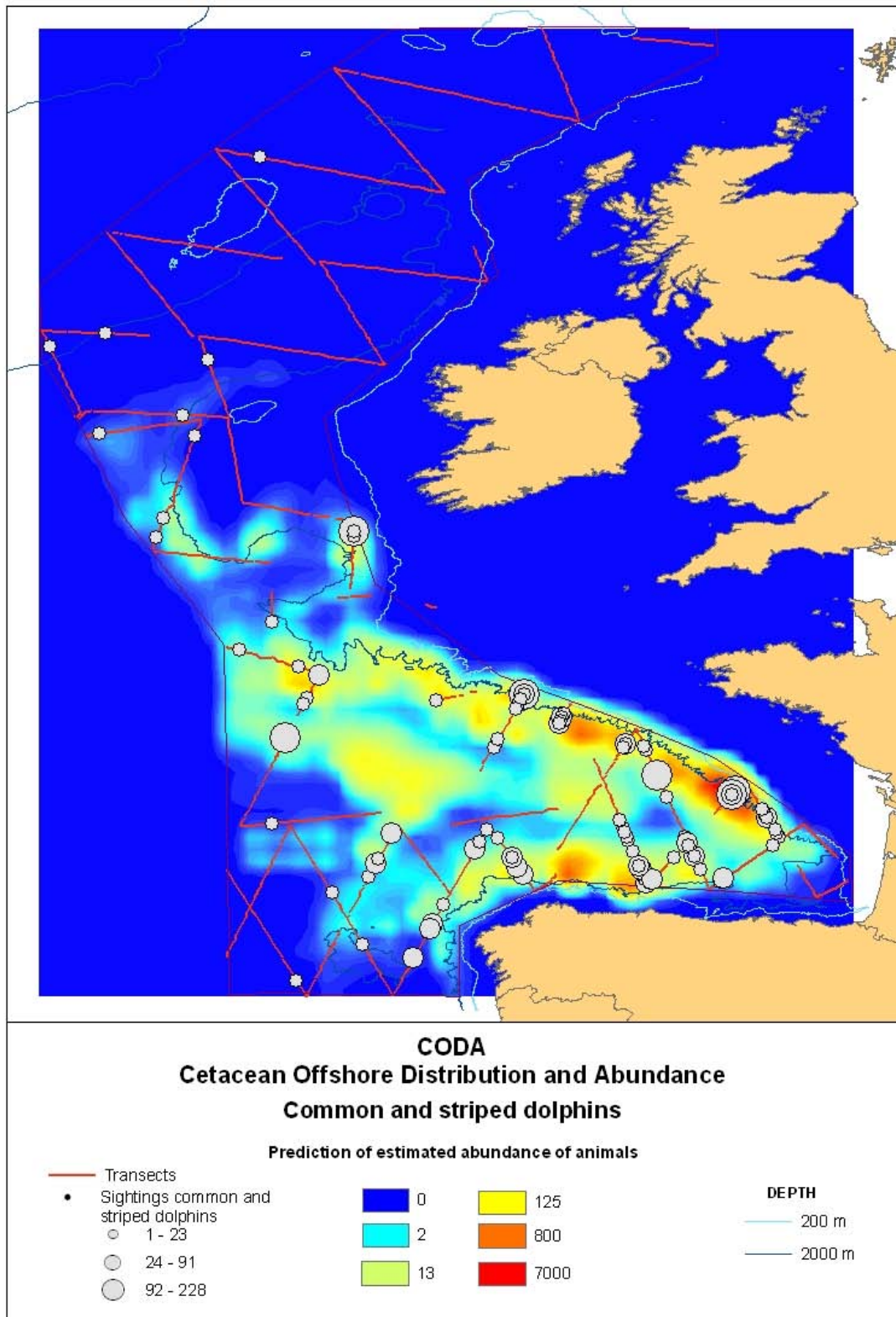


Figure 4: Surface map of smoothed predicted abundance of common and striped dolphins combined.

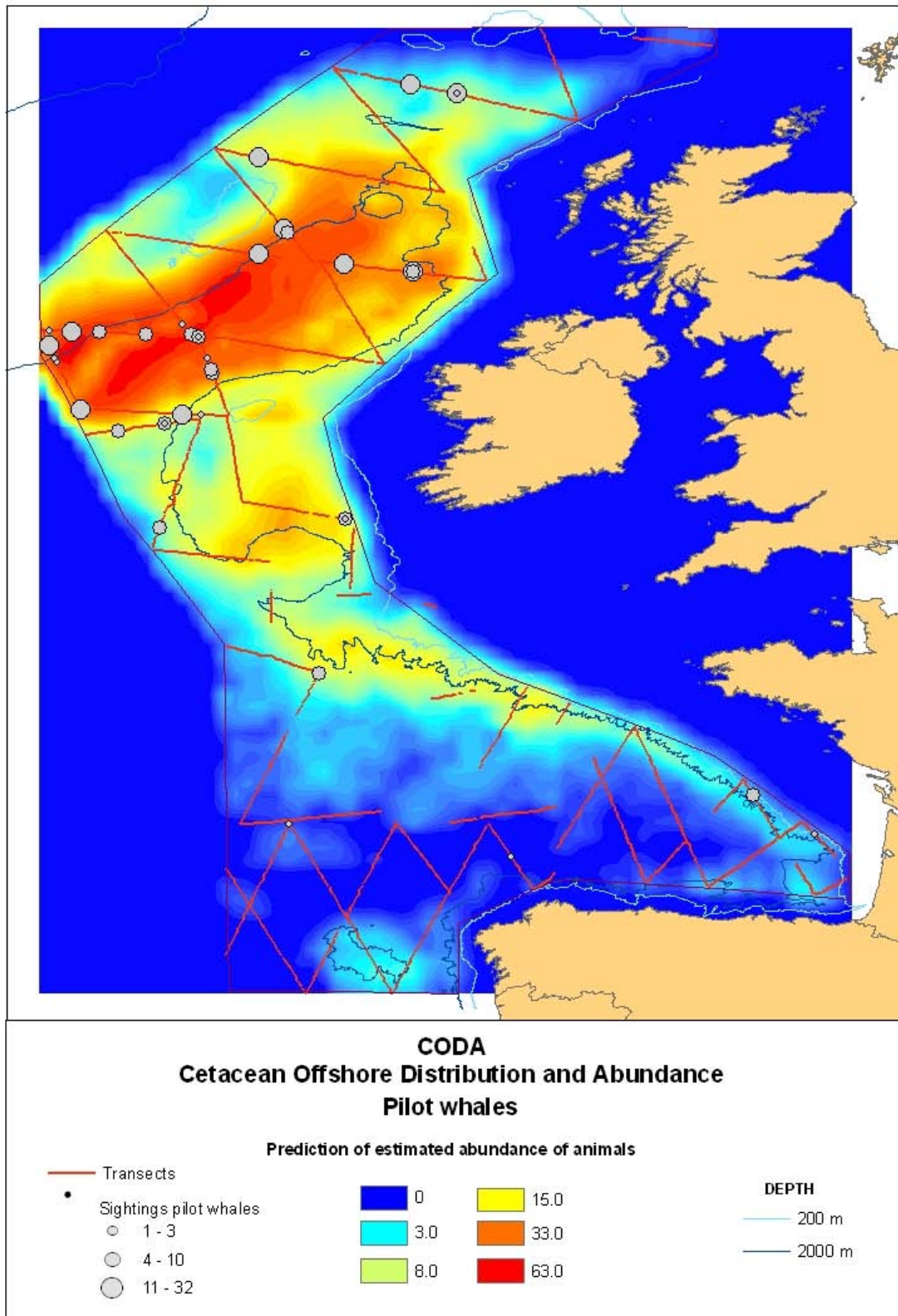


Figure 5: Surface map of smoothed predicted abundance of long-finned pilot whale.

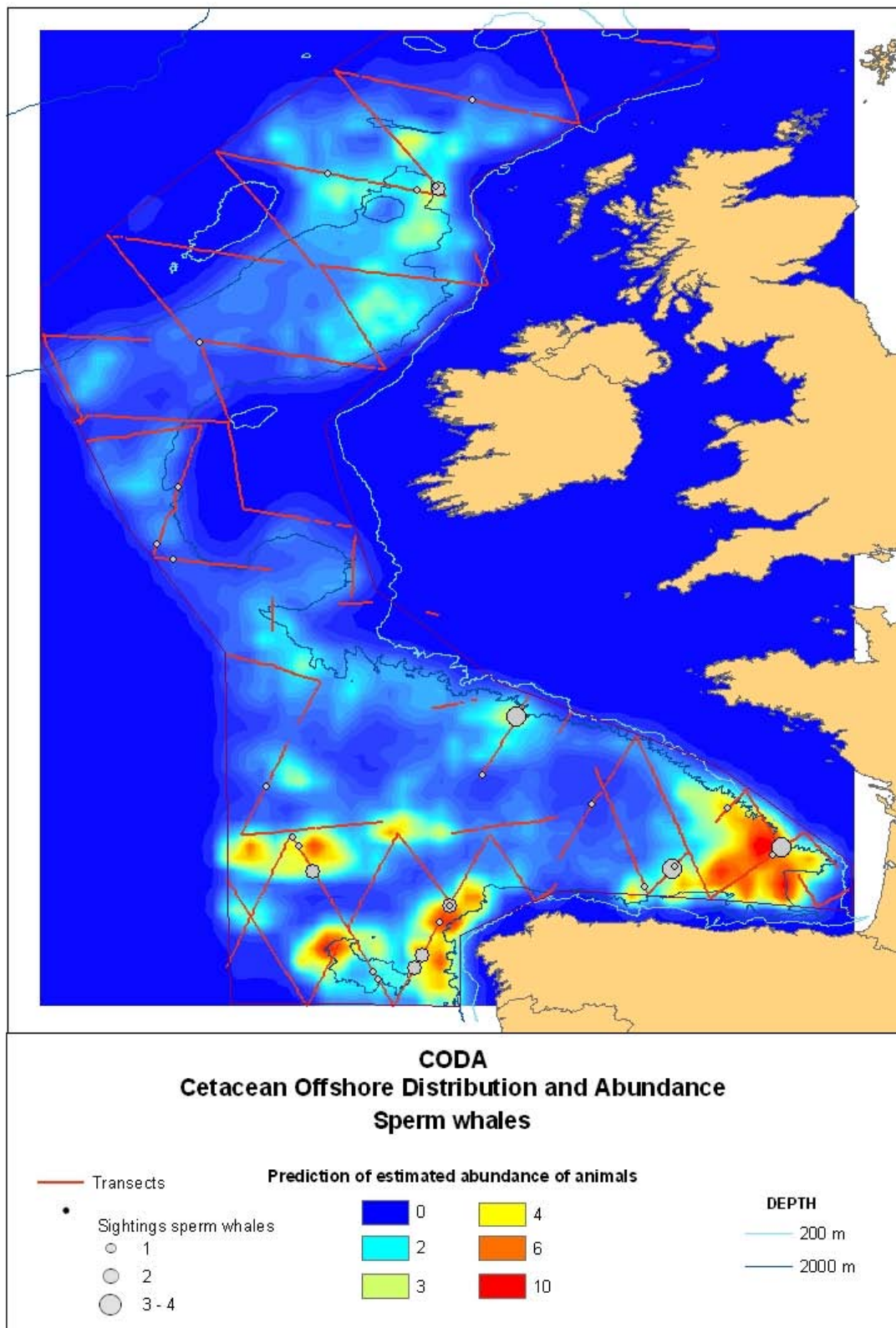


Figure 6: Surface map of smoothed predicted abundance of sperm whale.

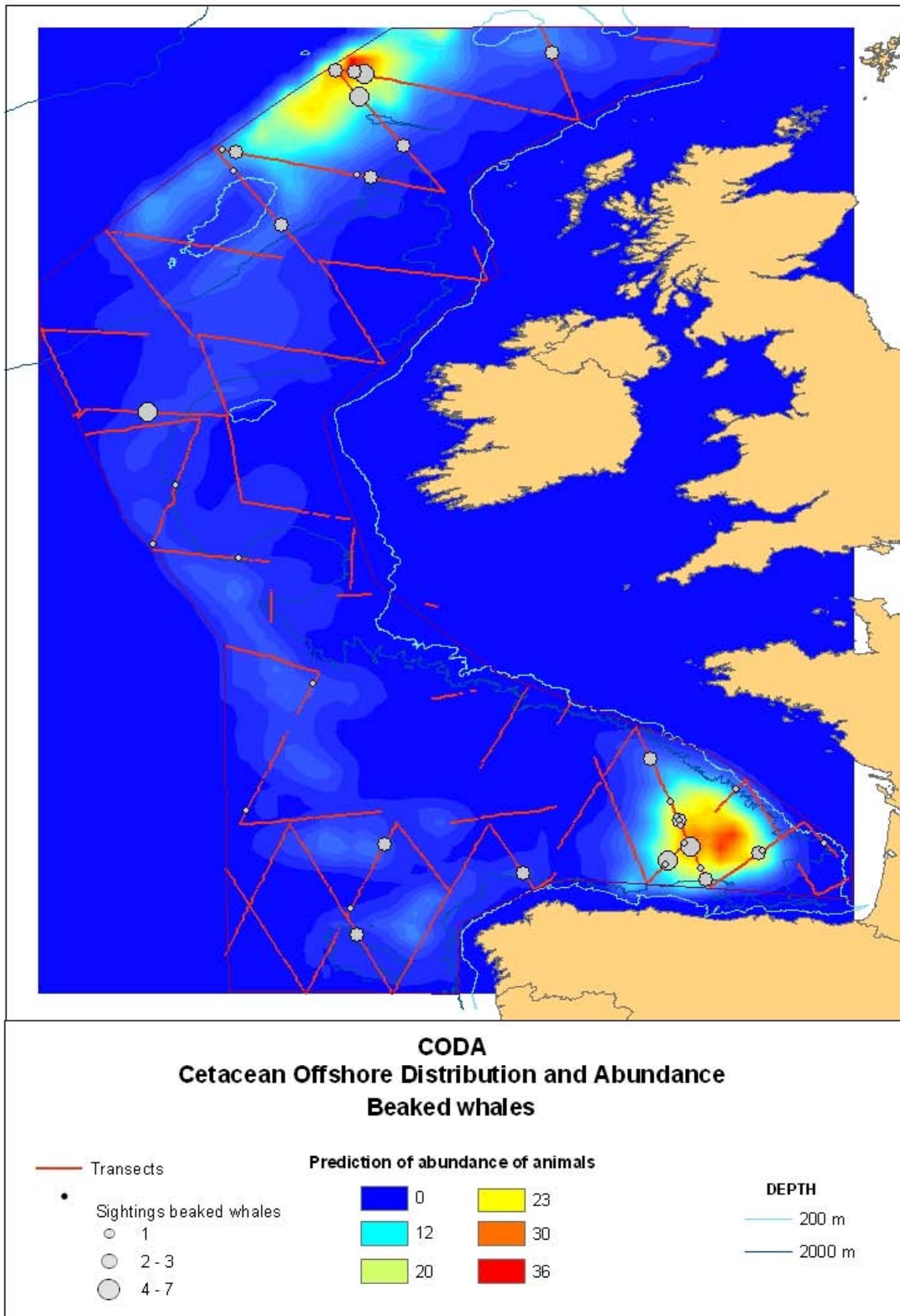


Figure 7: Surface map of smoothed predicted abundance of beaked whales.

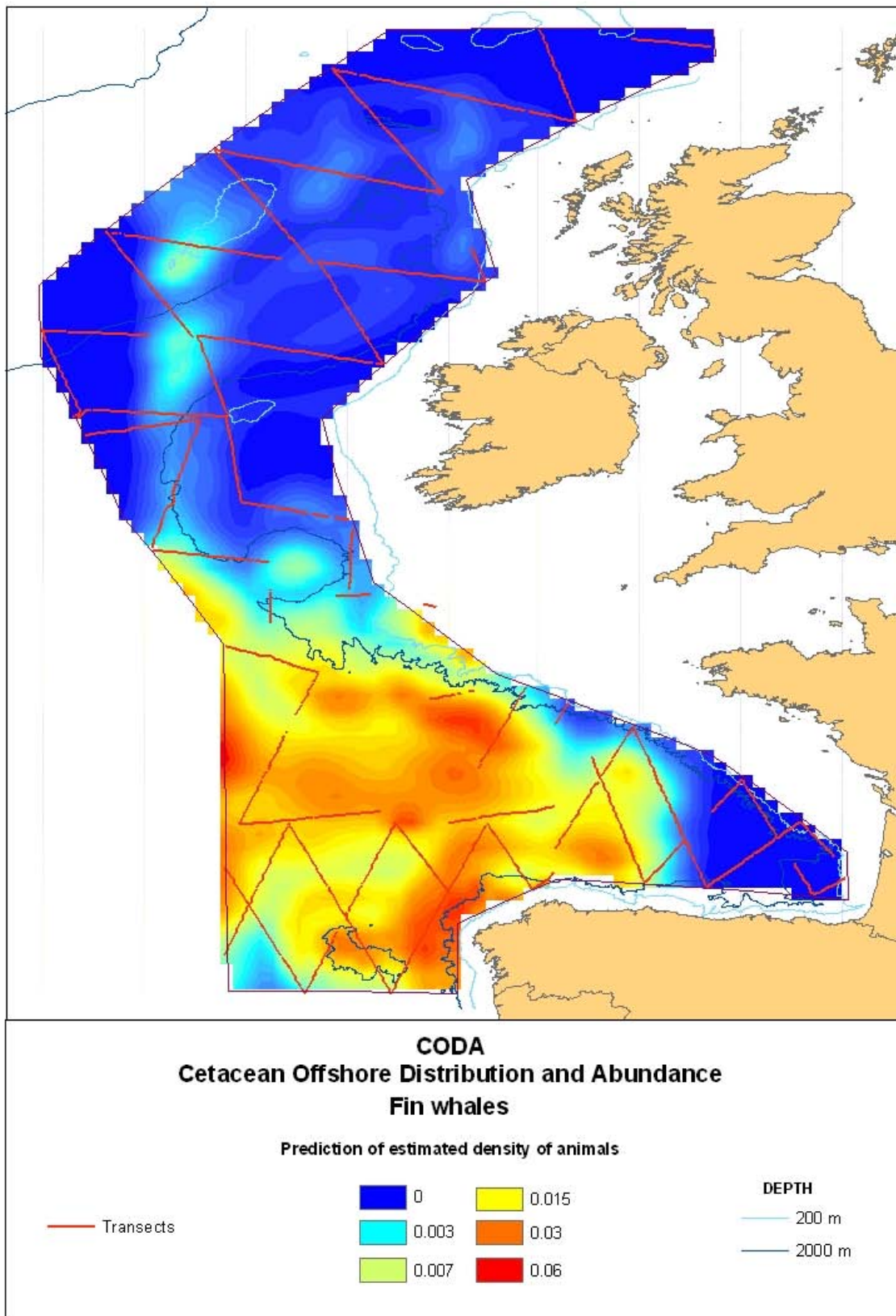


Figure 8: Surface map of smoothed predicted abundance of fin whale.

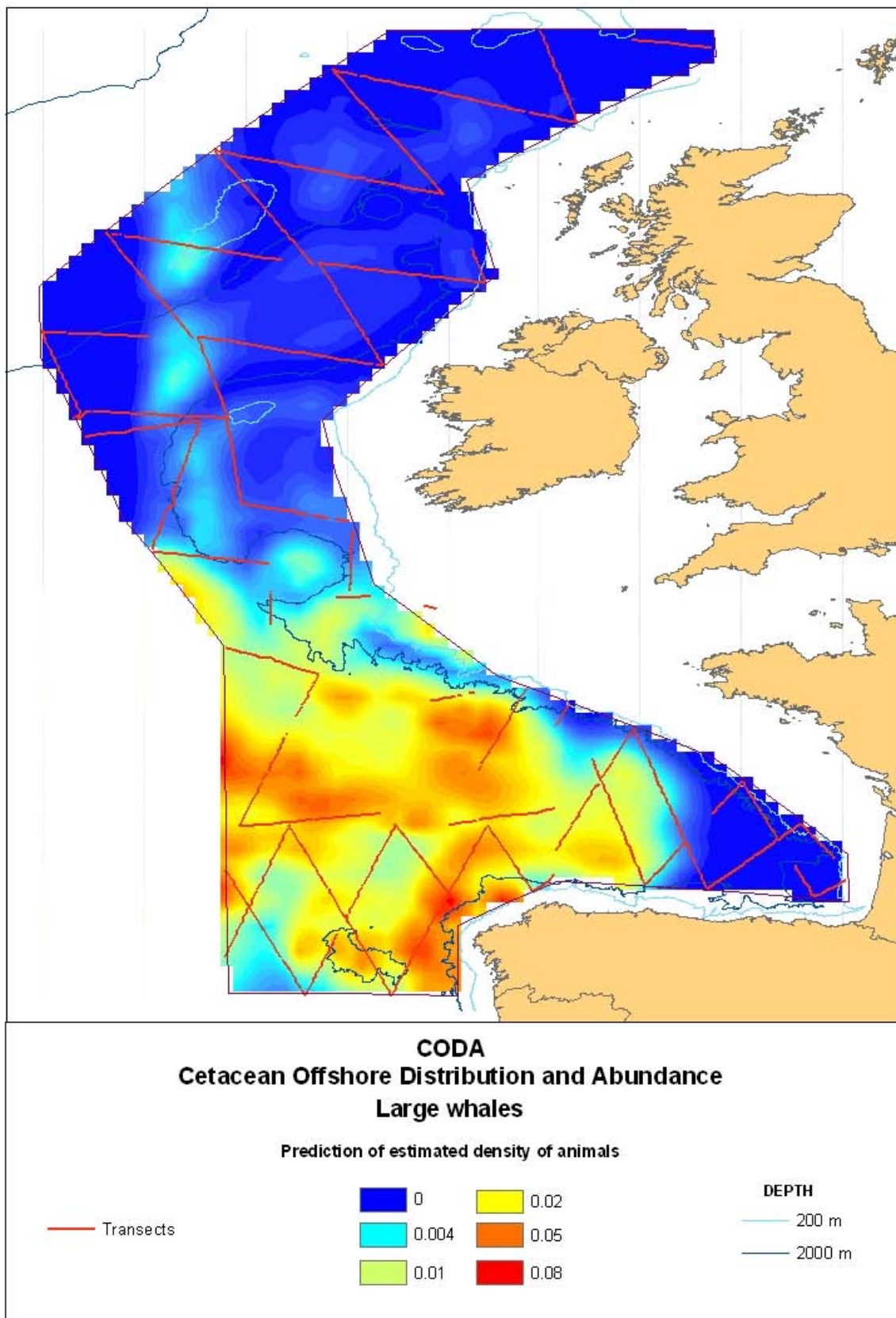


Figure 9: Surface map of smoothed predicted abundance of large baleen whales.