Appendix I[1]

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

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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. The objectives of the Cetacean Offshore Distribution and Abundance in the European Atlantic project (CODA) are 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 will also develop 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 the main species found in the surveyed area.

SURVEY METHODS

The study area was divided into four strata (Figure 1) and was surveyed by five ships[2] during July 2007. Realised search effort is shown in Figure 2. 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

[1] A version of this Appendix containing preliminary estimates of abundance was presented to the IWC Scientific Committee in Chile, June 2008. The ms has been revised and the estimates have been updated.
[2] The survey was planned with one ship per stratum but due to engine failure, two ships covered stratum 2.

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.

ANALYSIS

The analysis was based on the methodology developed by Borchers *et al*. (1998) and Borchers *et al.* (2006) known as Mark-recapture Distance Sampling (MRDS). In trial configuration 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 $\boldsymbol{z}$, $p_1(x,z)$ 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 θ_i'= (θ_{i0}, …, θ_{iQi})' represents the Q_i parameters of the detection function of observer i (i=1,2). Using a Horvitz-Thompson-like estimator, abundance is then given by

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

where n_1 is the number of detections made by observer 1 (some of which may have been seen by observer 2) and $p_1.(\boldsymbol{z})$ represents the integration over the range of x.

When animals occur in groups, an estimate of individual abundance is obtained by replacing the numerator in equation (1) with the group size, s_{j1}, where s_{j1} is the size of the jth detected group.

$$\hat{N}_{1_{indiv}} = \sum_{j=1}^{n_1} \frac{s_{j1}}{p_{1.}(z_j \mid \hat{\theta})}$$

Estimates of mean group size are obtained as

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

Group sizes are required for all groups detected by observer 1 in order to estimate mean group size and hence individual abundance. In practice, it may be that group size cannot be estimated without error and may be biased. However, groups tracked by observer 2 (and therefore observed for longer) were believed to have more reliable estimates of group size. Therefore, using only duplicate detections a correction factor can be estimated which can then be used to correct bias in observer 1's estimates of group size. The correction factor was estimated as (summing over duplicate observations only)

$$\hat{c}_{s_1} = \frac{\sum s_{j1}(2)}{\sum s_{j1}(1)}$$

The variance of these all estimators can be estimated using a transect-based bootstrap procedure. For simpler models (those not requiring school size correction) variance was based on the empirical variance in estimated density between samples (Innes *et al*. 2002).

For some species there were not enough duplicate sightings to be able to implement this approach. In this case, a Conventional Distance Sampling (CDS) approach (Buckland *et al.*, 2001) was used. All analyses were carried out in DISTANCE 6 Release 4 (Thomas et al., 2006). The best models were chosen through comparison of the Akaike Information Criterion (AIC, Akaike, 1973). The fit of models was examined using Goodness of Fit Tests and QQ-plots.

RESULTS

The survey areas and effort achieved in each stratum are shown in Table 1. Tables 2 summarises the numbers of sightings in each stratum for species where sample size was sufficient for a mark-recapture line transect (MRLT) analysis. For bottlenose dolphin, minke whale and beaked whale there were sufficient sightings only for a conventional line transect (CLT) sampling approach.

For all species, data collected during Beaufort sea state ≤4 were used. Truncation was necessary for some species to be able to fit reliable detection function models. However, truncation of observer 2 detections within distances at which observer 1 detection probability is greater than zero is likely to result in positively biased abundance estimates. 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 sea state, swell, glare, visibility, cue, sightability, precipitation and cloud cover.

Mark-Recapture Line Transect Estimates

Common and striped dolphin

For estimating the detection function for common and striped dolphins, data for both species were pooled because their size, group sizes and behaviour are very similar and therefore no differences in detectability were expected between them. Perpendicular distance was truncated at 3,000 m, discarding two observations (1.3%).

The full independence method was applied (Laake & Borchers 2004) because common and striped dolphins responded strongly to the survey vessel, generally moving towards (Figure 3). The best detection function model included perpendicular distance, cue (2 factor levels) and Beaufort (6 factor levels) as covariates. The fitted detection function is given in Figure 4.

The group size correction factor for both common and striped dolphins was estimated as 1 (i.e. no correction) for Blocks 1 and 2, and 1.767 (CV=0.181) for Blocks 3 and 4. Estimates of abundance for the whole area were 118,264 (CV=0.38) common dolphins, 61,364 (CV=0.93) striped dolphins, and 224,166 (0.48) common and striped dolphins, combined. Estimates for each block are given in Table 3.

Pilot whales

Perpendicular distance data were truncated at 4,000 m, removing two tracker sightings at 4079 and 4585 m, both sightings of long-finned pilot whales that took place in stratum 2 (R/V Germinal). A full independence model was fitted to sightings of long and short-finned pilot whale sightings combined because there was some evidence of attraction to the ships (Figure 3). The best detection function model included Primary platform (factor) and sightability in addition to perpendicular distance as covariates. The fitted detection function is given in Figure 4. A separate detection function was fitted to the long-finned pilot whale data only; the best model included the covariates perpendicular distance, visibility and sightability.

The estimates of abundance for the whole area were 26,778 (CV=0.34) pilot whales (both species), and 25,101 (CV=0.33) long-finned pilot whales. Estimates for each block are given in Table 3.

Sperm whale

Initial analysis of the duplicate data to look for responsive movement showed that there was no apparent movement of sperm whales away from or towards the survey ships (Figure 3). Therefore, the point independence method was applied (Laake & Borchers 2004). Data were truncated at 3,500 m, discarding four observations. The best model of the detection function included only perpendicular distance as a covariate. The fitted detection function is given in Figure 4. The abundance of sperm whales in the whole survey area was 2,091 (CV=0.34). Estimates for each block are given in Table 3.

Fin and Sei whales

A detection function was fitted to all species in the large baleen whale category, comprising fin, sei, blue and fin or sei whale. A full independence model was used because there was some evidence of responsive movement of fin whales to the survey vessels (Figure 3). A truncation distance of 4,000 m was applied. The best detection function model included sightability and primary platform height in addition to perpendicular distance. The fitted detection function is given in Figure 4. A group size correction factor was not applied because almost all observations were of single animals.

The abundance estimates for the whole area were 7,625 (0.21) fin whales, 366 (0.33) sei whales and 8,237 (CV=0.20) large baleen whales. Estimates for each block are given in Table 4.

Unidentified large whales

Many sightings of large whales, seen predominately as distant blows, could not be identified to species and were coded “W?”. The use of this code varied between vessels; observers in Block 2 were more cautious than other observers and tended to apply the W? code when no features other than the whale blow were observed. The W? category was excluded from the large baleen whale analysis because it was possible that it included some sperm whales, which would be expected to have a different detection probability. Therefore, a separate detection function was generated for code W?.

The data were truncated at 6,000 m removing two outlying observations. The final sample size was 159 observations; 97 Primary, 86 Tracker and 24 Duplicates. A full independence model was fitted because of some evidence of responsive movement. The best detection function model included perpendicular distance and cloud cover (as a continuous variable). A group size correction factor was not applied because almost all observations were of single animals.

However, the assumption could be made that all unidentified large whales (code W?) were large baleen whales; coded on the other ships as fin, sei, fin/sei or blue whales with an ID certainty of low or medium. Estimates were made based on this assumption: (i) pooling large baleen whales and W?; and (ii) making the further assumption that the majority of W? sightings were fin whales, pooling fin whale (FW) and W?. A detection function for (i) was fitted to the data after truncation at 6,000m. A full independence model was chosen and the best detection function model included perpendicular distance, cloud cover and primary platform height as covariates. Estimates are given in Table 4.

Conventional distance sampling estimates

Bottlenose dolphin

The perpendicular distance data were truncated at 1,200 m and a half-normal model with cluster size in addition to perpendicular distance as covariates was selected as the best model for the detection function (Figure 5). Total abundance of bottlenose dolphins in the survey area was estimated to be 19,295 (CV=0.25). Estimates of abundance by block are given in Table 5.

Minke whale

The data were truncated at 1400m limiting sample size to 22 observations. A hazard rate model fitted to perpendicular distance data only was selected as the best model for the detection function (Figure 5). Total abundance of minke whales in the survey area was estimated to be 6,765 (CV=0.99). Estimates of abundance by block are given in Table 5.

Beaked whales

The three species of beaked whales (Cuvier’s, Sowerby’s and Northern bottlenose) and the “unidentified beaked whale” category were pooled together. Data were truncated at 1400 m, discarding three observations (6.7%). A half-normal model fitted to 42 observations with perpendicular distance and Beaufort sea state (2 levels) as covariates was the best fitting detection function (Figure 5). Total abundance of beaked whales in the survey area was estimated to be 6,992 (CV=0.25). Estimates of abundance by block are given in Table 5.

DISCUSSION

A minimum of 13 species was recorded during the survey, including at least three species of beaked whale and killer whale (*Orcinus orca*). Sighting conditions during the summer of 2007 were relatively poor, especially in the northern sector, and problems with the survey ship in block 2 reduced the time available for survey. Nevertheless, almost 10,000km of survey effort was achieved, enabling abundance estimates to be calculated for fin, sei, minke, pilot, sperm and beaked whales, and common, striped and bottlenose dolphins.

The abundance estimates presented here are the first for some species in these waters. Overall, blocks 2 and 4 (Bay of Biscay) tended to have the highest densities of cetaceans in offshore waters. Block 2 had the highest density of small delphinids (common, striped and bottlenose dolphins). Large baleen whales, especially fin whales, were most commonly seen off the Galician coast (block 3), although high densities were also found in block 2. Most of the sightings of pilot whales and minke whales occurred in the northern block (block 1) west of the UK.

The abundance estimate for fin whale is likely a considerable underestimate because it does not include any of the large number of unidentified large whale (W?) sightings, many of which were likely to have been fin whales. However, including W? sightings generates an overestimate of fin whale abundance. One way to account for this would be to prorate unidentified large whale abundance in proportion to the abundance of identified whales.

Abundance for beaked and minke whales and for bottlenose dolphin, estimated with CDS methods, are likely underestimates because animals missed on the transect line were not corrected for; there was no evidence of attraction to the survey ships. This bias is likely to be particularly high for beaked whales, which have long dive durations.

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Table 1. Block sizes and survey effort (km) searched by the shipboard surveys. The columns headed % Beaufort show the percentages of effort at or below the indicated sea states.

Block	**Vessel code**	**Surface area (km^2)**	**Total effort (km) Beaufort<6**	**% Beaufort**				
				≤ 4	≤ 3	≤ 2	≤ 1	= 0
1	MC	348 722	3408.77	100	69.4	35.4	6.9	0.9
2	RA+GE	336 407	2296.87	97.8	61.1	16.7	4.5	0
3	CS	160 537	2180.45	99.9	67.2	23.8	13.3	0.4
4	IN	121 872	1765.37	94.1	62.4	24.9	9.7	0

Table 2. Sample sizes available for fitting detection functions. Numbers of schools detected within the truncation distance of the transect line by observer 1 (primary), observer 2 (tracker) and both (i.e. duplicates) while on search effort. Data from sea states 0-4 were used in all cases.

Species	**Seen by**	**Number of sightings**
Common, striped and common/striped dolphin	Tracker	173
	Primary	165
	Duplicate	73
Long-finned pilot whale	Tracker	59
	Primary	46
	Duplicate	19
Long and short-finned pilot whale	Tracker	62
	Primary	49
	Duplicate	21
Large baleen whales (fin, sei, fin/sei, blue)	Tracker	223
	Primary	204
	Duplicate	92
Sperm whale	Tracker	47
	Primary	31
	Duplicate	17

Table 3: Estimates of abundance and density (animals/km^2) using the MRDS approach for odontocetes. Figures in parentheses are CVs. Figures in square brackets are 95% confidence intervals.

Species	Block	Animal abundance	Animal density (animals/km^2)
Common dolphin	1	3,546 (0.76)	0.010 (0.76)
	2	53,638 (0.54)	0.159 (0.54)
	3	12,378 (1.23)	0.077 (1.23)
	4	48,701 (0.51)	0.400 (0.51)
	Total	**118,264 (0.38) [56,915 – 246,740]**	**0.122 (0.38)**
Striped dolphin	1	519 (1.05)	0.0015 (1.05)
	2	33,254 (1.57)	0.099 (1.57)
	3	7,546 (0.62)	0.047 (0.62)
	4	20,045 (0.56)	0.165 (0.56)
	Total	**61,364 (0.93) [12,323 – 305,568]**	**0.063 (0.93)**
Common and striped dolphins	1	4,065 (0.67)	0.012 (0.67)
	2	115,398 (0.80)	0.343 (0.80)
	3	24,551 (0.66)	0.153 (0.67)
	4	80,152 (0.37)	0.658 (0.37)
	Total	**224,166 (0.48)** [90,979 – 552,331]	**0.232 (0.48)**
Long-finned pilot whale	1	18,709 (0.37)	0.054 (0.37)
	2	5,566 (0.75)	0.016 (0.75)
	3	194 (0.88)	0.001 (0.88)
	4	632 (1.1)	0.005 (1.1)
	Total	**25,101 (0.33) [13,251 - 47,550]**	**0.026 (0.33)**
Pilot whale (long and short-finned)	1	22,034 (0.37)	0.063 (0.37)
	2	4,148 (0.55)	0.012 (0.55)
	3	238 (0.91)	0.001 (0.91)
	4	358 (0.91)	0.003 (0.91)
	Total	**26,778 (0.34) [13,835 – 51,831]**	**0.028 (0.34)**
Sperm whale	1	363 (0.46)	0.001 (0.46)
	2	759 (0.52)	0.002 (0.52)
	3	560 (0.55)	0.003 (0.55)
	4	409 (0.55)	0.003 (0.55)
	Total	**2,091 (0.34) [1,077 – 4,057]**	**0.002 (0.34)**

Table 4: Estimates of abundance and density (animals/km^2) using the MRDS approach for baleen whales. Figures in parentheses are CVs. Figures in square brackets are 95% confidence intervals.

Species	Block	Animal abundance	Animal density (animals/km^2)
Fin whale	1	248 (0.45)	0.001 (0.45)
	2	3,668 (0.34)	0.011 (0.34)
	3	3,113 (0.22)	0.019 (0.22)
	4	595 (0.72)	0.005 (0.72)
	Total	**7,624 (0.21)** **[5,028 – 11,563]**	**0.008 (0.21)**
Sei whale	1	0	0
	2	0	0
	3	366 (0.33)	0.002 (0.33)
	4	0	0
	Total	**366 (0.33)** **[176 – 762]**	**0.0004 (0.33)**
Large baleen whales	1	250 (0.44)	0.0007 (0.44)
	2	3,853 (0.33)	0.011 (0.33)
	3	3,529 (0.22)	0.022 (0.22)
	4	605 (0.72)	0.005 (0.72)
	Total	**8,237 (0.20)** **[5,476 – 12,390]**	**0.008 (0.20)**
Unidentified large whale	1	352 (0.43)	0.001 (0.43)
	2	5,997 (0.43)	0.018 (0.43)
	3	226 (0.32)	0.001 (0.32)
	4	26 (0.71)	0.0002 (0.71)
	Total	**6,601 (0.40)** **[3,003 – 14,512]**	**0.007 (0.40)**
Large baleen whales + Unidentified large whale	1	574 (0.27)	0.002 (0.27)
	2	9,648 (0.37)	0.029 (0.37)
	3	3,636 (0.19)	0.022 (0.19)
	4	693 (0.70)	0.006 (0.70)
	Total	**14,550 (0.26)** **[8,561 - 24,729]**	**0.015 (0.26)**
Fin whale + Unidentified large whale	1	574 (0.27)	0.002 (0.27)
	2	9,493 (0.37)	0.028 (0.37)
	3	3,207 (0.19)	0.020 (0.19)
	4	693 (0.70)	0.006 (0.70)
	Total	**13,966 (0.27)** **[8,088 – 24,119]**	**0.014 (0.27)**

Table 5: Conventional distance sampling abundance estimates for bottlenose dolphin, minke whale and beaked whales. Figures in parentheses are CVs. Figures in square brackets are 95% confidence intervals.

Species	Block	Animal abundance	Animal density (animals/km^2)
Bottlenose dolphin	1	5,709 (0.35)	0.016 (0.35)
	2	11,536 (0.33)	0.034 (0.33)
	3	876 (0.82)	0.005 (0.82)
	4	1,174 (0.45)	0.010 (0.45)
	Total	**19,295 (0.25)** **[11,842 – 31,440]**	**0.020 (0.25)**
Minke whale	1	5,547 (1.03)	0.016 (1.03)
	2	1,218 (1.04)	0.004 (1.04)
	3	0	0
	4	0	0
	Total	**6,765 (0.99)** **[1,239 – 36,925]**	**0.007 (0.99)**
Beaked whales	1	3,512 (0.34)	0.011 (0.34)
	2	785 (0.43)	0.002 (0.43)
	3	597 (0.55)	0.004 (0.55)
	4	2,097 (0.45)	0.017 (0.45)
	Total	**6,992 (0.25)** **[4,287-11,403]**	**0.007 (0.25)**

Figure 1. Survey blocks. The vessels that surveyed each block were: Block 1 = *Mars Chaser*, Block 2 = *Rari* & *Germinal*, Block 3 = *Cornide de Saavedra* and Block 4 = *Investigador*.

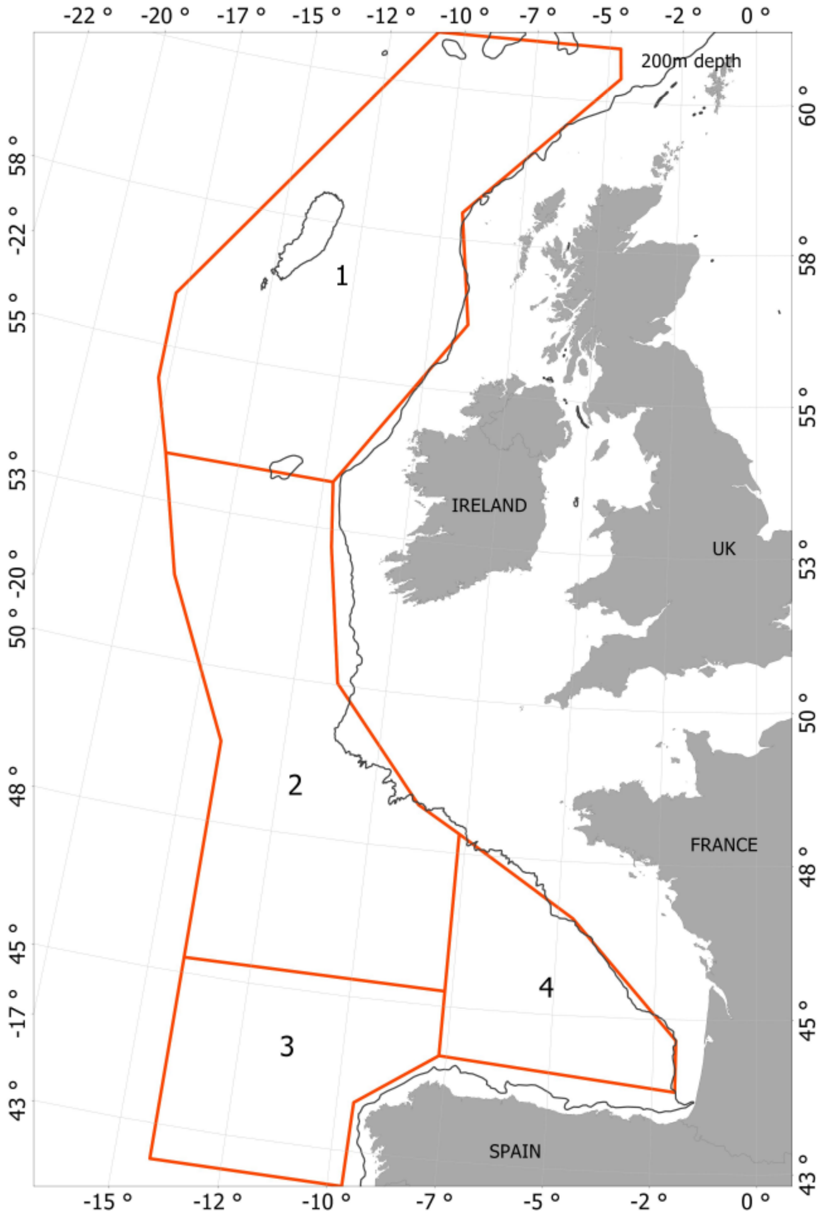


Figure 2. Realised search effort.

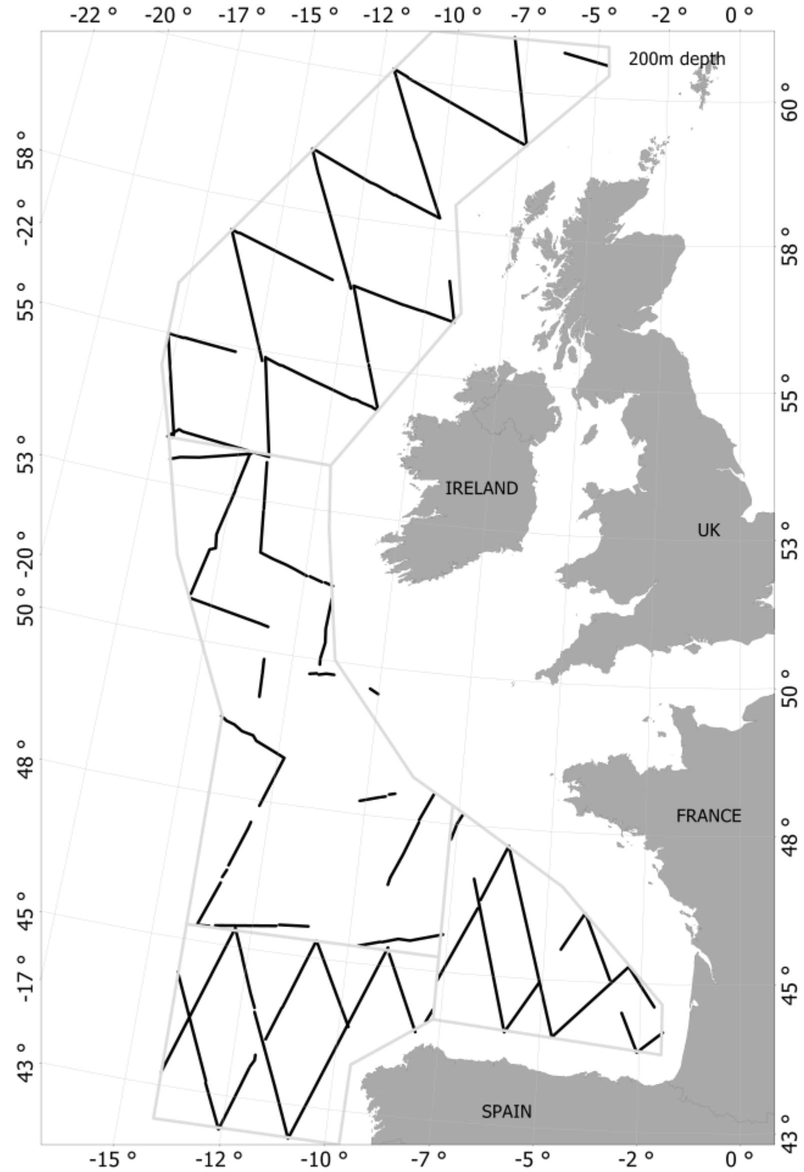


Figure 3: Plots of perpendicular distances of duplicates at the time they were seen by the tracker (x-axis) and then by the primary (y-axis). The dotted line corresponds to no movement in relation to the trackline. Points above the line correspond to animals moving away from the trackline, those below correspond to movement towards the trackline. CD = common dolphin; CD = striped dolphin; CS = common or striped dolphin; FW = fin whale; SP = sperm whale; LF = long-finned pilot whale.

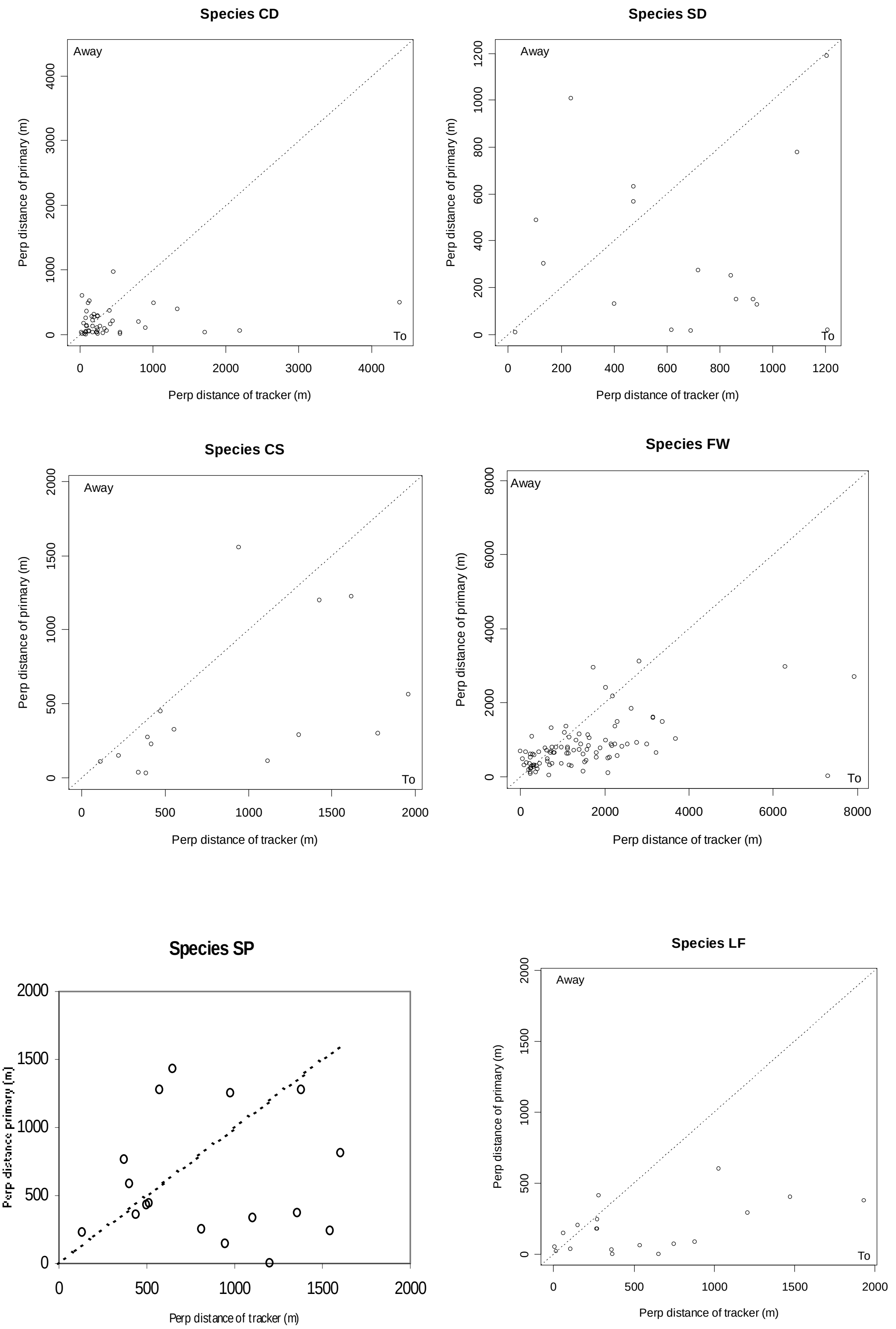
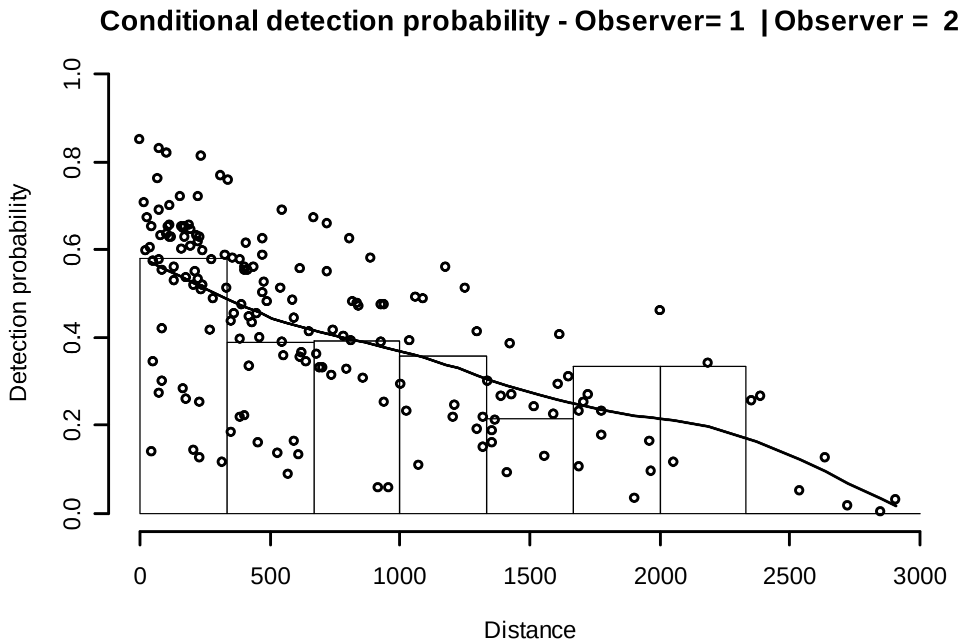
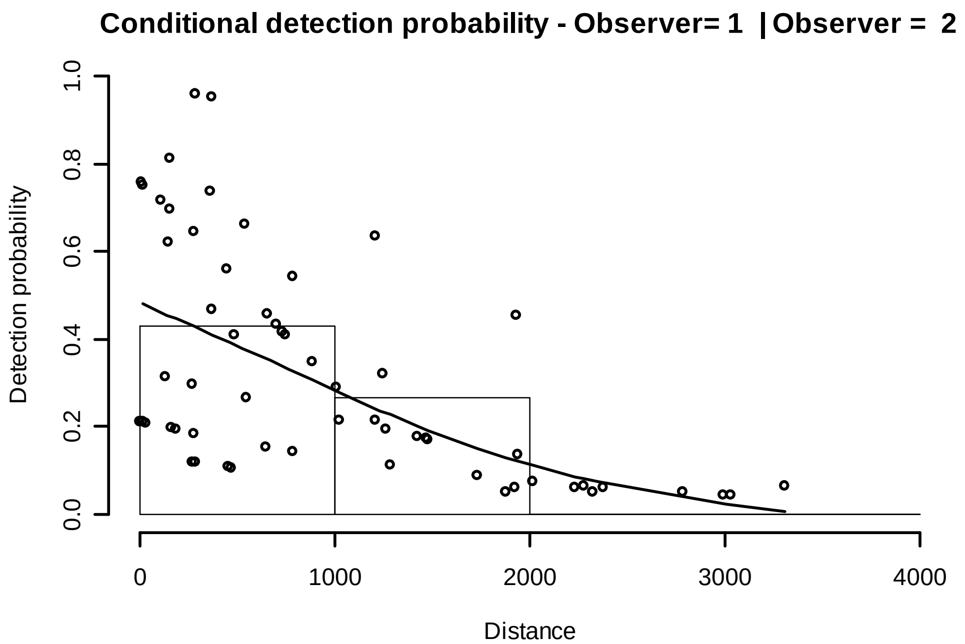


Figure 4. Plots of conditional detection probability for species analysed using MRDS. The histograms are the proportions of observer 2 (Tracker) detections that were seen by observer 1 (Primary). The line is the average fitted detection function. The points are the estimated probability of detection of each observation (given its explanatory variable values and perpendicular distance) for observer 2. Distances are in metres.

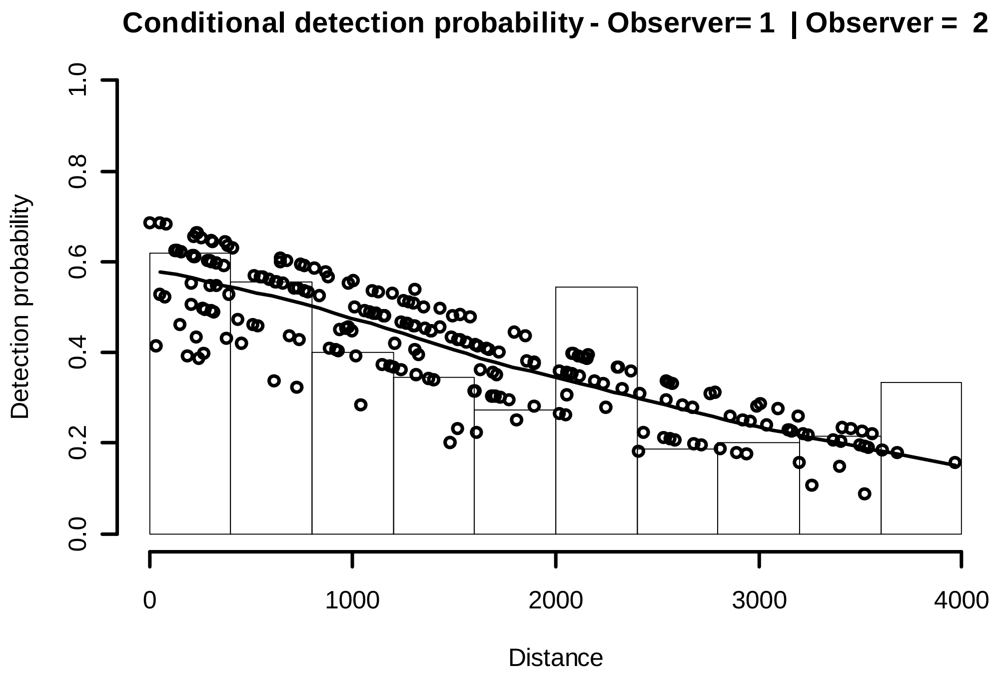
Common and striped dolphins



Pilot whale (long and short-finned)



Large baleen whales (fin, sei, fin/sei and blue)



Sperm whale

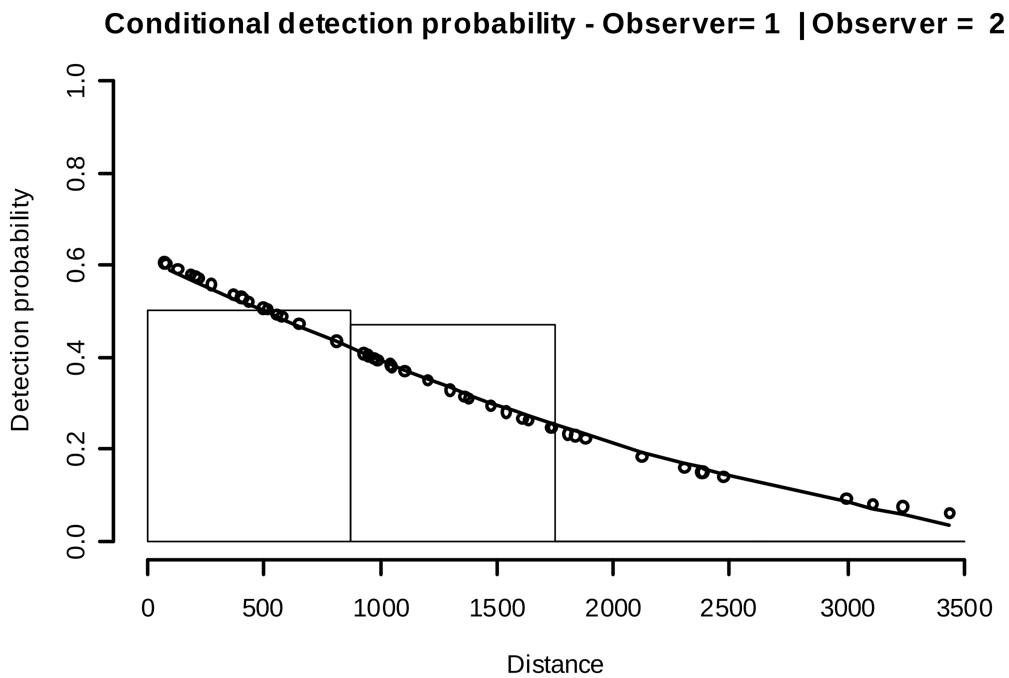
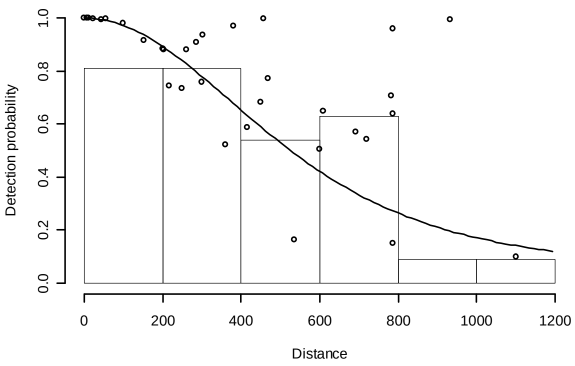
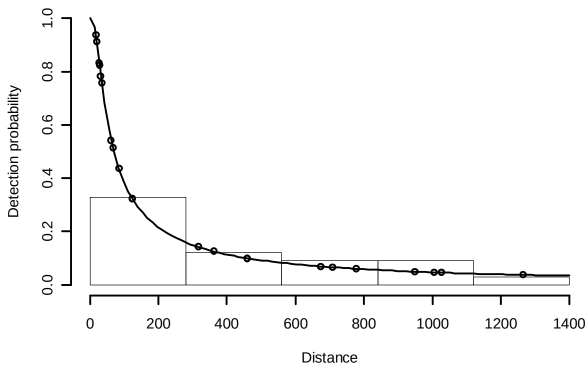


Figure 5. Distribution of perpendicular distances and fitted detection functions for species analysed using conventional distance sampling.

Bottlenose dolphin



Minke whale



Beaked whales