

1 **Distribution and habitat use modelling from satellite tracking data of humpback whales**  
2 **in Brazil agree with shipboard survey data modelling**

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17 Short title: humpback whale distribution from tracking data

18 **Abstract**

19 Statistical modelling of animal distribution has been widely applied to explain how mobile species  
20 use their habitats. The distribution and habitat use of humpback whales *Megaptera novaeangliae* off  
21 the eastern coast of Brazil have previously been investigated by modelling visual survey data. Here  
22 we modelled their distribution in their breeding range using individual tracking data to compare  
23 ecological inferences with those from previous models from line transect data. A Generalized  
24 Estimating Equation framework was used to model the tracking data and pseudo-absences as  
25 functions of spatial covariates. Covariates considered were latitude and longitude, sea surface

26 temperature (SST), current and wind speeds near the surface, distances to shelf-break and the coast,  
27 sea bottom depth and slope, and a factor variable representing “shelter”. Two modelling exercises  
28 were developed: a Habitat Use Model (HUM) and a Distribution Model (DIM). Covariates retained  
29 in the selected HUM were SST, distance to coast and shelf-break, current and wind speeds, and  
30 shelter. Covariates retained in the selected DIM were latitude/longitude, current speed, and distances  
31 to shelf-break and coast. The modelled relationships between whale occurrence and environmental  
32 covariates using tracking data were similar to those using line transect data. Distribution maps were  
33 also similar, supporting higher densities around the Abrolhos Archipelago and to its south. We  
34 showed that habitat use and distribution of this population in the area could be similarly inferred by  
35 modelling either line transect or tracking data. Using these two approaches in conjunction can  
36 strengthen the understanding of important ecological aspects of animal populations.

37 Key words: *Megaptera novaeangliae*, ecology, conservation, marine mammals, population recovery.

## 38 1. INTRODUCTION

39 Animal distribution and habitat use result from animals exploiting resources to meet their ecological  
40 requirements, from their physiological constraints and the effects of the environment on them  
41 (Matthiopoulos & Aarts 2010). Data on where animals are distributed and how they use the  
42 environment can inform the management of human activities to avoid conflicts. In that context,  
43 distribution models are useful tools to support the identification of areas that require management  
44 (Runge et al. 2015). Because different types of data for studying species' spatial ecology may be  
45 available, it is important to explore whether similar inferences about distribution and habitat use are  
46 obtained. Animal distribution data obtained through different methods within an area of interest  
47 could, for example, complement each other to improve the spatial extent of information available.

48 Population distribution and habitat use can be explored using a range of data types and analytical  
49 methods, with outputs partially depending on the nature of the data used (Redfern et al. 2006; Aarts  
50 et al. 2008). Line transect sampling, for example, is designed to estimate density and abundance, and  
51 the data can be used to infer distribution and habitat use through spatial modelling methods (Miller  
52 et al. 2013, Roberts et al. 2016). In line transect surveys, animals are detected along transects and the  
53 effective search areas of those transects are estimated from detection distances using distance  
54 sampling (Buckland et al. 2001). Line transect data are therefore counts of animals detected in units  
55 of sampled space.

56 Animal tracking data, commonly acquired using animal-borne tags, can also be used to investigate  
57 the distribution and habitat use of animals. For marine mammals, developments to improve equipment  
58 and the increasing availability of analysis tools have facilitated their application (Aarts et al. 2008,  
59 Russell et al. 2016, Jonsen 2016, Trudelle et al. 2016, Elith et al. 2020, Carter et al. 2022). In contrast  
60 to line transect surveys, for which the data are both locations where animals were detected and,  
61 crucially, where they were not, the sampling units in tracking studies are individual animals, and the  
62 data are formed by a series of observed locations of the tracked individuals. That means that the

63 portion of space that is sampled is only that which is visited by those animals, meaning that there is  
64 no information in the data about places that are not visited. Another important difference between the  
65 two data types is that line transect data are a snapshot of the location of animals at the time of the  
66 survey (i.e. it is cross-sectional data), while tracking data consists of a set of repeated measurements  
67 of the location of a sample of animals that have been telemetered (i.e. it is longitudinal data, on  
68 multiple individuals). Despite the above differences, the analysis of contrasting data types can provide  
69 different views of a species underlying distribution (Matthiopoulos et al. 2022)

70 For telemetry tracking data to be useful for habitat use and distribution modelling, the design of  
71 analysis and interpretation of results must consider many potential biases (Elith et al. 2020). For  
72 example, the distribution of locations can be greatly influenced by the distribution of tag deployments,  
73 resulting in tagging location bias (Block et al. 2011). Also important is the serial autocorrelation in  
74 locations along tracks because observations are naturally space-time series (Matthiopoulos & Aarts  
75 2010). It is crucial to consider whether tracked individuals represent a small portion of the population  
76 for which inferences are intended, meaning that although the sample size of locations may appear  
77 large (i.e. many locations), sample sizes for individuals can be small (i.e. few animals). That also  
78 raises concerns regarding whether tracked animals realistically represent their population with respect  
79 to distribution and habitat use (Sequeira et al. 2019).

80 Animal distribution and habitat use can be inferred using a presence-absence approach. However,  
81 that requires information on both where animals were present (i.e. places surveyed where animals  
82 were detected) and where animals were absent (i.e. places surveyed with no animals detected).  
83 Because of the lack of information on real absences in tracking data (e.g. Pirotta et al. 2011), “pseudo-  
84 absence” locations, which represent the available habitat not-visited, are needed for presence-absence  
85 distribution modelling of tracking data (Elith et al. 2020). When using pseudo-absences, the number  
86 of absences to include in the models is controlled by the user, therefore the ratio of pseudo-absence  
87 per presence to be used must be decided. That decision should be guided by model “coefficient

88 stability analysis” (when alternative models with an increasing number of pseudo-absences per  
89 presence are ran to visually investigate the stability of the output coefficients; see Supporting  
90 Information S4 in Ventura et al. 2019), while ensuring that pseudo-absences have the corresponding  
91 fraction of the weight of a presence in the models (i.e. the weighted sum of presences equals the  
92 weighted sum of pseudo-absences; Barbet-Massin et al. 2012).

93 A decision about how to define the area of inference is also required. Some studies have used a  
94 percentage of kernel density estimates to represent habitats frequently used by the animals (e.g.  
95 Pendoley et al. 2014, Mei et al. 2017, Thorne et al. 2017); that percentage is, again, user-controlled.  
96 Adopting a pre-defined area, where the distribution and habitat use of a population have already been  
97 studied using different data, can contribute to a better understanding of how those animals relate to  
98 their environment.

99 Most humpback whale *Megaptera novaeangliae* populations are recovering after the end of global  
100 commercial whaling (Zerbini et al. 2019) and the population breeding in coastal waters of Brazil  
101 during winter and spring is no exception (Bortolotto et al. 2016, Wedekin et al. 2017). However, the  
102 coincident increase in human activities in Brazilian coastal waters, especially those related to oil and  
103 gas production (Bortolotto et al. 2017), means that there is a need to understand how these activities  
104 may affect distribution and habitat use to inform whether management actions may be necessary to  
105 avoid impact on the population. Distribution of this population in the area was investigated in the past  
106 using descriptive analysis (Zerbini et al. 2006, Martins et al. 2001, 2013, Castro et al. 2014, Gonçalves  
107 et al. 2018), from a difference in densities within line transect survey blocks (Andriolo et al. 2010) or  
108 for very restricted areas (Martins et al. 2001, Gonçalves et al. 2018). Analysis of line transect data to  
109 investigate the distribution of humpback whales off the coast of Brazil has shown that density was  
110 strongly related to sea temperature and bathymetric features (Bortolotto et al. 2017, Pavanato et al.  
111 2018). Telemetry data for the species in the area has been used to investigate the relative usage of  
112 protected areas (Castro et al. 2014) and movements (Zerbini et al. 2006), but not distribution.

113 Here we present distribution and habitat use models of telemetry tracking data of humpback whales  
114 in Brazil and compare model outputs with those from a study using line-transect survey data (i.e.  
115 Bortolotto et al. 2017). Comparing the results on distribution and habitat from different approaches  
116 can strengthen the understanding of important ecological aspects of animal populations, especially  
117 when results support each other. Therefore, management actions, such as spatial planning of natural  
118 resources exploration (e.g. oil exploration, fishing), and the need for conservation strategies for  
119 populations may be better informed.

## 120 **2. MATERIALS & METHODS**

121 The area of inference for modelling humpback whale distribution and habitat use in this study was  
122 determined by adapting the survey area from Bortolotto et al. (2017), originally comprising the  
123 continental shelf from 5°S to 23°S, to allow a direct comparison. The original area was restricted  
124 considering both the extent of spatial covariates available and the distribution of tagging locations.  
125 Since in a presence/pseudo-absence approach for spatial modelling the area of inference is assumed  
126 to be the habitat available for the animals (Aarts et al. 2008), and because the tagging locations were  
127 not distributed evenly within the original study area (Figure 1), the northernmost portion of the  
128 original area, originally extending north to Natal (Fig. 4 in Bortolotto Ret al. 2017), was excluded to  
129 minimize the chances of failing to meet that assumption.

### 130 ***2.1. Data acquisition: whale tracking***

131 From 2003 to 2012, satellite-linked telemetry tags were attached to adult humpback whales along the  
132 coast of Brazil. Tagging operations occurred every year between August and December except for  
133 2004, when no tagging happened (Supplement, Table S1). Animals were tagged only in good weather  
134 conditions, calm seas, and light to moderate winds (i.e. sea state less than 4 in the Beaufort scale).

135 Implantable (n = 108) and LIMPET (Low Impact Minimum Percutaneous Electronic Transmitter;  
136 n = 5) tags from Wildlife Computers (Redmond, WA, USA) were used. Implantable tags were

137 attached to the animals using a carbon fiber pole or with an Air Rocket Transmitter System (ARTS;  
138 Heide-Jørgensen et al. 2001); LIMPET tags were attached using a crossbow (Andrews et al. 2008).  
139 The targeted tag location on the animal was the base of the dorsal fin because this area is most  
140 frequently exposed when animals surface to breathe, maximizing the chances of transmitter-satellite  
141 signal linking. The tagging boat approached target animals to distances between 3 and 10 m. When  
142 the pole was used, a maximum distance of 5 m was required. Photographs of the tagged animal's tail  
143 fluke, dorsal fin and attached tag were taken for individual identification and quality control of  
144 tagging methods. Tracking data from tagged whales were obtained via the Argos satellite system  
145 ([www.argos-system.org](http://www.argos-system.org), *Collecte Localisation Satellites SA*), and tags were programmed to transmit  
146 in various duty cycles (e.g. transmitting every second/other day, every four days; Supplement, Table  
147 S1), to maximize the longevity of animal tracking. Sexes were genetically identified from skin  
148 biopsies collected with crossbow and a modified dart (Dalla Rosa et al. 2008).

## 149 ***2.2. Tracking data processing***

150 Because the present whale tracks were obtained via the Argos satellite system, which uses “Doppler-  
151 based positioning” (Lopez et al. 2015), each location was estimated with an associated uncertainty.  
152 To minimize the number of unrealistic locations, a speed filter was applied to the whale tracking data,  
153 implemented with R package *trip* and assuming a maximum swimming speed of 12 km h<sup>-1</sup> for  
154 humpback whales (Garrigue et al. 2010). To reduce the occurrence of long gaps between locations,  
155 for which no information was available, tracks were split into two or more if time gaps were longer  
156 than 10 days. To account for irregular time intervals and uncertainty in estimated locations, humpback  
157 whale tracks were re-estimated using a hierarchical form of a “first-Difference-Correlated-Random  
158 Walk model” (DCRW; Jonsen 2016). That model was fitted with R package *bsam* (Version 1.1.2;  
159 Jonsen 2016) and used to predict two locations per day (i.e. time step of 12 hours) for each track.  
160 Default *bsam* package model diagnostics and plots of predicted locations *versus* original locations  
161 were inspected to check for both model convergence and whether derived locations were aligned with

162 observed locations. Data from individuals for which the model did not converge were discarded from  
163 the analysis. A summary of the data used in the analysis is presented in Table 1 (see Supplement,  
164 Table S1, for details). The uncertainty associated with the estimated locations was not considered in  
165 the distribution and habitat use models.

166 Because the objectives here were related to investigating distribution in the breeding area and to  
167 compare results to a previous study, derived locations beyond the limits of the survey area, in offshore  
168 waters or during migration, for example, were censored from the dataset (Figure 1) before the  
169 distribution models were built.

### 170 **2.3. Covariates**

171 Environmental covariate values used in presence/pseudo-absence spatial models were extracted from  
172 published datasets for the post-processed track locations. Candidate covariates considered in the  
173 models were chosen to permit comparison to a previous modelling study using line transect data from  
174 humpback whales in the same region (Bortolotto et al. 2017). Current speed close to the surface  
175 (Curr.sp) values were extracted from the *OSCAR Third Degree Sea Surface Velocity* dataset (ESR,  
176 2009), with resolution  $0.33 \times 0.33^\circ$  (latitude  $\times$  longitude) in 5-day intervals. Daily values for sea  
177 surface temperature (SST), with resolution  $0.01 \times 0.01^\circ$ , were extracted from *JPL MUR SST project*  
178 dataset (JPL MUR MEaSURES Project, 2010). Daily wind speed at the surface of the sea (Wind.sp)  
179 values were extracted from the *Era-Interim* dataset (Dee et al. 2011), with horizontal resolution  
180  $0.125 \times 0.125^\circ$ . Depth values were extracted from ETOPO1 (Amante & Eakins 2009), for which the  
181 resolution is  $0.1 \times 0.1^\circ$ . Slope was derived from ETOPO1. Distances from coast (Dist.coast) and from  
182 the shelf break (Dist.shelf), represented here by the 500 m depth contour, were measured with the  
183 *gDistance* function, *rgeos* R package (version 0.3-26; Bivand & Rundel 2017). To represent regions  
184 within the area where animals could be sheltered from rougher weather and colder waters, a factor  
185 covariate for “shelter” was created by combining values of SST and wind speed in six classes, defined



186 by quantiles of these covariates, *sensu* Bortolotto et al. (2017). The logarithm of depth was used in  
187 the models.

188 Values for the dynamic covariates (i.e. Curr.sp, SST and Wind.sp) were obtained by matching the  
189 timestamps of each location with the nearest (in time and horizontal space) covariate value.

#### 190 ***2.4. Data analysis and modelling***

191 Processed track locations were considered as presences in spatial models. To provide contrasting data,  
192 pseudo-absences were generated randomly within the survey area to represent where animals could  
193 have been, assuming that the survey area was accessible to all tagged animals. To select the most  
194 appropriate ratio of presence to pseudo-absences, different scenarios (i.e. 1:1, 1:3, 1:5 and 1:10) were  
195 explored to verify model “coefficients stability” (see Supporting Information S4 in Ventura et al.  
196 2019). In every model scenario, weighting was applied so the weight of pseudo-absences followed  
197 the corresponding fraction, to ensure that the number of presences was equal to the sum of the weights  
198 of the pseudo-absences. The model fitted to the data with five pseudo-absences per presence produced  
199 the same fitted coefficients as with ten, but different from smaller ratios (1:1 and 1:3), indicating that  
200 five pseudo-absences per presence was sufficient to represent the underlying background of the  
201 inference area. To match a set of five pseudo-absences to one specific presence, all locations within  
202 a set of five pseudo-absences were given the same timestamp as the corresponding presence.

203 Covariate pairs that were strongly correlated ( $> 0.7$ ), or that had high ( $> 10$ ; Hair et al. 2014) variance  
204 inflation factor scores (*vif* function, *car* R package) when together in a model, were not included  
205 simultaneously in the same model.

206 Two objectives guided the inclusion of candidate covariates in the spatial models. For the Distribution  
207 Model (DIM), the objective was to create the best distribution map as possible, so all available  
208 covariates were considered. For the Habitat Use Model (HUM), the objective was to investigate the

209 relationship of whale occurrence and important ecological characteristics, and all covariates but  
210 geographic position (latitude and longitude) were considered.

211 To compare the present models with those in Bortolotto et al. (2017), latitude and longitude were not  
212 considered in the HUM. This procedure was adopted because these covariates have no logical  
213 biological interpretation for habitat use, and because they were both strongly correlated with SST.  
214 The DIM included those covariates as potential explanatory terms because its objective was to  
215 identify those features that describe most variability in whale occurrence and to generate the best  
216 predictive map for potentially informing management. The present DIM map was created to be  
217 compared to the AEM map in Bortolotto et al. (2017).

218 Presence vs. pseudo-absence was modelled as a binomial random variable, with probability of  
219 presence a smooth function of the continuous covariates, first within a Generalized Additive Model  
220 (GAM; Wood 2017) framework and then fitting the GAM using a Generalized Estimating Equation  
221 (GEE; Hardin & Hilbe 2002) approach to account for possible autocorrelation, as detailed below.  
222 Continuous covariates were included in the models using b-splines, and a logit link function was used.  
223 Weighted regression was used, where presences were assigned a weight of 1 and pseudo-absences a  
224 weight of 0.2. Model fitting was done using software R (R Core Team, 2017), with functions specified  
225 below.

226 For each of the DIM and HUM, covariate selection proceeded in three stages. First, the full model  
227 (i.e. model with all candidate covariates) was fitted, with the number and location of each b-spline  
228 knot selected using the Spatially Adaptive Local Smoothing Algorithm (SALSA; Walker et al. 2011),  
229 implemented with the *MRSea* R package (version 1.0.beta; Scott-Hayward et al. 2017). The  
230 maximum number of knots were restricted to eight for one-dimensional smoothers and to 20 for two-  
231 dimensional smoothers (i.e. for geographic position), to prevent overfitting of smooth terms

232 (Wood 2017). Continuous covariates for which no knot was indicated as significant, at  $\alpha = 0.05$ , were  
233 not considered in subsequent steps.

234 In the second stage, a backwards covariate selection process was followed. The model from the first  
235 step was refitted using a GEE to accommodate residual autocorrelation. For this, the data were  
236 organized in correlation panels, with a panel for each set of presences within a track (one panel per  
237 track) and a different panel for each pseudo-absence (one panel per pseudo-absence). Using this panel  
238 structure was congruent with the assumption that model residuals within a track were correlated, but  
239 that residuals in different tracks were not, and that residuals for pseudo-absences were mutually  
240 independent. Model fitting used the *geeglm* function within the *geepack* R package (version 1.2-1;  
241 Højsgaard et al. 2006). The fitted model's QICu score (Pan, 2001) was calculated. Then, a series of  
242 models were fitted, leaving one covariate out at a time, and QICu scores were calculated for each of  
243 these models. The model with the lowest QICu score was retained. If this model had fewer covariates  
244 than the full model, then the process was repeated to drop another covariate. This was repeated until  
245 dropping covariates did not result in any further decrease in QICu.

246 In the third stage, the statistical significance of remaining covariates was assessed using marginal p-  
247 values, via the function *getPvalues* from *MRSea* R package (Scott-Hayward et al., 2017). Any  
248 covariates that were non-significant using an  $\alpha$ -level of 0.05 were dropped and the GEE re-fitted.

249 For the selected DIM and HUM, model performance was verified with Receiver Operating  
250 Characteristic (ROC) curves and confusion matrices, as per Pirotta et al. (2011), using R package  
251 *ROCR* (version 1.0-7; Sing et al. 2009). The ROC and confusion matrix can be used to calculate  
252 percentages of false positives and false negatives expected for the model, by comparing the predicted  
253 values to the observed.

254 For comparison to the distribution maps presented in Bortolotto et al. (2017), prediction grids  
255 (8 by 8 km cells) containing covariate values from 2008 and 2012 (the years for which distribution

256 models from sighting data were developed in that study) were used for predictions using the selected  
257 DIM. The contribution of each covariate in the final HUM was visualized with partial plots, with  
258 confidence intervals based on the GEE estimated uncertainty, adapting custom R code from Pirotta  
259 et al. (2011).

### 260 **3. RESULTS**

261 Data from 113 tags, deployed from 2003 to 2012, were available for the analysis. Model outputs from  
262 package *bsam* (e.g. posterior densities and model convergence plots) indicated poor model fit and/or  
263 convergence for whale tracks with less than 12 locations or less than five days of tracking. Those  
264 tracks were therefore excluded from the analysis. After filtering, interpolated locations from 87 tracks  
265 were available for investigating distribution and habitat use (Figure 1), comprising 62 tracks from  
266 females (mothers with calves), 19 from males and six from animals of unidentified sex (Table 1).  
267 Because five pseudo-absences were created per each presence (i.e. interpolated locations within the  
268 survey area;  $n = 3,071$ ), 15,355 pseudo-absences were used, totaling 18,426 locations to be modelled.

269 The final HUM model included smooth terms for current speed, SST, wind speed, coast distance and  
270 distance to the shelf-break, and the factor variable shelter (Table 2). As a result of using GEEs for  
271 dealing with autocorrelation in the data, confidence intervals for fitted relationships between the  
272 response variable and the covariates were very wide (i.e. high uncertainty), except for SST (Figure  
273 2). Depth had no statistically significant knots when the full model was fitted with SALSA and was  
274 not considered further. The fitted relationship for the SST covariate showed a clear peak around 24-  
275 25°C (Figure 2), similar to Bortolotto et al. (2017).

276 The final DIM included latitude and longitude, current speed, and distances to coast and shelf break  
277 (Supplement, Table S4). Shelter and wind had no significant knots at the first step of covariate  
278 selection, and depth had a non-significant marginal p-value in the last step of covariate selection for  
279 the DIM (Table 2). Overall, higher probabilities of encountering whales were predicted for the region

280 around the Abrolhos archipelago and to the south, supporting findings from Bortolotto et al. (2017)  
281 (Figure 3). For 2008, 74.7% of the tracking data model predictions that were above the median  
282 (median = 0.44) spatially overlapped with line transect model predictions above the median  
283 (median = 4.01). For 2012, 73.7% of the tracking data model predictions that were above the median  
284 (median = 0.41) overlapped with line transect model predictions above the median (median = 5.11).  
285 However, clear differences were observed at a smaller scale: in the Abrolhos Bank region, a patch of  
286 predicted lower probability of occurrence for both 2008 and 2012 overlapped with the area presenting  
287 the highest densities from Bortolotto et al. (2017).

288 Models performed better than random, with confusion matrices indicating 66.2% of correct  
289 predictions for the HUM, and 63.1% for the DIM, and with the area under the ROC curve (AUC),  
290 0.691 and 0.732, respectively (Table 3).

#### 291 **4. DISCUSSION**

292 We investigated the distribution and habitat use of humpback whales off Brazil with spatial models  
293 applied to locations obtained through animal tracking and to spatial covariates. To generalize our  
294 results to other whale populations, they should be interpreted in light of several important specificities  
295 of the population studied here. For instance, the increasing abundance of this recovering population  
296 (Zerbini et al. 2019, Bortolotto et al., 2021) may have an effect on their distribution and on how they  
297 use their habitats in the area, which was not possible to evaluate here because of the nature of the  
298 individual tracking data. Also, because here we considered whales on a breeding area, the unbalance  
299 in the reproductive stage (or animal sex) in our tracked animals (see Results; Supplement Table S1)  
300 very likely prevents them from accurately representing the population in general. That is because,  
301 animals in different reproductive stages are known to use their habitat differently (Cartwright et al.  
302 2012, Derville et al. 2018). The scale of the dynamic environmental predictors (e.g., current speed,  
303 SST) and the effect of environmental variability in other systems, such as their feeding grounds, must  
304 also be considered. However, here we focus in describing mainly the differences in the

305 implementation and interpretation of modelling of either data from individual tracking or from line  
306 transect sampling.

### 307 *Model considerations and constraints*

308 Spatiotemporal correlation in track locations and other common issues in applying presence/absence  
309 modelling for distribution and habitat use (Aarts et al. 2008) were carefully considered in the analysis.  
310 Despite differences in the sampling unit of the tracking and survey data (individual vs. space) and  
311 statistical tools used, some of the outputs from modelling track locations in a presence/pseudo-  
312 absence modelling approach support findings from distribution models fitted to line transect data  
313 (Bortolotto et al. 2017). Although the uncertainty in most of the covariate-response (telemetry data)  
314 relations fitted here was much higher (Figure 2), SST showed a clear peak around the same range of  
315 temperatures in both the present study and in the line transect modelling (Supplement, Figure S3),  
316 which probably reflects how strongly habitat use for these animals is related to temperature in their  
317 breeding grounds (see Bortolotto et al. 2017 for a discussion on the role of SST for habitat use of  
318 humpback whales). The apparent agreement between the two methods is not only reassuring for what  
319 is known about habitat use for this population, but also shows that similar, possibly complementary,  
320 conclusions can be drawn on this regardless of which of the two methods is used, given enough  
321 sample size and careful consideration of potential bias sources. However, differences such as the  
322 patch of present lower probability of whale occurrence that overlapped with the area presenting the  
323 highest densities from Bortolotto et al. (2017), need to be considered at smaller scales.

324 It is important to note that, by creating pseudo-absences from random locations in the entire area, it  
325 was assumed that the entire survey area was available to the animals at any time (Soberón and  
326 Peterson 2005). However, this is an arbitrary decision and the available area from the animals'  
327 perspective could be different (Aarts et al. 2008, Hazen et al. 2021). For example, an animal tagged  
328 in the vicinity of the Abrolhos archipelago (Figure 1) would take at least two days to reach the

329 southernmost portion of the survey area, swimming in a straight line at 12 km h<sup>-1</sup> (i.e. the maximum  
330 travel speed [Garrigue et al. 2010] used as a criteria in the data pre-processing/filtering).

331 The restriction of the area of inference (survey area) in comparison to that of Bortolotto et al. (2017;  
332 compare north extents of the upper and the lower panels of Figure 3) was adopted to reduce the effects  
333 of violating the area availability assumption (Hazen et al. 2021). Further restrictions could be  
334 investigated at the expense of inferring over a smaller region and considering fewer data. Another  
335 possibility to reduce issues from non-uniformly distributed tagging locations could be to truncate the  
336 first days from each track. This was not adopted here because many tracks presented relatively short  
337 periods of locations within the survey area and such truncation would eliminate a substantial amount  
338 of information from the dataset. The extent of the area of inference also has a major influence on  
339 where pseudo-absences are randomly placed to represent the background environment where animals  
340 were not observed. The restriction of the area considered in this study potentially also minimized the  
341 effects related to that issue, because areas further north from the limits of the survey area (Figure 1)  
342 were visited by only two animals (out of 113). Also, because of imbalance in the tagging locations  
343 and number of animals tagged across years (Table 1) data from all years were pooled to model  
344 distribution. Therefore, it was impossible to evaluate temporal variation in distribution and habitat  
345 use patterns. Data were assumed to be representative for the population as a whole and for the period  
346 between 2003 to 2013. Year was not considered as a covariate in the analysis and inferences presented  
347 here must be interpreted as the overall distribution pattern for that population. Investigating temporal  
348 variation in distribution could help understanding the potential expansion of population range in the  
349 breeding area (Pavanato et al. 2018), but spatiotemporally balanced data within the area of inference  
350 is needed for that. One possible option is to restrict the area of inference in ways that allow meeting  
351 the above criteria, at the expense, again, of inferring over a much-reduced area. There is evidence that  
352 this population was increasing at near the upper limit of the rate expected during the period considered  
353 here (Wedekin et al. 2017), and we suggest that the potentially resulting distributional shifts would

354 be better assessed with line transect data modelling (Supplement, Table S5). To investigate the  
355 potential expansion of the breeding range, however, tracking data could indicate areas used by  
356 animals that were not designed to be surveyed.

357

358 The first step of covariate selection (i.e. observing “robust standard errors” from model fitting with  
359 SALSA) led to discarding of covariates that were not estimated precisely enough to be considered  
360 significant, even before the residual autocorrelation was accounted for. Because serial autocorrelation  
361 may cause non-important covariates to appear more significant (Aarts et al. 2008), GEEs permit  
362 realistic estimation of uncertainty for covariate-response relations. However, such fitted relations can  
363 be difficult to interpret (Pirodda et al. 2011), especially for those covariates with wide confidence  
364 intervals in their fitted relationships (Figure 2). The second step of covariate selection (observing the  
365 *QICu* scores) had been used in previous studies analyzing similar data to the present and is a  
366 reasonable way to account for the residual auto-correlation issue (Pirodda et al. 2011, Jones et al.  
367 2017). The last step of covariate selection (marginal *p-values*) was the final check for contribution of  
368 covariates to the models. The combination of the three criteria adopted improves the chances of only  
369 retaining important covariates related to animal distribution. Despite the above criteria, all covariates  
370 but SST presented large confidence intervals in their fitted relationships (Figure 2), precluding  
371 detailed interpretation of those results.

### 372 ***Habitat use from humpback whale tracking data***

373 Like the model used to investigate habitat use in Bortolotto et al. (2017), latitude and longitude were  
374 not considered in the HUM. The present final HUM adds wind speed to the already identified  
375 important covariates related to habitat use of humpback whales in the area (Martins et al. 2001,  
376 Bortolotto et al. 2017, Pavanato et al. 2018). However, the combination of SST and wind speed,  
377 represented by shelter, had been already identified as important in the line transect models. Using



378 autoregressive models applied to line transect data, Pavanato et al. (2018) identified bathymetry and  
379 distance to the shore to be related to the occurrence of humpback whale groups in the area. Wind  
380 speed was also considered as a candidate covariate in that study, but it was not retained in that final  
381 model. In the present study, it is unclear what is the relation between wind and whale occurrence from  
382 the partial plot for that covariate (Figure 2) or from its estimated coefficients (Supplement, Table S3).  
383 Looking at the fitted coefficients for shelter (Figure 2), wind seems to be important when the water  
384 is relatively colder, which agrees well with the results found from modelling line transect data.  
385 However, present results for shelter suggest a contradicting interpretation of its importance than from  
386 the line transect data models from Bortolotto et al. (2017) which is likely due to the high uncertainty  
387 in the shelter coefficients (Figure 2). Other covariates in the final HUM include current speed and  
388 distance from the shelf and to the shore, which may be related to calf survival probabilities, protection  
389 against predators or in habitat selection for specific reproduction-related groups (Corkeron & Connor  
390 1999, Félix & Botero-Acosta 2011). Here, tracking data were used to investigate the population  
391 distribution overall, therefore sex and other individual characteristics were not incorporated in the  
392 models. The reason for not using this information was that there is no clear way to allocate sex and  
393 other individual characteristics to pseudo-absences within the GEEs framework. One option would  
394 be to fit models separately for males and females because this information is available (Supplement,  
395 Table S1). However, sex was unbalanced in the present data with most animals being females.  
396 Distribution patterns found in Bortolotto et al. (2017) and now supported here, are consistent with  
397 what could be expected for population distribution driven by female habitat selection.

398 Alternative approaches to investigate habitat use from tracking data include inferring animal  
399 behavior, which can be related to specific biological and environmental features (McClintock et al.  
400 2015, Jonsen 2016, Roncon et al. 2018, Jonsen et al. 2019). There are also methods to study spatial  
401 distribution from tagging data which do not require creating pseudo-absences, such as point process  
402 models (Johnson et al. 2013) or by considering animal tracks in a grid over the study area as a result

403 of a Markov process (Whitehead & Jonsen 2013). Movement models can be used to quantify the  
404 relationship between covariates and the probability of animals being in specified behavioral states  
405 (Roncon et al. 2018, Jonsen et al. 2019), therefore, to investigate habitat use, not necessarily from a  
406 spatial perspective. In that sense, direct comparisons to line transect models (Table S5) as presented  
407 here would be more challenging. For instance, that type of models would be very useful to investigate  
408 habitat use in more dynamic systems, such humpback whale feeding grounds where whales are  
409 constantly tracking suitable foraging conditions (Bamford et al. 2022) in relation to highly dynamic  
410 ocean features (i.e. upwellings, eddies, fronts). Management implications

411 It is certainly important to investigate the potential effect of human activities on the occurrence of  
412 whales in the area (Pavanato et al. 2018). To evaluate that, data from before the presence of such  
413 activities are needed, or drastic enough changes in the distribution or intensity of them must happen  
414 before being able to identify a redistribution, coinciding with the change in activities. However, that  
415 the two methods considered here agreed in terms of distribution and habitat use inferences, means  
416 that either could be used to informing conservation or management actions. Alternatively, a simpler  
417 analysis of overlap between whale distribution and the distribution of potential harmful human  
418 activities (Martins et al. 2013) could also contribute to such investigation.

419 Modelling animal distribution using line transect data may have some important advantages in data  
420 collection, survey design and modelling techniques, such as being able to control the places visited  
421 in the survey design (Table S5 **Error! Reference source not found.**). Line transect surveys also allow  
422 deriving abundance estimates when the assumptions of distance sampling are dealt with (Buckland  
423 et al. 2015). In contrast, satellite tagging of whales allows data to be collected remotely, meaning that  
424 the field work necessary for the method is restricted to that of tagging the animals. Also, the data may  
425 allow different approaches for investigating habitat use and distribution, because they include  
426 information about movement of individuals over time (Matthiopoulos & Aarts 2010). Because close  
427 proximity to the animal is required for tagging, other useful detailed information may also be

428 simultaneously collected. For example, it is common to collect skin and blubber biopsies during the  
429 tagging procedure. Important information such as sex, hormone levels and contaminants can be  
430 determined from those samples (Heide-Jørgensen et al. 2006, Reisinger et al. 2014). Tagging whales  
431 is a more invasive field procedure (Alves et al. 2010, Andrews et al. 2019), but provides data that are  
432 impossible to obtain from line transect surveys only.

433 The two methods compared here are complementary and may be used in conjunction to expand the  
434 spatiotemporal coverage of studies on distribution or habitat use, therefore providing better  
435 information to evaluate the need of, and for implementing conservation and management actions  
436 when needed. Survey efforts to investigate distribution of a population can be split between tagging  
437 some animals in one portion of the area of interest and surveying another portion, enhancing data  
438 collection while reducing logistical costs. Therefore, distribution and habitat use investigations  
439 aiming at informing conservation of large whales can be more easily and realistically implemented.

440

441 *Ethical considerations*

442 Tagging of animals were conducted under permits issued by the Brazilian Institute of the  
443 Environment and Renewable Natural Resources (IBAMA, permit #009/02/CMA/IBAMA;  
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655 **Table 1.** Summary of the data set (presences only) used for modelling distribution. (Max  
 656 locations = maximum number of locations per track within a year).

<b>Year</b>	<b>Tracks</b>	<b>Locations</b>	<b>Initial date</b>	<b>Ending date</b>	<b>Max locations</b>
2003	8	340	18-Oct	25-Dec	118
2005	11	359	11-Oct	27-Nov	83
2006	3	75	12-Oct	10-Nov	37
2007	7	281	08-Sep	18-Oct	78
2008	17	598	27-Aug	03-Nov	97
2009	9	399	14-Sep	09-Nov	98
2010	10	282	18-Sep	06-Nov	56
2011	8	314	29-Sep	20-Nov	63
2012	13	407	08-Aug	17-Dec	85
2013*	1	16	20-Aug	27-Aug	16
Total/Overall	87	3071	—	—	—

657 \*locations from a whale tagged in 2012, which was tracked for more than 300 days.

658 **Table 2.** Covariates retained in models for both present tracking data and for line transect data.  
 659 (HUM = Habitat Use Model, DIM = Distribution Model, AEM = Abundance Estimation Model from  
 660 Bortolotto et al. 2017).

Covariate	Tracking data (present)		Line transect data	
	HUM	DIM	HUM	AEM
Current speed	*	*	*	*
Depth				
Distance to shelf break	*	*	*	*
Distance to coast	*	*	*	*
Shelter	*		*	*
Slope				
SST	*		*	
Wind speed	*			*
Latitude and longitude	—	*	—	*

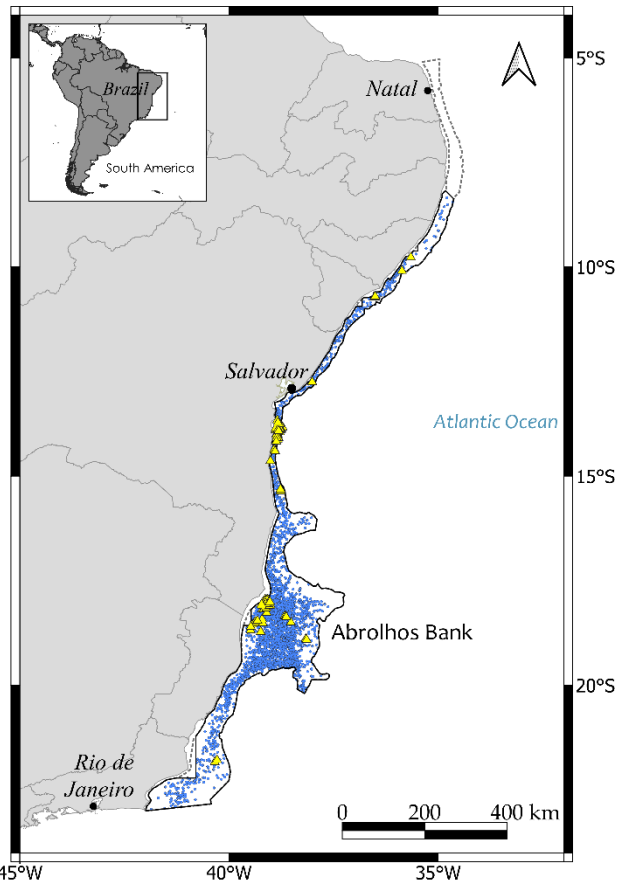
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662 **Table 3.** Performance of models fitted to telemetry tracking data of humpback whales. (HUM =  
 663 Habitat Use Model, DIM = Distribution Model, AUC = area under the ROC curve).

<b>Model</b>		<b>HUM</b>		<b>DIM</b>	
<b>Correctly predicted</b>		<b>66.2%</b>		<b>63.1%</b>	
<b>AUC</b>		<b>0.691</b>		<b>0.732</b>	
<b>Confusion matrices</b>		<b>Observed</b>		<b>Observed</b>	
	<b>Predicted</b>	<b>1</b>	<b>0</b>	<b>1</b>	<b>0</b>
	<b>1</b>	1871	5022	2330	6063
	<b>0</b>	1200	10333	741	9292
<b>Total observed</b>		3071	15355	3071	15355
		<b>1</b>	<b>0</b>	<b>1</b>	<b>0</b>
<b>Percent of observed</b>	<b>1</b>	60.9%	32.7%	75.9%	39.5%
	<b>0</b>	39.1%	67.3%	24.1%	60.5%

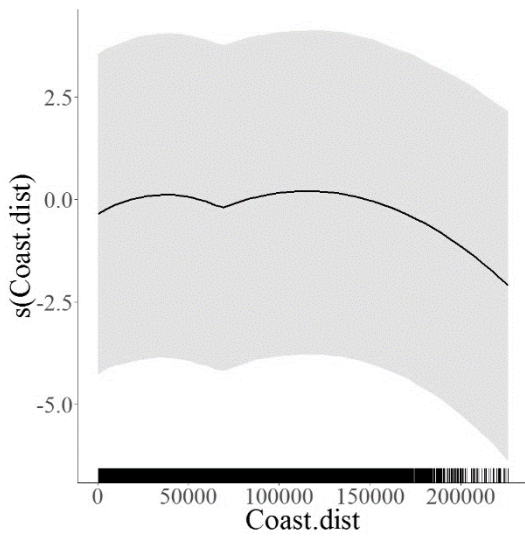
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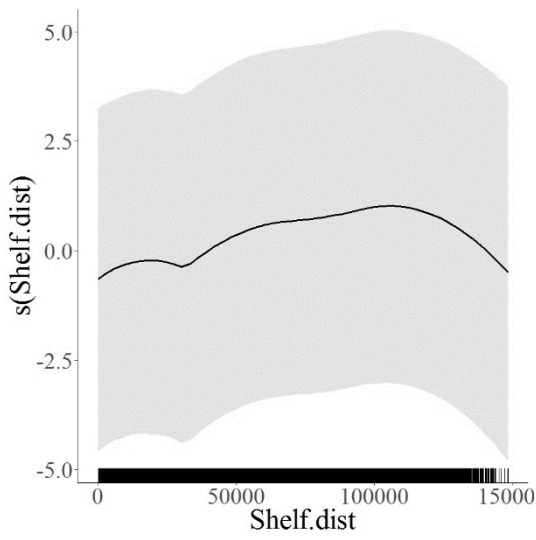
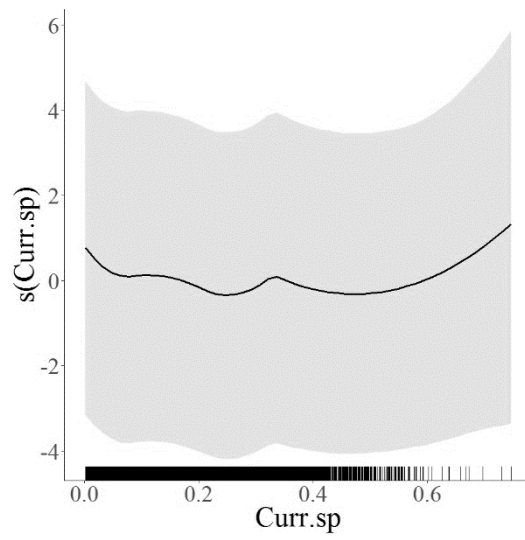


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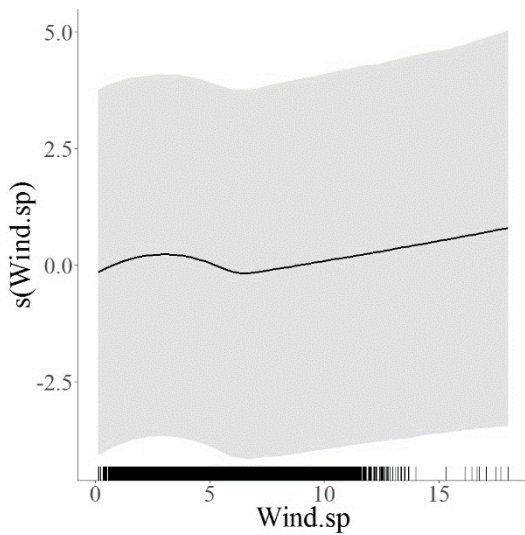
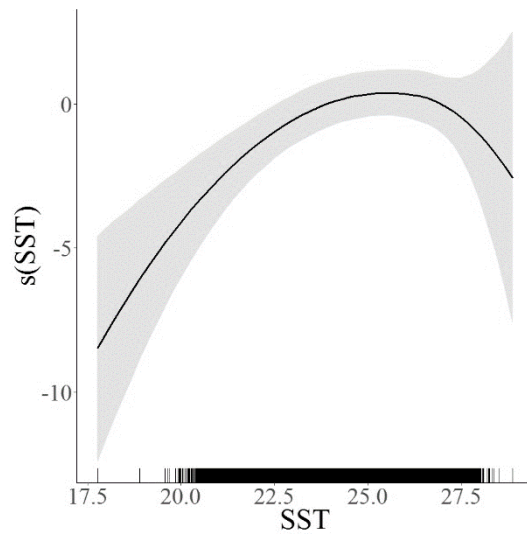
666 **Figure 1.** Humpback whale locations used in the distribution and habitat use analysis (blue dots) and  
 667 tagging locations (yellow triangles). The area of inference (black solid line) was adapted from  
 668 Bortolotto et al. (2017) (grey dotted line), considering the uneven tagging locations and  
 669 environmental covariates extent.



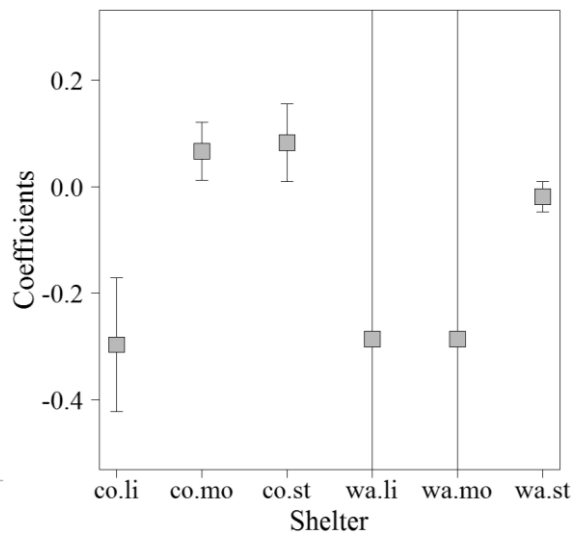
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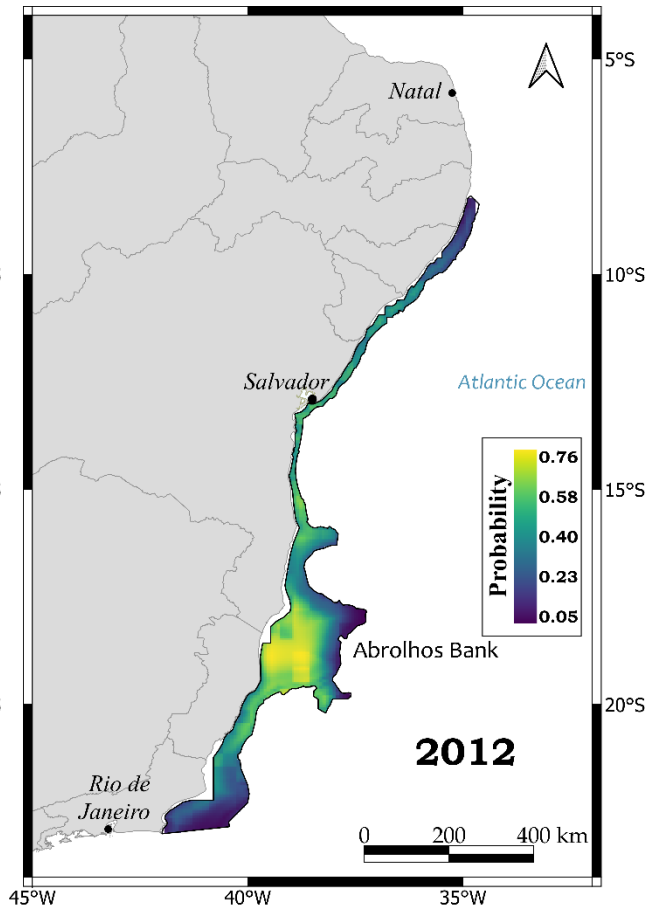
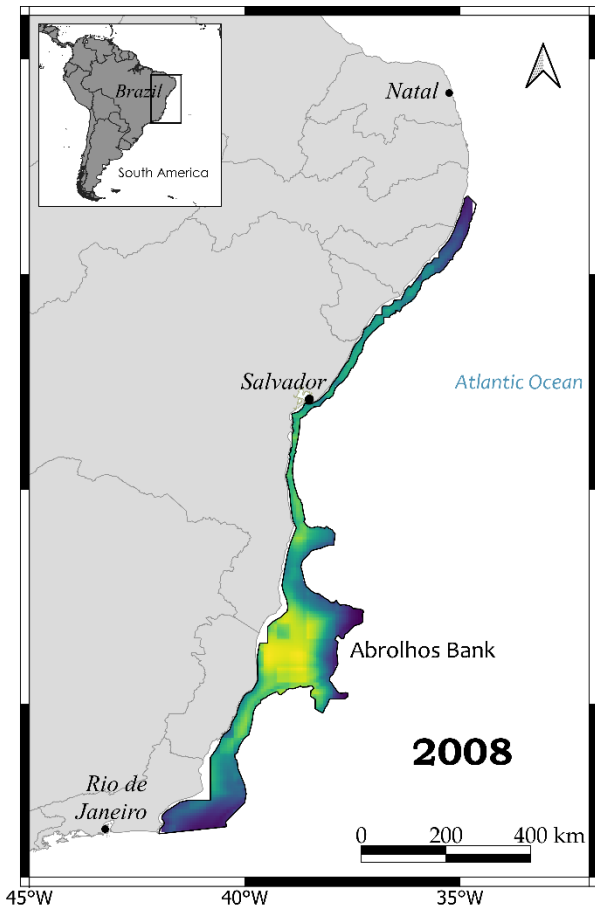


673 Figure 2. Fitted relationships for smooth functions of covariates in the final habitat use model (HUM).

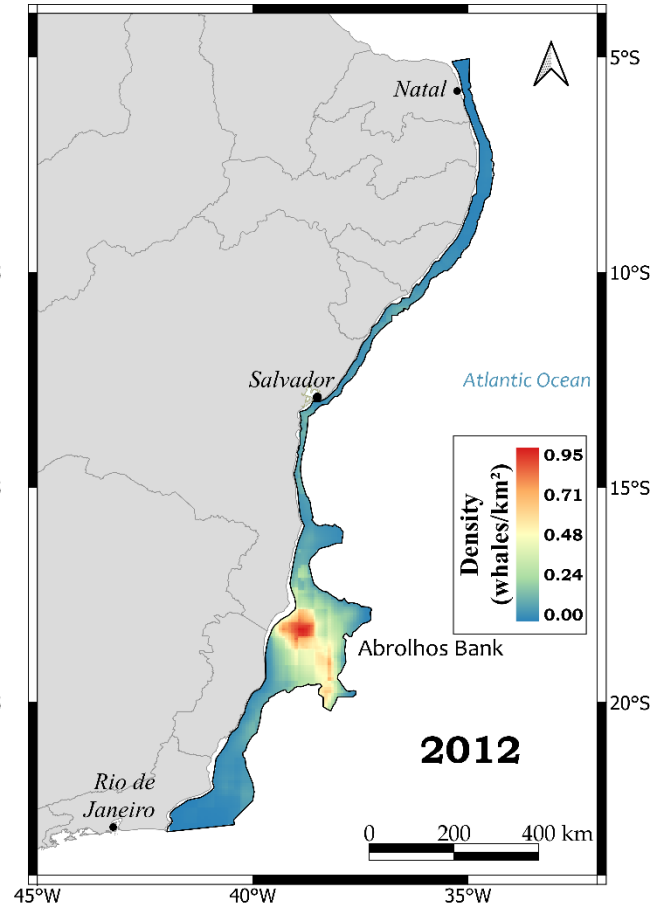
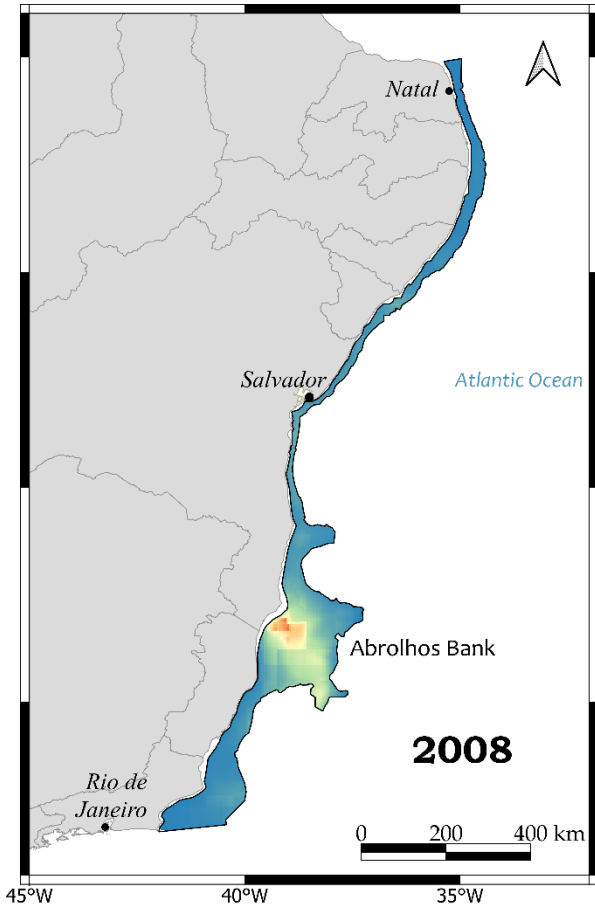
674 Error bars in the “Shelter” plot represent 95% normal confidence intervals. (co = cold, wa = warm,

675 li = light, mo = moderate, st = strong, Curr.sp = current speed, SST = sea surface temperature,  
676 Wind.sp = Wind speed, Coast.dist = distance to the coast, Shelf.dist = distance to the shelf-break).

677



678



679 **Figure 3.** Upper panel: Occurrence probability surfaces, predicted using the present distribution  
680 model (DIM) of tracking data; Lower panel: “AEM” (Abundance Estimation Model) maps adapted  
681 from Bortolotto et al. (2017), showing humpback whale density surfaces, for comparison. See  
682 Supplement, Figure S2, for uncertainty maps of present DIMs.

683