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Predictive Spatial Analysis of Marine Mammal Habitats

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14. ABSTRACT
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List of Acronyms

AIC Akaike Information Criterion
ASPE Average Squared Prediction Error
CART Classification and Regression Trees
CCA Canonical Correspondance Analysis
CHL Surface Chlorophyll
CV Coefficient of Variation
CZCS Coastal Zone Color Scanner
EEZ Exclusive Economic Zone
ER Encounter Rate
ESW Effective Strip Width
GAM Generalized Additive Model
GCV Generalized Cross Validation
GIS Geographic Information System
GLM Generalized Linear Model
GOM Gulf of Mexico
MLD Mixed Layer Depth
NASC Nautical Area Scattering Coefficient
NMDS Nonmetric Multidimensional Scaling
NOAA National Oceanic and Atmospheric Administration
NODE Navy OPAREA Density Estimate
NOH North of Hatteras
OPAREA Operating Area
PODAAC Physical Oceanography Distributed Active Archive Center
SDSS Spatial Decision Support System
SE Standard Error
SeaWIFS Sea-viewing Wide Field-of-view Sensor
SERDP Strategic Environmental Research and Development Program
SOH South of Hatteras
SSS Sea Surface Salinity
SST Sea Surface Temperature
SWFSC Southwest Fisheries Science Center
TD Thermocline Depth
TS Themocline Strength
UNCW University of North Carolina Wilmington
USWTR UnderSea Warfare Training Range

Keywords

Habitat models, cetaceans, SDSS, baleen whales, humpback whale, right whale, sperm whale, killer whales, pilot whales, common dolphins, bottlenose dolphins, harbor porpoise, GAM, GLM, beaked whales, marine mammals, pelagic species, niche, ordination, community structure, classification and regression trees, CART, group contrast mantel test, Northwest Atlantic, South Atlantic, Gulf of Mexico, ship based surveys, aerial surveys.

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Abstract

We developed a data management, statistical modeling and decision support system describing the habitat use of marine mammals in the North Atlantic and Gulf of Mexico. Our objective was to make this information available in a comprehensive and readily accessible manner to environmental planners and decision makers in the Navy and elsewhere. The system uses data on the distribution of marine mammals generated in dedicated surveys contained in the online OBIS-SEAMAP marine data archive (http://seamap.env.duke.edu). We used these data to develop predictive habitat models for guilds of marine mammals in these two regions. We delivered model outputs in an online, flexible Spatial Decision Support System (SDSS). The SDSS is a browser-based, interactive mapping application that enables the user to view the model results, together with the original survey effort and marine mammal observations. In our model development, we fitted a suite of multivariate statistical models (CART, GLM, GAM and Bayesian approaches) to observations from at-sea surveys, together with remotely sensed environmental data (bathymetry, sea-surface temperature, chlorophyll), as well as derived variables such as slope, temperature fronts and chlorophyll aggregations. In total, we generated 33 models, representing 16 cetacean guilds, using environmental data from the JPL physical oceanographic data archive (PO.DAAC). We present the model results as predictive maps for the likelihood of encounter with marine mammal guilds, together with estimates of the associated standard errors. The supplemental comparison of habitat models and Navy OPAREA Density Estimates (NODEs) to observation data revealed insufficient data in two Navy training areas for all but two species. Overall the NODE models performed better for data-rich species (bottlenose and spotted dolphins) than rare species (pilot whales and Risso's dolphins), but performance varied greatly among species. Users may delineate regions of interest within the SDSS and extract summary statistical outputs, such as histograms and model statistics, from these areas. The SDSS system also incorporates model results from a related SERDP project (SI-1391, NOAA Southwest Fisheries Science Center) and estimates of marine mammal density, generated by colleagues at Geomarine, Inc. This work represents an important step towards understanding marine mammal habitat use with respect to regions utilized by the U. S. Navy.

1.0 Objective

The objectives of our project were to: (1) develop and test the robustness of various models of marine mammal habitat suitability, as predicted by physical conditions of the marine environment; (2) design a hierarchical framework for analyzing patterns of marine mammal habitat suitability across seasonal time frames; (3) assemble a Spatial Decision Support System that allows Navy users to examine and analyze model outputs and original input data across multiple time scales; and (4) test how well predictive marine mammal habitat and density models perform at spatial scales relevant to Navy training exercises. In constructing models of marine mammal habitats, we focused on environmental parameters that are important determinants of the distribution of marine mammals and also readily measurable using existing technologies. Our intent was to provide the Navy with quantitative tools that will allow quantitative predictions of the presence of marine mammals in particular regions of interest.

Our work is a response to the pertinent SERDP statement of need (SON CSSON-04-02), which described a requirement for predictive models to be able to operate across a wide range of spatial scales (>1000 to < 100 nautical miles) and temporal scales ranging from years to daily time intervals. The modeling / forecasting system must also be sensitive to oceanographic dynamics across these same space and time scales. In this report, we address these challenging requirements in an explicit manner.

2.0 Background

To meet its statutory requirements under the Endangered Species Act and Marine Mammal Protection Act, the Navy requires analytical tools with which to predict the distribution of marine mammals at spatial and temporal scales relevant to training exercises. The Navy must be able to conduct such exercises to maintain readiness, and the best way to avoid potentially adverse effects on these protected species is to conduct exercises in times and areas where the probability of encountering marine mammals is low. We developed a novel analytical tool kit that will allow the Navy to predict the probability of encountering marine mammals at various spatial and temporal scales. Our research group has worked closely, particularly with respect to statistical approaches and product development, with the SERDP SI-1391 research group at the Southwest Fisheries Science Center, who recently completed a similar project (Barlow et al. 2009).

Spatial analysis of the distribution of marine mammals has lagged behind the study of terrestrial species due to the three-dimensional and fluid nature of this environment. Nevertheless, it is clear that features of their habitat control the distribution of these species. For example, physical forcing influences the distribution of marine mammals at multiple scales. At a large scale (thousands of km), the distribution of marine mammals frequently reflects the oceanographic domains and current systems that influence primary productivity and plankton biogeography (Ballance et al. 1997, Brodeur et al. 1999). At finer scales (tens to hundreds of km), the distribution of these animals is likely mediated by the dispersion and availability of their prey (Hunt and Schneider 1987, Fiedler et al. 1998). Prey distribution, in turn, is influenced by physical processes associated with gradients in bathymetry (Springer et al. 1996, Hunt et al. 1998, Mueter and Norcross 1999, Murawski and Finn 1988) and water temperature (Wildhaber and Crowder 1990, Swain and Kramer 1995, Hunt et al. 1996, Haury et al. 1978). Increasing evidence suggests that marine mammals and other upper trophic level predators concentrate within regions of enhanced productivity and prey aggregation frequently associated with specific bathymetric domains and water mass boundaries (Sund et al. 1981, Kenney and Winn 1986, Springer et al. 1996, Fiedler et al. 1998, Hunt et al. 1999, Polovina et al. 2000).

Only a few previous studies have attempted to elucidate relationships between marine mammal communities and their habitats in the U.S. Exclusive Economic Zone (e.g., Reilly and Fiedler 1994; Davis et al. 1998, Mullin et al. 1994; Hamazaki 2002, Waring et al. 1993). Despite these preliminary studies, our knowledge of the relationship between marine mammals and their habitats is still very poor and certainly insufficient to predict their presence in particular areas.

Traditional approaches to the study of marine mammal habitats have encountered analytical problems because many environmental variables are correlated with one another**.** As a simple example, the farther away from shore one gets, the deeper the water becomes. In this case, the data are clearly not independent, thus classical statistical techniques cannot (or should not) be used. There are, however, alternative statistical approaches capable of dealing with the lack of independence in the data as well as incorporating the location of the data *per se*. Many of these techniques are computationally intensive, so their use has spread only after the advent of sophisticated computer technology. Furthermore, very few scientists have adapted these techniques to the study of marine environments. New improvements in GIS software and remote sensing techniques now offer researchers the opportunity to gather, integrate and analyze a variety of spatial data from large study areas. We have exploited these advances in computation and data availability in our modeling exercises.

Marine mammals are predators at or near the top of the food chain. Therefore, it would be desirable to focus on biological components of their habitat to describe their patterns of distribution and abundance. For example, as noted above, it is likely that their distributions are determined by the distribution of prey (Hui 1985). Unfortunately, it is extremely difficult (and often impossible) to determine prey abundance and distribution in the ocean, even with commercially important species. We currently do not have the tools to determine the distribution and abundance of these prey species at scales that are relevant to either marine mammals or the Navy. Instead, therefore, we can predict the distribution and abundance of marine mammals by using *physical* environmental parameters that are readily measured using existing technologies. For example, the distributions of many prey species of marine mammals are limited by physical oceanographic features, such as water temperature (Murawski and Finn 1988). Many prey exhibit preferences for specific temperature/depth combinations and other species are found in nutrient-rich areas along temperature fronts, such as the edge of the Gulf Stream, and density fronts, such as river plumes (Olson and Backus 1985, Laurs et al. 1984). Not surprisingly, pelagic marine mammals are found along environmental discontinuities such as thermal fronts and bathymetric changes because these are areas that concentrate prey (e.g., Davis et al. 1998, Fiedler and Reilly 1994, Kenney and Winn 1986, Hui 1985). Although we cannot measure prey densities in these areas, we can identify and describe these areas using physical parameters such as SST and sea surface height. We have incorporated a variety of these physical parameters in our analysis.

Past research has used various quantitative approaches to describe marine mammal habitats. For example, Reilly and Fiedler (1994) and Fiedler and Reilly (1994) used canonical correspondence analysis (**CCA**, ter Braak 1985) to analyze cetacean habitats in the eastern tropical Pacific (ETP) and to examine the changes in these habitats over a 15-year time series. CCA is an indirect ordination based on weighted averages which are then constrained to be expressed as a linear combination of ancillary variables (*i.e.*, environmental data) presumed to be relevant to the data. This requires *a priori* knowledge about how the species respond to environmental variables. CCA assumes that species respond unimodally and symmetrically to environmental gradients, as well as have similar modes and standard deviations (ter Braak 1986). It arranges the data based only on patterns of similarity that are internal to the data derived from iteratively computing weighted averages for species from sample scores and samples from species scores (ter Braak 1985). CCA repeats this procedure until all coefficients and scores stabilize. However, a major drawback of CCA is that it assumes that the correct environmental variables have been measured.

A potentially less-biased approach is non-metric multidimensional scaling analysis (NMDS, Kruskal 1964). **NMDS** is also an indirect ordination but it is based on pairwise sample dissimilarities and is explicitly concerned with mapping the data in reduced data space such that the distances that separate the samples in ordination space reflect at least the rank ecological order of the data, if not their actual ecological distances. In contrast to CCA, NMDS makes no assumptions about linearity, requires no underlying model of species response to environmental gradients, and does not assume any inherent dimensionality in the data. Therefore, it provides a completely unbiased estimation of the trends in the data (Kruskal 1964). All samples are ordered simultaneously and the ordination is very specific to the samples used. NMDS arranges the samples by first assigning initial ordination scores randomly and computing the distances between all pairs of samples in ordination space. These distances are then compared to the ecological distances of the samples using a non-parametric rank regression. The goodness of fit is measured by computing a normalized, rescaled sum of squared deviations (stress) ranging from 0-100. The goal is then to iteratively move all of the samples (simultaneously) in ordination space such that stress is reduced and the value converges.

Hamazaki (2002) used standard clustering methods to classify cetaceans in the western North Atlantic into habitat groups as part of a predictive model. **Hierarchical Agglomerative Clustering** (Pielou 1984, Manly 1994) initially assumes each sample is one group. The two most similar samples are then joined to form a new group. This process is repeated, first joining pairs of samples and then successively joining groups into larger clusters until all samples are one group. To obtain the most accurate amounts of ecological similarity for relativized species abundance data, one can use a Bray-Curtis dissimilarity index (Bray and Curtis 1957) to calculate the ecological distance between groups (Bloom 1981; Legendre and Legendre 1998). However, there are other indices that can be used. Clustering methods are highly sensitive to linkage methods, thus the selection of linkage methods is important. If no one community is assumed to have been sampled more than any other community in the study area, an unweighted group averaging linkage method (Sneath and Sokal 1973, Pielou 1984) can be used. This technique joins groups based on the average pairwise distances for samples in two groups. The linkage method produces a dendrogram with relatively little chaining, uses information about all samples in each group to define joinings, and is monotonic in that there can be no reversals in the dendrogram (Pielou 1984). Because agglomerative methods are sensitive to outliers, which can affect the results of the clustering process by fusing these outliers with other samples and creating “bad” groups (Pielou 1984), the results of the cluster analysis should be corroborated by plotting the clusters using an ordination.

Torres et al. (2003) used classification and regression trees (**CART**; Venables and Ripley 1997) to elucidate and predict cetacean habitat in the western mid-Atlantic. CART divides the data set into several groups (e.g., species), each of which has a different predicted value of the response variable (e.g., environmental variable). The data are recursively partitioned such that the maximum deviance in the response variable is chosen at each split. The resulting subgroups are partitioned subsequently until the final groups are relatively homogeneous. CART makes none of the assumptions of linearity, normality, homogeneity of variances, or independence of the data that many other techniques would, thus is able to give robust results in terms of how the species are related to the environment. The habitats resulting from CART analyses can be easily mapped and the model predictions can be tested using a GIS and independent data reserved for model testing.

Generalized Linear Models (GLM) regression models mainly differ from linear models in that the dependent variables do not need to be normally distributed or have homogenous variances. The independent variables must be continuous and normally distributed. The model parameters are estimated using maximum likelihood instead of ordinary least-squares. Moses and Finn (1997), Waring et al. (2001) and Hamazaki (2002) used **logistic regression** analysis, a specialized type of GLM, to predict cetacean habitats in the western North Atlantic. Logistic regression best explains the patterns seen in the dependent variable using a sigmoidal (i.e., non-linear) probabilistic function (i.e., the dependent variable is binary) that switches from one group to another at a given threshold. The dependent variable in this case is either presence or absence of a species, and the model then predicts the probability of that species being present given certain environmental conditions and thresholds of that variable where the species would be present (Legendre and Legendre 1998). Gregr and Trites (2001) used **Poisson regression**, another specialized type of GLM, to predict the critical habitats of five whale species off coastal British Columbia. Poisson regression is used if instead of predicting the presence-absence of a species, one wants to use the abundance of a species.

Forney (2000) used **Generalized Additive Models** (GAMs) to reduce the uncertainty in estimating the abundance of two small cetacean species off California relative to environmental variables. GAMs have the advantage over GLMs in that the relationship between the dependent and independent variables is not constrained to be linear or of any other shape, thus reflecting the true relationships between observations. As with GLMs, data do not need to be unimodal, gaussian or have homogenous variances. In addition, GAMs can use smoothing functions to fit non-parametric functions (Hastie and Tibshirani 1990). However, the number of degrees of freedom one chooses to use in the smoothing algorithms and the smoothing functions themselves all have profound effects on the results.

However, none of these techniques explicitly consider the spatial arrangement of the data. Location (space) is dealt with by looking at the relationships between latitude and/or longitude (or their interaction term) and the given variables. By using distance matrices and calculating the distances between all pairs of samples, **Mantel** tests eliminate the need to arbitrarily define a point of origin (departure) from which to start making spatial comparisons and incorporate space *per se*. Mantel and partial Mantel tests (Mantel 1967) are non-parametric, linear regressions between two (or more, in the case of partial Mantel tests) variables in distance matrices, each of which emphasize the variation of the variable by considering the pair wise dissimilarities between sample locations. The advantages of this approach are that the methods: (1) are non-parametric, so they do not assume any underlying model and the data do not have to be independent; and (2) account explicitly for spatial dependencies in the data. This method is generally employed as a hypothesis testing technique, not as a map prediction tool.

We explored the use of these various alternative approaches to predicting marine mammal habitats, paying particular attention to the biases and constraints of different techniques, particularly with respect to the limitations of available data. As part of our work and that of our sister project (SI-1391), we produced a manuscript describing these alternative approaches in considerable detail (Redfern et al. 2006).

3.0 Materials and Methods

Technical Objective 1. Develop and test the robustness of spatio-temporal models of marine mammal distributions as predicted by physical conditions of the marine environment.

3.1 Data Sources

3.1.1 Marine Mammal Surveys

Our project encompassed the entire U.S. Exclusive Economic Zone along the Atlantic coast and Gulf of Mexico. We focused particular effort in areas known to be important for Navy training exercises areas (*e.g.* VA Capes, Cherry Point and Charleston/Jacksonville along the Atlantic coast) (Figure 1). This allowed us to focus on areas critical to the Navy's mission and provide guidelines on appropriate regional scales for model development. We delineated three regions to allow for a hierarchical modeling approach: (1) Gulf of Mexico; (2) Southeast Atlantic (Southeast); and (3) Northeast Atlantic (Northeast). In some models, especially where there were only a small number of observations, we combined the Southeast and Northeast into an East Coast (East) model. We also explored the effects of combining observations from the Gulf of Mexico and Atlantic into a single model. We used the 5-m contour as the near-shore boundary and used the exclusive economic zone (EEZ) as the offshore boundary. These three regions were delineated based on the biogeography of the area (Ekman, 1953, Angel, 1979, MacLeod, 2000). The boundary between Northeast and Southeast corresponds to the separation between temperate and sub-tropical ecosystems at the point at which the Gulf Stream veers offshore of Cape Hatteras (Figure 1).

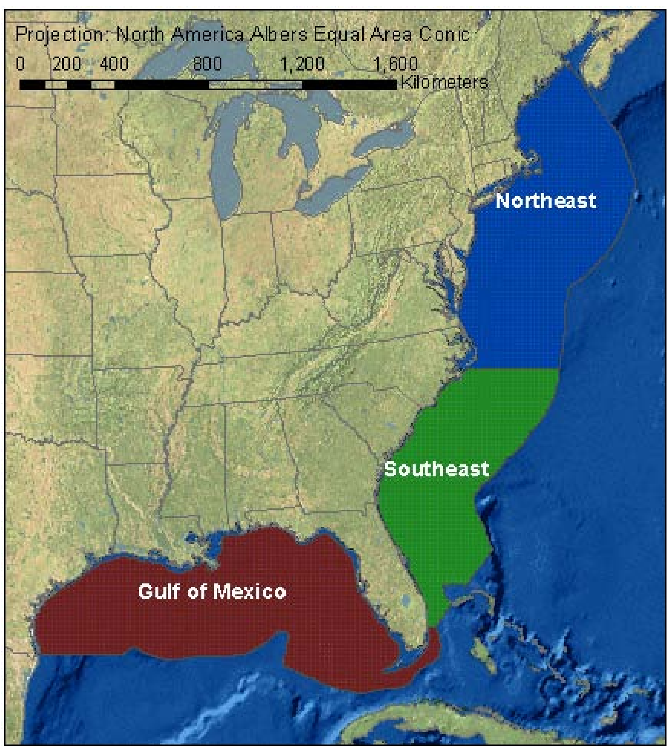

Figure 1. Study area including Gulf of Mexico, Southeast, and Northeast regions.

Within these three regions, we searched the online OBIS-SEAMAP data archive (http://seamap.env.duke.edu) for high quality data sets of marine mammal observations (Figure 2; also see Halpin et al. 2009). In general, we restricted our search to aerial and shipboard line-transect surveys of marine mammals, conducted primarily by NOAA researchers engaged in stock assessment surveys. These observations were augmented by similar surveys conducted by academic researchers, using essentially the same protocols. All these datasets included observations of survey effort (*i.e.* survey tracks) and were collected expert, professional observers; we did not use any opportunistic surveys. We restricted our search for marine mammal surveys to years after 1985, when the earliest available sea-surface temperature satellite records became available through the AVHRR Pathfinder.

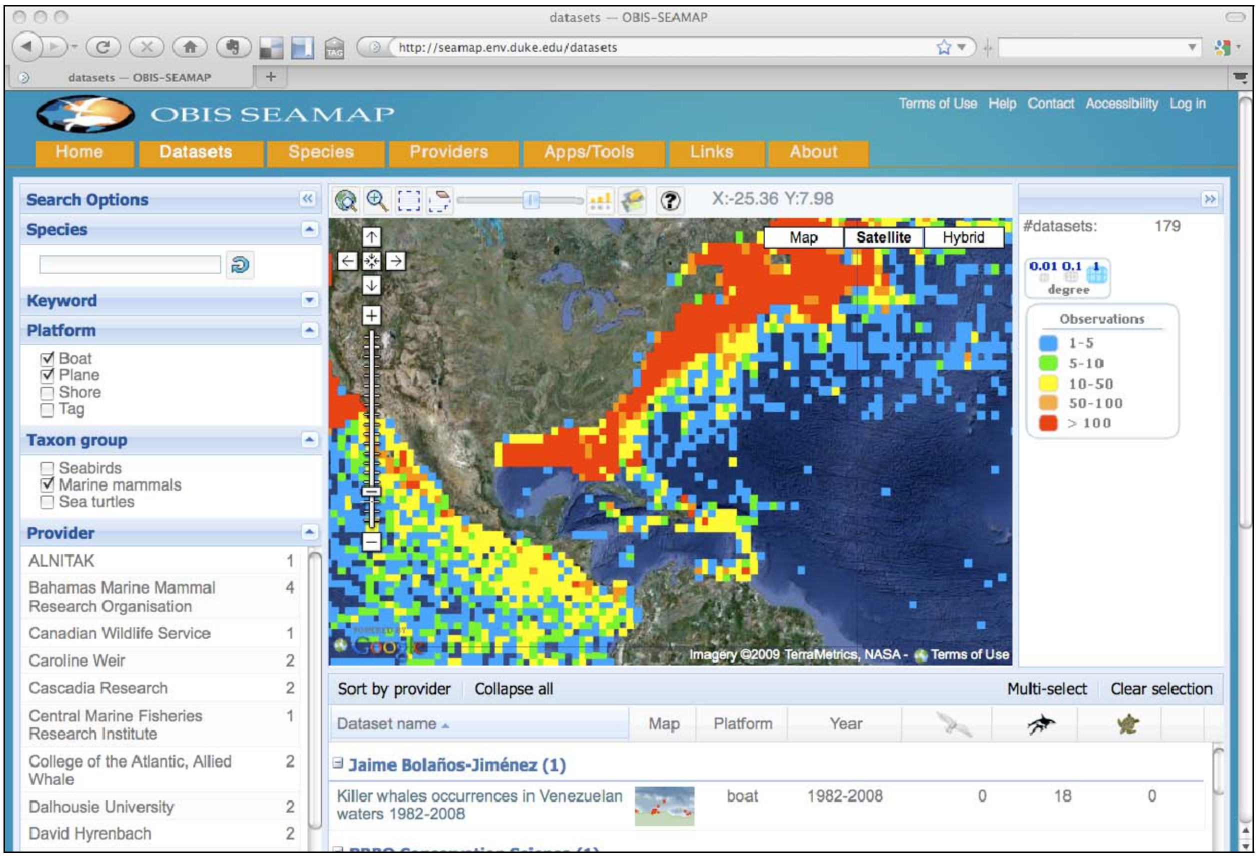

Figure 2. The OBIS-SEAMAP information system displays the spatial density of marine mammal observations based on aerial or shipboard platform surveys.

Thus, the data we used to predict habitat suitability for marine mammals came from government agencies and academic institutions that contributed to OBIS-SEAMAP. The two primary data sources were marine mammal surveys conducted by the Northeast Fisheries Science Center (NEFSC) in Woods Hole, MA and the Southeast Fisheries Science Center (SEFSC) in Miami, FL. Dr. Debra Palka and Lance Garrison, from NEFSC and SEFSC respectively, agreed to allow us to use these data in development and evaluation of our predictive models. The surveys spanned the years 1991 to 2007 and covered the entire Atlantic coast and Gulf of Mexico. These are the most extensive marine mammal survey data sets available within the U.S. east coast EEZ (Table 1).

Table 1. Survey datasets identified by provider, name, type of platform, begin/end date and number of marine mammals observed. Provider identifiers correspond to Dalhousie University (DU), Duke University Marine Lab (DUML), Northeast Fisheries Science Center (NEFSC), Southeast Fisheries Center (SEFSC), University of North Carolina Wilmington (UNCW) and the Years of the North Atlantic Humpback Whale (YoNAH) consortium.

Provider	Name	Platform	Begin	End	Mammals
DU	Sargasso cruise - sperm whale sightings	boat	2004-05-06	2004-06-15	11
DUML	Hatteras Eddy Cruise 2004	boat	2004-08-15	2004-08-19	20
	Summer 2004 and Winter 2005 Cape Hatteras	boat	2004-08-04	2005-02-02	70
	Vessel-Based Surveys for proposed Onslow Bay USWTR site	boat	2007-06-07	2007-11-20	23
NEFSC	Aerial Circle-Back Abundance Survey 2004	plane	2004-06-13	2004-07-12	287
	Aerial Survey - Experimental 2002	plane	2002-07-20	2002-08-10	332
	Aerial Survey - Summer 1995	plane	1995-08-05	1995-09-17	304
	Aerial Survey - Summer 1998	plane	1998-07-19	1998-08-20	422
	Harbor Porpoise Survey 1991	boat	1991-07-24	1991-08-27	770
	Harbor Porpoise Survey 1992	boat	1992-07-31	1992-09-05	1,238
	Joint Deepwater Systematics and Marine Mammal Survey	boat	2002-07-18	2002-08-01	105
	Marine Mammal Abundance Survey - Leg 1	boat	1995-07-10	1995-08-02	433
	Marine Mammal Abundance Survey - Leg 2	boat	1995-08-09	1995-09-05	153
	Marine Mammal Survey 1991-10	boat	1991-10-13	1991-10-24	80
	Marine Mammal Survey 1992	boat	1999-07-29	1999-08-27	1,021
	Marine Mammal Survey 1997	boat	1997-08-23	1997-09-04	60
	Marine Mammal Survey 1998, Part 1	boat	1998-07-08	1998-08-03	492
	Marine Mammal Survey 1998, Part 2	boat	1998-08-09	1998-08-31	309
	Mid-Atlantic Marine Mammal Abundance Survey 2004	boat	2004-06-24	2004-08-03	522
	Summer Marine Mammal Survey 1995, Part I	boat	1995-07-11	1995-08-01	150
	Summer Marine Mammal Survey 1995, Part II	boat	1995-08-07	1995-09-04	1,401
SEFSC	Atlantic Cetacean Survey 1992	boat	1992-01-04	1992-02-10	77
	Atlantic Cetacean Survey 1999	boat	1999-08-09	1999-09-25	236
	Atlantic surveys, 1998	boat	1998-07-09	1998-08-20	287
	Caribbean Survey 2000	boat	2000-02-17	2000-04-02	196
	Eastern Gulf of Mexico Marine Mammal Survey 1994	boat	1994-08-16	1994-09-08	305
	Gulf of Mexico Marine Mammal Survey 1992; Sightings	boat	1992-04-22	1992-06-07	270
	Gulf of Mexico Marine Mammal Survey 1993 (S)	boat	1993-05-04	1993-06-15	271
	Gulf of Mexico Marine Mammal Survey 1993 (W)	boat	1993-01-06	1993-02-12	45
	Gulf of Mexico Marine Mammal Survey 1994	boat	1994-04-16	1994-06-09	286
	Gulf of Mexico Shelf 2001	boat	2001-08-31	2001-09-28	225
	Mid-Atlantic Tursiops Surveys 1995 (1)	plane	1995-07-13	1995-07-23	47
	Mid-Atlantic Tursiops Surveys 1995 (3)	plane	1995-07-31	1995-08-13	46
	Mid-Mid Atlantic Tursiops Surveys 1995 (2)	plane	1995-07-24	1995-07-31	50
	Northern Gulf of Mexico Cetacean Survey 1998	boat	1998-09-07	1998-09-24	42
	Northern Gulf of Mexico Marine Mammal Survey 2000	boat	2000-09-07	2000-10-01	84
	Oceanic Gulf of Mexico Cetacean Survey 1996	boat	1996-04-17	1996-06-08	536
	Oceanic Gulf of Mexico Cetacean Survey 1997	boat	1997-04-17	1997-06-09	268
	Oceanic Gulf of Mexico Cetacean Survey 1999	boat	1999-04-23	1999-06-01	217
	Oceanic Gulf of Mexico Cetacean Survey 2000	boat	2000-04-20	2000-05-29	198
	Oceanic Gulf of Mexico Cetacean Survey 2001	boat	2001-04-18	2001-05-30	181
	Southeast Cetacean Aerial Survey 1992	plane	1992-01-20	1992-03-02	263
	Southeast Cetacean Aerial Survey 1995	plane	1995-01-27	1995-03-06	176
	Gomex Sperm Whale Survey 2000	boat	2000-06-28	2000-07-26	278
UNCW	2008 Right Whale Aerial Surveys	plane	2008-02-02	2008-06-14	565
	Aerial Survey 98-99	plane	1998-09-14	1999-10-30	177
	Aerial Surveys for proposed Onslow Bay USWTR site - Left	plane	2007-06-26	2007-12-11	10
	Aerial Surveys for proposed Onslow Bay USWTR site - Right	plane	2007-06-26	2007-12-11	16
	Marine Mammal Aerial Surveys 2006-2007	plane	2006-12-05	2007-05-02	929
	Marine Mammal Sightings, Southeastern US 2001	plane	2001-02-06	2001-03-02	402
	Right Whale Aerial Survey 05-06	plane	2005-10-27	2006-04-20	690

Provider	Name	Platform	Begin	End	Mammals
YoNAH	The Years of the North Atlantic Humpback Whale	boat	1992-01-15	1993-12-08	4,215

Despite this compilation of data sets, sample sizes were inadequate to build separate habitat suitability models for each species, so we grouped species at various taxonomic levels to create species *guilds*. Each guild was established using information on species distributions, interactions and other expert knowledge. Each guild was compared to the ordination results for validation. The final cetacean guilds we used in models of habitat suitability include: baleen whales (*Balaenoptera* spp.), humpback whale (*Megaptera novaeangliae*), right whale (*Eubalena glacialis*) beaked whales, sperm whale (*Physeter macrocephalus*), pygmy and dwarf sperm whales (*Kogia* spp.), killer whales, pilot whales (*Globicephala* spp.), Lags (*Lagenorhynchus* spp.), common dolphins (*Delphinus* spp.), striped dolphin (*Stenella coeruleoalba*), pantropical spotted dolphin (*Stenella attenuate*), spotted dolphin (*Stenella frontalis*), bottlenose dolphin (*Tursiops truncatus*), and harbor porpoise (*Phocoeana phocoena*) (Table 2).

Table 2. Taxonomic members of cetacean guilds

Guild name	**Scientific name**	**Common Name**
Baleen whales	*Balaenoptera* spp.	Baleen whales
	Balaenoptera acutorostrata	Minke whale
	Balaenoptera borealis	Sei whale
	Balaenoptera edeni	Bryde’s whale
	Balaenoptera musculus	Blue whale
	Balaenoptera physalus	Fin whale
Humpback whale	*Megaptera novaeangliae*	Humpback whale
Right whale	*Eubalena glacialis*	North Atlantic right whale
Beaked whales	*Berardius bairdii*	Baird's beaked whale
	Hyperodon ampullatus	North Atlantic bottlenose whale
	Mesoplodon spp.	Beaked whales
	Mesoplodon bidens	Sowerby’s beaked whale
	Mesoplodon densirostris	Blainville’s beaked whale
	Mesoplodon europaeus	Gervais’ beaked whale
	Mesoplodon mirus	True’s beaked whale
	Ziphiidae	Beaked whales
	Ziphius	Goose-beaked whales
	Ziphius cavirostris	Cuvier’s beaked whale
Sperm whale	*Physeter macrocephalus*	Sperm whale
Kogia	*Kogia* spp.	Kogia
	Kogia breviceps	Pygmy sperm whale
	Kogia sima	Dwarf sperm whale
Killer whale	*Orcinus orca*	Killer whale
	Feresa attenuate	Pygmy killer whale
	Peponocephala electra	Melon-headed whale
	Pseudorca crassidens	False killer whale
Pilot whales	*Globicephala* spp.	Pilot whales
	Globicephala macrorhynchus	Short-finned pilot whale

Guild name	Scientific name	Common Name
	Globicephala melas	Long-finned pilot whale
Lags	*Lagenorhynchus* spp.	White-beaked dolphins
	Lagenorhynchus acutus	Atlantic white-sided dolphin
	Lagenorhynchus albirostris	White-beaked dolphin
Common dolphins	*Delphinus* spp.	Common dolphin
	Delphinus delphis	Common dolphin
Stenella	*Stenella clymene*	Short-snouted spinner dolphin
	Stenella longirostris	Spinner dolphin
Stenella coeruleoalba	*Stenella coeruleoalba*	Striped dolphin
Stenella attenuata	*Stenella attenuata*	Pantropical spotted dolphin
Stenella frontalis	*Stenella frontalis*	Atlantic spotted dolphin
Tursiops truncatus	*Tursiops truncatus*	Bottlenose dolphin
Harbor porpoise	*Phocoena phocoena*	Harbor porpoise

3.1.2 Environmental Data

The environmental data layers we used to construct the habitat models are a combination of static, dynamic and derived variables (see Table 3), all of which have been shown to be useful predictor variables for marine mammal habitats (Redfern et al. 2006). The General Bathymetric Chart of the Oceans (GEBCO)[1] provides a 1-minute global bathymetric surface for the static variable depth. The 200 meter contour from this grid is used for deriving distance from the continental shelf with the ArcGIS function EucDistance. The final benthic variable, distance from shore, is taken as the Euclidean distance from the NOAA Global Self-consistent, Hierarchical, High-resolution Shoreline Database (GSHHS)[2]. All surface layers were converted to the Lambert Equal-Area projection for consistency the representation of area.

We retrieved temporally dynamic environmental data, such as sea-surface temperature and ocean surface chlorophyll, from various online oceanographic archives. These data were initially accessed via FTP from national data centers by developing automated batch processing data collection scripts. Standard scientific data formats such as NetCDF and HDF files were converted to ArcGIS grids for sampling both marine mammal observations and observer platform effort. The most recent version of our automated data sampling process retrieves these data using the OPeNDAP protocols and data transfer process, which can subset the data before transfer over the internet (Cornillon et al. 2003). The remotely sensed oceanographic covariates used to develop the predictive habitat models have limitations in terms of availability. We have summarized the availability of remotely sensed oceanographic data with respect in time to the observations (Figure 3). Continuous sea-surface temperature satellite data from various satellites, e.g. AVHRR Pathfinder, have been available since 1981, but remotely sensed chlorophyll measurements suffered a large gap between the Coastal Zone Color Scanner (1978 - 1986) and SeaWIFS (1997 – present).

[1] http://gebco.net
[2] http://ngdc.noaa.gov/mgg/shorelines/gshhs.html

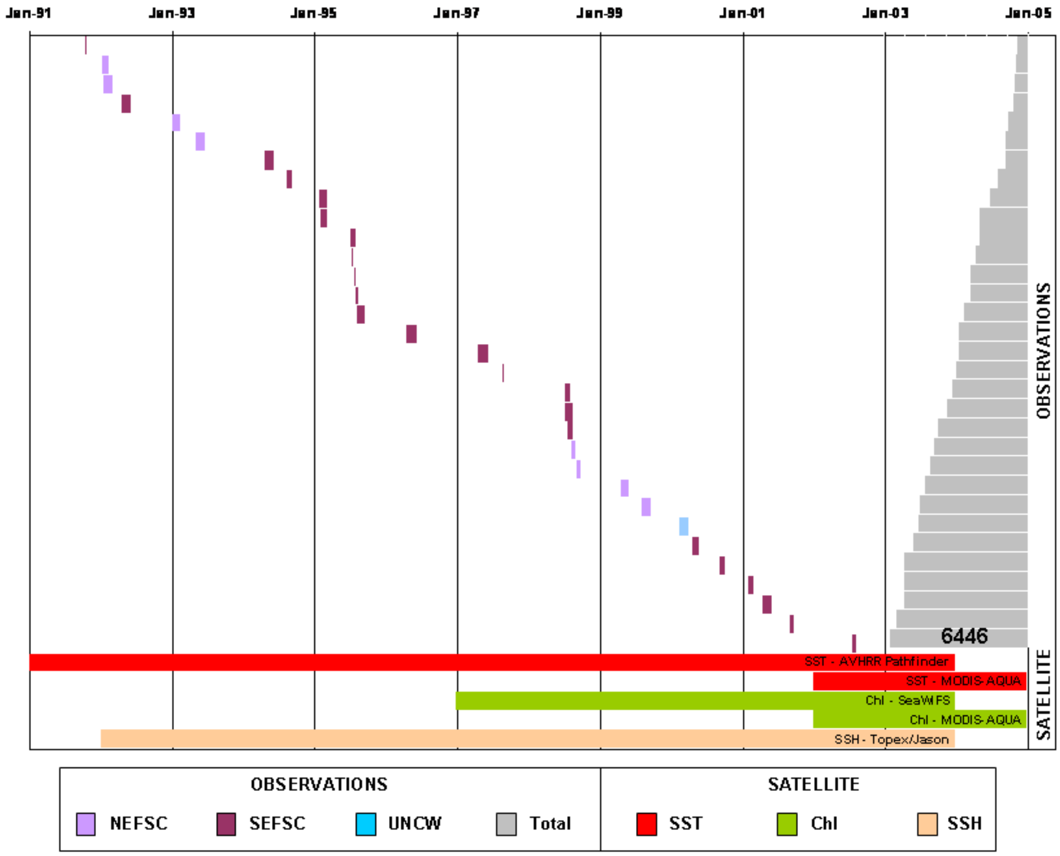

Figure 3. Availability of satellite data coincident in time with observations from specific dataset providers up to 2005. Cumulative observations are shaded in grey.

The Chlorophyll a product from the SeaWIFS satellite platform, also from JPL PO.DAAC, and the distance from a significant patches of high chlorophyll concentrations were similarly sampled. However, we did not use this data as a predictor variable in the habitat model since: the satellite was not operational until 1997 which would require us to discard of earlier observations, and oceanographic forecast models do not presently predict chlorophyll. In order for the fitted models to be useful for forecasting, similar environmental variables need to be available for future forecasting.

Table 3. Dynamic Oceanographic Satellite Data Extent and Resolution.

Variable	Satellite	Extent		Resolution		Source
		Time	Space	Time	Space	
SST	AVHRR Pathfinder	'85-'04	Global	8d/m	9km	JPL PODAAC
	MODIS-AQUA	'02-'05	Global	8d/m	4km	GSFC OceanColor
Chl	SeaWiFS	'97-'04	Global	8d/m	9km	GSFC OceanColor
	MODIS-AQUA	'02-'05	Global	8d/m	4km	GSFC OceanColor
SSH	Topex/Jason	'92-'04	Global	8d	9km	AVISO

In order to build reasonable environmental models we needed to synchronize the sampling of sea-surface temperatures (SST) with the same time periods when marine mammals where observed. In order to develop this time-synchronous data set, we sampled through the monthly and 8-day AVHRR Pathfinder SST version 5 satellite data product available through the JPL PO.DAAC[3] data center.

In addition to the development of time-synchronous SST data we also developed analytical products depicting oceanographic features such as sea-surface temperature fronts. Sea surface temperature fronts were developed by identifying areas of significant change in temperature gradient versus spatial distance. These distinctive ridges in surface temperature are assumed to relate to differences in water masses. In addition, these frontal areas are hypothesized to be potentially important in the development of highly productive areas and the aggregation of prey species. The boundaries between distinct temperature zones produce linear geographic features. In order to relate these linear features to marine mammal locations, a secondary analysis of the distance from fronts was calculated. A distance to SST front was further derived for each applicable time period within ArcGIS by: applying the BoundaryClean function to the SST, deriving the Slope, creating a binary raster grid for all values greater than one standard deviation above the mean slope, thinning this raster, using the PolyLine function to generate linear front features, and finally deriving the Euclidean distance from fronts using the EucDistance function.

Covariates of season and latitude from the observation date and location were used as predictor variables (Table 4). These seasonal and latitudinal covariates allow for more specific separation of species habitats based on seasonal or regional variations in marine mammal populations or seasonal migrations. The four seasons were developed as ordinal variables defined as: winter (1, December to February); spring (2, March to May), summer (3, June to August) and fall (4, September to November). Marine mammal observation effort and observer data are not evenly distributed across seasons in the Atlantic and Gulf of Mexico regions. Data analysis and model selection were often limited to summer seasons due to data limitations.

Table 4. Predictor variables used to fit habitat models.

Variable	**Category**	**Type**	**Resolution**	**Source**
Season	NA	Ordinal	NA	NA
Latitude	NA	Continuous	NA	NA
Depth	Static	Continuous	1 minute	GEBCO
Distance from Shelf (200m isobath)	Static, Derived	Continuous	1 minute	GEBCO
Distance from Coast	Static, Derived	Continuous	Vector	GSHHS
Sea-Surface Temperature (SST)	Dynamic	Continuous	8-day/Monthly, 4km	AVHRR Pathfinder (JPL PO.DAAC)
Distance to SST Fronts	Dynamic, Derived	Continuous	8-day/Monthly, 4km	AVHRR Pathfinder (JPL PO.DAAC)

[3] http://podaaB-www.jpl.nasa.gov/cgi-bin/dcatalog/fam_summary.pl?sst+pfsst

A 10km x 10km sampling grid was generated within the study area in order to consistently sample and aggregate the environmental covariates. This sampling grid was bounded with the 10m contour nearshore and the US Exclusive Economic Zone (EEZ) offshore and included regional Naval Operating Areas. Edge cells less than half the full (10km x 10km) size were removed to avoid slivers and sampling problems. The midpoints of these cells were then used to sample the underlying environmental data.

3.2 Modeling Framework

Developing marine mammal habitat model outputs followed five general steps: (1) gathering observations of marine mammals and associated survey effort; (2) sampling of date-synchronous environmental data; (3) fitting multivariate statistical models to the data; (4) predicting habitat from the models across a seascape with time-specific environmental conditions; and (5) presentation of results within a spatial decision support system (SDSS). We have summarized these processes by a conceptual workflow in Figure 4. Our incorporation of geospatial web services for gathering of the marine mammal datasets and remotely-sensed environmental imagery enabled a standardized, automated approach as new data became available online.

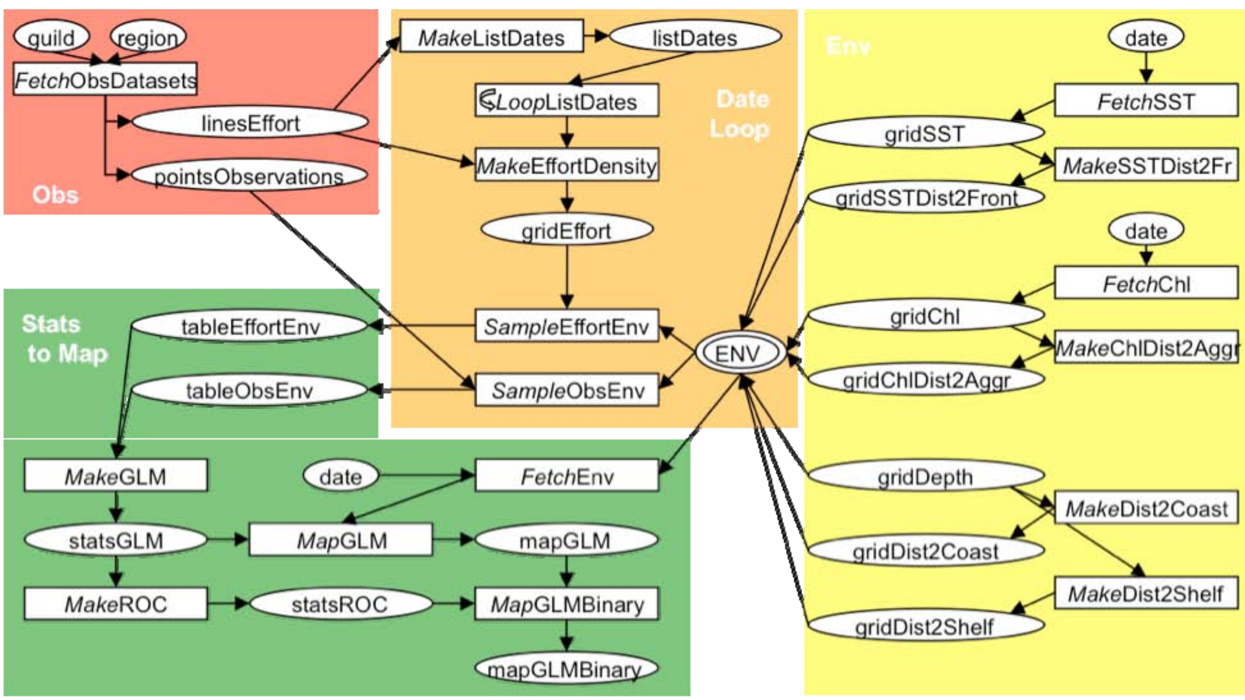

Figure 4. Scientific workflow to process survey effort and marine mammal observations with subsequent spatial sampling of date-synchronous environmental data and habitat modeling.

In our analysis, a lack of a visual observation of a marine mammal in a particular point in time and space cannot be considered a true absence, as animals could be present below the surface, In contrast, however, a confirmed sighting indicates a definite encounter in a particular habitat. Random sampling across the entire study area would under-predict presence in areas in which animals may have been present, but were simply not surveyed. Therefore, we used only the on-effort portions of ship and aerial survey tracks, or line segments, to sample the time-synchronous background environment for all marine mammal datasets. In addition to developing environmental data matched to time-synchronous observations of marine mammals, we developed an equal number of pseudo-absence data points to compare with the true observations. These pseudo-absence sampling locations were developed by sampling locations along on-effort survey tracks where no marine mammals were observed to provide a contrasting data set for analysis.

We used a table of environmental data containing absence or presence and the associated environmental data as the input to fit several multivariate logistic regression techniques: generalized linear model (GLM), generalized additive model (GAM) and a classification and regression tree (CART). As noted above, a GLM generally assumes a linear relationship between the environmental predictor and response, in this case likelihood of encounter varying between 0 (absence) and 1 (presence). A GAM allows for non-linear relationships, which can increase the predictive strength of the fit but also risks over-fitting the model and can introduce complexities not easily explained ecologically (Austin 2007). For both these techniques, we used the Akaike's Information Criterion (AIC) within the R statistical analysis software package to select the most parsimonious model amongst all possible variable combinations.

In contrast, the CART model method is based on a rule-based classification approach where the data are bifurcated based on the level deviance explained. We used minimal cross-validation error process to "prune" the CART decision trees for model selection. For a more in-depth review of these techniques see Redfern et al. (2006) for applications specific to marine mammals and Guisan and Zimmermann (2000) for habitat modeling in general.

Once we built the multivariate regression model based on the presence and pseudo-absence point data, we used this model to predict the likelihood of encounter across the seascape for a set of environmental conditions specific in time, such as the past, current or forecast conditions. When predicting likelihood of presence for a single point of data in multivariate space, the further the predictors are from the data used to build the model, the higher the associated error with that prediction. For instance, most of our survey data were observed in coastal waters. So if distance to shore is a significant variable distinguishing between presence and absence in the fitted model, the further offshore we moved beyond the surveyed area, the higher the prediction error. For this reason, we offered a prediction presence map masked by prediction error beyond 1 standard error.

We also felt that it might be useful to create a binary representation of predicted habitat, i.e. habitat and non-habitat. Receiver Operating Characteristic (ROC) curves can be used to define a cutoff value for conversion of a likelihood surface that continuously ranges from 0 to 1 into a binary surface of 0 and 1 (i.e. binary habitat vs. non-habitat areas) (Fielding and Bell 1997). These curves define the relationship between the fitted models prediction of false absence rates vs. false presence rates from the original data. A null model would theoretically form an equal relationship, or graphically a diagonal straight line, between false predictions of absence vs. presence. The greatest deviation from this relationship, i.e. the lowest rate of false absence vs. presence, determines the optimal cutoff. For species of particular concern (such as highly endangered right whales), this optimal cutoff may be too low for environmental management and can be shifted to make more allowance for falsely predicting absence but not presence.

In our final model selection we employed Generalized Additive Models or GAMs (Wood, 2006) to relate the environment to the presence of animals. Each cell from the sampling grid provided a row or record in of data set. The area of the cell was the offset and the amount of time observers spent in the cell surveying the weight. This weighting process allows datasets from both ship and aircraft to be utilized within the habitat modeling process, using time spent surveying as the common denominator. There are several methods available to fit models to data. GAMs allow for smoothed splines to be fit through each predictor variable. This process can potentially over-fit the data. We restricted this spline fitting process to 5 knots (i.e. inflection points) so that they are more ecologically sensible.

We linked probability of presence ($\hat{P}$) to the sum of predictor variables (*z*) over all cells (*i*) and predictors (*z*), using a logarithmic link function:

$$\hat{P}_i = \exp\left[\alpha + \sum_{k=1}^{q} s_k(z_{ik}) + \log(a_i)\right] + e_i \quad (1)$$

where the predictor variables, z_{ik} , fitted by a smoothing function s_k, are summed with offset (*a*) and error (*e*) terms.

We used a quasi-binomial distribution to model the binary response to allow for dispersion, i.e. many zeros or absences. Simpler models with fewer knots were encouraged with a slightly higher gamma term than the default (1.2) and the use of thin-plate splines with shrinkage (`bs='ts'`) was increased to prefer smoother fits with fewer knots. In practice, the R statistical modeling formulation is:

```
gam(presence ~ s(log(depth),k=5,bs='ts') + s(d2shelf2,k=5,bs='ts')
               + s(log(d2coast),k=5,bs='ts') + s(sst,k=5,bs='ts'),
    data=dat, family=quasibinomial(link='logit'), weights=eff, gamma=1.4)
```

We examined each model output for accuracy based on existing knowledge of species distributions, error rates and Generalized Additive Model (GAM) output. We first eliminated from consideration any models developed with fewer than 10 observations. Second, each model was compared with prior information regarding the distribution of species and guilds. This allowed us to identify models with highly erroneous predicted species distributions. Third, we examined models where some portion of the distribution had an especially high standard error. Finally, we reviewed the GAM results for each model, investigating the relationship between species distribution and each individual environmental parameter. Our review process allowed us to reject model outputs that were statistically weak or erroneous.

3.3 Ordination

We used the combined data set on the distribution of marine mammals from Maine to the Gulf of Mexico to examine macro-scale patterns of community structure. We applied non-metric dimensional scaling, group contrast mantel tests, and classification and regression trees to construct a Q-type ordination of the species data, test for group structure that exists within the ordination, and determine how these groups differed in environmental space. We constructed ordinations in the three regions identified above: the Gulf of Mexico, oceanic waters south of Cape Hatteras NC (Southeastern), and oceanic waters north of Cape Hatteras (Northeastern). We paid close attention to the beaked whales in the Northeastern region by testing the effect of adding or subtracting various species to this guild. We quantified the environmental relationships among groups in these communities, and for management purposes, we quantified the effect of identifying sightings at sea to different taxonomic levels.

We used methods laid out in Field et al. (1982), Clarke (1993), and Urban et al. (2002) to perform a multivariate analysis of these species data. We were working at significantly larger spatial scales than most community ecologists operate at, so we followed closely the methods of Urban et al. (2002). In short, after assembling the database(s), we performed a non-metric multidimensional scaling (NMDS) analysis of the community data, which we plotted on top of interpolated environmental surfaces. Following this ordination, we used group contrast Mantel tests and hierarchical clustering techniques to find optimal groupings in the species assemblages. Finally, we used classification and regression tree analysis to assess how these groups are different in environmental space.

At each sighting we extracted spatially and temporally specific environmental information (see Best et al., 2007 and 3.2 Modeling Framework). Specifically, we used R (Ihaka and Gentleman, 1996) to co-locate the position of the sighting with each of five environmental layers: (1) sea surface temperature (SST); (2) Chlorophyll concentration; (3) bottom depth; (4) distance to continental shelf; and (5) distance to shore. For the temporally dynamic layers, we took the SST and chlorophyll data from PODAAC (Best et al., 2007). For the static layers, we calculated derived variables, such as distances to specific features, using standard GIS processing techniques, e.g. Euclidean distance to a line feature. To perform a traditional multivariate analysis we assembled a sites-by-species matrix. First, we created a spatial layer of 50 km wide hexagons (Figure 5, Figure 6).

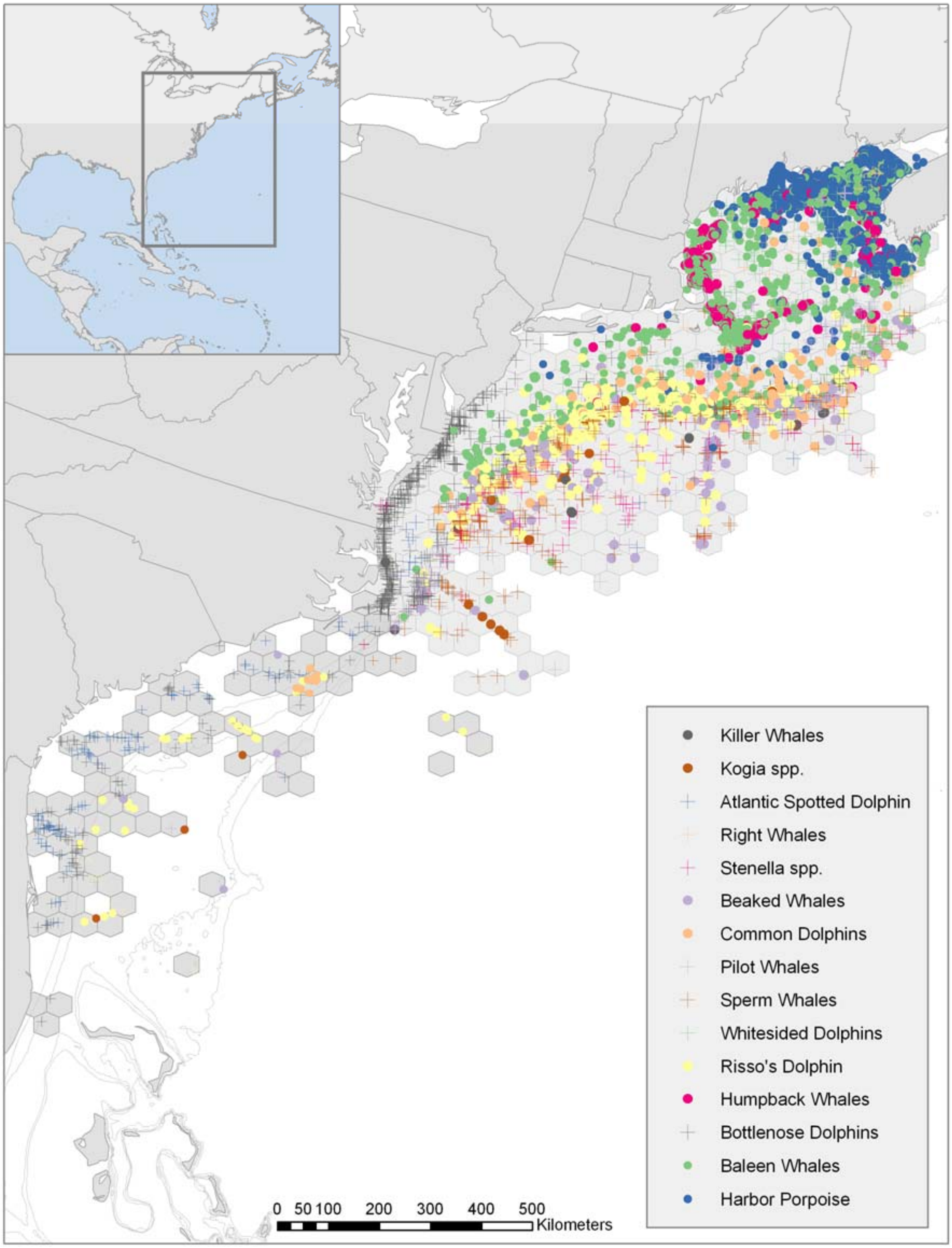

Figure 5. Overview figure for the Northeastern (NOH) and the Southeastern (SOH) regions. Sampling hexagons are depicted in light grey (NOH), and dark grey (SOH). Sightings are depicted at the taxonomic guild level with different color and symbols. Contour lines (200, 500, 1000, 2000 m) are shown in light grey.

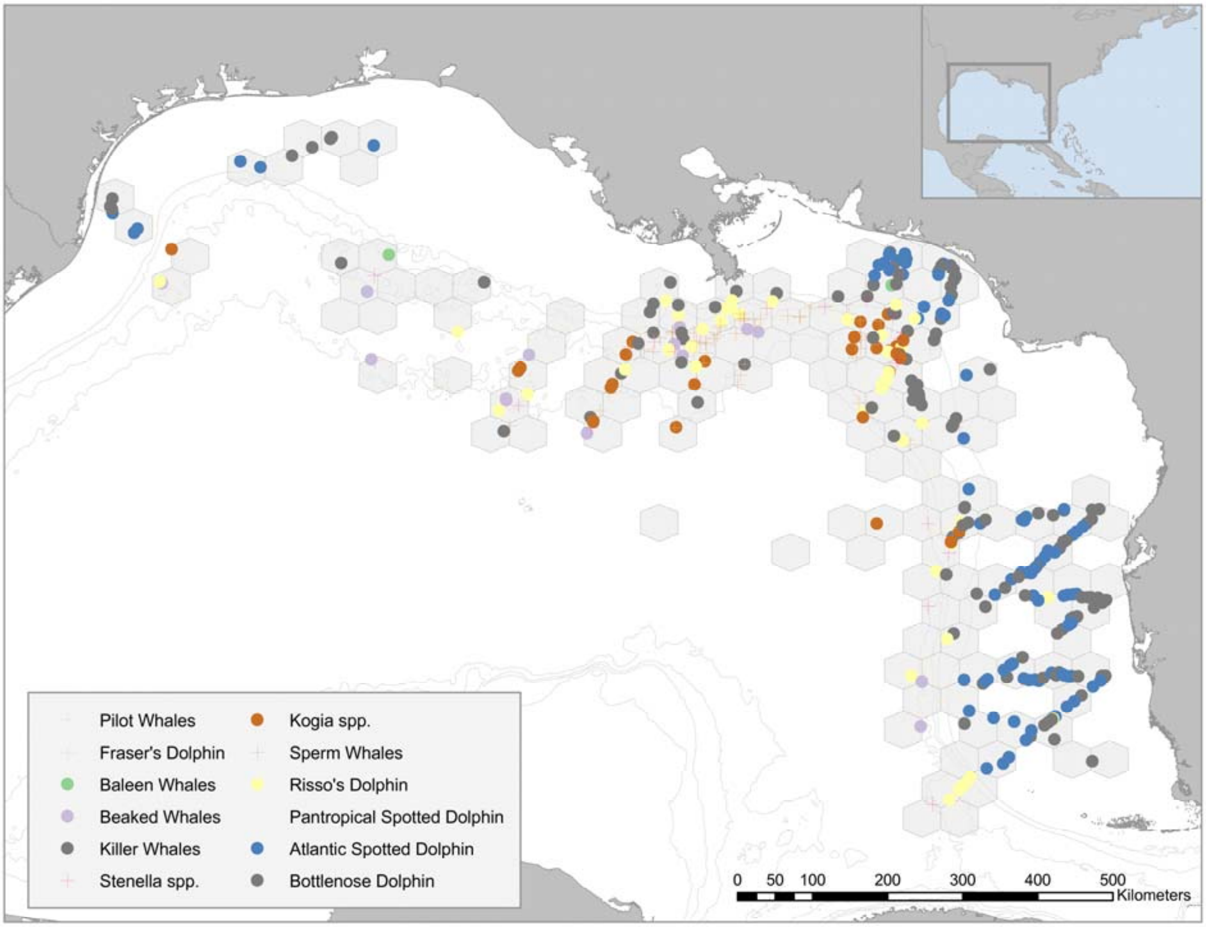

Figure 6. Overview figure for the Gulf of Mexico (GOM). Sampling hexagons are depicted in dark grey, and sightings are depicted at the taxonomic guild level with different color and symbols. Contour lines (200, 500, 1000, 2000 m) are shown in light grey.

We then intersected these hexagons with the sightings data to create a presence-absence data matrix comprised of site ID (rows) and species present on that site (columns). We created an index of sighting frequency or rarity, which was used to ensure convergence in certain ordinations. That is, in certain cases with a few sightings of extremely rare species, the ordination would fail to converge. We limited our ordination to the “summer” season, defined as June through August. We chose this temporal extent because most of the data originated in these months. We created a climatological average of the species composition during summer over all years. We acknowledge the crucial role time plays in marine systems, but the data are limited, especially in non-summer months and so we were unable to examine the temporal progression of species in ordination space over time (within and across years).

In this analysis we used the same three bio-geographic identified in Section 3.1.1: the Gulf of Mexico (GOM); Southeastern (SOH); and Northeastern (NOH); (Figure 5, Figure 6). For the NOH region we prepared data frames both with and without rare species (the latter defined as seen in fewer than 5% of the sites) (See Appendix C: Tabular Summary for Ordination Groups for a full description). The ordination for the GOM and SOH regions would only converge once rare species were removed (see next section for details).

We used the vegan package (http://cc.oulu.fi/~jarioksa/softhelp/vegan.html, last accessed 4 January 2009) in R (Ihaka and Gentleman, 1996) to perform a traditional Q-type analysis using non-metric multidimensional scaling (NMDS). NMDS uses distance algorithms to “place” species in ordination space; accordingly one needs a distance or dissimilarity matrix to complete the analysis. We used the Jaccard dissimilarity metric on the sites by species data frame. We then ran several exploratory NMDS analyses to assess dimensionality of the final solution. Specifically, we iterated from one to five dimensions for the ordination, and ran the algorithm until convergence was reached. We then plotted dimensions versus stress to look for ‘elbows,’ or places where increasing the dimensions fails to greatly reduce the stress (results not shown). In each of the ordinations, we settled on a three-dimensional solution. In summary, for the NOH region we ran a 3-D NMDS ordination for all species and for common species only (*i.e.* all rare species removed). For both SOH and GOM, we ran 3-D NMDS ordinations for common species only. (See summary tables in Appendix C: Tabular Summary for Ordination Groups. These tables include the “rarity” score of each species in each bio-geographic region).

One of our primary goals in this analysis was to determine whether or not natural groups existed in the marine mammal species data. Typically when performing this analysis, one looks for groups of sites and then the indicator species that characterize those sites (McCune et al., 2002). Alternatively, one can look for groups in the species data by examining the transpose of the sites by species matrix. We pursued the latter strategy, for two reasons: (1) we were using presence-absence data and indicator species analysis requires abundance data; and (2) for habitat modeling with data-poor species we were interested in whether natural groups exist that could increase our sample sizes. To find these groups, we iteratively conducted a group-contrast Mantel test (Urban et al., 2002) between the species distance in the sites-by-species matrix and the group distance generated by hierarchical agglomerative clustering with the goal of finding the highest Mantel R value. A high Mantel R, or correlation value, represents the optimal number of groups in the data in species space.

Our process was as follows. First, we created a species distance matrix using the Jaccard measure of dissimilarity. This distance matrix shows how dissimilar species are from one another in terms of their position in species space. Second, we created a group membership vector using hierarchical agglomerative clustering with group average linkages. This vector denotes which species belongs to which group. Finally, we ran a Mantel test between these two distance matrices and recorded the Mantel R coefficient. In other words, this test determines whether the distance in species space corresponds to the distance between groups, thereby highlighting the “among” to “within” group contrast. In theory, there are an optimal number of groups that maximizes the correlation between these distances. To estimate this maximum, we iterated over all possible numbers of groups, i.e., from two groups up to the number of species seen in the region, recording the Mantel R at each point. (Though we did not use the p-values, the Mantel R values were generated with n=10,000 randomizations.) Plotting Mantel R against the number of groups yields the “optimal” number of groups present in the species data (Figure 7). Following this finding, we then created the actual group membership vector by specifying the number of groups in the k-means clustering algorithm. This grouping is used in two subsequent analyses: 1) to denote group membership in the ordinations; and 2) the classification and regression tree (CART) analysis of environmental differences among groups in species space.

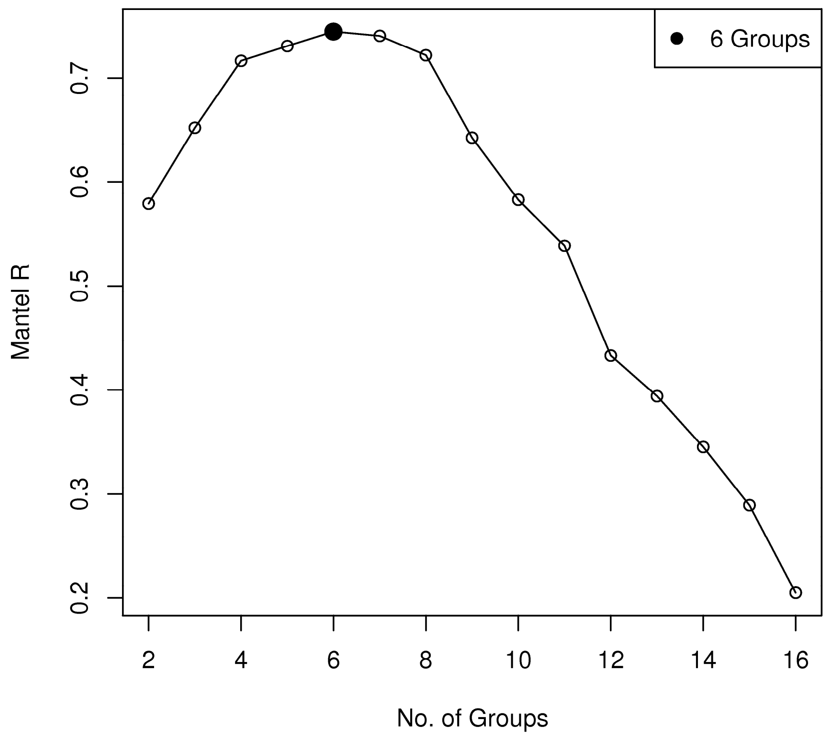

Figure 7. Results from iterative group contrast Mantel tests between distance in species space and group space (see text for details). In this example, we ran this test incrementing upward the number of potential groups in the species data from 2 to the total number of species seen in the region. At each step, the Mantel R coefficient was recorded, and we chose the highest R to correspond to the "optimal" number of groups present in the species data. Here 6 groups were chosen.

Once group membership was determined we ran a series of classification and regression tree (CART) analyses (*sensu* Urban et al. 2002) to determine which environmental factors patterned the different groups. Before running the CART, we merged the group membership vector with the raw environmental data for each species sighting. We used the rpart library in R (Ihaka and Gentleman, 1996) to create classification trees depicting group membership as a function of the environmental variables. This yields a summary of the groups in the data, and the quantitative values of the variables that controlled the split, e.g. group 2 is found in water deeper than 185 m, while group 1 is found in water shallower than 185 m, etc. All of these data exhibit varying degrees of spatial autocorrelation, so we used partial Mantel tests to test group membership as predicted by the environmental variables while controlling for spatial autocorrelation (Urban et al., 2002). These tests help to determine whether species in the same groups are also found in similar environments.

Several of the species present in the three regions are fairly cryptic and are particularly difficult to identify to the species level. This is especially true for some of the beaked whales (MacLeod, 2000, Macleod et al., 2006, Macleod and Mitchell, 2006). Due to this problem, and sometimes to increase the statistical power of surveys, researchers often lump beaked whales (Waring et al., 2001). We tested the effects of classifying sightings at different taxonomic levels by running the NOH ordination first with all sightings were at the species level and then when sightings were lumped at higher taxonomic levels. For example, we examined three species groups of beaked whales separately (Sowerby's, Cuvier's and unknown beaked whales) and then lumped all beaked whales together in one group.

3.4 Spatial Decision Support System

To facilitate the use and analysis of the model outputs by environmental planners and other researchers, we developed a single, online interface that allows visualization of the outputs, together with a toolbox for analyses. We developed a browser-based spatial decision support system (SDSS) that enables viewing of original survey effort, marine mammal observations, and model results (http://seamap.env.duke.edu/prod/serdp/serdp_map.php; The complete online help is available in the page, under [Help] tab; Figure 8).

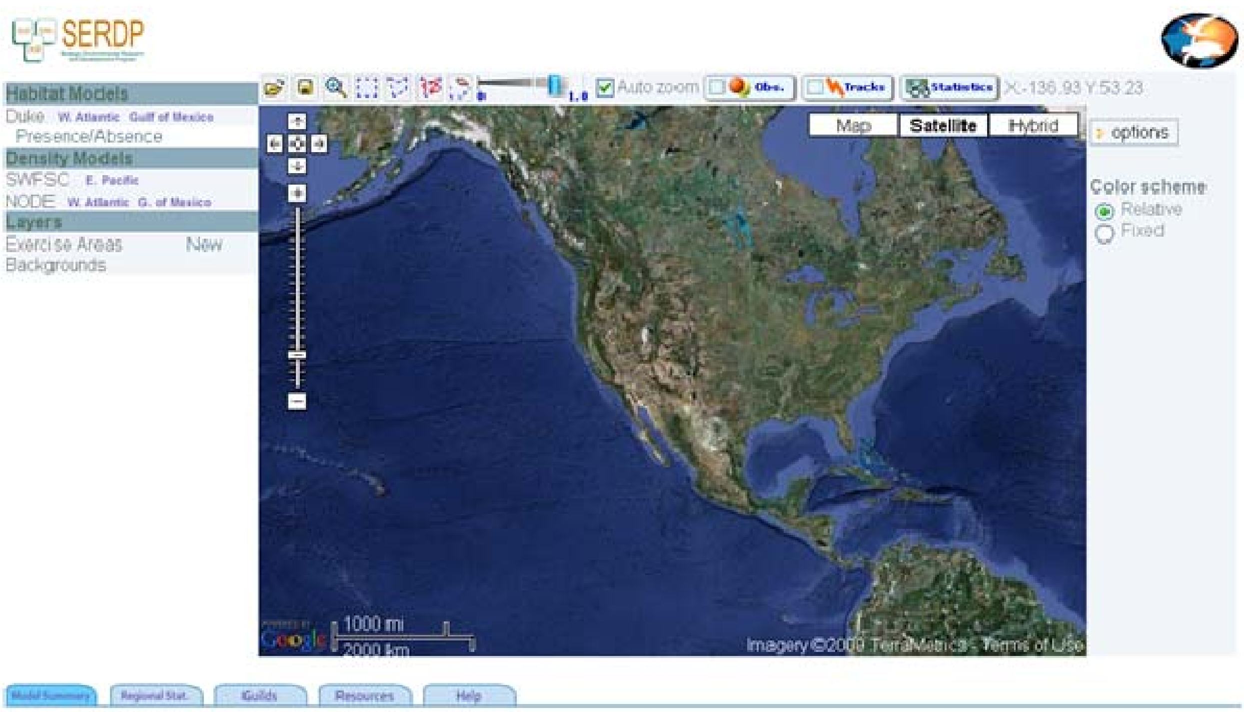

Figure 8. The SDSS interface. The left-hand side panel frames the model outputs in a hierarchical structure. The central part of the interface is the main map based on Google Maps above which lies a toolbar to various functions. Map options and legends are placed in the right-hand side panel.

In the SDSS, the model outputs are structured in a hierarchy of guild, season and region. A folder-like navigation menu helps users to find a model output of their interest, which is then overlaid on the satellite imagery provided by Google (Figure 9). Upon selection of a particular model output, relevant information such as the guild name, a list of contributing datasets, basic statistics of the model and supporting graphs is presented. The map can be color-coded by binary habitat index, which is useful when asking a question such as "where is the habitat of this species?" as well as habitat suitability indices (Figure 10). In addition, the standard error of the output can be mapped.

It is particularly valuable to visualize observations and survey efforts along with the model output. The SDSS is built on a database that stores all the observations and survey effort data used in the calculations. Each user can turn on/off the observations and efforts and identify points or lines to obtain detailed information (Figure 11). The list of contributing datasets provides links to a Dataset Page on the OBIS-SEAMAP web site where users can obtain the complete metadata of each dataset and download the observation data if further analyses are required.

Figure 9. The navigational menu shown to a model output level. Each entry works as a toggle; opening and hiding a tree beneath it.

Figure 10. The output is color-coded by habitat suitability index ("Prediction"), binary habitat index or standard error. To change the color, click [options] button and select the preferred color-coding option from "Output type."

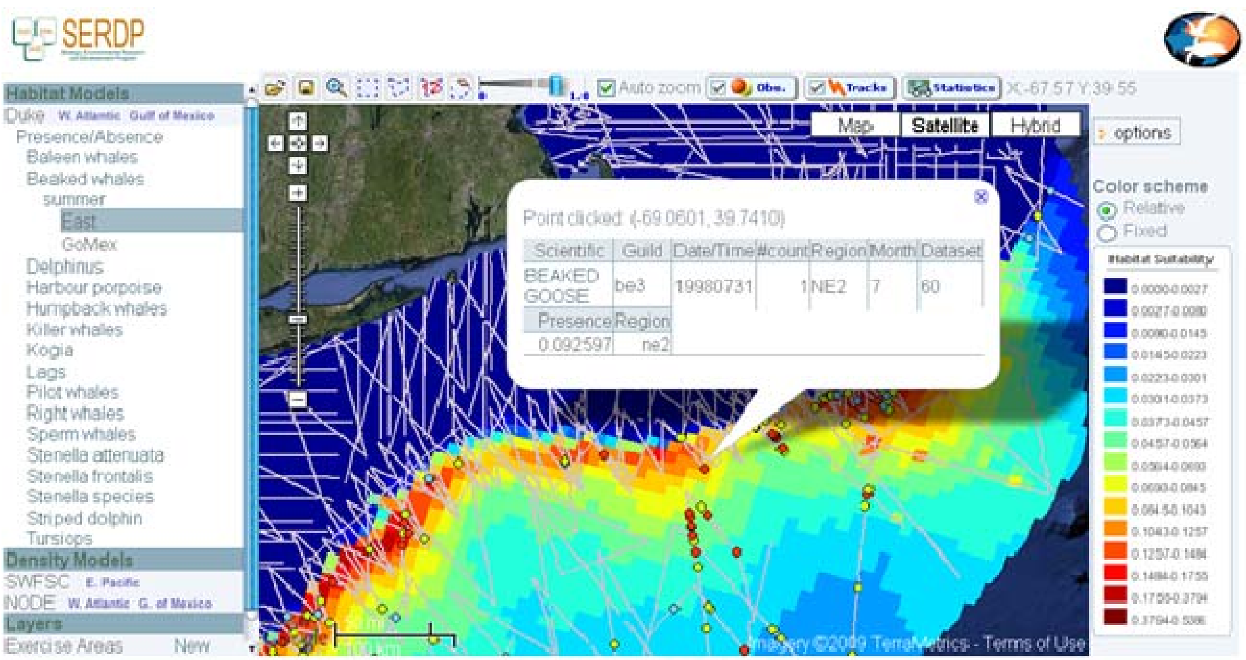

Figure 11. Observations and effort that were used in the model can be mapped along with the output. To turn them on/off, the user will toggle the button [Obs.] and [Tracks] in the toolbar. To identify an observation point or a line, click on it. Then, a popup window with the information of the clicked point/line will appear.

The model outputs, observations and efforts can be mapped over the entire project area (North Atlantic and Gulf of Mexico), but it may be of particular interest for some users to focus on areas of specific Navy training activities. Therefore, the SDSS is equipped with polygon drawing tools that allow users to draw any shape of an area on the map (Figure 12). In addition, thirteen naval exercise areas are pre-loaded in the SDSS and users can simply select and map one of them (Figure 12). Once the area is specified, whether it is a hand-delineated area or pre-loaded exercise area, observations and efforts are filtered to those within the area. The statistics of the output in that area is calculated dynamically and presented with histograms (frequency of habitat suitability index and cumulative area), giving the user fine-tuned supporting data for making planning decisions (Figure 13). As planning and decision-making processes may take a long time, it is useful if the customized map can be saved for later use. Thus, the map state in the SDSS, including the selected model, the area drawn, calculated statistics, can be saved and restored (Figure 14). This feature also saves users' time when the past map can be applied to a new planning with modifications.

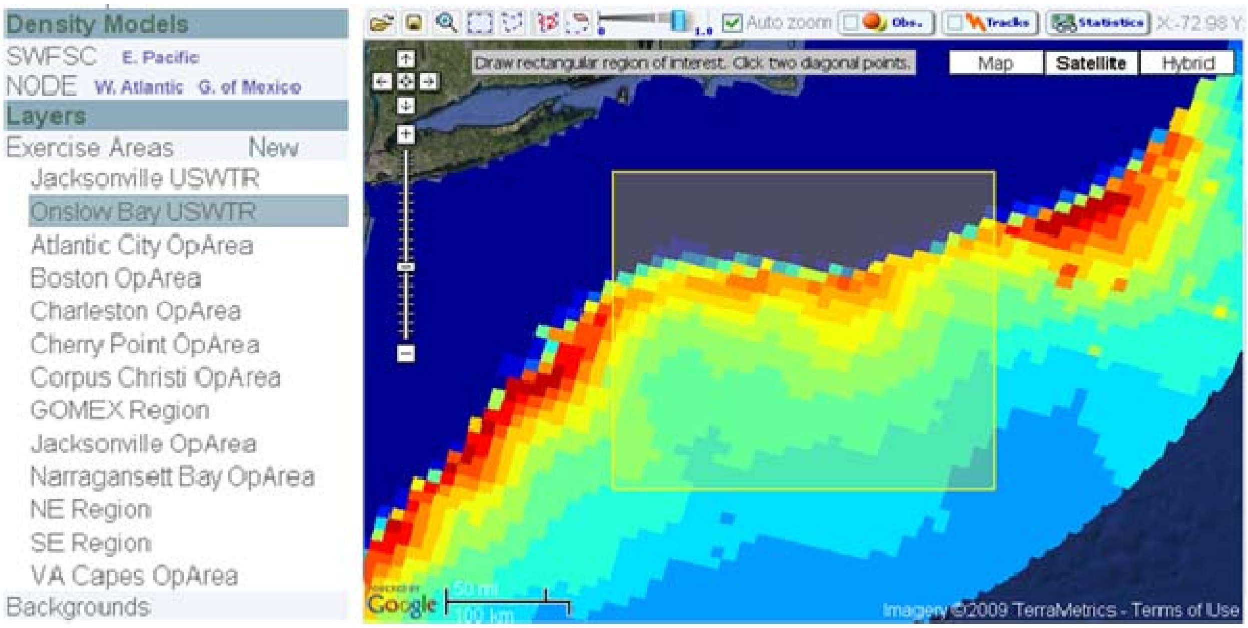

Figure 12. (Right) The polygon drawing tools allow users to interactively delineate areas of interest. The user can click one of the three drawing tools to activate it. Then, locate the vertices by clicking on the map. (Left) Pre-loaded Navy exercise areas can be used as an area of interest. To select and map one of them, expand "Exercise Areas" and click on one of the areas listed.

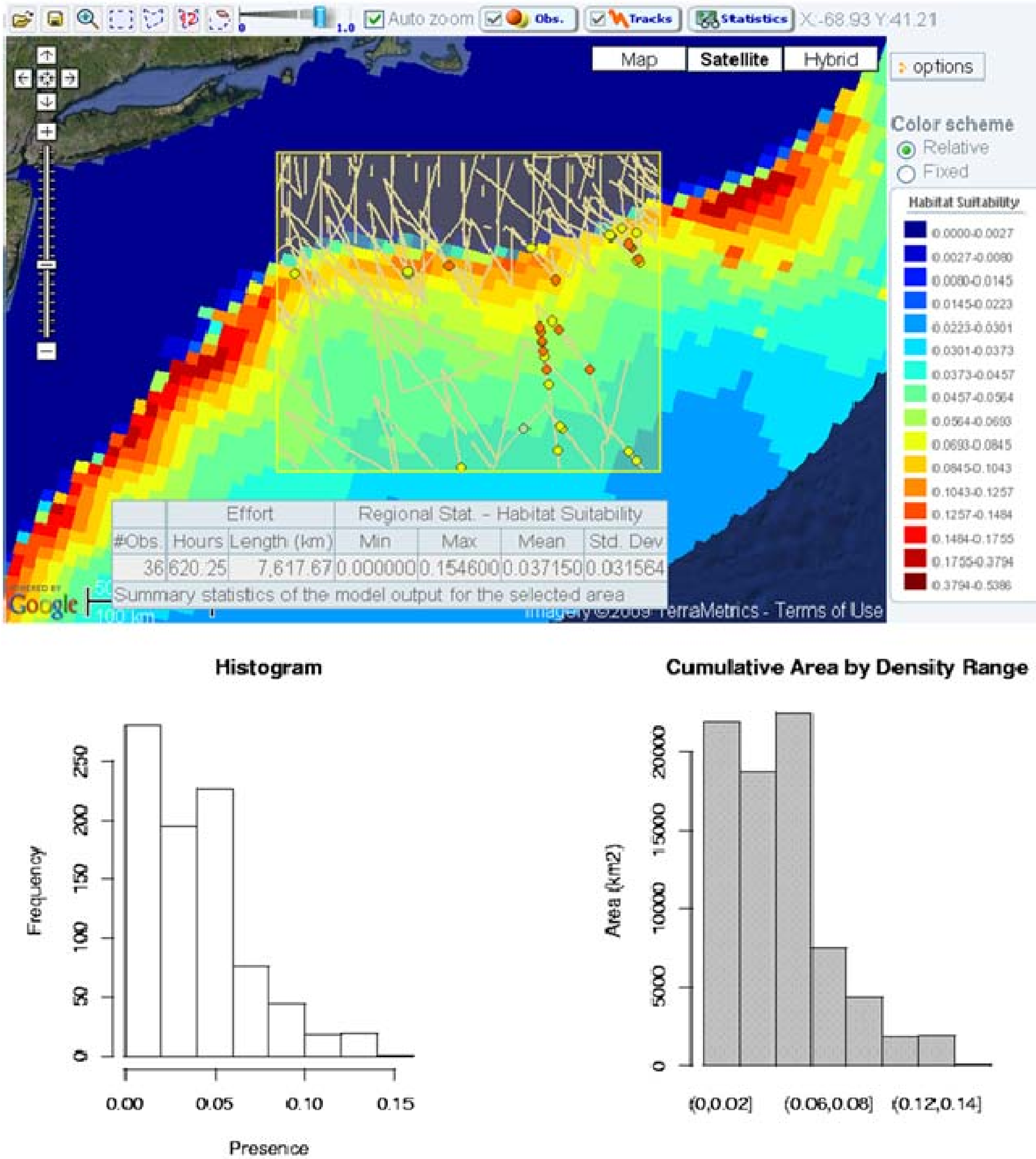

Figure 13. (Above) The summary statistics within the area of interest is calculated and the results are shown at the bottom of the map. (Bottom) Two histograms, frequency of the habitat suitability index (left) and cumulative area (right), are also presented. To get the summary statistics within an area, first draw an area of interest or select one of the pre-loaded Navy exercise areas. Then, click [Statistics] in the toolbar.

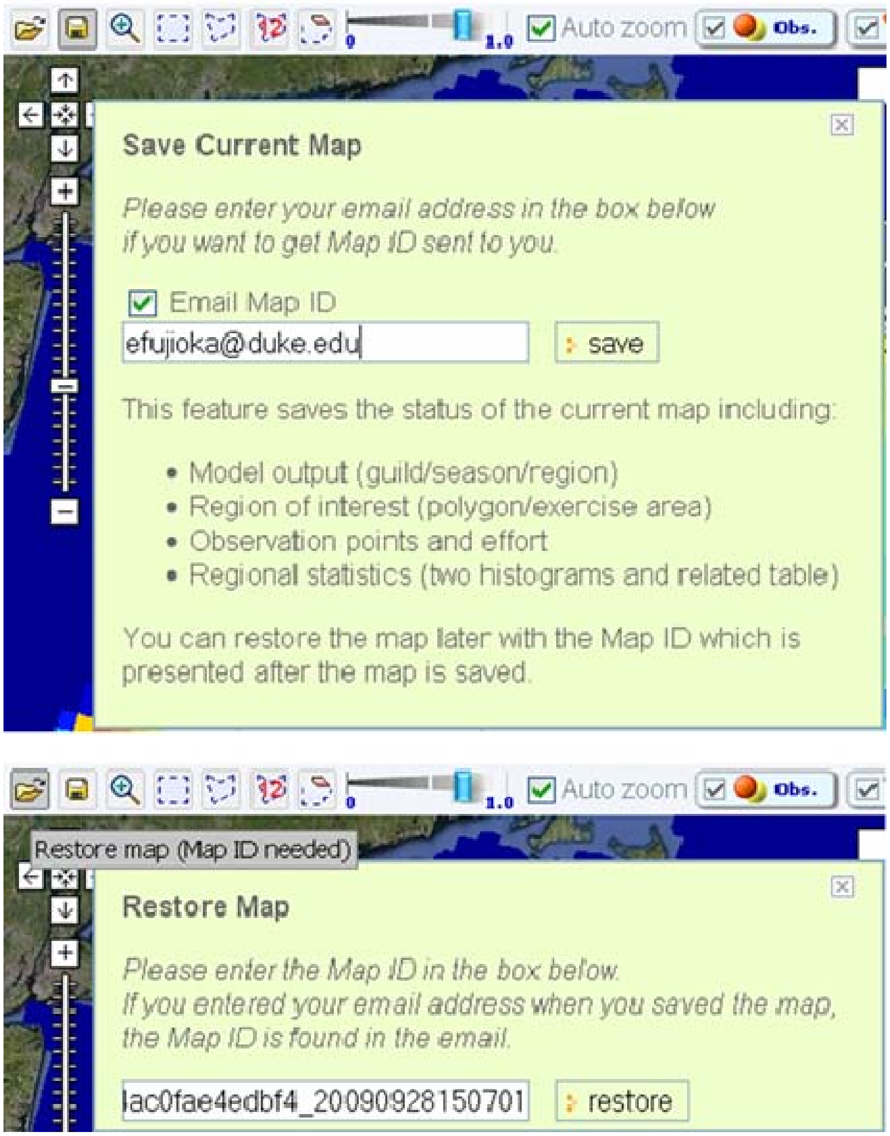

Figure 14. The map state can be saved and restored for later uses. (Above) To save the map state, the user can click the [Save current map] button in the toolbar. In the dialog that appears, enter your email address and click [Save] button. A map identification is sent to the address specified, which is required to restore the map. (Bottom) To restore the map, click [Restore map] button in the toolbar, enter the map identification and click [restore] button.

The SDSS also incorporates model outputs from two related SERDP projects (NOAA Southwest Fisheries Science Center Project SI-1391 and the Navy Oparea Density Estimates), allowing users to compare multiple models within a consistent, efficient interactive interface. The model outputs from the three projects are incorporated into the navigation menu. The same features described above (polygon drawing, filtering, statistics with histograms) can be applied to these outputs in the same manners and operations, which is particularly productive when producing reports in a standardized format.

3.5 Model Validation

The focus of this component of the project was to examine how well broad-scale marine mammal habitat and density models performed at small scales. To address this question we compared the relative density of marine mammals in two relatively small areas of the southeastern U.S. to modeled outputs of presence and density. This approach provides information about the performance of our modeled outputs at scales relevant to Navy training activities. Specifically, we compared relative densities in these two areas to outputs of the Duke marine mammal habitat models and the Navy OPAREA Density Estimates (NODEs); both sets of models were designed to capture species distribution patterns over a very broad area (*e.g.* the entire eastern U.S. EEZ). It was necessary to construct these models over a broad region due to data limitations, a common problem in modeling the distribution of marine mammals. As noted elsewhere in this report, for most areas of the US EEZ, and particularly in offshore areas, there are too few marine mammal sightings to create models at a fine scale.

We used two independent data sets to validate our model outputs. Coincidental to our marine mammal habitat modeling efforts, the Navy initiated a project to monitor marine mammals at two proposed Under Sea Warfare Training Ranges (USWTR) off the southeastern U.S. coast (Figure 15). The monitored areas of the two sites are both approximately 6,000 km^2 in extent. The first USWTR site lies approximately 50 miles off Onslow Bay, North Carolina and the second site is 35 miles off Jacksonville, Florida. Researchers at Duke University and the University of North Carolina Wilmington (UNCW) are conducting dedicated marine mammal surveys in these two areas. Duke researchers conduct the shipboard surveys and UNCW conducts aerial surveys in this monitoring program. The surveys collect data on all marine mammal species observed in these two areas.

The USWTR monitoring project provided an opportunity to investigate how well the habitat suitability models and the NODE density models capture the distribution of cetaceans in these two areas of particular Navy interest. Before these monitoring studies began very few surveys had been conducted in either area and almost no data was available during the winter months. As such, the Duke habitat models and the NODE models were developed using very sparse cetacean data from these regions. Comparing the model outputs with these recent observational data allows us to evaluate the performance of these models at a very fine-scale.

Monitoring surveys began at the Onslow Bay site in June 2007 and in January 2009 at Jacksonville. At both sites standardized aerial and shipboard line transect surveys were conducted along ten 74-nm tracklines. Shipboard surveys for cetaceans were conducted from the flying bridge of two offshore fishing vessels. Aerial surveys were conducted from a Cessna Skymaster aircraft at an altitude of approximately 305m. Observations followed standard distance sampling methods for cetaceans, similar to those employed in Barlow (2006).

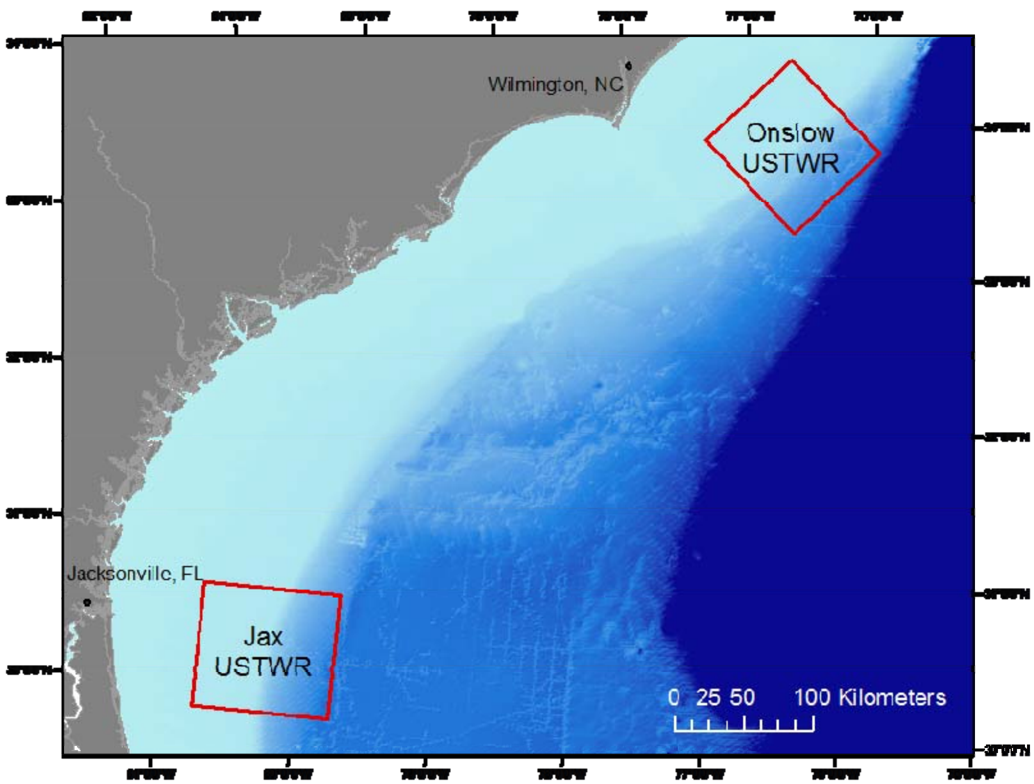

Figure 15. Locations of two monitoring sites from which marine mammal survey data were used to validate model outputs.

We used observations from the ship and aerial surveys to calculate estimates of relative density for each combination of species and season. Separate estimates were made for shipboard and aerial data. We restricted our analysis of shipboard to data to Onslow Bay; too few shipboard survey observations were available from Jacksonville. Only data collected during on-effort portions of surveys were included in the analysis. We removed any portion of the surveys occurring in Beaufort Sea State > 3 because of the reduction in sightability in higher sea states. We used a grid with an 8-km resolution as the analysis unit. For each cell, we calculated the length of on-effort track line and number of individuals marine mammals observed. We repeated this step for each species for which adequate observation data were available and calculated a relative density value for each cell.

We organized the data cumulatively by season, but if there were not at least two complete on-effort survey passes though a given cell, that cell was removed from analysis. This step was necessary to eliminate areas with insufficient survey effort. For some species there was adequate survey coverage but the sightings rate was too low to conduct an analysis (*i.e.* sightings only occurred in one cell during a given season).

We retrieved modeled density and habitat data directly from the Duke habitat suitability models and the NODE models through the SDSS. We extracted a value from the model outputs for each analysis unit. We used the NODE models to assess all species/season combinations. Due to the more limited availability of habitat models, we restricted our comparison of model outputs to sightings of bottlenose dolphins (*Tursiops truncatus*) in winter, summer and fall.

We calculated Spearman correlation coefficients to examine the relationship between the model outputs and observational data for each combination of site and season. Spearman rank correlation is a non-parametric technique that relies on rank order to assess correlation. Values range from -1 to +1 with negative values indicating repulsion and positive values indicative of attraction. We calculated coefficients for each cumulative season, site and species combination for which adequate data was available.

4.0 Results and Discussion

4.1 Ordination

Ordination analyses were conducted and results are presented here for the three geographic subregions (NOH, SOH and GOM). Of the three regions, NOH contained the most data both in terms of effort (not depicted) and species observations. Due to the relative richness of this data set, therefore, we were able to conduct ordinations on both the complete dataset and as well as with the rare species removed, allowing us to draw an interesting point of comparison. Rare species are often of management interest and it is instructive to see which other species these are (or more typically are not) sighted with. However their inclusion tended to make most species seem average, even in cases where structure naturally exists, that is the presence of the rare outliers makes other more common species clump together in ordination space (results not shown). The species are fairly well split along axis 1, with most of the squid eating species (Kenney and Winn, 1986) to the right (positive along Axis 1), and most of the fish and plankton eating species (Kenney and Winn, 1986) to the left (negative along Axis 1) (Figure 16). Certain species are distant from others in ordination space; these include Atlantic spotted dolphin, the *Kogia* spp. and pilot whales (Figure 16). The fish and plankton eating species are somewhat more tightly clustered than the squid eating species (Figure 16).

Six groups were delineated in the cluster analysis – two large groups and four small ones (Figure 16). One group, comprised of common dolphins, Atlantic white-sided dolphins, Harbor porpoise, minke whales, fin whales, humpback whales, and Northern right whales are tracking cooler, more productive, inshore waters (Figure 16). The “offshore” species are all Odontocetes: bottlenose dolphins, Risso’s dolphins, sperm whales, striped dolphins, striped dolphins, pilot whales, and beaked whales. The remaining four groups were each comprised of a single species: 1) Cuvier’s beaked whales; 2) Sowerby’s beaked whales; 3) *Kogia* spp.; and 4) Atlantic spotted dolphins (Figure 16).

By depicting the environmental data as fitted surfaces, we can observe the relative position of the groups and the species within those groups with greater clarity. The inshore species are in the highest productivity waters (Figure 16 a), and are fairly clumped. These species are in the coolest areas and closest to shore (Figure 16 b, c). However, even though the grouping between inshore and offshore is apparent, subtleties exist in the response to chlorophyll levels. For example, although the offshore group is seen in warmer waters (Figure 16 b, c), there is a distinct gradient in the response to chlorophyll. At one end of this gradient are those species seen in the least productive waters (Bottlenose and Risso's dolphins) and at the other end seen in more productive waters (beaked whales and pilot whales) (Figure 16 a). With respect to chlorophyll and sea surface temperature, common dolphins, pilot whales and fin whales are seen approximately midway between the inshore and offshore groups, with fin whales seen closest to the center of the onshore group (Figure 16 a, b). In summary, most, but not all, toothed whales and dolphins are seen father offshore, in warmer, deeper, less productive waters, while all baleen whales and three dolphin species are seen closer to shore, in cooler, shallower, more productive waters (Figure 16).

No baleen whales are present in the SOH during summer. In contrast, this region is dominated by a smaller number of odontocete species, many of which are quite spread out in species space (Figure 17). Three groups exist in the ordination, although the main group seems the most defined (green circles in Figure 17). This group consists of pilot whales, bottlenose dolphins, Risso's dolphins, spotted dolphins and common dolphins. In particular, three species are typically observed alone: Pantropical spotted dolphin; *Kogia* spp., and beaked whales (Figure 17). In general, the main group tends to be in warmer, lower productivity waters that are closer to shore (Figure 17). Pantropical spotted dolphins are seen in cooler, more productive waters farther from shore (Figure 17). *Kogia* spp. are seen in the deepest and warmest waters (Figure 17).

The GOM has the greatest diversity of species and the ordination results were less striking than the other two areas in terms of differences between groups. Like the SOH region, species in the GOM region were comprised entirely of odontocetes. However, unlike the SOH, there was more discernable structure and grouping in the GOM (Figure 18). One particularly important variable in the GOM is depth (Davis et al., 1998, Baumgartner et al., 2001, Davis et al., 2002). In the GOM, surveys were conducted across a large depth gradient (Figure 6). Most species in the GOM were observed in waters shallower than 1050 m; species found in the deepest waters included: rough-toothed dolphins, Pantropical spotted dolphins, sperm whales, and melon-headed whales (Figure 18 d). Two species are clear outliers and were seen typically by themselves: killer whales and Atlantic spotted dolphins (Figure 18).

Seven groups were delineated in the GOM (Figure 18). The largest group was comprised of bottlenose dolphins, Risso's dolphins, *Kogia* spp., spinner dolphins, striped dolphins, sperm whales, and Pantropical spotted dolphins (orange circles in Figure 18). Smaller multiple species groups included: (a) melon headed whales, and rough toothed dolphins (dark green circles in Figure 18); and (b) Clymeme dolphins, dwarf sperm whales, and beaked whales (purple circles in Figure 18).

Most of the species in the GOM occur in relatively low productivity (0.2 - 0.3 mg/m^3 chlorophyll) waters (Figure 18 a). There is a concave shape to the chlorophyll response, with Atlantic spotted dolphins and Clymene dolphins occurring in the most productive waters, yet the former is found in relatively cool waters, while the latter occurs in relatively warm waters (Figure 18 a, b). In comparison the two outliers (Atlantic spotted dolphins and killer whales) were seen in similarly productive waters, with killer whales seen in waters about 0.5°C warmer, and 10-12 km farther offshore (Figure 18 a, b, c). Bottlenose dolphins are also somewhat isolated in species space and occur frequently in productive onshore waters (Figure 18 a, c).

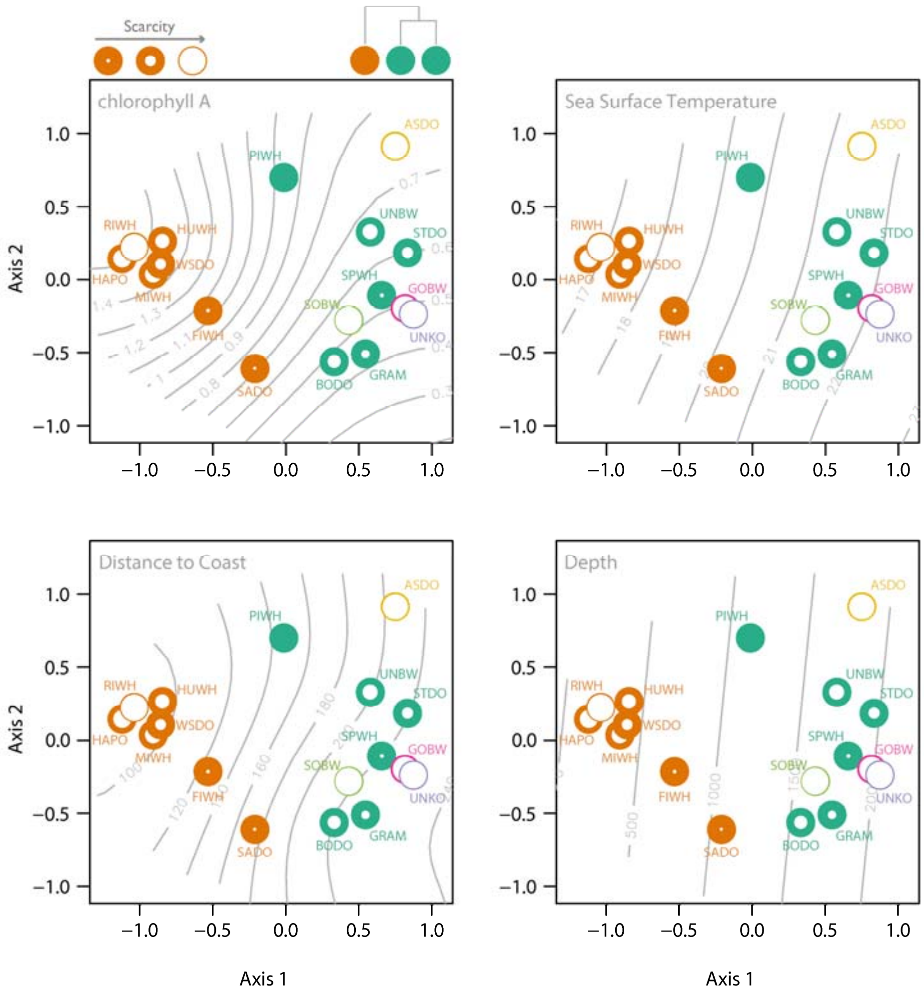

Figure 16. Plot of NOH species in ordination space (1st two axes) overlaid on a fitted environmental surface (grey contour lines). Plots from left to right and top to bottom: chlorophyll a (mg per m^{-3}); sea surface temperature (°C); distance to coast (km); and depth (m). Species location is marked with two circles, an outer colored one, and an inner white one. Note small legend at upper left: (1) size of inner circle corresponds to rarity level, i.e. a fully colored in circle is abundant, while circles with a thin colored outline are rare; (2) color corresponds to grouping from group contrast Mantel tests. Species are labeled as follows: ASDO, Atlantic Spotted Dolphin; BODO, Bottlenose Dolphin; FIWH, Fin Whale; GOBW, Cuvier's Beaked Whale; GRAM, Risso's Dolphin; HAPO, Harbor Porpoise; HUWH, Humpback Whale; MIWH, Minke Whale; PIWH, Pilot Whale; RIWH, Right Whale; SADO, Common Dolphin; SOBW, Sowerby's Beaked Whale; SPWH, Sperm Whale; STDO, Striped Dolphin; UNBW, Unidentified Beaked Whale; UNKO, Pygmy or Dwarf Sperm Whale; WSDO, Atlantic White-Sided Dolphin.

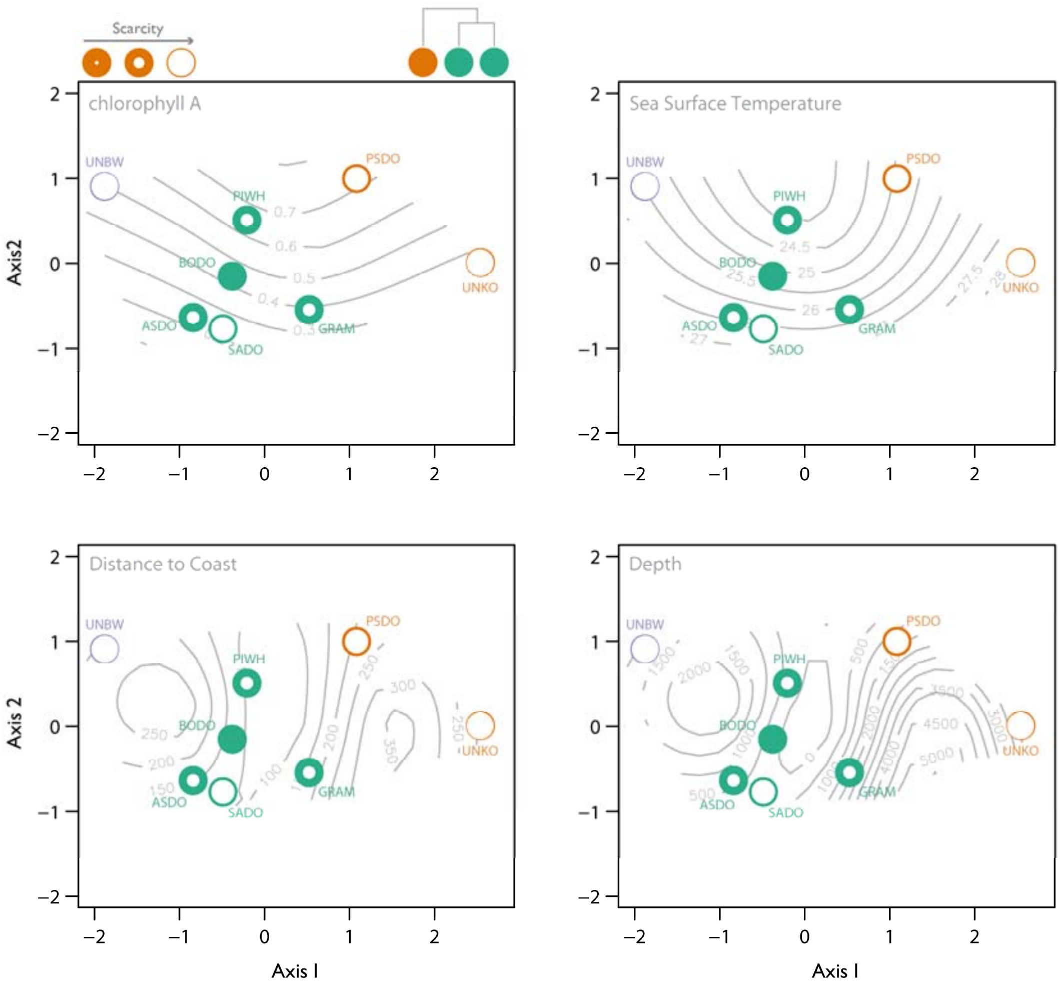

Figure 17. Plot of SOH species in ordination space (1st two axes) overlaid on a fitted environmental surface (grey contour lines). Species are colored and labeled as in Figure 16, except for PSDO, Pantropical Spotted Dolphin.

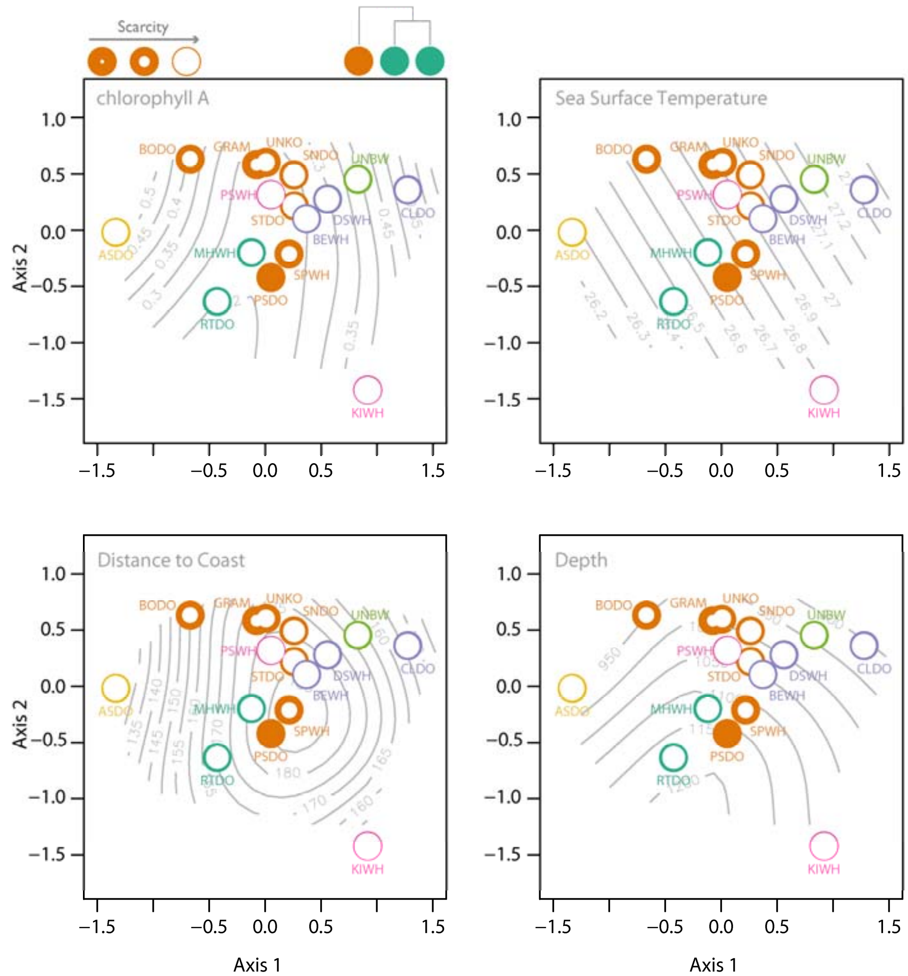

Figure 18. Plot of GOM species in ordination space (1st two axes) overlaid on a fitted environmental surface (grey contour lines). Species are colored as in Figure 16. Species are labeled as follows: ASDO, Atlantic Spotted Dolphin; BEWH, Beaked Whale (*Mesoplodon* spp.); BODO, Bottlenose Dolphin; CLDO, Clymene Dolphin; DSWH, Dwarf Sperm Whale; GRAM, Risso's Dolphin; KIWH, Killer Whale; MHWH Melon-Headed Whale; PSDO, Pan-Tropical Spotted Dolphin; PSWH, Pygmy Sperm Whale; RTDO, Rough-Toothed Dolphin; SNDO, Spinner Dolphin; SPWH, Sperm Whale; STDO, Striped Dolphin; UNBW, Unidentified Beaked Whale (*Ziphiidae*); UNKO, Pygmy or Dwarf Sperm Whale.

In the NOH we identified two dominant groups (depicted with orange and dark green colors in Figure 16) differentiated along a sea surface temperature gradient, with the onshore group being found in waters cooler than 19.3°C. This observation was reflected in the Mantel results - with SST having the highest correlation with group difference (Table 5). In the SOH, the primary split in the CART was along a depth gradient (split at 718 m), with a secondary split at SST values of 29.1°C. The Pantropical spotted dolphins and *Kogia* spp. were seen primarily offshore (Table 5). In the Mantel results, the strongest correlations between group membership and the environment were among distance to shelf (Mantel R = 0.284), and depth (Mantel R = 0.332, Table 5). The greatest environmental structuring among the groups occurred in the GOM (Figure 18). In terms of sighting frequency on unique sites, groups 2 and 6 are the largest groups in the GOM. Group 2 is comprised of striped dolphin, *Kogia* spp., spinner dolphin, Pan-tropical spotted dolphin, sperm whales, bottlenose dolphin, Risso's dolphin, while group 6 is comprised of killer whales and pygmy sperm whales (Figure 18). Generally group 2 is arrayed along an increasing depth gradient as follows: bottlenose dolphin, *Kogia* spp., Risso's dolphin, spinner dolphin, striped dolphin, sperm whale, Pan-tropical spotted dolphin. Pygmy sperm whales are seen in depths between spinner dolphin and striped dolphin, while killer whales are seen in deeper waters (Figure 18). The strongest patterning variables in the CART analysis were depth and distance to coast, which matched the Mantel results (Table 5). (We include the full graphical summaries of the CART for each region in Appendix D: Graphical CART Results.)

Table 5. Mantel correlations between group membership and the five environmental variables for each of the three regions. Due to the large size of the NOH dataset, we calculated a bootstrapped Mantel R, which is reported along with 5% confidence intervals.

Region	**Variable**	**Mantel R**	**CI**
NOH	chlorophyll A	-0.008	(-0.06, 0.07)
	Depth	0.286	(0.21, 0.37)
	d2coast	0.288	(0.21, 0.36)
	d2shelf	-0.032	(-0.09, 0.03)
	SST	0.371	(0.28, 0.46)
SOH	Variable	Mantel R	p-value
	chlorophyll A	-0.051	NS
	Depth	0.284	0.0009
	d2coast	0.208	0.0007
	d2shelf	0.332	0.0001
	SST	0.046	NS
GOM	Variable	Mantel R	p-value
	chlorophyll A	-0.046	NS
	Depth	0.083	0.001
	d2coast	0.035	0.06
	d2shelf	0.027	NS
	SST	-0.011	NS

We found that grouping species at higher taxonomic levels caused significant shifts in the previously identified groups (Figure 18). For example, when we lumped beaked whales together they fell generically into the "offshore" group (Figure 18), but when we analyzed the data at the species level, Cuvier's and Sowerby's beaked whales emerged as separate groups (Figure 16). Lumping beaked whales across taxonomic levels obscures real ecological distinctions among these species (Figure 19); identified at the species level, beaked whales exhibit distinct ecological niches (Figure 16). In addition, there are other subtle differences with the right whales and pilot whales changing their group membership slightly, though in each case (split vs. lumped) these two species are distant from the other group members (Figure 19).

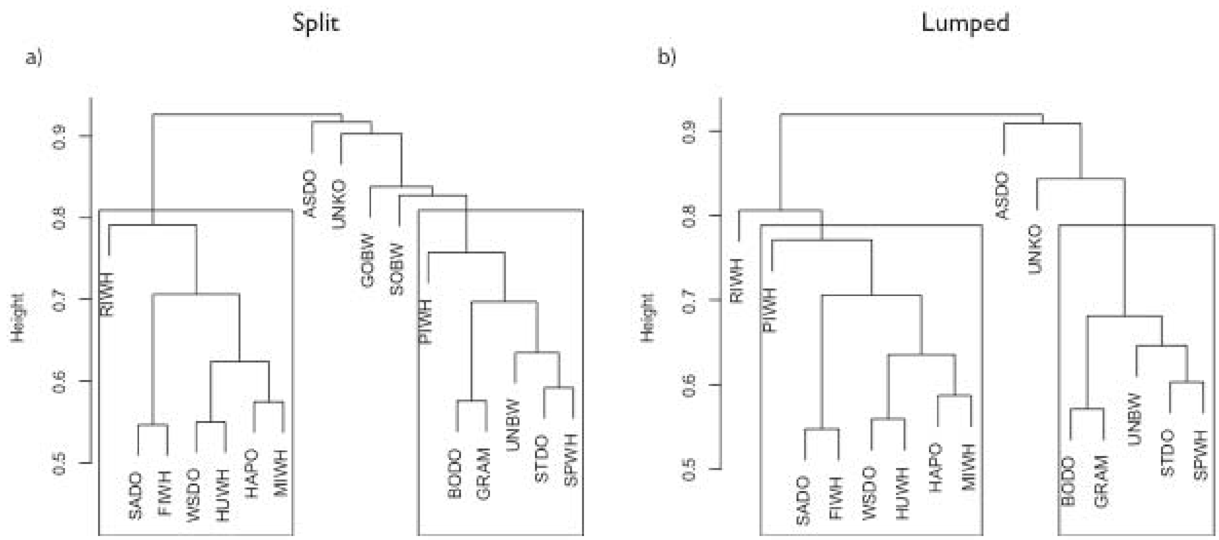

Figure 19. Dendrogram resulting from hierarchical k-means clustering, using a group average linkage for the common species sighted in the NOH region. Six groups were identified using group-contrast Mantel tests (see text for details); rectangles surround groups containing more than one species, e.g., pygmy sperm whales comprised a group. In (b) the dendrogram is a result of lumping sightings across taxonomic levels, *i.e.* all beaked whales are the "same" species in the ordination. Note especially how lumping the beaked whales moves all sightings into the "offshore" group (b).

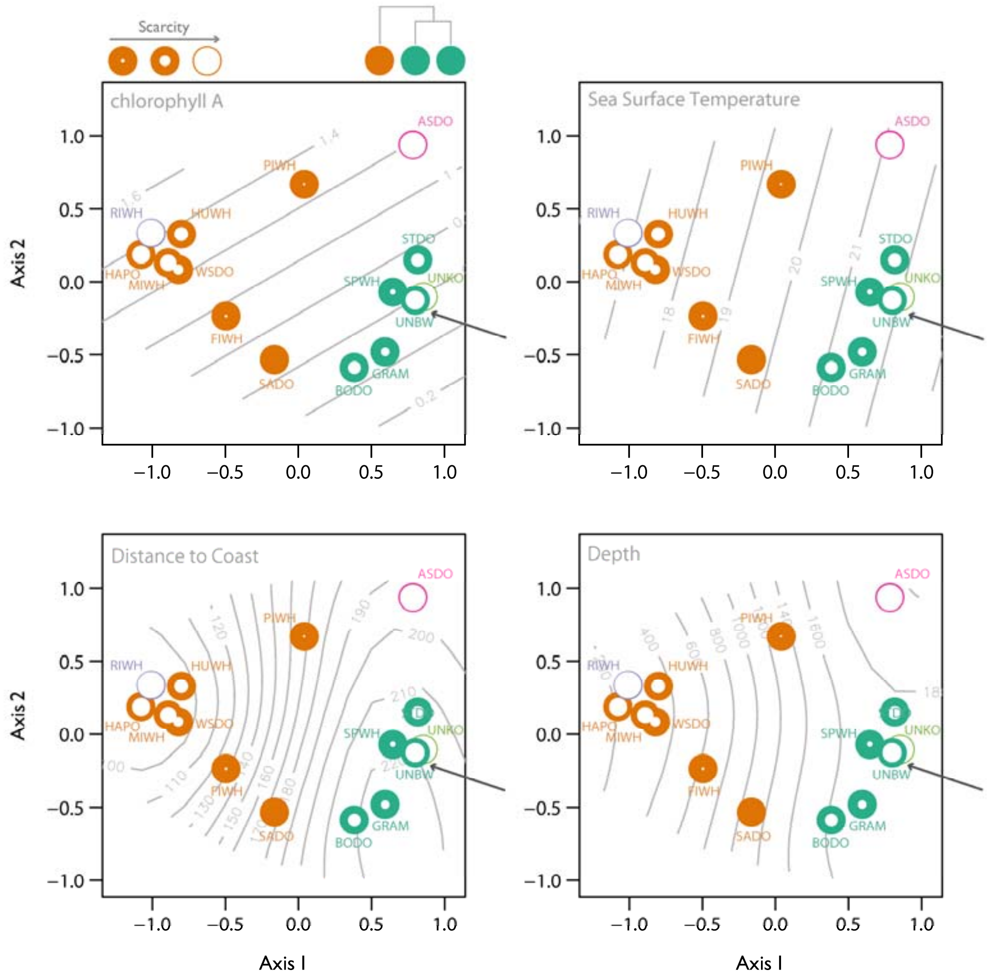

Figure 20. The same plot as Figure 16 except sightings were lumped across taxonomic levels. Grouping follows Figure 19 b. Dark grey arrows denote the new position of "Beaked whales." Compare this to the positions of Cuvier's and Sowerby's Beaked whales in Figure 16.

In the NOH region, the most obvious signal in the ordination is the clear distinction between the "onshore" and "offshore" species groups. The onshore species occur in cooler, shallower, more productive waters; in clear contrast with the offshore group (Figure 16). These splits are consistent with the diet-based partitioning (planktivores, teuthivores and piscivores) used in Kenney and Winn (1986), which showed high use areas in the western Gulf of Maine as a major feeding ground. In Kenney and Winn's analysis, humpback whales, fin whales, right whales, white-sided dolphins, and minke whales primarily used the inshore areas – all these species are piscivorous save for the right whale. Our results also include harbor porpoise and common dolphins in this group. The baleen whales are known to feed on prey concentrated in the Gulf of Maine, such as sand lance (*Ammodytes* spp.). Harbor porpoise are a coastal species, and this population does not leave the Gulf of Maine during the summer months (Read et al., 1993). Harbor porpoise are consistently seen in the coolest, shallowest, most productive waters, which is consistent with their life history strategy (Read and Hohn, 1995) and a diet comprised primarily of herring (Smith and Gaskin, 1974, Smith and Read, 1992). Right whales feed on copepods, but group with the other large baleen whales (Figure 16). Their primary prey, *Calanus finmarchicus* is an important prey species for many fish species in the Gulf of Maine (Baumgartner et al., 2007), which helps explain their grouping.

In the NOH region, the offshore group is comprised solely of odontocetes, quite similar to the baseline from Kenney and Winn (1986). Kenney and Winn refer to this group as the teuthivores, and, although it is less compact then the piscivores, their diet-based partition is closely aligned with our grouping results (Figure 16). The pilot whales, identified only to the genus level in field surveys, are approximately split between the onshore and offshore groups (Figure 16). This placement is likely a compromise between the long-finned pilot whales, typically seen in colder more productive waters, and short-finned pilot whales typically seen in warmer oligotrophic waters (Payne and Heinemann, 1993). Pilot whales group with the offshore species, but their apparent distance from other members in the group (beaked whales, striped dolphin, sperm whale, Risso's dolphin, and bottlenose dolphin) could owe to this effect. The coastal ecotype of bottlenose dolphins (Hersh and Duffield, 1990) is not represented in these data in the NOH region. Indeed, Torres et al. (2003) found any bottlenose dolphin seen farther than 34 km from the shore is classified as the offshore ecotype, and the placement here puts bottlenose dolphin well offshore of that distance (Figure 16). Bottlenose dolphins are considered primarily piscivores, but the offshore ecotype is also known to eat squid (Barros and Odell, 1990). In addition the stomach contents of the offshore ecotype frequently contain remains from deep-water fish families (Mead and Potter, 1990). This may help explain why the piscivorous bottlenose dolphins are grouped with the squid-eaters.

Previous work on sperm and beaked whales (Waring et al., 2001) has noted that while these are shelf-edge species (Kenney and Winn, 1986), sperm whales are more widespread than beaked whales and are typically seen in close proximity to the edges of warm core rings (Waring et al., 1993; 2001). Waring et al. (2001) found that sperm whales were typically seen in warmer waters than beaked whales; however their analysis lumped beaked whales across species. Here we found that Sowerby's beaked whales were seen in cooler waters than sperm whales, but that Cuvier's beaked whales were seen in warmer waters than sperm whales, suggesting there is fine-scale habitat partitioning between these two deep diving squid-eating species. The distinctions between beaked whales observed here, *i.e.* Sowerby's found in cooler waters than Cuvier's beaked whales, are similar to previous reports (MacLeod, 2000; Macleod et al., 2006). In addition, both Sowerby's and Cuvier's beaked whales cluster into their own unique single-species groups. Sowerby's beaked whales are smaller than Cuvier's beaked whales and it has been suggested that size differences may lead to prey partitioning among beaked whales (MacLeod and D'Amico, 2006).

Our findings are also similar to a previous cluster analysis in this area conducted by Hamazaki (2002). Hamazaki found two primary groups, with two subgroups in each. He named these groups "Mid-Atlantic" and "North-Atlantic," with "Mid-Atlantic Offshore," "Mid-Atlantic Shelf," "North-Atlantic Nearshore," and "North-Atlantic Shelf" subgroups (Hamazaki, 2002). These major groupings are very similar in terms of species membership to the ones presented here. First, his analysis uncovered four groups, but ours had six. Second, beaked whales were lumped in Hamazaki (2002), whereas we split them in our analysis. In cases where we can identify individuals to the species level among beaked whales, it is clear these species occupy their own niche (Figure 16). Common dolphins are present in our onshore piscivorous group, whereas Hamazaki (2002) placed this species in an offshore separate group - the “Mid-Atlantic Shelf” group (although of all the species in our onshore group, common dolphins are closest to the offshore group). Finally, similar to the results of Hamazaki (2002), bottlenose dolphin and Risso’s dolphin are located close to each other in our ordination space (Figure 16). It should be noted that the data used in Hamazaki (2002) are not as spatially comprehensive as the ones used here. For example, no right whales were present in his dataset, although they are present in the Gulf of Maine and Bay of Fundy in the summertime.

The SOH was the poorest area in terms of sample size, due to a lack of survey effort. Perhaps as a result, the results from this area were the simplest and, as a result, inference into community structure here is most difficult. Groups emerged from the data in this region (Figure 17), but the spacing within groups south of Cape Hatteras no doubt reflects the paucity of sightings. For example, whereas Risso’s dolphin and bottlenose dolphin were closely grouped in the other two areas (Figure 16, Figure 18), here they are found farther apart. The onshore ecotype of bottlenose dolphin are not well represented in these surveys (Figure 17 c); indeed while they are the most abundant in this survey, it has been found that most bottlenose dolphins migrate north of Cape Hatteras, and hence into the NOH region, in summertime (Torres et al., 2005). Similar to the results from the NOH region, in the SOH beaked whales cluster out into their own distinct niche (Figure 17).

The richest and most complex structure in the ordination results was seen in the GOM (Figure 18). This region had the highest species diversity, the largest number of groups (7) and significant structuring in environmental space (Figure 18). Depth was an important patterning variable (Figure 18), which corresponds well with previous work on distributions in the GOM (Baumgartner, 1997; Davis et al., 1998; Baumgartner et al., 2001; Mullin and Fulling, 2004). Past surveys have led to a good understanding of the role of depth in partitioning marine mammal species in the GOM, with the approximate shallow to deep gradient as follows: shelf species (Atlantic spotted dolphin and bottlenose dolphin), upper slope species (Risso’s dolphin, short finned pilot whales), lower slope species (*Kogia*, rough-toothed dolphins, spinner dolphins and sperm whales), and oceanic species (striped dolphins, melon-headed whales, Pan-tropical spotted dolphin, Clymene dolphins and beaked whales) (Davis et al., 1998; Baumgartner et al., 2001; Davis et al., 2002). As with most pelagic species, although a clear trend exists, there is overlap within these groups, *e.g.* Figure 2 in Davis et al. (1998). Within this overlap in species space species tend to separate on subsequent environmental variables, *e.g.* Risso’s and *Kogia* overlap in depth, but differ in slope and zooplankton biomass with Risso’s seen in high slope environments, while *Kogia* are typically seen in areas of higher zooplankton biomass (Baumgartner, 1997; Baumgartner et al., 2001). Similarly, Davis et al. (1998) noted that, in cases where species overlap in environmental space, *e.g.* oceanic dolphins and sperm whales, physiology dictates that the shallow-diving dolphins are restricted to upper portions of the water column (Williams et al., 1993) and sperm whales can dive to greater depths.

In general, the depth partitioning we observed in the GOM is consistent with previous work (Davis et al., 1998; Baumgartner et al., 2001; Davis et al., 2002), with a few exceptions. Rough toothed dolphins were seen in deeper waters than other lower slope species (Figure 18) and

Clymene dolphins and beaked whales were seen in shallower waters than other oceanic species (Figure 18). Differences between our results and those in previous studies may be due to scale. Several previous studies examined only part of the Gulf of Mexico, *e.g.* the western continental slope (Davis et al., 1998), northern oceanic GOM (Davis et al., 2002), or the continental shelf (Fulling et al., 2003), whereas the data we analyzed covers a larger area (Figure 6). Some of the differences may reflect the effects of seasonality in the marine mammal community and/or in survey effort, leading to certain species being seen more frequently in the summer (Mullin and Fulling, 2004) or the spring (Jefferson and Schiro, 1997).

We ignored time, both within and across years, because we were deliberately trying to generate a baseline snapshot and understanding of community structure in marine mammals across a large spatial gradient and we were limited by the availability of data. We chose to focus on summer because that was the richest seasonal data periodset. Research cruises are typically conducted during summer because this is the season with the best weather, which leads to better sighting conditions. Obviously it would be desirable to examine both seasonal and inter-annual variation in our ordination results, but at present there is insufficient data to conduct such analyses.

4.2 Seasonal Data Limitations

When available marine mammal observation data are subdivided by monthly or seasonal time periods important trends emerge. Figures 21 and 22 depict the distribution of available observer effort and observation data arrayed by guilds versus monthly time periods. Figures 23 and 24 highlights this same comparison for three guilds; *Tursiops*; Beaked Whales and Baleen Whales. An important trend that emerges from this temporal data gap analysis is the distinct difference in the availability of data for late fall, winter and early spring time periods. This trend is due to a lower rate of data collection conducted during winter versus summer seasons. This fundamental temporal trend in data collection effort directly limits our ability to construct models for many marine mammal guilds in non-summer seasons. Tables 6 and 7 in sections 4.3 and 4.4 provide a listing of model results by guilds and seasons for the Gulf of Mexico and Atlantic coast regions respectively. The lower numbers of successful models constructed for marine mammal guilds in fall, spring and winter seasons are due primarily to this uneven trend in data availability by season.

Without data for the desired season and region, a predictive model cannot be sufficiently built. Understanding the distribution of species data in time and place is therefore necessary, not only for constraining existing modeling exercises, but also for planning future survey activities in order to fill the gaps. In Figures 21 through 24, all survey effort (blue lines) and observations (red dots) are summarized by guild and season. Marginal totals of effort (in hours) and observations (n) are tallied, providing total observations and effort per season and per guild across seasons. These data are pulling from the 53 datasets described earlier (Table 1), inclusive of all observations and effort within the clipped study area (Figure 1).

Not surprisingly, the majority of survey effort occurs in the summer (260 hours) and spring (220 hours) versus fall (69 hours) and winter (73 hours). With less survey effort, there are fewer opportunities for observation. For winter, only *Tursiops* has at least 100 sightings and 9 of the 16 guilds have fewer than 10 observations. Fall is less bleak with 5 guilds (humpback whales, harbour porpoise, *Stenella frontalis,* and *Tursiops*) having over 100 observations, despite 4 hours less survey effort than winter. The distribution of survey effort is also more widespread in the fall, likely capturing the broader migratory ranges of the animals. For summer, 11 of the 16 guilds have observations in excess of 100, while spring only has 4 guilds in this more abundant category.

Species with the lowest number of observations across all seasons are also the most rare for this area and cryptic: killer whales (n=67), right whales (n=77), *Stenella* species (n=124), striped dolphin (n=195), *Kogia* (n=205) and beaked whales (n=251). When making such comparisons, it is useful to keep in mind the number of individual species contributing to a given guild (Table 2). While beaked whales are some of the most cryptic and rare species, the guild is lumped with 10 species. When comparing observations here to input presences in the models (Table B-1), there may be fewer presences than observations if more than one observation occurred in a given cell for that guild and season.

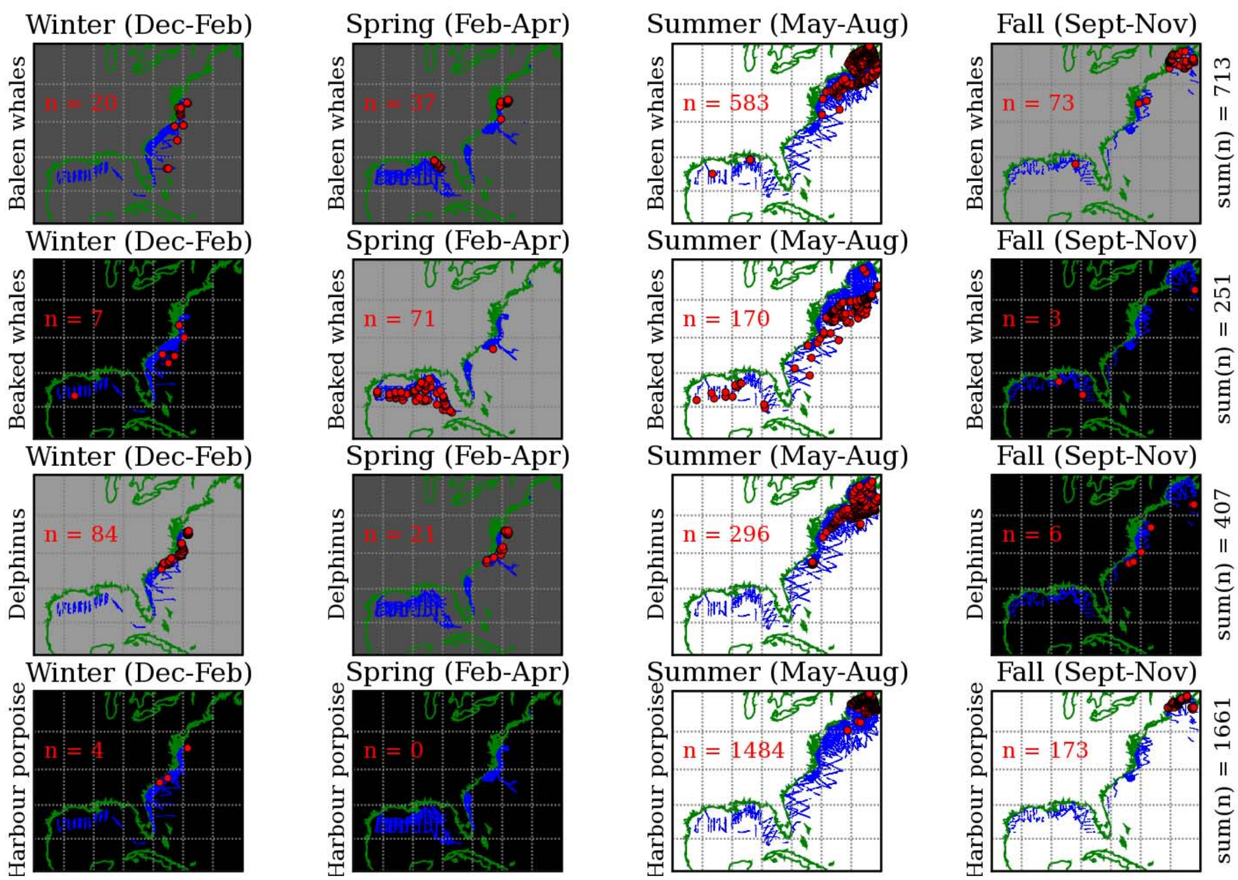

Figure 21. Data availability (part 1 of 4) for Baleen whales, Beaked whales, *Delphinus* and Harbour porpoise by season with marginal totals of observations (n) and effort (e). Blue lines are effort and red dots observation. Background color corresponds with obs < 10 (black), 10-49 (dark grey), 50-99 (light grey), 100+ (white).

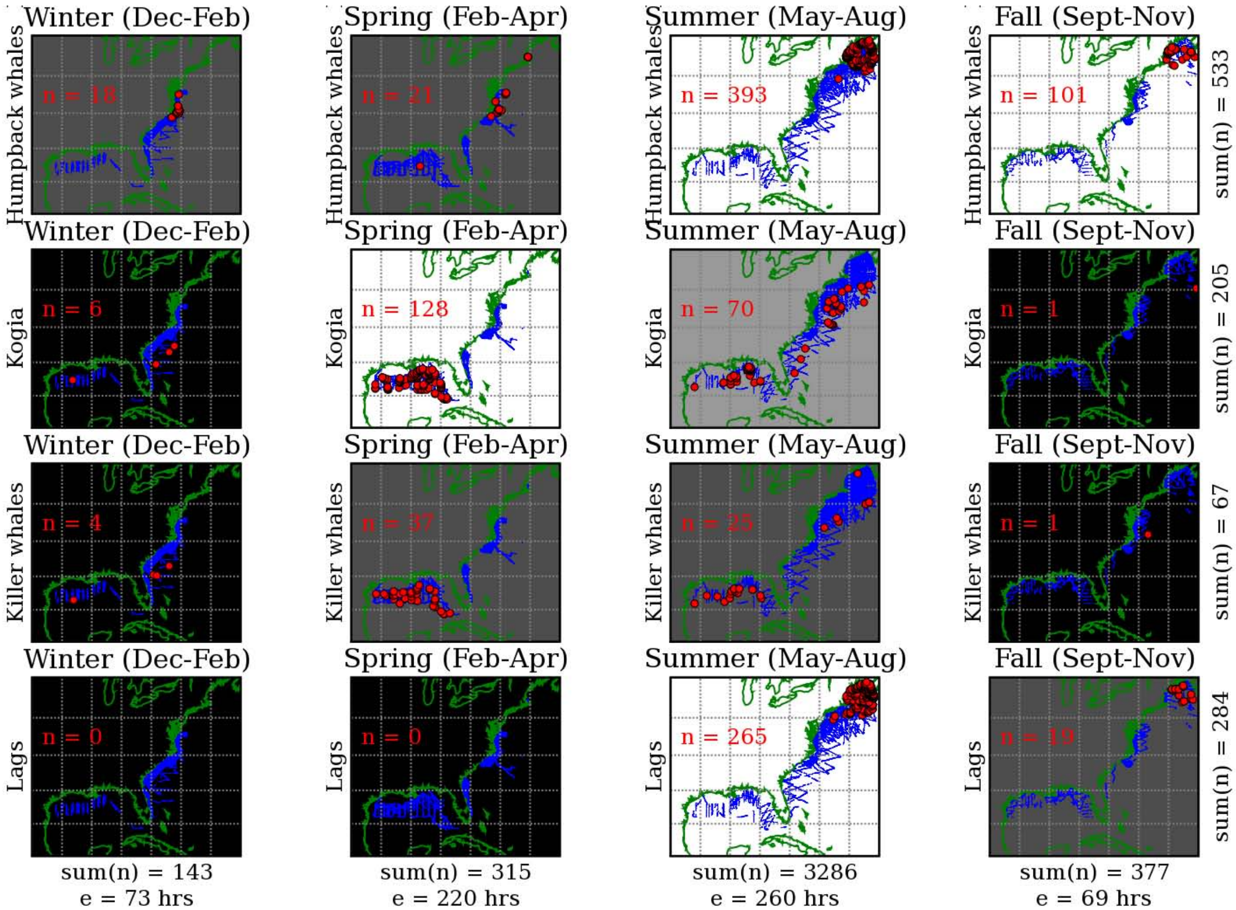

Figure 22. Data availability (part 2 of 4) for Humpback whales, Kogia, Killer whales and Lags by season with marginal totals of observations (n) and effort (e). Blue lines are effort and red dots observation. Background color corresponds with obs < 10 (black), 10-49 (dark grey), 50-99 (light grey), 100+ (white).

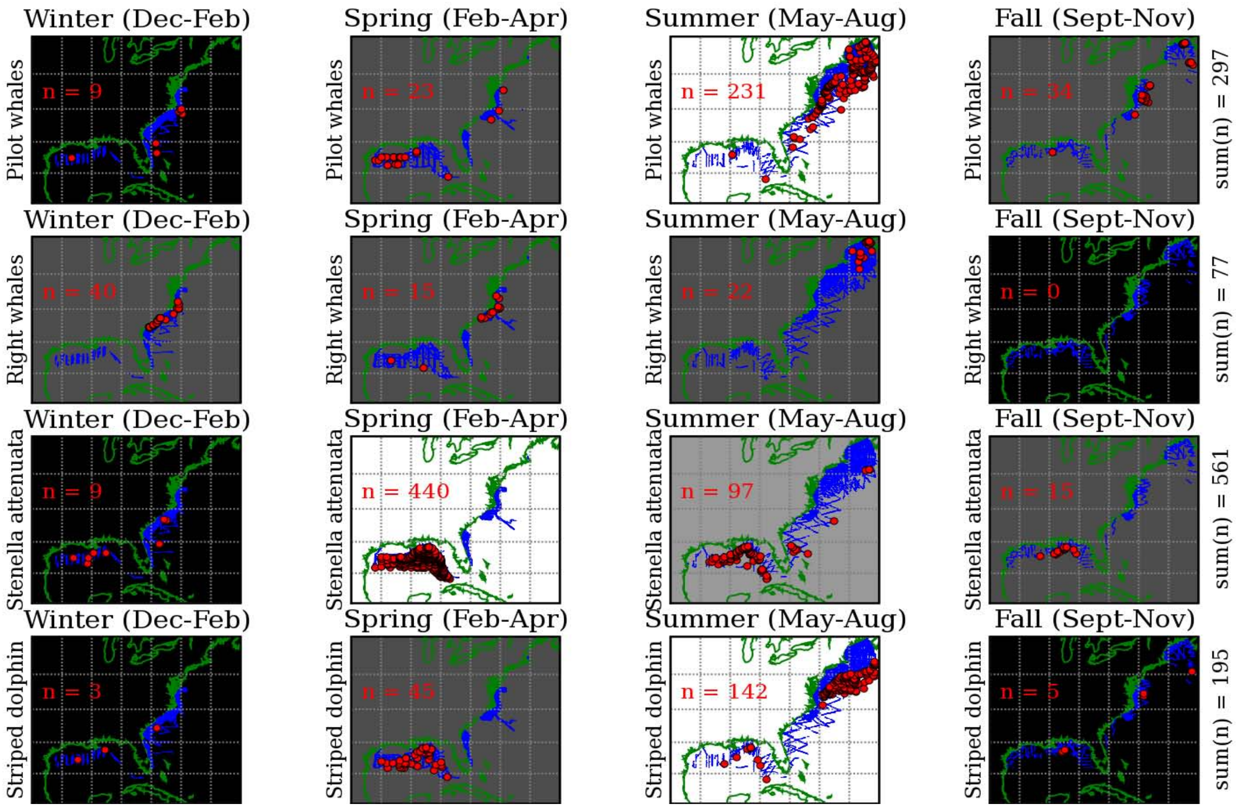

Figure 23. Data availability (part 3 of 4) for Pilot whales, Right whales, *Stenella attenuata* and Striped dolphin by season with marginal totals of observations (n) and effort (e). Blue lines are effort and red dots observation. Background color corresponds with obs < 10 (black), 10-49 (dark grey), 50-99 (light grey), 100+ (white).

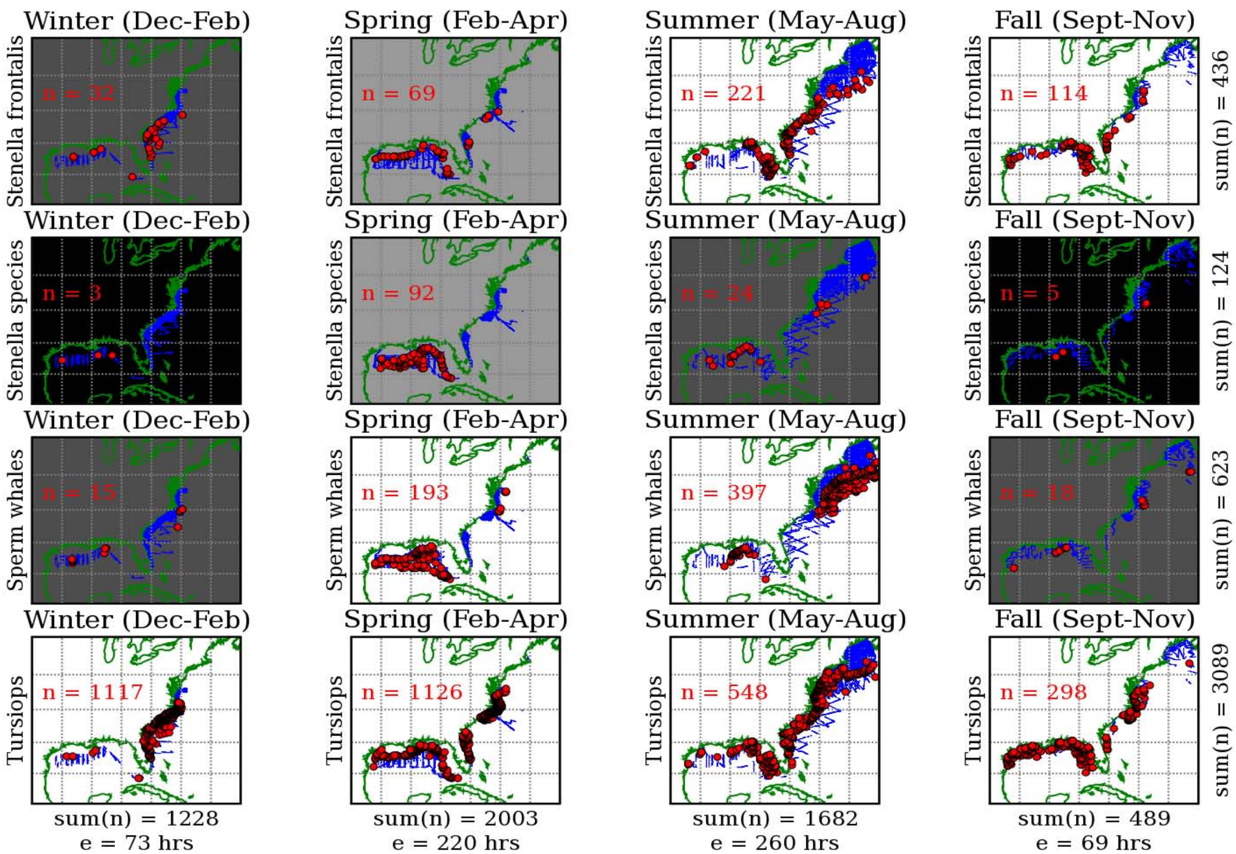

Figure 24. Data availability (part 4 of 4) for *Stenella frontalis*, *Stenella*, Sperm whales and *Tursiops* by season with marginal totals of observations (n) and effort (e). Blue lines are effort and red dots observation. Background color corresponds with obs < 10 (black), 10-49 (dark grey), 50-99 (light grey), 100+ (white).

4.3 Final Models for the Gulf of Mexico

A total of 65,104.5 km (280.8 days) of effort data were available for model building in the Gulf of Mexico, all of which are based from ship-based surveys.

The figures and tables in Appendix B present the habitat suitability model results for nine cetacean guilds in the Gulf of Mexico. The nine guilds include: beaked whales, sperm whale, killer whales, *Kogia*, *Stenella*, *Stenella attenuata*, *Stenella frontalis*, *Stenella coeruleoalba*, and *Tursiops truncatus*. Each guild converged in the summer season except *Stenella coeruleoalba*. No guild converged for the winter season, and only a few models converged during the fall and spring seasons (Table 6).

Table 6. Gulf of Mexico model by season.

Guild	Season			
	Summer	**Fall**	**Winter**	**Spring**
Beaked whale	X			
Sperm whale	X			
Killer whales	X			
Kogia	X			
Stenella	X			
Stenella attenuata	X			X
Stenella frontalis	X	X		X
Stenella coeruleoabla				X
Tursiops truncatus	X	X		

The Atlantic spotted dolphin (*Stenella frontalis*) occurs primarily from the continental shelf waters (10-200 m deep) to the slope waters (< 500 m deep) in the Gulf of Mexico (Fulling *et al*. 2003; Mullin and Fulling 2004), and has been seen in the Gulf of Mexico in all seasons (Waring *et al*. 2008). The fall *S. attenuata* model for the Gulf of Mexico shows the highest probability of suitable habitat along the entirety of the continental shelf within the model area. The GAM plot of depth illustrates the negative response between deep water and suitable habitat, and a positive response between shallower water and suitable habitat.

Sperm whales are present year round in the Gulf of Mexico (Mullin *et al*, 1994; Hansen *et al*. 1996; Mullin and Hoggard 2000). Ship based and aerial surveys indicate sperm whales are widely distributed only in waters greater than 200 meters in the northern Gulf of Mexico, (Waring *et al*. 2008), however they aggregate around the continental shelfbreak and canyon regions (Davis *et al*. 1998; Baumgartner *et al*. 2001; Jochens *et al*. 2006). The summer sperm whale model for the Gulf of Mexico shows the probability of highest suitable habitat for sperm whales along the shelfbreak off the Mississippi delta, Desoto Canyon, and western Florida. The depth GAM plot indicates a negative response to shallow waters (less than 1000 meters) and a positive response to deeper waters (greater than 1000 m).

Although beaked whale sightings in the Gulf of Mexico are scarce, they have been sighted in all seasons (Waring *et al*. 2008). They are widely distributed in the deeper waters of the Gulf of Mexico. The summer beaked whale model for the Gulf of Mexico shows highest probability of suitable habitat in the waters offshore of the shelf break in the central and western part of the model area. As shown in the GAM plot, depth is the only variable the produced a response. There is a negative response between shallow water and suitable habitat, and a positive response between deeper water and suitable habitat.

4.4 Final Models for the Atlantic

A total of 258,693.1 km (341.4 days) of effort data were available for model building in the US Atlantic EEZ. Aerial surveys comprised 50,575.8 km (218.2 days) of effort, whereas 208,117.3 km (123.2 days) came from ship-based surveys.

The figures and tables in Appendix B present the habitat suitability values for 11 guilds in the Atlantic Ocean. The 11 guilds include: baleen whales, humpback whales, right whales, beaked whales, sperm whales, pilot whales, lags, common dolphins, *Stenella coeruleoalba*, *Tursiops truncatus*, and *Phocoena phocoena* (Table 7). Two guilds, *Tursiops truncatus* and Harbor porpoise, were modeled in respective subregions because of the local intensity of sighting data. *Tursiops truncatus* were modeled in the Northeast and Southeast subregions while Harbor porpoise were only modeled in the Northeast subregion.

Table 7. Atlantic Ocean guilds by season.

Guild	**Season**			
	Summer	**Fall**	**Winter**	**Spring**
Baleen whales	X	X		
Humpback whale	X	X	X	
Right whale	X			
Beaked whales	X			
Sperm whale	X	X		
Pilot whales			X	
Lags	X			
Common dolphins	X			
Stenella coeruleoalba	X			
Tursiops truncatus (Northeast)		X		X
Tursiops truncatus (Southeast)	X		X	X
Phocoena phocoena (Northeast)	X	X		

4.4.1 East

The North Atlantic right whale (*Eubalaena glacialis*) occurs in the Gulf of Maine year round but is observed in large aggregations during the spring and summer months (Cole *et al.* 2007, Baumgartner and Mate 2005, Winn *et al.* 1986). The modeled summer habitat is consistent with decades of summer right whale observations in the Gulf of Main. Further, the GAM plots for the model demonstrate a strong response with depth and sea surface temperature, which is consistent with the whale's well documented, discrete foraging grounds (Baumgartner *et al.* 2003).

In the Atlantic, beaked whales are observed primarily offshore, along the continental shelf break (Waring *et al.* 2001, Palka 2006, MacLeod *et al.* 2006). This distribution is reflected in the summer GAM results which confirm a strong association with deep water habitat. The most robust habitat occurs just east of the shelf break which corresponds well with the limited observation data available for this deep foraging species.

4.4.2 Northeast Atlantic

The distribution of harbor porpoise in the Gulf of Maine is well documented, especially during the summer months. In summer, harbor porpoise occur in the northern reaches of the Gulf of Maine in waters less than 150m deep (Gaskin 1977, Kraus *et al.* 1983, Palka 1995). The species proximity to shore and preference for shallow depths is reflected in the GAM plots for the summer habitat model.

There are two genetically distinct morphotypes of *Tursiops truncatus* in U.S. Atlantic waters (Duffield *et al*. 1983), offshore and coastal forms. The offshore form is generally distributed along the outer continental shelf while the coastal form is continuously distributed along U.S. east coast from Florida to south of Long Island, NY (Waring *et al*. 2009). The spring *Tursiops truncatus* models in the Northeast represent suitable habitat for the coastal form only as offshore data were not available for this guild. The GAM plots show a positive response to shallow waters and mid-latitudes.

4.4.3 Southeast Atlantic

In the southeastern Atlantic, the spring *Tursiops truncatus* model reflects habitat preference for the coastal form as offshore data were not available for this guild. The GAM plots show a positive response to shallow waters. There is also a small positive response to sea surface temperature between approximately 16 and 21 Celsius.

4.5 Model Validation

In general, our ability to evaluate the performance of the two model types was hindered by a lack of empirical data in both Onslow Bay and Jacksonville. We should note that one of the criteria used to select these two potential USWTR sites was a low density of marine mammals, to avoid potentially adverse effects from Naval training activities in these areas.

We had sufficient survey data from the two monitoring areas to evaluate model performance in a robust fashion for only two species: bottlenose and spotted dolphins (*Stenella frontalis*). In addition, we were able to compare survey data from spotted dolphins only with the NODE model output, because there were too few data to construct a habitat suitability model for this species in the Atlantic (see Table B-1). We were able to make some tentative evaluations of model outputs for Risso’s dolphins (*Grampus griseus*) and pilot whales (*Globicephela* spp.) in Onslow Bay, albeit with very limited data. Two additional species, minke whales (*Balaenoptera acutorostrata*) and rough-toothed dolphins (*Steno bredanensis*), were observed in the two monitoring areas, but only very rarely; we did not attempt to validate model outputs for these two rare species.

In general, the NODE models performed better for data-rich species (bottlenose and spotted dolphins) than rare species (pilot whales and Risso’s dolphins), but performance varied greatly among species (Tables 8 and 9). Outside the spring and summer months, there were very few observations and our comparisons in these other seasons should be treated with caution. In spring and summer, the NODE model outputs demonstrated a general positive relationship with the relative density estimates, particularly with the aerial survey data sets that contained a larger number of observations (Table 8). This was most pronounced for the NODE model outputs of spotted dolphins in spring at the Onslow Bay site (Table 8), although with r_s values of 0.45, the correlation is not particularly robust.

Bottlenose dolphins were the only species with sufficient data to compare both NODE and habitat models (Tables 9-11). Using the aerial survey data, the two models performed similarly at the Jacksonville site with significant r_s values of 0.22 for the NODE model and 0.21 for the habitat models. In Onslow Bay, the density models ($r_s = 0.28$) slightly outperformed the habitat models ($r_s = 0.23$), although in spring the habitat model values were negatively correlated with bottlenose dolphin relative density.

We also compared the observed relative densities of bottlenose dolphins at both sites with the binary assessment of habitat, derived from our habitat suitability models. In summer, 50 8-km cells contained bottlenose dolphin sightings; the binary habitat model correctly predicted 27 of these cells. In spring, 27 cells contained sightings, but none of these cells were identified as habitat by the binary habitat model. In winter, 13 cells contained sightings, but again the binary habitat model failed to predict occurrence in any of these cells. Essentially, the spring and winter models failed to capture this offshore component of the habitat of bottlenose dolphins. In contrast the summer model was more accurate, because more observations were available for development of the original model. Once again, our take home message is that more data results in better models.

Appendix E includes visual representations of the relative density and modeled values for each combination of variables for which data were available, including species for which no formal statistical analysis was possible.

Table 8. Spearman correlation coefficients describing the relationship between relative density estimates derived from (a) aerial surveys and (b) ship-based surveys and NODE density estimates at the Onslow Bay USWTR monitoring site. (Significant p-values in bold.)

		Winter			Spring			Summer			Fall		
	Species	r_s	p-value	n	r_s	p-value	n	r_s	p-value	n	r_s	p-value	n
a.	Bottlenose Dolphins	0.02	0.8172	97	0.26	**0.0077**	101	0.28	**0.0048**	100	0.26	**0.0105**	99
	Spotted Dolphins	0.26	**0.0094**	97	0.45	**0.0001**	101	0.15	0.1423	100			
	Risso's Dolphins							-0.06	0.5714	100			
	Pilot Whales				0.11	0.2866	101	0.25	**0.0121**	100			
b.	Bottlenose Dolphins				-0.15	0.6576	11	-0.05	0.5082	84	0.41	0.0583	22
	Spotted Dolphins				0.3	0.3701	11	0.21	0.0582	84	0.45	**0.0371**	22
	Risso's Dolphins							-0.04	0.7412	84			
	Pilot Whales							0.21	0.0566	84			

Table 9. Spearman correlation coefficients describing the relationship between relative density estimates from aerial surveys and NODE density estimates at the Jacksonville USWTR monitoring site. (Significant p-values in bold.)

	Winter			Summer		
Species	r_s	p-value	n	r_s	p-value	n
Bottlenose Dolphins	-0.1	0.2989	101	0.22	**0.0162**	120
Spotted Dolphins	0.22	**0.0239**	101	0.25	**0.0057**	120

Table 10. Spearman correlation coefficients describing the relationship between relative density estimates derived from (a) aerial surveys and (b) ship-based surveys data and habitat suitability models at the Onslow Bay USWTR monitoring site. (Significant p-values in bold.)

		Winter			Spring			Summer		
	Species	r_s	p-value	n	r_s	p-value	n	r_s	p-value	n
a.	Bottlenose Dolphins	-0.01	0.9424	97	-0.23	**0.0235**	101	0.23	**0.0211**	100
b.	Bottlenose Dolphins				0.3	0.3631	11	0.07	0.5082	84

Table 11. Spearman correlation coefficients describing the relationship between relative density estimates derived from aerial surveys and habitat suitability models at the Jacksonville USWTR monitoring site. (Significant p-values in bold.)

	Winter			Summer		
Species	r_s	p-value	n	r_s	p-value	n
Bottlenose Dolphins	0.14	0.1717	101	0.21	**0.0226**	120

5.0 Conclusions and Implications for Future Research/Implementation

We constructed habitat suitability models for 20 guilds of marine mammals in the Gulf of Mexico and Atlantic Ocean. We believe that these models will allow the Navy and other parties to predict the probability of occurrence of these marine mammal species over broad areas of interest. After evaluating a variety of modeling approaches independently, we concur with Barlow et al. (2009) that General Additive Models "offer a robust framework for predictive modeling of cetacean density, as long as sufficient observations of each species are available and the surveys adequately characterize the full range of oceanographic variability." We also agree that remotely sensed environmental observations can be used effectively to predict the distribution and density of marine mammals at sea.

Our Spatial Decision Support System hosts the results of our modeling work, together with model outputs from our sister project in the Pacific (SI-1391) and the NODE model outputs of spatial variation in marine mammal density in the Atlantic. These products are publically available over the web in an interactive format that allows users to download model outputs, view input data, examine model diagnostics and query data sets. We believe that the SDSS offers a powerful tool to a wide variety of potential users both within and outside the Navy community. As noted below, the true value of the SDSS will depend on its acceptance and use within the Navy, NOAA and scientific communities.

Despite having access to the vast majority of line transect surveys conducted by NOAA and academic institutions, there were significant gaps in spatial and temporal coverage of marine mammal distribution in the Atlantic and Gulf of Mexico EEZ. These data gaps severely limited our ability to construct models of habitat suitability for many species. The Gulf of Maine and Gulf of Mexico have had the benefit of major research efforts on cetaceans, but no similar effort has occurred for the area south of Cape Hatteras. Accordingly, there is a stark need for more surveys in the southeastern U.S. In addition, we stress the need for more data collection outside the summer season in all areas. Most surveys are conducted in summer, when sighting conditions are best, but this limits our understanding of the distribution of marine mammals in other seasons. In some cases, traditional surveys can be conducted in other seasons to address this need. In other situations, it will be necessary to develop alternative methods of obtaining insight into distribution and estimating density, using passive acoustic monitoring and other means. This will be a major challenge for our field in the coming decades.

Almost by definition, data are very limited for rare species, which are often of particular concern to the Navy and other ocean users. Here we specifically highlight the need for better information on the distribution of beaked whales in the Atlantic and Gulf of Mexico, particularly at the species level. Our work showed important differences in the habitat preferences of different species of beaked whales; more work is needed in this area and, again, novel techniques will be needed to address this data limitation. We hope that our work will help to spur further research efforts into the ecology and conservation of beaked whales and other species discussed herein.

The availability of data restricted our modeling efforts to predicting the habitat suitability of marine mammals at a fairly coarse scale. Neither our models of habitat suitability nor the

NODES models of density were particularly successful at predicting the occurrence of cetaceans at a fine scale in two areas of particular Navy interest. Both of these areas were in the southeastern U.S., where data are particularly limited. Not surprisingly, the models performed best when developed for data-rich species. Thus, our analysis (and that of our sister project) indicates that, when adequate data are available, we can construct models that accurately capture the distribution and density of marine mammals at various scales. When data are sparse, the models perform poorly. In such cases, there may be no alternative to conducting dedicated monitoring programs, using a suite of techniques to describe the distribution and density of marine mammals.

We also recognize that there is considerable interest, both within and outside the Navy, in understanding the distribution and density of marine mammals in areas that have yet to be surveyed. Almost no survey effort has been expended in Atlantic waters outside the U.S. EEZ, for example, so our knowledge of marine mammals in these waters is almost non-existent. We caution that it is impossible to predict the distribution or density in such areas, at least with the present tools at our disposal. Such knowledge can come only from dedicated surveys or data collection programs using platforms of opportunity.

6.0 Transition Plan

We hope that the models of marine mammal habitat preferences we developed here will be useful to environmental planners from the Navy. As noted above, our model outputs and those from SI-1391 are publically accessible at http://serdp.env.duke.edu/ in the form of a Spatial Decision Support System (SDSS).

We agree fully with the principals from SI-1391 that there is a critical need to transition the SDSS to a permanent web site maintained by some entity with a commitment to maintain the software over a long term. NOAA is in an excellent position to host this online resource, particularly because it is the agency that permits many of the activities that could potentially affect marine mammal populations. We are ready to work with NOAA to make this transition.

We believe strongly that, whoever hosts the SDSS, it should remain publically and freely available to a variety of users. As noted in Barlow et al. (2009) many potential users have been identified for this software tool. Together with our colleagues from the Southwest Fisheries Science Center, we identified a partial list of potential users at a joint planning meeting between the SWFSC and Duke teams which includes: Navy, Air Force, Coast Guard, Army Corps of Engineers, Minerals Management Service, National Science Foundation, National Marine Fisheries Service Science Centers and Regional Offices, universities, and oil exploration companies.

We have been working with our colleagues from the SWFSC to develop a transition plan for the outcomes of our two research programs. Together with the lead PI on SI-1391 (Barlow) we have participated in seminars describing the SERDP projects at NOAA and to the Inter-Agency Working Group on Marine Mammals. Ultimately, however, it is up to the Navy and NOAA to decide how best to use the resources in the SDSS and what, if any, further refinement of this information is necessary. We are ready and able to assist, but the impetus must come from two these federal agencies.

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Appendix A: List of Scientific/Technical Publications

A.1 Journal Publications

Best, B.D., P.N. Halpin, E. Fujioka, A.J. Read, S.S. Qian, L.J. Hazen, and R.S. Schick. 2007. Geospatial web services within a scientific workflow: Predicting marine mammal habitats in a dynamic environment. Ecological Informatics 2:210-223.

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Schick, R.S., P.N. Halpin, A.J. Read, D. Urban, B.D. Best, C.P. Good, J.E. Roberts, E.A. LaBrecque, C. Dunn, and L.P. Garrison. *In review*. Community Structure in Pelagic Marine Mammals at Large Spatial Scales as Revealed by Multivariate Ordination. Marine Ecology Progress Series.

A.2 PhD Dissertations

Schick, R.S. (2009) Animal Movement in Pelagic Ecosystems: From Communities to Individuals. Ph.D. Dissertation, University Program in Ecology, Duke University, Durham, NC.

Good, C.P. (2009) Spatial Ecology of the North Atlantic Right Whale (*Eubalaena glacialis*). Ph.D. Dissertation, University Program in Ecology, Duke University, Durham, NC.

A.3 Conference Proceedings

Schick, R.S., Loarie, S.R., Halpin, P.N., Read, A.J., Slay, C.S., Kraus, S.D., Mate, B.R., Baumgartner, M.F., and Clark, J.S. Estimating habitat suitability in the migratory corridor of NW Atlantic Right Whales. The Annual Meeting of the North Atlantic Right Whale Consortium, New Bedford, MA, November 5-6, 2008.

Schick, R.S., Clark, J.S., Loarie, S.R., Colchero, F., Best, B.D., Boustany, A., Conde, D.A., Halpin, P.N., Joppa, L.N., McCellan, C.M., Read, A.J., Slay, C.S., Kraus, S.D., Mate, B.R., and Baumgartner, M.F. Understanding Movement Data and Movement Processes: what is the state of the art? The Third International Biologging Science Symposium, Pacific Grove, CA, September 1-5, 2008.

Appendix B: Detailed Model Results

Table B-1. Summary status of all attempted models by combination of region, guild and season. Data with less than cells containing observations (N < 5) were skipped. Some failed to converge. Of those that converged, many were considered invalid by expert opinion. Presences (1s) and absences (0s) are listed. Deviance explained, adjusted r-squared, maximum value from fitted model, maximum value from prediction, and optimum binary cutoff value from ROC.

Region	Guild	Season	Status	1s	0s	R^2	Dev. Expl.	Max Fit	Max Predict	ROC Opt.
Gulf of Mexico										
	Baleen whales	Fall	N < 5	1	944					
		Spring	Invalid	8	4,809	0.03	0.35	0.08	0.10	0.01
		Summer	N < 5	1	1,403					
		Winter	N < 5	0	605					
	Beaked whales	Fall	N < 5	2	943					
		Spring	Invalid	56	4,761	0.09	0.11	0.16	0.07	0.00
		Summer	Valid	13	1,391	0.27	0.37	0.67	0.09	0.01
		Winter	N < 5	1	604					
	Delphinus	Fall	N < 5	0	945					
		Spring	N < 5	0	4,817					
		Summer	N < 5	0	1,404					
		Winter	N < 5	0	605					
	Harbor porpoise	Fall	N < 5	0	945					
		Spring	N < 5	0	4,817					
		Summer	N < 5	0	1,404					
		Winter	N < 5	0	605					
	Humpback whales	Fall	N < 5	0	945					
		Spring	N < 5	1	4,816					
		Summer	N < 5	0	1,404					
		Winter	N < 5	0	605					
	Killer whales	Fall	N < 5	0	945					
		Spring	Invalid	31	4,786	0.26	0.23	0.23	0.03	0.00
		Summer	Valid	14	1,390	0.03	0.10	0.06	0.04	0.01
		Winter	N < 5	1	604					
	Kogia	Fall	N < 5	0	945					
		Spring	Invalid	91	4,726	0.04	0.07	0.19	0.11	0.03
		Summer	Valid	29	1,375	-0.04	0.07	0.03	0.03	0.01
		Winter	N < 5	1	604					

Region	Guild	Season	Status	1s	0s	R^2	Dev. Expl.	Max Fit	Max Predict	ROC Opt.
Gulf of Mexico										
	Lags	Fall	N < 5	0	945					
		Spring	N < 5	0	4,817					
		Summer	N < 5	0	1,404					
		Winter	N < 5	0	605					
	Pilot whales	Fall	N < 5	1	944					
		Spring	Invalid	17	4,800	0.00	0.06	0.02	0.00	0.00
		Summer	N < 5	2	1,402					
		Winter	N < 5	2	603					
	Right whales	Fall	N < 5	0	945					
		Spring	N < 5	2	4,815					
		Summer	N < 5	0	1,404					
		Winter	N < 5	0	605					
	Risso's dolphin	Fall	N < 5	1	944					
		Spring	Invalid	117	4,700	0.09	0.12	0.40	0.99	0.06
		Summer	Invalid	31	1,373	0.32	0.18	0.27	0.47	0.00
		Winter	N < 5	0	605					
	Rough-toothed dolphin	Fall	N < 5	4	941					
		Spring	Failed	15	4,802					
		Summer	Invalid	9	1,395	0.03	0.07	0.05	0.05	0.01
		Winter	N < 5	0	605					
	Sperm whales	Fall	Invalid	7	938	0.03	0.49	0.27	0.27	0.00
		Spring	Failed	128	4,689					
		Summer	Valid	40	1,364	0.25	0.29	0.50	0.44	0.03
		Winter	Invalid	7	598	-0.03	0.09	0.05	0.06	0.01
	Stenella attenuata	Fall	Invalid	15	930	-0.18	0.26	0.16	0.32	0.00
		Spring	Valid	342	4,475	0.15	0.09	0.23	0.16	0.04
		Summer	Valid	71	1,333	0.24	0.19	0.27	0.27	0.01
		Winter	Failed	6	599					
		Fall	Valid	73	872	-0.29	0.15	0.15	0.20	0.03
		Spring	Valid	43	4,774	0.19	0.37	0.24	0.24	0.01
		Summer	Valid	69	1,335	0.49	0.41	0.43	0.43	0.01
		Winter	Invalid	6	599	0.02	0.26	0.28	0.62	0.02

Region	Guild	Season	Status	1s	0s	R^2	Dev. Expl.	Max Fit	Max Predict	ROC Opt.
	Stenella species	Fall	N < 5	2	943					
		Spring	Failed	76	4,741					
		Summer	Valid	15	1,389	0.26	0.26	0.33	0.25	0.00
		Winter	N < 5	3	602					
	Striped dolphin	Fall	N < 5	2	943					
		Spring	Valid	44	4,773	0.02	0.09	0.05	0.05	0.01
		Summer	Invalid	10	1,394	0.70	0.54	0.58	0.74	0.00
Gulf of Mexico										
	Striped dolphin	Winter	N < 5	2	603					
	Tursiops	Fall	Valid	160	785	0.71	0.30	0.93	0.99	0.16
		Spring	Invalid	157	4,660	0.05	0.28	0.33	0.65	0.03
		Summer	Valid	102	1,302	0.22	0.24	0.56	0.57	0.05
		Winter	Invalid	7	598	-0.07	0.22	0.03	0.03	0.02
East										
	Baleen whales	Fall	Valid	47	1,817	0.30	0.37	0.37	0.39	0.03
		Spring	Invalid	16	2,857	0.41	0.66	0.93	1.00	0.00
		Summer	Valid	372	8,706	0.18	0.27	0.58	0.61	0.04
		Winter	Invalid	16	3,886	0.45	0.50	0.56	1.00	0.00
	Beaked whales	Fall	N < 5	1	1,863					
		Spring	N < 5	1	2,872					
		Summer	Valid	121	8,957	0.16	0.28	0.35	0.54	0.01
		Winter	Invalid	6	3,896	-0.03	0.17	0.05	0.72	0.00
	Delphinus	Fall	Invalid	6	1,858	0.16	0.48	0.34	0.42	0.00
		Spring	Invalid	19	2,854	-0.03	0.06	0.04	0.14	0.01
		Summer	Valid	187	8,891	-0.12	0.21	0.17	0.17	0.01
		Winter	Invalid	49	3,853	-0.10	0.38	0.54	0.58	0.02
	Harbour porpoise	Fall	Invalid	46	1,818	0.00	0.50	0.43	0.44	0.03
		Spring	N < 5	0	2,873					
		Summer	Invalid	396	8,682	0.47	0.55	0.92	0.92	0.06

Region	Guild	Season	Status	1s	0s	R^2	Dev. Expl.	Max Fit	Max Predict	ROC Opt.
		Winter	N < 5	3	3,899					
	Humpback whales	Fall	Valid	27	1,837	0.69	0.62	0.78	0.78	0.03
		Spring	Invalid	11	2,862	0.01	0.13	0.26	0.27	0.01
		Summer	Valid	153	8,925	0.38	0.42	0.57	0.56	0.03
		Winter	Valid	11	3,891	0.46	0.48	0.60	0.80	0.23
	Killer whales	Fall	N < 5	1	1,863					
		Spring	N < 5	0	2,873					
		Summer	Invalid	7	9,071	-0.01	0.25	0.02	0.02	0.00
		Winter	N < 5	3	3,899					
	Kogia	Fall	N < 5	1	1,863					
		Spring	N < 5	0	2,873					
		Summer	Invalid	26	9,052	0.03	0.17	0.93	0.83	0.00
		Winter	N < 5	4	3,898					
	Lags	Fall	Invalid	15	1,849	-0.03	0.35	0.15	0.17	0.00
		Spring	N < 5	0	2,873					
		Summer	Valid	151	8,927	0.15	0.31	0.24	0.17	0.02
		Winter	N < 5	0	3,902					
	Pilot whales	Fall	Invalid	22	1,842	0.05	0.22	0.15	0.16	0.01
		Spring	N < 5	3	2,870					
East										
	Pilot whales	Summer	Invalid	156	8,922	0.08	0.06	0.15	0.14	0.07
		Winter	Valid	7	3,895	0.00	0.31	0.07	0.08	0.00
	Right whales	Fall	N < 5	0	1,864					
		Spring	Failed	13	2,860					
		Summer	Valid	17	9,061	0.02	0.32	0.26	0.12	0.00
		Winter	Invalid	16	3,886	0.98	0.88	1.00	0.68	0.05
	Risso's dolphin	Fall	Invalid	7	1,857	0.84	0.59	0.83	0.15	0.00
		Spring	N < 5	3	2,870					
		Summer	Invalid	231	8,847	0.25	0.27	0.98	0.98	0.06
		Winter	Invalid	7	3,895	0.99	0.94	1.00	1.00	0.00
	Rough-toothed dolphin	Fall	N < 5	1	1,863					
		Spring	N < 5	0	2,873					
		Summer	N < 5	3	9,075					

Region	Guild	Season	Status	1s	0s	R^2	Dev. Expl.	Max Fit	Max Predict	ROC Opt.
	Sperm whales	Winter	N < 5	1	3,901					
		Fall	Valid	7	1,857	0.26	0.54	0.37	0.59	0.00
		Spring	Invalid	8	2,865	-0.62	0.42	0.19	0.69	0.02
		Summer	Valid	224	8,854	0.22	0.29	0.31	0.30	0.02
	Stenella attenuata	Winter	Invalid	5	3,897	0.71	0.77	0.90	1.00	0.02
		Fall	N < 5	0	1,864					
		Spring	N < 5	0	2,873					
		Summer	Invalid	11	9,067	-0.02	0.24	0.06	0.04	0.00
	Stenella frontalis	Winter	N < 5	3	3,899					
		Fall	Invalid	22	1,842	0.51	0.46	0.63	0.93	0.03
		Spring	Invalid	6	2,867	-0.01	0.05	0.03	0.03	0.00
		Summer	Invalid	107	8,971	0.10	0.25	0.67	0.93	0.01
	Stenella species	Winter	Invalid	23	3,879	-0.02	0.07	0.03	0.03	0.00
		Fall	N < 5	2	1,862					
		Spring	N < 5	0	2,873					
		Summer	Invalid	6	9,072	-0.01	0.12	0.01	0.01	0.00
	Striped dolphin	Winter	N < 5	0	3,902					
		Fall	N < 5	3	1,861					
		Spring	N < 5	0	2,873					
		Summer	Valid	115	8,963	0.20	0.29	0.43	0.13	0.03
	Tursiops	Winter	N < 5	1	3,901					
		Fall	Invalid	80	1,784	0.16	0.19	1.00	1.00	0.04
		Spring	Invalid	429	2,444	0.35	0.20	0.98	0.98	0.25
		Summer	Invalid	298	8,780	0.38	0.26	0.94	1.00	0.04
		Winter	Invalid	591	3,311	0.54	0.24	0.92	1.00	0.11
Northeast										
	Harbor porpoise	Fall	Valid	46	1,138	0.55	0.60	0.93	0.38	0.00
		Spring	N < 5	0	1,087					

Region	Guild	Season	Status	1s	0s	R^2	Dev. Expl.	Max Fit	Max Predict	ROC Opt.
		Summer	Valid	396	7,298	0.47	0.50	0.89	0.89	0.05
		Winter	N < 5	1	843					
	Tursiops	Fall	Valid	41	1,143	0.33	0.21	0.36	0.36	0.09
		Spring	Valid	204	883	0.53	0.31	0.88	0.88	0.20
		Summer	Invalid	210	7,484	0.47	0.35	0.96	0.99	0.02
		Winter	Invalid	113	731	0.77	0.64	0.98	1.00	0.03
Southeast										
	Tursiops	Fall	Invalid	39	641	0.47	0.34	0.57	1.00	0.07
		Spring	Valid	225	1,561	0.25	0.17	0.68	0.83	0.14
		Summer	Valid	88	1,296	0.50	0.22	0.91	0.97	0.06
		Winter	Valid	478	2,580	0.41	0.14	0.72	0.90	0.26

Gulf of Mexico

Beaked whales | Summer | Gulf of Mexico

Number of presences: 13
Number of absences: 1391
R squared: 0.270033
Deviance explained: 0.371218
ROC optimum: 0.667173
Maximum fit: 0.00983088
Maximum prediction: 0.0882899
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -46.175      5.174  -8.925   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F p-value
s(log(depth))   1.973e+00 1.973e+00    41.34  <2e-16 ***
s(log(d2shelf)) 1.774e-06 1.774e-06 2.04e-07      NA
s(log(d2coast)) 2.201e-06 2.201e-06 4.01e-05      NA
s(sst)          1.924e+00 1.924e+00   111.91  <2e-16 ***
s(lat)          3.466e-05 3.466e-05 1.38e-04      NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =   0.27   Deviance explained = 37.1%
GCV score = 0.00091915  Scale est. = 0.00091338  n = 1404
```

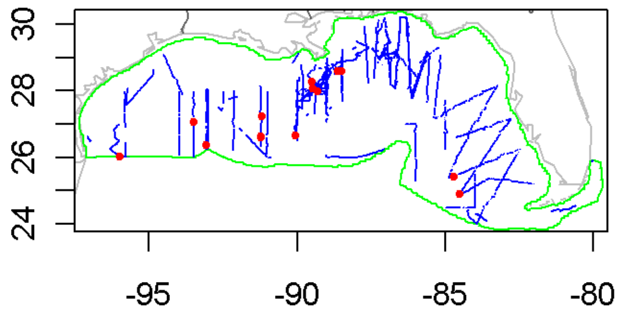


Figure B-1. Map of points of observational sightings and tracks of survey effort for Beaked whales guild during Summer season in Gulf of Mexico region.

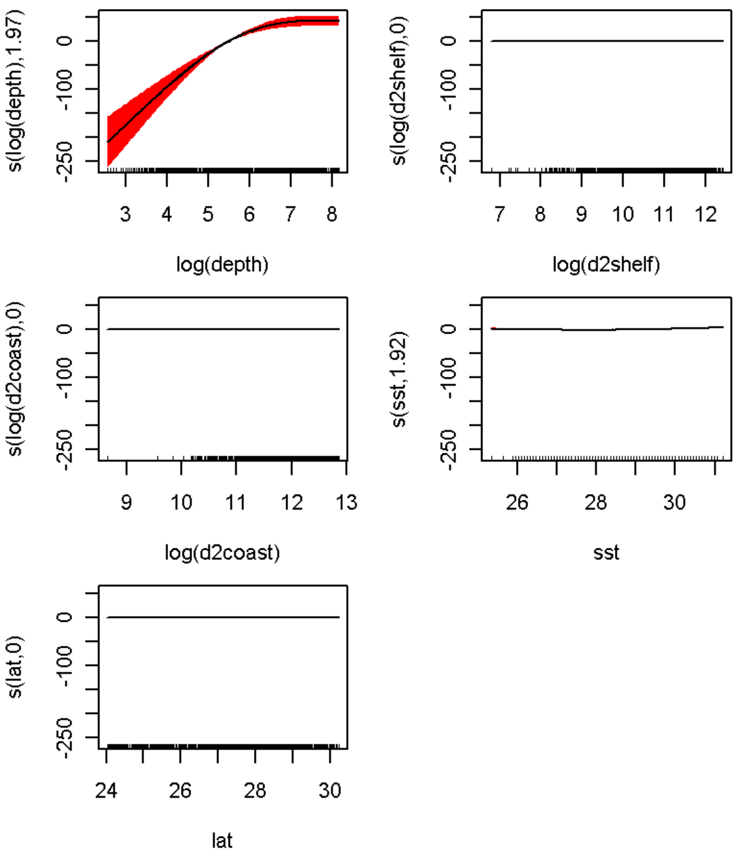


Figure B-2. Terms plot of predictors to GAM model fit for Beaked whales guild during Summer season in Gulf of Mexico region.

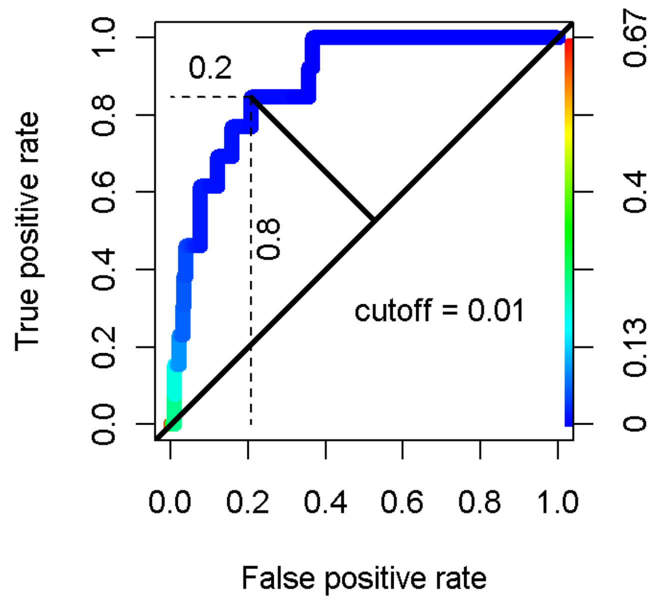


Figure B-3. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Beaked whales guild during Summer season in Gulf of Mexico region.

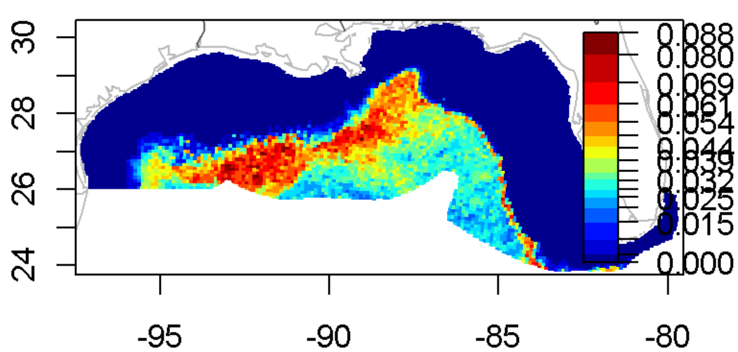


Figure B-4. Map of mean predicted habitat for Beaked whales guild during Summer season in Gulf of Mexico region.

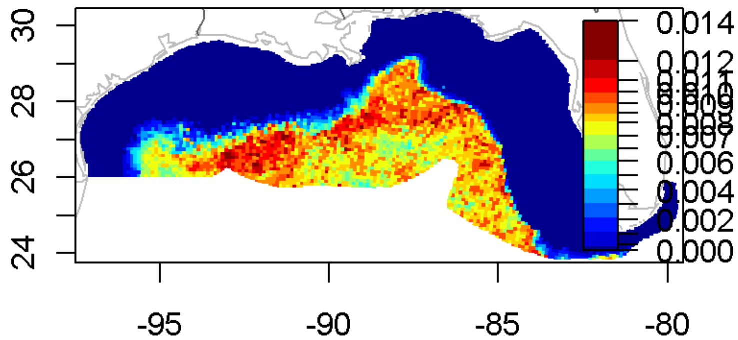


Figure B-5. Map of standard error of habitat for Beaked whales guild during Summer season in Gulf of Mexico region.

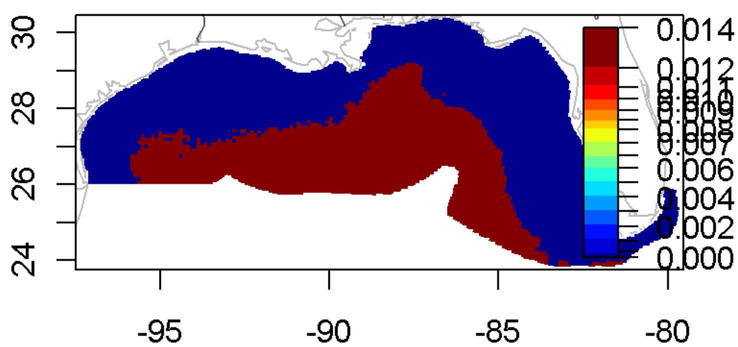


Figure B-6. Map of binary habitat (cutoff determined by ROC) for Beaked whales guild during Summer season in Gulf of Mexico region.

Killer whales | Summer | Gulf of Mexico
Number of presences: 14
Number of absences: 1390
R squared: 0.0313822
Deviance explained: 0.0973328
ROC optimum: 0.0611983
Maximum fit: 0.01223
Maximum prediction: 0.0400034
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -5.1302     0.1425     -36   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   9.318e-01 9.318e-01   50.191 9.95e-12 ***
s(log(d2shelf)) 8.615e-05 8.615e-05 3.50e-05       NA
s(log(d2coast)) 6.696e-01 6.696e-01    4.912  0.04034 *
s(sst)          8.579e-01 8.579e-01   10.541  0.00204 **
s(lat)          5.678e-06 5.678e-06 3.26e-06       NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.0314   Deviance explained = 9.73%
GCV score = 0.0010354  Scale est. = 0.0010308  n = 1404
```

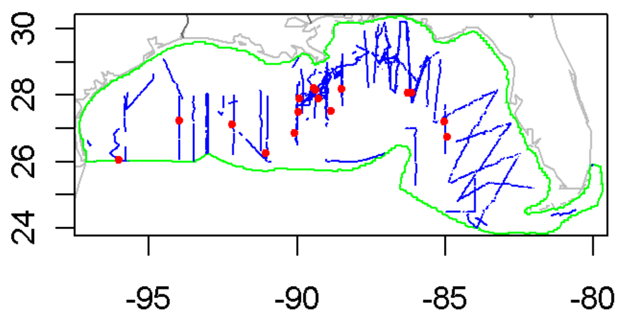


Figure B-7. Map of points of observational sightings and tracks of survey effort for Killer whales guild during Summer season in Gulf of Mexico region.

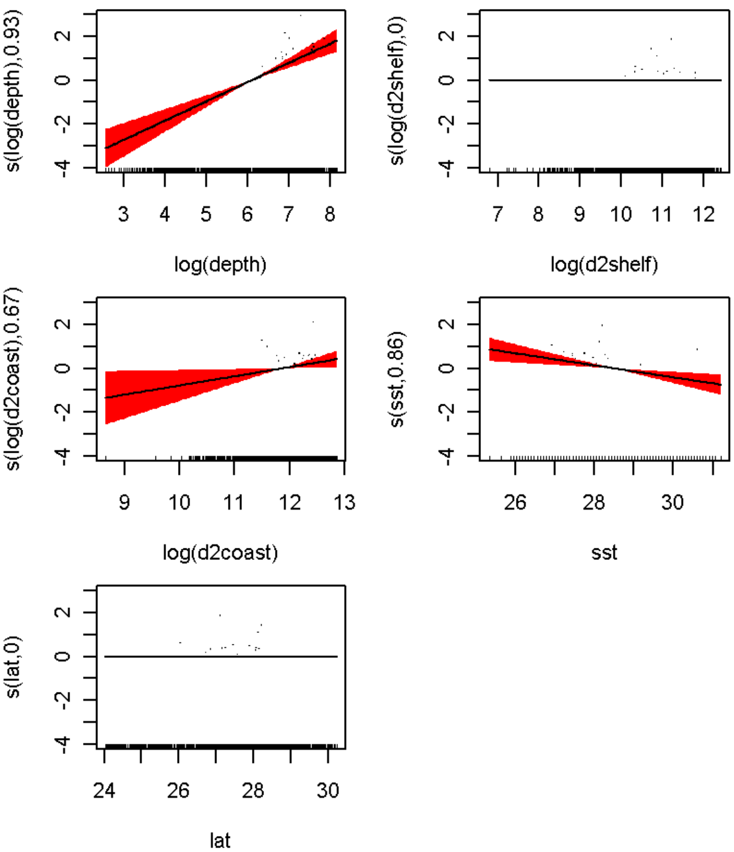


Figure B-8. Terms plot of predictors to GAM model fit for Killer whales guild during Summer season in Gulf of Mexico region.

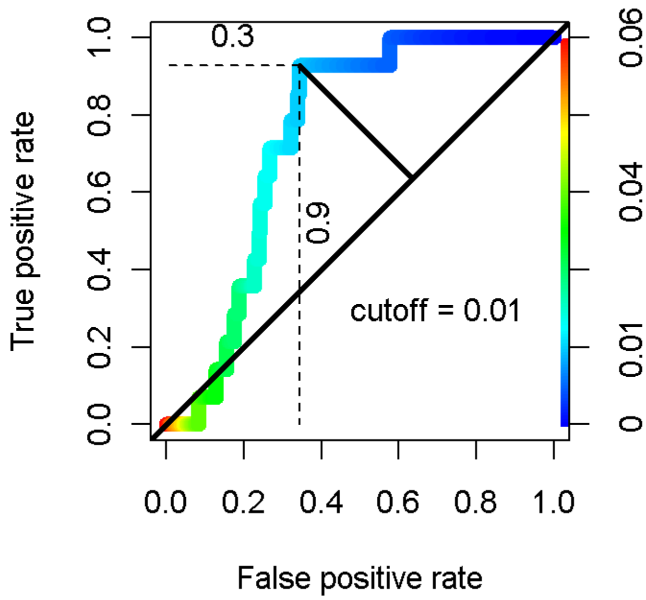


Figure B-9. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Killer whales guild during Summer season in Gulf of Mexico region.

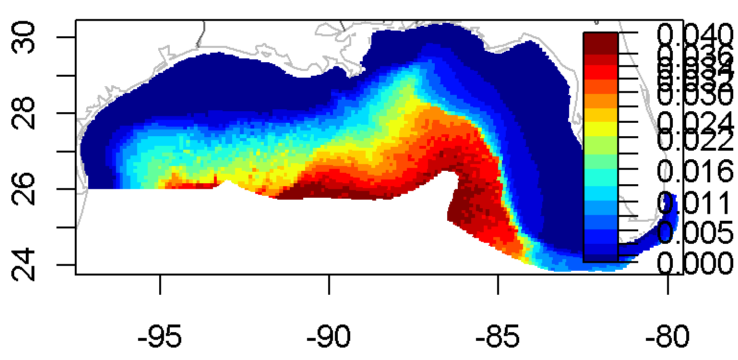


Figure B-10. Map of mean predicted habitat for Killer whales guild during Summer season in Gulf of Mexico region.

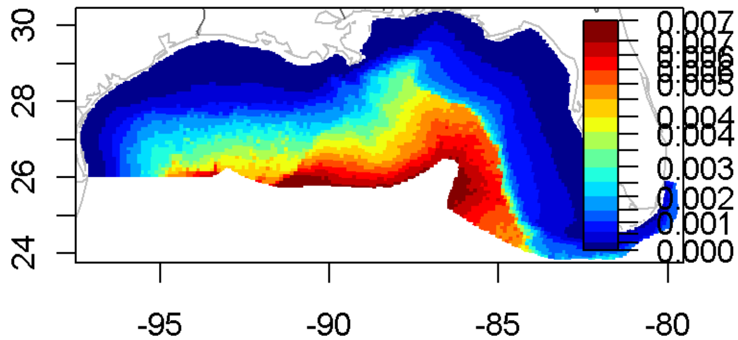


Figure B-11. Map of standard error of habitat for Killer whales guild during Summer season in Gulf of Mexico region.

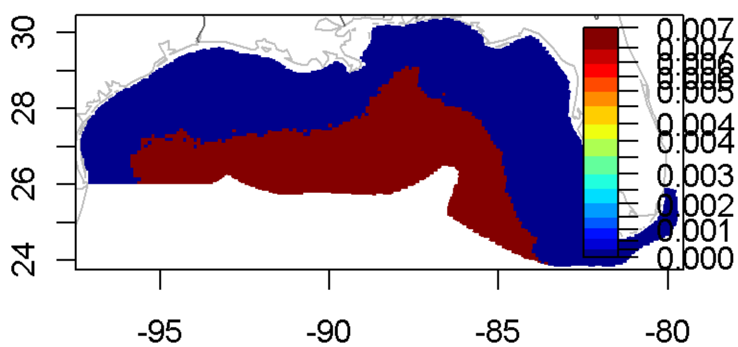


Figure B-12. Map of binary habitat (cutoff determined by ROC) for Killer whales guild during Summer season in Gulf of Mexico region.

Kogia | Summer | Gulf of Mexico
Number of presences: 29
Number of absences: 1375
R squared: -0.0428955
Deviance explained: 0.0658001
ROC optimum: 0.0280834
Maximum fit: 0.0105476
Maximum prediction: 0.0280833
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -5.6069     0.3417  -16.41   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   1.908e+00 1.908e+00   12.426 6.79e-06 ***
s(log(d2shelf)) 3.559e-06 3.559e-06 1.79e-06       NA
s(log(d2coast)) 5.422e-06 5.422e-06 1.43e-05       NA
s(sst)          1.622e-05 1.622e-05 6.43e-05       NA
s(lat)          6.359e-01 6.359e-01    2.788    0.107
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  -0.0429   Deviance explained = 6.58%
GCV score = 0.0013421  Scale est. = 0.001336  n = 1404
```

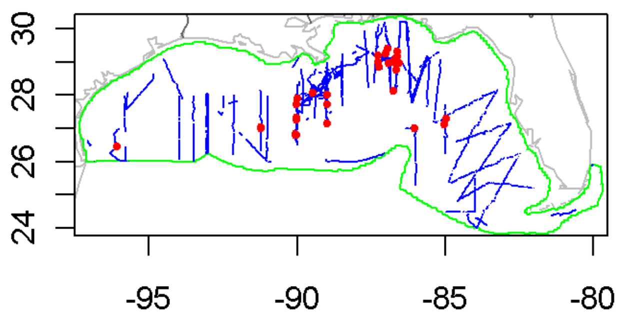


Figure B-13. Map of points of observational sightings and tracks of survey effort for Kogia guild during Summer season in Gulf of Mexico region.

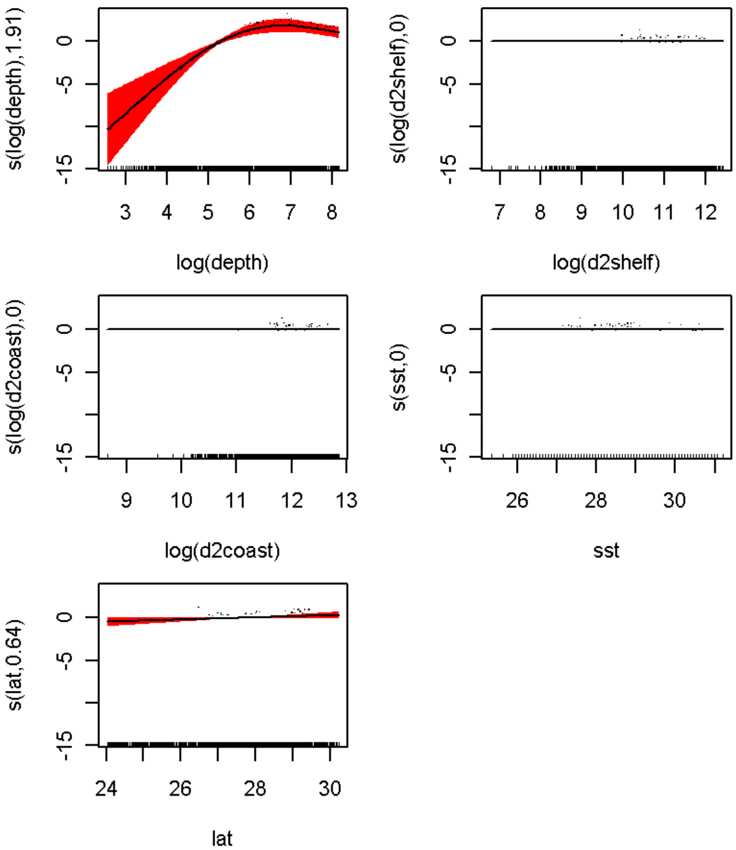


Figure B-14. Terms plot of predictors to GAM model fit for Kogia guild during Summer season in Gulf of Mexico region.

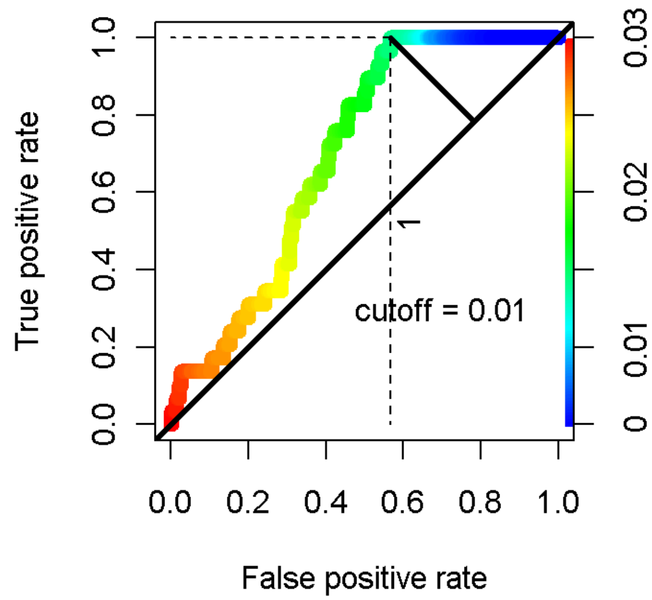


Figure B-15. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Kogia guild during Summer season in Gulf of Mexico region.

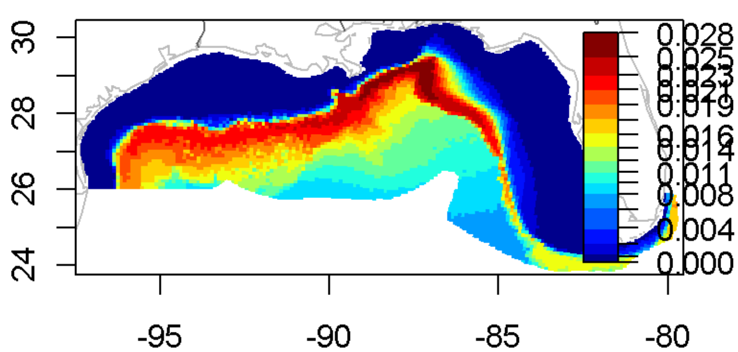


Figure B-16. Map of mean predicted habitat for Kogia guild during Summer season in Gulf of Mexico region.

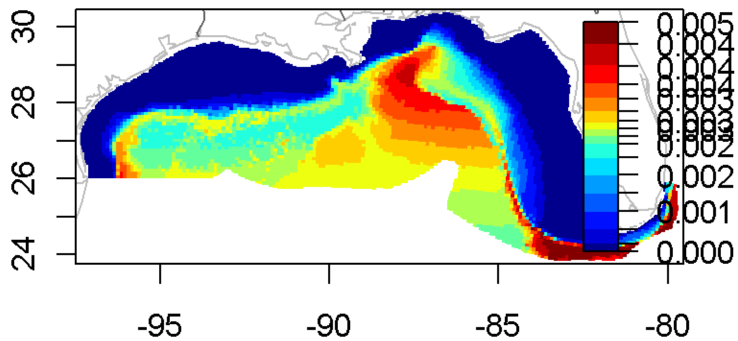


Figure B-17. Map of standard error of habitat for Kogia guild during Summer season in Gulf of Mexico region.

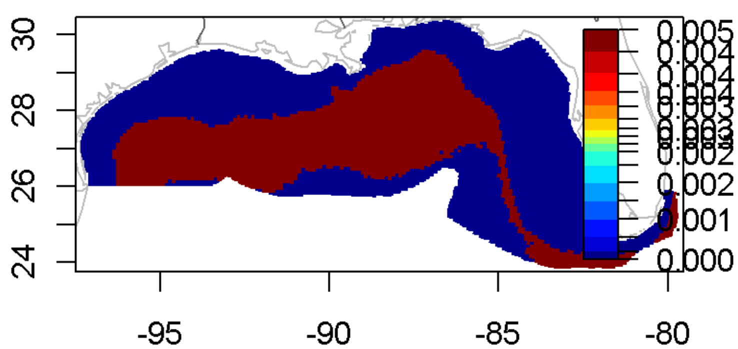


Figure B-18. Map of binary habitat (cutoff determined by ROC) for Kogia guild during Summer season in Gulf of Mexico region.

Sperm whales | Summer | Gulf of Mexico
Number of presences: 40
Number of absences: 1364
R squared: 0.247522
Deviance explained: 0.290869
ROC optimum: 0.50429
Maximum fit: 0.0281774
Maximum prediction: 0.435584
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -4.7000     0.2256  -20.83   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   9.322e-01 9.322e-01   44.898 1.14e-10 ***
s(log(d2shelf)) 6.975e-01 6.975e-01    4.692   0.0430 *
s(log(d2coast)) 8.073e-06 8.073e-06 2.56e-06       NA
s(sst)          9.863e-01 9.863e-01  182.846  < 2e-16 ***
s(lat)          1.770e+00 1.770e+00   29.319 5.50e-12 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.248   Deviance explained = 29.1%
GCV score = 0.0031407  Scale est. = 0.0031191  n = 1404
```

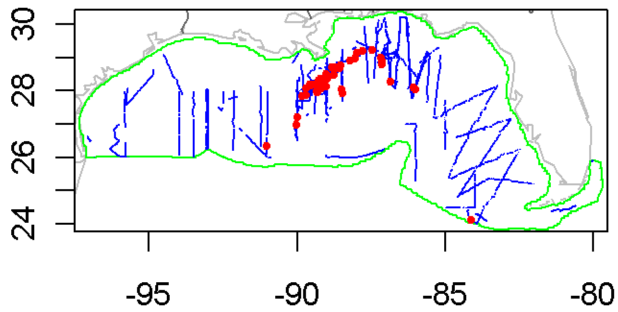


Figure B-19. Map of points of observational sightings and tracks of survey effort for Sperm whales guild during Summer season in Gulf of Mexico region.

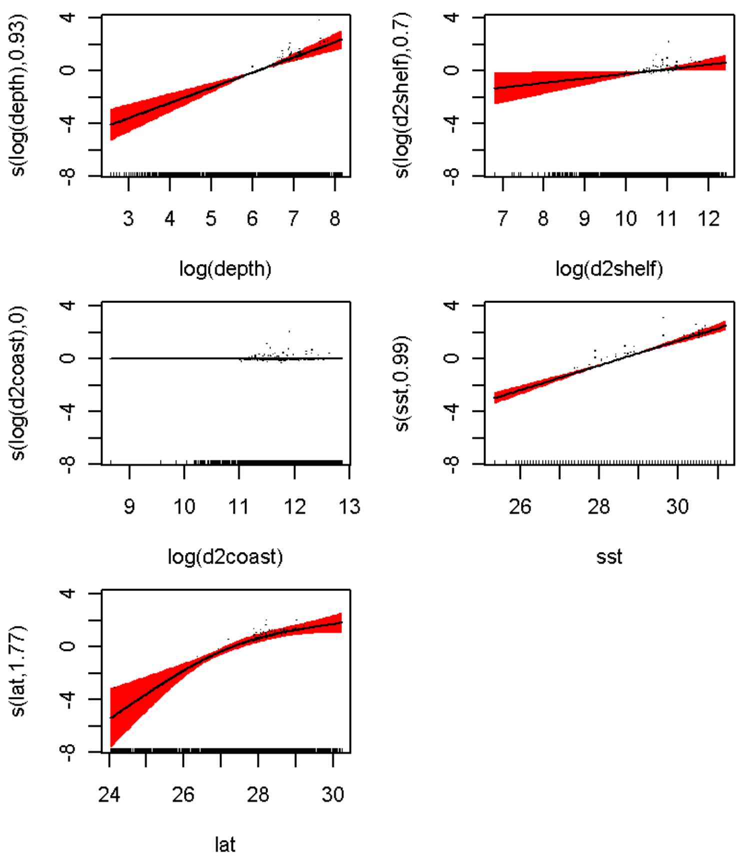


Figure B-20. Terms plot of predictors to GAM model fit for Sperm whales guild during Summer season in Gulf of Mexico region.

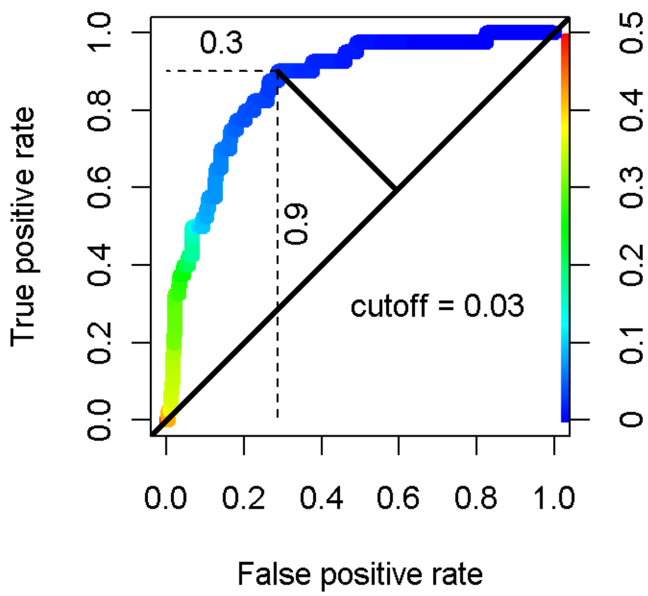


Figure B-21. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Sperm whales guild during Summer season in Gulf of Mexico region.

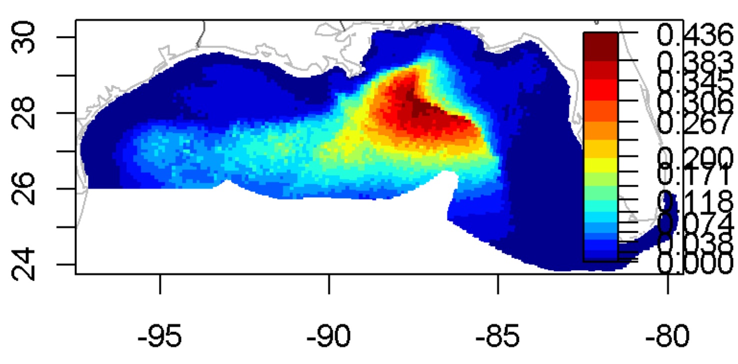


Figure B-22. Map of mean predicted habitat for Sperm whales guild during Summer season in Gulf of Mexico region.

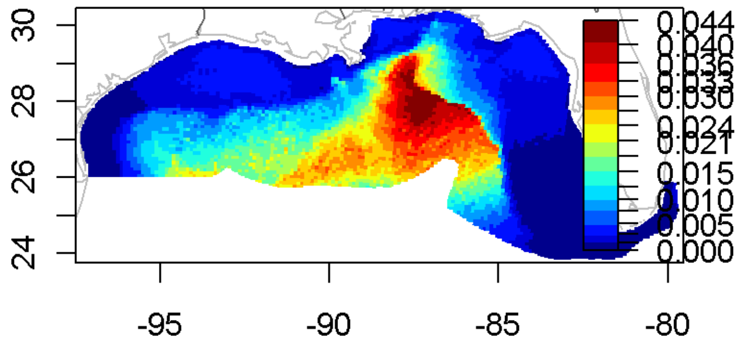


Figure B-23. Map of standard error of habitat for Sperm whales guild during Summer season in Gulf of Mexico region.

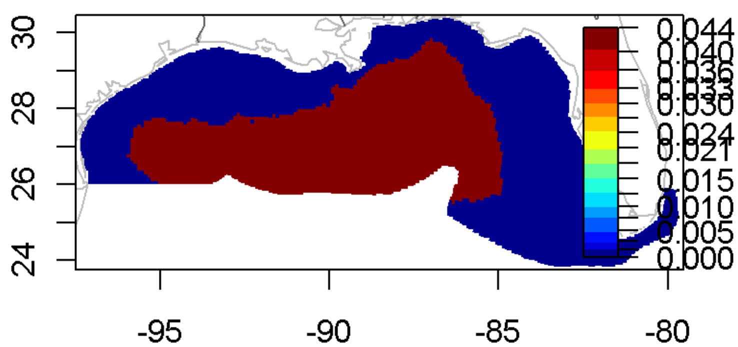


Figure B-24. Map of binary habitat (cutoff determined by ROC) for Sperm whales guild during Summer season in Gulf of Mexico region.

Stenella attenuata | Spring | Gulf of Mexico
Number of presences: 342
Number of absences: 4475
R squared: 0.152654
Deviance explained: 0.0982559
ROC optimum: 0.259881
Maximum fit: 0.066543
Maximum prediction: 0.2572
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 5, bs = 'ts') + s(d2shelf2, k = 5,
    bs = 'ts') + s(log(d2coast), k = 5, bs = 'ts') + s(sst, k =
5,
    bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -5.6042     0.8578  -6.533  7.1e-11 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                    edf   Ref.df        F  p-value
s(log(depth))   3.88293 3.882933    38.78  < 2e-16 ***
s(d2shelf2)     0.00139 0.001390 0.000271       NA
s(log(d2coast)) 2.45909 2.459086    46.63  < 2e-16 ***
s(sst)          0.91743 0.917425    14.88 0.000188 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.153   Deviance explained = 9.83%
GCV score = 0.0042591  Scale est. = 0.0042459  n = 4817
```

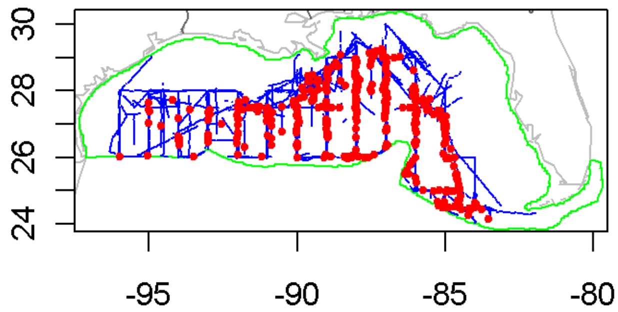


Figure B-25. Map of points of observational sightings and tracks of survey effort for Stenella attenuata guild during Spring season in Gulf of Mexico region.

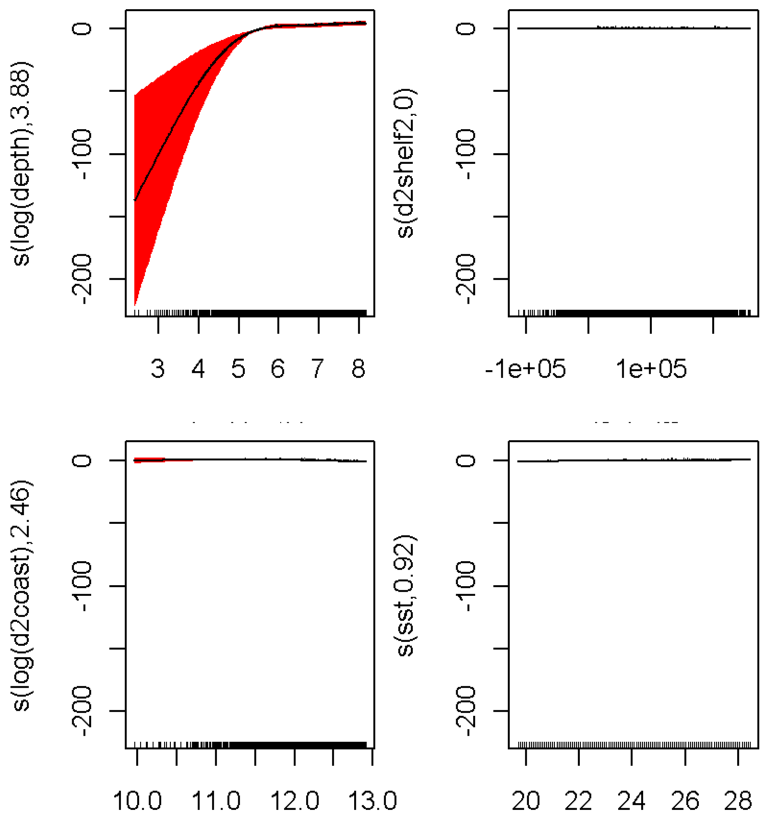


Figure B-26. Terms plot of predictors to GAM model fit for Stenella attenuata guild during Spring season in Gulf of Mexico region.

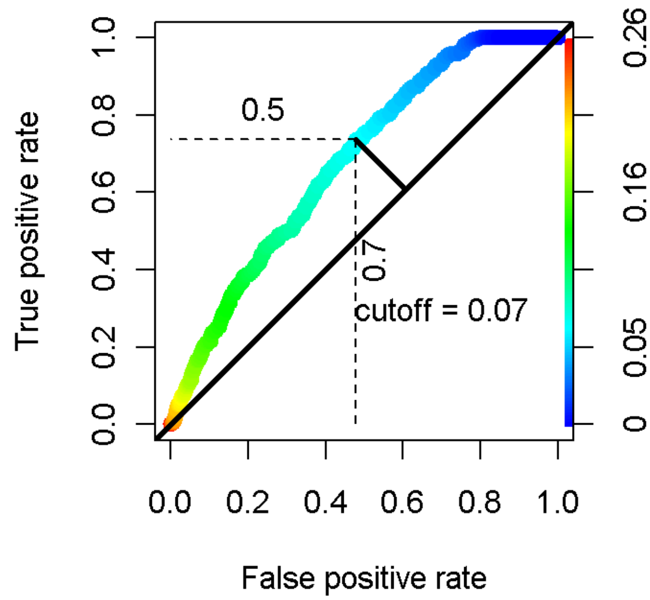


Figure B-27. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Stenella attenuata guild during Spring season in Gulf of Mexico region.

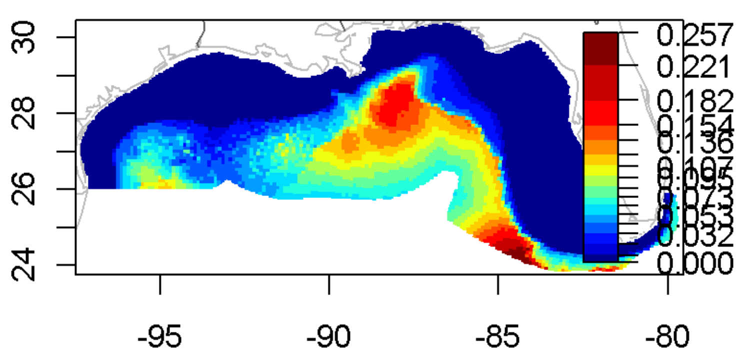


Figure B-28. Map of mean predicted habitat for Stenella attenuata guild during Spring season in Gulf of Mexico region.

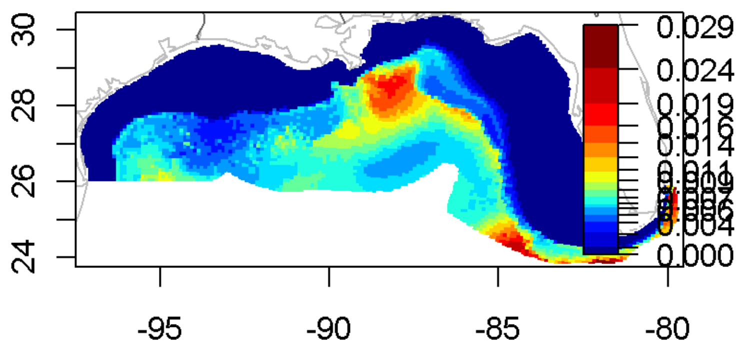


Figure B-29. Map of standard error of habitat for Stenella attenuata guild during Spring season in Gulf of Mexico region.

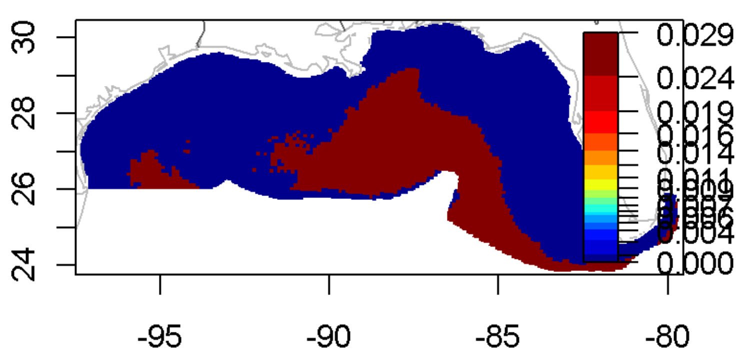


Figure B-30. Map of binary habitat (cutoff determined by ROC) for Stenella attenuata guild during Spring season in Gulf of Mexico region.

Stenella attenuata | Summer | Gulf of Mexico
Number of presences: 71
Number of absences: 1333
R squared: 0.132048
Deviance explained: 0.169337
ROC optimum: 0.157851
Maximum fit: 0.0338501
Maximum prediction: 0.997923
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 5, bs = 'ts') + s(d2shelf2, k = 5,
    bs = 'ts') + s(log(d2coast), k = 5, bs = 'ts') + s(sst, k =
5,
    bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   -9.712      5.507  -1.763    0.078 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   2.9290954 2.9290954   12.781 4.24e-08 ***
s(d2shelf2)     0.7126343 0.7126343    4.041  0.05716 .
s(log(d2coast)) 2.2924112 2.2924112    4.570  0.00756 **
s(sst)          0.0009615 0.0009615 6.93e-05       NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.132   Deviance explained = 16.9%
GCV score = 0.0027733  Scale est. = 0.0027486  n = 1404
```

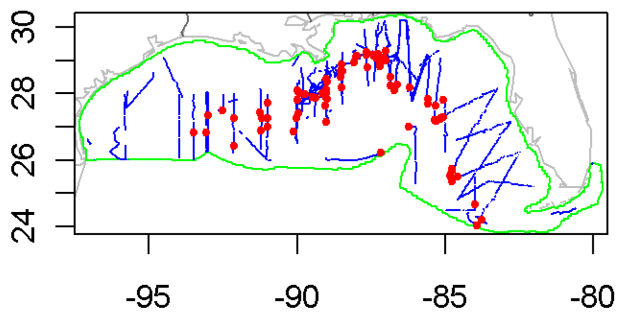


Figure B-31. Map of points of observational sightings and tracks of survey effort for Stenella attenuata guild during Summer season in Gulf of Mexico region.

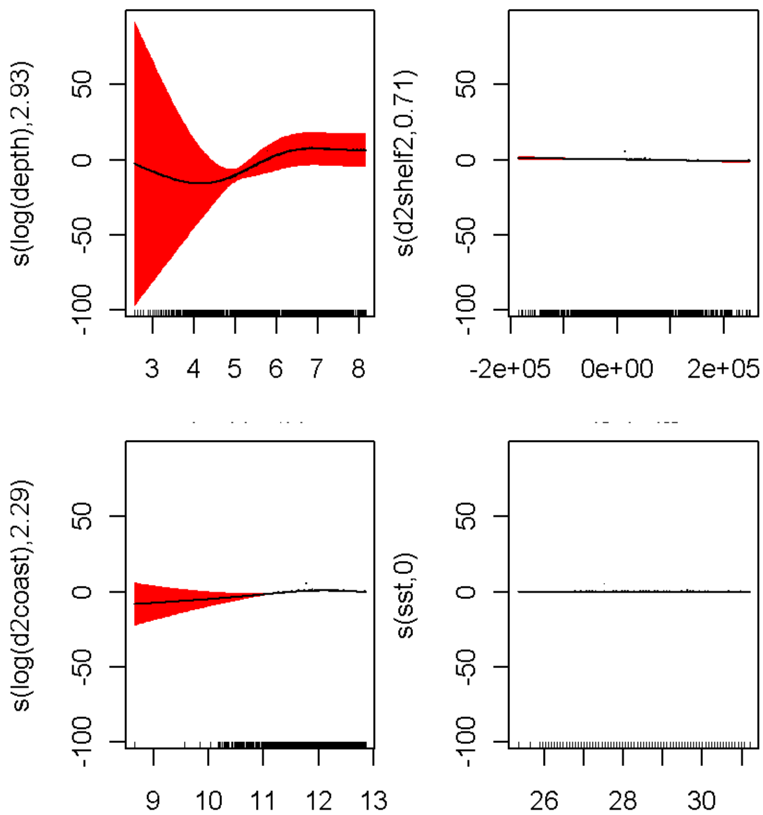


Figure B-32. Terms plot of predictors to GAM model fit for Stenella attenuata guild during Summer season in Gulf of Mexico region.

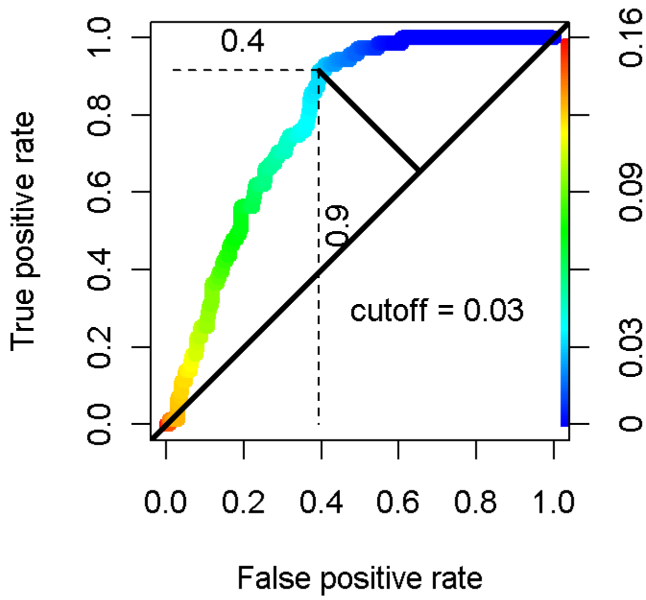


Figure B-33. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Stenella attenuata guild during Summer season in Gulf of Mexico region.

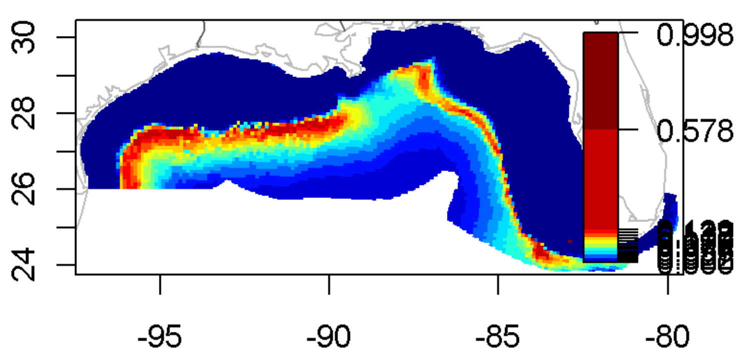


Figure B-34. Map of mean predicted habitat for Stenella attenuata guild during Summer season in Gulf of Mexico region.

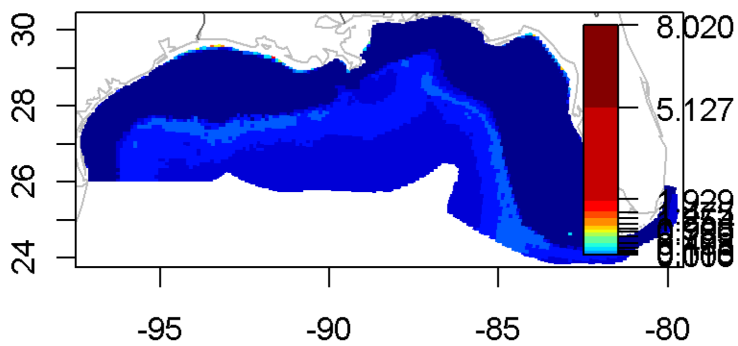


Figure B-35. Map of standard error of habitat for Stenella attenuata guild during Summer season in Gulf of Mexico region.

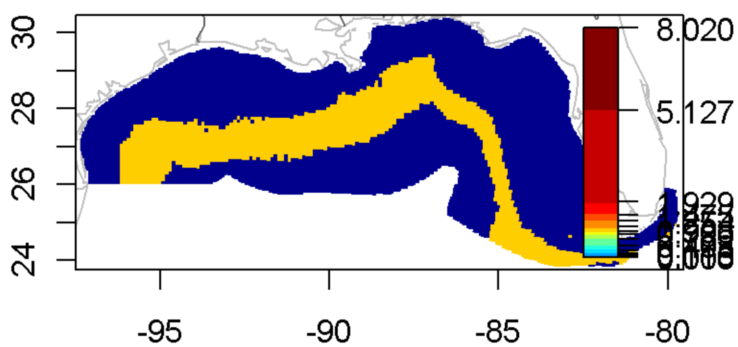


Figure B-36. Map of binary habitat (cutoff determined by ROC) for Stenella attenuata guild during Summer season in Gulf of Mexico region.

Stenella frontalis | Fall | Gulf of Mexico
Number of presences: 73
Number of absences: 872
R squared: -0.293357
Deviance explained: 0.153402
ROC optimum: 0.146437
Maximum fit: 0.0256421
Maximum prediction: 0.196969
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -5.3545     0.4178  -12.81   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   1.941e+00 1.941e+00   20.487 3.14e-09 ***
s(log(d2shelf)) 9.537e-06 9.537e-06 2.26e-05       NA
s(log(d2coast)) 7.128e-01 7.128e-01    4.879   0.0390 *
s(sst)          1.359e-05 1.359e-05 2.02e-04       NA
s(lat)          7.059e-01 7.059e-01    4.717   0.0423 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  -0.293   Deviance explained = 15.3%
GCV score = 0.001768  Scale est. = 0.0017533  n = 945
```

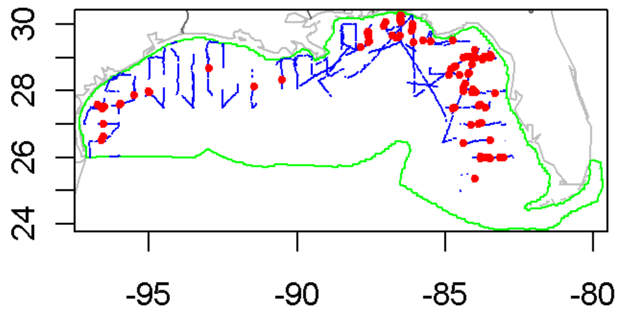


Figure B-37. Map of points of observational sightings and tracks of survey effort for Stenella frontalis guild during Fall season in Gulf of Mexico region.

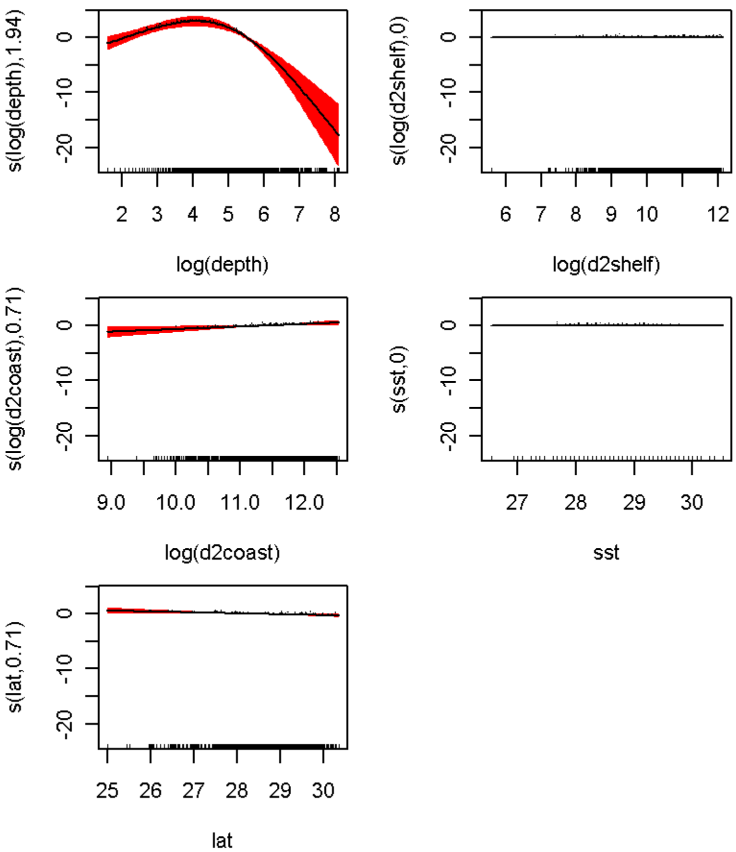


Figure B-38. Terms plot of predictors to GAM model fit for Stenella frontalis guild during Fall season in Gulf of Mexico region.

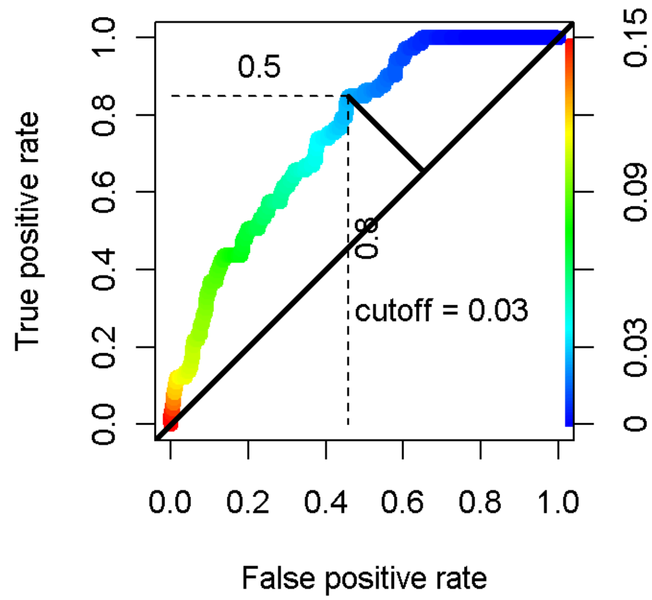


Figure B-39. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Stenella frontalis guild during Fall season in Gulf of Mexico region.

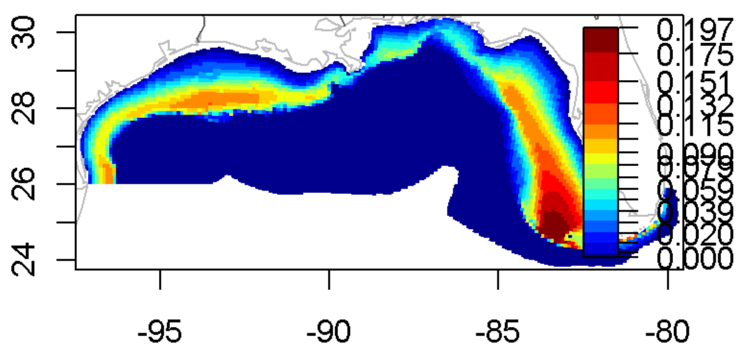


Figure B-40. Map of mean predicted habitat for Stenella frontalis guild during Fall season in Gulf of Mexico region.

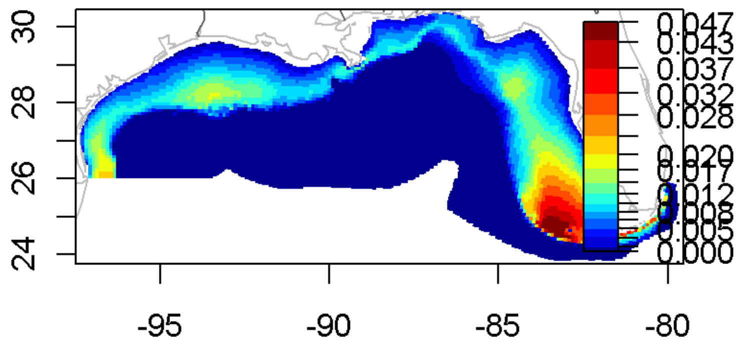


Figure B-41. Map of standard error of habitat for Stenella frontalis guild during Fall season in Gulf of Mexico region.

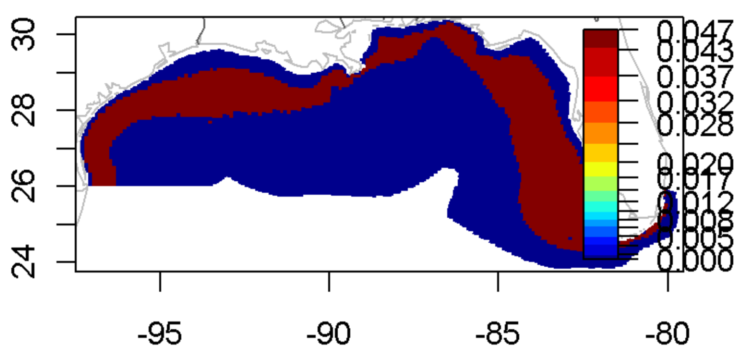


Figure B-42. Map of binary habitat (cutoff determined by ROC) for Stenella frontalis guild during Fall season in Gulf of Mexico region.

Stenella frontalis | Spring | Gulf of Mexico
Number of presences: 43
Number of absences: 4774
R squared: 0.188883
Deviance explained: 0.369799
ROC optimum: 0.242346
Maximum fit: 0.00540961
Maximum prediction: 0.242433
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -12.1936     0.6565  -18.57   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                     edf   Ref.df       F  p-value
s(log(depth))   1.968251 1.968251 198.469  < 2e-16 ***
s(log(d2shelf)) 0.925370 0.925370  23.554 2.63e-06 ***
s(log(d2coast)) 1.999714 1.999714  39.568  < 2e-16 ***
s(sst)          0.005962 0.005962   0.006       NA
s(lat)          1.999409 1.999409  60.513  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.189   Deviance explained =   37%
GCV score = 0.00055813  Scale est. = 0.00055649  n = 4817
```

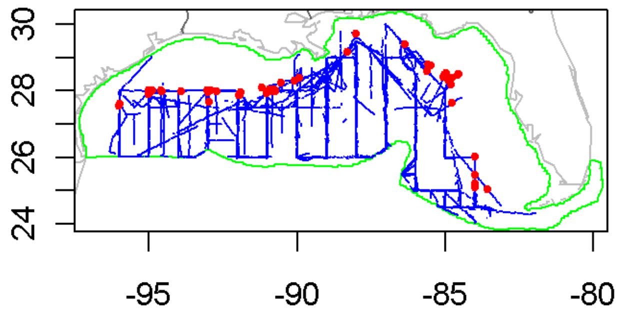


Figure B-43. Map of points of observational sightings and tracks of survey effort for Stenella frontalis guild during Spring season in Gulf of Mexico region.

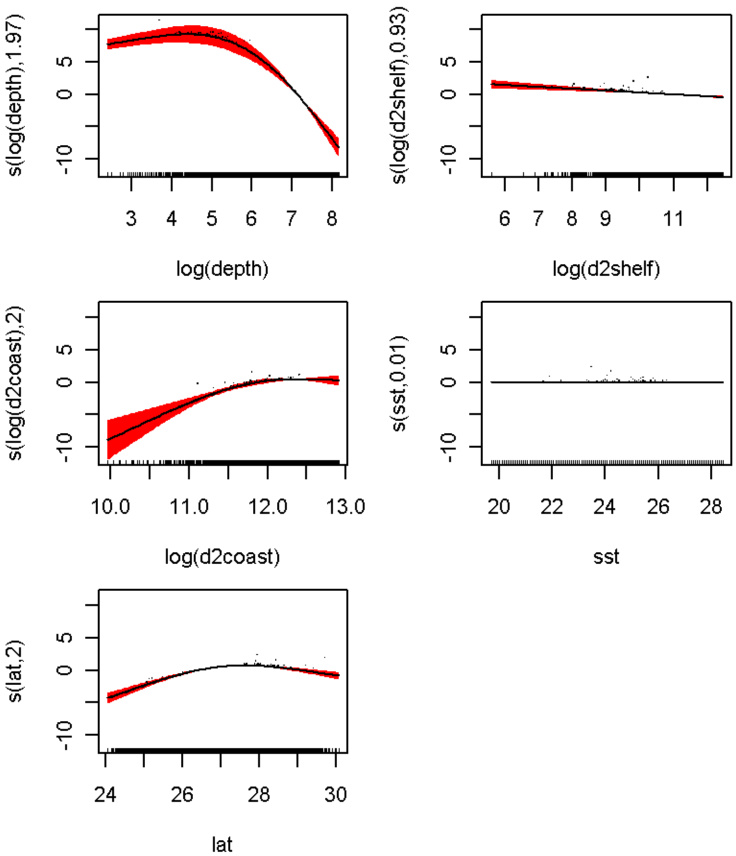


Figure B-44. Terms plot of predictors to GAM model fit for Stenella frontalis guild during Spring season in Gulf of Mexico region.

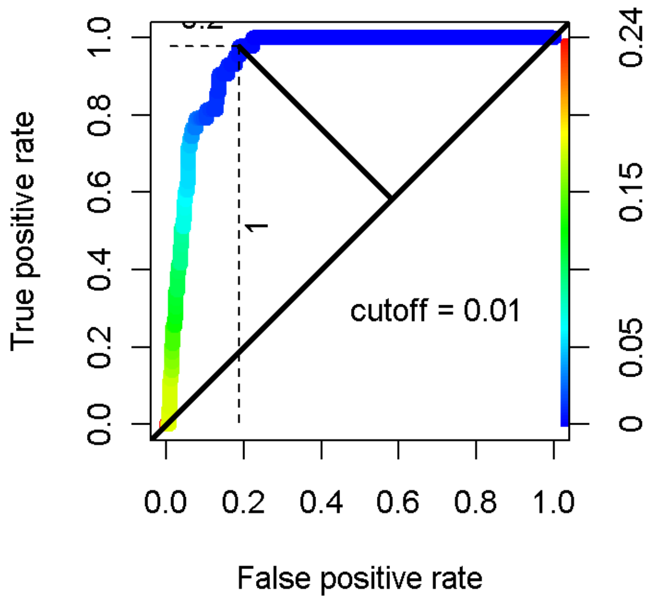


Figure B-45. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Stenella frontalis guild during Spring season in Gulf of Mexico region.

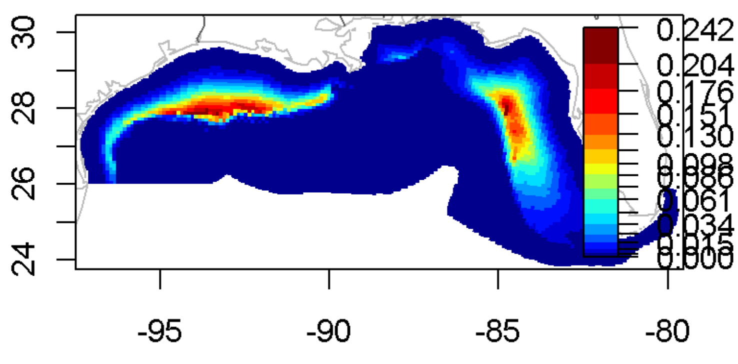


Figure B-46. Map of mean predicted habitat for Stenella frontalis guild during Spring season in Gulf of Mexico region.

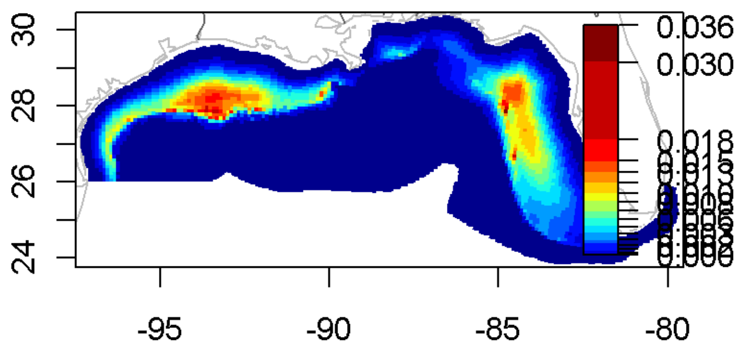


Figure B-47. Map of standard error of habitat for Stenella frontalis guild during Spring season in Gulf of Mexico region.

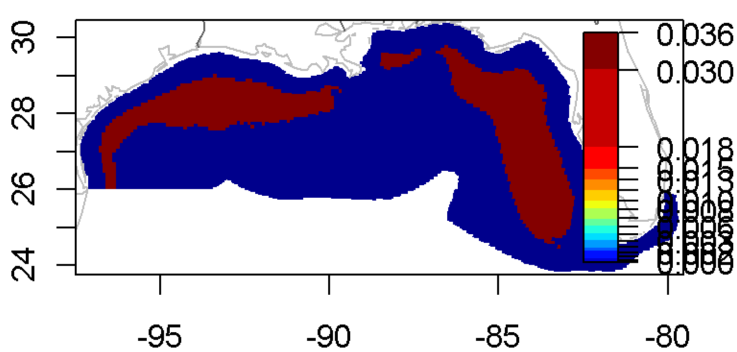


Figure B-48. Map of binary habitat (cutoff determined by ROC) for Stenella frontalis guild during Spring season in Gulf of Mexico region.

Stenella frontalis | Summer | Gulf of Mexico
Number of presences: 69
Number of absences: 1335
R squared: 0.491978
Deviance explained: 0.413624
ROC optimum: 0.425924
Maximum fit: 0.0128391
Maximum prediction: 0.429672
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -18.792      2.005  -9.374   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   1.988e+00 1.988e+00   48.291  < 2e-16 ***
s(log(d2shelf)) 9.733e-01 9.733e-01   60.416 3.02e-14 ***
s(log(d2coast)) 2.769e-06 2.769e-06 1.45e-06       NA
s(sst)          8.423e-06 8.423e-06 3.44e-05       NA
s(lat)          1.920e+00 1.920e+00    9.487 0.000105 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.492   Deviance explained = 41.4%
GCV score = 0.0015603  Scale est. = 0.0015485  n = 1404
```

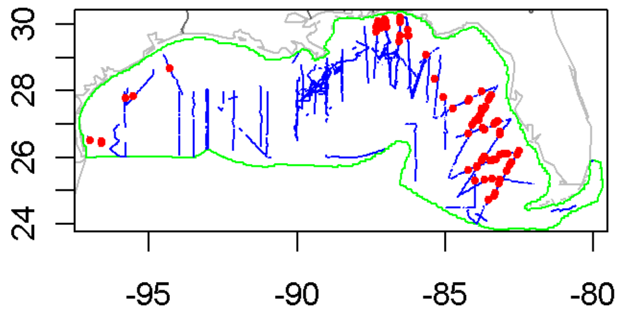


Figure B-49. Map of points of observational sightings and tracks of survey effort for Stenella frontalis guild during Summer season in Gulf of Mexico region.

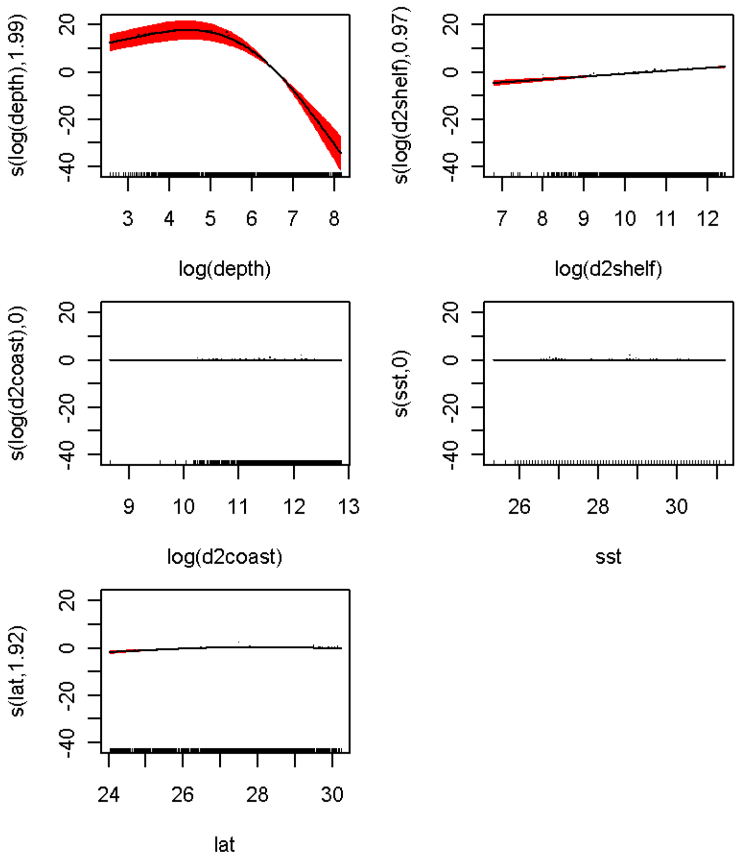


Figure B-50. Terms plot of predictors to GAM model fit for Stenella frontalis guild during Summer season in Gulf of Mexico region.

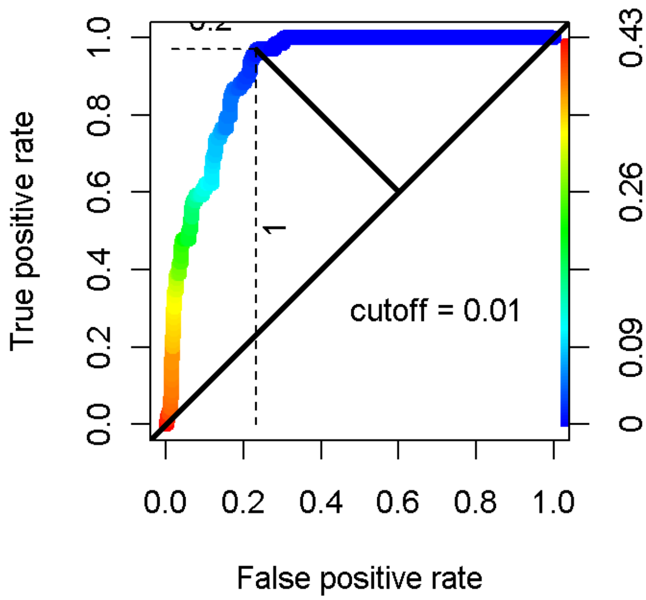


Figure B-51. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Stenella frontalis guild during Summer season in Gulf of Mexico region.

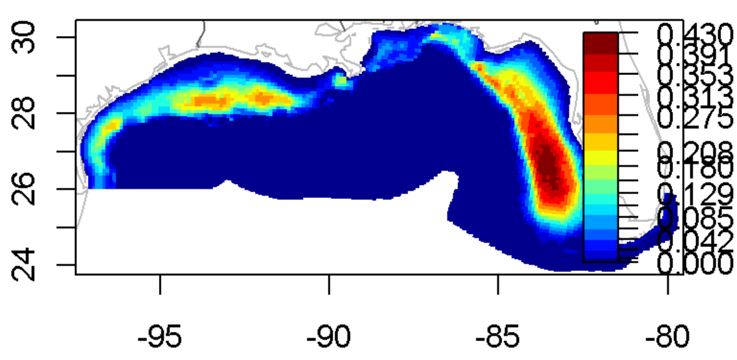


Figure B-52. Map of mean predicted habitat for Stenella frontalis guild during Summer season in Gulf of Mexico region.

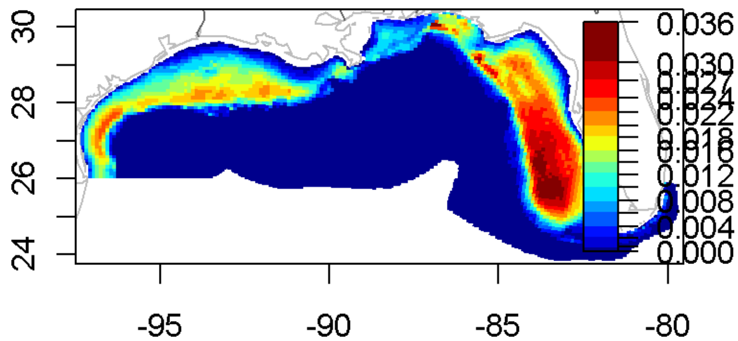


Figure B-53. Map of standard error of habitat for Stenella frontalis guild during Summer season in Gulf of Mexico region.

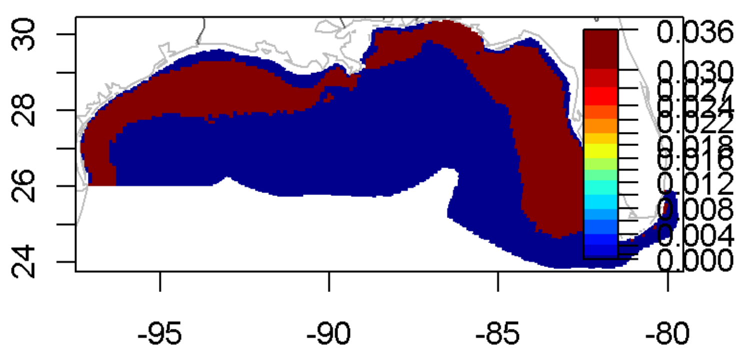


Figure B-54. Map of binary habitat (cutoff determined by ROC) for Stenella frontalis guild during Summer season in Gulf of Mexico region.

<u>Stenella species | Summer | Gulf of Mexico</u>
Number of presences: 15
Number of absences: 1389
R squared: 0.260497
Deviance explained: 0.262424
ROC optimum: 0.329093
Maximum fit: 0.00203911
Maximum prediction: 0.251118
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -6.5404     0.3812  -17.16   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   9.616e-01 9.616e-01    35.80 5.04e-09 ***
s(log(d2shelf)) 2.042e-06 2.042e-06 5.12e-09       NA
s(log(d2coast)) 2.760e-05 2.760e-05 4.74e-05       NA
s(sst)          9.788e-01 9.788e-01   115.43  < 2e-16 ***
s(lat)          1.950e+00 1.950e+00    15.04 4.59e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =   0.26   Deviance explained = 26.2%
GCV score = 0.0015767  Scale est. = 0.0015668  n = 1404
```

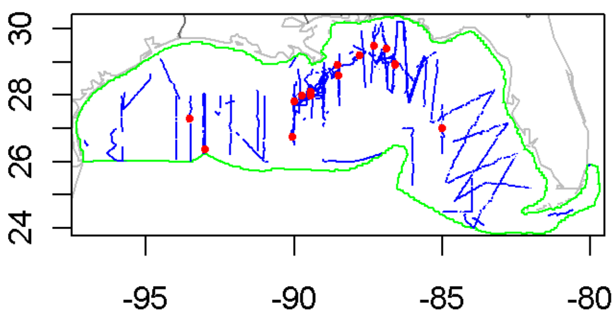


Figure B-55. Map of points of observational sightings and tracks of survey effort for Stenella species guild during Summer season in Gulf of Mexico region.

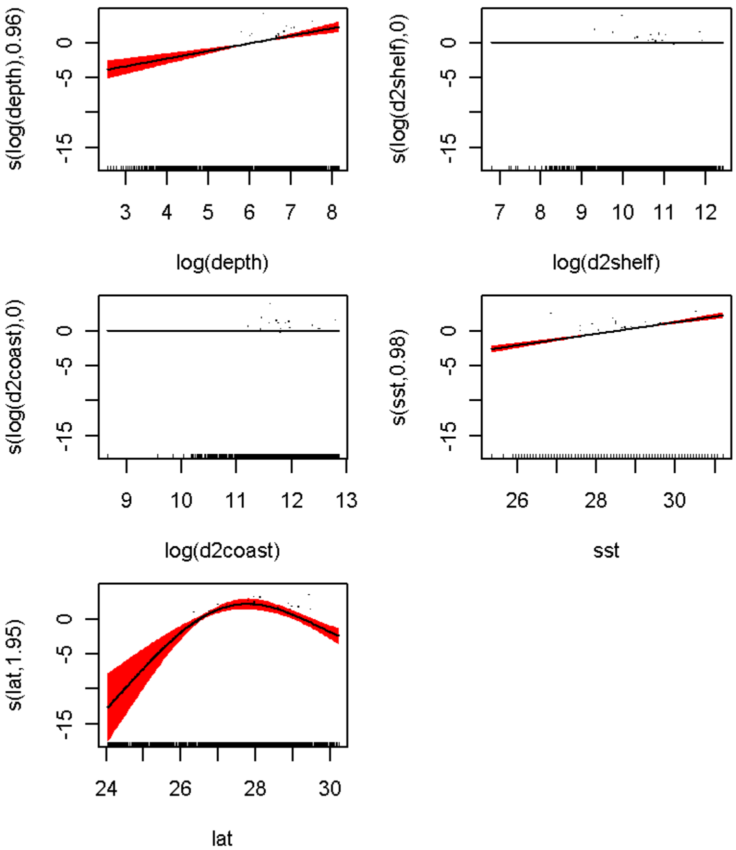


Figure B-56. Terms plot of predictors to GAM model fit for Stenella species guild during Summer season in Gulf of Mexico region.

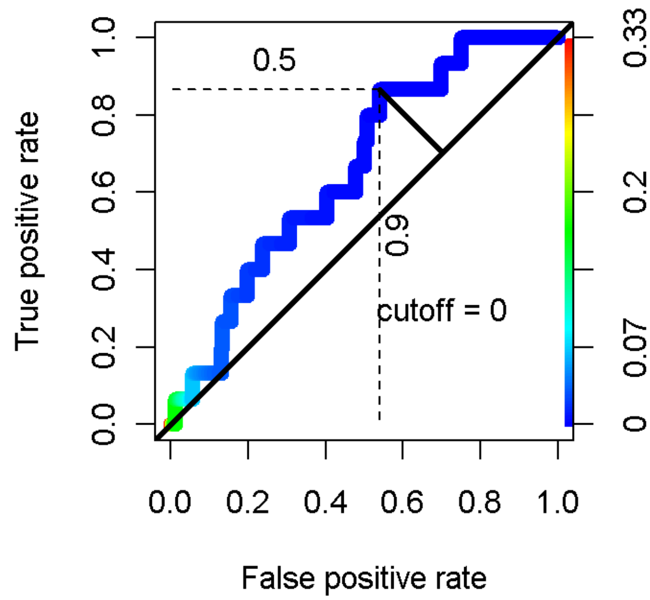


Figure B-57. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Stenella species guild during Summer season in Gulf of Mexico region.

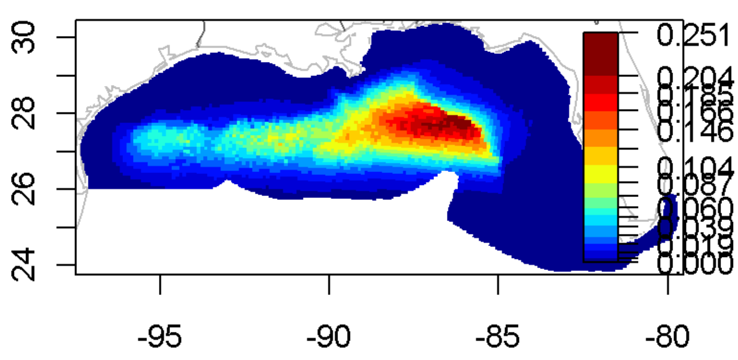


Figure B-58. Map of mean predicted habitat for Stenella species guild during Summer season in Gulf of Mexico region.

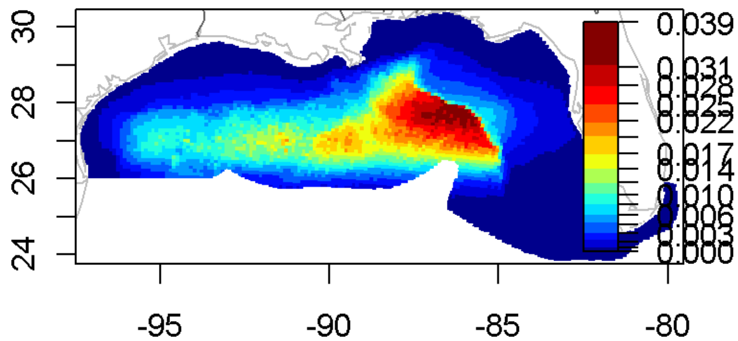


Figure B-59. Map of standard error of habitat for Stenella species guild during Summer season in Gulf of Mexico region.

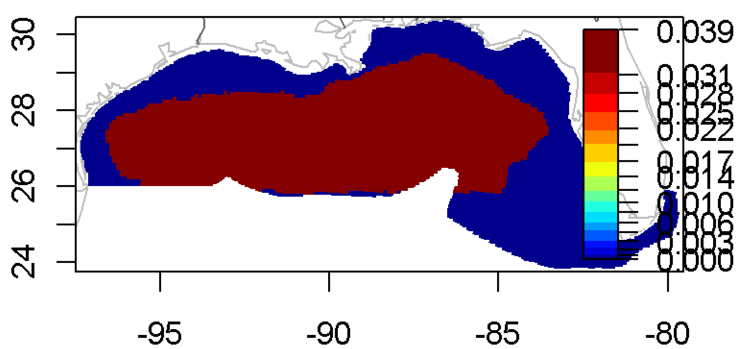


Figure B-60. Map of binary habitat (cutoff determined by ROC) for Stenella species guild during Summer season in Gulf of Mexico region.

Striped dolphin | Spring | Gulf of Mexico
Number of presences: 44
Number of absences: 4773
R squared: 0.0183192
Deviance explained: 0.0841211
ROC optimum: 0.0492344
Maximum fit: 0.00532561
Maximum prediction: 0.0495035
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 5, bs = 'ts') + s(d2shelf2, k = 5,
    bs = 'ts') + s(log(d2coast), k = 5, bs = 'ts') + s(sst, k =
5,
    bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -5.52232    0.08098  -68.19   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                   edf Ref.df      F  p-value
s(log(depth))   0.8763 0.8763 23.964 3.55e-06 ***
s(d2shelf2)     0.1110 0.1110  0.289       NA
s(log(d2coast)) 0.9275 0.9275 59.762 9.39e-14 ***
s(sst)          3.8793 3.8793 36.011  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.0183   Deviance explained = 8.41%
GCV score = 0.00070347  Scale est. = 0.00070168  n = 4817
```

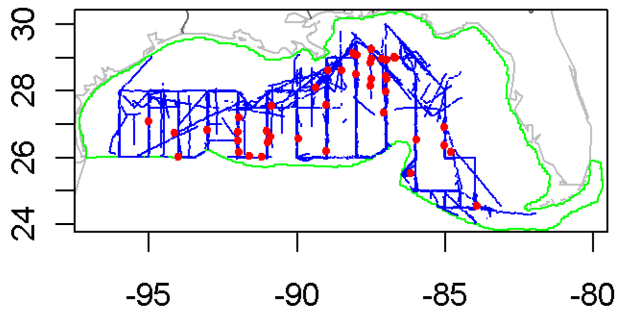


Figure B-61. Map of points of observational sightings and tracks of survey effort for Striped dolphin guild during Spring season in Gulf of Mexico region.

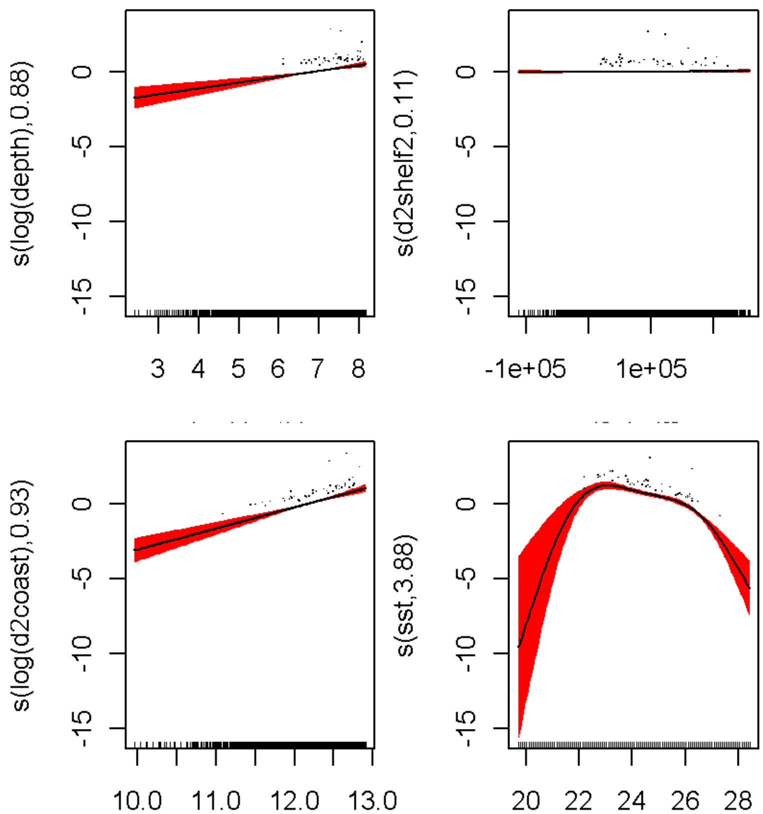


Figure B-62. Terms plot of predictors to GAM model fit for Striped dolphin guild during Spring season in Gulf of Mexico region.

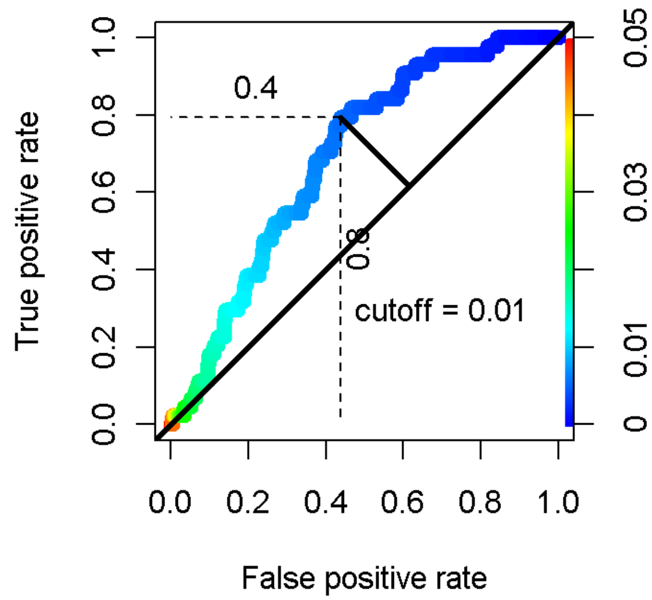


Figure B-63. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Striped dolphin guild during Spring season in Gulf of Mexico region.

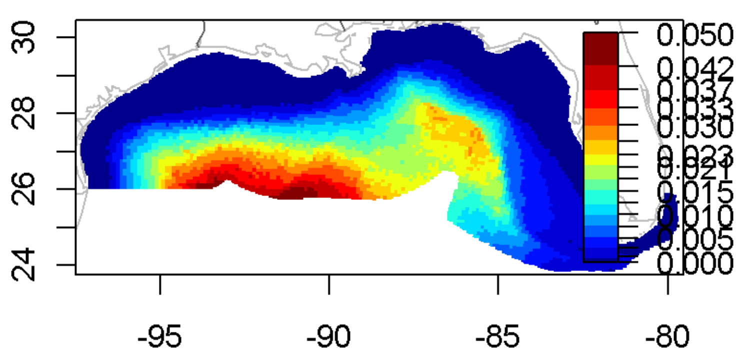


Figure B-64. Map of mean predicted habitat for Striped dolphin guild during Spring season in Gulf of Mexico region.

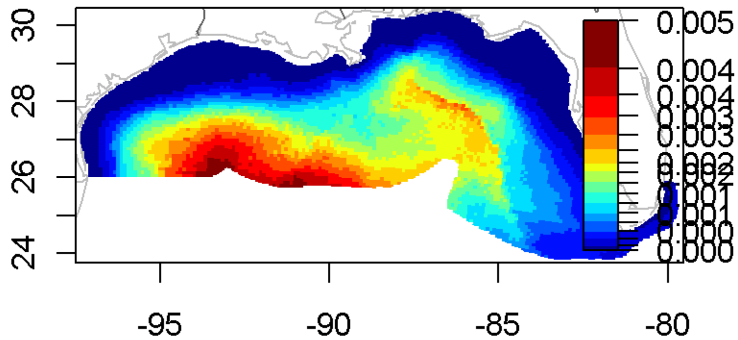


Figure B-65. Map of standard error of habitat for Striped dolphin guild during Spring season in Gulf of Mexico region.

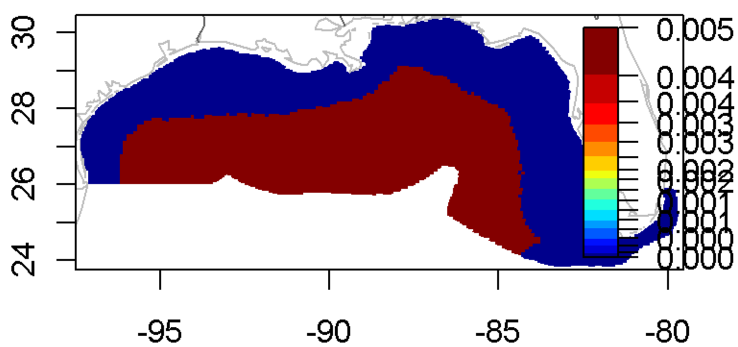


Figure B-66. Map of binary habitat (cutoff determined by ROC) for Striped dolphin guild during Spring season in Gulf of Mexico region.

Tursiops | Fall | Gulf of Mexico
Number of presences: 160
Number of absences: 785
R squared: 0.707445
Deviance explained: 0.301947
ROC optimum: 0.929315
Maximum fit: 0.160285
Maximum prediction: 0.989978
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -2.0266     0.1134  -17.88   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   0.9630687 0.9630687  135.809  < 2e-16 ***
s(log(d2shelf)) 0.0004748 0.0004748 0.000407       NA
s(log(d2coast)) 0.4377039 0.4377039    1.522       NA
s(sst)          0.9605369 0.9605369   21.976 4.52e-06 ***
s(lat)          1.8932847 1.8932847   17.033 1.09e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.707   Deviance explained = 30.2%
GCV score = 0.005287  Scale est. = 0.0052341  n = 945
```

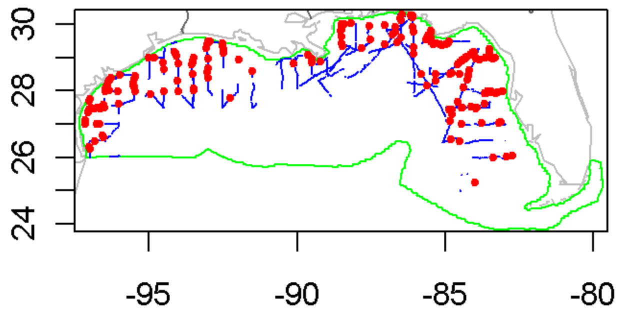


Figure B-67. Map of points of observational sightings and tracks of survey effort for Tursiops guild during Fall season in Gulf of Mexico region.

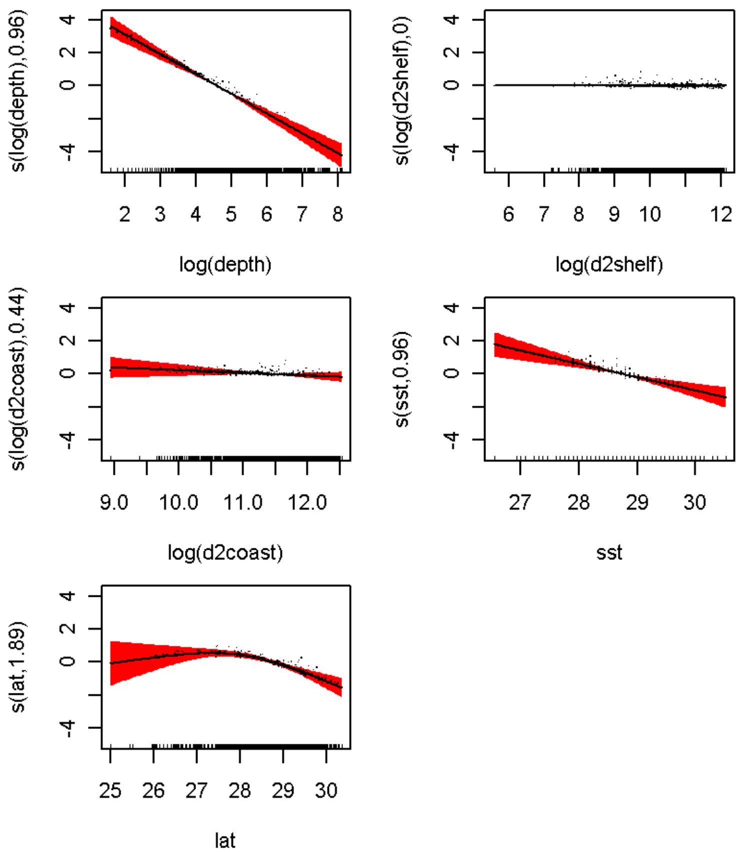


Figure B-68. Terms plot of predictors to GAM model fit for Tursiops guild during Fall season in Gulf of Mexico region.

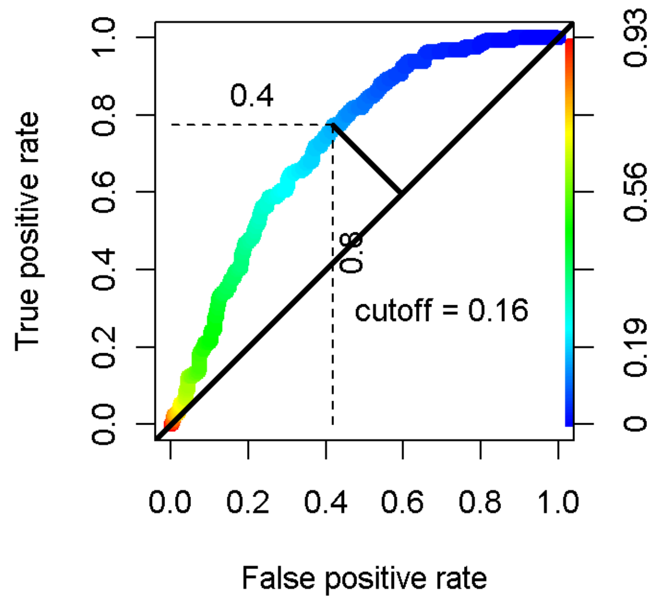


Figure B-69. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Tursiops guild during Fall season in Gulf of Mexico region.

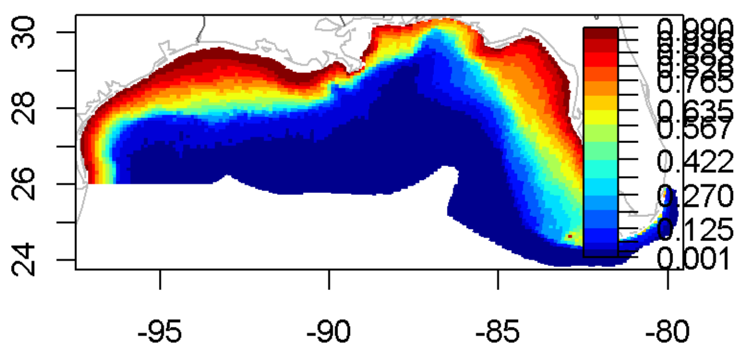


Figure B-70. Map of mean predicted habitat for Tursiops guild during Fall season in Gulf of Mexico region.

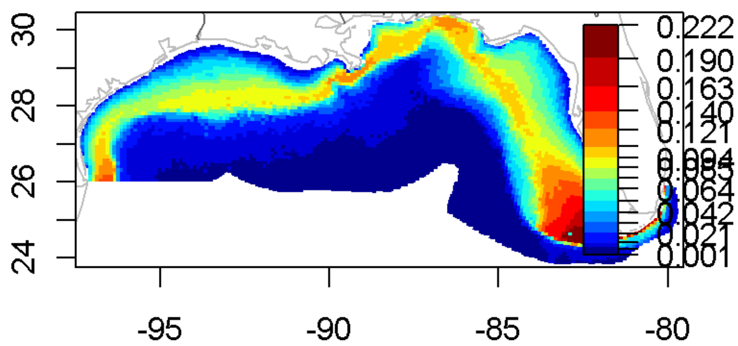


Figure B-71. Map of standard error of habitat for Tursiops guild during Fall season in Gulf of Mexico region.

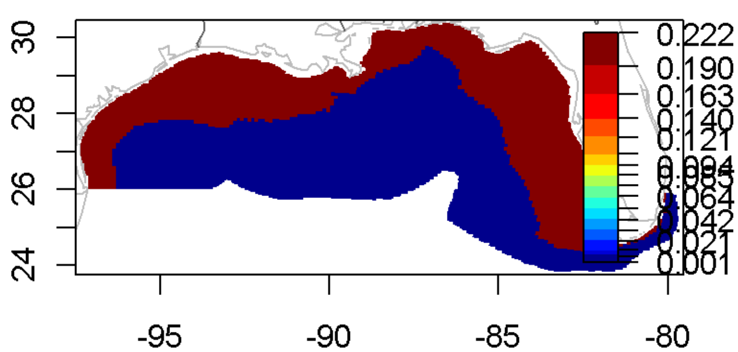


Figure B-72. Map of binary habitat (cutoff determined by ROC) for Tursiops guild during Fall season in Gulf of Mexico region.

Tursiops | Summer | Gulf of Mexico
Number of presences: 102
Number of absences: 1302
R squared: 0.220096
Deviance explained: 0.239817
ROC optimum: 0.560228
Maximum fit: 0.0523544
Maximum prediction: 0.572905
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -3.8493     0.1619  -23.78   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   1.999e+00 1.999e+00    89.81  < 2e-16 ***
s(log(d2shelf)) 1.971e+00 1.971e+00    70.15  < 2e-16 ***
s(log(d2coast)) 1.573e-05 1.573e-05 7.63e-06       NA
s(sst)          9.405e-01 9.405e-01    19.06 2.15e-05 ***
s(lat)          2.953e-05 2.953e-05 1.41e-04       NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =   0.22   Deviance explained =   24%
GCV score = 0.0034859  Scale est. = 0.0034595  n = 1404
```

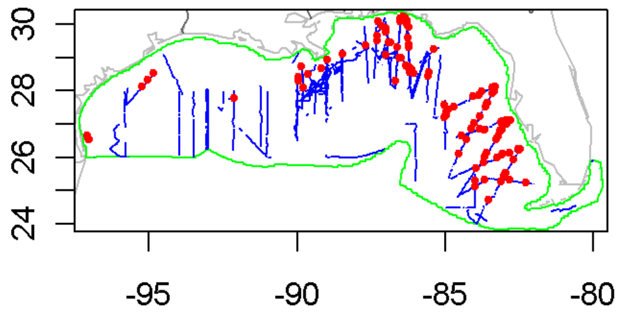


Figure B-73. Map of points of observational sightings and tracks of survey effort for Tursiops guild during Summer season in Gulf of Mexico region.

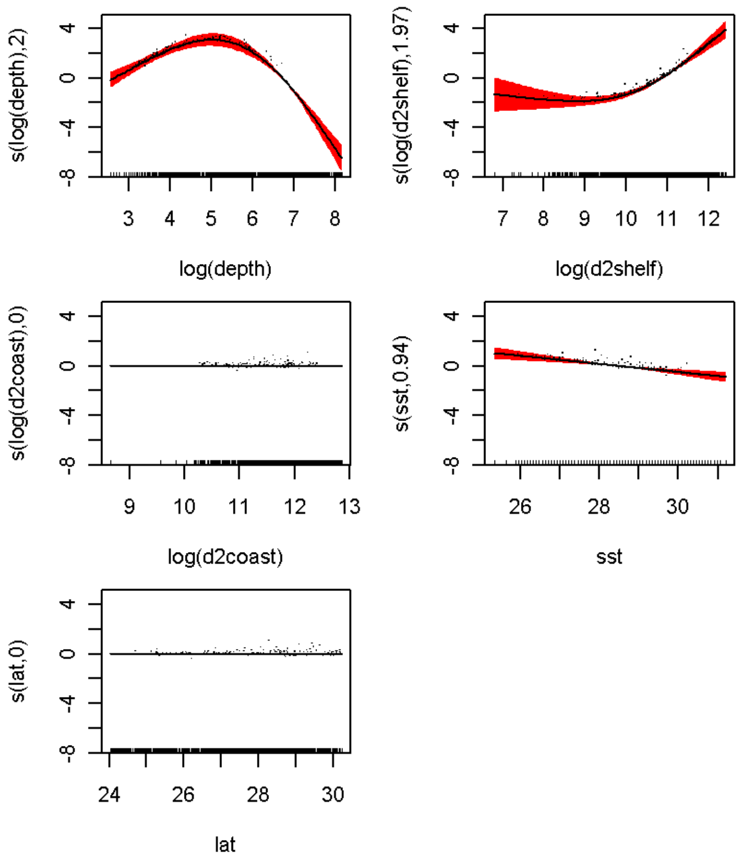


Figure B-74. Terms plot of predictors to GAM model fit for Tursiops guild during Summer season in Gulf of Mexico region.

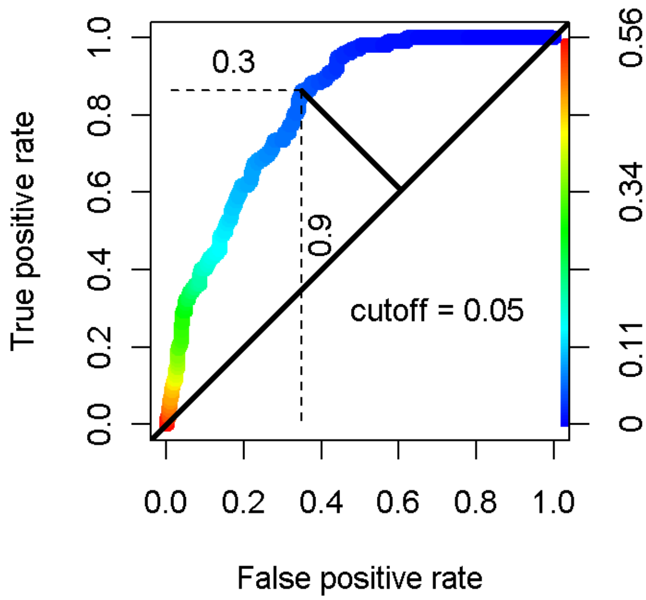


Figure B-75. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Tursiops guild during Summer season in Gulf of Mexico region.

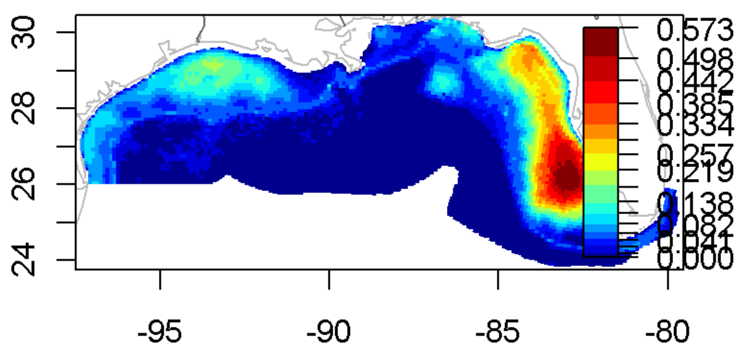


Figure B-76. Map of mean predicted habitat for Tursiops guild during Summer season in Gulf of Mexico region.

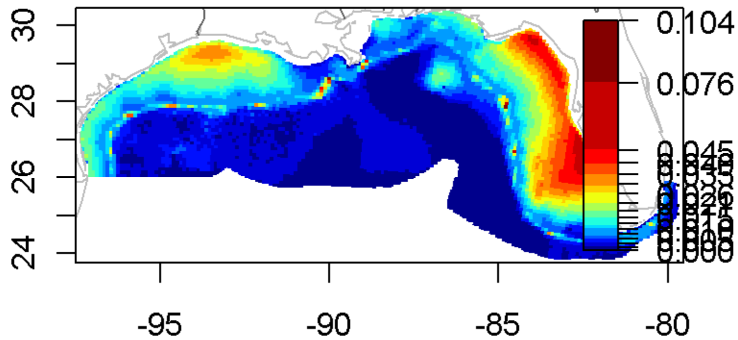


Figure B-77. Map of standard error of habitat for Tursiops guild during Summer season in Gulf of Mexico region.

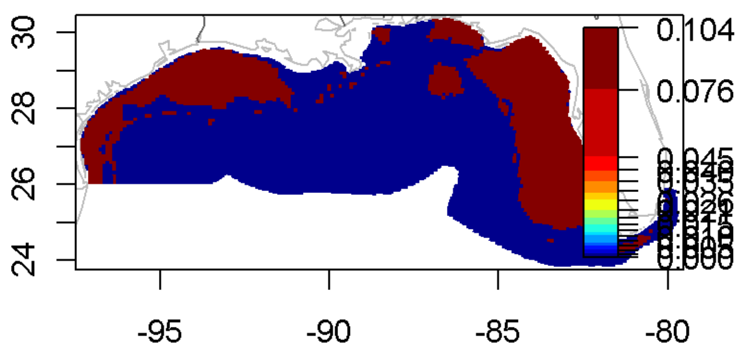


Figure B-78. Map of binary habitat (cutoff determined by ROC) for Tursiops guild during Summer season in Gulf of Mexico region.

East

Baleen whales | Fall | East
Number of presences: 47
Number of absences: 1817
R squared: 0.304059
Deviance explained: 0.365696
ROC optimum: 0.369921
Maximum fit: 0.0295519
Maximum prediction: 0.389591
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -4.9462     0.1594  -31.02   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   2.488e-06 2.488e-06 2.74e-06       NA
s(log(d2shelf)) 8.826e-01 8.826e-01    21.83 9.26e-06 ***
s(log(d2coast)) 1.945e+00 1.945e+00    26.83 6.09e-12 ***
s(sst)          7.860e-01 7.860e-01    18.87 7.63e-05 ***
s(lat)          8.327e-01 8.327e-01    44.88 7.74e-10 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.304   Deviance explained = 36.6%
GCV score = 0.00094118  Scale est. = 0.00093613  n = 1826
```

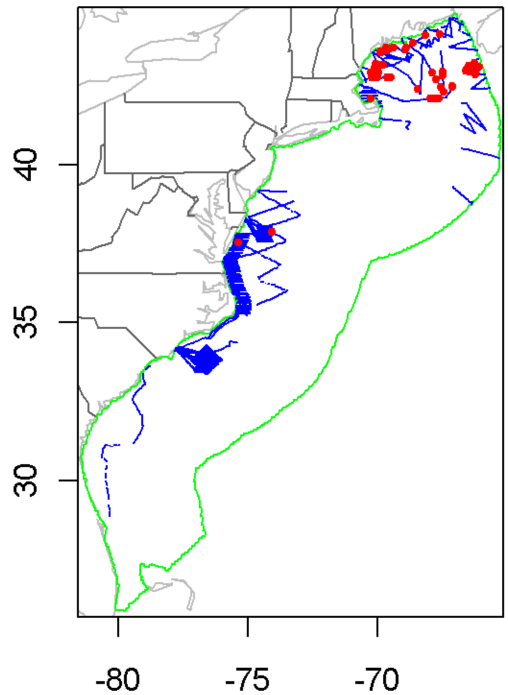


Figure B-79. Map of points of observational sightings and tracks of survey effort for Baleen whales guild during Fall season in East region.

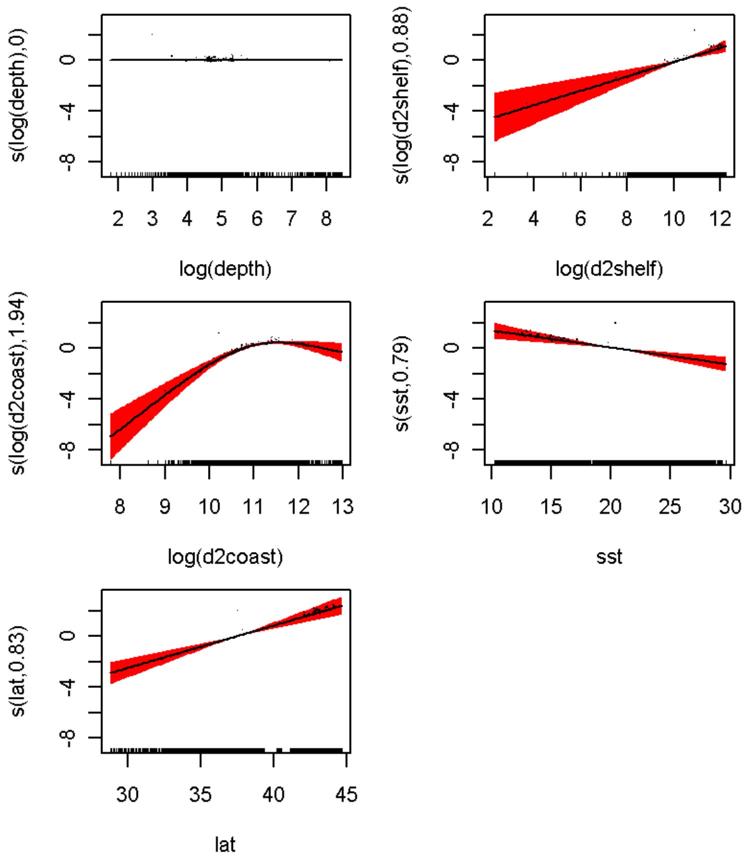


Figure B-80. Terms plot of predictors to GAM model fit for Baleen whales guild during Fall season in East region.

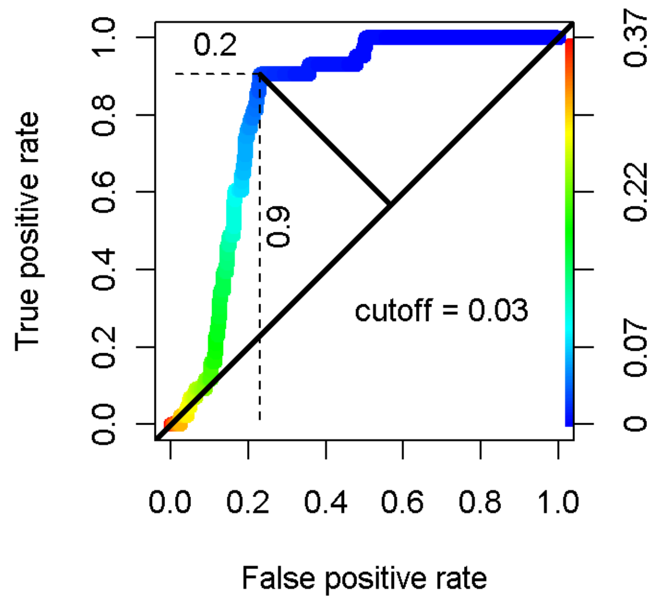


Figure B-81. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Baleen whales guild during Fall season in East region.

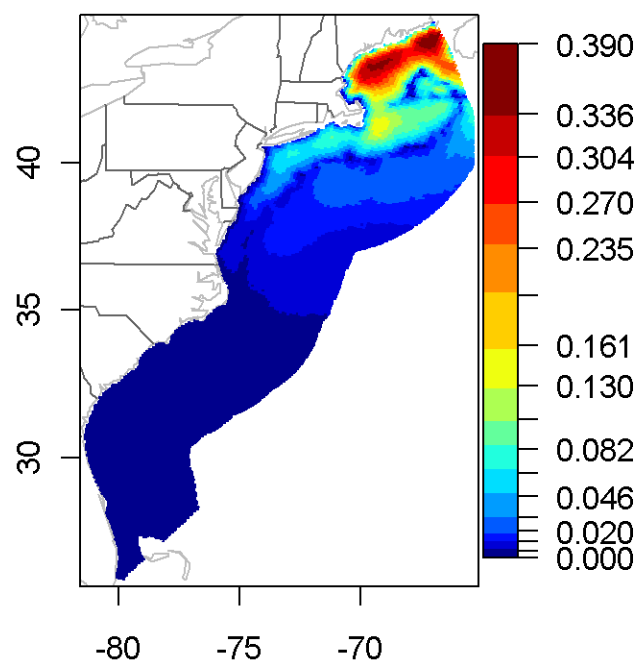


Figure B-82. Map of mean predicted habitat for Baleen whales guild during Fall season in East region.

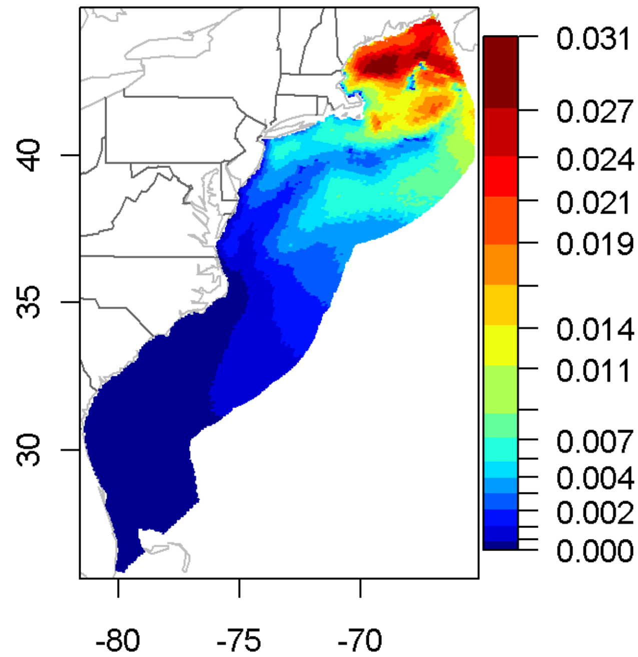


Figure B-83. Map of standard error of habitat for Baleen whales guild during Fall season in East region.

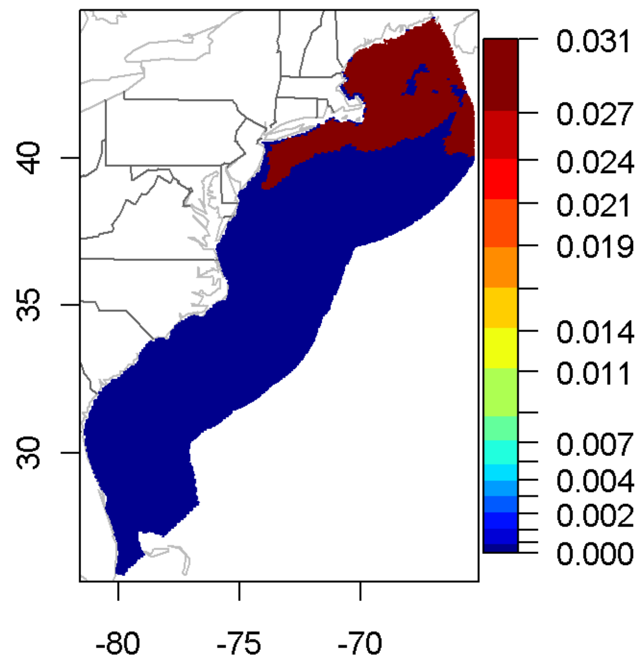


Figure B-84. Map of binary habitat (cutoff determined by ROC) for Baleen whales guild during Fall season in East region.

Baleen whales | Summer | East
Number of presences: 372
Number of absences: 8706
R squared: 0.182955
Deviance explained: 0.266012
ROC optimum: 0.581464
Maximum fit: 0.0400907
Maximum prediction: 0.606017
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   -4.938      0.192  -25.72   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                     edf   Ref.df       F p-value
s(log(depth))   0.002105 0.002105   0.006      NA
s(log(d2shelf)) 1.989983 1.989983 208.749  <2e-16 ***
s(log(d2coast)) 1.948299 1.948299 145.425  <2e-16 ***
s(sst)          1.967542 1.967542  55.649  <2e-16 ***
s(lat)          1.733880 1.733880 159.550  <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.183   Deviance explained = 26.6%
GCV score = 0.0016006  Scale est. = 0.0015977  n = 8663
```

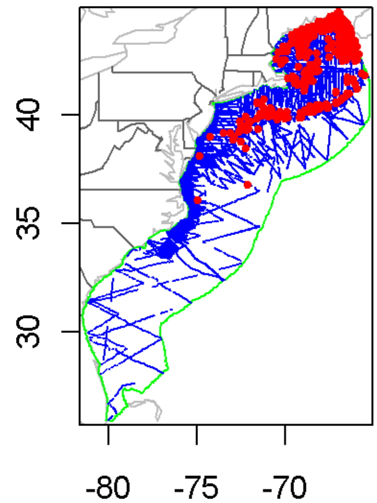


Figure B-85. Map of points of observational sightings and tracks of survey effort for Baleen whales guild during Summer season in East region.

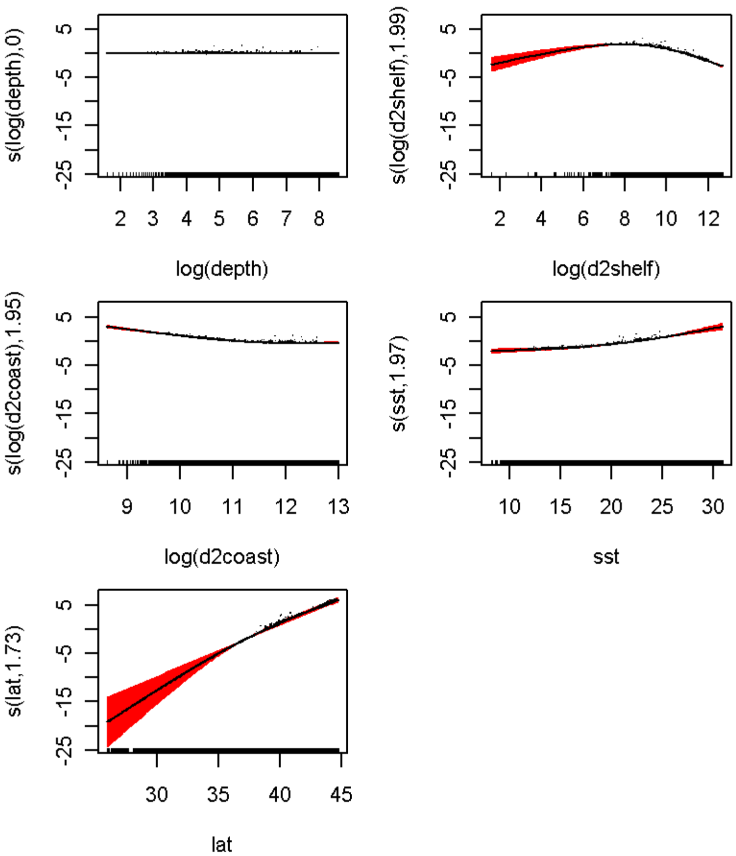


Figure B-86. Terms plot of predictors to GAM model fit for Baleen whales guild during Summer season in East region.

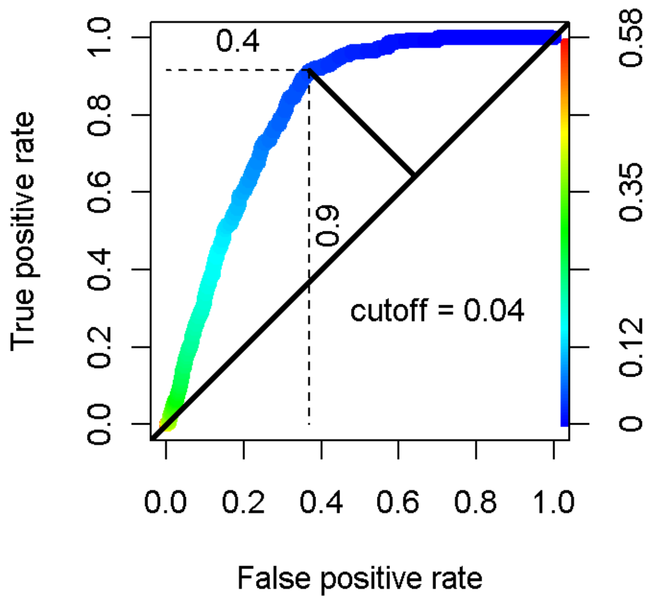


Figure B-87. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Baleen whales guild during Summer season in East region.

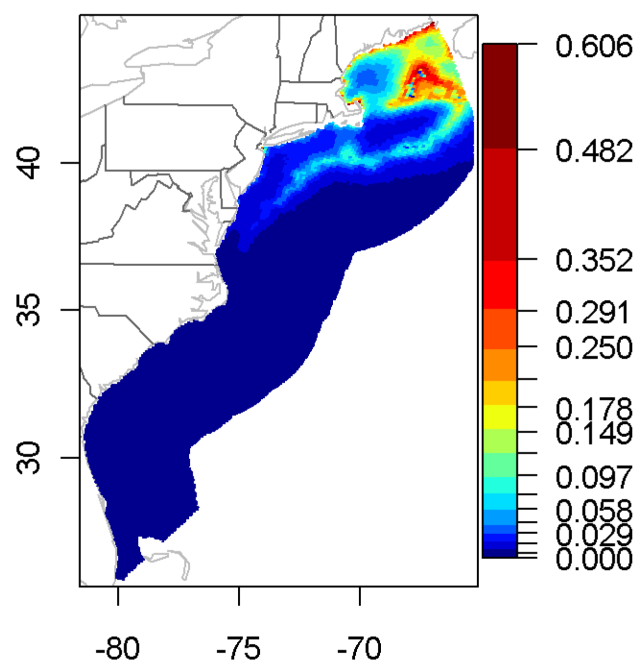


Figure B-88. Map of mean predicted habitat for Baleen whales guild during Summer season in East region.

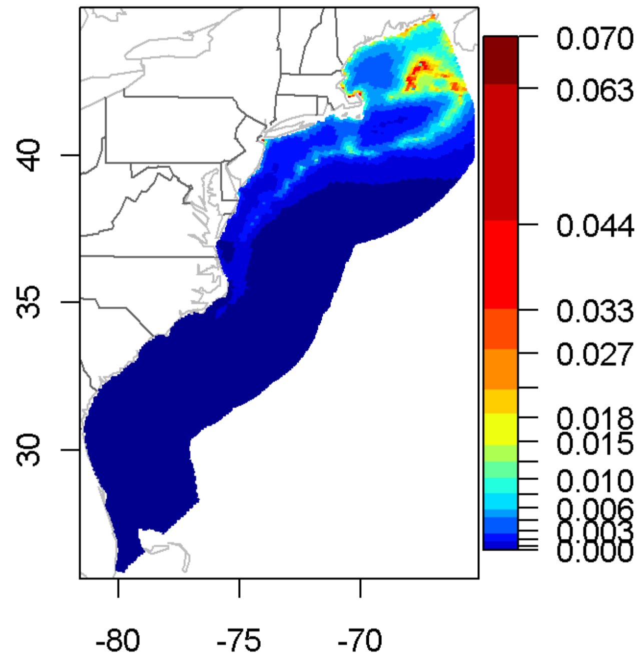


Figure B-89. Map of standard error of habitat for Baleen whales guild during Summer season in East region.

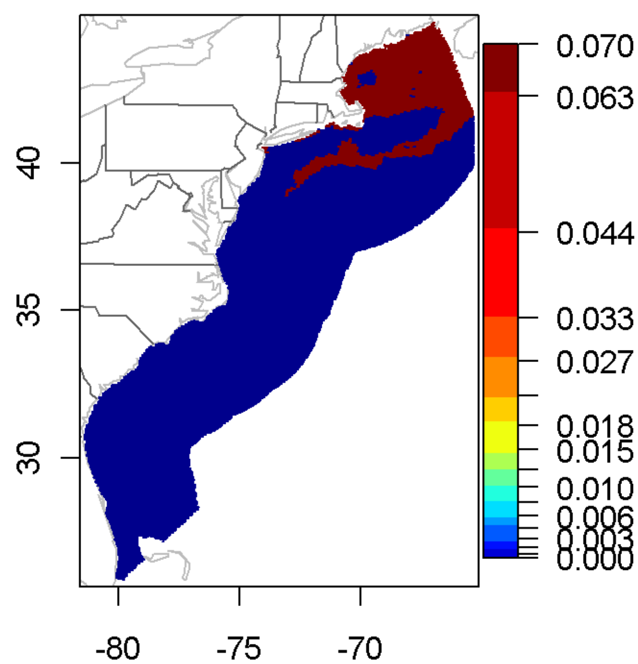


Figure B-90. Map of binary habitat (cutoff determined by ROC) for Baleen whales guild during Summer season in East region.

Beaked whales | Summer | East
Number of presences: 121
Number of absences: 8957
R squared: 0.164088
Deviance explained: 0.2796
ROC optimum: 0.351673
Maximum fit: 0.011717
Maximum prediction: 0.538619
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -9.0990     0.3951  -23.03   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                  edf Ref.df     F  p-value
s(log(depth))   1.983  1.983 91.30  < 2e-16 ***
s(log(d2shelf)) 1.952  1.952 57.04  < 2e-16 ***
s(log(d2coast)) 1.991  1.991 46.10  < 2e-16 ***
s(sst)          1.964  1.964 46.51  < 2e-16 ***
s(lat)          1.992  1.992 35.99 3.07e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.164   Deviance explained =   28%
GCV score = 0.00098768  Scale est. = 0.00098545  n = 8663
```

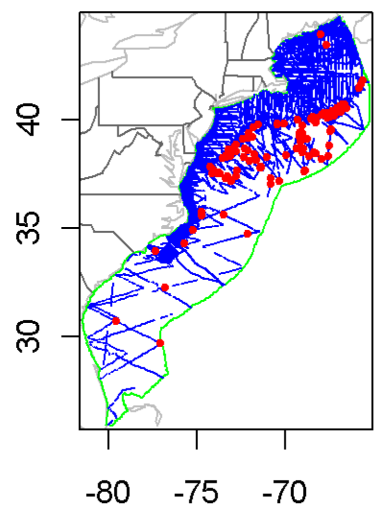


Figure B-91. Map of points of observational sightings and tracks of survey effort for Beaked whales guild during Summer season in East region.

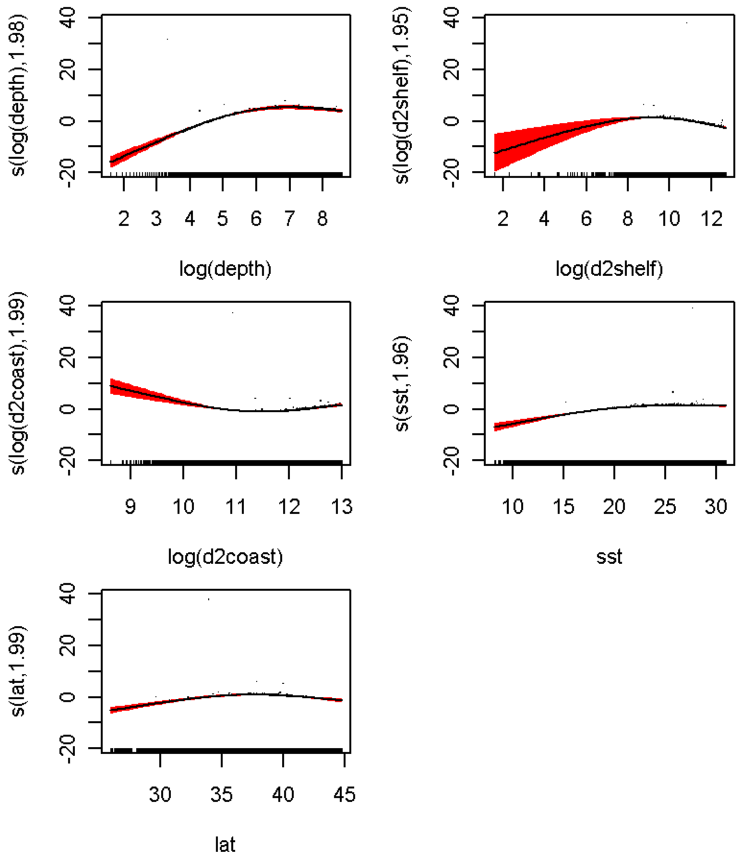


Figure B-92. Terms plot of predictors to GAM model fit for Beaked whales guild during Summer season in East region.

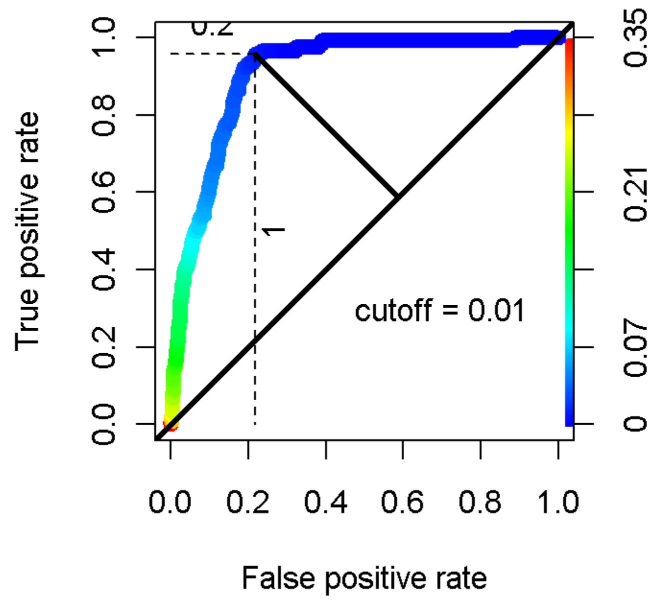


Figure B-93. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Beaked whales guild during Summer season in East region.

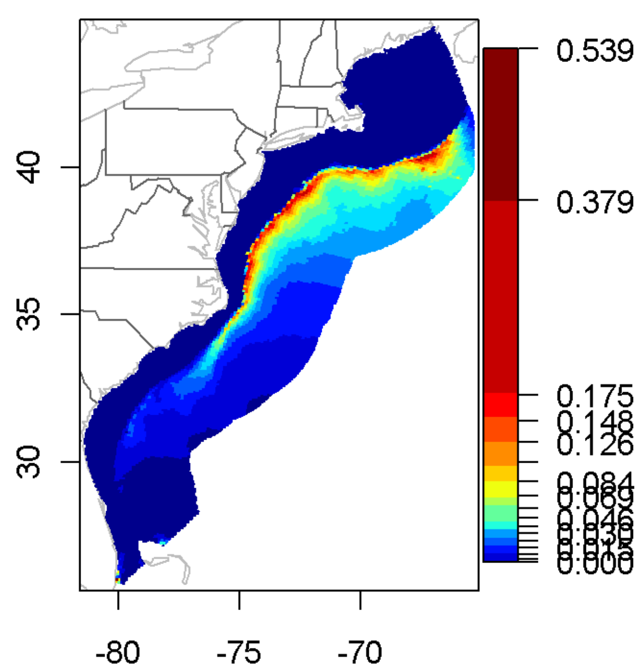


Figure B-94. Map of mean predicted habitat for Beaked whales guild during Summer season in East region.

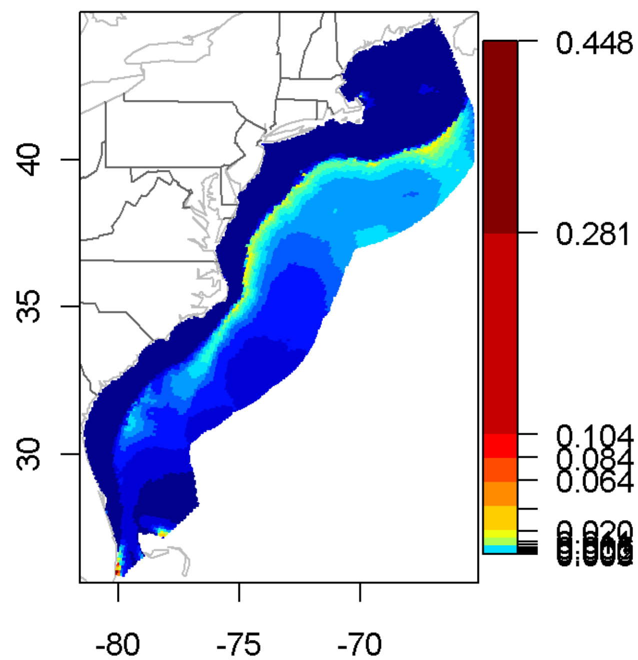


Figure B-95. Map of standard error of habitat for Beaked whales guild during Summer season in East region.

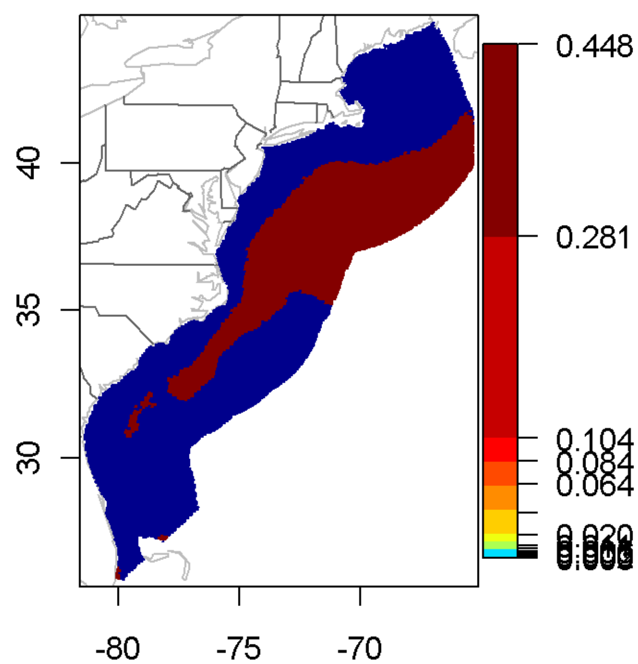


Figure B-96. Map of binary habitat (cutoff determined by ROC) for Beaked whales guild during Summer season in East region.

Delphinus | Summer | East
Number of presences: 187
Number of absences: 8891
R squared: -0.12386
Deviance explained: 0.213347
ROC optimum: 0.170433
Maximum fit: 0.0135978
Maximum prediction: 0.171273
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -7.0982     0.2456   -28.9   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F p-value
s(log(depth))   8.504e-01 8.504e-01     8.94 0.00443 **
s(log(d2shelf)) 1.976e+00 1.976e+00   138.45 < 2e-16 ***
s(log(d2coast)) 1.972e+00 1.972e+00    67.08 < 2e-16 ***
s(sst)          1.960e+00 1.960e+00   106.73 < 2e-16 ***
s(lat)          4.902e-06 4.902e-06 7.24e-05      NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  -0.124   Deviance explained = 21.3%
GCV score = 0.00067322  Scale est. = 0.00067214  n = 8663
```

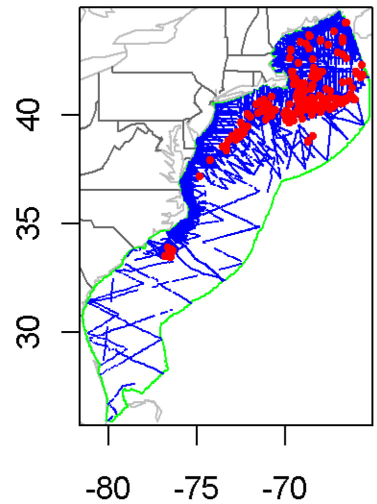


Figure B-97. Map of points of observational sightings and tracks of survey effort for Delphinus guild during Summer season in East region.

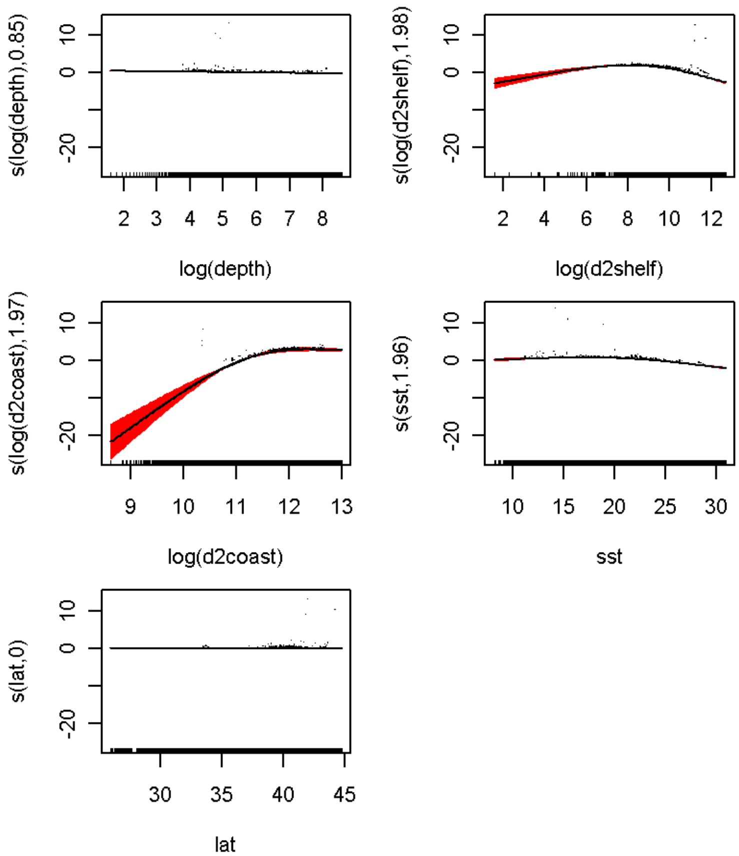


Figure B-98. Terms plot of predictors to GAM model fit for Delphinus guild during Summer season in East region.

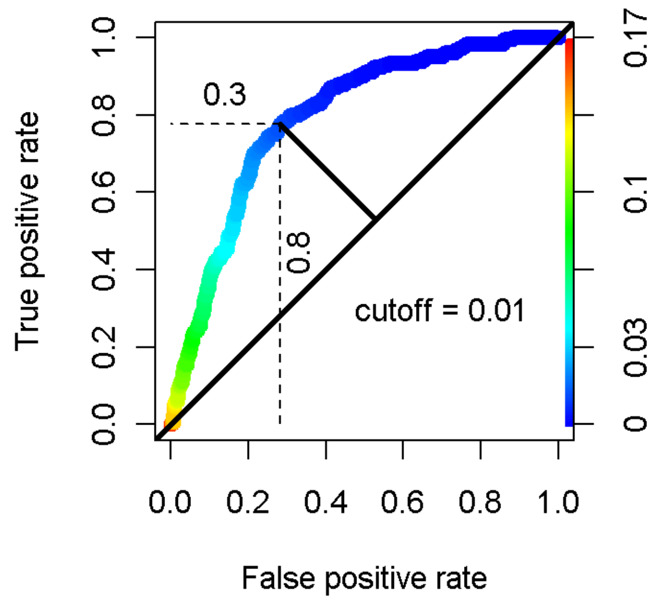


Figure B-99. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Delphinus guild during Summer season in East region.

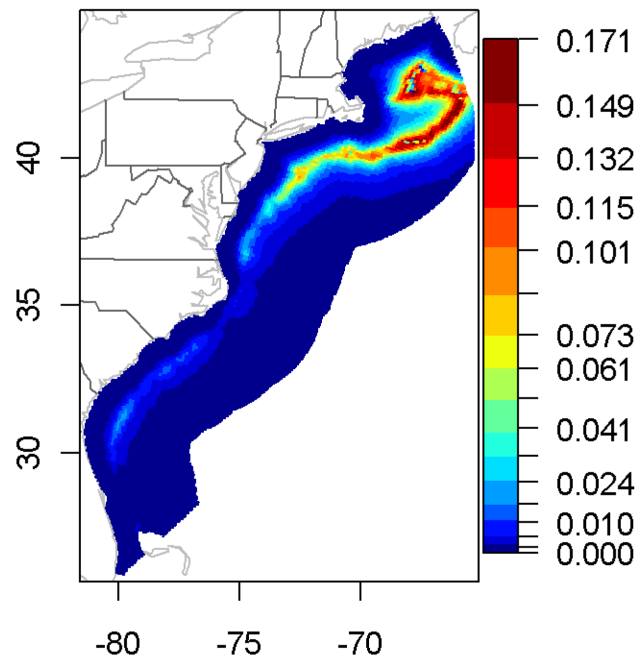


Figure B-100. Map of mean predicted habitat for Delphinus guild during Summer season in East region.

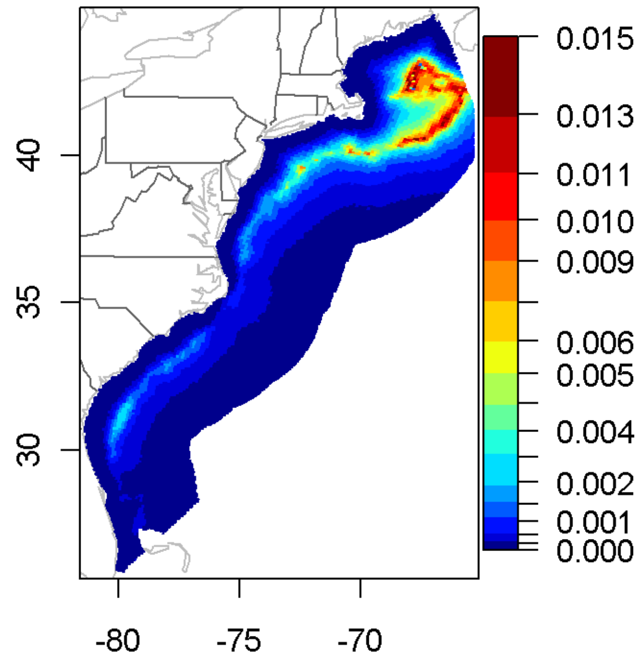


Figure B-101. Map of standard error of habitat for Delphinus guild during Summer season in East region.

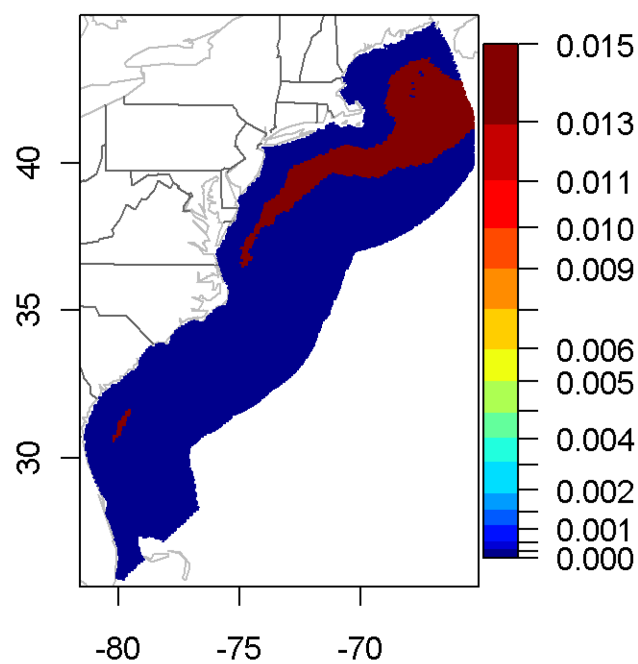


Figure B-102. Map of binary habitat (cutoff determined by ROC) for Delphinus guild during Summer season in East region.

Humpback whales | Fall | East
Number of presences: 27
Number of absences: 1837
R squared: 0.694947
Deviance explained: 0.622913
ROC optimum: 0.776822
Maximum fit: 0.031984
Maximum prediction: 0.776822
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -113.53      11.91  -9.533   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:
                      edf    Ref.df        F p-value
s(log(depth))   1.997e+00 1.997e+00   119.04  <2e-16 ***
s(log(d2shelf)) 9.819e-01 9.819e-01    76.66  <2e-16 ***
s(log(d2coast)) 1.544e-06 1.544e-06 6.95e-05      NA
s(sst)          3.340e-06 3.340e-06 1.40e-04      NA
s(lat)          1.983e+00 1.983e+00    81.63  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) =  0.695   Deviance explained = 62.3%
GCV score = 0.00063626  Scale est. = 0.00063253  n = 1826
```

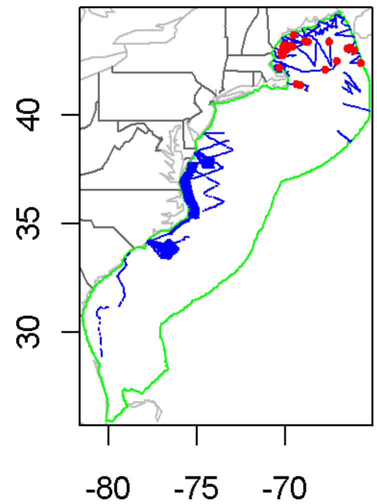


Figure B-103. Map of points of observational sightings and tracks of survey effort for Humpback whales guild during Fall season in East region.

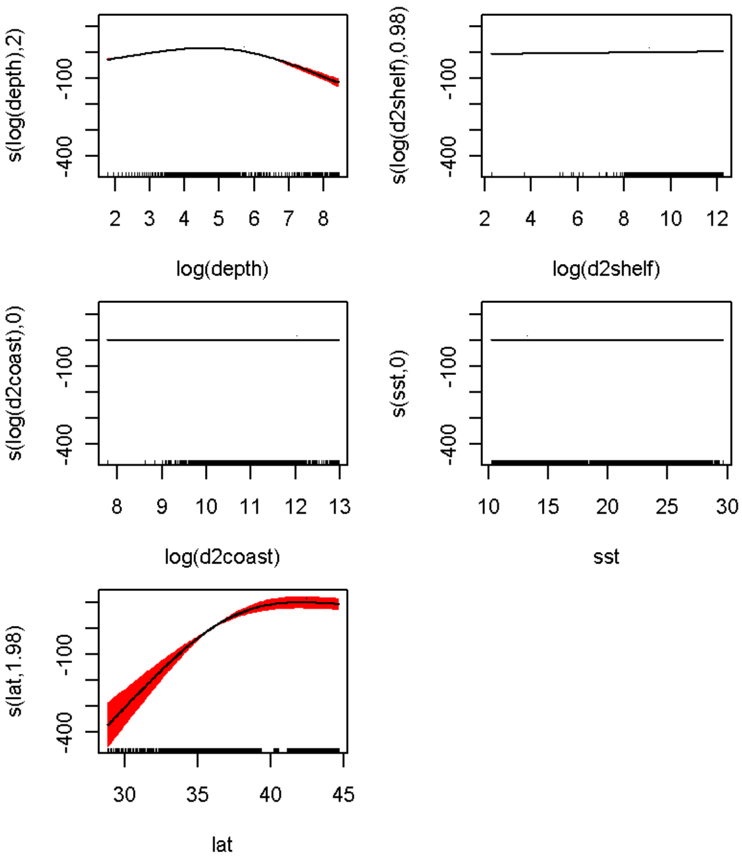


Figure B-104. Terms plot of predictors to GAM model fit for Humpback whales guild during Fall season in East region.

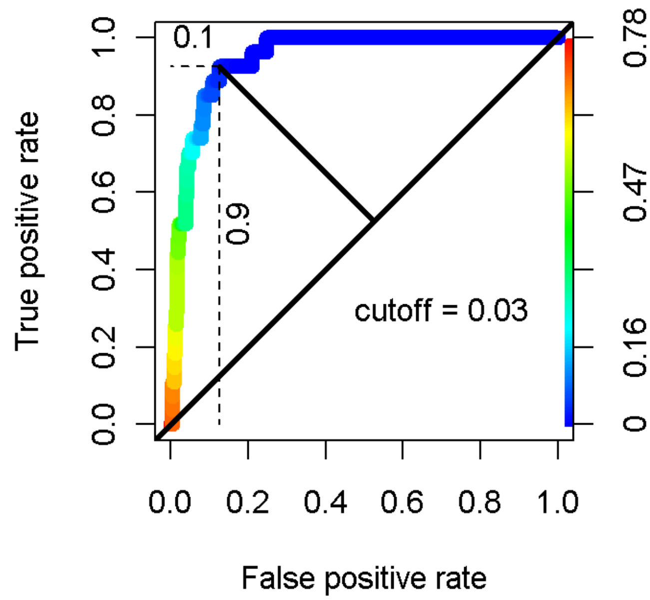


Figure B-105. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Humpback whales guild during Fall season in East region.

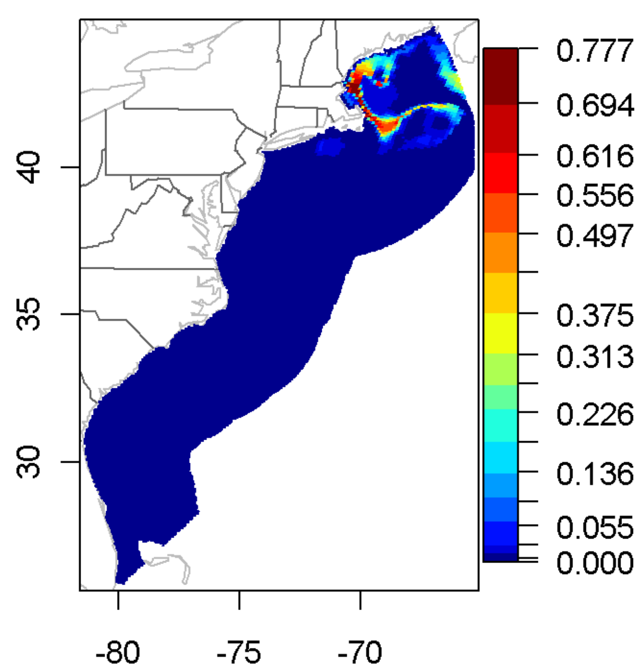


Figure B-106. Map of mean predicted habitat for Humpback whales guild during Fall season in East region.

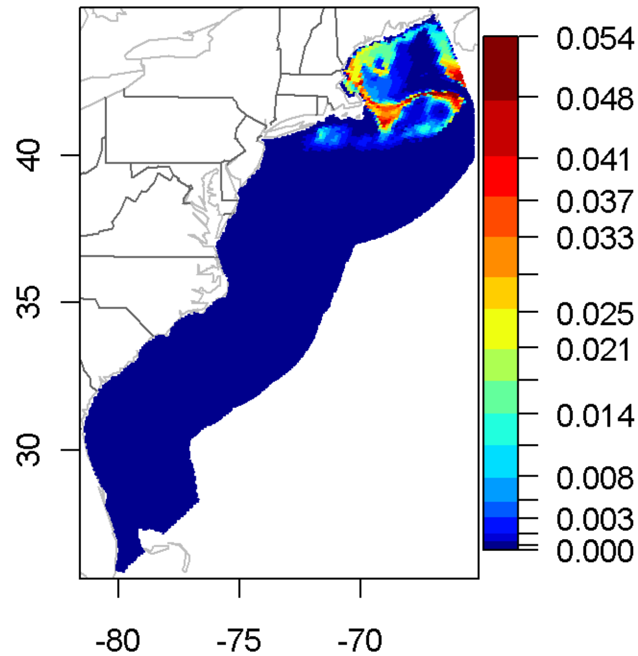


Figure B-107. Map of standard error of habitat for Humpback whales guild during Fall season in East region.

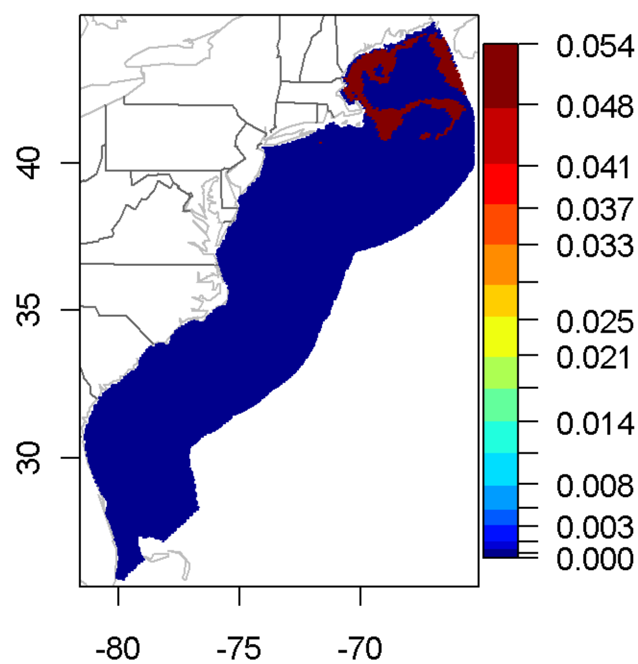


Figure B-108. Map of binary habitat (cutoff determined by ROC) for Humpback whales guild during Fall season in East region.

Humpback whales | Summer | East
Number of presences: 153
Number of absences: 8925
R squared: 0.379949
Deviance explained: 0.417218
ROC optimum: 0.569111
Maximum fit: 0.0319719
Maximum prediction: 0.555827
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -48.853      2.316  -21.09   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                   edf Ref.df      F  p-value
s(log(depth))   1.9935 1.9935 199.49  < 2e-16 ***
s(log(d2shelf)) 0.9991 0.9991 333.66  < 2e-16 ***
s(log(d2coast)) 0.9576 0.9576  30.98 4.75e-08 ***
s(sst)          1.9533 1.9533  78.39  < 2e-16 ***
s(lat)          1.9864 1.9864 132.39  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =   0.38   Deviance explained = 41.7%
GCV score = 0.0010055  Scale est. = 0.0010037  n = 8663
```

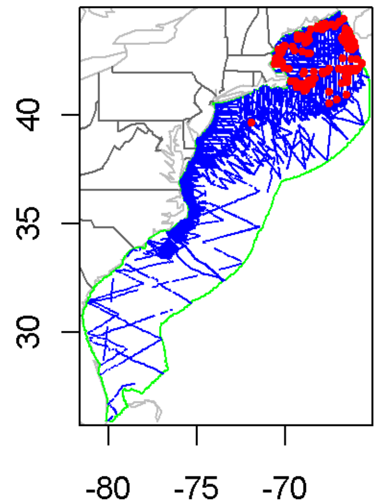


Figure B-109. Map of points of observational sightings and tracks of survey effort for Humpback whales guild during Summer season in East region.

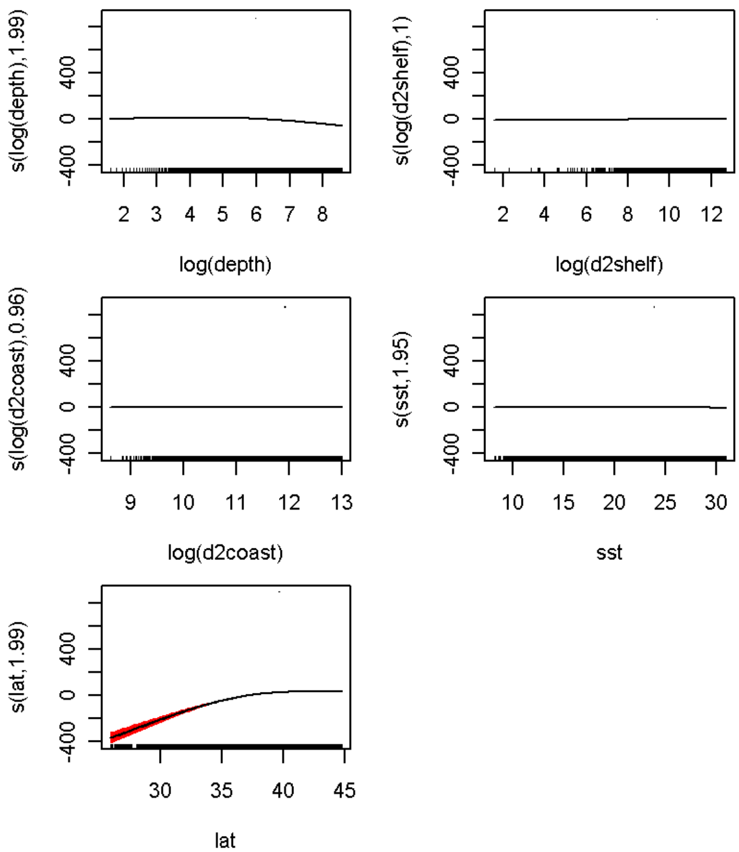


Figure B-110. Terms plot of predictors to GAM model fit for Humpback whales guild during Summer season in East region.

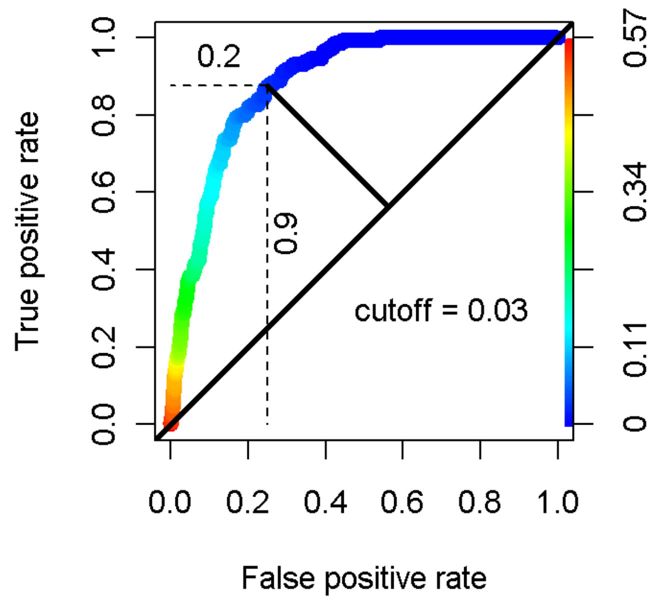


Figure B-111. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Humpback whales guild during Summer season in East region.

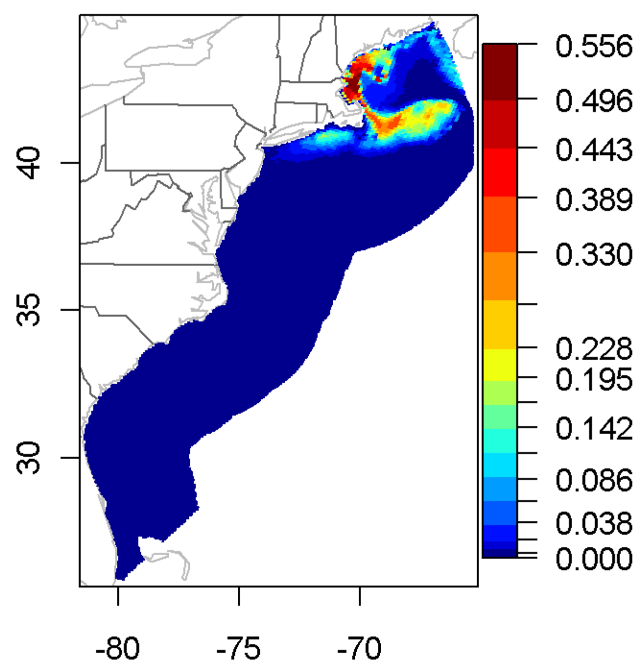


Figure B-112. Map of mean predicted habitat for Humpback whales guild during Summer season in East region.

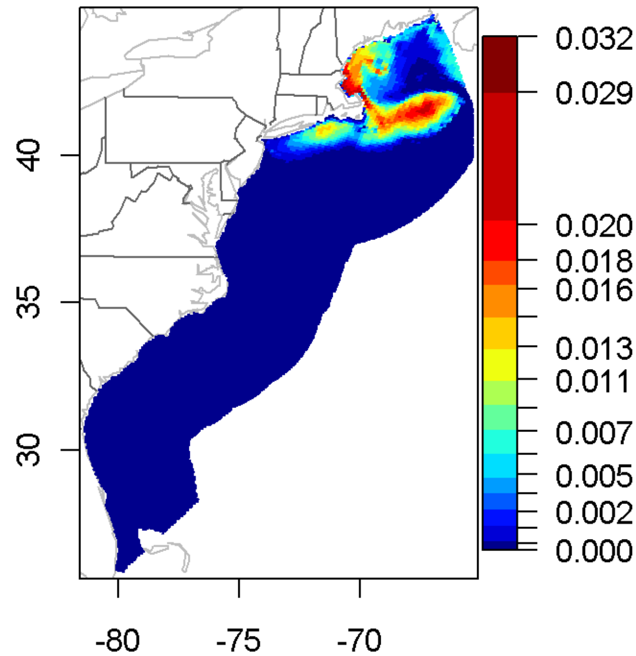


Figure B-113. Map of standard error of habitat for Humpback whales guild during Summer season in East region.

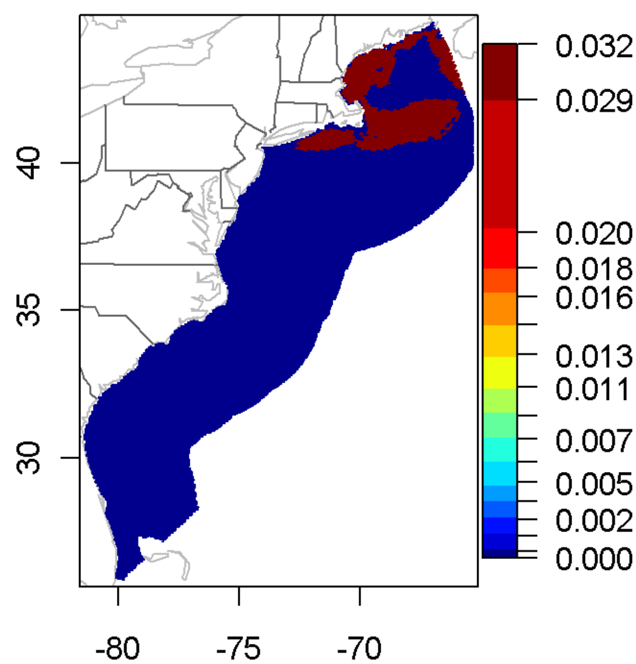


Figure B-114. Map of binary habitat (cutoff determined by ROC) for Humpback whales guild during Summer season in East region.

Humpback whales | Winter | East
Number of presences: 11
Number of absences: 3891
R squared: 0.456624
Deviance explained: 0.478758
ROC optimum: 0.599348
Maximum fit: 0.231581
Maximum prediction: 0.799905
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -23.8600     0.9411  -25.35   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F p-value
s(log(depth))   1.293e-06 1.293e-06 0.000136      NA
s(log(d2shelf)) 1.995e+00 1.995e+00    65.11  <2e-16 ***
s(log(d2coast)) 1.989e+00 1.989e+00   118.39  <2e-16 ***
s(sst)          1.240e-06 1.240e-06 0.000388      NA
s(lat)          1.998e+00 1.998e+00   223.31  <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.457   Deviance explained = 47.9%
GCV score = 0.00031276  Scale est. = 0.00031107  n = 2337
```

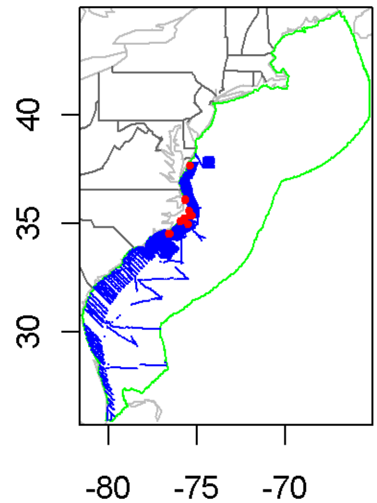


Figure B-115. Map of points of observational sightings and tracks of survey effort for Humpback whales guild during Winter season in East region.

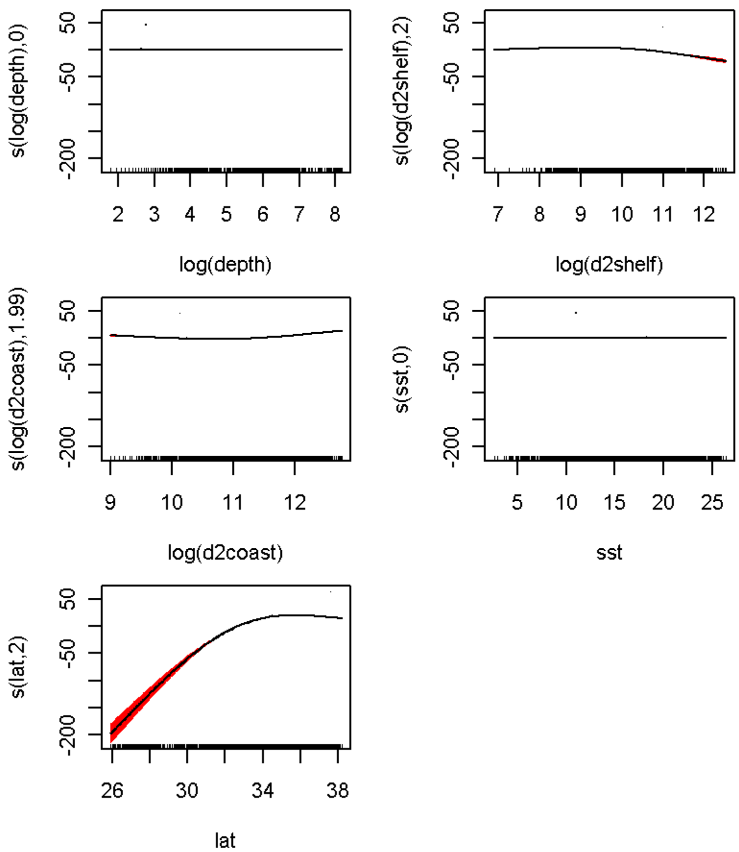


Figure B-116. Terms plot of predictors to GAM model fit for Humpback whales guild during Winter season in East region.

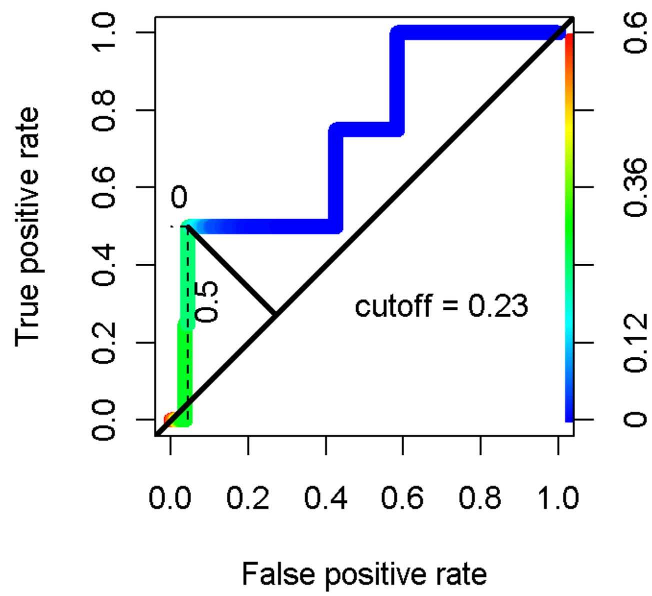


Figure B-117. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Humpback whales guild during Winter season in East region.

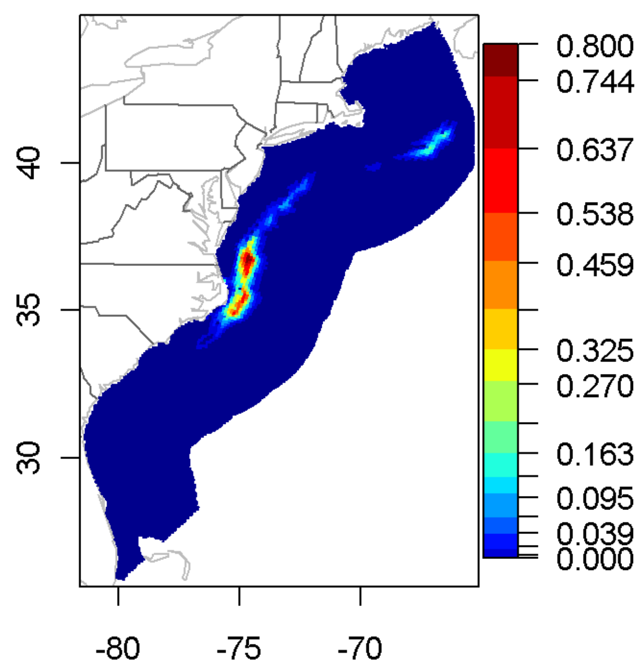


Figure B-118. Map of mean predicted habitat for Humpback whales guild during Winter season in East region.

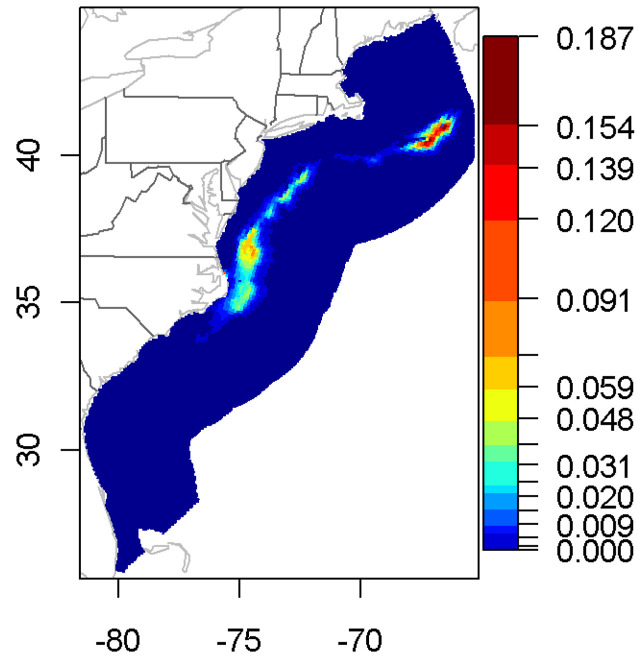


Figure B-119. Map of standard error of habitat for Humpback whales guild during Winter season in East region.

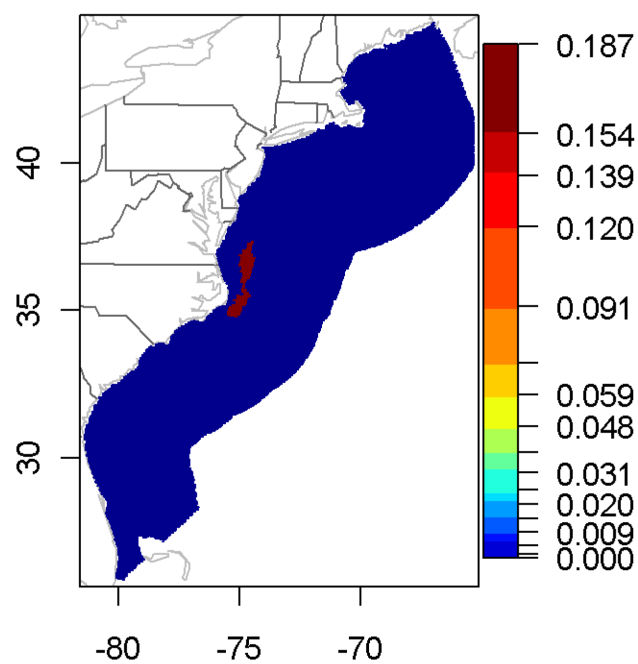


Figure B-120. Map of binary habitat (cutoff determined by ROC) for Humpback whales guild during Winter season in East region.

Lags | Summer | East
Number of presences: 151
Number of absences: 8927
R squared: 0.146137
Deviance explained: 0.313246
ROC optimum: 0.238948
Maximum fit: 0.0198197
Maximum prediction: 0.166888
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -9.4389     0.4409  -21.41   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df      F  p-value
s(log(depth))   1.946e+00 1.946e+00 18.117 2.08e-08 ***
s(log(d2shelf)) 2.585e-06 2.585e-06  0.001       NA
s(log(d2coast)) 1.965e+00 1.965e+00 23.325 1.11e-10 ***
s(sst)          1.975e+00 1.975e+00 85.731  < 2e-16 ***
s(lat)          9.729e-01 9.729e-01 96.167  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.146   Deviance explained = 31.3%
GCV score = 0.0008083  Scale est. = 0.00080698  n = 8663
```

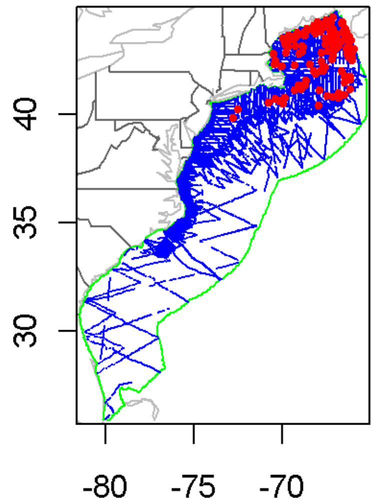


Figure B-121. Map of points of observational sightings and tracks of survey effort for Lags guild during Summer season in East region.

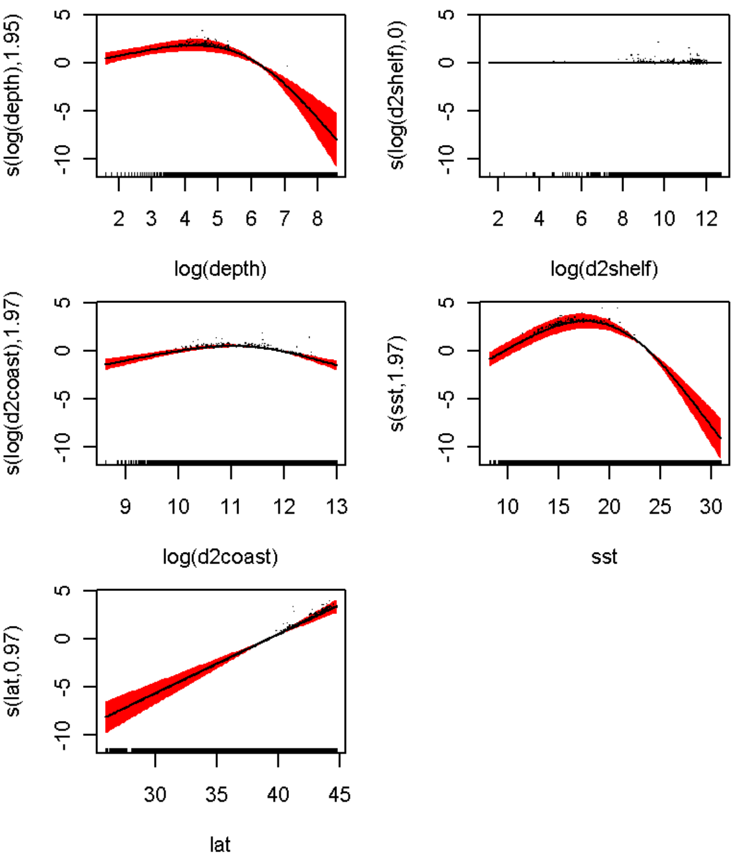


Figure B-122. Terms plot of predictors to GAM model fit for Lags guild during Summer season in East region.

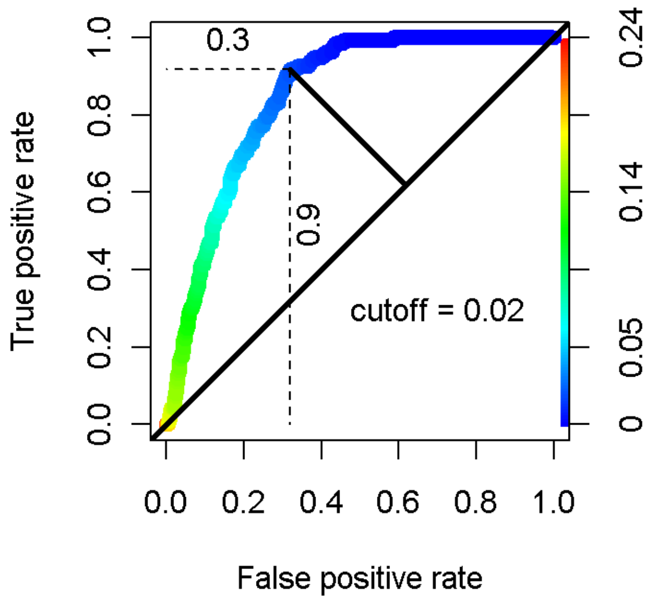


Figure B-123. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Lags guild during Summer season in East region.

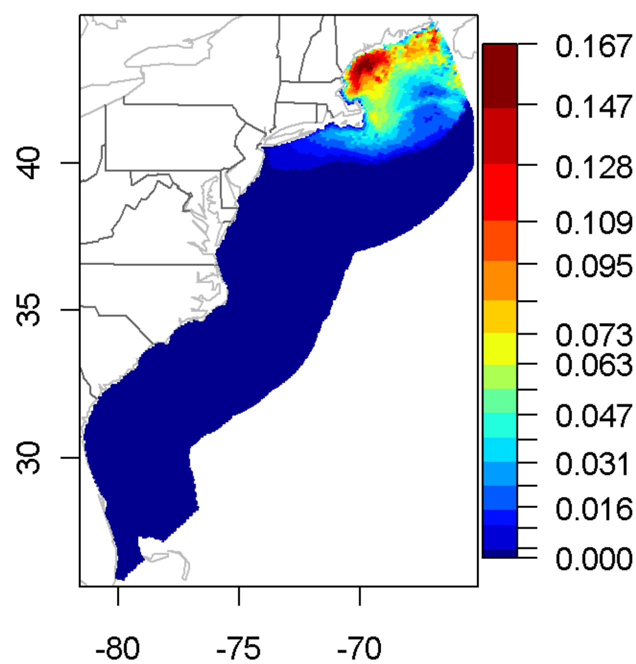


Figure B-124. Map of mean predicted habitat for Lags guild during Summer season in East region.

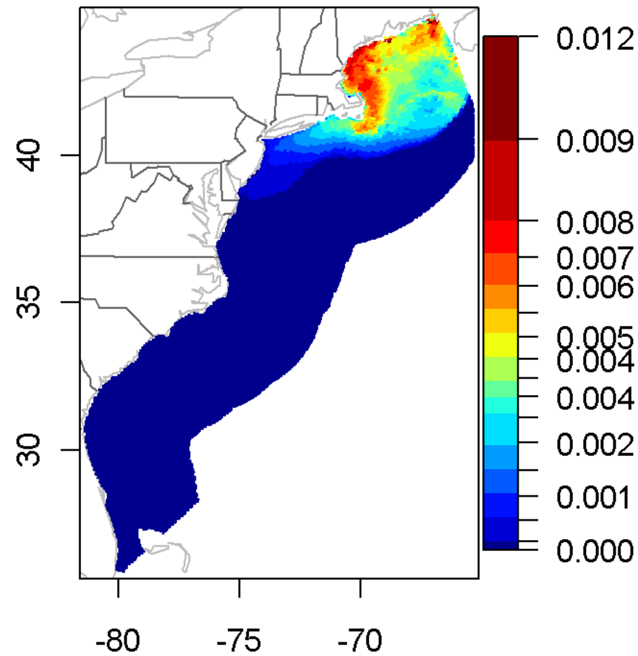


Figure B-125. Map of standard error of habitat for Lags guild during Summer season in East region.

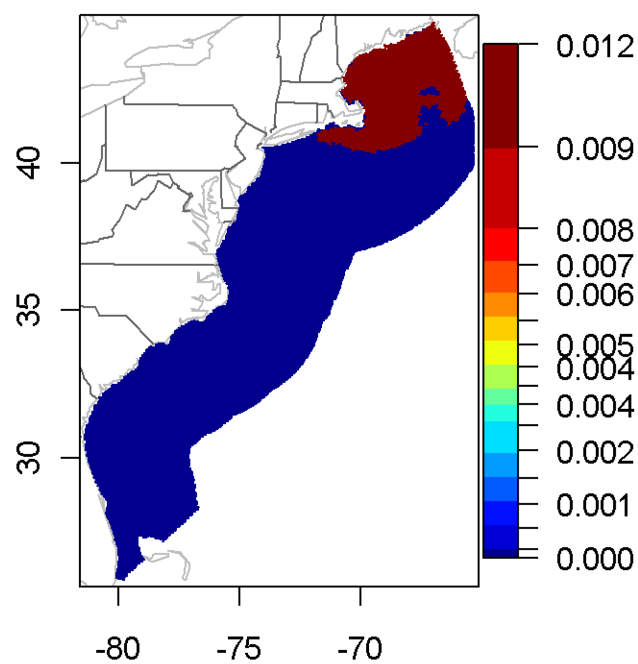


Figure B-126. Map of binary habitat (cutoff determined by ROC) for Lags guild during Summer season in East region.

Pilot whales | Winter | East
Number of presences: 7
Number of absences: 3895
R squared: 0.00342482
Deviance explained: 0.306854
ROC optimum: 0.0677613
Maximum fit: 3.06132e-06
Maximum prediction: 0.0766173
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -59.094      4.703  -12.56   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F p-value
s(log(depth))   1.974e+00 1.974e+00    51.09  <2e-16 ***
s(log(d2shelf)) 1.267e-07 1.267e-07 1.76e-07      NA
s(log(d2coast)) 1.989e+00 1.989e+00    60.53  <2e-16 ***
s(sst)          6.488e-08 6.488e-08 1.85e-07      NA
s(lat)          5.425e-07 5.425e-07 3.02e-06      NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.00342   Deviance explained = 30.7%
GCV score = 0.00013347  Scale est. = 0.00013296  n = 2337
```

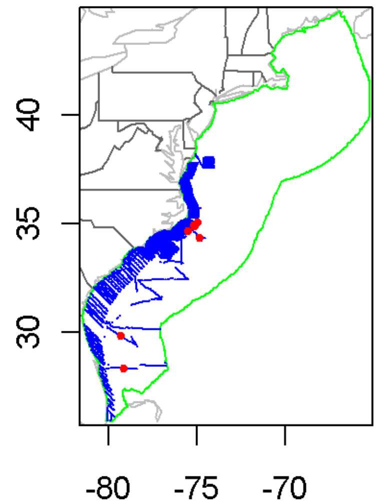


Figure B-127. Map of points of observational sightings and tracks of survey effort for Pilot whales guild during Winter season in East region.

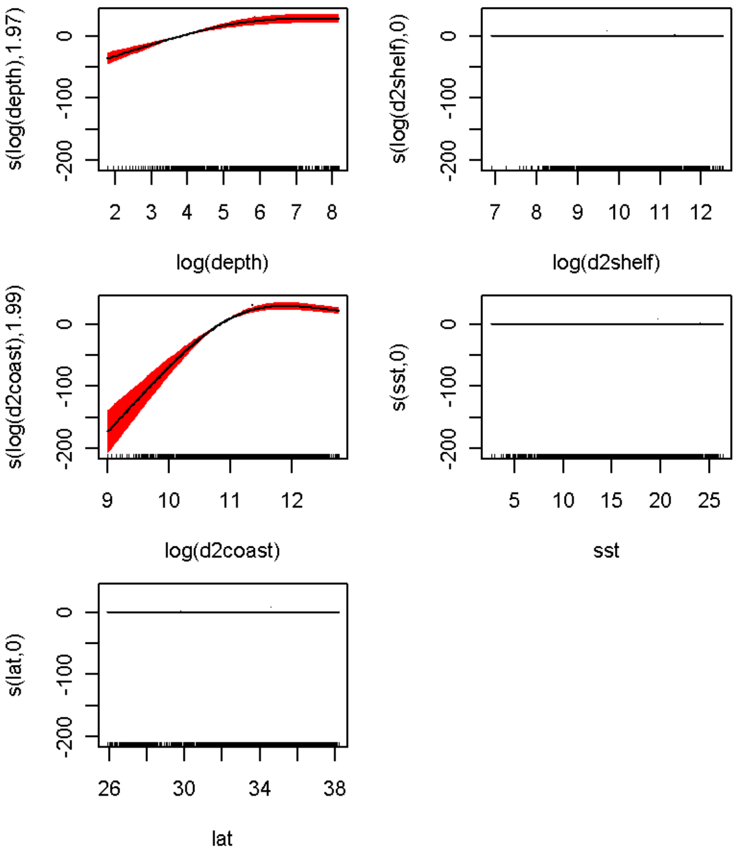


Figure B-128. Terms plot of predictors to GAM model fit for Pilot whales guild during Winter season in East region.

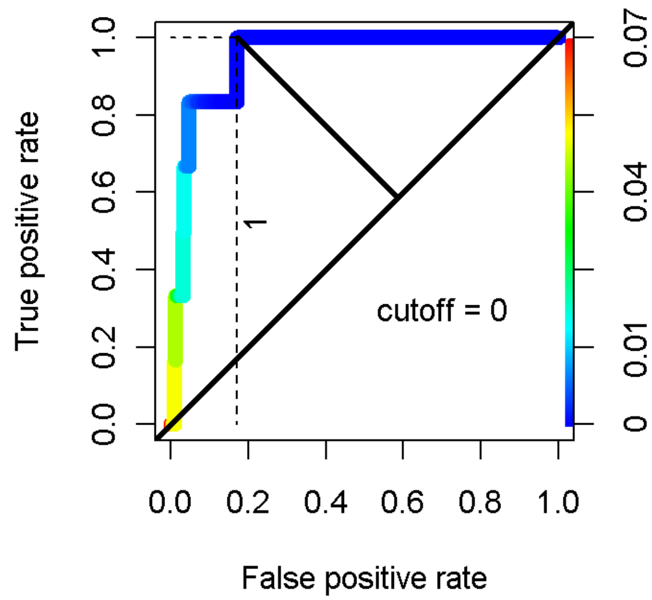


Figure B-129. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Pilot whales guild during Winter season in East region.

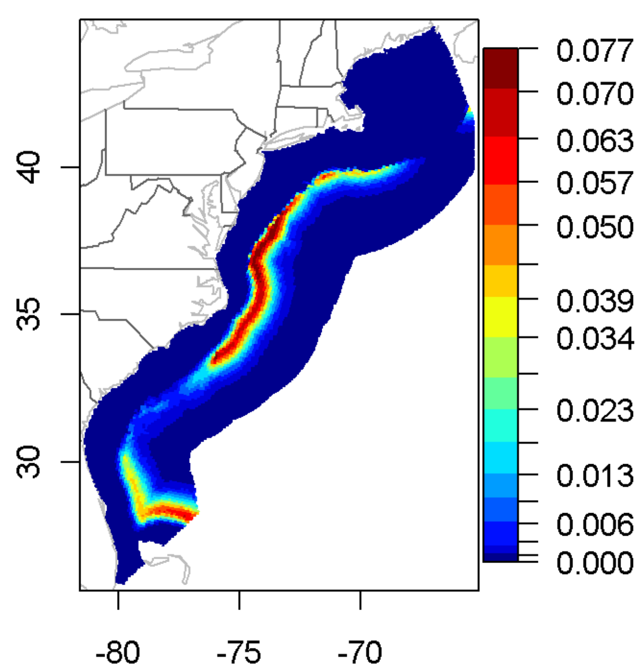


Figure B-130. Map of mean predicted habitat for Pilot whales guild during Winter season in East region.

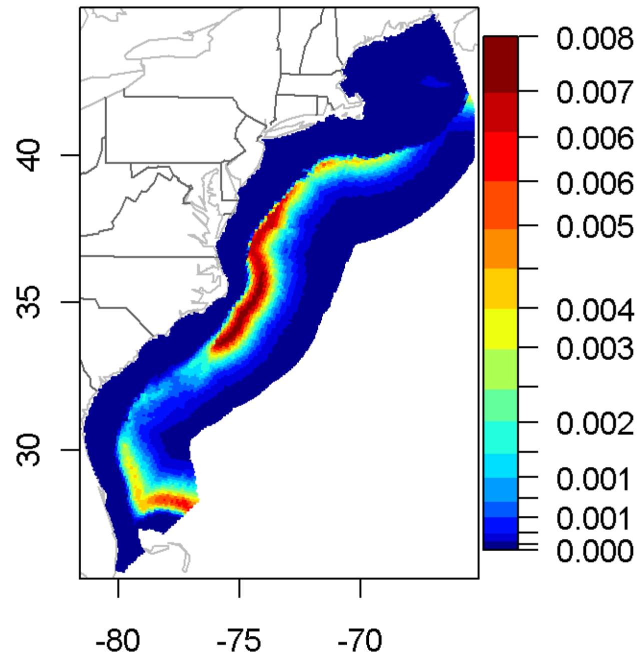


Figure B-131. Map of standard error of habitat for Pilot whales guild during Winter season in East region.

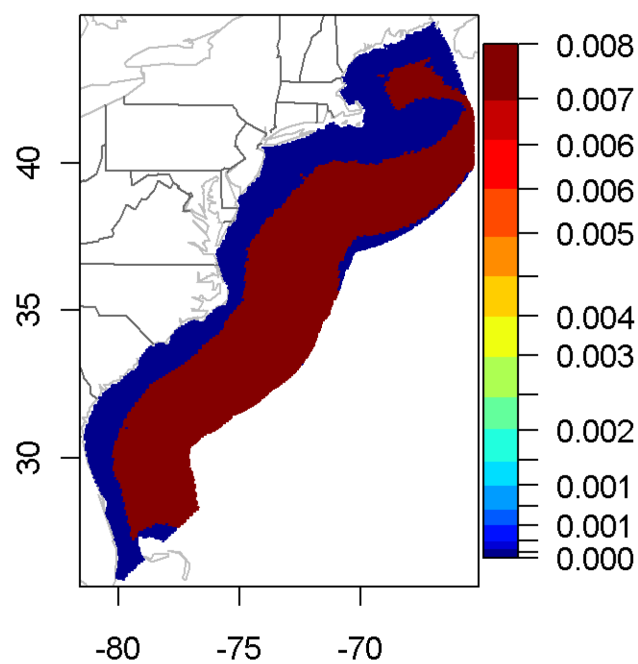


Figure B-132. Map of binary habitat (cutoff determined by ROC) for Pilot whales guild during Winter season in East region.

Right whales | Summer | East
Number of presences: 17
Number of absences: 9061
R squared: 0.0164802
Deviance explained: 0.323434
ROC optimum: 0.260051
Maximum fit: 1.85983e-05
Maximum prediction: 0.116522
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -26.367      1.293  -20.39   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                     edf   Ref.df        F p-value
s(log(depth))   1.999927 1.999927    83.11  <2e-16 ***
s(log(d2shelf)) 0.003881 0.003881 0.000138      NA
s(log(d2coast)) 1.872193 1.872193    87.02  <2e-16 ***
s(sst)          1.991079 1.991079   249.68  <2e-16 ***
s(lat)          0.999380 0.999380   577.88  <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.0165   Deviance explained = 32.3%
GCV score = 7.2929e-05  Scale est. = 7.281e-05  n = 8663
```

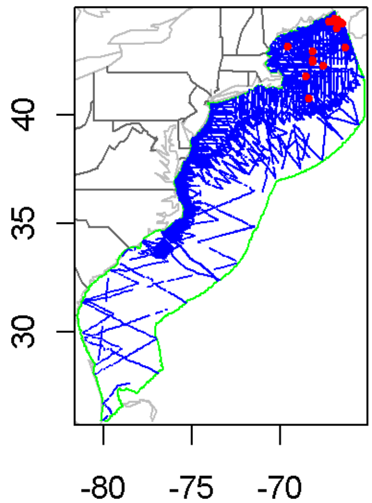


Figure B-133. Map of points of observational sightings and tracks of survey effort for Right whales guild during Summer season in East region.

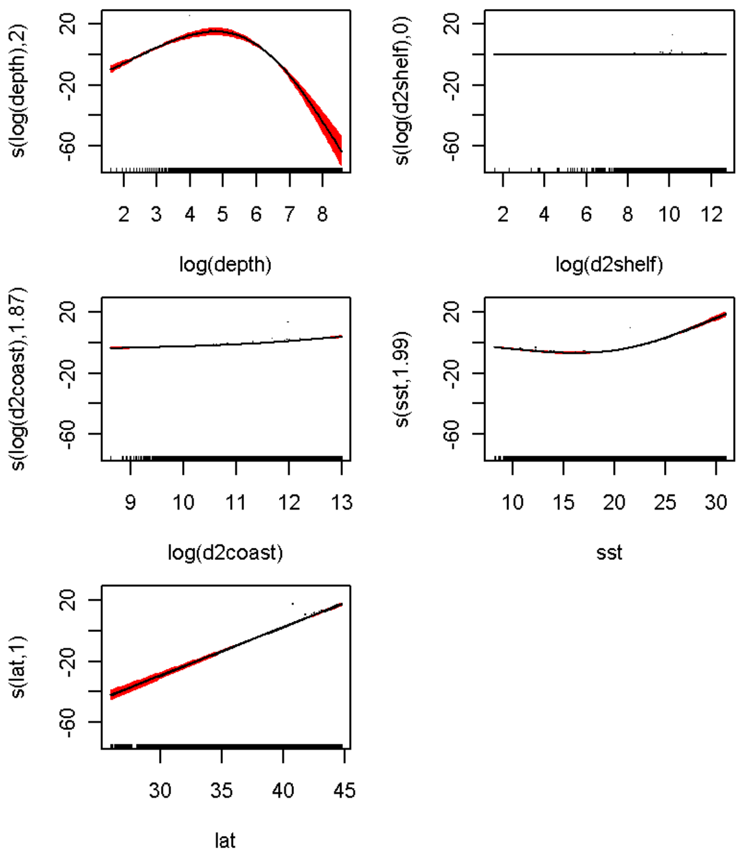


Figure B-134. Terms plot of predictors to GAM model fit for Right whales guild during Summer season in East region.

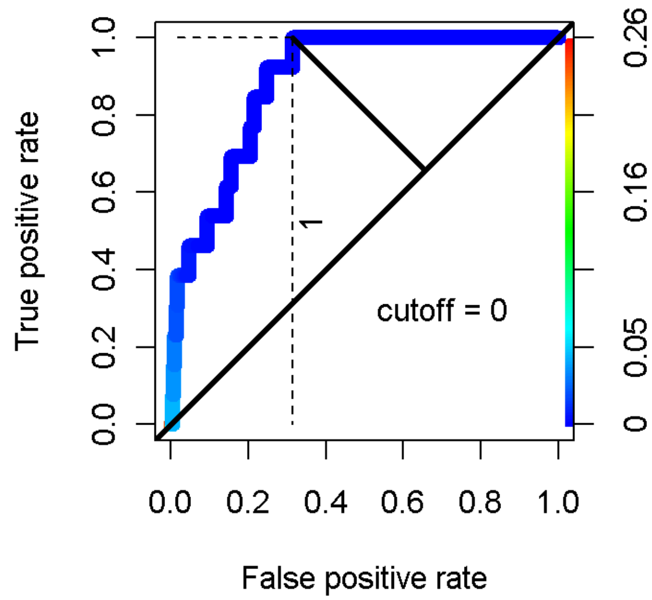


Figure B-135. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Right whales guild during Summer season in East region.

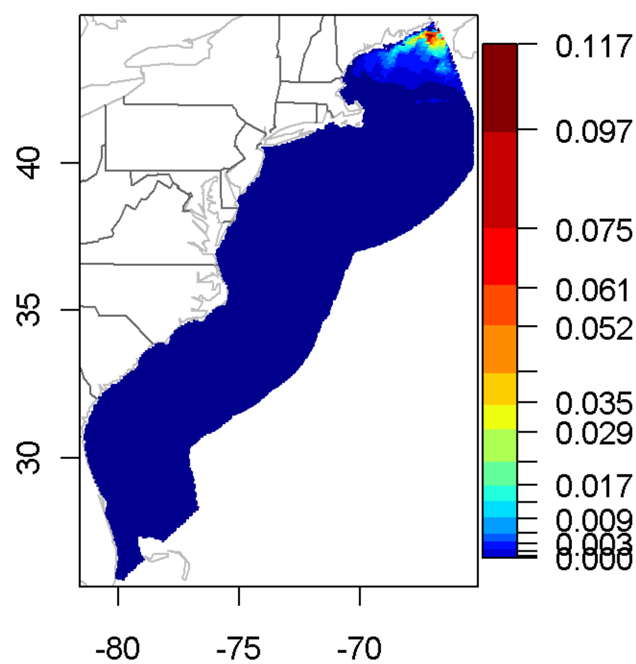


Figure B-136. Map of mean predicted habitat for Right whales guild during Summer season in East region.

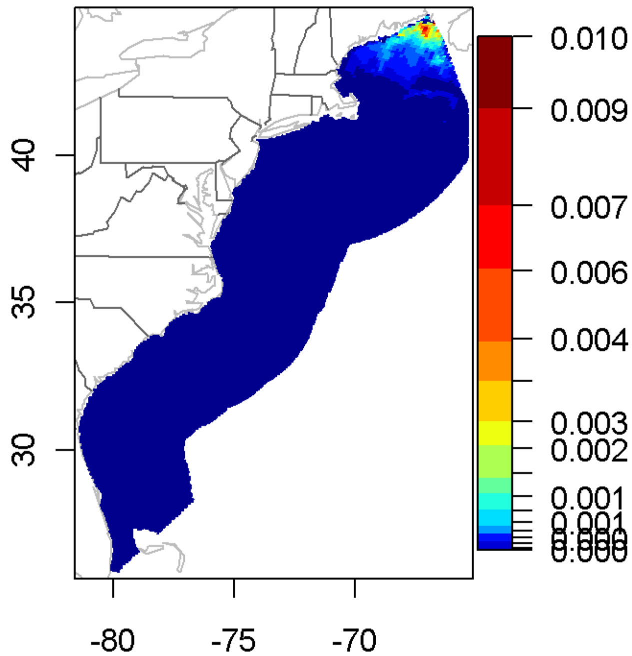


Figure B-137. Map of standard error of habitat for Right whales guild during Summer season in East region.

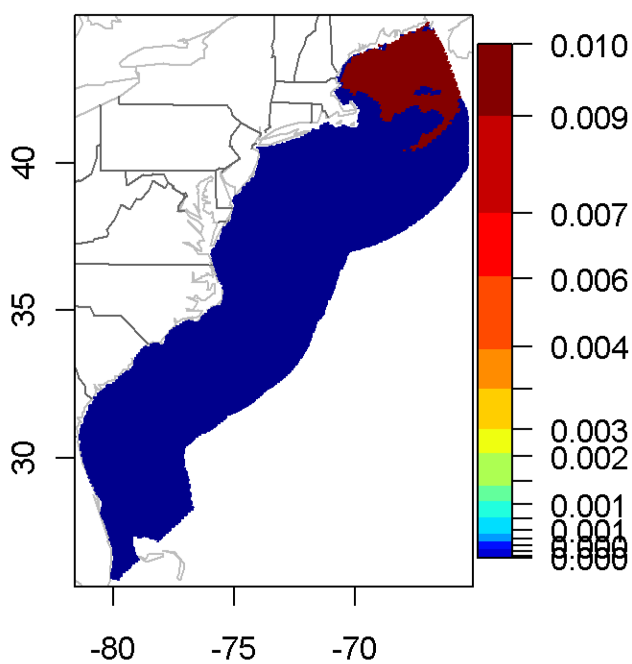


Figure B-138. Map of binary habitat (cutoff determined by ROC) for Right whales guild during Summer season in East region.

Sperm whales | Fall | East
Number of presences: 7
Number of absences: 1857
R squared: 0.256727
Deviance explained: 0.541766
ROC optimum: 0.367947
Maximum fit: 6.55695e-08
Maximum prediction: 0.587177
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -1911.3      138.4  -13.81   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F p-value
s(log(depth))   1.994e+00 1.994e+00   117.63  <2e-16 ***
s(log(d2shelf)) 3.847e-08 3.847e-08 1.72e-06      NA
s(log(d2coast)) 1.991e+00 1.991e+00    65.45  <2e-16 ***
s(sst)          3.324e-08 3.324e-08 1.39e-05      NA
s(lat)          2.332e-08 2.332e-08 2.27e-06      NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.257   Deviance explained = 54.2%
GCV score = 0.00013594  Scale est. = 0.00013528  n = 1826
```

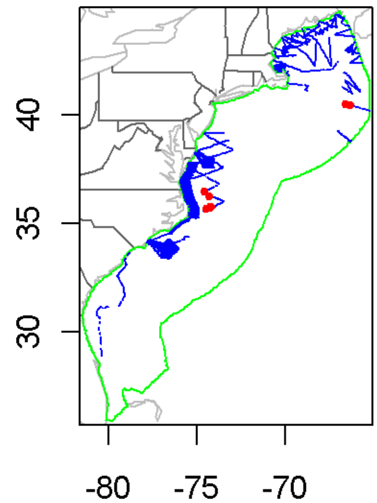


Figure B-139. Map of points of observational sightings and tracks of survey effort for Sperm whales guild during Fall season in East region.

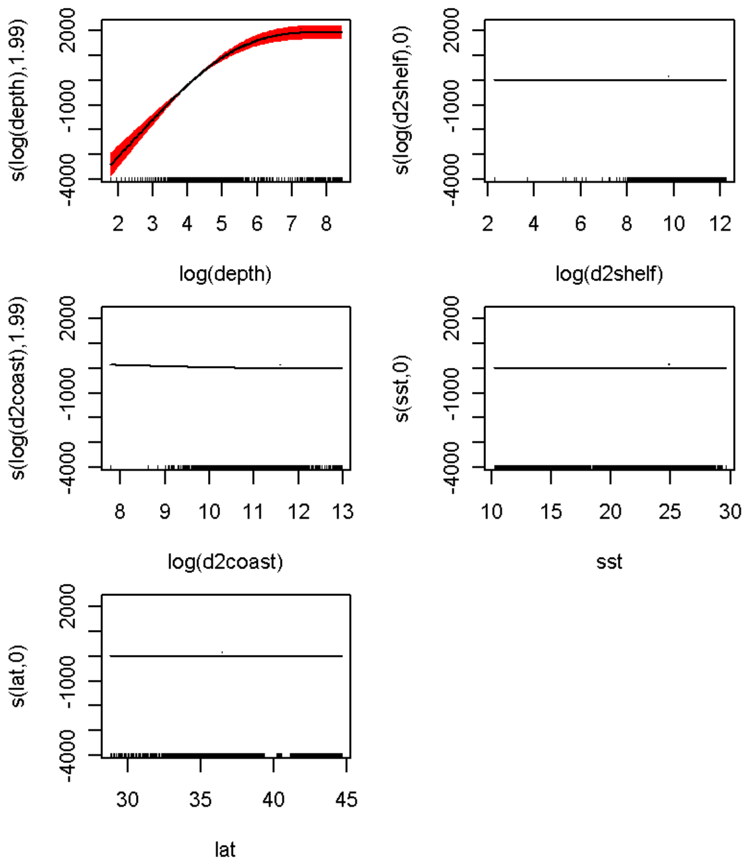


Figure B-140. Terms plot of predictors to GAM model fit for Sperm whales guild during Fall season in East region.

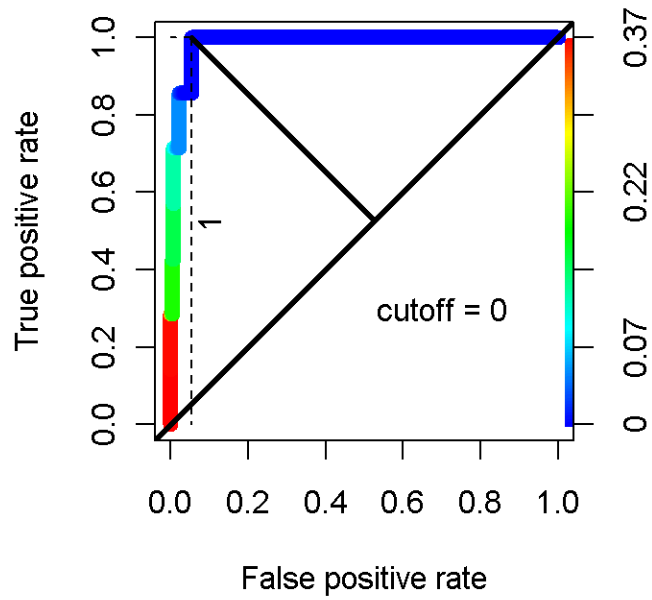


Figure B-141. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Sperm whales guild during Fall season in East region.

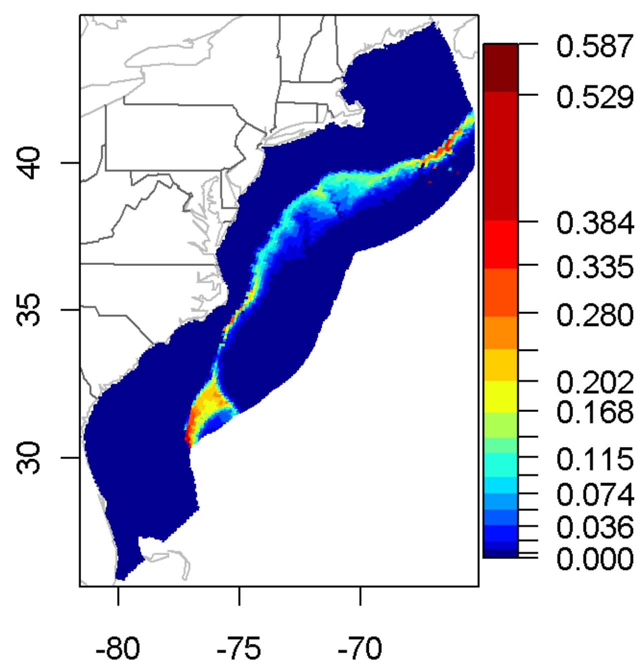


Figure B-142. Map of mean predicted habitat for Sperm whales guild during Fall season in East region.

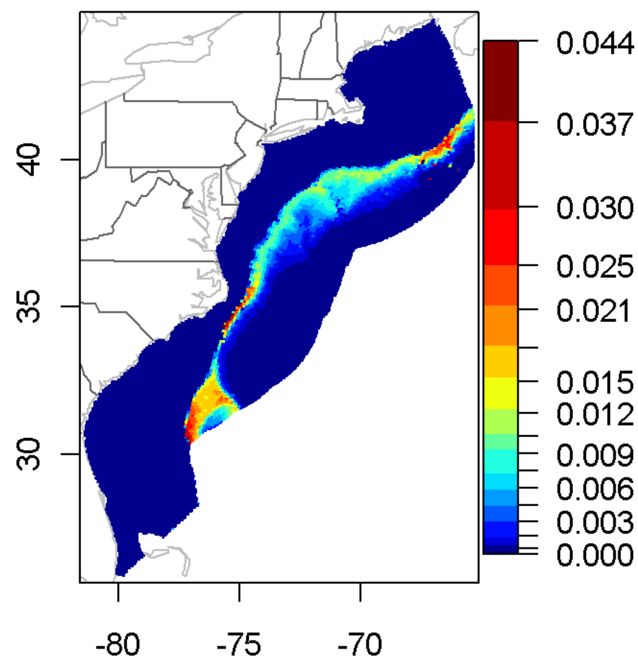


Figure B-143. Map of standard error of habitat for Sperm whales guild during Fall season in East region.

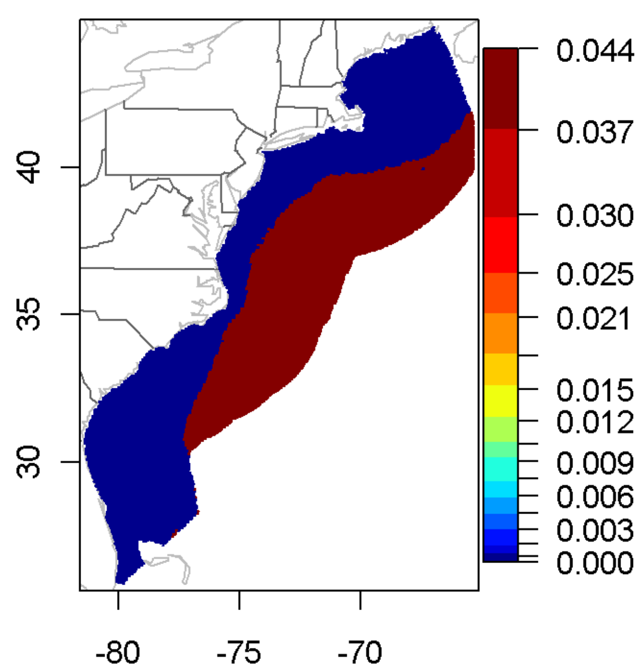


Figure B-144. Map of binary habitat (cutoff determined by ROC) for Sperm whales guild during Fall season in East region.

Sperm whales | Summer | East
Number of presences: 224
Number of absences: 8854
R squared: 0.222786
Deviance explained: 0.289096
ROC optimum: 0.311711
Maximum fit: 0.0183464
Maximum prediction: 0.298253
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -10.210      0.601  -16.99   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                   edf Ref.df       F  p-value
s(log(depth))   1.0590 1.0590 173.998  < 2e-16 ***
s(log(d2shelf)) 0.8499 0.8499   7.363   0.0095 **
s(log(d2coast)) 1.9871 1.9871  84.283  < 2e-16 ***
s(sst)          1.9687 1.9687  30.834 6.87e-14 ***
s(lat)          1.9908 1.9908  71.189  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.223   Deviance explained = 28.9%
GCV score = 0.0014359  Scale est. = 0.0014332  n = 8663
```

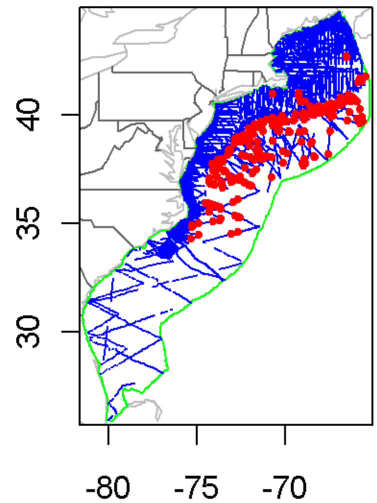


Figure B-145. Map of points of observational sightings and tracks of survey effort for Sperm whales guild during Summer season in East region.

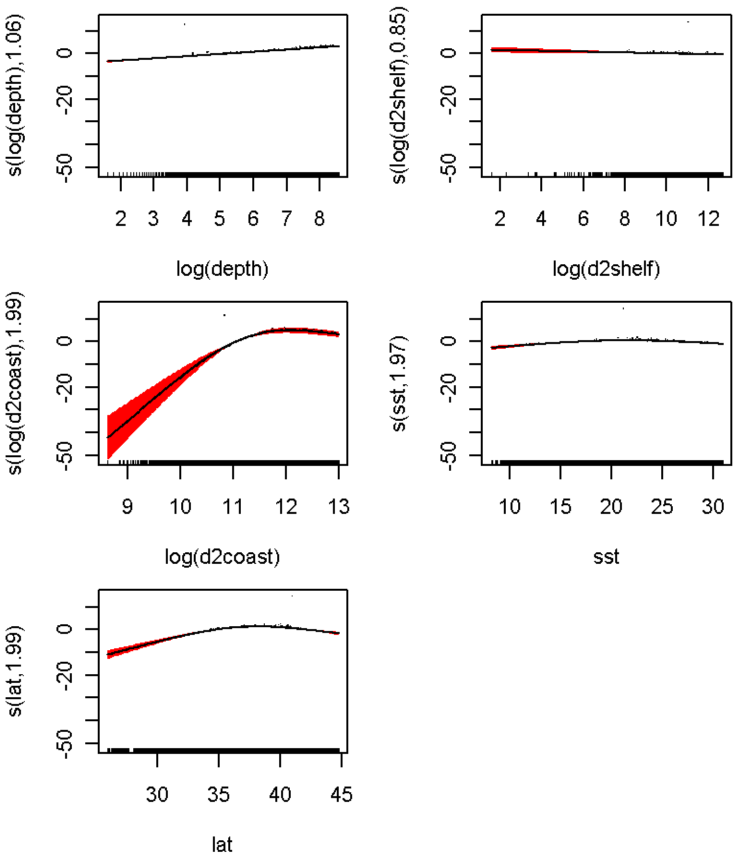


Figure B-146. Terms plot of predictors to GAM model fit for Sperm whales guild during Summer season in East region.

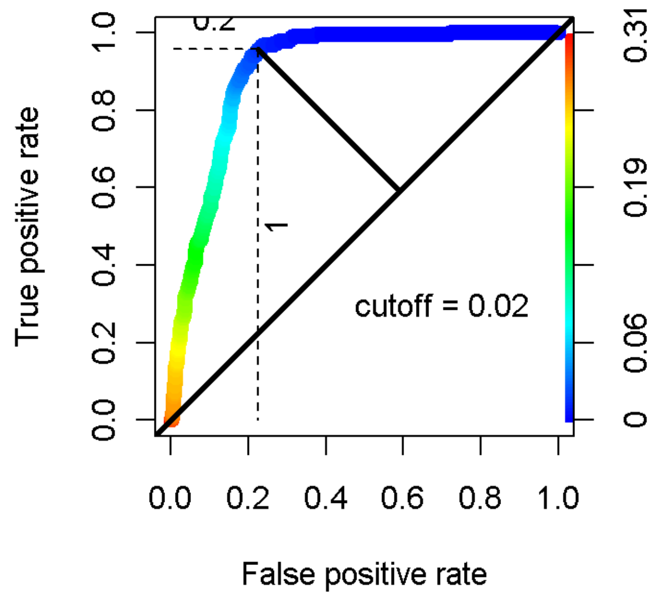


Figure B-147. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Sperm whales guild during Summer season in East region.

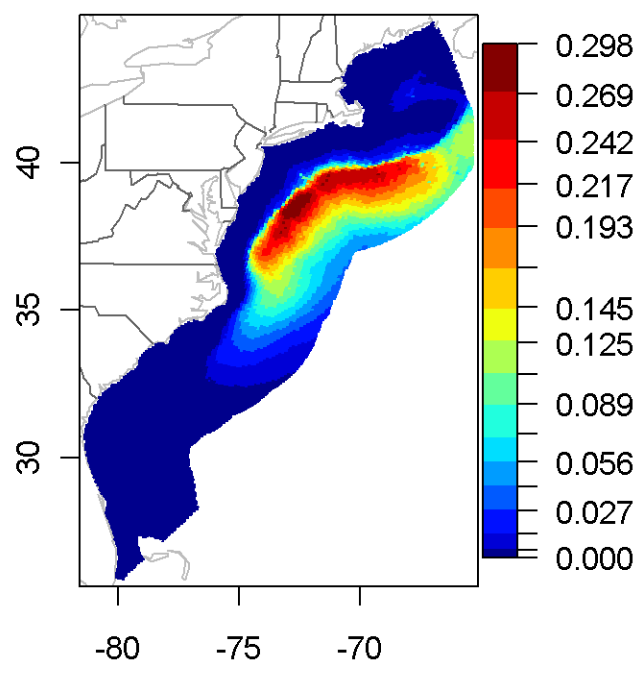


Figure B-148. Map of mean predicted habitat for Sperm whales guild during Summer season in East region.

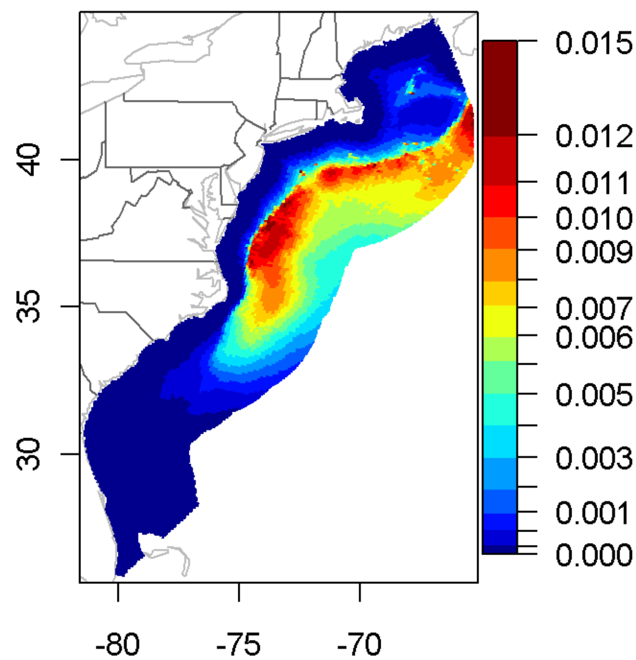


Figure B-149. Map of standard error of habitat for Sperm whales guild during Summer season in East region.

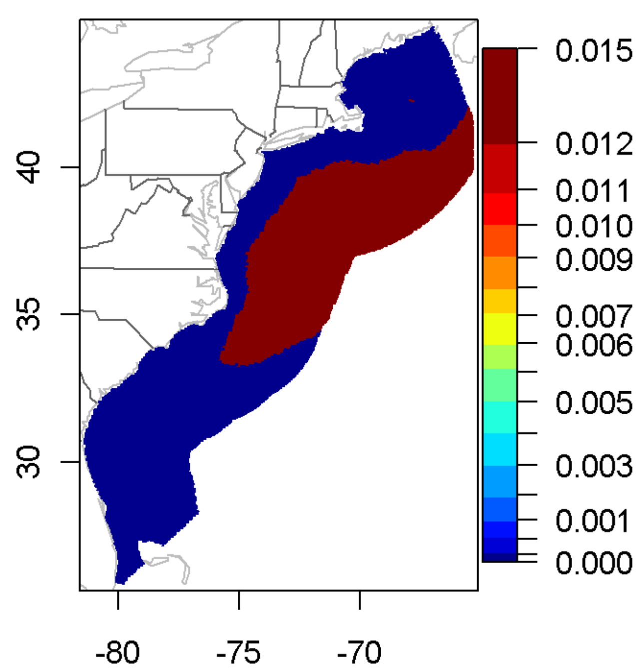


Figure B-150. Map of binary habitat (cutoff determined by ROC) for Sperm whales guild during Summer season in East region.

Striped dolphin | Summer | East
Number of presences: 115
Number of absences: 8963
R squared: 0.20261
Deviance explained: 0.288715
ROC optimum: 0.429463
Maximum fit: 0.0267239
Maximum prediction: 0.128321
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -8.3534     0.3645  -22.92   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                     edf   Ref.df        F  p-value
s(log(depth))   1.998444 1.998444    68.00  < 2e-16 ***
s(log(d2shelf)) 1.999386 1.999386    20.76 1.02e-09 ***
s(log(d2coast)) 0.005406 0.005406 0.000262       NA
s(sst)          1.896727 1.896727   116.63  < 2e-16 ***
s(lat)          1.991887 1.991887    61.88  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.203   Deviance explained = 28.9%
GCV score = 0.00094318  Scale est. = 0.00094144  n = 8663
```

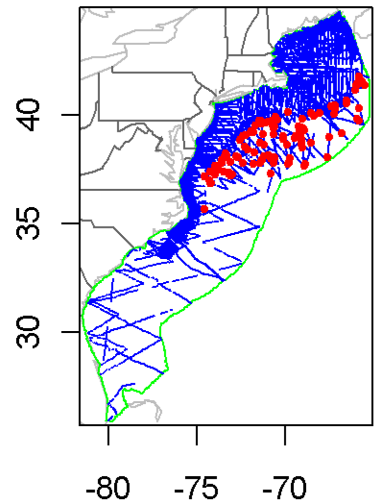


Figure B-151. Map of points of observational sightings and tracks of survey effort for Striped dolphin guild during Summer season in East region.

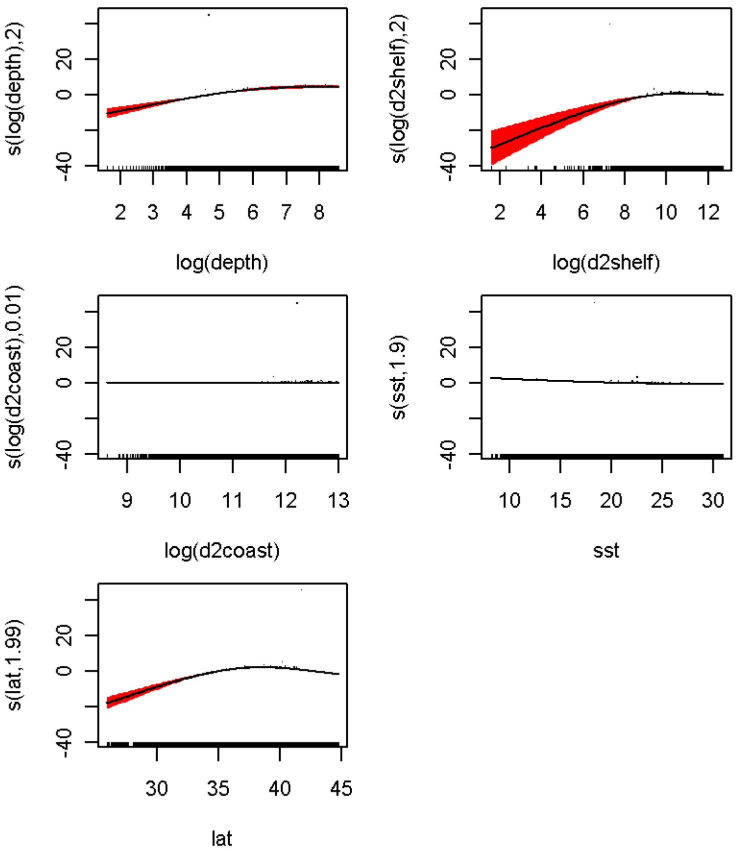


Figure B-152. Terms plot of predictors to GAM model fit for Striped dolphin guild during Summer season in East region.

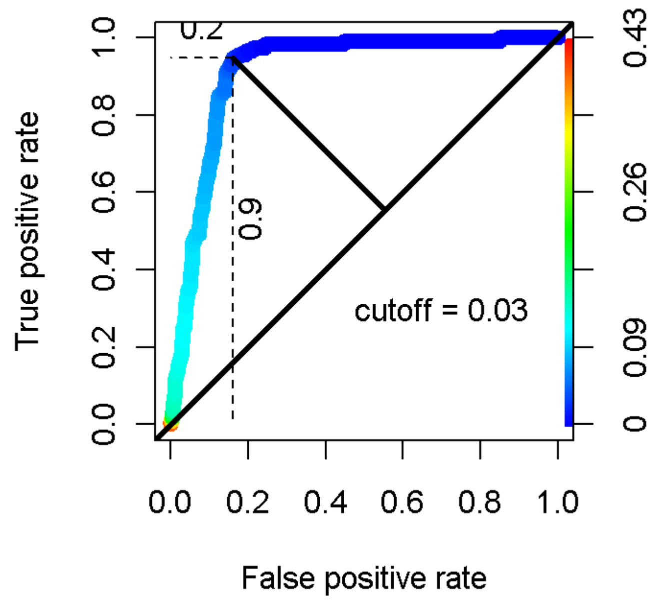


Figure B-153. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Striped dolphin guild during Summer season in East region.

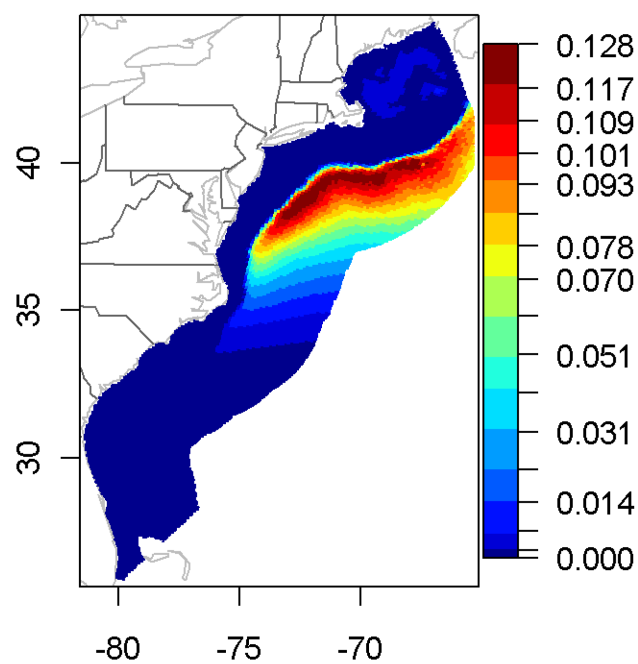


Figure B-154. Map of mean predicted habitat for Striped dolphin guild during Summer season in East region.

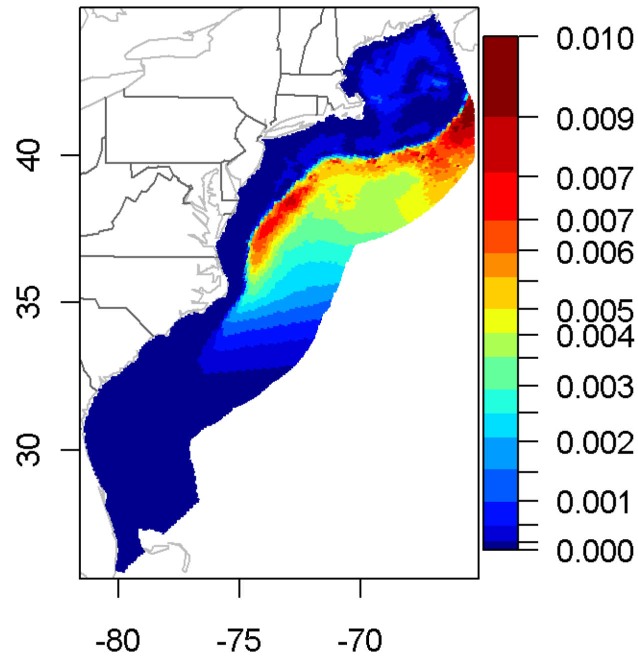


Figure B-155. Map of standard error of habitat for Striped dolphin guild during Summer season in East region.

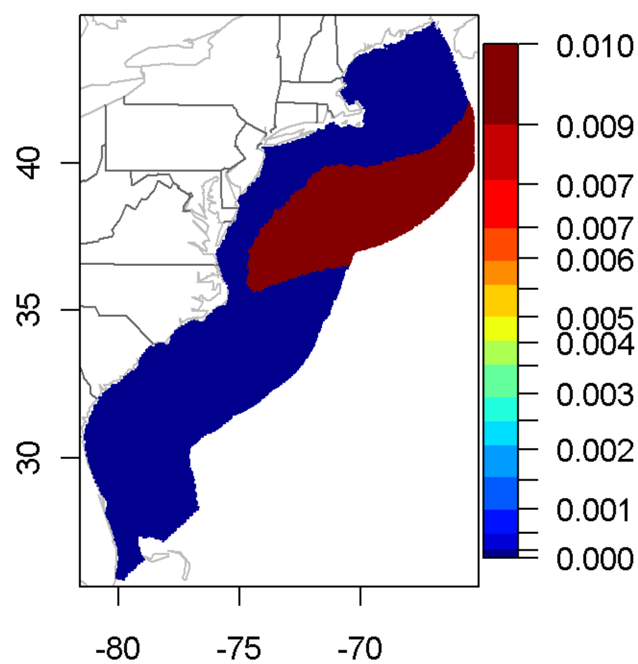


Figure B-156. Map of binary habitat (cutoff determined by ROC) for Striped dolphin guild during Summer season in East region.

Northeast

Harbor porpoise | Fall | Northeast

Number of presences: 46
Number of absences: 1138
R squared: 0.553125
Deviance explained: 0.598956
ROC optimum: 0.931982
Maximum fit: 0.00103759
Maximum prediction: 0.382668
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -49.039      3.708  -13.23   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                   edf Ref.df      F p-value
s(log(depth))   1.9946 1.9946  60.25  <2e-16 ***
s(log(d2shelf)) 1.9400 1.9400 108.72  <2e-16 ***
s(log(d2coast)) 0.9927 0.9927 105.27  <2e-16 ***
s(sst)          1.9799 1.9799  94.61  <2e-16 ***
s(lat)          0.9970 0.9970 154.06  <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.553   Deviance explained = 59.9%
GCV score = 0.0004492  Scale est. = 0.00044295  n = 1151
```

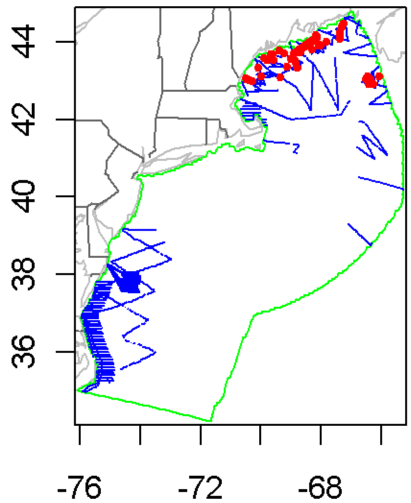


Figure B-157. Map of points of observational sightings and tracks of survey effort for Harbor porpoise guild during Fall season in Northeast region.

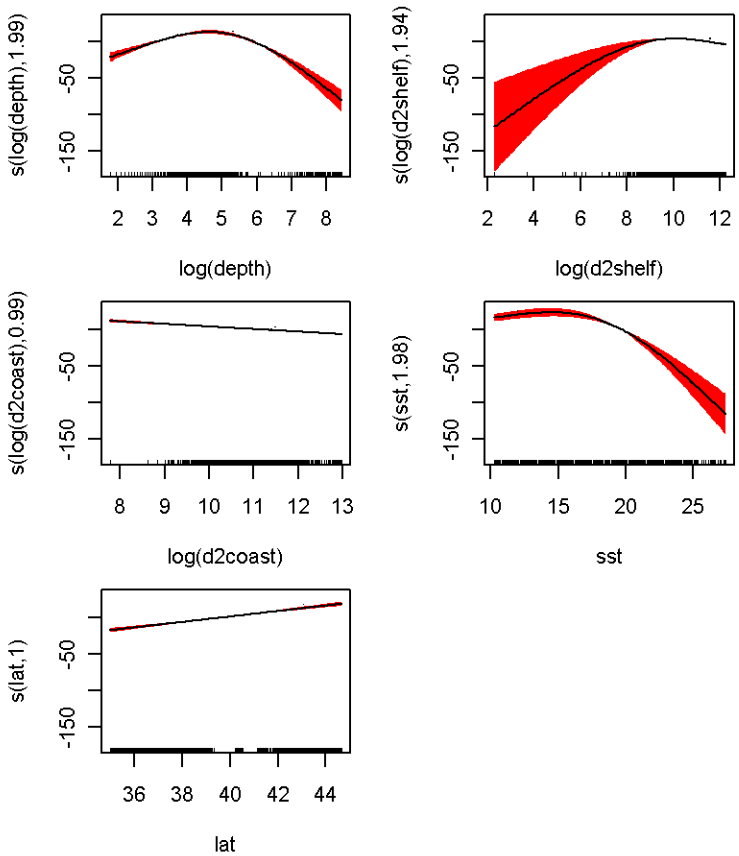


Figure B-158. Terms plot of predictors to GAM model fit for Harbor porpoise guild during Fall season in Northeast region.

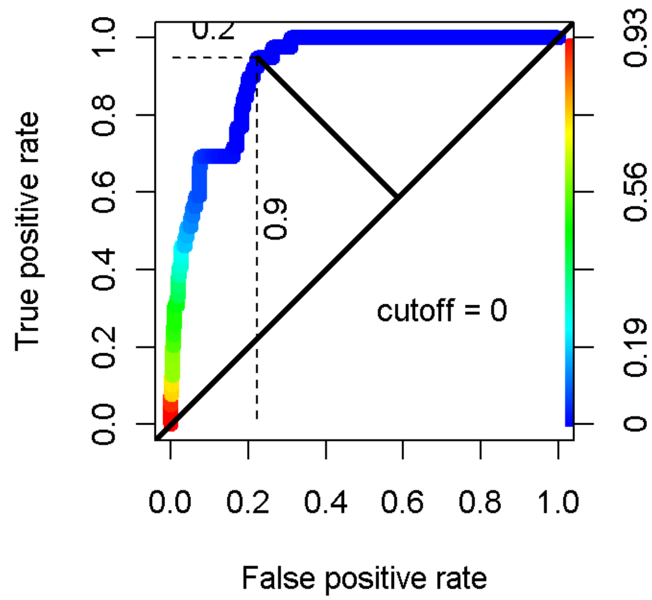


Figure B-159. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Harbor porpoise guild during Fall season in Northeast region.

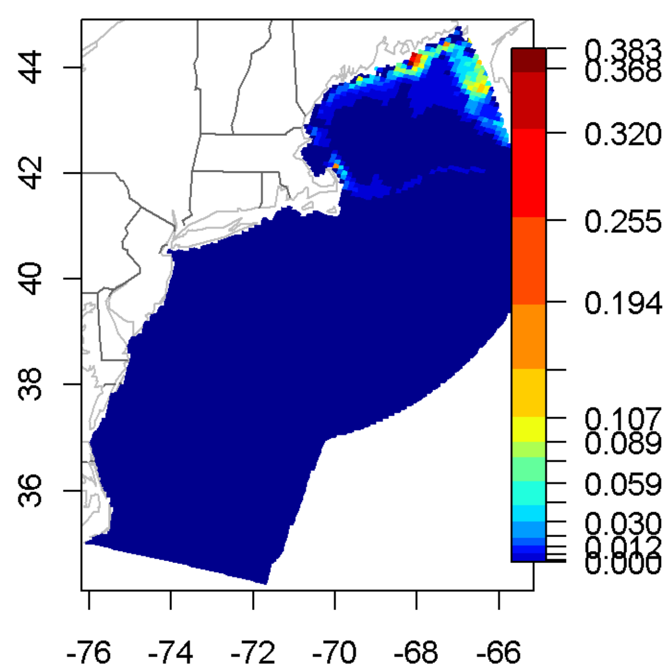


Figure B-160. Map of mean predicted habitat for Harbour porpoise guild during Fall season in Northeast region.

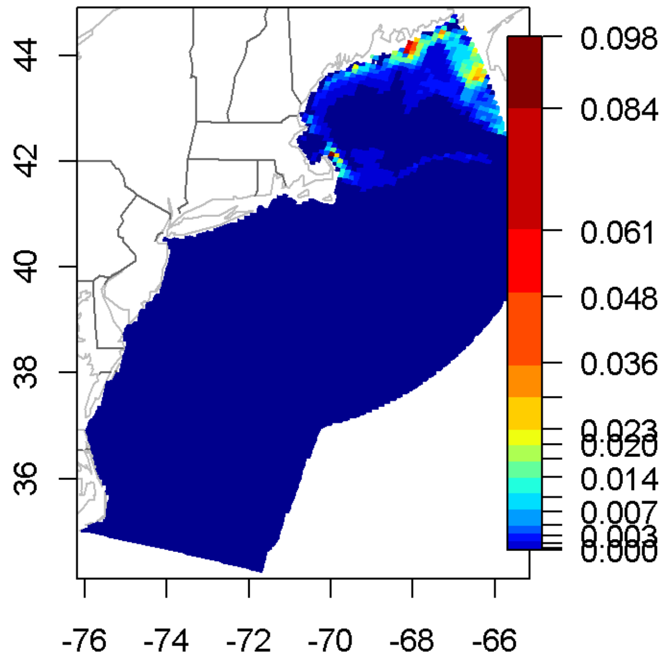


Figure B-161. Map of standard error of habitat for Harbor porpoise guild during Fall season in Northeast region.

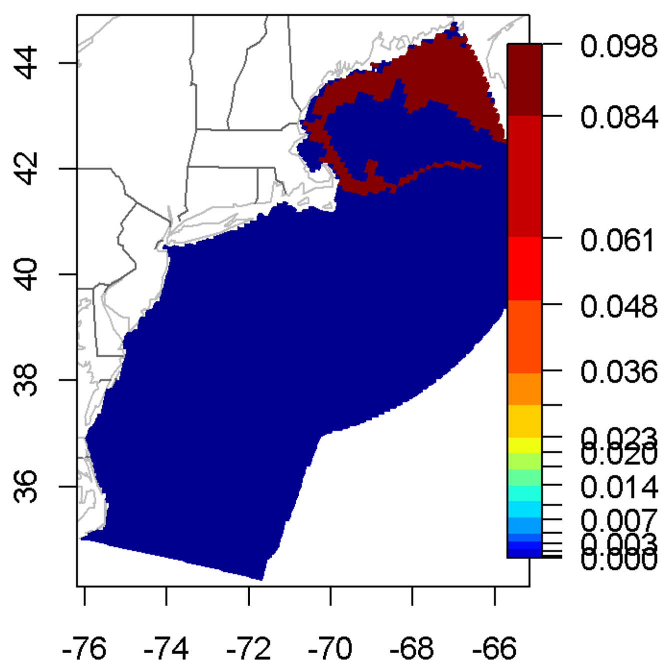


Figure B-162. Map of binary habitat (cutoff determined by ROC) for Harbour porpoise guild during Fall season in Northeast region.

Harbor porpoise | Summer | Northeast
Number of presences: 396
Number of absences: 7298
R squared: 0.47423
Deviance explained: 0.501926
ROC optimum: 0.885258
Maximum fit: 0.0484198
Maximum prediction: 0.885256
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -7.5617     0.1952  -38.74   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   8.700e-01 8.700e-01   25.959 1.52e-06 ***
s(log(d2shelf)) 2.704e-05 2.704e-05    0.002       NA
s(log(d2coast)) 8.351e-01 8.351e-01   22.441 1.05e-05 ***
s(sst)          2.225e-03 2.225e-03 0.000401       NA
s(lat)          9.924e-01 9.924e-01  909.103  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.474   Deviance explained = 50.2%
GCV score = 0.0011955  Scale est. = 0.0011944  n = 7282
```

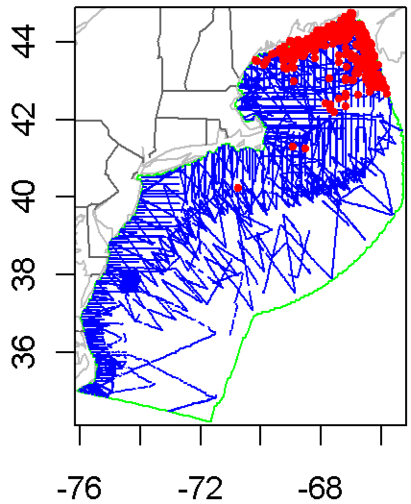


Figure B-163. Map of points of observational sightings and tracks of survey effort for Harbour porpoise guild during Summer season in Northeast region.

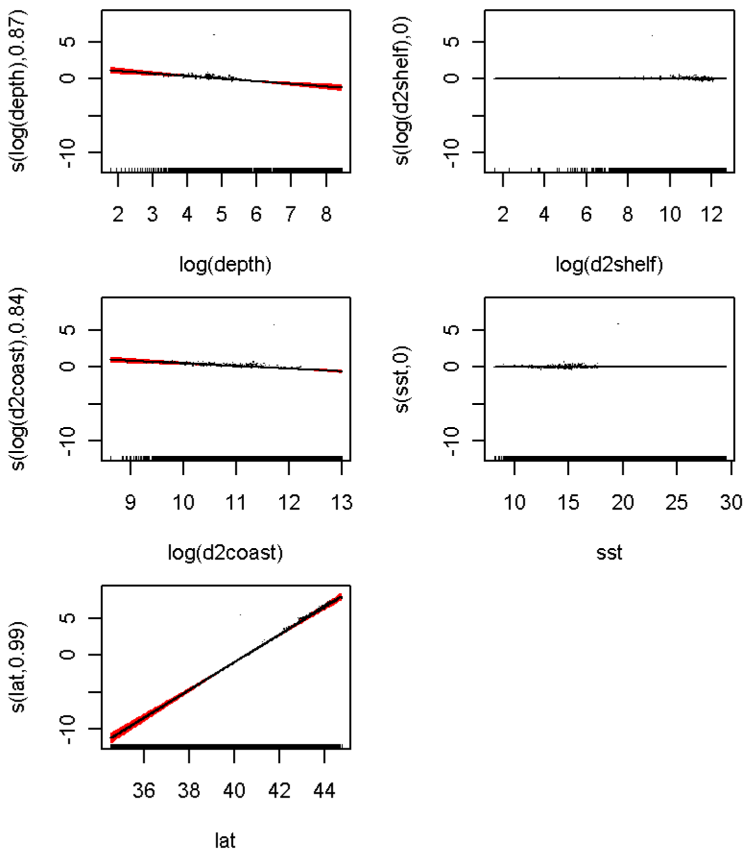


Figure B-164. Terms plot of predictors to GAM model fit for Harbor porpoise guild during Summer season in Northeast region.

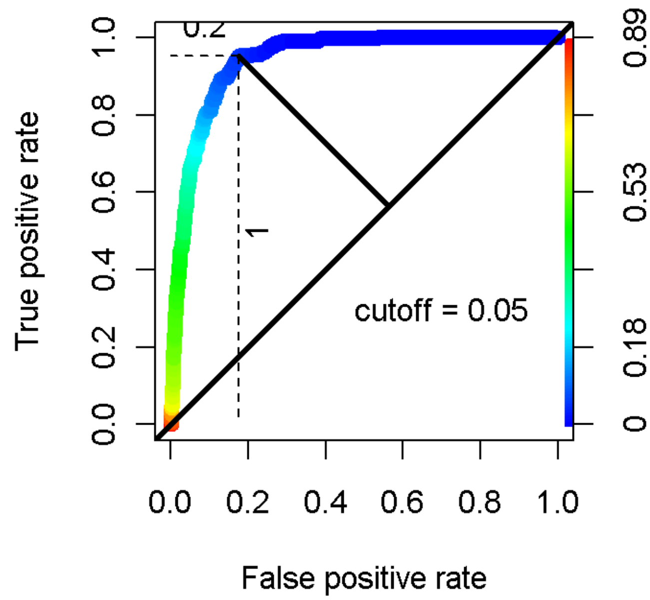


Figure B-165. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Harbor porpoise guild during Summer season in Northeast region.

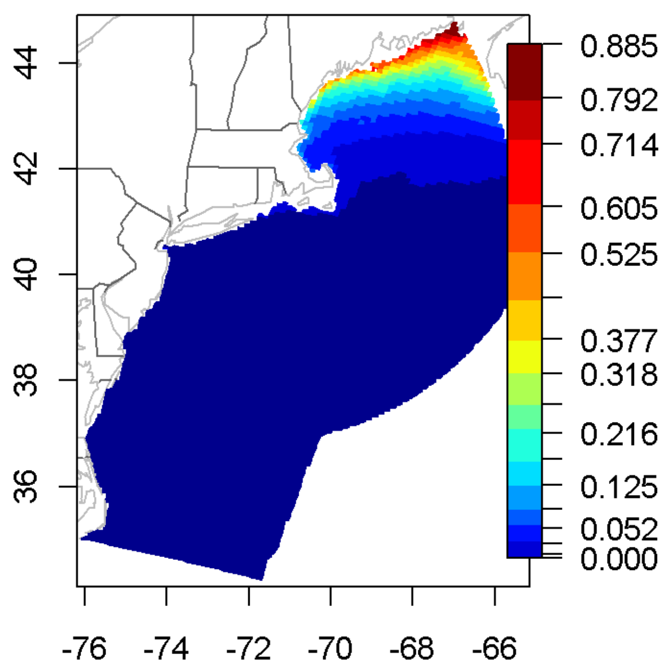


Figure B-166. Map of mean predicted habitat for Harbour porpoise guild during Summer season in Northeast region.

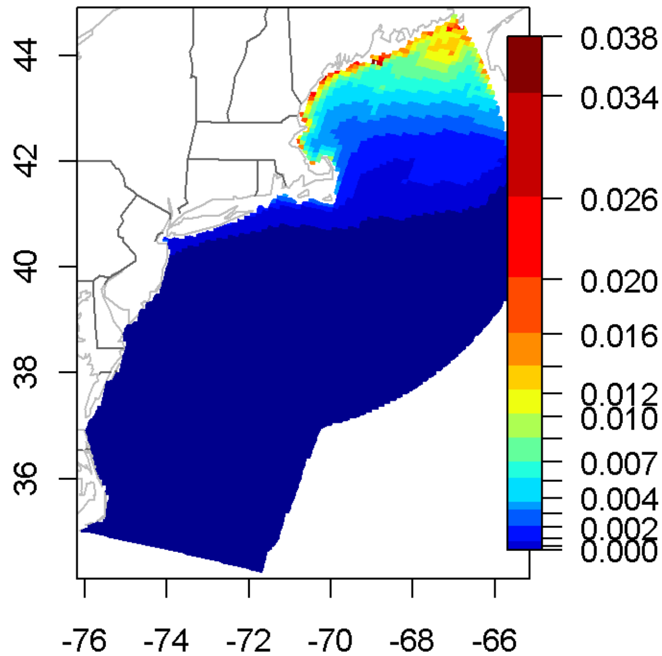


Figure B-167. Map of standard error of habitat for Harbor porpoise guild during Summer season in Northeast region.

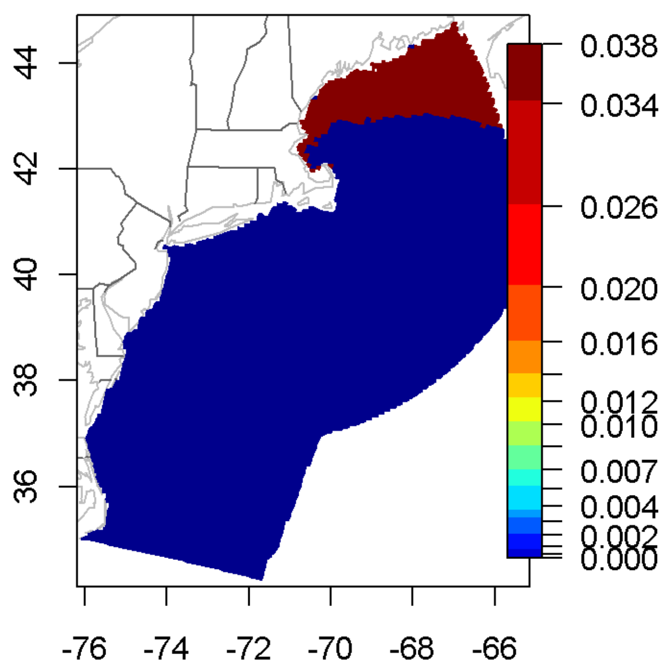


Figure B-168. Map of binary habitat (cutoff determined by ROC) for Harbour porpoise guild during Summer season in Northeast region.

Tursiops | Fall | Northeast
Number of presences: 41
Number of absences: 1143
R squared: 0.329845
Deviance explained: 0.21473
ROC optimum: 0.35694
Maximum fit: 0.0937174
Maximum prediction: 0.359095
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -4.2077     0.1883  -22.34   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   7.471e-01 7.471e-01    10.31  0.00344 **
s(log(d2shelf)) 3.908e-06 3.908e-06 1.54e-05       NA
s(log(d2coast)) 8.700e-01 8.700e-01    29.87 2.96e-07 ***
s(sst)          9.694e-01 9.694e-01    35.51 5.37e-09 ***
s(lat)          9.239e-01 9.239e-01    21.18 8.98e-06 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =   0.33   Deviance explained = 21.5%
GCV score = 0.0012847  Scale est. = 0.0012756  n = 1151
```

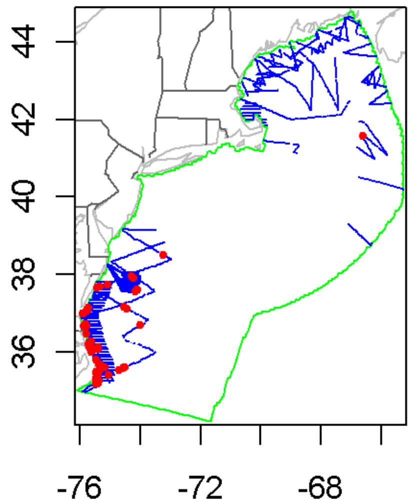


Figure B-169. Map of points of observational sightings and tracks of survey effort for Tursiops guild during Fall season in Northeast region.

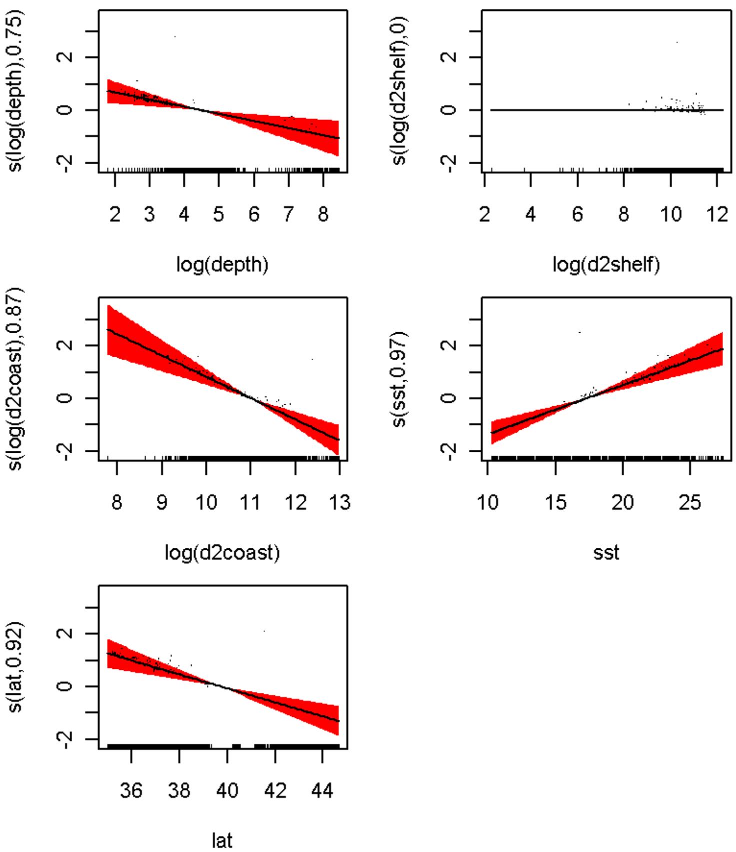


Figure B-170. Terms plot of predictors to GAM model fit for Tursiops guild during Fall season in Northeast region.

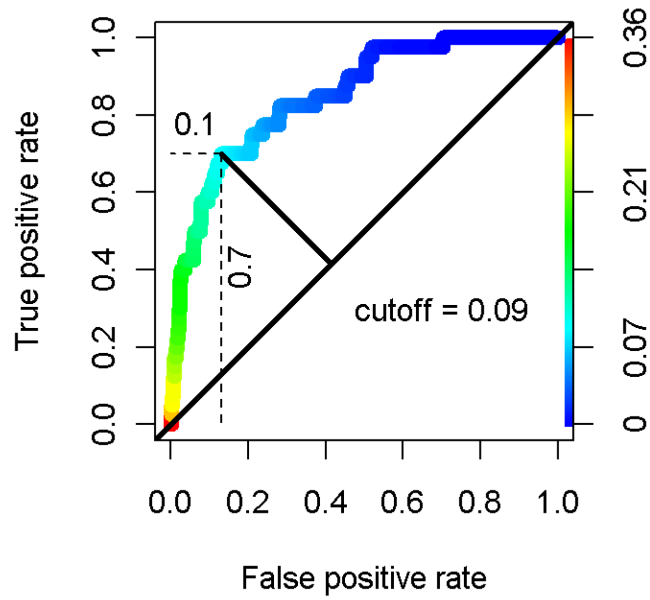


Figure B-171. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Tursiops guild during Fall season in Northeast region.

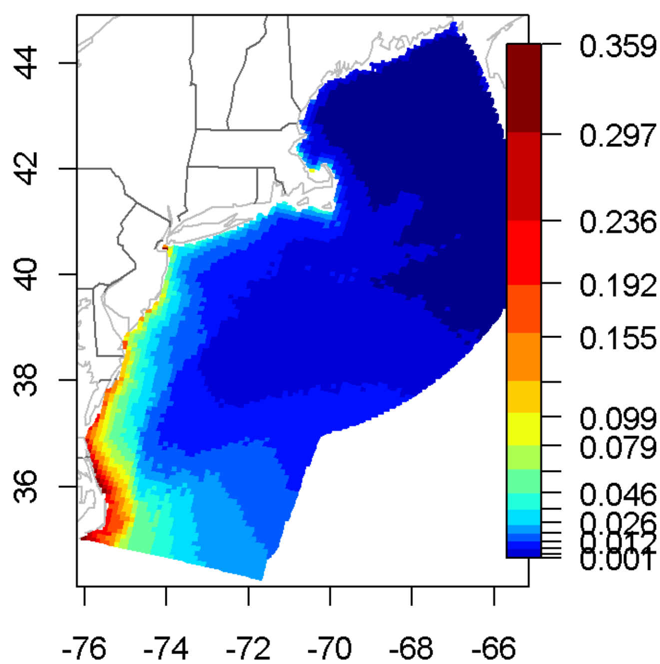


Figure B-172. Map of mean predicted habitat for Tursiops guild during Fall season in Northeast region.

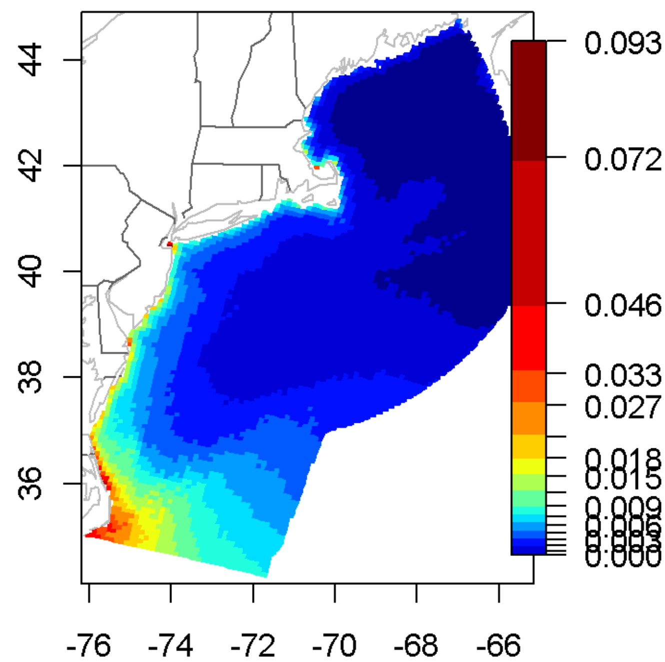


Figure B-173. Map of standard error of habitat for Tursiops guild during Fall season in Northeast region.

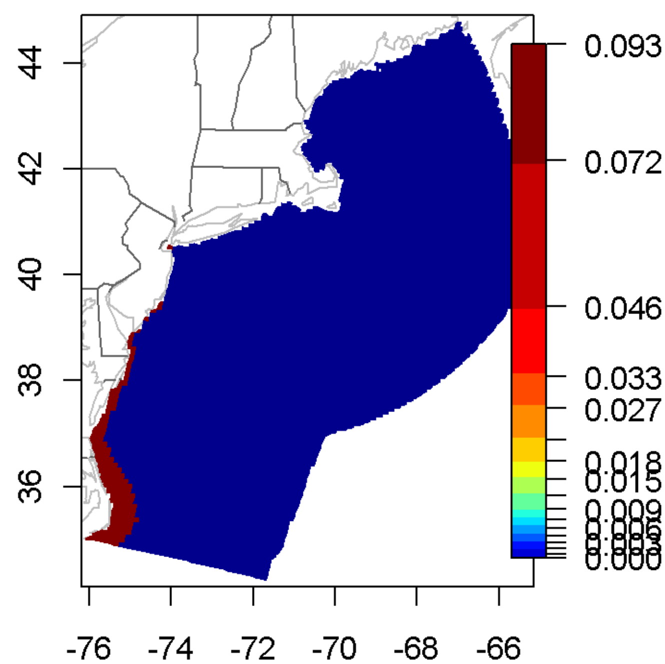


Figure B-174. Map of binary habitat (cutoff determined by ROC) for Tursiops guild during Fall season in Northeast region.

Tursiops | Spring | Northeast
Number of presences: 204
Number of absences: 883
R squared: 0.534618
Deviance explained: 0.307366
ROC optimum: 0.879142
Maximum fit: 0.198772
Maximum prediction: 0.879141
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -2.1827     0.1316  -16.58   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   9.301e-01 9.301e-01   43.961 2.07e-10 ***
s(log(d2shelf)) 7.443e-01 7.443e-01    6.834   0.0155 *
s(log(d2coast)) 1.418e-05 1.418e-05 1.25e-05       NA
s(sst)          2.307e-05 2.307e-05 4.46e-05       NA
s(lat)          1.000e+00 1.000e+00  150.346  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.535   Deviance explained = 30.7%
GCV score = 0.0032111  Scale est. = 0.0031898  n = 996
```

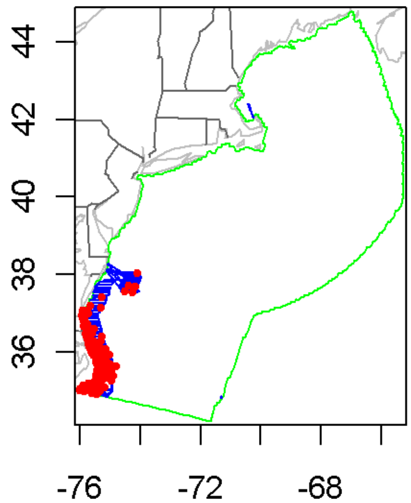


Figure B-175. Map of points of observational sightings and tracks of survey effort for Tursiops guild during Spring season in Northeast region.

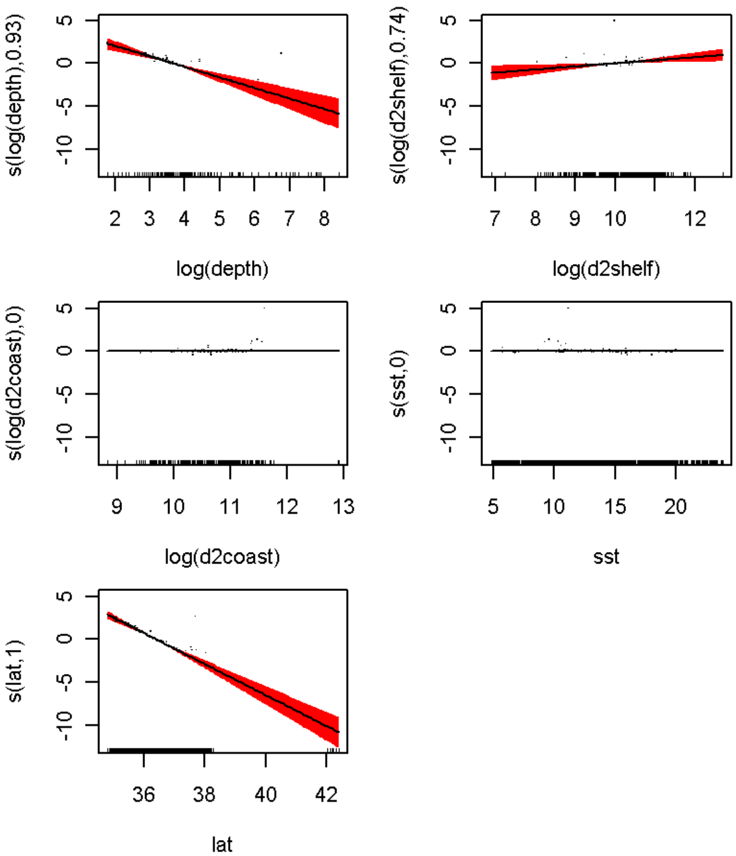


Figure B-176. Terms plot of predictors to GAM model fit for Tursiops guild during Spring season in Northeast region.

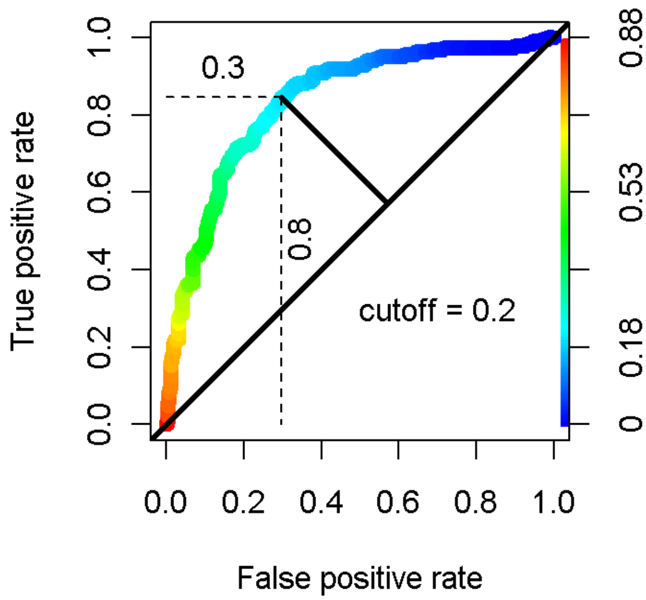


Figure B-177. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Tursiops guild during Spring season in Northeast region.

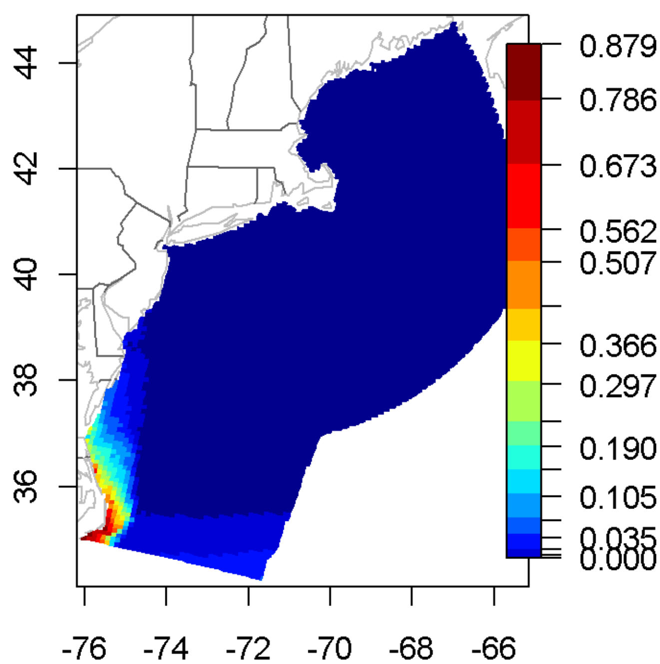


Figure B-178. Map of mean predicted habitat for Tursiops guild during Spring season in Northeast region.

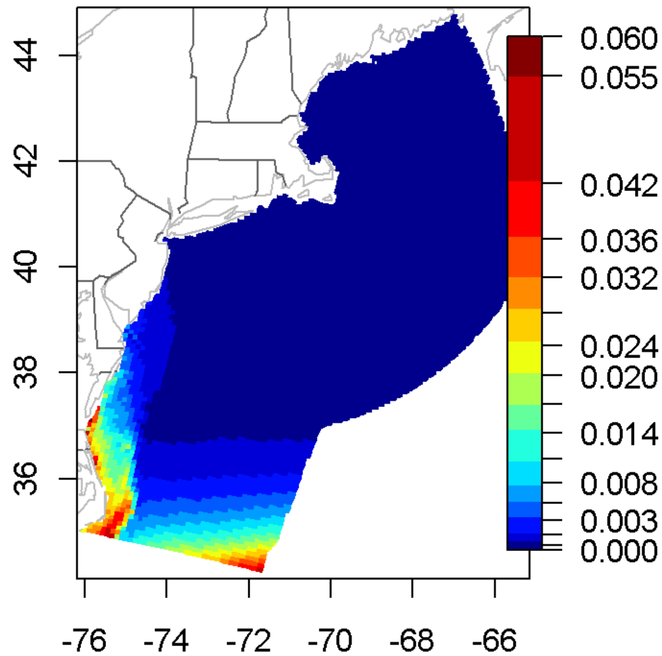


Figure B-179. Map of standard error of habitat for Tursiops guild during Spring season in Northeast region.

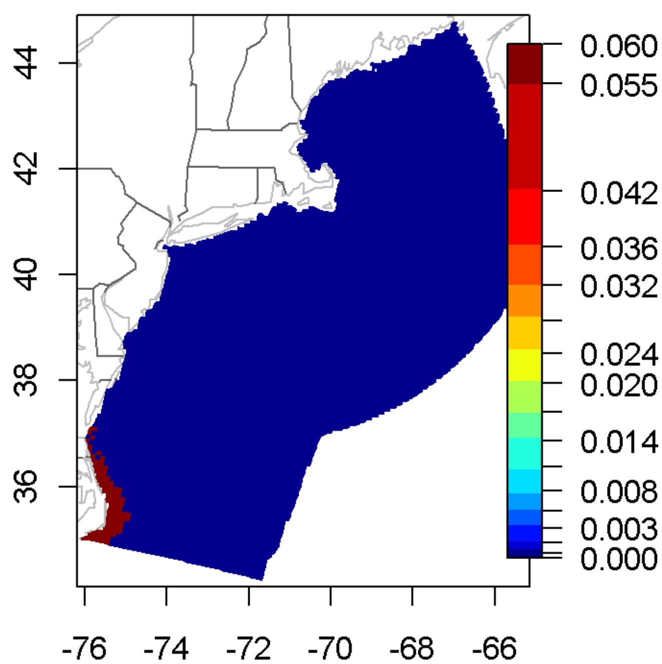


Figure B-180. Map of binary habitat (cutoff determined by ROC) for Tursiops guild during Spring season in Northeast region.

Southeast

Tursiops | Spring | Southeast

Number of presences: 225
Number of absences: 1561
R squared: 0.245593
Deviance explained: 0.171944
ROC optimum: 0.683688
Maximum fit: 0.143033
Maximum prediction: 0.831208
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -2.4201     0.1512  -16.01   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F  p-value
s(log(depth))   9.463e-01 9.463e-01    41.76 3.72e-10 ***
s(log(d2shelf)) 9.084e-01 9.084e-01    21.20 9.96e-06 ***
s(log(d2coast)) 1.146e-05 1.146e-05 1.46e-05       NA
s(sst)          1.966e+00 1.966e+00    35.08 2.13e-15 ***
s(lat)          5.240e-06 5.240e-06 3.08e-05       NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.246   Deviance explained = 17.2%
GCV score = 0.0022768  Scale est. = 0.0022636  n = 1494
```

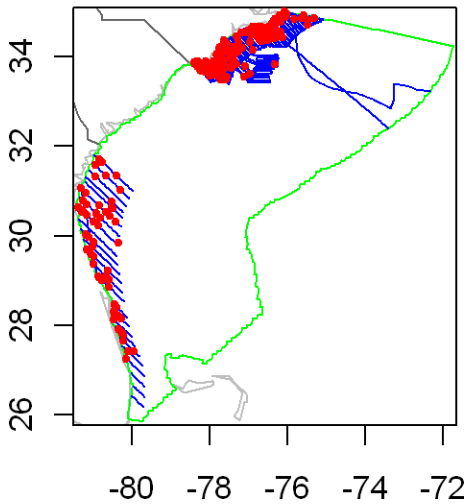


Figure B-181. Map of points of observational sightings and tracks of survey effort for Tursiops guild during Spring season in Southeast region.

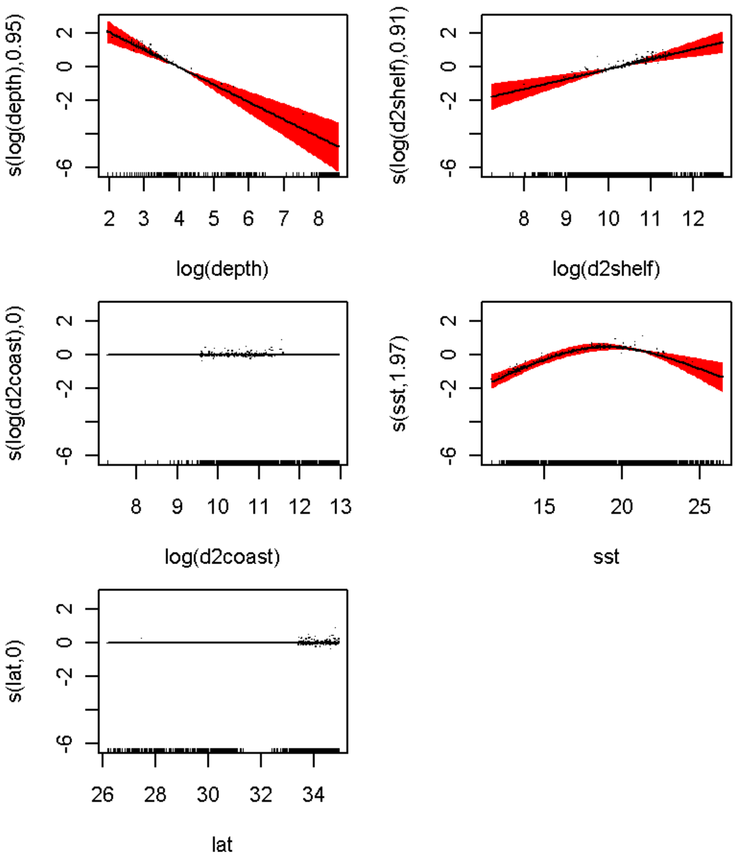


Figure B-182. Terms plot of predictors to GAM model fit for Tursiops guild during Spring season in Southeast region.

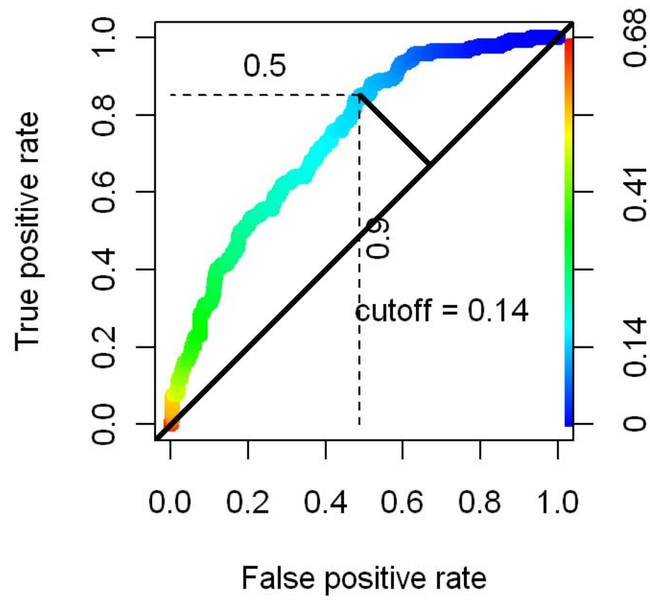


Figure B-183. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Tursiops guild during Spring season in Southeast region.

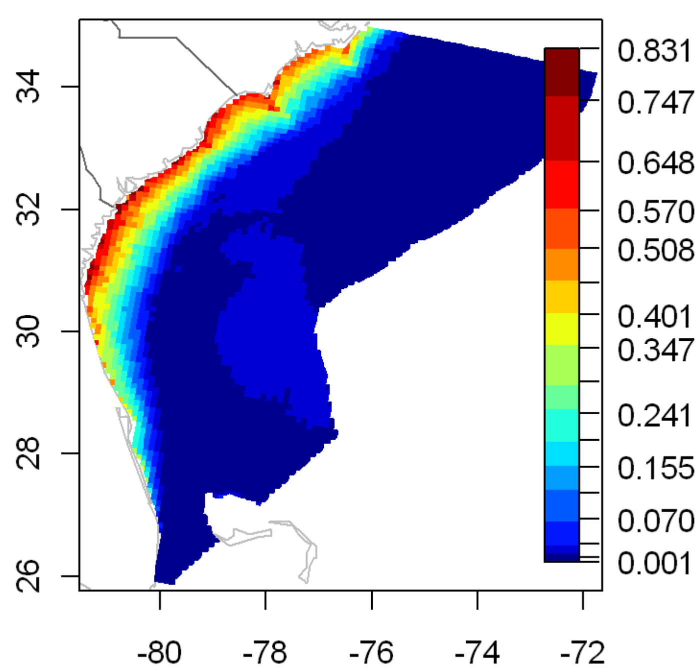


Figure B-184. Map of mean predicted habitat for Tursiops guild during Spring season in Southeast region.

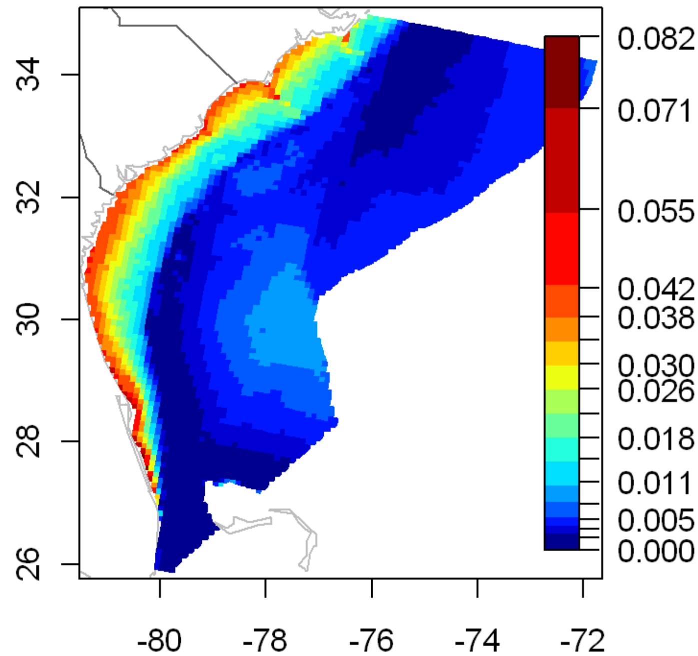


Figure B-185. Map of standard error of habitat for Tursiops guild during Spring season in Southeast region.

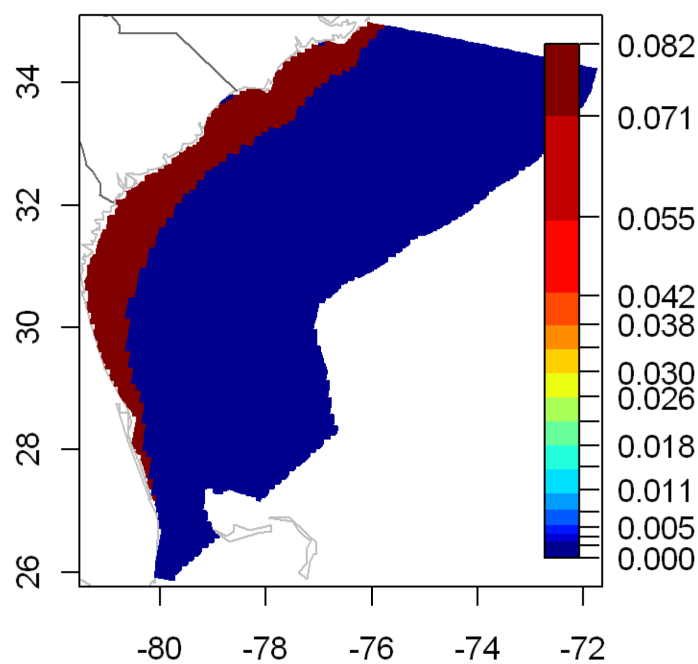


Figure B-186. Map of binary habitat (cutoff determined by ROC) for Tursiops guild during Spring season in Southeast region.

Tursiops | Summer | Southeast
Number of presences: 88
Number of absences: 1296
R squared: 0.848148
Deviance explained: 0.461247
ROC optimum: 0.913564
Maximum fit: 0.0463153
Maximum prediction: 0.997267
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 5, bs = 'ts') + s(d2shelf2, k = 5,
    bs = 'ts') + s(log(d2coast), k = 5, bs = 'ts') + s(sst, k =
5,
    bs = 'ts') + s(lat, k = 5, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -19.064      9.273  -2.056     0.04 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                     edf   Ref.df        F  p-value
s(log(depth))   3.976526 3.976526   82.452  < 2e-16 ***
s(d2shelf2)     3.698444 3.698444    5.714 0.000233 ***
s(log(d2coast)) 3.997330 3.997330   65.135  < 2e-16 ***
s(sst)          0.001072 0.001072 0.000201       NA
s(lat)          3.692411 3.692411   45.675  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.848   Deviance explained = 46.1%
GCV score = 0.0031254  Scale est. = 0.0030588  n = 1381
```

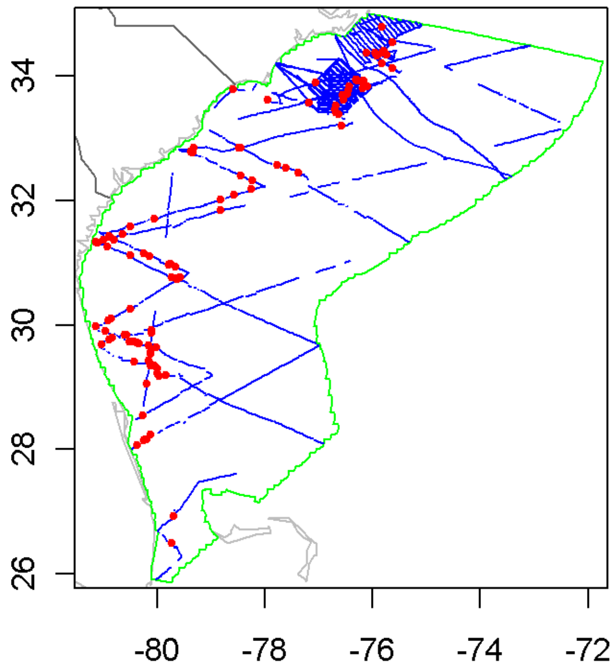


Figure B-187. Map of points of observational sightings and tracks of survey effort for Tursiops guild during Summer season in Southeast region.

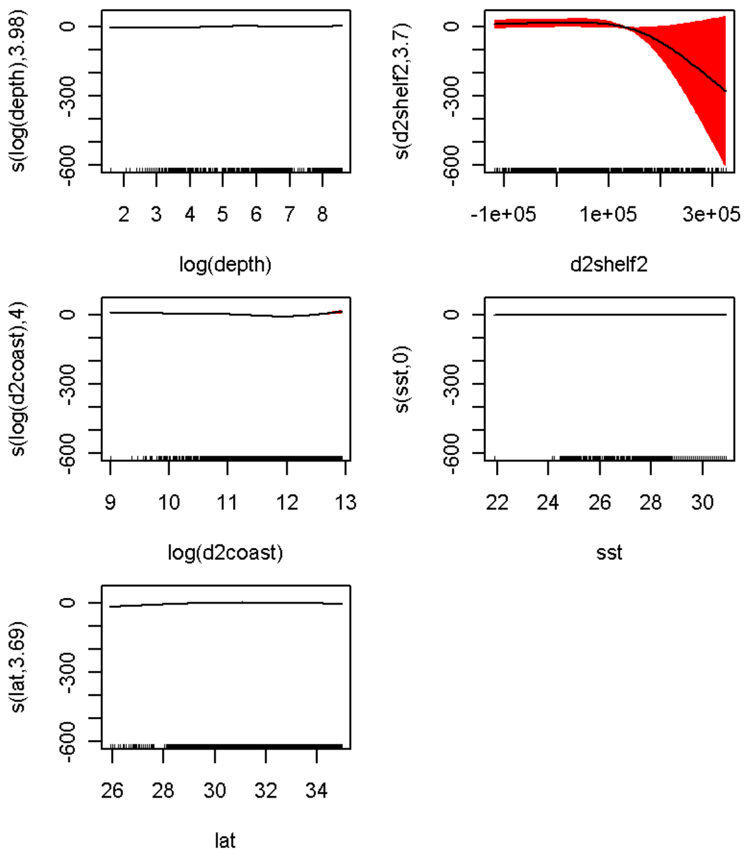


Figure B-188. Terms plot of predictors to GAM model fit for Tursiops guild during Summer season in Southeast region.

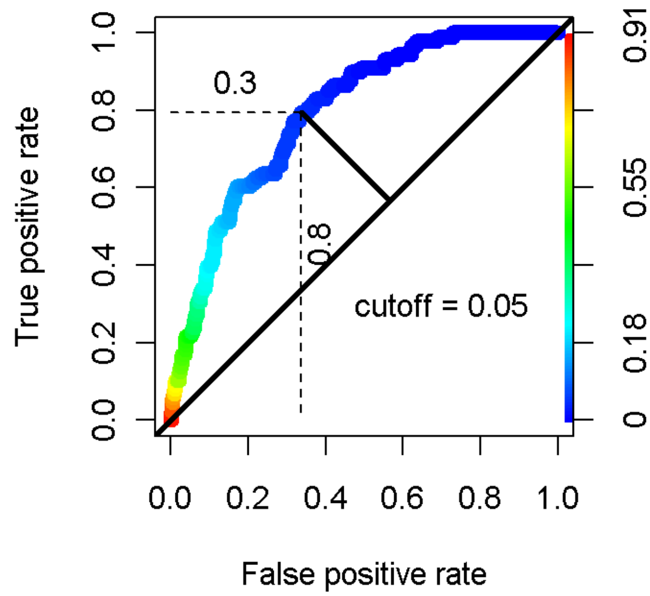


Figure B-189. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Tursiops guild during Summer season in Southeast region.

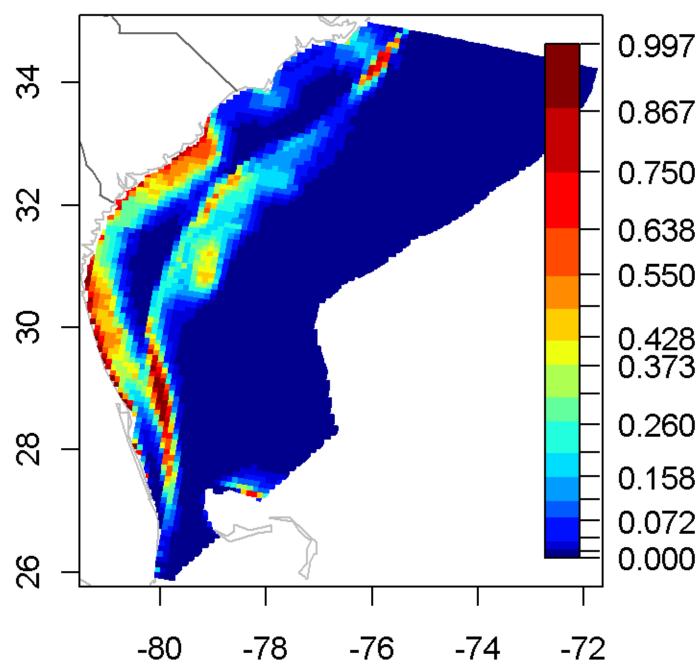


Figure B-190. Map of mean predicted habitat for Tursiops guild during Summer season in Southeast region.

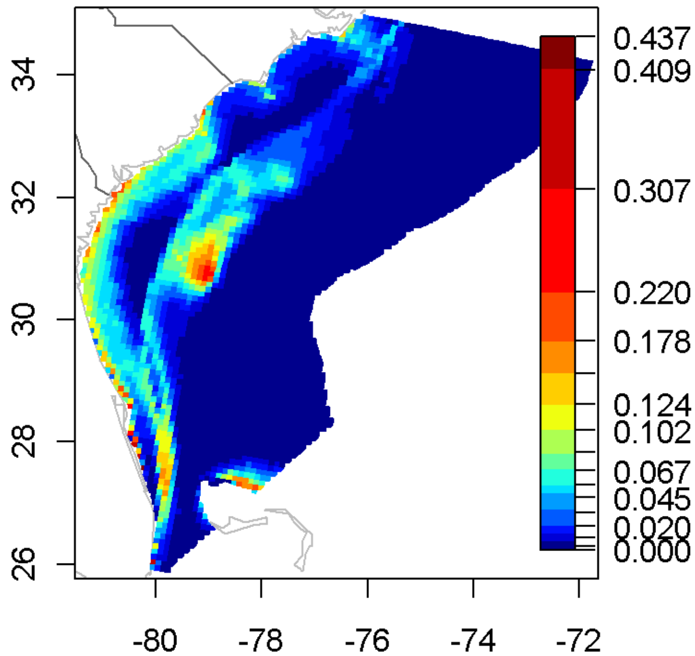


Figure B-191. Map of standard error of habitat for Tursiops guild during Summer season in Southeast region.

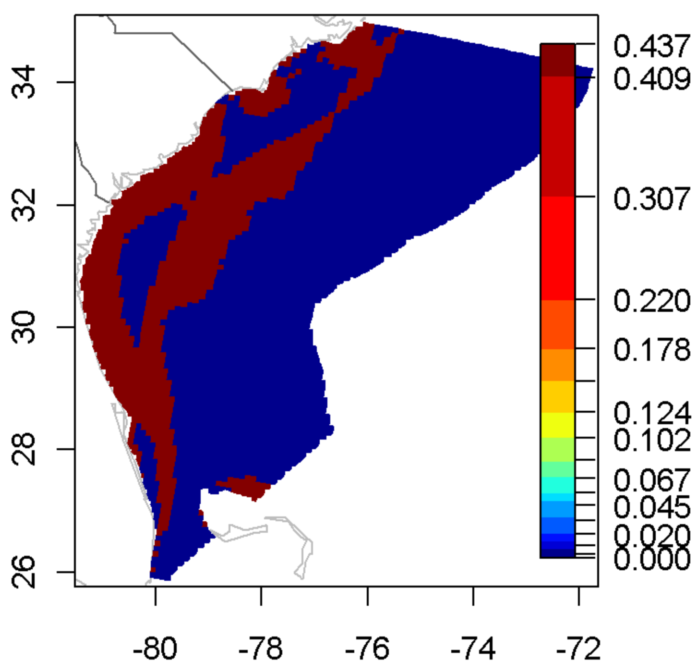


Figure B-192. Map of binary habitat (cutoff determined by ROC) for Tursiops guild during Summer season in Southeast region.

Tursiops | Winter | Southeast
Number of presences: 478
Number of absences: 2580
R squared: 0.408352
Deviance explained: 0.144186
ROC optimum: 0.720022
Maximum fit: 0.258801
Maximum prediction: 0.900581
Model text summary:

```
Family: quasibinomial
Link function: logit

Formula:
presence ~ s(log(depth), k = 3, bs = 'ts') + s(log(d2shelf),
    k = 3, bs = 'ts') + s(log(d2coast), k = 3, bs = 'ts') +
s(sst,
    k = 3, bs = 'ts') + s(lat, k = 3, bs = 'ts')

Parametric coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.73701    0.06621  -26.23   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Approximate significance of smooth terms:
                      edf    Ref.df        F p-value
s(log(depth))   1.997e+00 1.997e+00    73.03 < 2e-16 ***
s(log(d2shelf)) 3.675e-04 3.675e-04 5.84e-05      NA
s(log(d2coast)) 5.947e-06 5.947e-06 2.18e-07      NA
s(sst)          8.836e-01 8.836e-01    10.26 0.00211 **
s(lat)          8.041e-06 8.041e-06 8.44e-06      NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R-sq.(adj) =  0.408   Deviance explained = 14.4%
GCV score = 0.0027303  Scale est. = 0.0027197  n = 1811
```

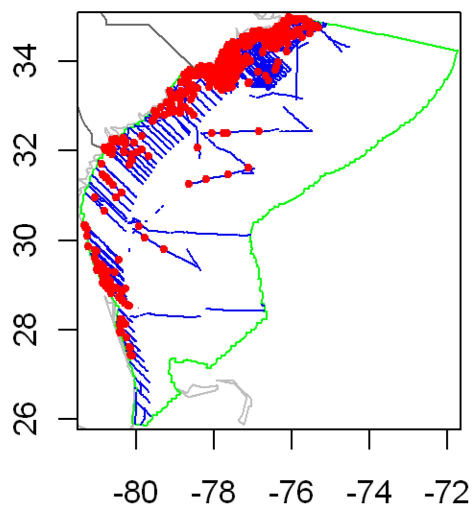


Figure B-193. Map of points of observational sightings and tracks of survey effort for Tursiops guild during Winter season in Southeast region.

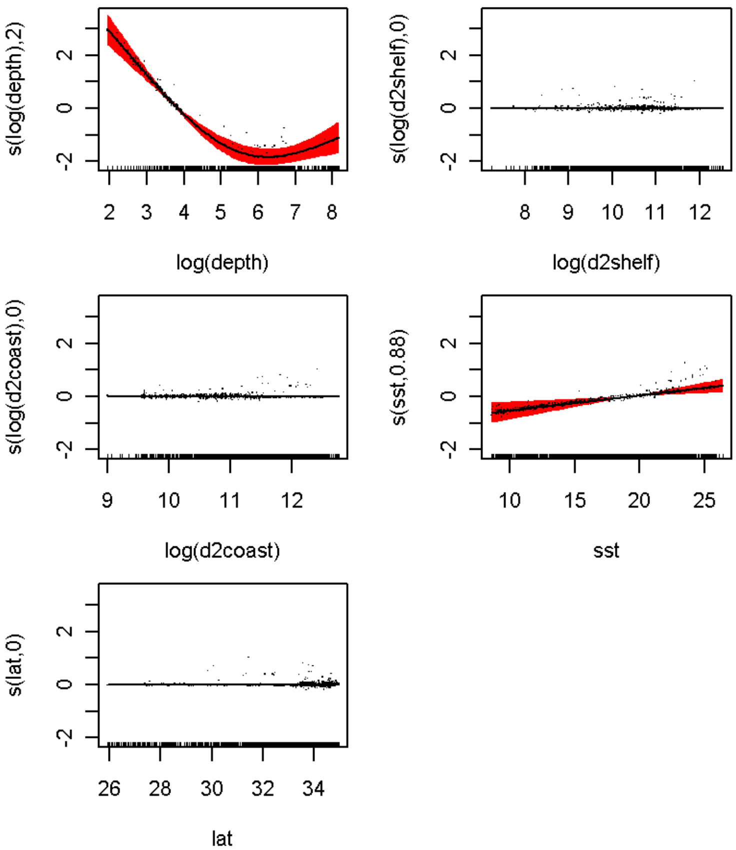


Figure B-194. Terms plot of predictors to GAM model fit for Tursiops guild during Winter season in Southeast region.

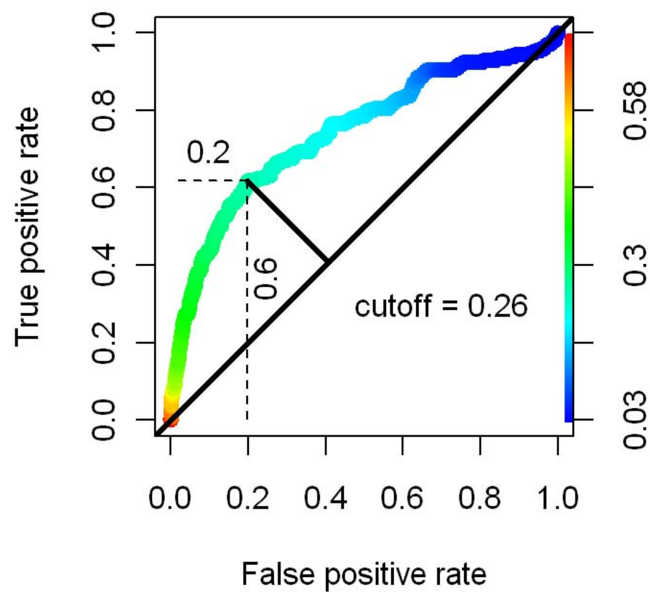


Figure B-195. Receiver operator characteristic (ROC) curve to determine optimal cutoff for binary habitat for Tursiops guild during Winter season in Southeast region.

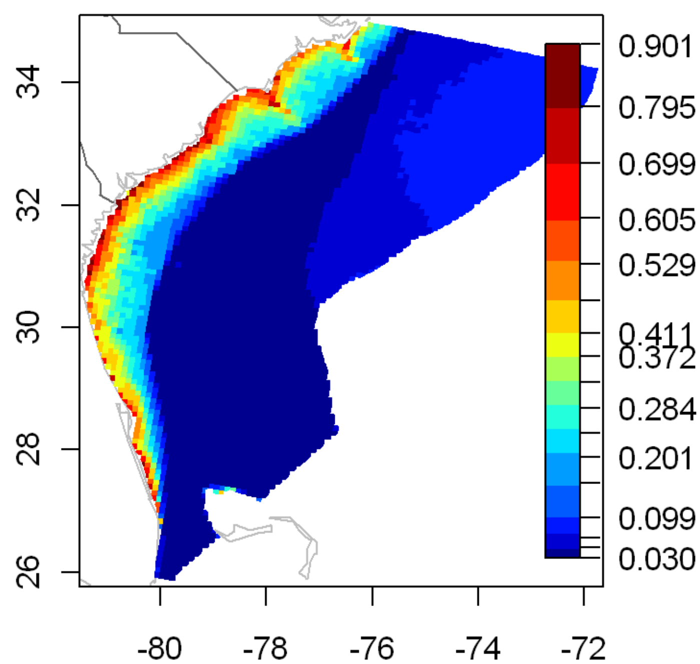


Figure B-196. Map of mean predicted habitat for Tursiops guild during Winter season in Southeast region.

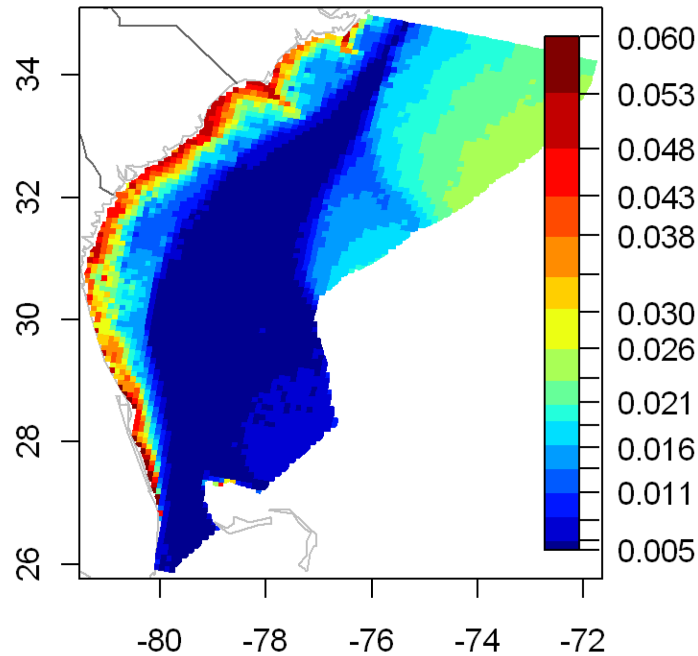


Figure B-197. Map of standard error of habitat for Tursiops guild during Winter season in Southeast region.

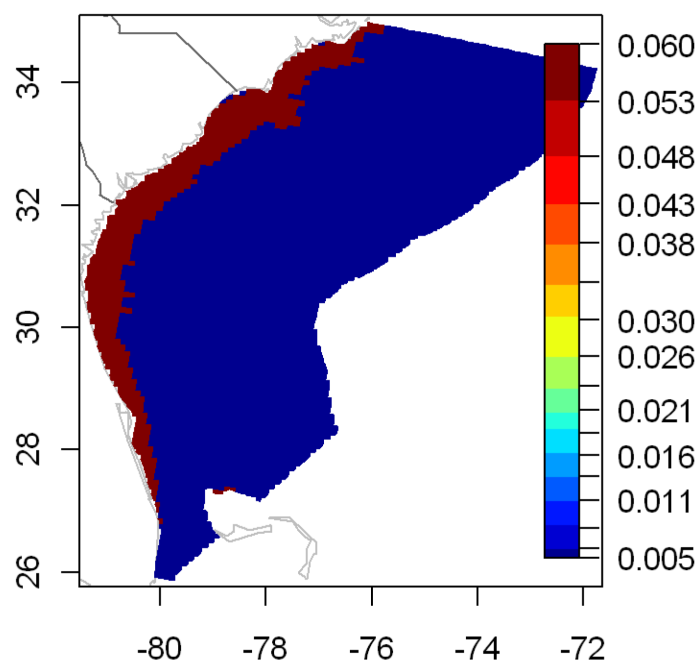


Figure B-198. Map of binary habitat (cutoff determined by ROC) for Tursiops guild during Winter season in Southeast region.

Appendix C: Tabular Summary for Ordination Groups

Table C-1. Summary table of the data in the NOH Ordination. Table includes information on species name, % rarity, and group membership identifier.

sptsn	Rank	Common name	rarity (%)	Group ID
180417	Species	Rough-toothed Dolphin	1	1
180426	Species	Bottlenose Dolphin	23	2
180434	Species	Striped Dolphin	27	2
180457	Species	Risso's dolphin	30	2
180464	Genus	Pilot Whales	35	2
180489	Species	Sperm Whale	37	2
180493	Family	beaked whales	20	2
180429	Species	Long-snouted Spinner Dolphin	1	3
180469	Species	Killer Whale	1	3
180430	Species	Pantropical Spotted Dolphin	1	4
180492	Species	Dwarf Sperm Whale	0	4
180435	Species	Clymene Dolphin	1	5
180466	Species	Short-finned Pilot Whale	1	5
180438	Species	Common Dolphin	34	6
180443	Species	Atlantic White-sided Dolphin	29	6
180473	Species	Harbor Porpoise	20	6
180524	Species	Minke Whale	21	6
180527	Species	Fin Whale	35	6
180530	Species	Humpback Whale	25	6
180537	Species	Northern Right Whale	8	6
180461	Species	Pygmy Killer Whale	1	7
180463	Species	False Killer Whale	2	8
180490	Genus	Pygmy Sperm Whales	7	9
180491	Species	Pygmy Sperm Whale	1	10
180508	Species	True's beaked whale	0	10
180498	Species	Cuvier's beaked whale	9	11
180506	Genus	Beaked Whales	2	12
180515	Species	North Atlantic beaked whale	7	13
180517	Species	Blainville's beaked whale	1	14
180526	Species	Sei Whale	4	15
552460	Species	Atlantic Spotted Dolphin	8	16

Table C-2. Summary table of the data in the NOH Ordination - rare species removed. Table includes information on species name, and group membership identifier.

sptsn	Rank	Common name	Group ID
180426	Species	Bottlenose Dolphin	1
180434	Species	Striped Dolphin	1
180457	Species	Risso's dolphin	1
180464	Genus	Pilot Whales	1
180489	Species	Sperm Whale	1
180493	Family	beaked whales	1
180438	Species	Common Dolphin	2
180443	Species	Atlantic White-sided Dolphin	2
180473	Species	Harbor Porpoise	2
180524	Species	Minke Whale	2
180527	Species	Fin Whale	2
180530	Species	Humpback Whale	2
180537	Species	Northern Right Whale	2
180490	Genus	Pygmy Sperm Whales	3
180498	Species	Cuvier's beaked whale	4
180515	Species	North Atlantic beaked whale	5
552460	Species	Atlantic Spotted Dolphin	6

Table C-3. Summary table of the data in the SOH Ordination - rare species removed. Table includes information on species name, and group membership identifier.

sptsn	Rank	Common name	% Sites Observed	Group ID
180426	Species	Bottlenose Dolphin	50	1
180438	Species	Common Dolphin	15	1
180457	Species	Risso's dolphin	30	1
180464	Genus	Pilot Whales	35	1
552460	Species	Atlantic Spotted Dolphin	40	1
180430	Species	Pantropical Spotted Dolphin	15	2
180490	Genus	Pygmy Sperm Whales	10	2
180493	Family	beaked whales	10	3

Table C-4. Summary table of the data in the GOM Ordination - rare species removed. Table includes information on species name, and group membership identifier.

sptsn	Rank	Common name	% Sites Observed	Group ID
180417	Species	Rough-toothed Dolphin	13	1
180459	Species	Melon-headed Whale	15	1
180426	Species	Bottlenose Dolphin	29	2
180429	Species	Long-snouted Spinner Dolphin	15	2
180430	Species	Pantropical Spotted Dolphin	54	2
180434	Species	Striped Dolphin	13	2
180457	Species	Risso's dolphin	35	2
180489	Species	Sperm Whale	27	2
180490	Genus	Pygmy Sperm Whales	23	2
180435	Species	Clymene Dolphin	12	3
180492	Species	Dwarf Sperm Whale	12	3
180506	Genus	Beaked Whales	10	3
180469	Species	Killer Whale	6	4
180491	Species	Pygmy Sperm Whale	6	4
180493	Family	beaked whales	12	5
552460	Species	Atlantic Spotted Dolphin	12	6

Appendix D: Graphical CART Results

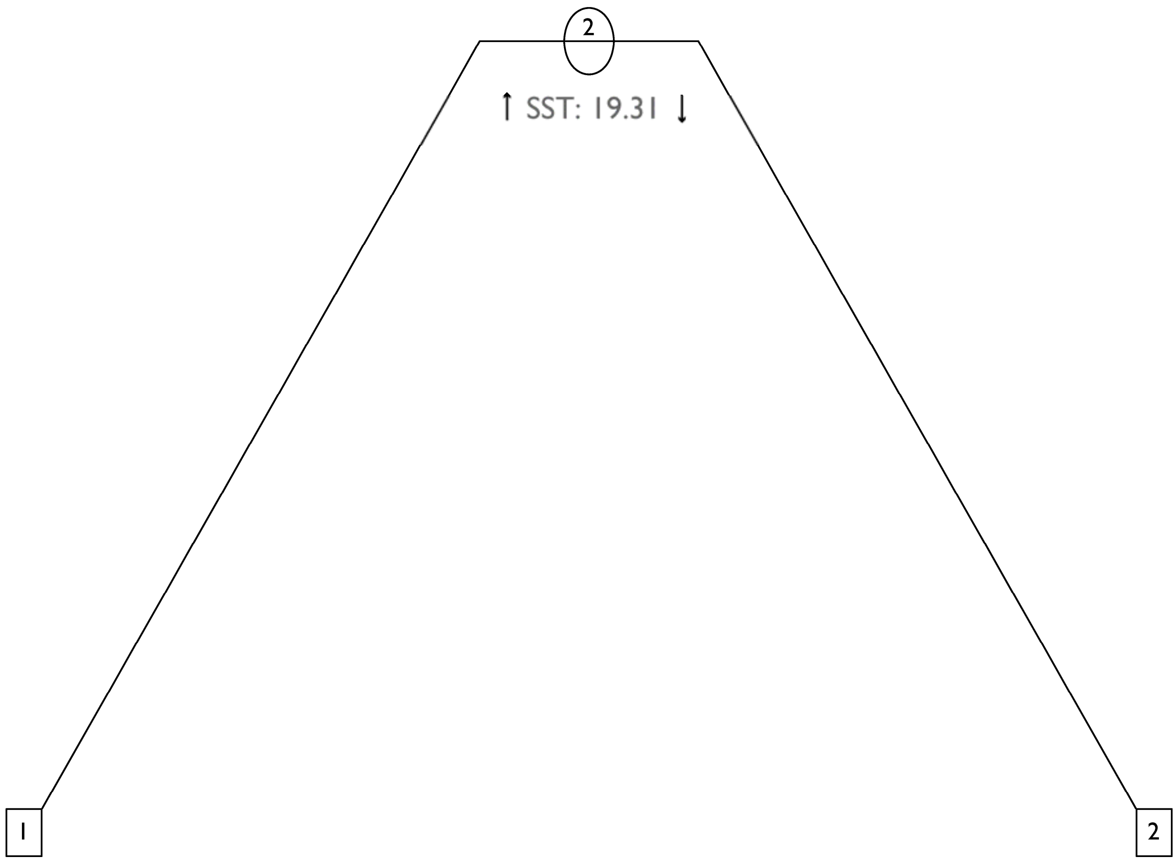


Figure D-1. Classification and regression tree for the two dominant groups present in the North of Hatteras Ordination. Text surrounded by arrows indicates the environmental variable governing the split and its direction, e.g. nodes to the right of an SST split with an up arrow are seen in warmer waters. Group 1 is found in waters warmer than 19.31°C, while group 2 is found in waters cooler than 18.8°C. Species in group 2 include all of the baleen whales, as well as white-sided dolphins and Harbor porpoise.

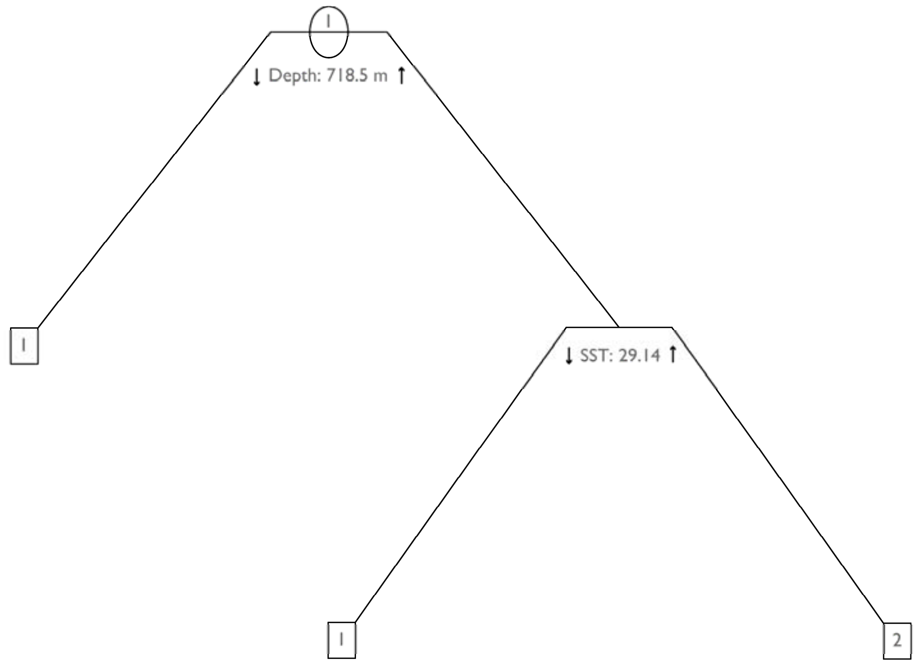


Figure D-2. Classification and regression tree for the two dominant groups present in the South of Hatteras Ordination. Text surrounded by arrows indicates the environmental variable governing the split and its direction, e.g. nodes to the right of an SST split with an up arrow are seen in warmer waters. Essentially all of the species are seen in group 1, with two smaller groups having vastly fewer sightings. The groups split along a depth and temperature gradient, with group 2 (Pantropical spotted dolphins and Pygmy sperm whales) being found farther offshore and in warmer waters.

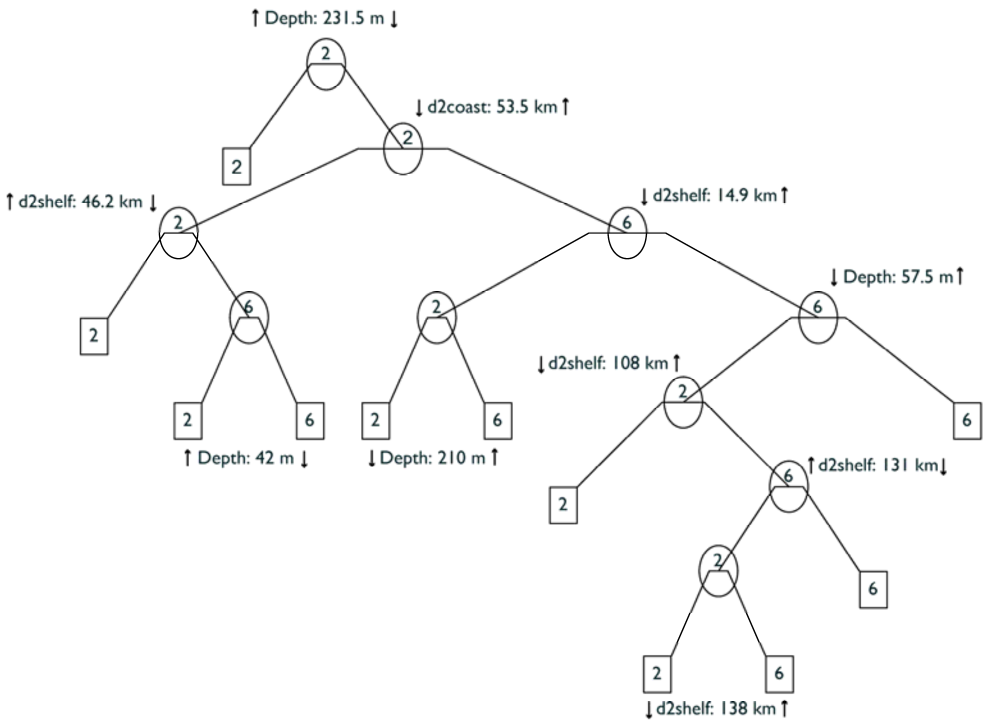


Figure D-3. Classification and regression tree for the two dominant groups present in the Gulf of Mexico Ordination. Symbology as in Figure D-1. Group 2 is typically found offshore in waters deeper than 232 m, while group 6, comprised solely of Atlantic Spotted Dolphins, is found in waters deeper than 38.5 m, and shallower than 232 m.

Appendix E: Model Validation Results

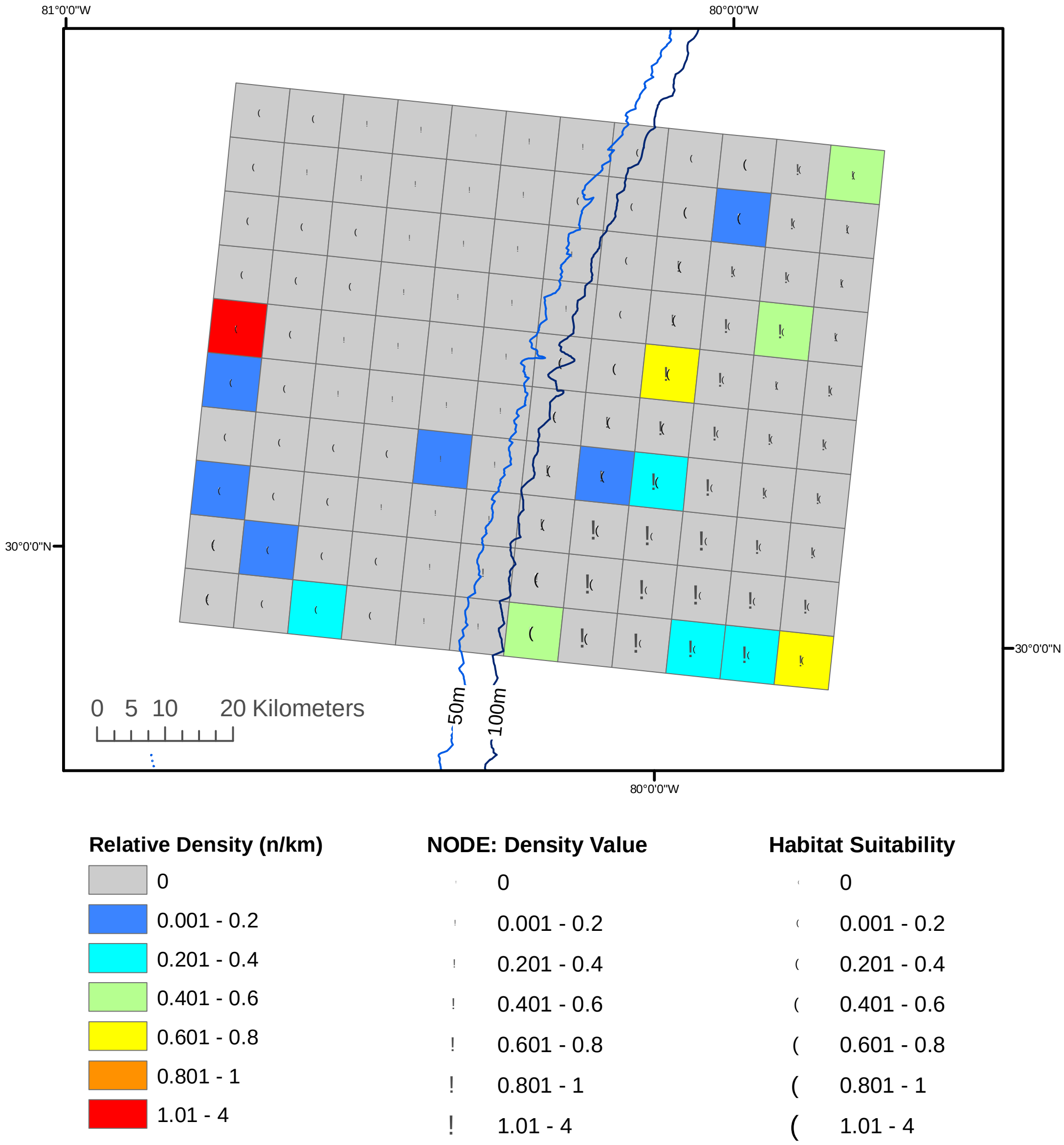


Figure E-1. Survey zone for the proposed Jacksonville USWTR illustrating bottlenose dolphin relative density values based on summer aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

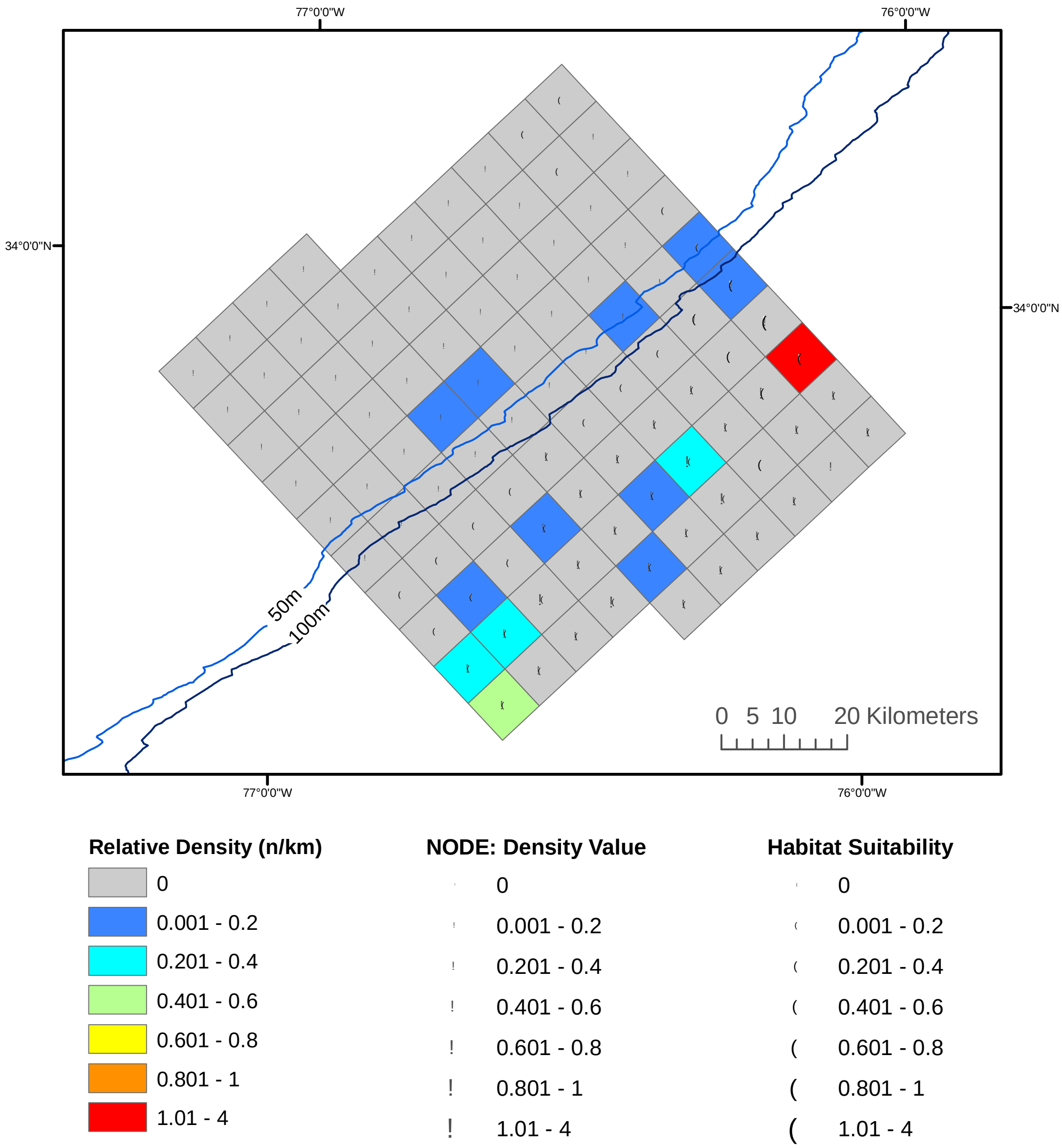


Figure E-2. Survey zone for the proposed Onslow Bay USWTR illustrating bottlenose dolphin relative density values based on summer aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

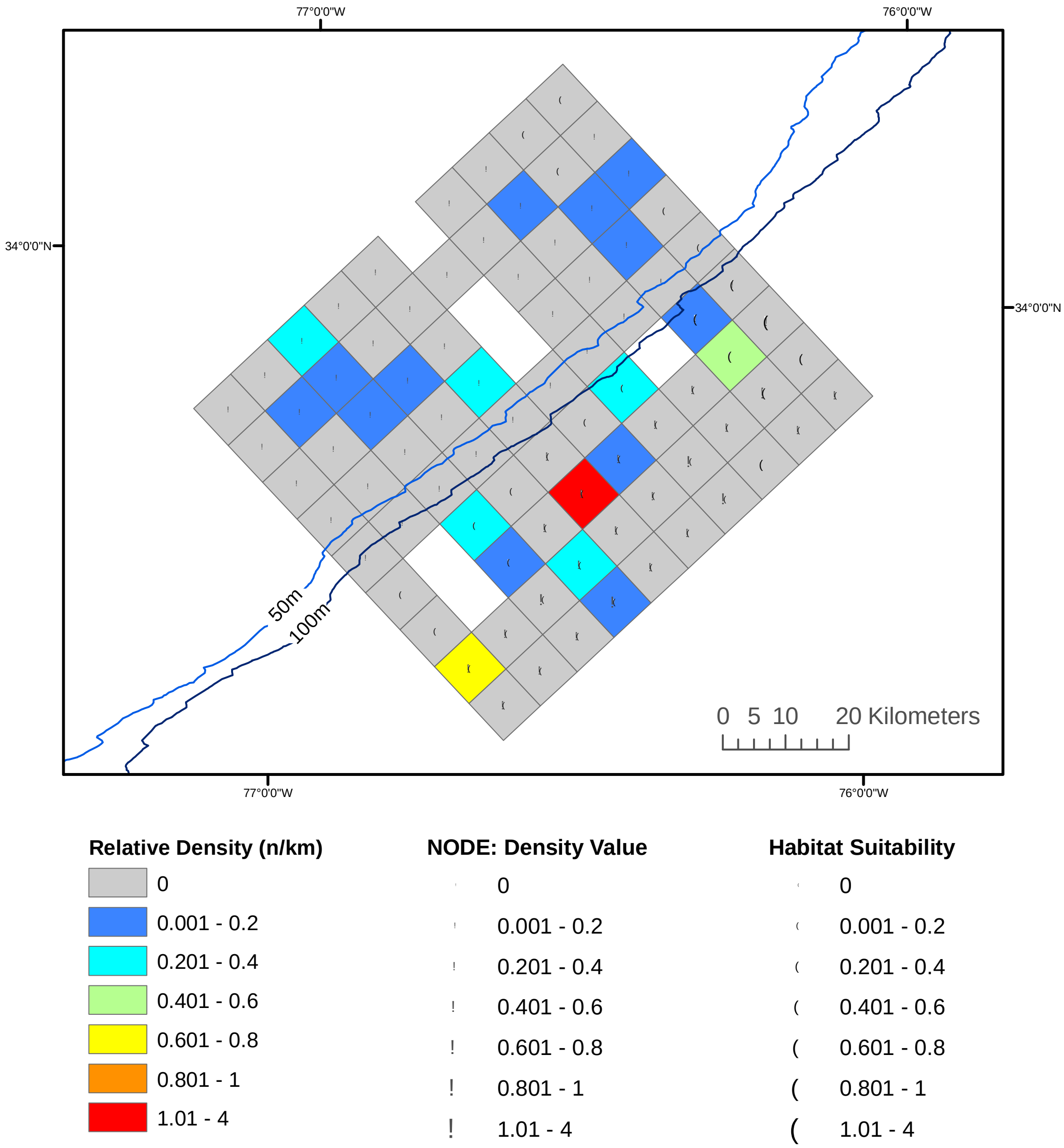


Figure E-3. Survey zone for the proposed Onslow Bay USWTR illustrating bottlenose dolphin relative density values based on summer ship surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

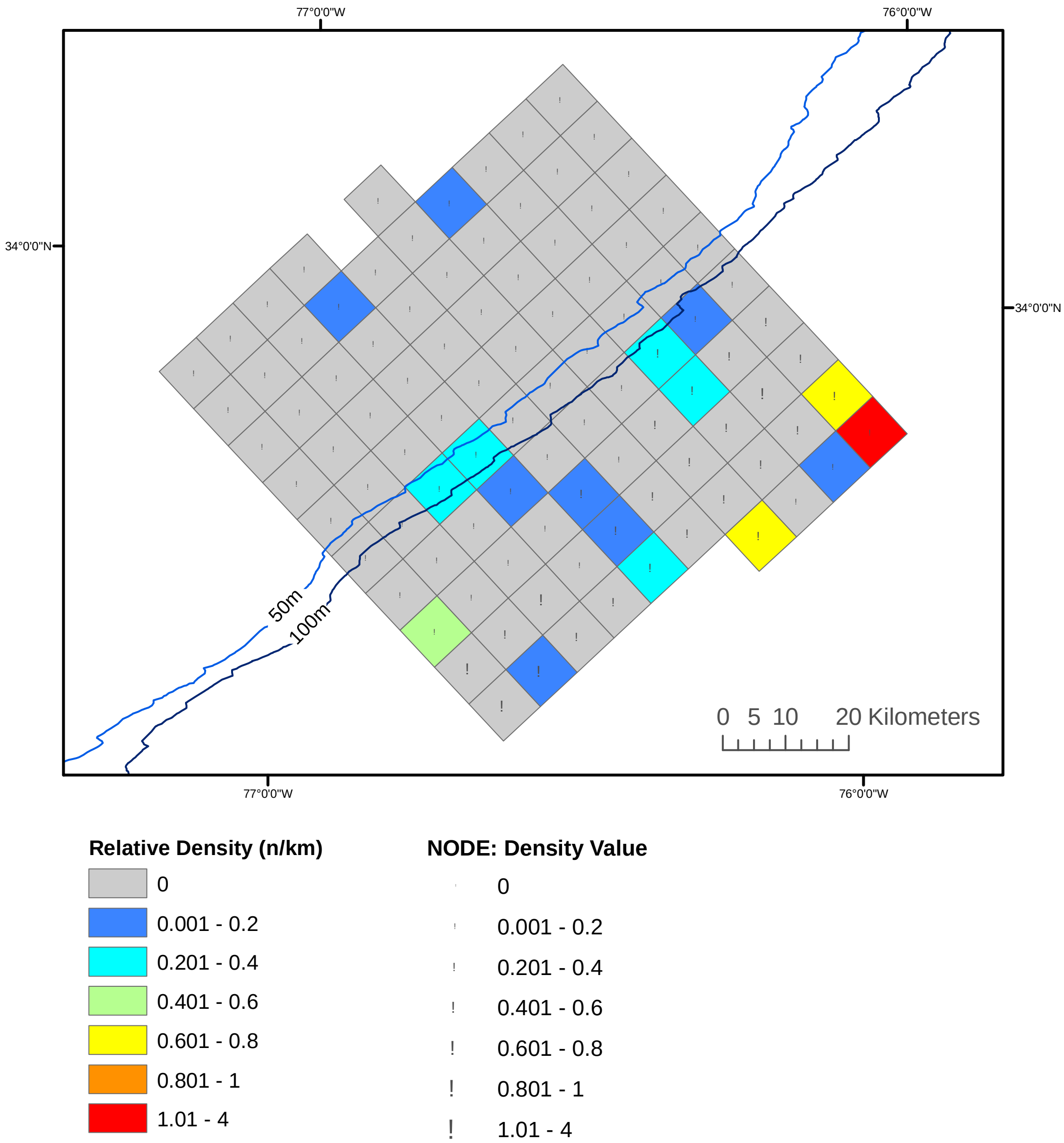


Figure E-4. Survey zone for the proposed Onslow Bay USWTR illustrating bottlenose dolphin relative density values based on fall aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

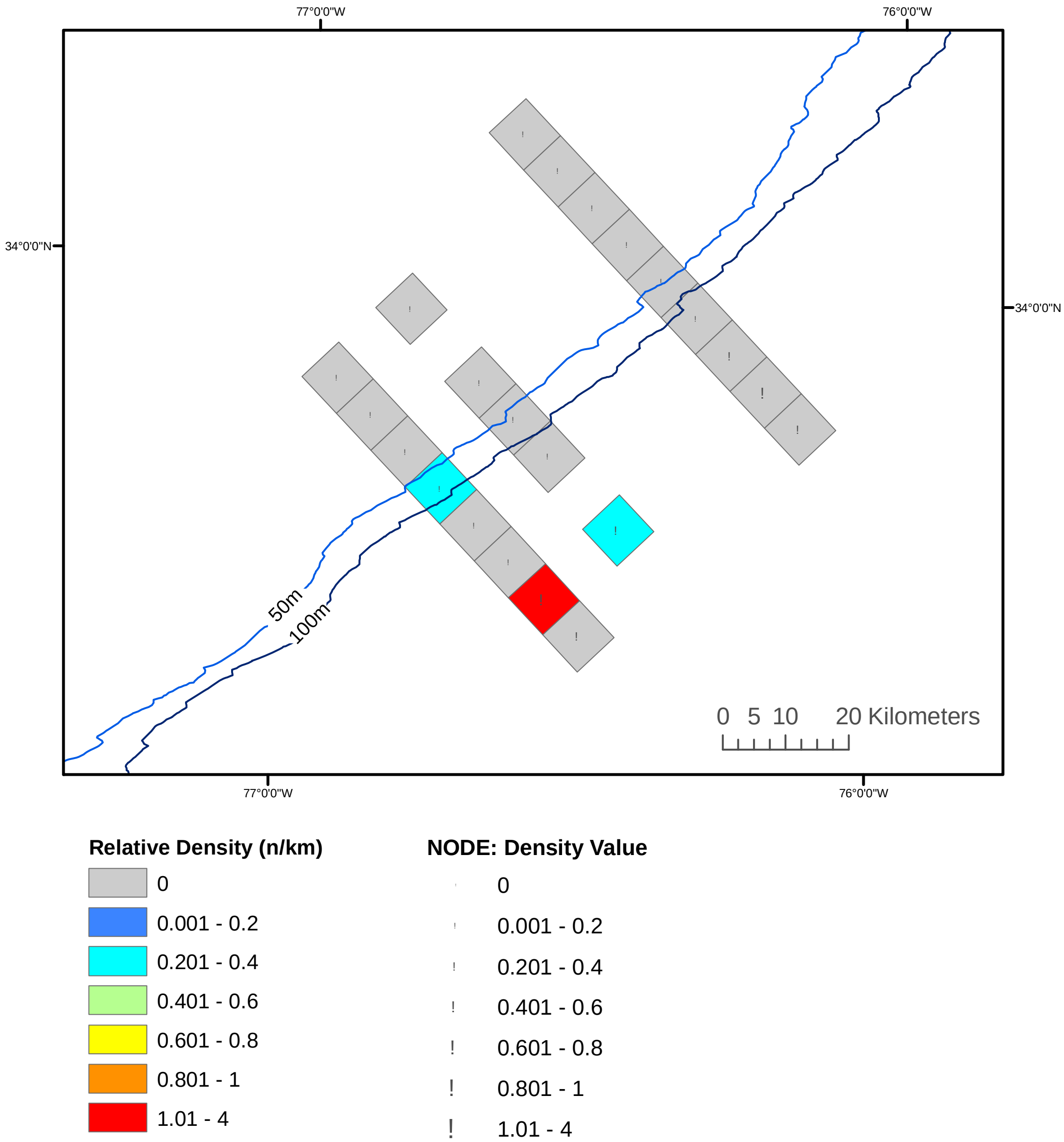


Figure E-5. Survey zone for the proposed Onslow Bay USWTR illustrating bottlenose dolphin relative density values based on fall ship surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

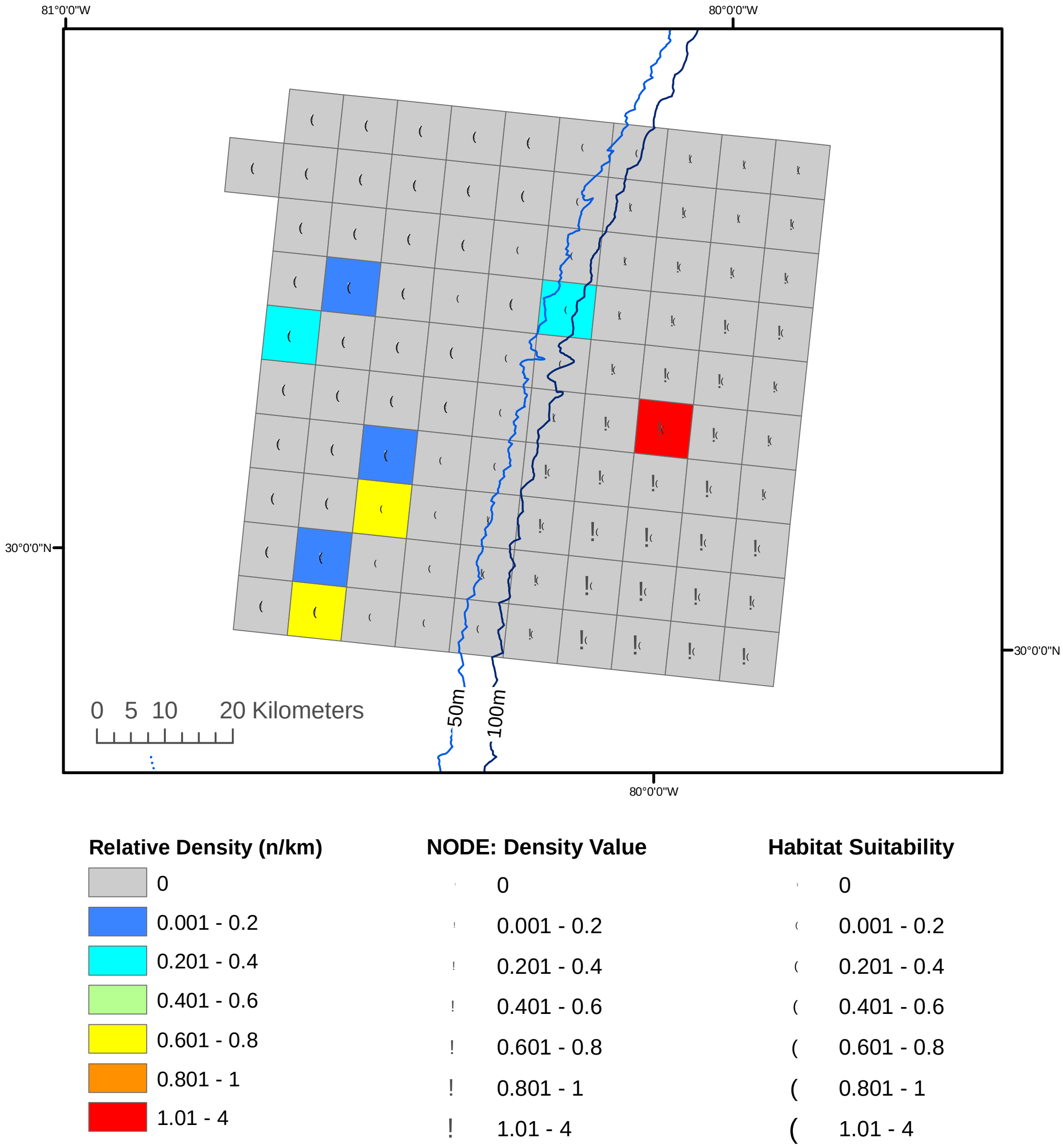


Figure E-6. Survey zone for the proposed Jacksonville USWTR illustrating bottlenose dolphin relative density values based on winter aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

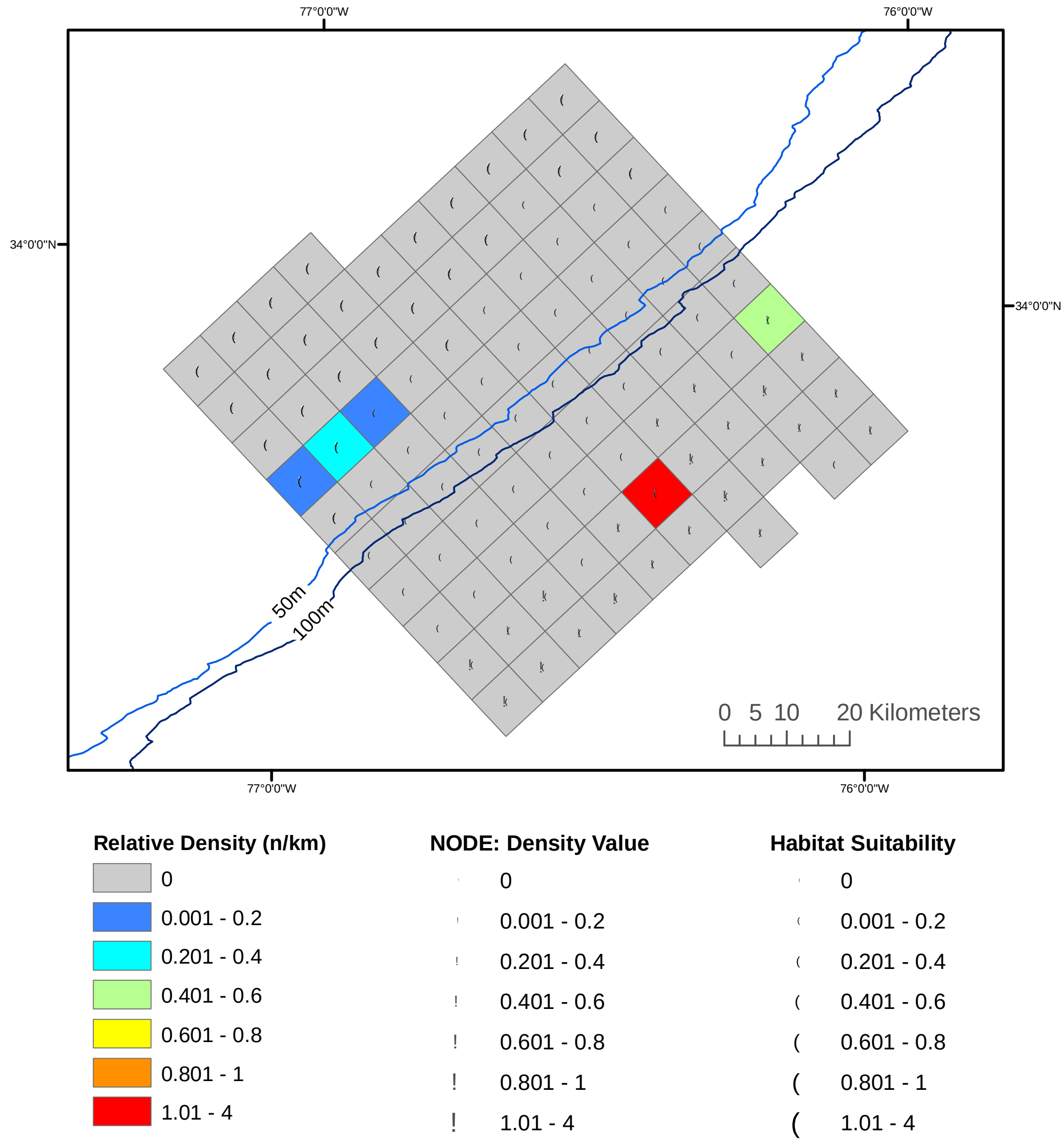


Figure E-7. Survey zone for the proposed Onslow Bay USWTR illustrating bottlenose dolphin relative density values based on winter aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

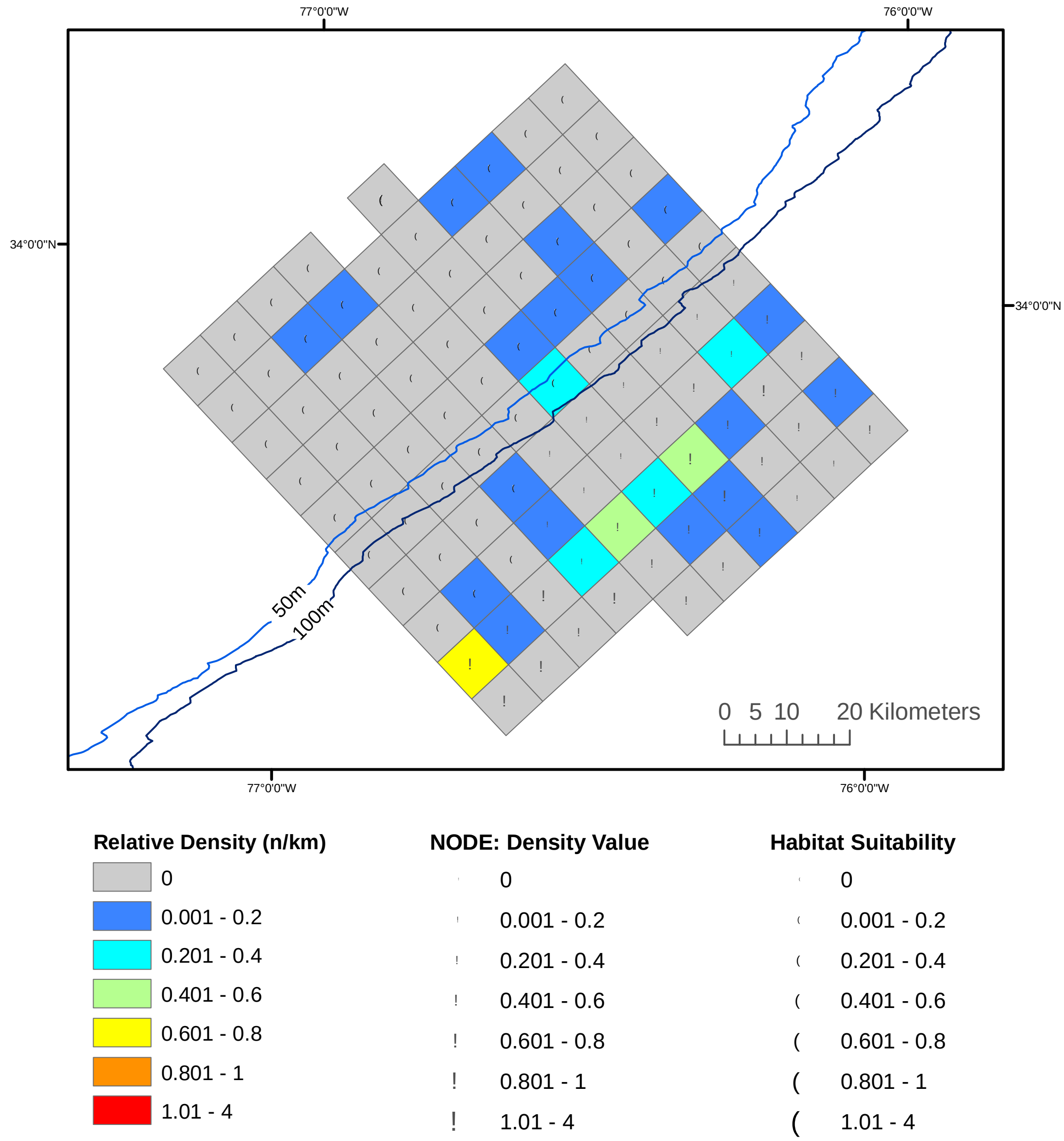


Figure E-8. Survey zone for the proposed Onslow Bay USWTR illustrating bottlenose dolphin relative density values based on spring aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

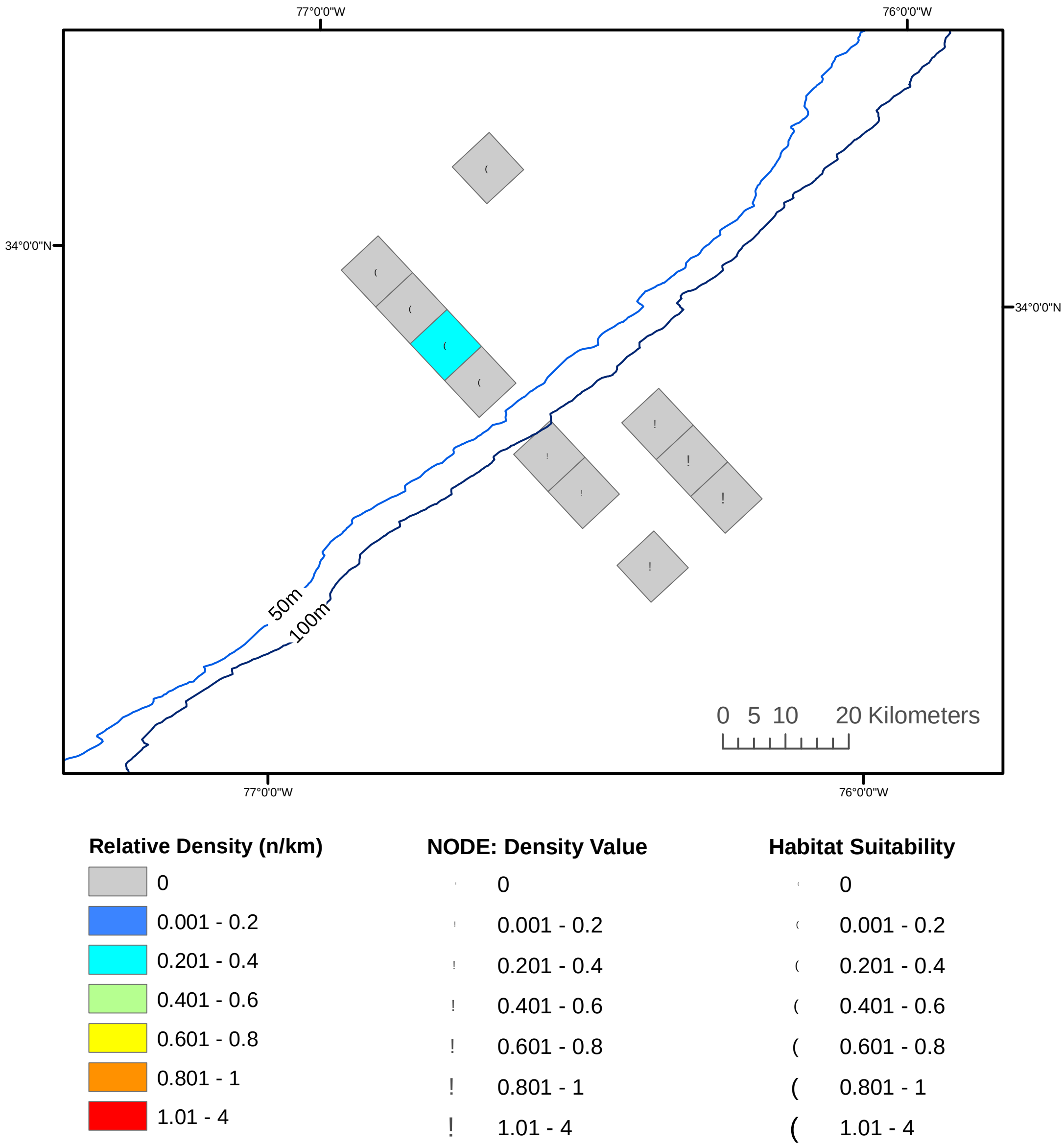


Figure E-9. Survey zone for the proposed Onslow Bay USWTR illustrating bottlenose dolphin relative density values based on spring ship surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

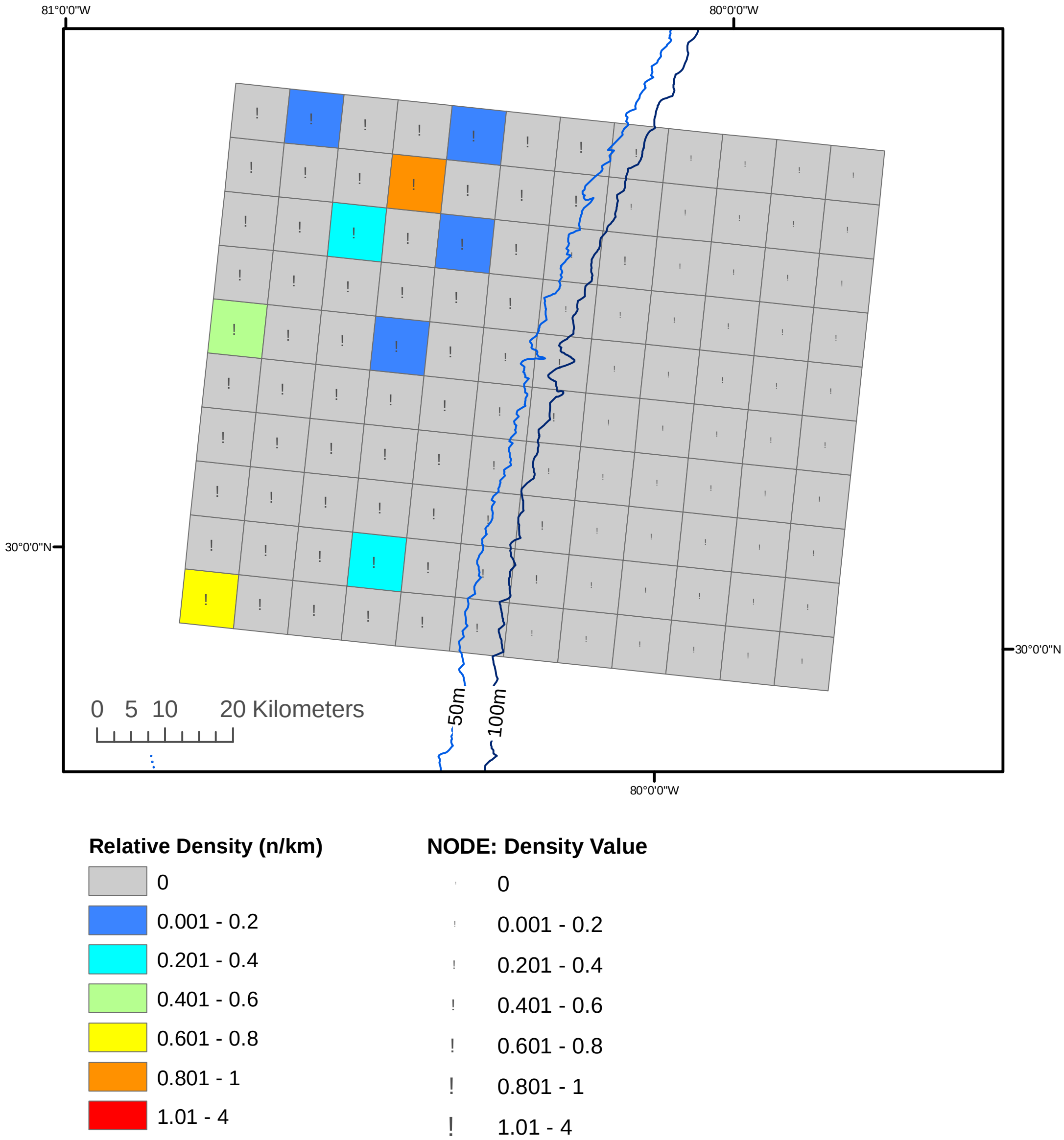


Figure E-10. Survey zone for the proposed Jacksonville USWTR illustrating spotted dolphin relative density values based on summer aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

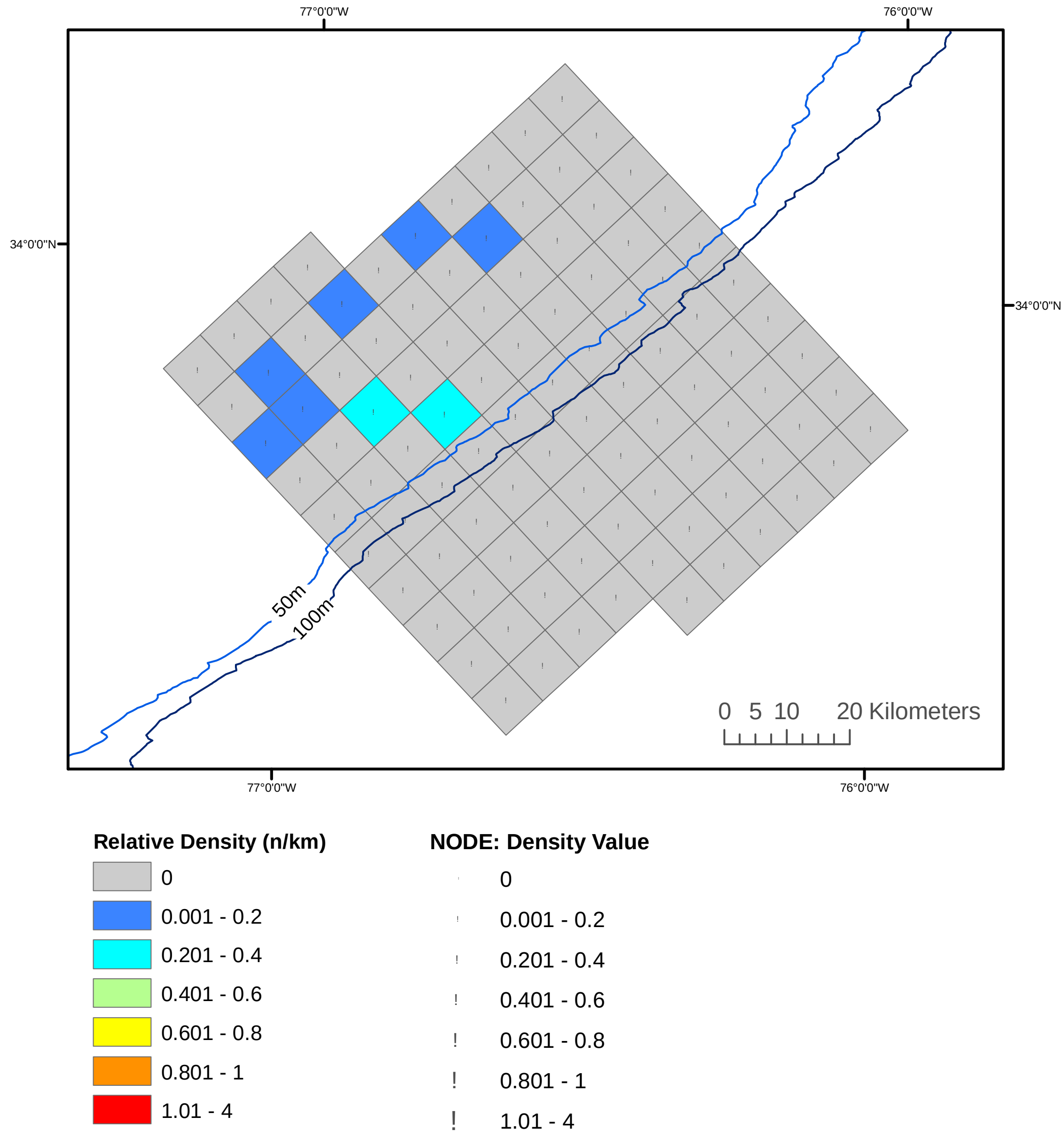


Figure E-11. Survey zone for the proposed Onslow Say USWTR illustrating spotted dolphin relative density values based on summer aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

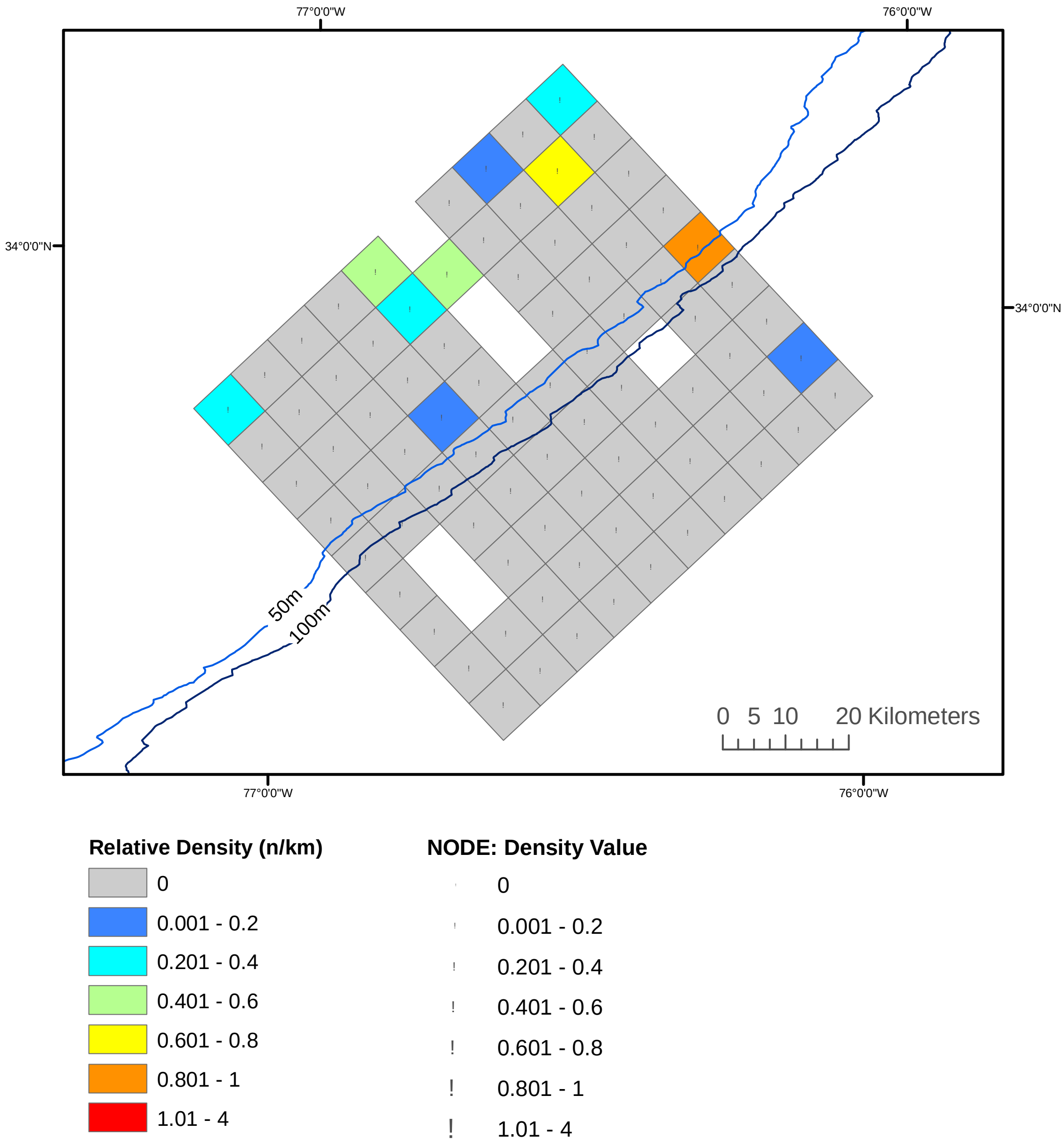


Figure E-12. Survey zone for the proposed Onslow Say USWTR illustrating spotted dolphin relative density values based on summer ship surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

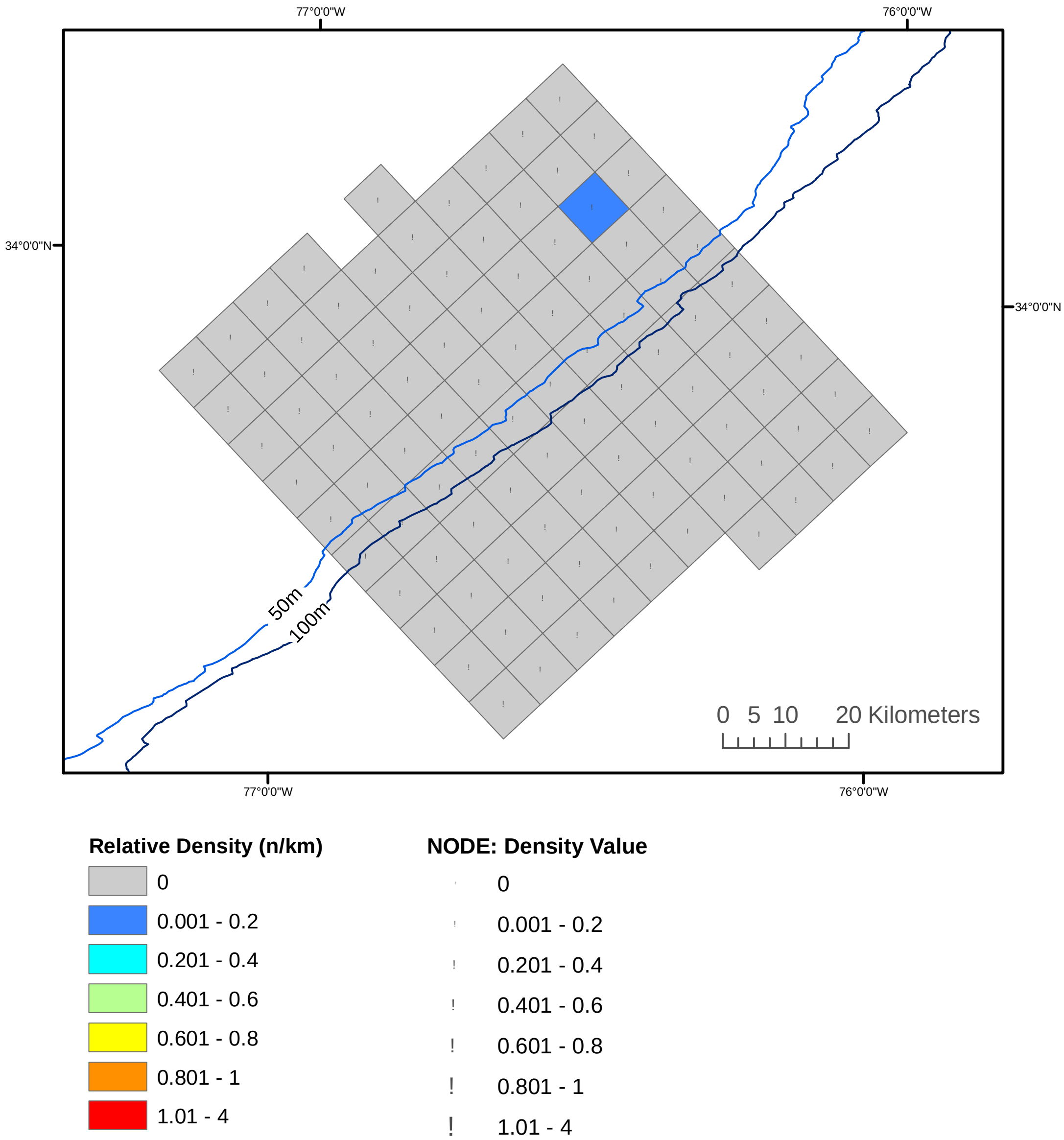


Figure E-13. Survey zone for the proposed Onslow Say USWTR illustrating spotted dolphin relative density values based on fall aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

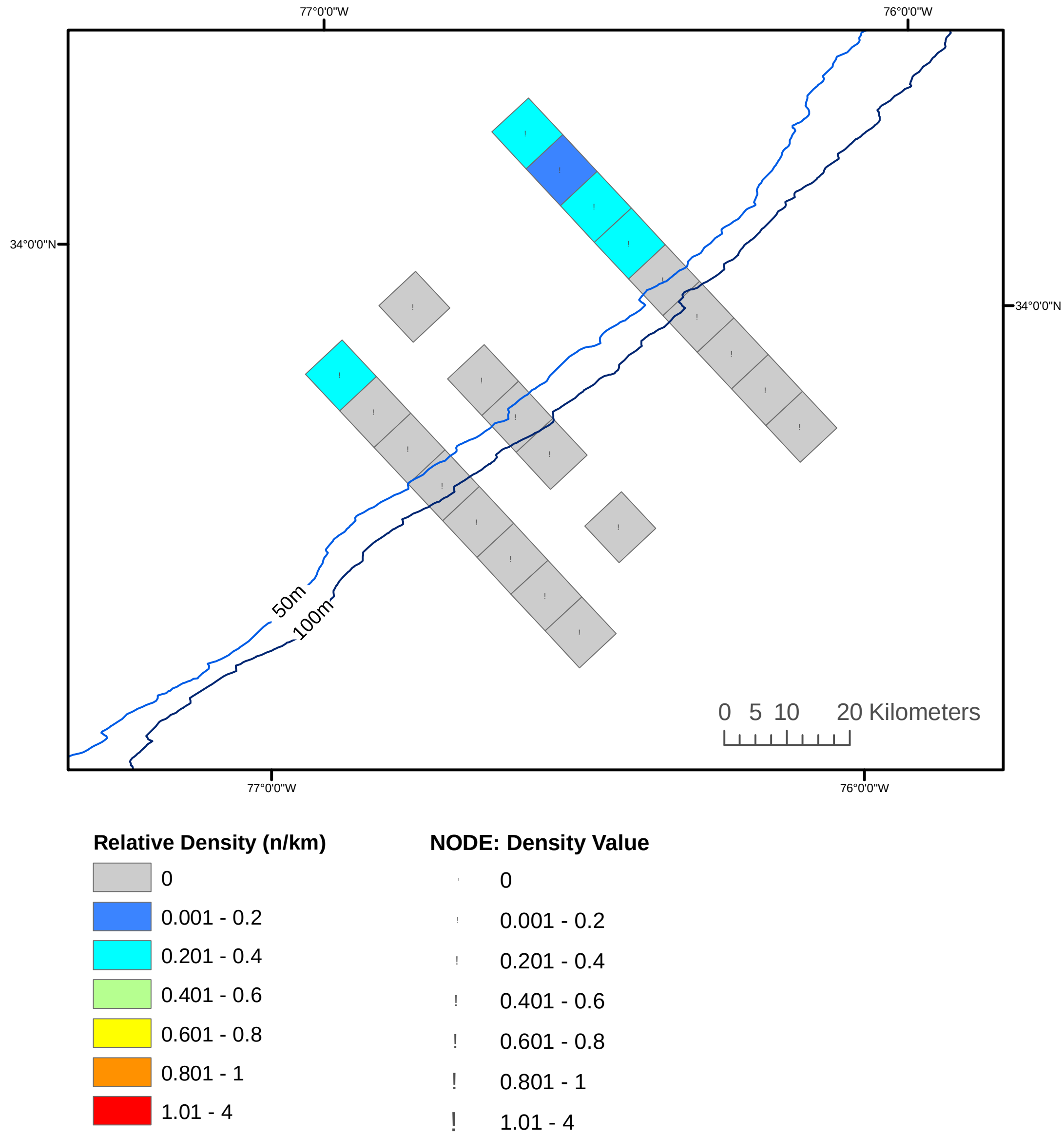


Figure E-14. Survey zone for the proposed Onslow Say USWTR illustrating spotted dolphin relative density values based on fall ship surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

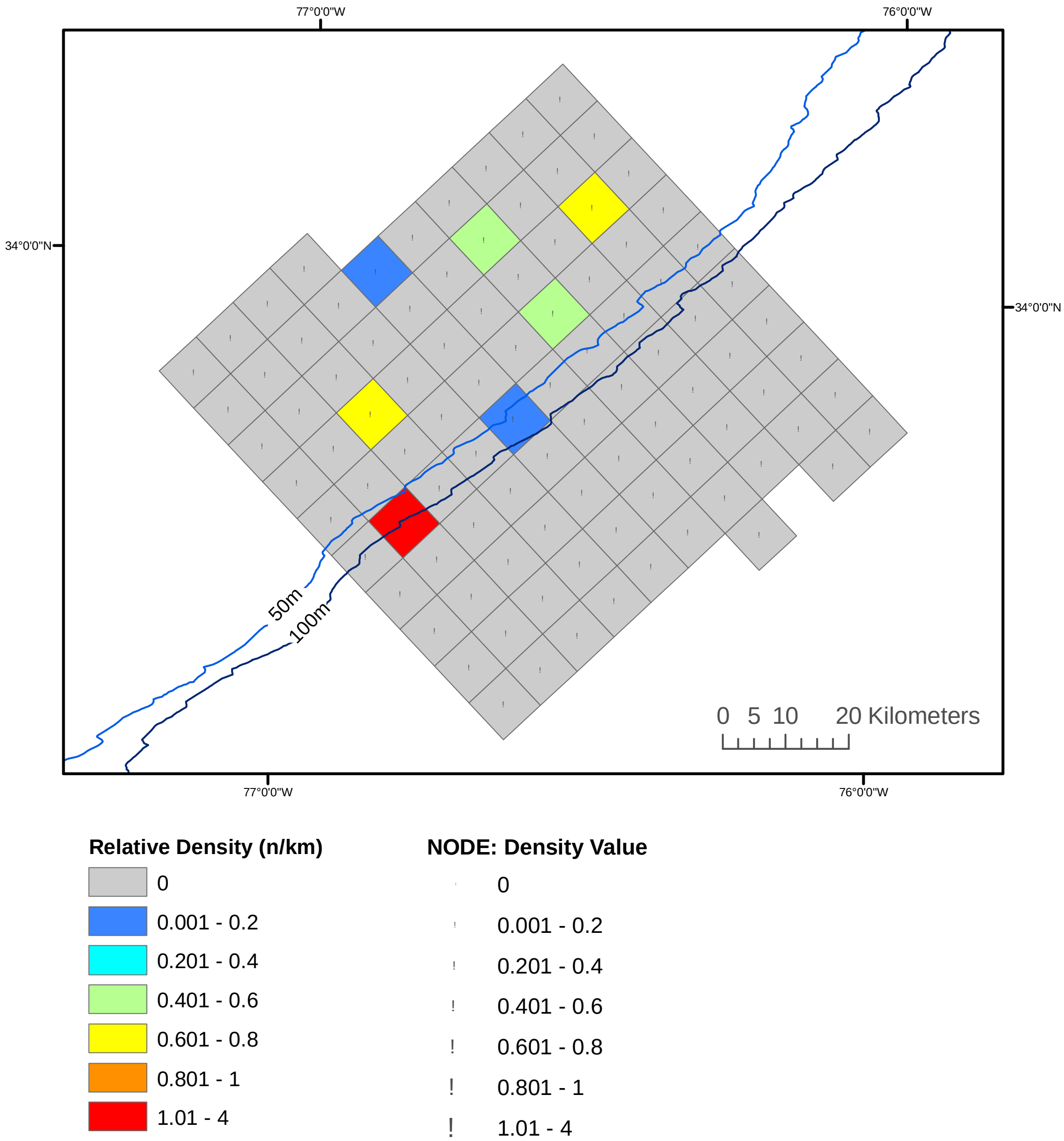


Figure E-15. Survey zone for the proposed Onslow Say USWTR illustrating spotted dolphin relative density values based on winter aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

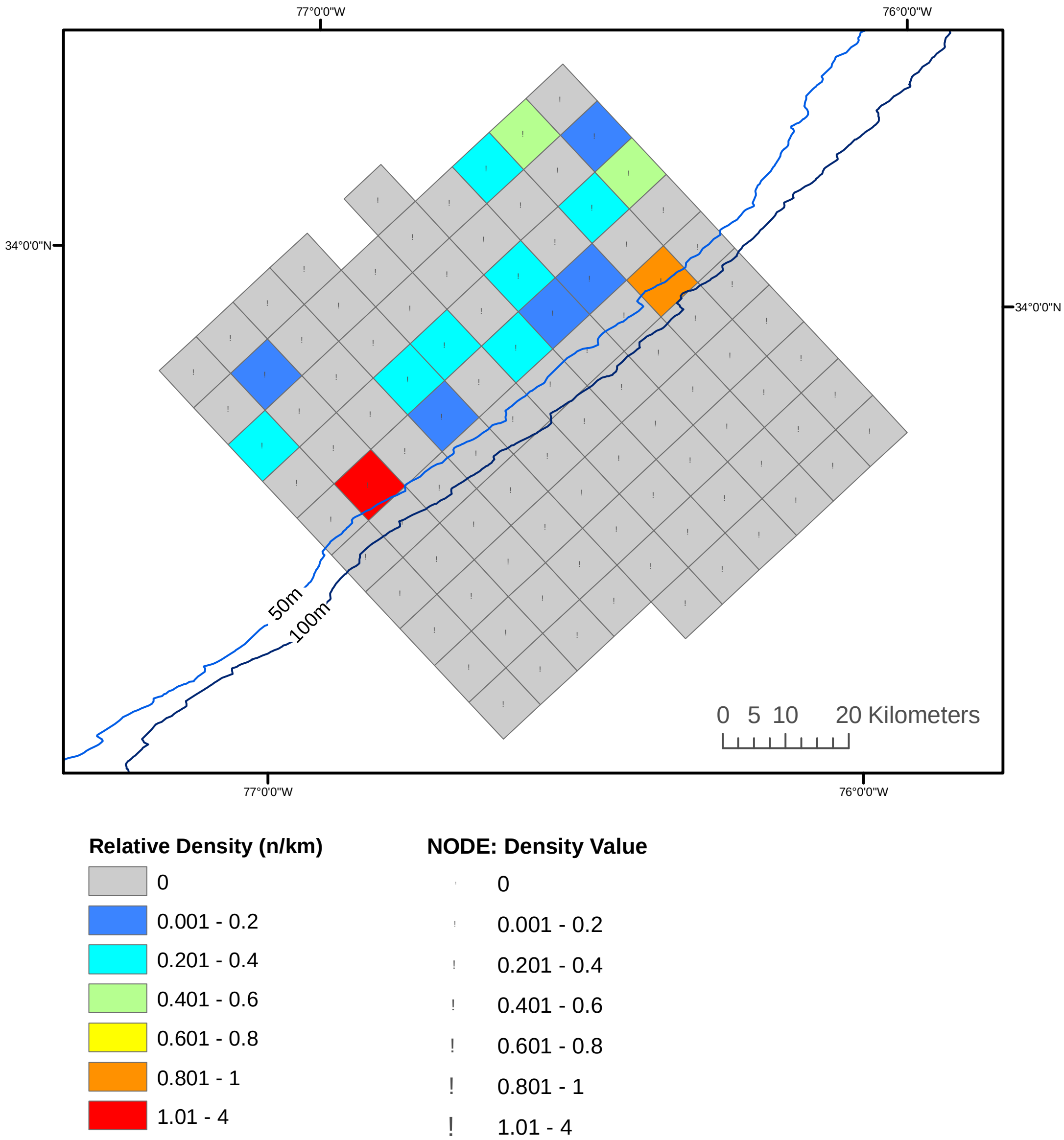


Figure E-16. Survey zone for the proposed Onslow Bay USWTR illustrating spotted dolphin relative density values based on spring aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

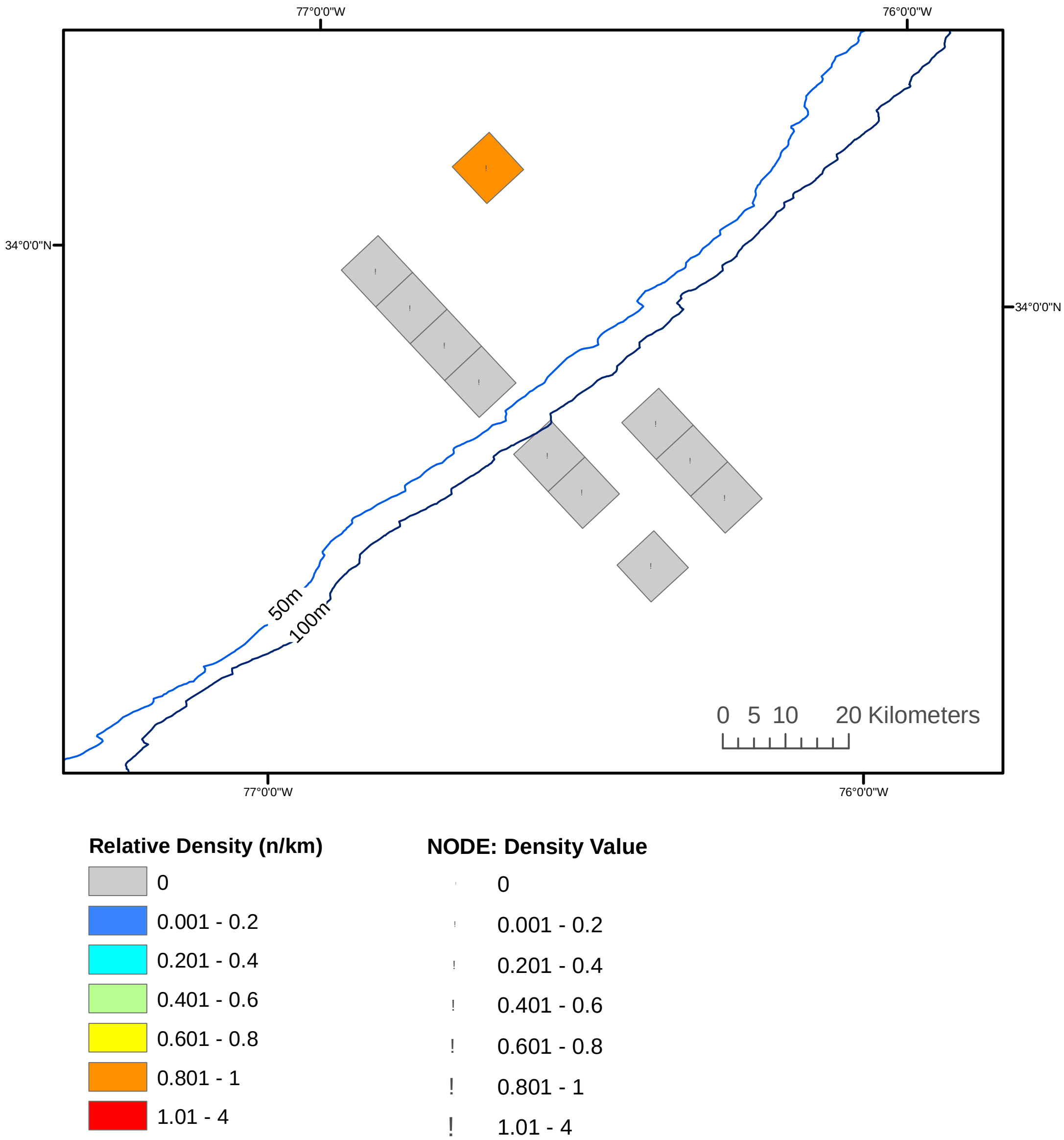


Figure E-17. Survey zone for the proposed Onslow Bay USWTR illustrating spotted dolphin relative density values based on spring aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

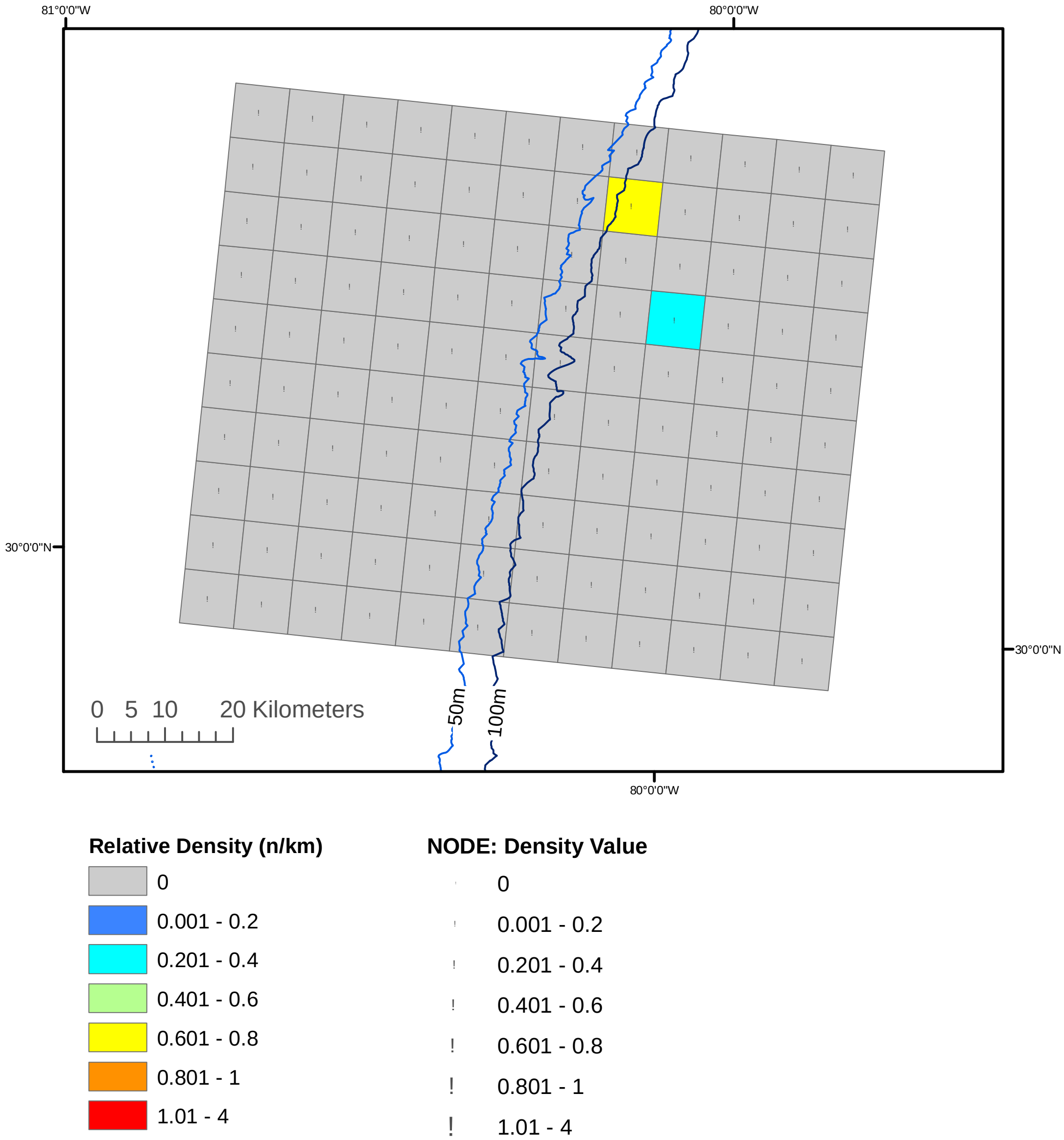


Figure E-18. Survey zone for the proposed Jacksonville USWTR illustrating Risso's dolphin relative density values based on summer aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

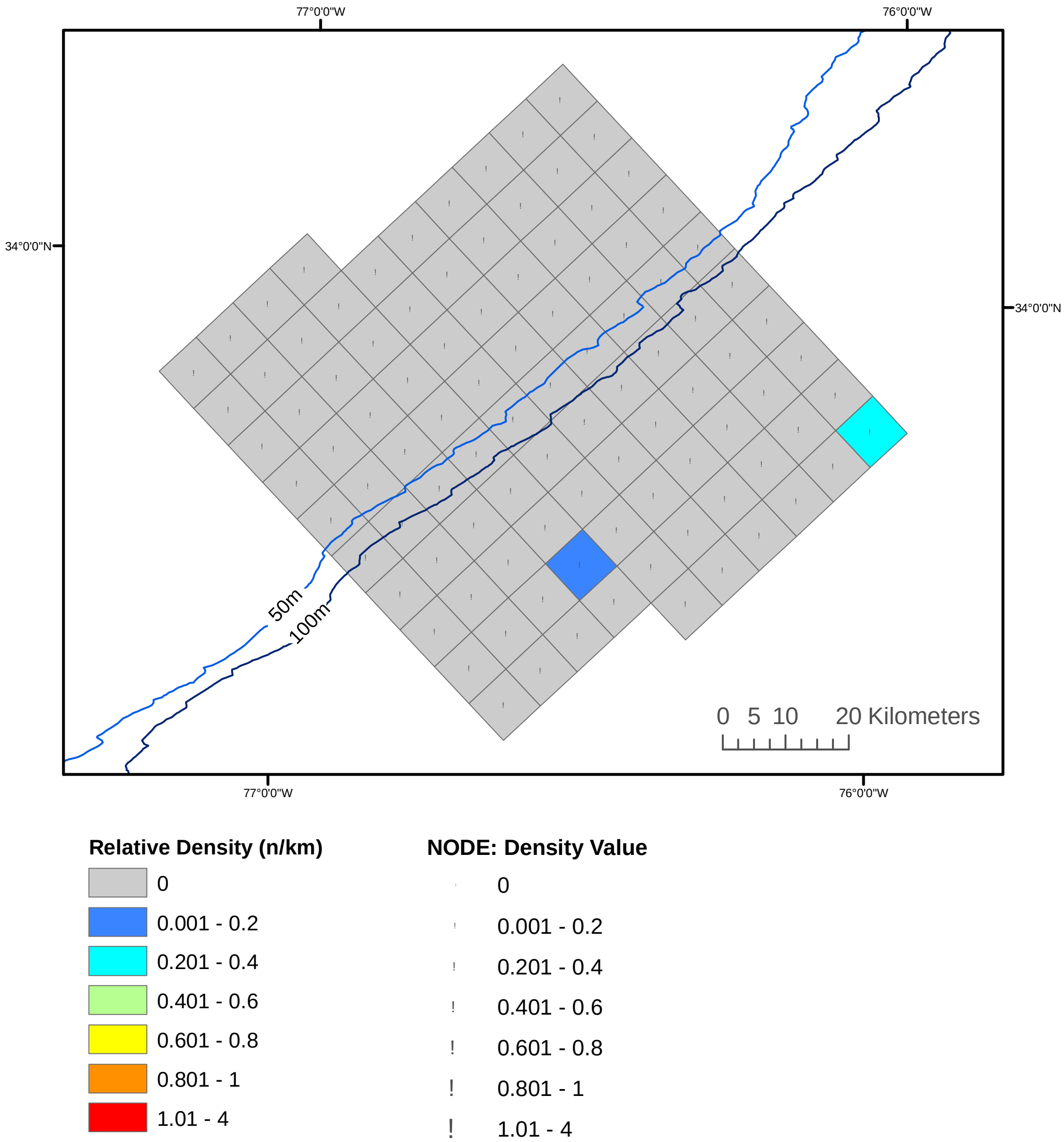


Figure E-19. Survey zone for the proposed Onslow Bay USWTR illustrating Risso's dolphin relative density values based on summer aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

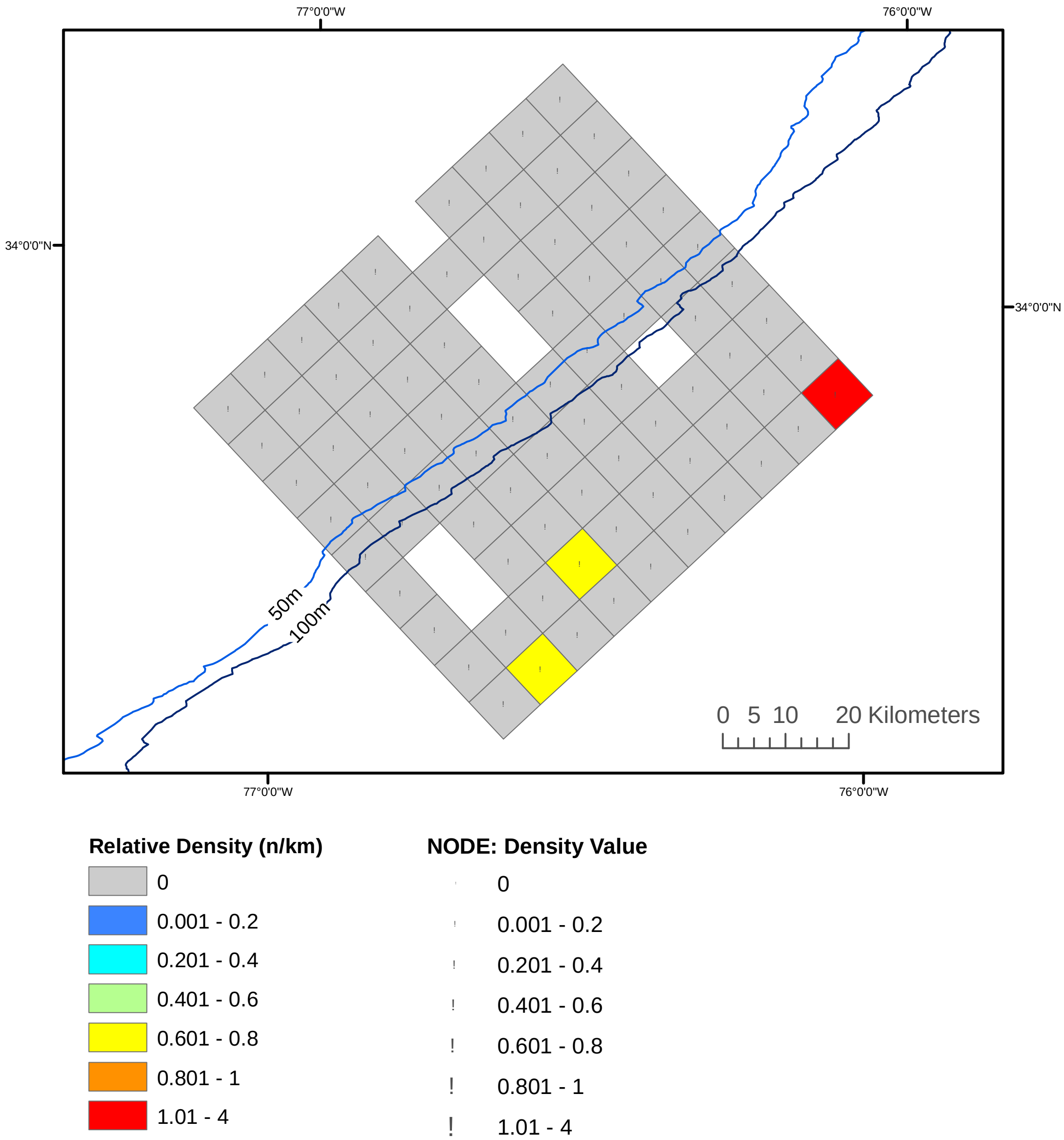


Figure E-20. Survey zone for the proposed Onslow Bay USWTR illustrating Risso's dolphin relative density values based on summer ship surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

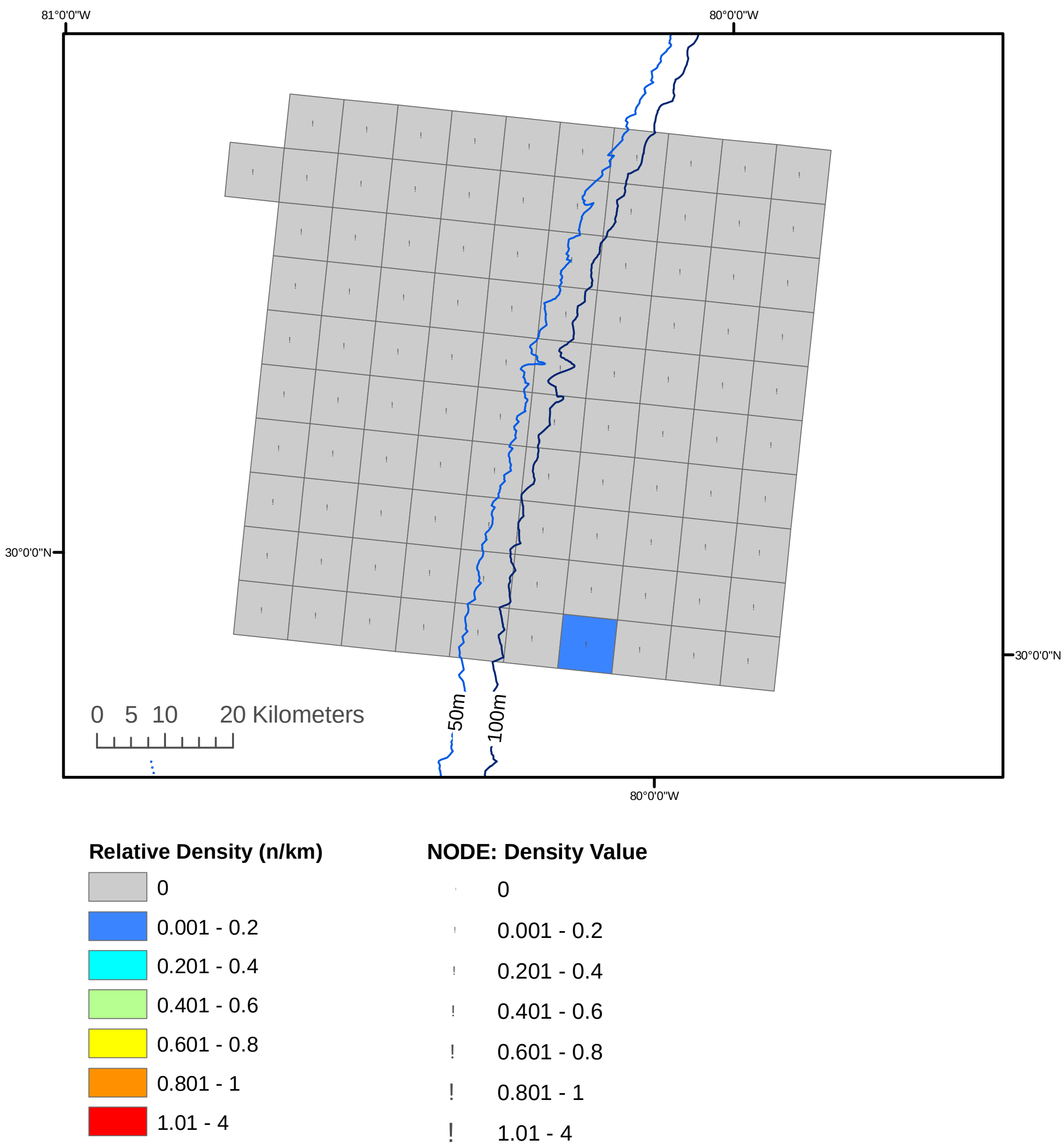


Figure E-21. Survey zone for the proposed Jacksonville USWTR illustrating Risso's dolphin relative density values based on winter aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

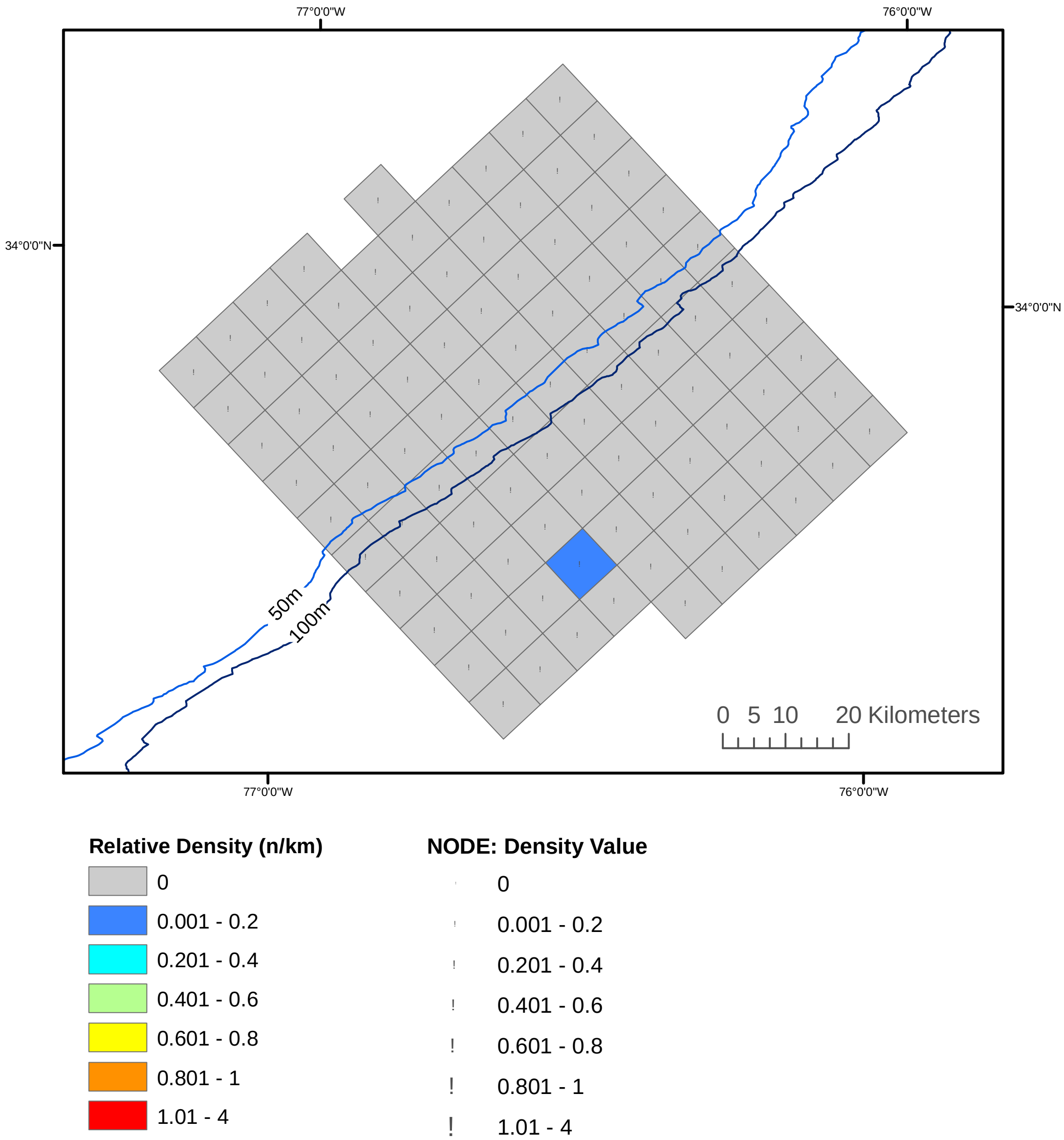


Figure E-22. Survey zone for the proposed Onslow Bay USWTR illustrating Risso's dolphin relative density values based on spring aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

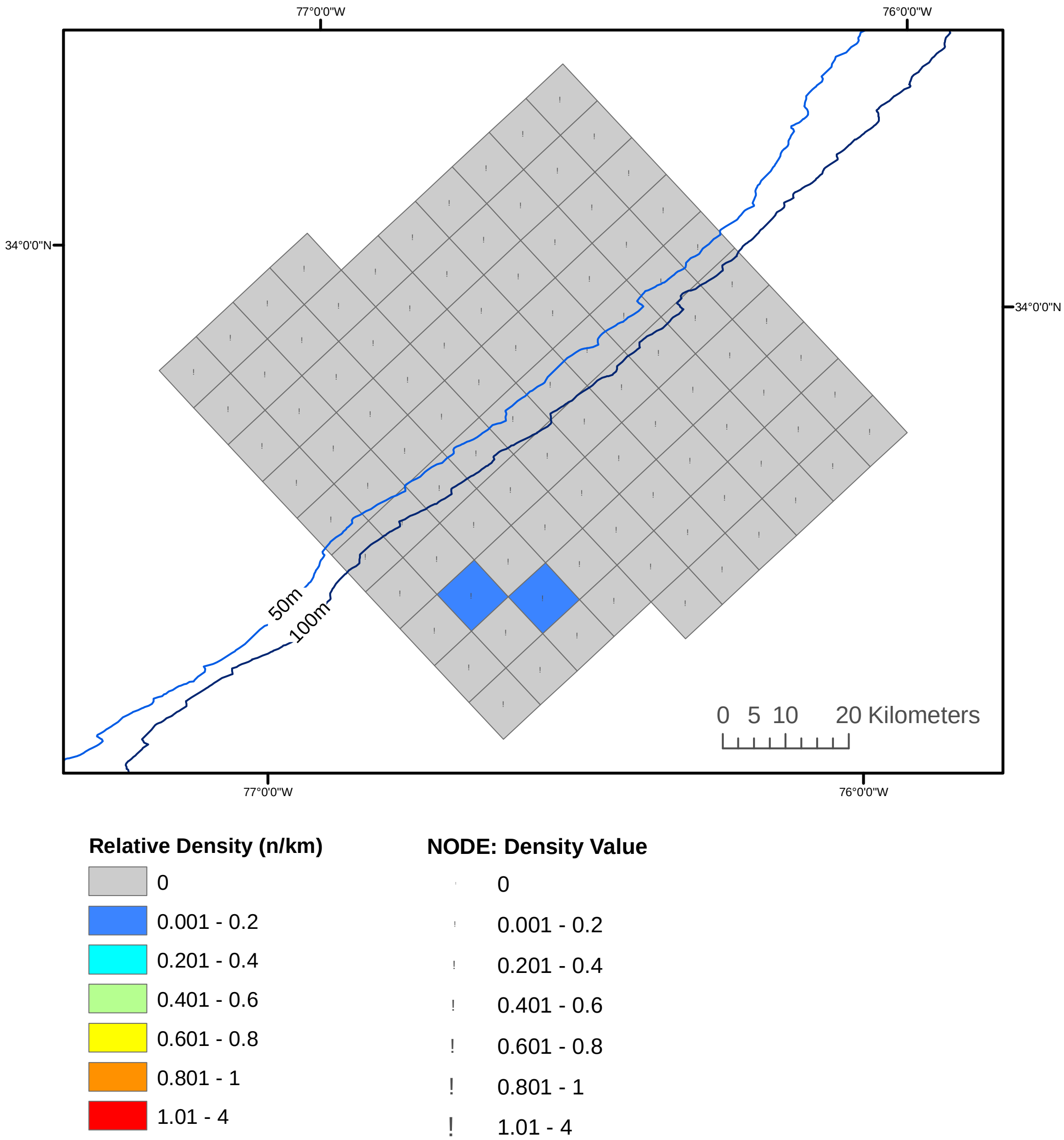


Figure E-23. Survey zone for the proposed Onslow Bay USWTR illustrating rough-toothed dolphin relative density values based on summer aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

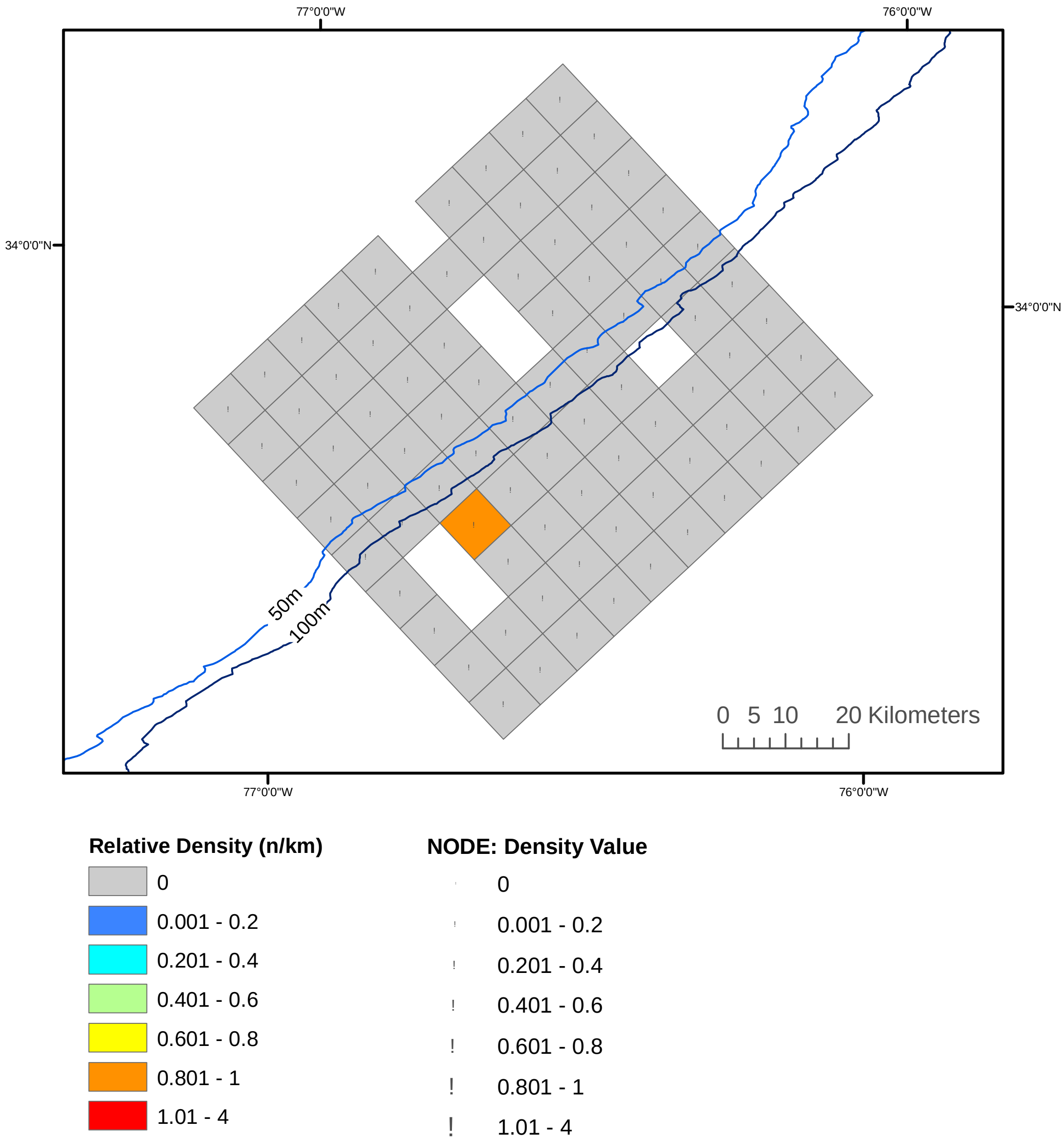


Figure E-24. Survey zone for the proposed Onslow Bay USWTR illustrating rough-toothed dolphin relative density values based on summer ship surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

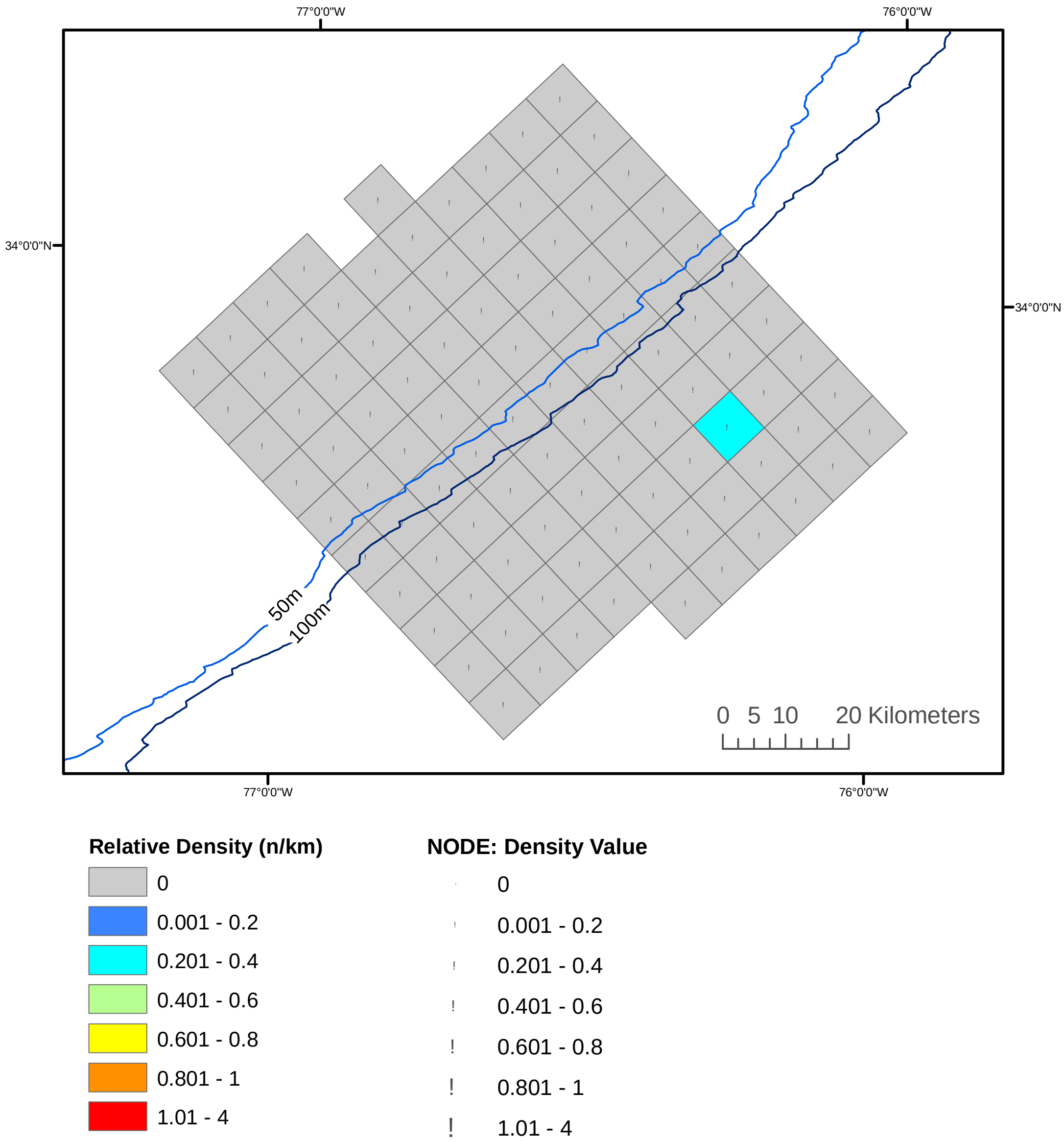


Figure E-25. Survey zone for the proposed Onslow Bay USWTR illustrating rough-toothed dolphin relative density values based on spring aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

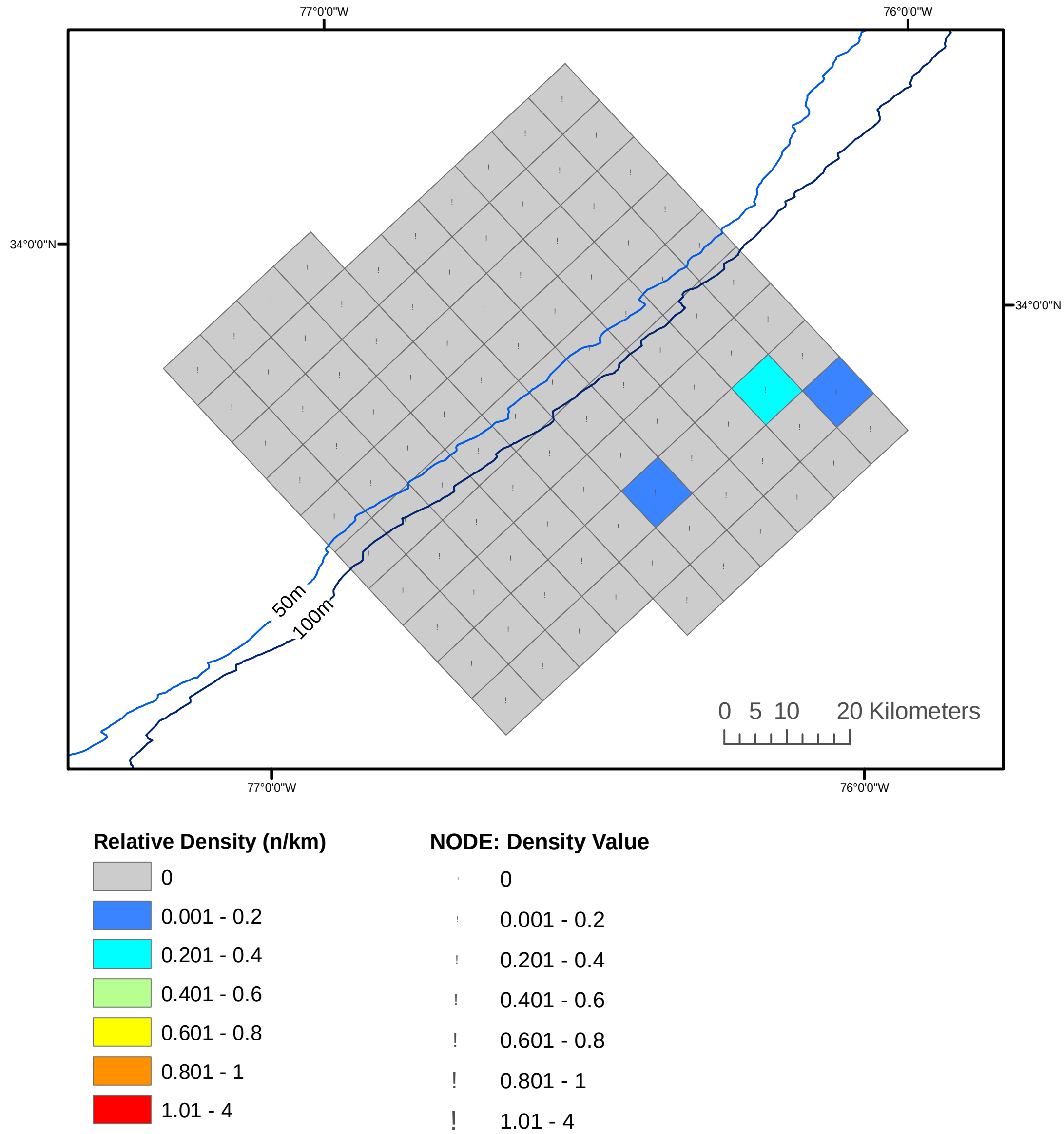


Figure E-26. Survey zone for the proposed Onslow Bay USWTR illustrating pilot whales relative density values based on summer aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

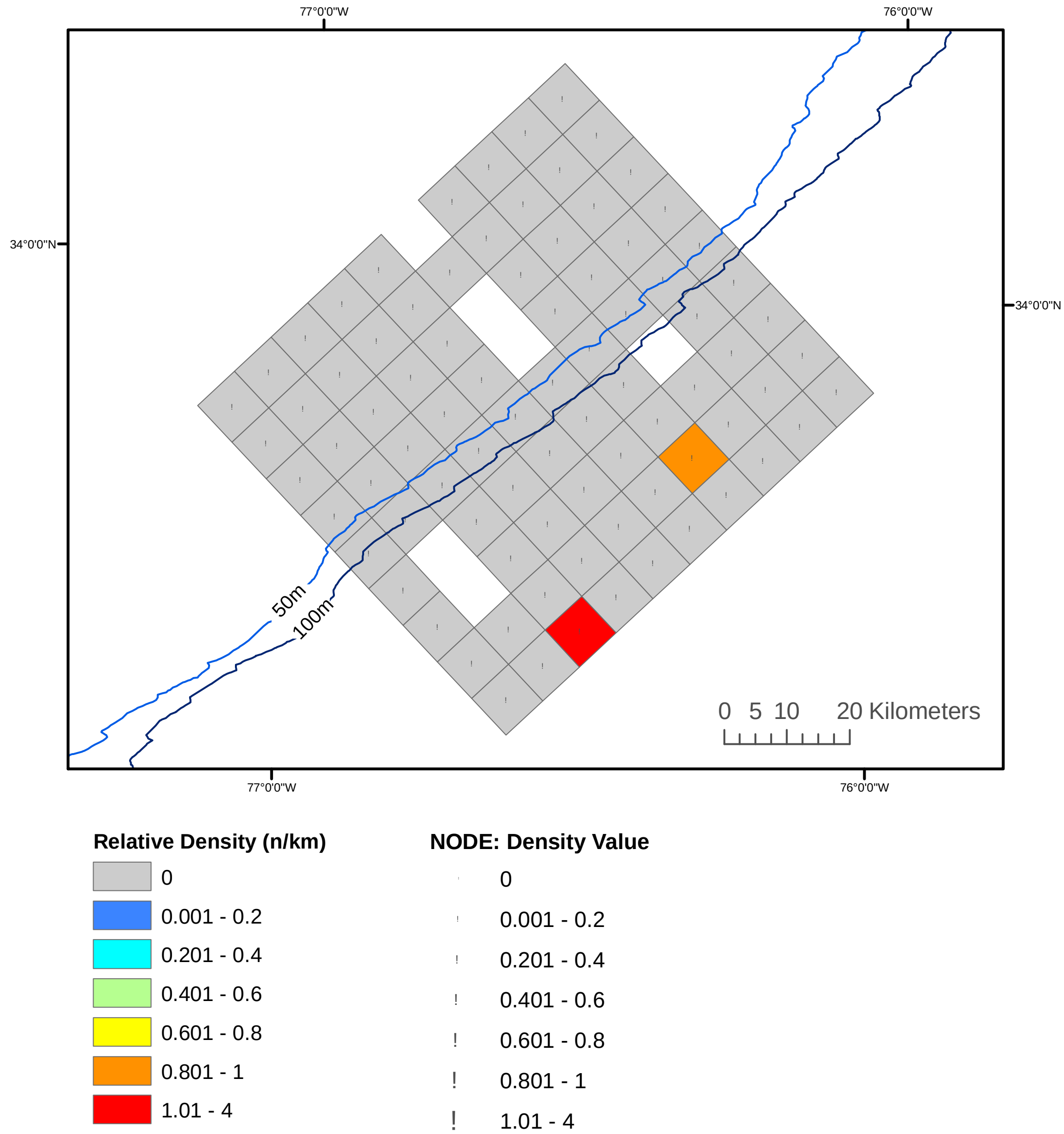


Figure E-27. Survey zone for the proposed Onslow Bay USWTR illustrating pilot whales relative density values based on summer ship surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.

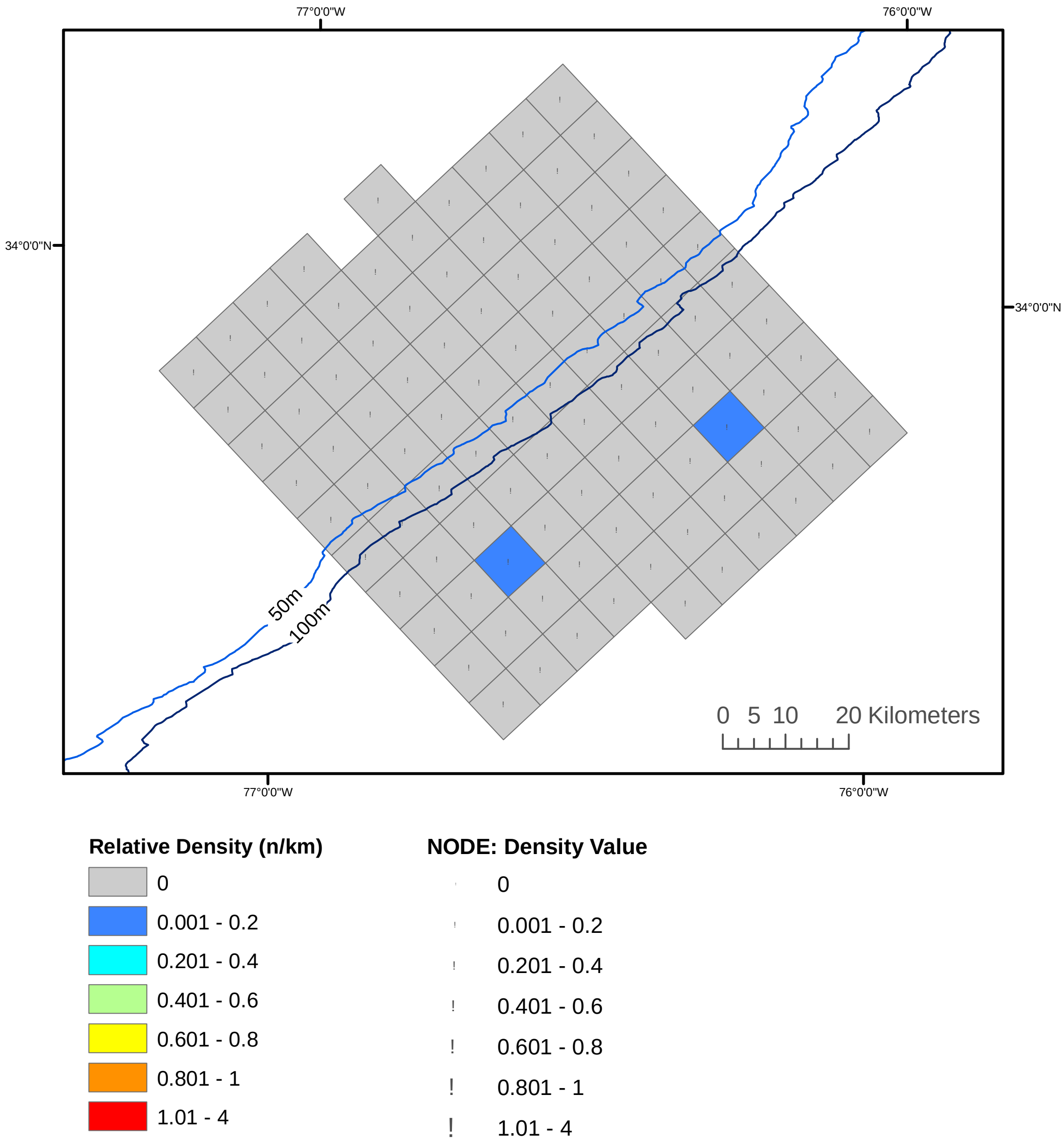
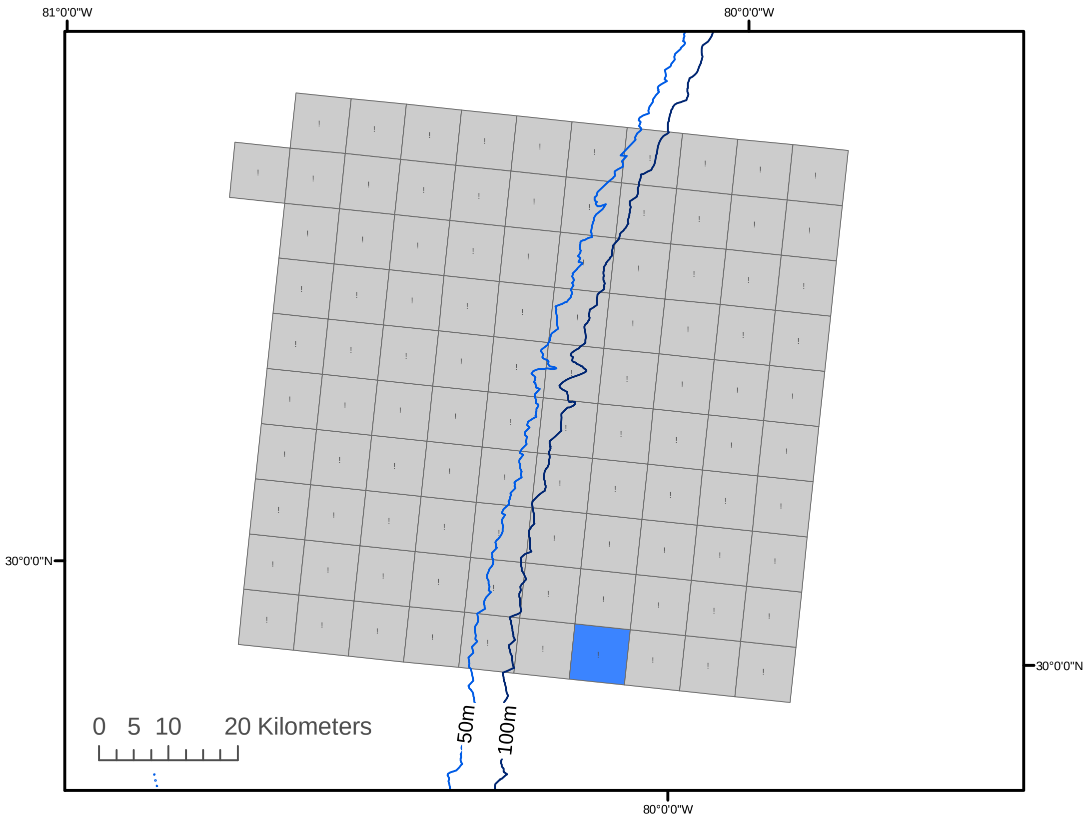


Figure E-28. Survey zone for the proposed Onslow Bay USWTR illustrating pilot whales relative density values based on spring aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.



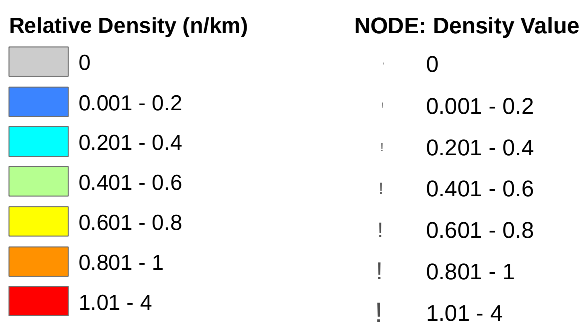


Figure E-29. Survey zone for the proposed Jacksonville USWTR illustrating minke whales relative density values based on winter aerial surveys. Solid colored circles represent concomitant NODE values and hollow circles represent habitat suitability values. The 50m and 100m depth contours are provided for reference.