

# Modelling abundance hotspots for data-poor Irish Sea rays

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## Abstract

Skates and rays represent one of the most vulnerable components of fish communities in temperate demersal fisheries such as the Irish Sea. They also tend to be data poor in comparison to commercially exploited teleost fish. Spatial management has been suggested as an important tool to protect these species, but requires an understanding of the abundance distribution, and the relationship the abundance distribution has with the environment at both adult and juvenile life history stages. Here we modelled bottom trawl survey data using delta log-normal boosted regression trees on to derive rays' spatial abundance, and environmental links. The modelling approach allowed the development of high resolution predictive maps of abundance of four skate and ray species targeted by fishing activity: thornback, spotted, cuckoo and blonde rays. The distributions of these species were driven by a general preference for sand and coarser substrates as well as higher salinities, temperatures and currents speeds. Spatial comparisons between abundance distributions and locations of skate and ray commercial landings indicated that the main hotspots for the investigated species are outside of the main commercial fishing areas and overlap with potential MPAs proposed for wider ecosystem protection. The method offers a useful tool for selecting potential MPA's to assist the management and conservation of data-poor species.

## Keywords

Boosted regression trees; data poor; elasmobranch; skates; rays

# 1 Introduction

## 1.1 Managing data-poor elasmobranch stocks

Most elasmobranch species are large-bodied, slow-growing and inherently vulnerable to overfishing, due to their low fecundity and late maturation (Holden, 1974, 1973; Musick et al., 2000). Several factors preclude the use of standard methods for stock assessment of elasmobranchs: data (particularly on age-structure and fecundity) are typically scarce or of poor quality (Ellis et al., 2010; Fahy, 1989; Gallagher, 2000), and landings are often reported for groups of species rather than for individual species. These problems are particularly compelling in Ireland where the actual species composition and age structure of ray catches is masked in bulked landings that are commercially boxed by size and value (Fahy, 1991). Ray catches are often not identified at the species level, or are misidentified (Fahy, 1991; ICES WGEF, 2010, 2009) (e.g. blonde rays (*Raja brachyura*) are often misidentified as spotted rays (*Raja montagui*)). Long-term, species-specific assessments are impeded by low and variable catch rates of rarer skate species (Ellis et al., 2010; ICES WGEF, 2010, 2009) and by inappropriate survey design (Ellis et al., 2010) leading to errors in abundance estimation (Brander, 1981; Casey and Myers, 1998; Myers and Worm, 2005).

Improved stock assessment for elasmobranchs has been a high priority since the start of the century (Chevolot et al., 2008; Ellis et al., 2005b; Heessen, 2003). The Johannesburg Declaration of 2002 (United Nations, 2002) committed governments to restore fisheries to maximum sustainable yield (MSY) by 2015 (European Commission, 2008). This typically involves managing the total allowable catch (TACs) of individual species. For Irish Sea skates and rays this approach is currently unfeasible, as biologically appropriate management units have not been defined (Ellis et al., 2010). For mainly bycatch species such as skates and rays, single-species TACs are unlikely to be effective as they can often increase discarding (ICES WGEF, 2012). It has been shown

that discard mortality of rays from the fishing fleet is already very high (Shephard et al., 2015).

Where management reference points are unknown, as in the case of blonde ray, the International Council for the Exploration of the Sea (ICES) prescribes a precautionary 20% annual TAC reduction (ICES WGLIFE, 2012; NWWRAC, 2012a). Whilst recent ICES advice based on abundance estimates recommended a 36% reduction for thornback and cuckoo ray, a 20% *increase* was recommended for spotted ray (ICES WGEF, 2012). Such examples highlight the inconsistencies that might arise in a mixed ray fishery managed under single-species TACs. Precautionary TAC reductions could increase the pressure on the already precarious Irish Sea ray fishing sector which has collapsed from its 1931 peak (ICES, 2014) with only a few Irish vessels currently taking the majority of the landings of thornback (*Raja clavata*), spotted, blonde and cuckoo ray (*R. naevus*) (Gerritsen, H., Marine Institute, pers. comm.).

## **1.2 Addressing management problems with spatial approaches**

Marine Protected Areas (MPAs) are often implemented to achieve conservation goals (Agardy, 2000; European Commission, 2008; Waitt Foundation, 2014), and have been demonstrated to be effective for elasmobranch species (Edgar et al., 2014). The ICES Working Group for Elasmobranch Fisheries (WGEF) recommends that such management interventions be implemented as effort restrictions or closures (spatial or seasonal), particularly to protect nursery and spawning grounds (ICES WGEF, 2012). Consultation with fishers has indicated that spatial management methods are considered to be the most effective approach (Fitzpatrick, M., pers. comm.; NWWRAC (2013)).

Whilst spatial management of skates and rays could be valuable (Ellis et al., 2008; Speed et al., 2010), its application is hampered by incomplete knowledge of specific ecologically important habitats (nursery and spawning areas) (Ellis et al., 2010).

Identifying such areas may help resolve the 'choke species' problem, whereby declines of certain species (especially cuckoo and blonde ray (NWWRAC, 2012b)) result in catch

limit restrictions being imposed on the entire species group. Protecting the most vulnerable species through spatial management of their nursery or spawning areas could allow catch limits for other species to be relaxed, such that most resilient species could be sustainably harvested.

Various modelling approaches can help identify the best areas to be protected with permanent/seasonal closures or technical measures such as minimum landing sizes. For example, the program Marxan (Ball and Possingham, 2003) finds the smallest areas required to meet its objective (e.g. protect nurseries) but performs badly with poor or absent data (Vincent et al., 2004) leading to over-large MPAs and avoidance of coasts (Loos, 2006) (where rays are often present). Maximum Entropy (MaxEnt) methods (Elith et al., 2011; Phillips et al., 2004) model species distributions from presence-only data, but cannot utilise abundance data, when available. Generalised Linear and Additive Models (GLMs & GAMs) are commonly used in a two-step procedure (e.g. De Raedemaeker et al. (2012) and references therein), first by modelling the presence/absence, then by modelling the presence-only abundance, and finally joining the two models (Guisan and Zimmermann, 2000; Martin et al., 2012).

Boosted Regression Trees (BRTs) could provide more robust predictions than GLMs and GAMs (Lo et al., 1992), with less variance (oversensitivity to noise leading to overfitting/imprecision) and bias (false assumptions in the algorithm leading to underfitting/inaccuracy), with a lower risk of misspecification and the ability to model complex interactions. In addition, BRTs are unaffected by multicollinearity, missing predictor values and outliers (see comparative evaluation in Abeare (2009)). They use machine learning to add increasingly small predictor-response relationships into one model to account for high proportions of variability despite complex multivariate relationships (Elith et al., 2008).

### 1.3 Ray habitat preferences and the study area

The four rays considered in this study have small distributional ranges (McEachran and Miyake, 1990; Stehmann and Bürkel, 1984). Juveniles remain nearly sedentary (Holden, 1975; Steven, 1936) but adults migrate inshore to feed, and also to mate and spawn in the spring/summer period (Steven, 1932; Walker et al., 1997). Such site-fidelities and habitat preferences make these rays species good candidates for spatial management (Hilborn et al., 2004; Kaiser et al., 2004).

Peak recreational angling landings for all species occur in certain small areas (Fahy and O'Reilly, 1990). Larger specimens have especially localized distributions (Fahy and O'Reilly, 1990), and find shelter in refuges that harbour high biodiversity (Shephard et al., 2012) and allow them to reach their maximum weight (Fahy, 1991; Ryland and Ajayi, 1984). Anglers often catch particularly large rays, partially because they fish where trawlers can't operate (Ryland and Ajayi, 1984). Commercial landings are highest off the Southeast coast of Ireland (Gallagher, 2000; Hillis and Grainger, 1990) and peak in August to December (Fahy, 1989; Gallagher, 2000).

## 2 Aims

We present a modelling approach for spatial management of data-poor stocks (cuckoo, thornback, blonde and spotted rays in the Irish Sea), using Boosted Regression Trees to map species abundances in relation to environmental correlates, and to identify ecologically important abundance hotspots. We then investigate how these models can be used to aid in MPA design. Finally, we assess the robustness of this approach by comparing our results with available data on.

## 3 Methods

### 3.1 Database selection and processing

The Irish Sea is a well-mixed shallow shelf sea that tapers to a deeper (100m) central channel, with very shallow ( $\leq 5\text{m}$ ) sandbanks running parallel to the coast that create 20-30m deep channels some 7-12km from shore (Connor et al., 2006; Vincent et al., 2004). Tidal bed stress is generally low to moderate except off a few particular headlands (Connor et al., 2006). The substrate is largely a sandy/gravel mix, generally coarser at depth, with rocks north west off Anglesey and a large mud bank running parallel to the south east coast of Northern Ireland, corresponding to locally lower bed stresses. Environmental data used in our analysis are described in Table 2.

Depth, substrate and temperature are known to correlate with elasmobranch abundance (Ellis et al., 2005a; Kaiser et al., 2004; Martin et al., 2012) but other potentially pertinent variables were also included in the analysis (the BRT modelling approach, described below, does not penalise for additional variables). QGIS mapping software (Quantum GIS Development Team, 2014) was used to interpolate environmental data points to a surface of Voronoi polygons, then to append their values to the highest resolution dataset (depth grids covering the whole Irish Sea ( $n = 391,568$ )). Distance to shore was calculated using raster proximity analysis. Substrate categories were converted from descriptive Folk classifications (Folk, 2013, 1954) to median grain size (SearchMESH, 2014), and inputted as a continuous factor to the model.

We downloaded catch per unit effort (CPUE, in numbers per hour) data for all rays caught in ICES area VIIa (Irish Sea) by standardised survey trawls (International Groundfish Survey and Bottom Trawl Survey) from 1993 to 2012 from the ICES Database of Trawl Surveys (ICES, 2012). To maximise the spatial coverage of the analysis, these data were averaged across all years. Cuckoo, thornback, blonde or spotted rays were present in 1645 of the 3341 half-hour trawls, the midpoints of which

were used as the map locations for those data. This generated 1447 site locations, many of which were closely located because the surveys aim to re-sample the same sites (see end of section 3.2).

Neither standard linear correlations nor GAMs showed clear strong relationships between any one month of temperature/salinity and CPUE, therefore only data collected in September were selected for each data source, as ICES trawls were predominantly conducted in September. Correlations between environmental variables were minimal ( $R^2 < 0.4$ ) and did not represent a problem for BRTs, which are robust towards autocorrelation between independent variables (Abeare, 2009).

**Table 1: Physical oceanographic datasets used during modelling, and their sources**

<b>Environmental Dataset</b>	<b>Spatial Resolution</b>	<b>Source</b>
Depth	275x455m grids	EMODnet (European Marine Observation and Data Network)(EMODnet, 2014)
Average Monthly sea bottom temperatures 2010-2012 (°C)	1185x1680m	Marine Institute, 2014 ( <a href="http://www.marine.ie/Home/site-area/data-services/data-services">http://www.marine.ie/Home/site-area/data-services/data-services</a> )
Average Monthly sea bottom salinities 2010-2012 (ppm)		
Maximum monthly 2 dimensional velocity ( $m.s^{-1}$ )		
Substrate (grain size in mm)	~250m minimum	British Geological Survey, 2011 (British Geological Survey, 2011)
Distance to shore (m)	275x435m grids	via European coastline layer (freely available)

### 3.2 Preliminary analyses

To determine if the ICES trawl survey stations sampled the full range of the environmental conditions in the Irish Sea, the distribution of environmental data collected from ICES sites was compared to the higher resolution environmental datasets.

The extremely low (<10m) and high (>50m) depths and hence also areas close to, and far (>15km) from shore are underrepresented in the trawl station data. No maximum

two-dimensional velocities above  $1.5 \text{ m}\cdot\text{s}^{-1}$  were recorded, reflecting that the few headlands known to feature high bed stress were not sampled.

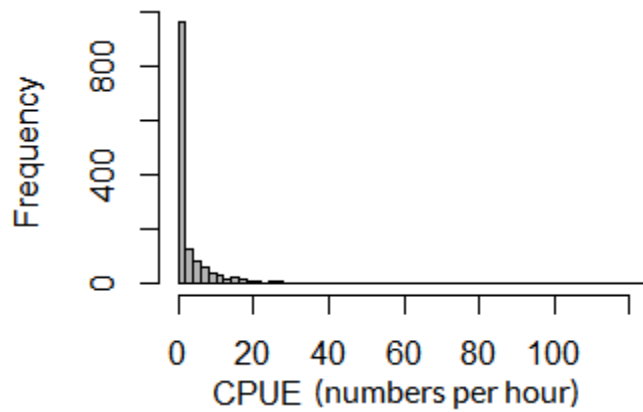
Kolmogorov-Smirnov tests on all variables showed that the environmental data from the trawls were not representative of the Irish Sea as a whole ( $p < 2.2 \times 10^{-16}$  for all variables). Variance tests showed that trawl survey variances were different to those from the full Irish Sea environmental dataset, with distance to shore and temperature being the most representative. These results are unsurprising given the restricted distribution of the survey stations, but were not considered to be problematic: areas in the Irish Sea poorly sampled by trawls can be readily identified, and conclusions drawn from such areas can be treated with less confidence (see histograms in supplementary material, Figure 22).

Care must be taken to ensure spatial data are not auto-correlated (Miller, 2012; Redfern et al., 2006). Analysis of the residuals of a GAM of CPUE as explained by latitude and longitude showed a normal error distribution (using 'mgcv' package (see packages section in references) in R (R Core Team, 2013)). A Mantel test ('vegan' package) on the same data showed that the model had sufficiently accounted for spatial autocorrelation in the raw data, and that the residuals were not auto-correlated (Mantel correlation 0.078,  $p=0.001$ ).

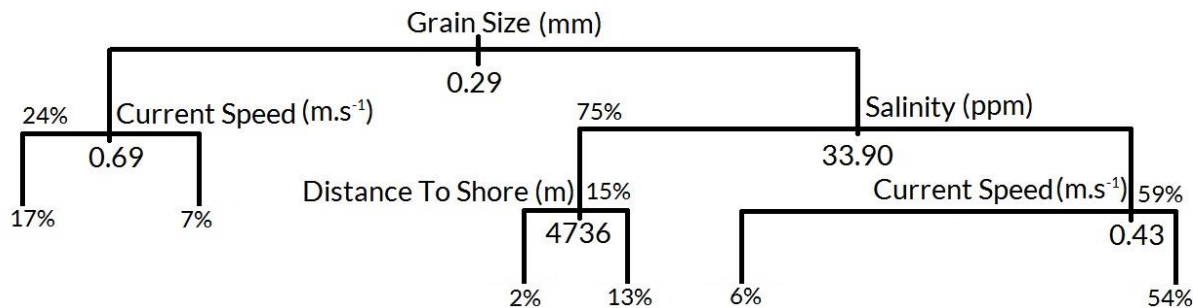
### 3.3 Modelling approach

Boosted Regression Trees were used to identify the combination of environmental variables that best described the observed variation in distribution and abundance of the rays, and to predict their abundances across the Irish Sea, using a custom written R function 'gbm.auto' (see Supplementary Information) which uses R packages 'gbm', 'dismo', and Elith *et al.*'s (2008) functions 'calibration', 'roc' and 'gbm.predict.grids'. Data exploration indicated that the CPUE data were zero-inflated with a long tailed distribution (most trawls caught nothing, and very few caught many specimens (Figure 9)).





**Figure 1: Histogram of CPUE of all rays**



**Figure 2: First tree produced by the binomial BRT. Variables and their split values are in black, above (right branch) and below (left branch) which sub-branches are split, as calculated by the model to maximise predictive power. Percentages refer to total number of sites within that split.**

Hence, a two-step (delta) process was followed: modelling the probability of zero/non-zero catch (presence/absence) with binomial BRTs, separately modelling the non-zero catch (abundance) with Gaussian BRTs, then joining each model into one CPUE metric (per Lo et al. (1992)).

Tree-based models use a series of rules to partition the predictor space into regions with the most homogeneous responses to predictors, via binary splits at specific values for each variable (the split points, see Figure 10). Regression tree-based models then fit the mean response for observations in that region, assuming normally distributed errors. Boosting posits that averaging many rough predictors is easier than finding a highly

accurate one, and iteratively fits decision trees to the training data, progressively focusing on the remaining poorly modelled observations, which are the hardest to predict. The first BRT maximises the predictive performance (known as predictive deviance, a measure of the predictive power of a model); the second is fitted to the residuals of the first and the model updated with both trees (terms) before fitting the third to *its* residuals, and so on (all from Elith et al. (2008)). The relative contribution of any one explanatory variable ( $x_j$ ) is based on how often it is selected to split individual trees, weighted by the squared improvement to the model ( $I_j^2$ ) resulting from the sum of these trees (i.e. from  $m=1$  to  $M$  the total number of trees):

$$\hat{I}_j^2 = \frac{1}{M} \sum_{m=1}^M I_j^2 (Tm)$$

where  $I_j^2$  is the relative influence of input variable  $j$  for individual tree  $Tm$  (Friedman and Meulman, 2003; Harma, 2013) – see bar plots in Section 4.1.

Binomial BRTs on presence/absence data were performed for each species and all species together. To minimise predictive error we examined a combination of BRT fitting parameters: tree complexity and learning rate. Tree complexity, also known as interaction depth, fits a model with  $n$ -way interactions, i.e.  $n$  nodes on the trees. We examined tree complexities of  $n$  equals either two or five. Learning rate, also known as shrinkage parameter, determines the contribution of each tree to the growing model, with smaller contributions causing the BRT process to progress more gradually, generate more trees, and usually achieve greater accuracy. We examined learning rates of either 0.01 or 0.005. Another fitting parameter, bag fraction, controls for stochasticity within the model by specifying the proportion of data drawn at random, without replacement, from the full training set, to be used for each successive tree (Elith et al., 2008; Ridgeway, 2006) . Bag fraction was set at 0.5 as recommended by Elith et al. (2008). To find the combination of parameters resulting in the minimum predictive error, we tried different combinations of learning rate, in case the larger rate – which runs the BRT faster, producing less trees – resulted in a better or an equally well performing model

with more simplicity. Similarly, different tree complexities were assessed. An example of one (of the many) trees generated internally within BRT models is shown in Figure 10. The stochasticity introduced by the bag fraction, combined with the small learning rate, causes many hundreds or thousands of these trees to be generated, varying each time, with each contributing only a small amount to the final modelled relationship.

The best combination of tree complexity and learning rate was chosen for each species and the grouped data, based on the BRT model's correlation score between training data and testing data (with proportion of each defined by bag fraction). The effects of simplifying these models were then tested, as recommended by Elith *et al.* (2008), using 'gbm.simplify' from the 'dismo' package, which removes predictors one by one then tests if the model's training data correlation score improves without them, compared to the previous best model. Simplified models are discarded if they confer no improvement, which is often the case. The final BRT model was then used to predict the presence/absence probability (0 to 1) for each species at each environmental grid site across the Irish Sea, based on that site's environmental variables.

For the Gaussian BRT, the abundance data (Figure 9) were log transformed ( $\ln(\text{CPUE} + 1)$ ) as is typical for standardising catch and effort data that is characterised by long-tailed positive distributions (Froeschke and Drymon, 2013; Lo *et al.*, 1992; Punt *et al.*, 2000). The BRT process was then performed on them with the same parameters as above, except with a Gaussian distribution (Maunder and Punt, 2004; Punt *et al.*, 2000). To transform the data back to their original scale, they were log-reversed and also bias corrected using Duan's Smearing Estimator (Duan, 1983), resulting in a predicted abundance score for each presence-only value. Duan's Smearing Estimator estimates the expected value of the error distribution, which would otherwise be unknown and lead to inaccuracy if simply reversing the log using exponents. Resulting presence-only values were then multiplied by the presence/absence predictions from the previous stage to give a predicted CPUE per site that incorporates the probability of occurrence into the

predicted abundance (Cass-Calay and Schmidt, 2009; Froeschke and Froeschke, 2011; Lo et al., 1992). The final outputs are thus abundance probability maps per species for the whole Irish Sea, based on the environmental variables (see Figure 11 for conceptual diagram). In addition, abundance hotspots were generated from the 'all species' surface by displaying only predicted CPUE values above an arbitrary 50% of the highest predicted abundance. Finally these results were compared to existing and proposed MPAs, and to Irish ray landings data (Gerritsen, H., Marine Institute, Pers. Comm.), to investigate the ability of our approach to identify potential MPAs from the modelled abundance surfaces (Figure 14 and Figure 15).

## **4 Results**

The training data correlation scores were high for all tests (binomial/Gaussian: all: 0.79/0.76, cuckoo: 0.77/0.67, thornback: 0.72/0.72, blonde: 0.65/0.84, spotted: 0.82/0.83). These results indicate confidence in the outputs of the BRT analyses.

### **4.1 Influential Variables and Partial Dependence Plots**

Variable influence plots and plots of predictive deviance vs the three most influential environmental variables are shown for the 'all species' group and for blonde rays only (Figures 3 and 4); additional plots for all species are in the supplementary material (Figure 17 to Figure 21). Higher predictive deviance scores indicate the range of environmental conditions within which there is a relatively high probability of occurrence or a higher predicted abundance. For the 'all species' group (Figure 12), substrate was the most influential predictor of presence, with rays showing a weak-positive preference for grain sizes above 0.3mm (sand and coarser), and preferences for more saline, warmer waters with higher current speeds. When rays were present their abundances were equally explained by salinity and temperature, with higher predicted abundance in water above 34ppm and 15°C respectively.

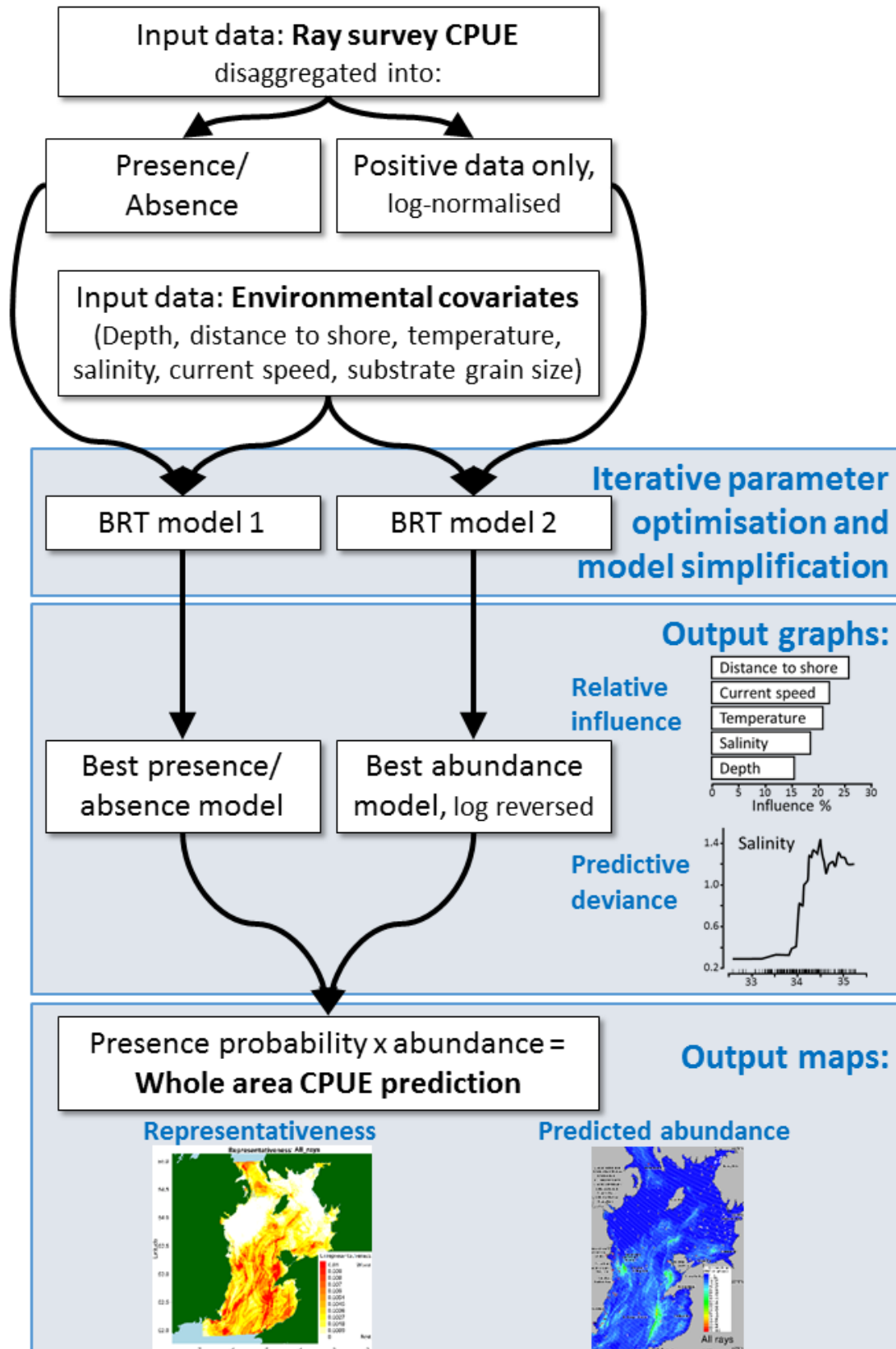
Cuckoo ray presence was best predicted by depth (especially >70m) and current speed (>1m/s), while its abundance was mostly affected by distance to shore (especially 17 to 30km) (supplementary information). Reportedly cuckoo ray are most common at depths of 70-100m (Wheeler, 1978; Whitehead et al., 1984), away from shore (Marine Institute, 2012), and prefer sand (Ellis et al., 2005a). Grain size was found not to be an important predictor of cuckoo ray presence or abundance, most likely reflecting that substrates in the Irish Sea are quite homogenous, largely comprising a sandy/gravel mix (Connor et al., 2006; Vincent et al., 2004).

Thornback presence related strongly to temperature (strong preference for warmer water) and salinity (peak at 34.5ppm), with abundance related principally to temperature, depth and salinity (supplementary information). Thornback rays are usually found 10 to 300m deep, with adults usually 16 to 24 km offshore (Fahy and O'Reilly, 1990; Stehmann and Bürkel, 1984) and juveniles inshore (Ellis et al., 2005a). All prefer gravel and pebbles, intermediate to strong two-dimensional velocities (Martin et al., 2012), and usually occur on sandbanks extending from adjacent shallows rather than more dynamic distinct banks, especially for juveniles (Kaiser et al., 2004).

Both the presence and abundance of Blonde rays (Figure 13) were explained by distance to shore (slight preference for >40km, peak abundance at 22km), depth (aversion to depths between 40 and 100m) and current speed (preference for higher). The species' reported preference for calm coastal shallows was not detected, however, predicted distributions were consistent with previous reports of their occurrence offshore on distinct sandbanks (Kaiser et al., 2004; Martin et al., 2012).

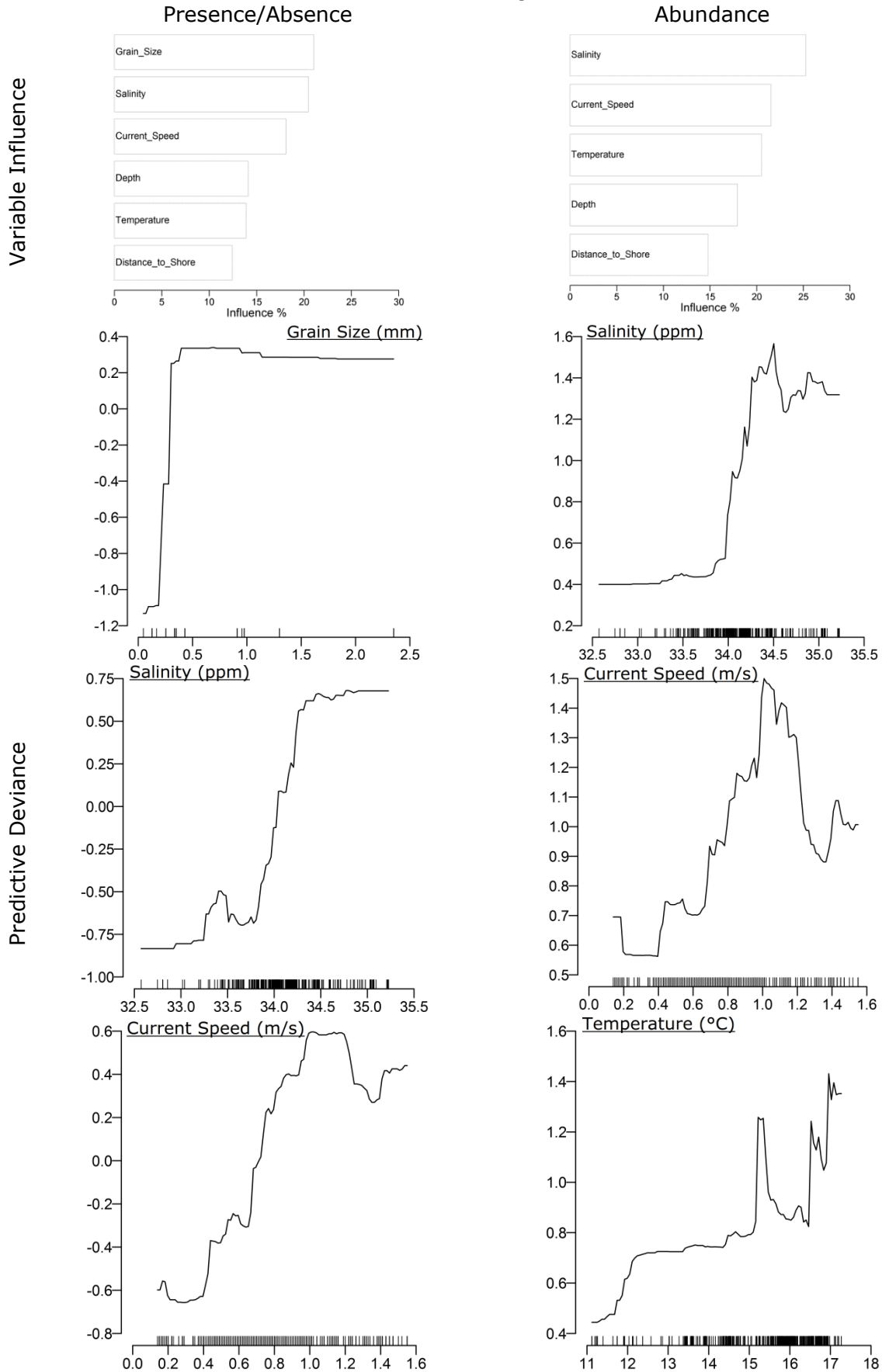
Spotted ray presence and abundance were predicted by salinity (strong preference for >34.3ppm), current speed (gentle peak around 1m/s) and distance to shore (peak around 25km), (Figure 17 to Figure 21). This concurs with published literature indicating that juvenile spotted rays are found further offshore (Southern Irish Sea

and St. George's Channel) than other young rays, whereas adults are commonly found 30 to 150m deep, preferring sandy substrates (Ellis et al., 2005a; Fahy and O'Reilly, 1990; Martin et al., 2012).



**Figure 3: Conceptual diagram summarising the Boosted Regression Tree (BRT) modelling approach used to spatially represent ray abundance**

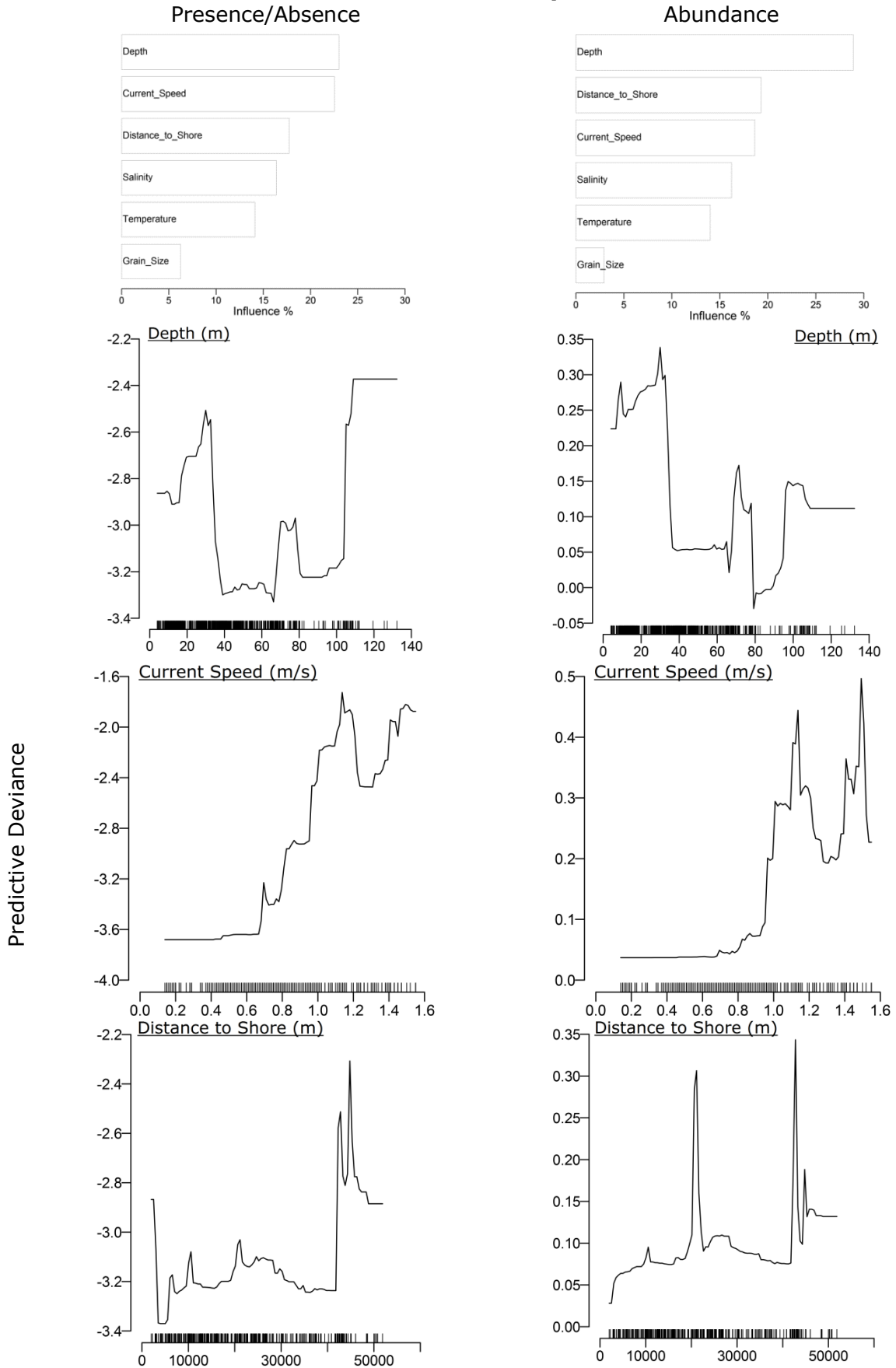
## All Rays



**Figure 4: Relative influence (%) of environmental variables on all ray BRT outputs, and BRT partial dependence plots showing relationships of environmental variables to ray presence/abundance. Tick marks indicate the distribution of the predictors.**



## Blonde Ray



**Figure 5: Relative influence (%) of environmental variables on blonde ray BRT outputs, and BRT partial dependence plots showing relationships of environmental variables to ray presence/abundance. Tick marks indicate the distribution of the predictors.**

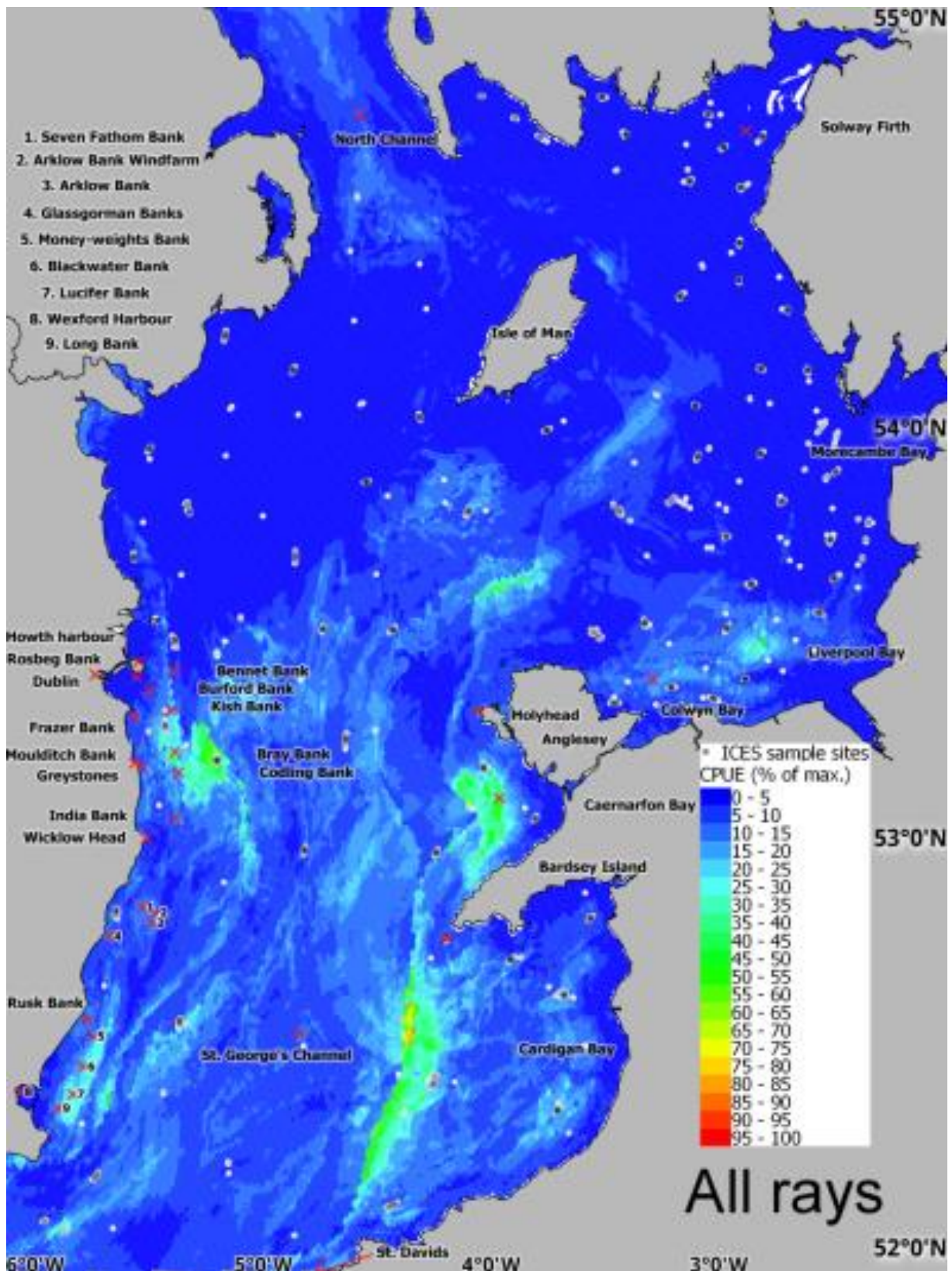


Figure 6: BRT predicted surface of 'all species' ray group, with ICES sampling stations (greyscale gradient indicates sampling frequency per site) and Irish Sea locations (red crosses). Colour gradient indicates sites' predicted ray abundance as a proportion of global maximum.

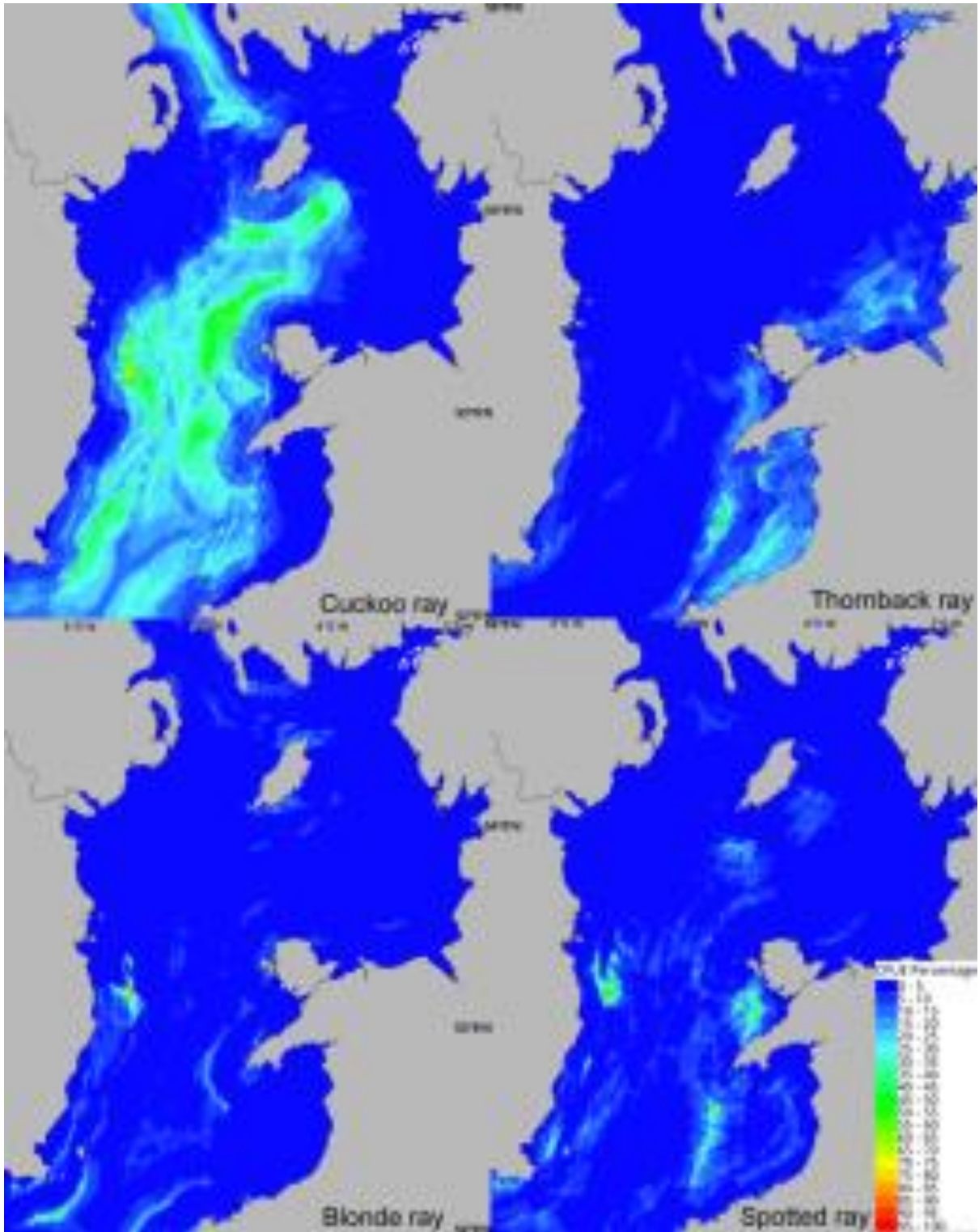


Figure 7: BRT predicted surfaces for cuckoo, thornback, blonde and spotted ray, with colour gradients as a proportion of each species' individual maximum CPUE.

## 4.2 Predicted surfaces

For all species combined, the model predicts low abundances in the *Nephrops* ground around Dublin which is characterised by muddy substrate, low current speed, and also in the shallow waters of the North East Irish Sea, from Solway Firth down to Morecambe Bay. Peak abundances are predicted within a band of water 30-50m deep outside of the Welsh bays running from Holyhead to Bardsey Island to St. Davids. Within the Irish regional sea limit, peaks are along the same depth band, arcing from Codling to Long Bank, around and inside the 20-30m deep channels created by the shallow ( $\leq 5\text{m}$ ) coastal-running central (Kish, Bray, Codling, India) and southern (Rusk, Money-weights, Blackwater, Lucifer, Long) Irish banks (Figure 5).

The predicted distribution of cuckoo rays (Figure 6) shows the strong influence of distance to shore and depth, with highest abundances occurring in the deeper ( $\sim 100\text{m}$ ) central St George's and North channels, and off the eastern Irish coast, as previously suggested (Fahy and O'Reilly, 1990). Higher abundance is also predicted for the Bray and Kish Banks.

Predicted thornback ray abundances (Figure 6) show a strong bias towards the shallow South-eastern bays (Liverpool, Colwyn, Caernarfon and especially Cardigan) where they are known to form local sub-populations spreading from such bays (Fitzmaurice et al., 2003). Predicted abundance is low in the north and the central channels, consistent with their reported near-shore preference (Fahy and O'Reilly, 1990; Stehmann and Bürkel, 1984), and their strong relationship with temperature (supplementary information). There was little rise in abundance around the distinct sandbanks north of Wicklow Head (Kaiser et al., 2004), but reportedly high abundances at Greystones (Fahy and O'Reilly, 1990) were not predicted.

Blonde ray predicted abundances show the underlying influence of distance to shore through the bands which track the coastline. Their preference for distinct sandbanks is

evident (Ellis et al., 2005a; Kaiser et al., 2004), with peaks over the Bray and Codling Banks, and low abundances in higher current speed areas with hard substrate such as off Anglesey. This matches the results of similar work from the English Channel (Martin et al., 2012).

High spotted ray abundances are predicted inside Caernarfon and outside Cardigan Bay, contributing to this pattern alongside thornback ray (Figure 14). Abundances otherwise suggest spotted ray are to be found across much of the Irish Sea, less so on the muddy *Nephrops* ground and along the shallow North-eastern coast. They prefer intermediary depths as expected (Ellis et al., 2005a; Fahy and O'Reilly, 1990), with a small patch of high abundance on the Kish / Bray / Codling Banks, and the southern banks.



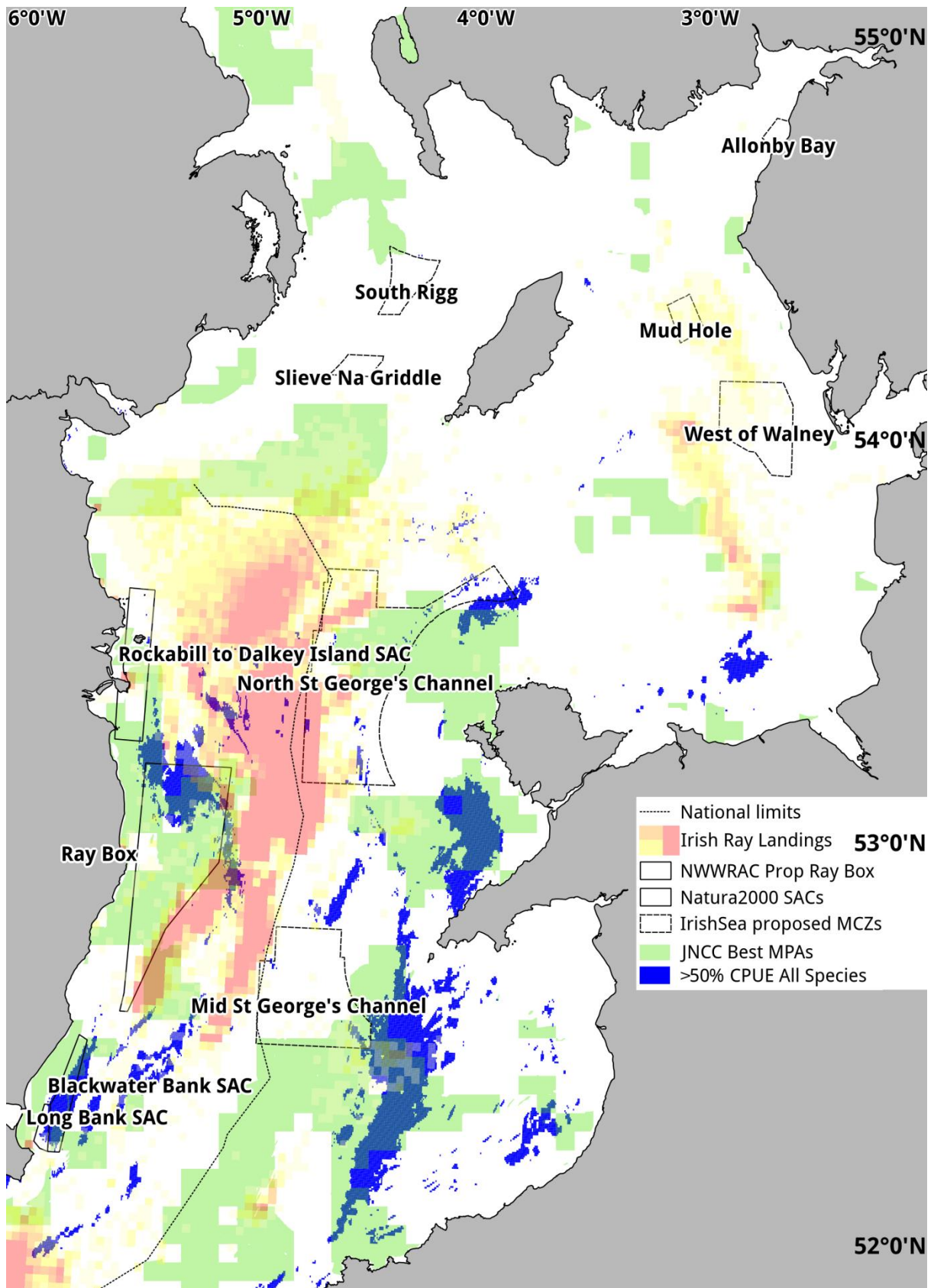


Figure 8: Predicted abundance hotspots for all ray species (group) above 50% of the maximum CPUE (blue) in the Irish Sea, overlaid with JNCC auto-computed best MPAs for various management goals (green), 2006-2012 annually-averaged Irish ray fisheries landings (red gradient), existing and proposed management areas (boxes) and the Irish/UK national limits (dotted line).

### 4.3 Spatial management areas

This study explores the viability of combining data for a group of species, and managing them by protecting the most vulnerable member (based on a productivity susceptibility analysis (McCully et al., 2013)). Abundance hotspots for all species (Figure 16, blue shading) consist of a few large patches and numerous smaller bands and independent areas. The large patches overlap most of the high abundance areas for blonde ray and the peak abundance areas for cuckoo ray, covering the extreme peak and offshore band in Cardigan Bay for thornback ray, and the patches edging Cardigan and Caernarfon Bay for spotted ray. The area off the Bray / Codling banks features high abundance for all species except thornback ray (Figure 15).

In the western Irish Sea, most of the northern hotspot and almost all of the southern overlaps with existing / proposed management areas (Figure 16, boxes, and green shading). The southern hotspot is subject to minimal ray fishing (Figure 16, yellow-red gradient), possibly as a consequence of their distance from Howth, the home port for most boats exploiting rays in the Irish Sea (Gallagher, 2000) as well as the protection provided by surrounding sandbanks . The northern hotspot is similarly protected on its western flank, but subject to increasingly intense fishing going eastward. High ray catches by the fleet co-occur only with hotspots at the patches extending north-east and south-east from the northern hotspot.

Elsewhere in the Irish Sea many hotspot areas don't overlap with conservation-designated areas, such as the hotspots in Liverpool Bay, much of Cardigan Bay, the thin hotspots in the channel and south west, and many of the small spots in the north.

## 5 Discussion

### 5.1 Overview

The delta log-normal BRT approach synthesises numerous input variables, weighs their relative importance to the dependant variable, and produces complex output predictions. This is especially valuable for data-poor species like blonde rays (ICES WGLIFE, 2012), for which we have generated high resolution predictions leading to spatial management advice for the whole Irish Sea from only 668 survey catches. The method produces maps of predicted species abundances as related to environmental correlates, requiring little post-processing in mapping software, and allowing easy comparisons with existing spatial management zones. Areas of ecological importance are clear (Figure 14), and abundance hotspots can be easily produced based on managerial threshold choices e.g. CPUE (Figure 16). The method effectively discriminates the influence of environmental variables on the abundance of these rays (Figure 12 and Figure 13). These outputs underpin the predicted surfaces but are themselves important results for improving our understanding of the habitat preferences of these species.

The unrepresentativeness of surveyed environmental variable ranges noted in some areas does not undermine the general conclusions of the study, but highlights the need for caution when drawing conclusions from the least represented areas, i.e. extreme shallows and depths, very near and 25-40km from shore, and areas with fast current. Several poorly sampled shallow, near-shore, and fast current areas are likely to be co-located. They may also act as *de facto* refugia (Shephard et al., 2012), being neither sampled by the survey nor fished by the fleet. In future studies, information on the abundance of rays in these areas could potentially be obtained from angling record data while accounting for the limitations of using fisheries dependent data to derive estimates of abundance through appropriate standardisation methods (e.g. Maunder and Punt (2004)).



The survey was not specifically designed for the purposes of this study, but to provide age-based stock abundance information for other commercial fish species to support analytical assessments. However, it remains the only substantial source of distribution data for our study species. It was necessary to average both the biological and environmental data across all the study years. Therefore, interannual changes in species distributions in response to environmental or fishery related changes are not captured in the analysis and the predicted distributions represent averaged conditions rather than the current situation. While environmental variability in some datasets (depth, distance to shore, substrate) is minimal, other environmental parameters (temperature, salinity, current speed) may be more variable, and hence more likely to exert temporal changes in distributions. Revision of derived maps that incorporate updated data is therefore advised when using this method to inform spatial management.

Many of the relationships between species abundance and environmental variables that are described by the model agree with those previously reported (especially for cuckoo ray and spotted ray). This provides some indirect validation of the ability of the model to accurately predict the distribution and abundance of those species. It also indicates that the habitat preferences of the species in question are generally consistent across study areas. However, the habitat preferences of blonde ray appear to show variation between study areas, highlighting the influence of local environmental variability on abundance distributions and the dangers of extrapolating from one geographic area to another (Kaiser et al., 2004; Martin et al., 2012).

Fishing activity is likely to influence the distribution and abundance of rays, and could lead to lower abundance in habitats that are otherwise favourable. Similarly, areas of low fishing activity act as *de facto* refugia. Fishing activity is likely to coincide with certain habitat features. Fishing pressure was not considered as an explanatory variable in this analysis, so it should be borne in mind that apparent relationships between abundance and environmental variables (such as substrate type) may actually reflect a correlation with fishing patterns. The survey mostly recorded moderately low abundances of rays in

the general areas of high fishing landings, suggesting that low abundances *could* be associated with commercial fishing, however the small discrete areas where maximum landings were reported by the fishery were not surveyed, so it is not possible to confirm this. In order to disentangle species specific habitat requirements from the effects of fishing on abundance, fishing effort could be included as a variable in the model. While this was beyond the scope of the current study, it warrants further research. In its current form, the model is useful for predicting where areas of high ray abundance occur, but does not provide insight into whether this is driven by habitat characteristics or the absence of fishing.

## 5.2 Spatial overlap of protected areas

The most vulnerable species (Figure 15, blonde ray) and the species with the most precautionary ICES catch advice (cuckoo ray) would both be protected by the closure of abundance hotspots identified here (Figure 16), suggesting that this method can be used to manage groups of differentially vulnerable, data-poor species. Alternatively, protecting hotspots generated by abundance probability maps for blonde or cuckoo ray (Figure 4) would also protect some of the less vulnerable members of the group.

The BRT abundance hotspots closely align with a number of areas previously recommended for protection. The UK's Joint Nature Conservancy Council's (JNCC) Marxan analysis of 19 environmental, biological, and anthropogenic datasets resulted in a map of the minimum protected area recommended to meet conservation targets for nationally-important marine wildlife (green shading in Figure 16. (Vincent et al., 2004)), particularly in terms of biodiversity and fisheries objectives. These areas generally overlap with all the BRT abundance hotspots. The southern hotspot overlaps the Blackwater Bank SAC (Special Area of Conservation) which protects a polychaete and amphipod species complex that is a rich food source for rays (especially juveniles) (Ajayi, 1982; Farias et al., 2006). Furthermore, it is enclosed by sandbanks and is not impacted by trawling (Marine Institute, 2013), suggesting that this is an attractive *de facto* refuge (Shephard et al., 2012). The northern hotspot is mostly covered by the

North Western Waters Regional Advisory Council's (NWWRAC) proposed temporary closed area ("ray box") and has been identified as an important nursery and spawning ground by the fishing industry (NWWRAC, 2013). The agreement between the abundance hotspots and previous expert advice further reinforces the potential viability of the BRT method as a tool to generate MPA candidates. It also highlights that protected areas chosen based on the abundance of key indicator species can have broad and persistent benefits for many species (Babcock et al., 2010; Barrett et al., 2007). Designing MPAs around specific 'concern' species is a recognised method for managing multi-species fisheries (Hilborn et al., 2004; Myers and Worm, 2005; Stelzenmüller et al., 2013), thus basing MPAs on the hotspots known to protect the most vulnerable species in this group could be an highly effective conservation strategy.

The high-resolution spatial variability in predicted abundances (Figure 14 and Figure 15) reveals the complex interplay of underlying environmental variables, resulting in a few large hotspot areas, and many small fragments (blue shading, Figure 16). While these hotspots can be readily converted into seemingly viable MPA candidates, other considerations often dictate designation of MPAs. Hotspot areas identified via the delta-BRT approach may be suboptimal MPAs for several reasons: planning and enforcing many smaller areas requires more work and cost than does a few larger areas, and non-compliance by the fishing sector is easier and more likely, hence making policing harder and costlier (Agardy et al., 2011). The fragment MPAs may be smaller than the thresholds required by species for persistence, abundance or occupancy of an area (Rhodes et al., 2008), or their home ranges (Agardy et al., 2011). While networks of small sanctuaries may maximize recruitment of fish into surrounding areas (GESAMP, 1996), this is more true for broadcast spawners (Halpern and Warner, 2003; Shanks et al., 2003) than sedentary species like the rays considered here (Kaiser et al., 2004; McEachran and Miyake, 1990), however small MPAs may be effective in protecting such species (Buxton et al., 2006), if consideration of their migratory behaviours is beneficial to MPA planning (Sale et al., 2005).

Conservation plans should begin with a clearly defined aim (Kelleher, 1999), and balance the conservation benefit of candidate areas versus their maintenance cost, in order to identify the optimal MPA (Klein et al., 2013). For example, if the abundance hotspot map was intended to focus on nursery areas, counts of adult females could be heavily weighted to tailor the BRT analysis towards them. An ideal MPA consists of a highly protected core area surrounded by a buffer zone (Kelleher, 1999), but reserve selection algorithms such as Marxan can help select the optimal size and number of MPAs to balance area closures against negative social impacts (Ball and Possingham, 2003; Harborne, 2009). In reality, an MPA's conservation objective is more likely to be the protection of the whole ecosystem or a significant species group rather than a single species (Kelleher, 1999; Stelzenmüller et al., 2013), although protecting notable species or nursery/spawning areas may be a key priority (Halpern and Warner, 2003; Kelleher, 1999).

The proposed method should be considered as a valuable tool for MPA selection, and could be especially useful if tailored to specific subsets of species data, e.g. to protect spawning grounds by focusing on mature females. Pairing the output of this method with information regarding home range size (Buxton et al., 2006), thresholds of minimum viable habitat size (Kelleher, 1999; Rhodes et al., 2008), migration patterns (Buxton et al., 2006; Hilborn et al., 2004), spawning substrate preferences (Lindholm et al., 2001), and water movement patterns (for broadcast spawners) (Shanks et al., 2003) could offer a powerful tool for conservation. Selection of a threshold CPUE percentage should be driven by the underlying biology of the species, such as  $F_{MSY}$  (Zhou et al., 2012). Any such measures could be incorporated into a management strategy evaluation that considers the ramifications of area closures on the future of the stocks, and weighs these against the impact on the fishery, e.g. Wiegand et al. (2011).

### 5.3 Further work

Fishermen's knowledge of their targeted stocks' habitat preferences is difficult to incorporate into traditional fisheries stock assessments (Johannes, 2003; Soto, 2006) but could be highly valuable (Hind, 2012; Johannes et al., 2000). Developing a qualitative interface to the statistical model (for example through use of hand-drawn maps and social scoring metrics) would enable delta log-normal BRTs to generate predicted abundance surfaces from fishermen's knowledge.

The addition of survey data covering the most heavily fished areas would improve the representativeness of the outcomes for high CPUE areas, and thus increase confidence in the results in general. Including fishing pressure would strengthen the model further, addressing the key limitation of this study as it stands, and allowing the full potential of the method to be realised.

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## **7 Author contributions**

Conceived and designed analyses: SD RO DGR MJC DB. Performed analyses: SD. Wrote paper: SD RO DB MC DR.

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## 8.1 R functions and packages used

calibration, roc, and gbm.predict.grids: from Elith et al. (2008) appendix, built upon Friedman's work (Friedman, 2001).

gbm: Ridgeway, G. 2013. gbm: Generalised Boosted Regression Models. R package version: 2.1. <http://cran.r-project.org/package=gbm>

dismo: Hijmans, R.L., Phillips, S., Leathwick, J. and Elith, J. 2103. dismo: Functions for species distribution modelling, that is, predicting entire geographic distributions from occurrences at a number of sites. R package version: 0.9-3. <http://cran.r-project.org/package=dismo>

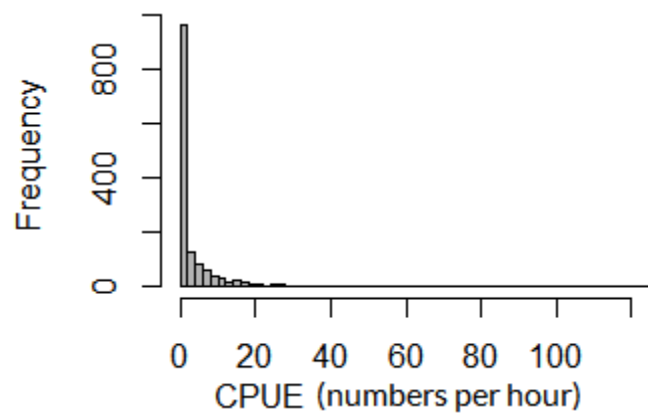
mgcv: Wood, S.N. 2011. MgcV: Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society (B) 73(1):3-36. <http://CRAN.R-project.org/package=mgcv>

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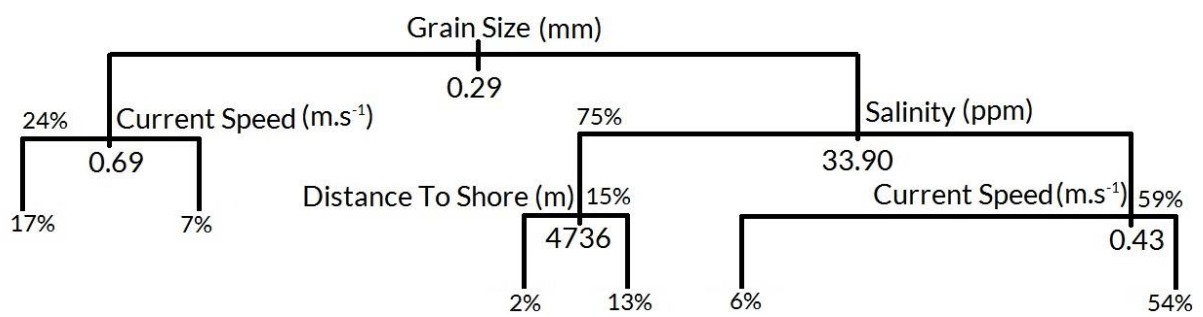
## 9 Figures (see Supplementary Material for full resolution versions)

**Table 2: Physical oceanographic datasets used during modelling, and their sources**

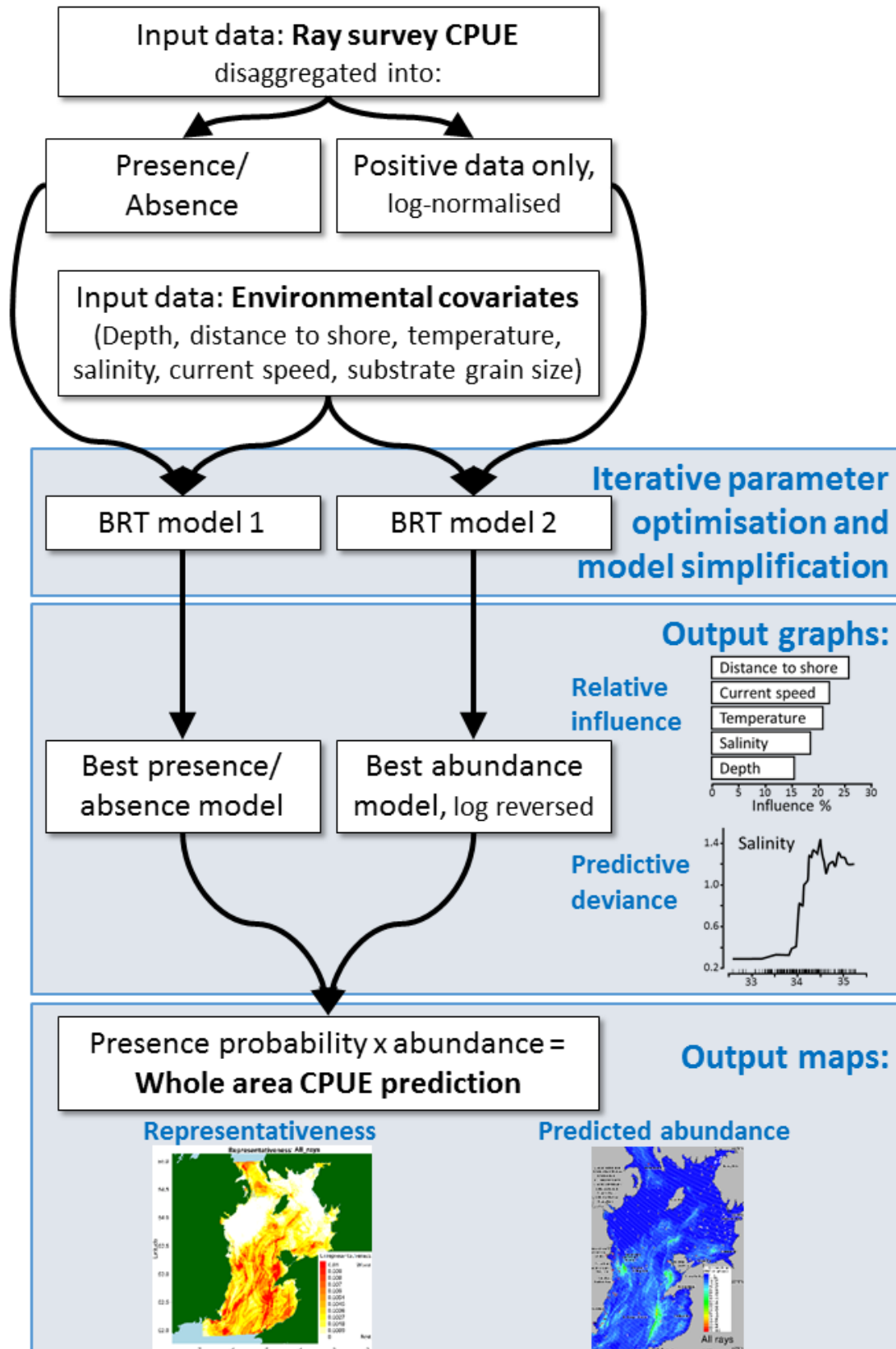
<b>Environmental Dataset</b>	<b>Spatial Resolution</b>	<b>Source</b>
Depth	275x455m grids	EMODnet (European Marine Observation and Data Network)(EMODnet, 2014)
Average Monthly sea bottom temperatures 2010-2012 (°C)	1185x1680m	Marine Institute, 2014 ( <a href="http://www.marine.ie/Home/site-area/data-services/data-services">http://www.marine.ie/Home/site-area/data-services/data-services</a> )
Average Monthly sea bottom salinities 2010-2012 (ppm)		
Maximum monthly 2 dimensional velocity (m.s <sup>-1</sup> )		
Substrate (grain size in mm)	~250m minimum	British Geological Survey, 2011 (British Geological Survey, 2011)
Distance to shore (m)	275x435m grids	via European coastline layer (freely available)



**Figure 9: Histogram of CPUE of all rays**

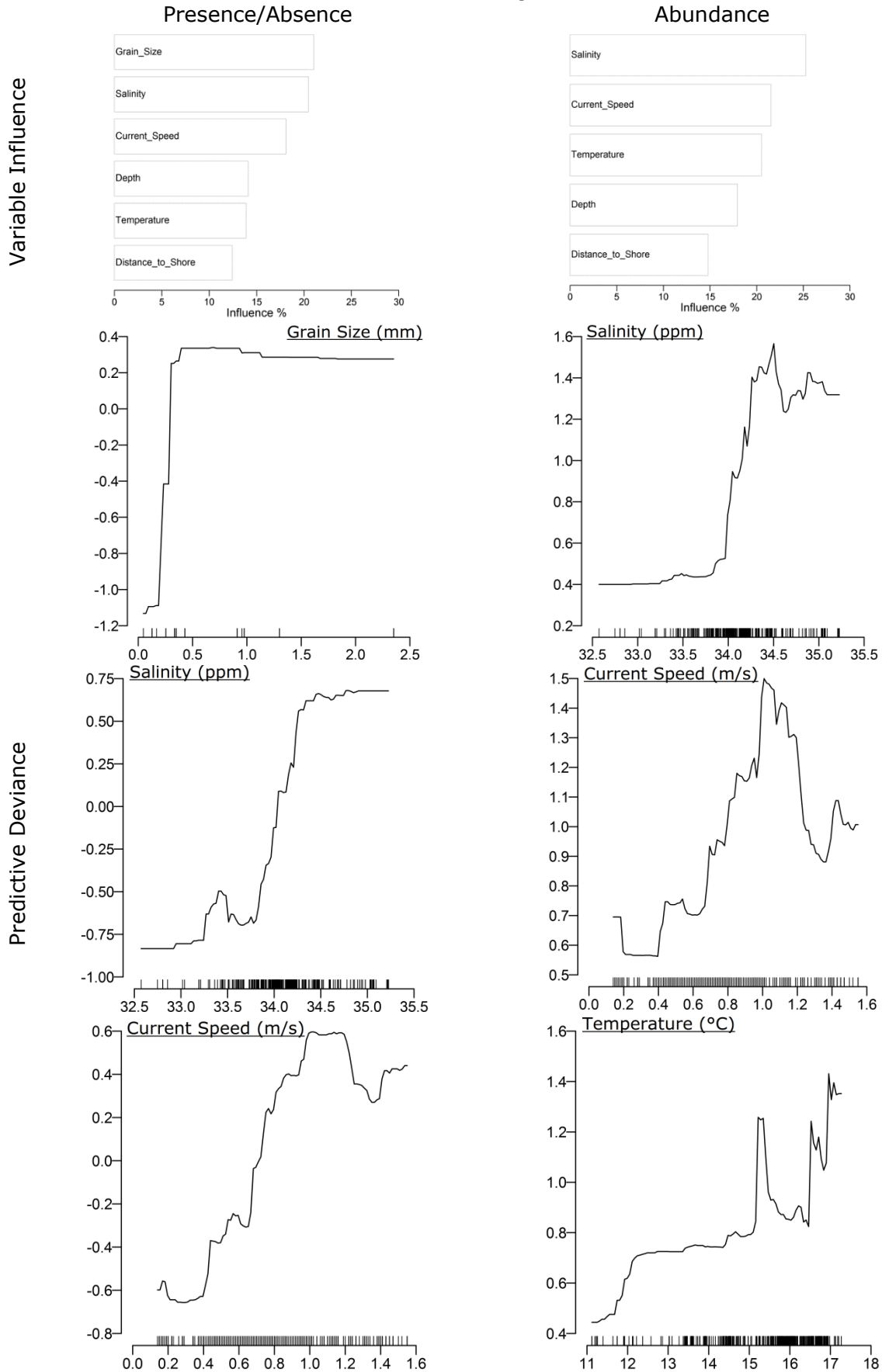


**Figure 10: First tree produced by the binomial BRT. Variables and their split values are in black, above (right branch) and below (left branch) which sub-branches are split, as calculated by the model to maximise predictive power. Percentages refer to total number of sites within that split.**



**Figure 11: Conceptual diagram summarising the Boosted Regression Tree (BRT) modelling approach used to spatially represent ray abundance**

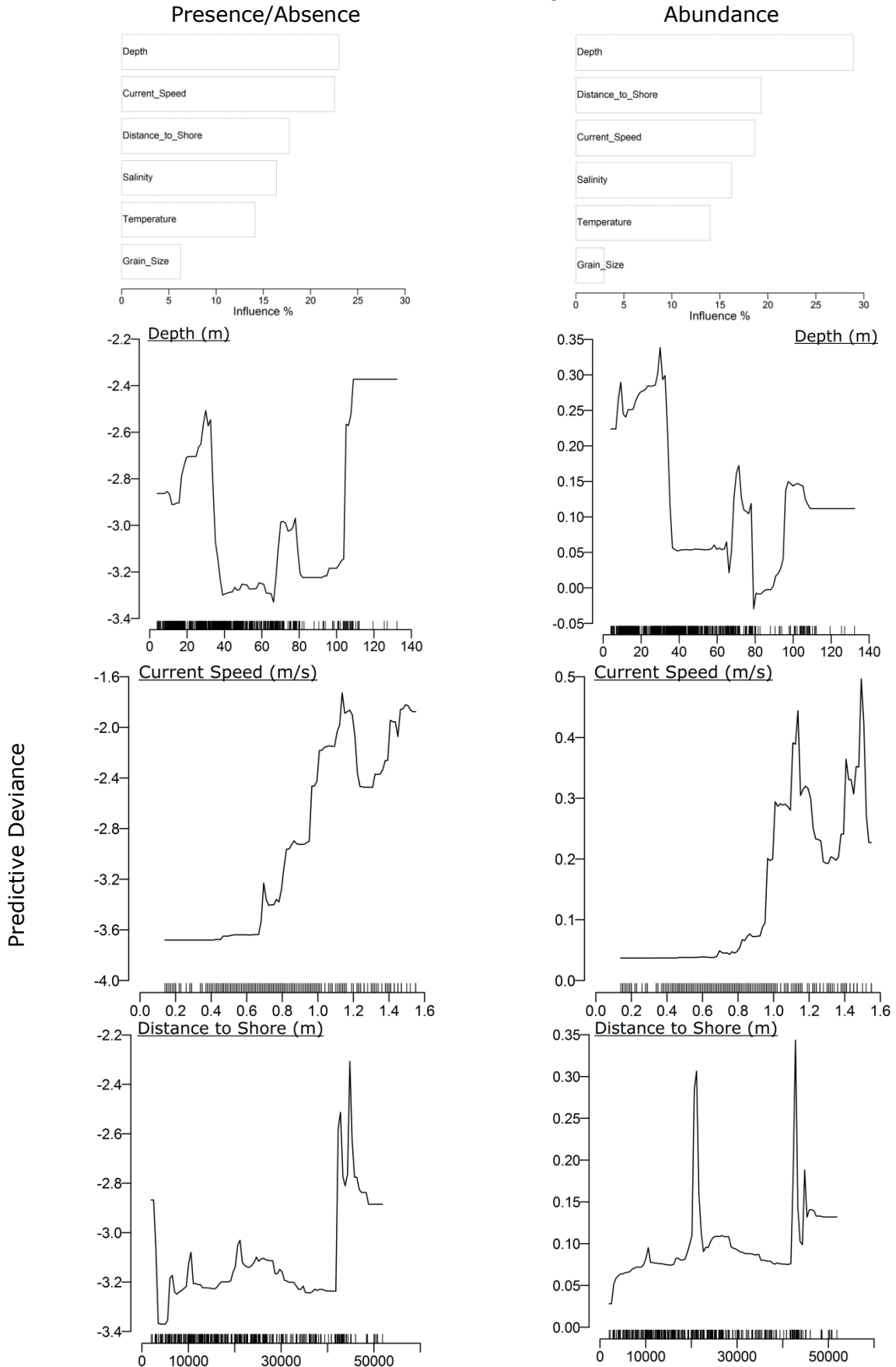
## All Rays



**Figure 12: Relative influence (%) of environmental variables on all ray BRT outputs, and BRT partial dependence plots showing relationships of environmental variables to ray presence/abundance. Tick marks indicate the distribution of the predictors.**



## Blonde Ray



**Figure 13: Relative influence (%) of environmental variables on blonde ray BRT outputs, and BRT partial dependence plots showing relationships of environmental variables to ray presence/abundance. Tick marks indicate the distribution of the predictors.**

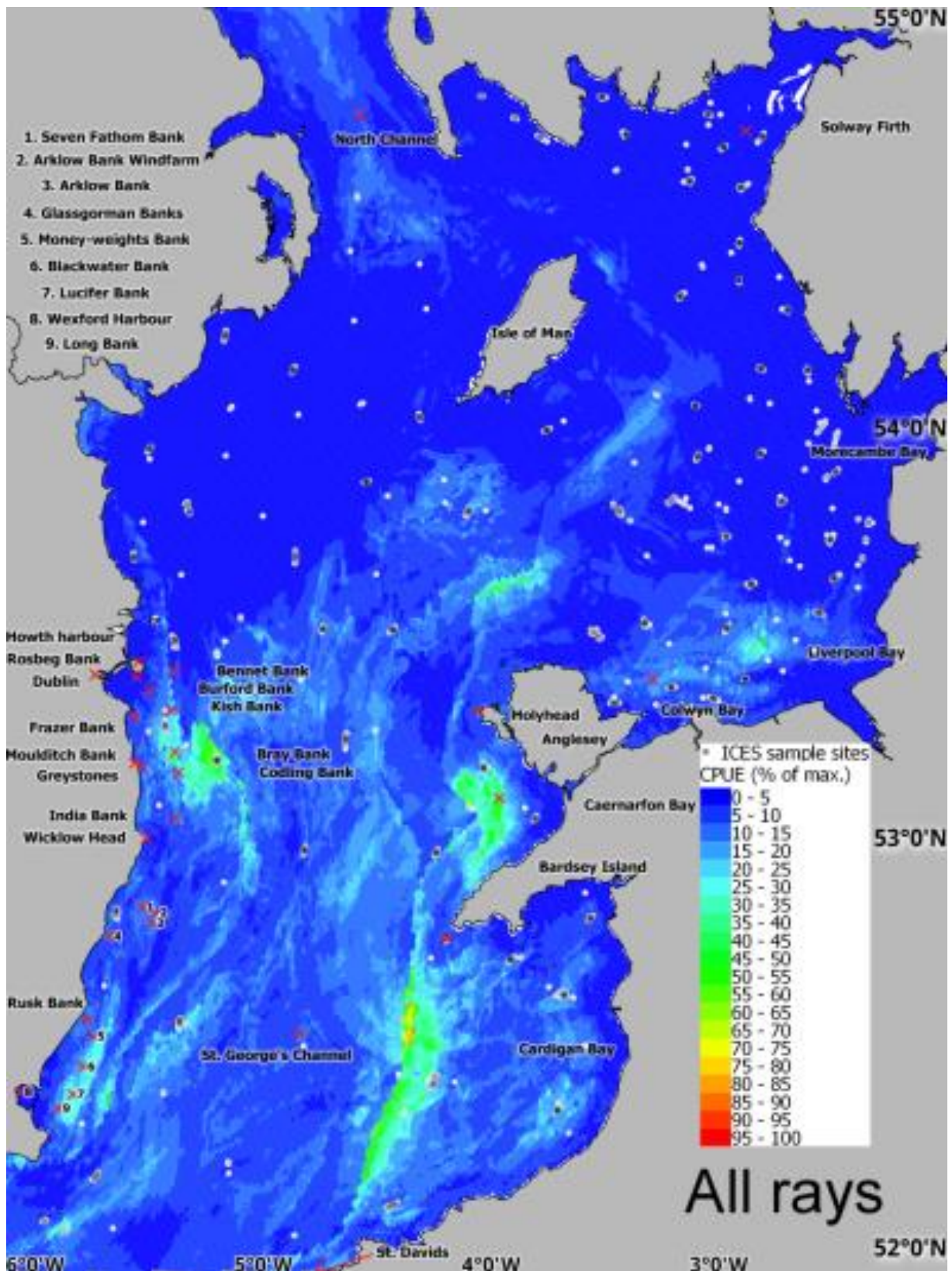


Figure 14: BRT predicted surface of 'all species' ray group, with ICES sampling stations (greyscale gradient indicates sampling frequency per site) and Irish Sea locations (red crosses). Colour gradient indicates sites' predicted ray abundance as a proportion of global maximum.

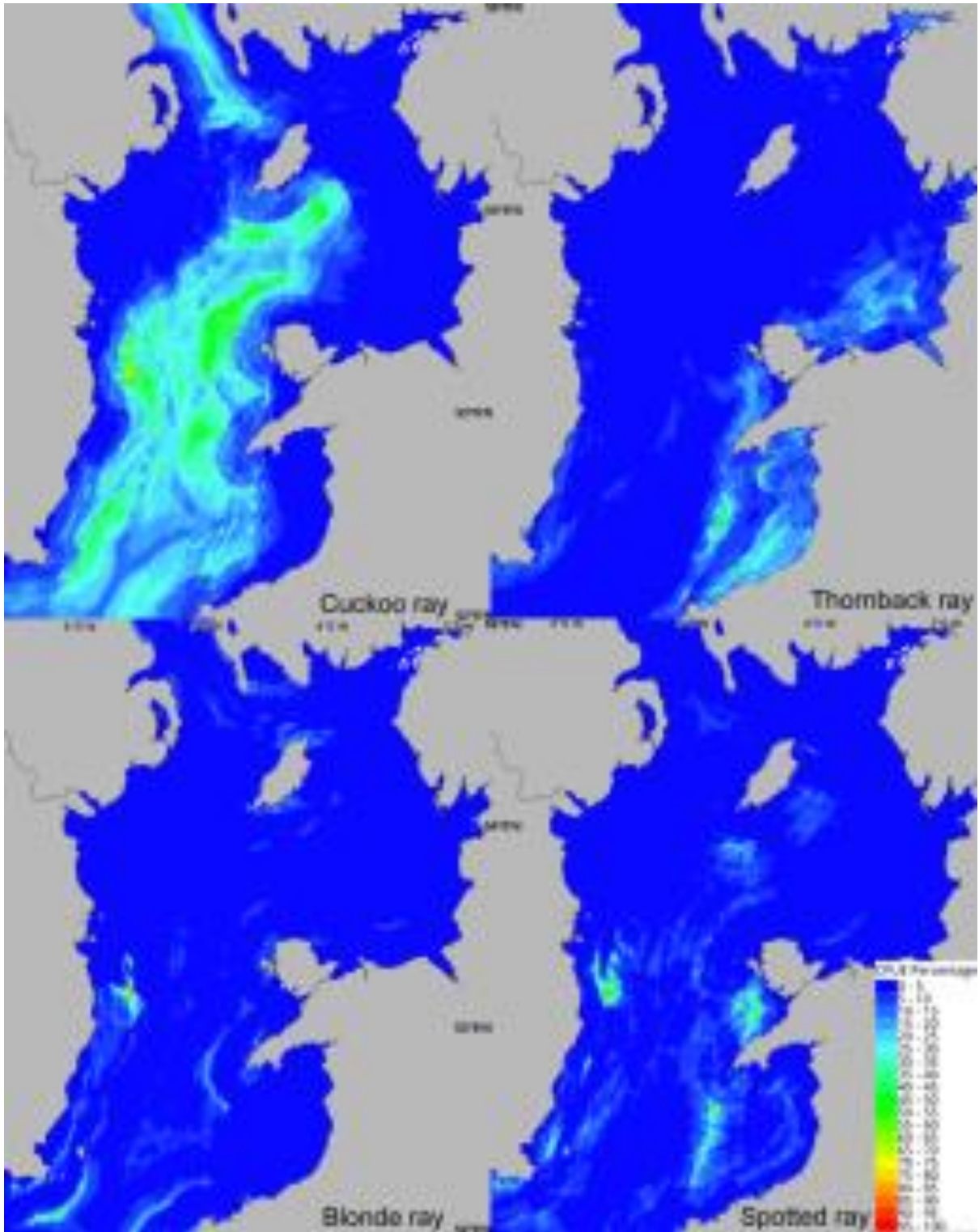


Figure 15: BRT predicted surfaces for cuckoo, thornback, blonde and spotted ray, with colour gradients as a proportion of each species' individual maximum CPUE.



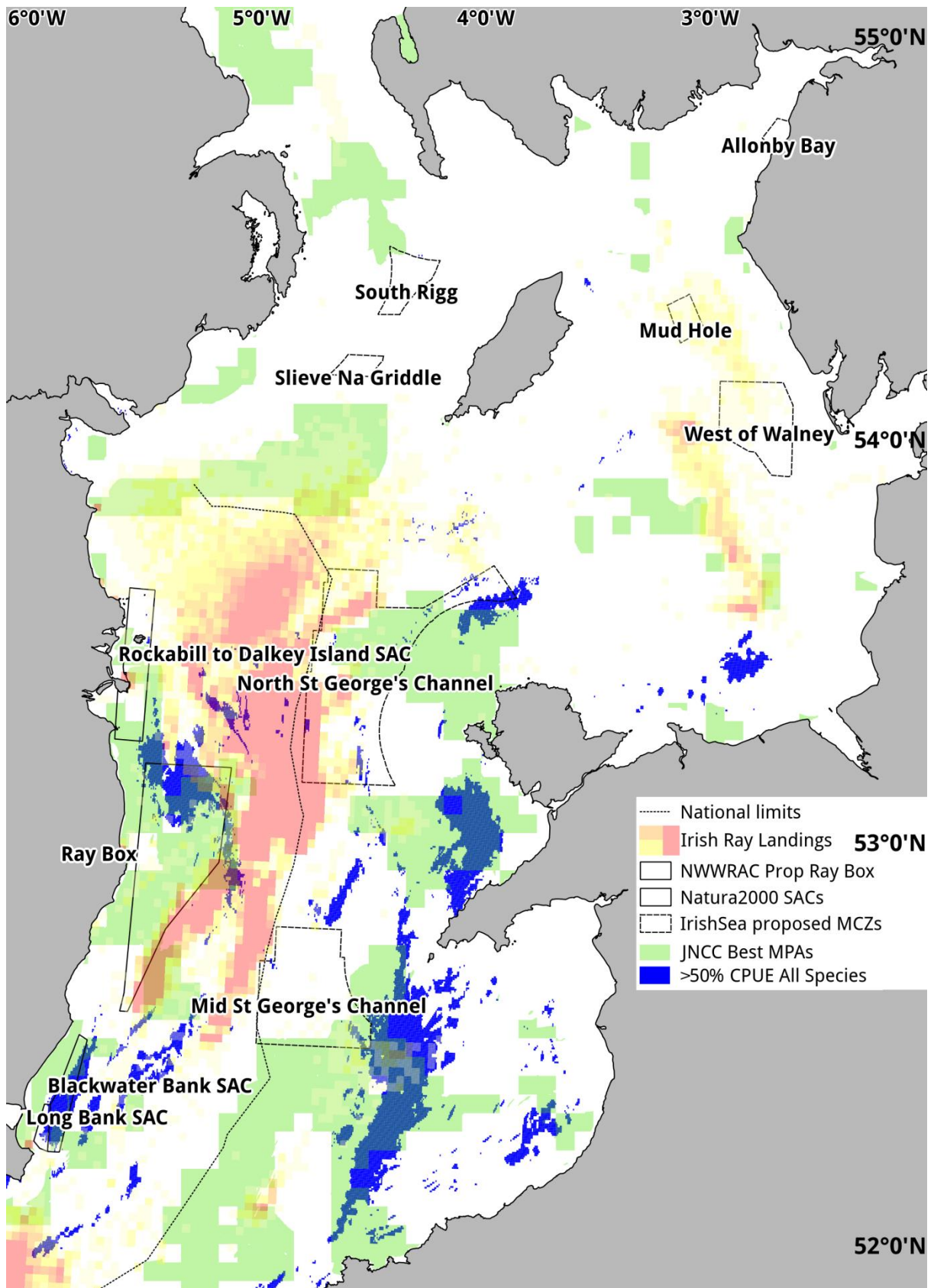
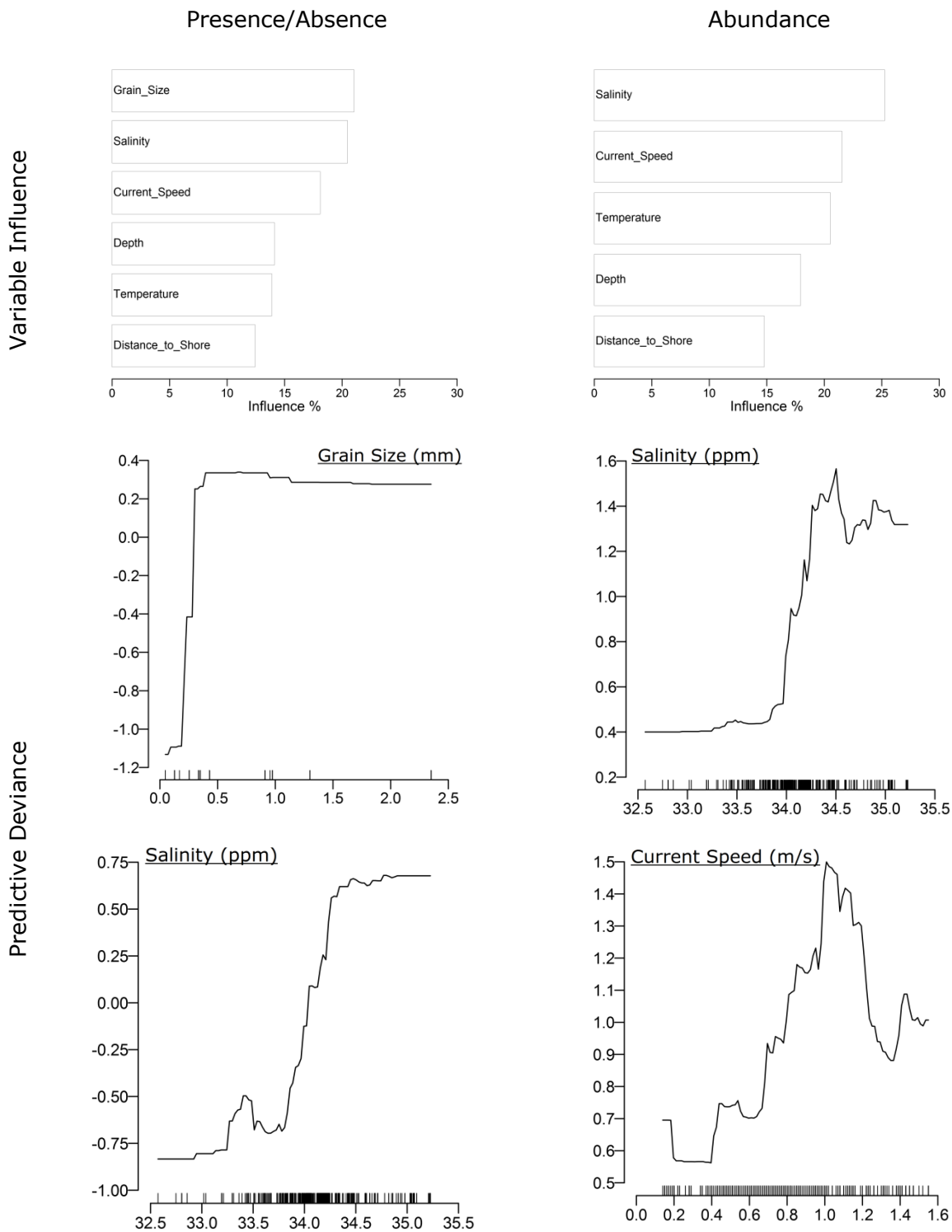
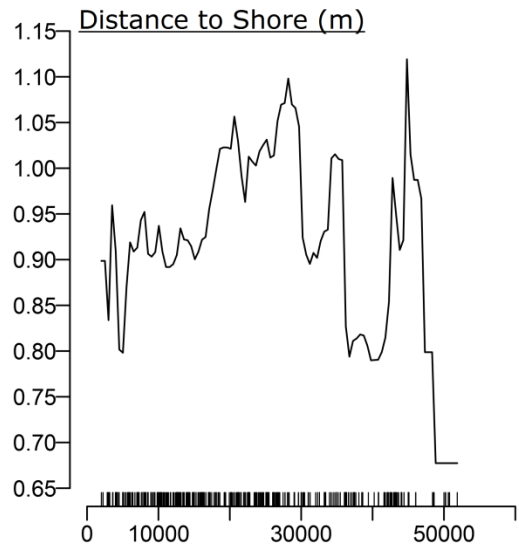
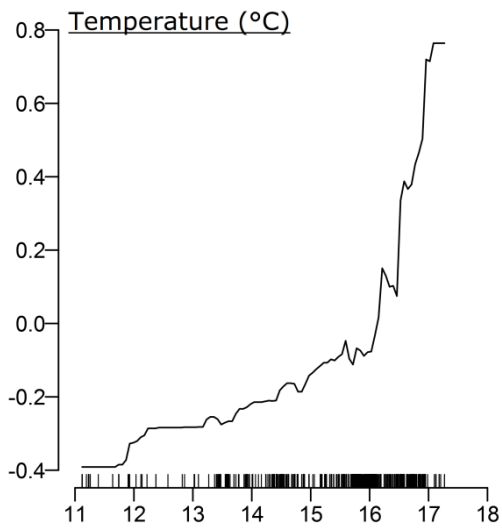
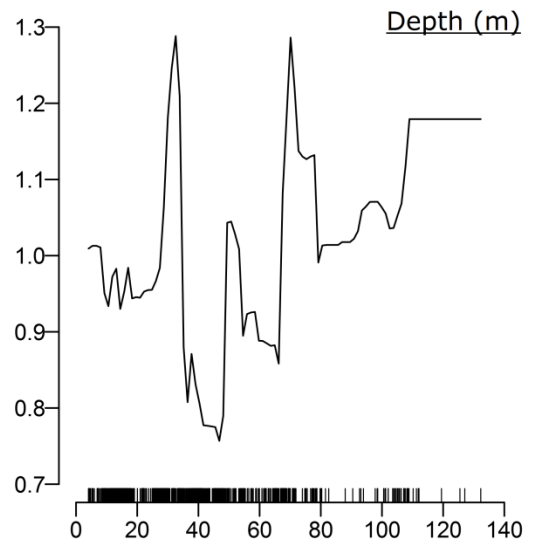
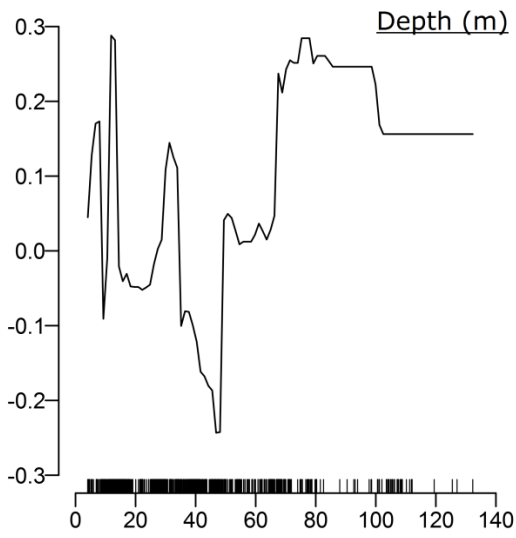
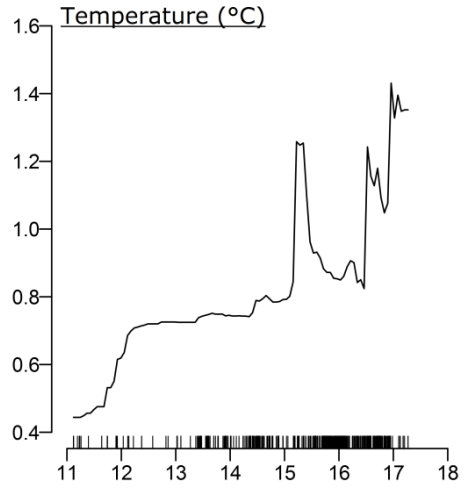
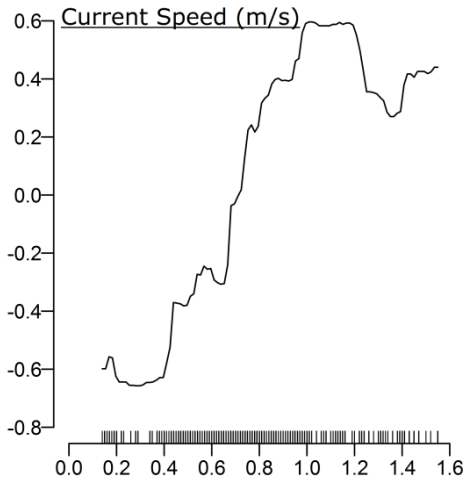


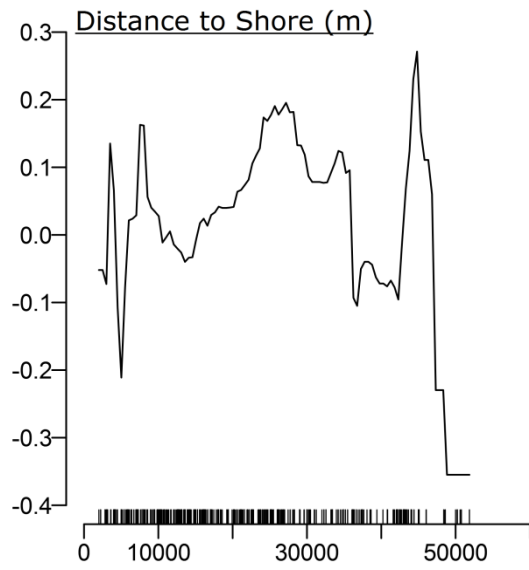
Figure 16: Predicted abundance hotspots for all ray species (group) above 50% of the maximum CPUE (blue) in the Irish Sea, overlaid with JNCC auto-computed best MPAs for various management goals (green), 2006-2012 annually-averaged Irish ray fisheries landings (red gradient), existing and proposed management areas (boxes) and the Irish/UK national limits (dotted line).

# 10 Supplementary Figures (see separate document for full resolution versions)

## All Rays







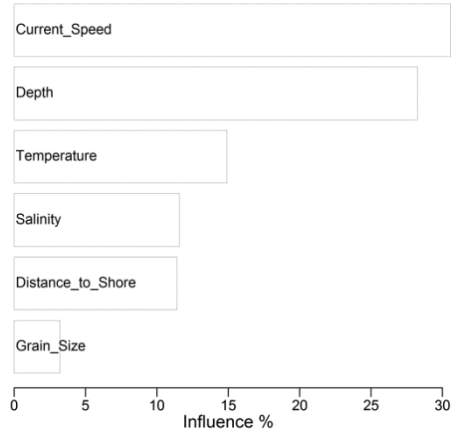
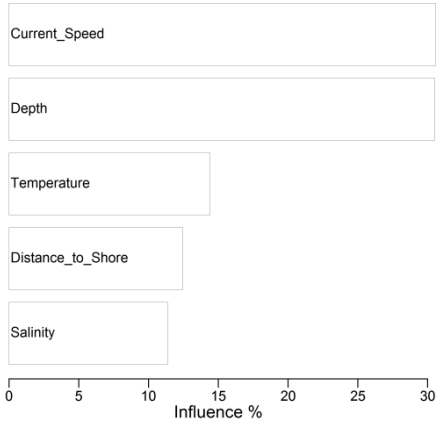
**Figure 17: Relative influence (%) of environmental variables on all ray BRT outputs, and BRT partial dependence plots showing relationships of environmental variables to ray presence/abundance. Tick marks indicate deciles of the distribution of the predictors.**

# Cuckoo Ray

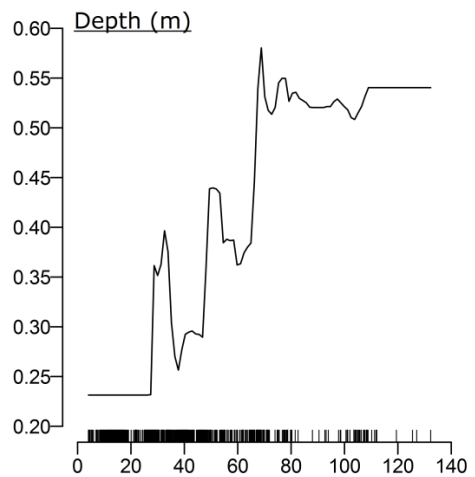
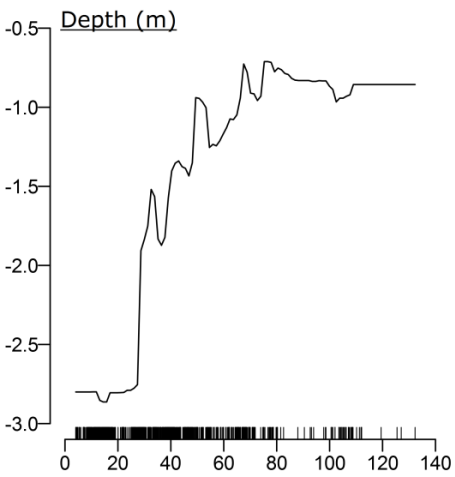
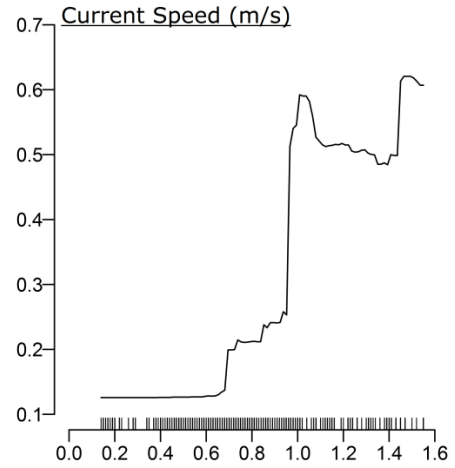
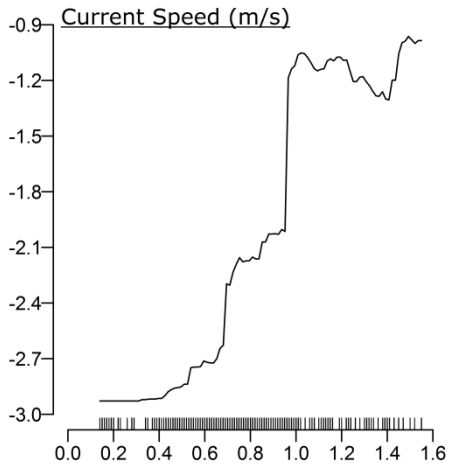
## Presence/Absence

## Abundance

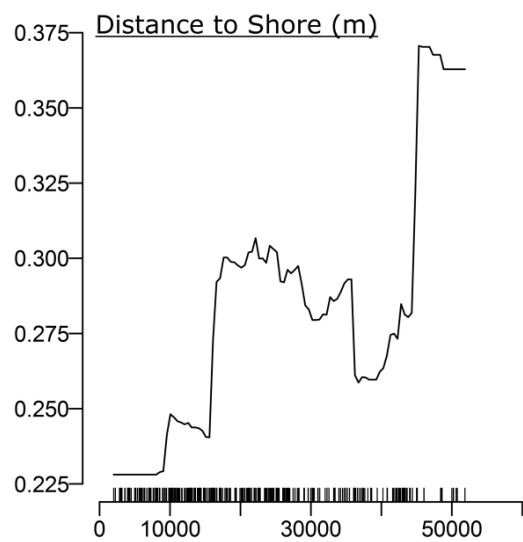
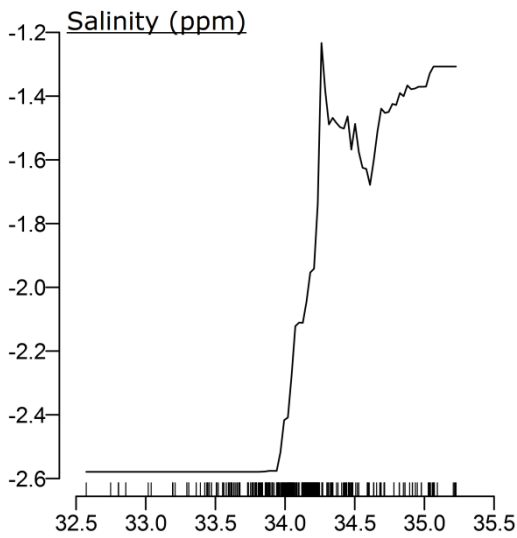
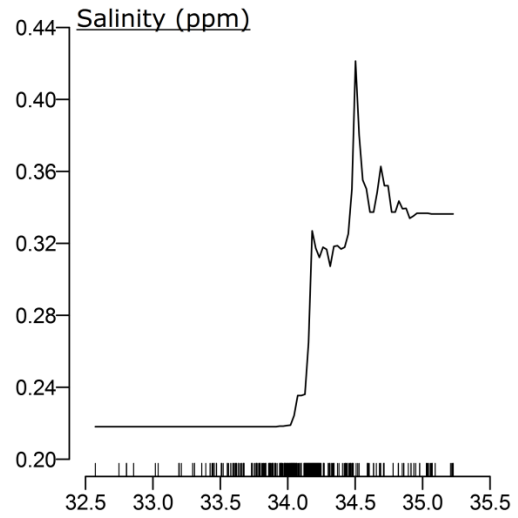
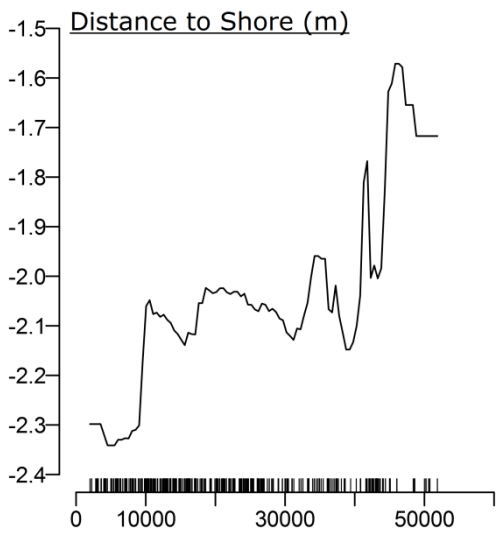
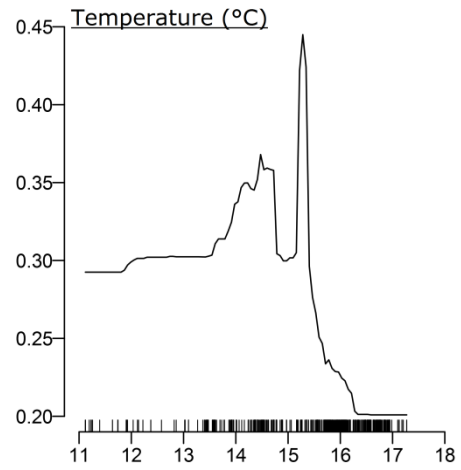
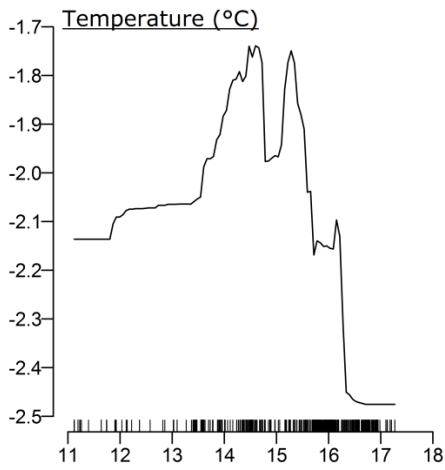
Variable Influence

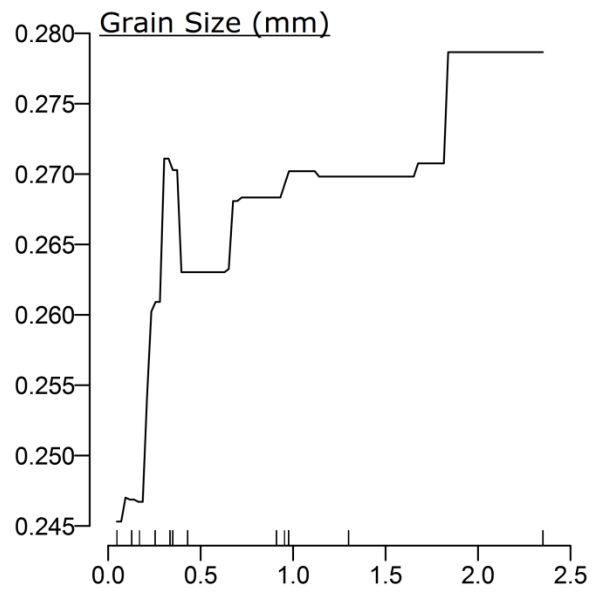


Predictive Deviance



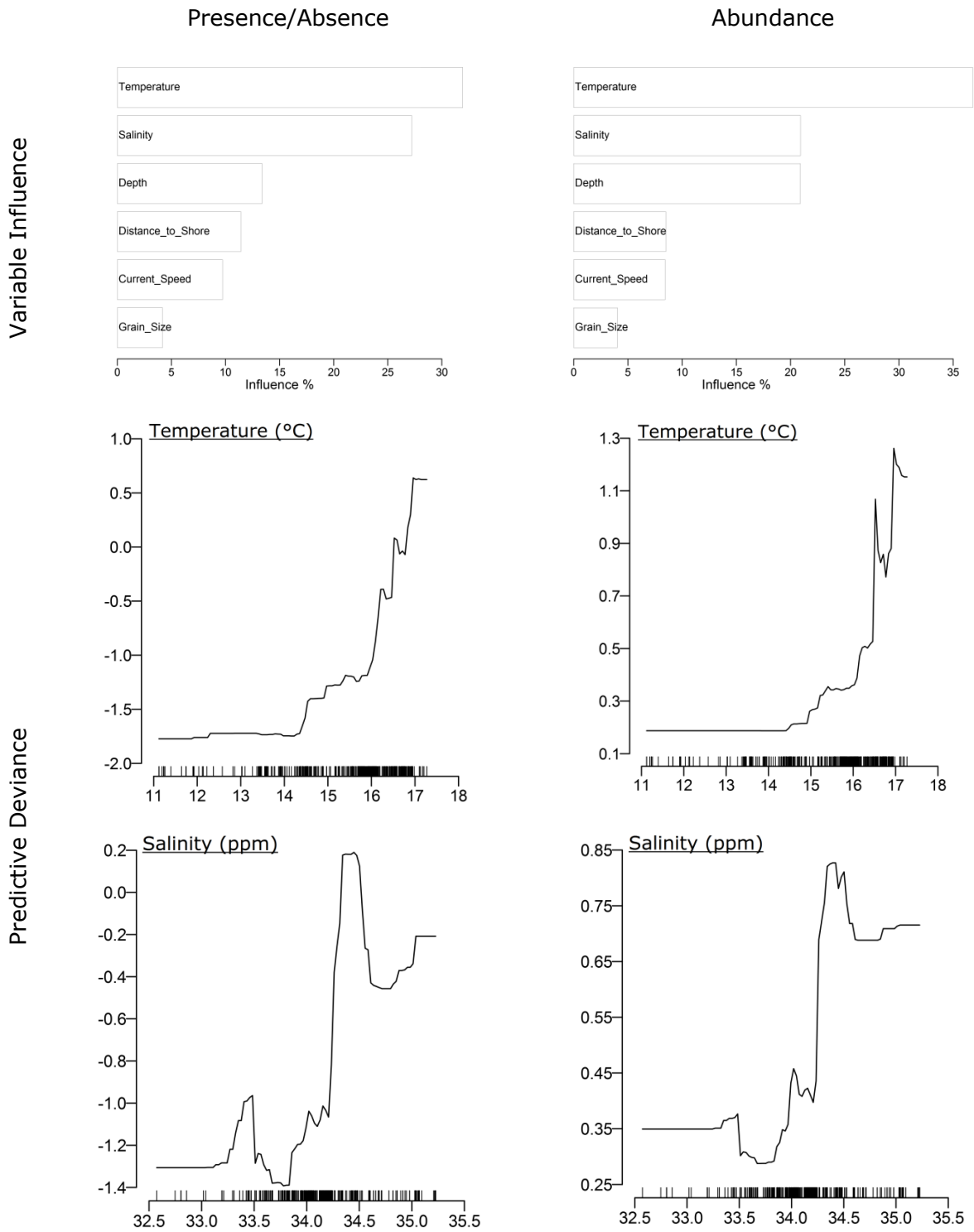


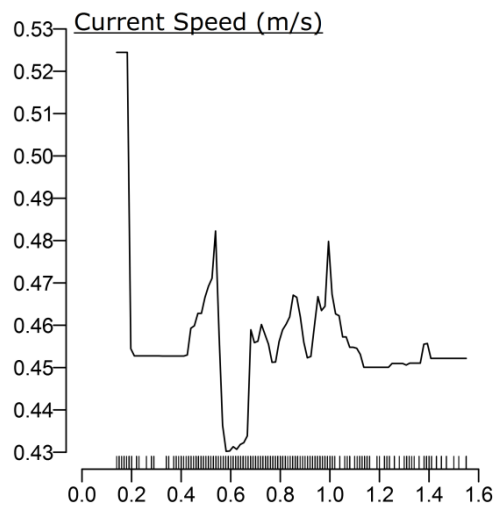
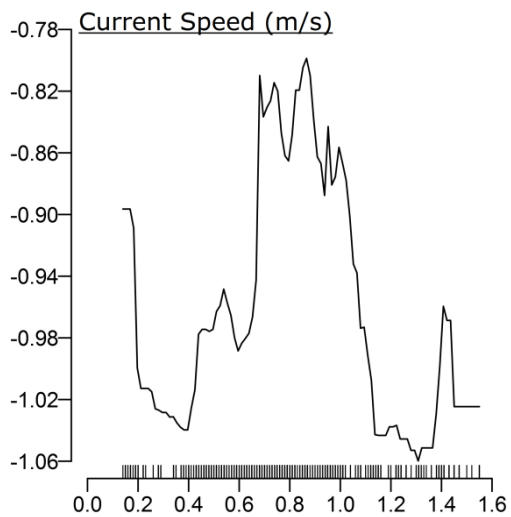
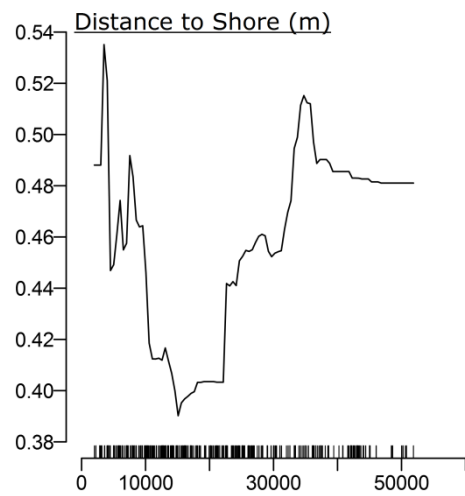
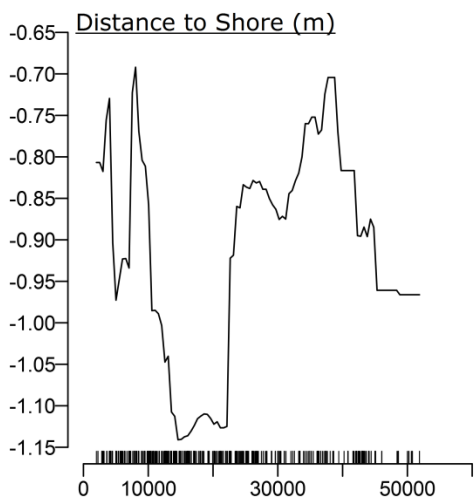
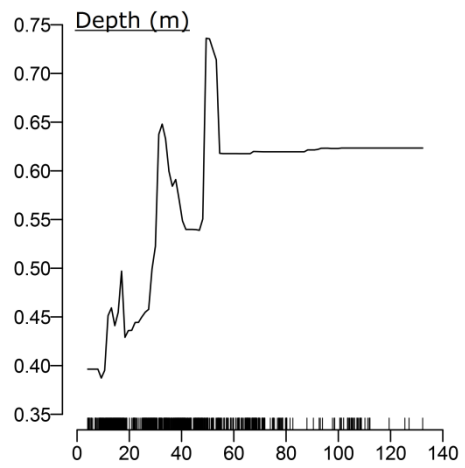
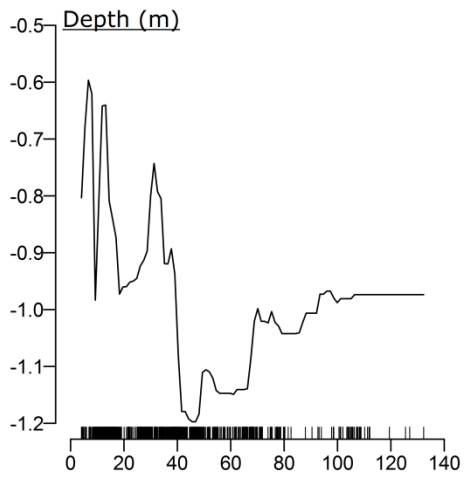


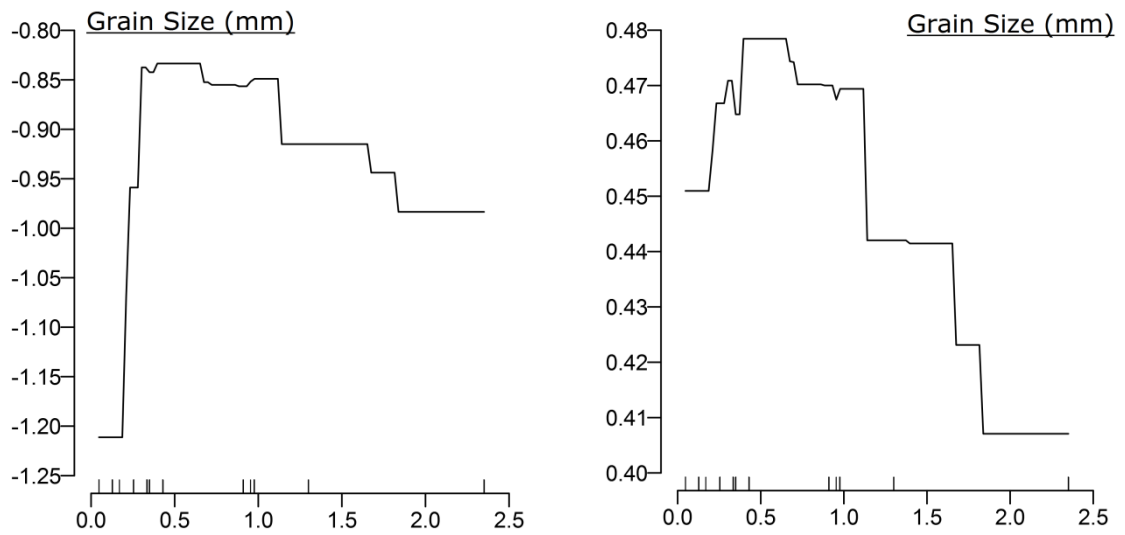


**Figure 18: Relative influence (%) of environmental variables on cuckoo ray BRT outputs, and BRT partial dependence plots showing relationships of environmental variables to ray presence/abundance. Tick marks indicate deciles of the distribution of the predictors.**

# Thornback Ray

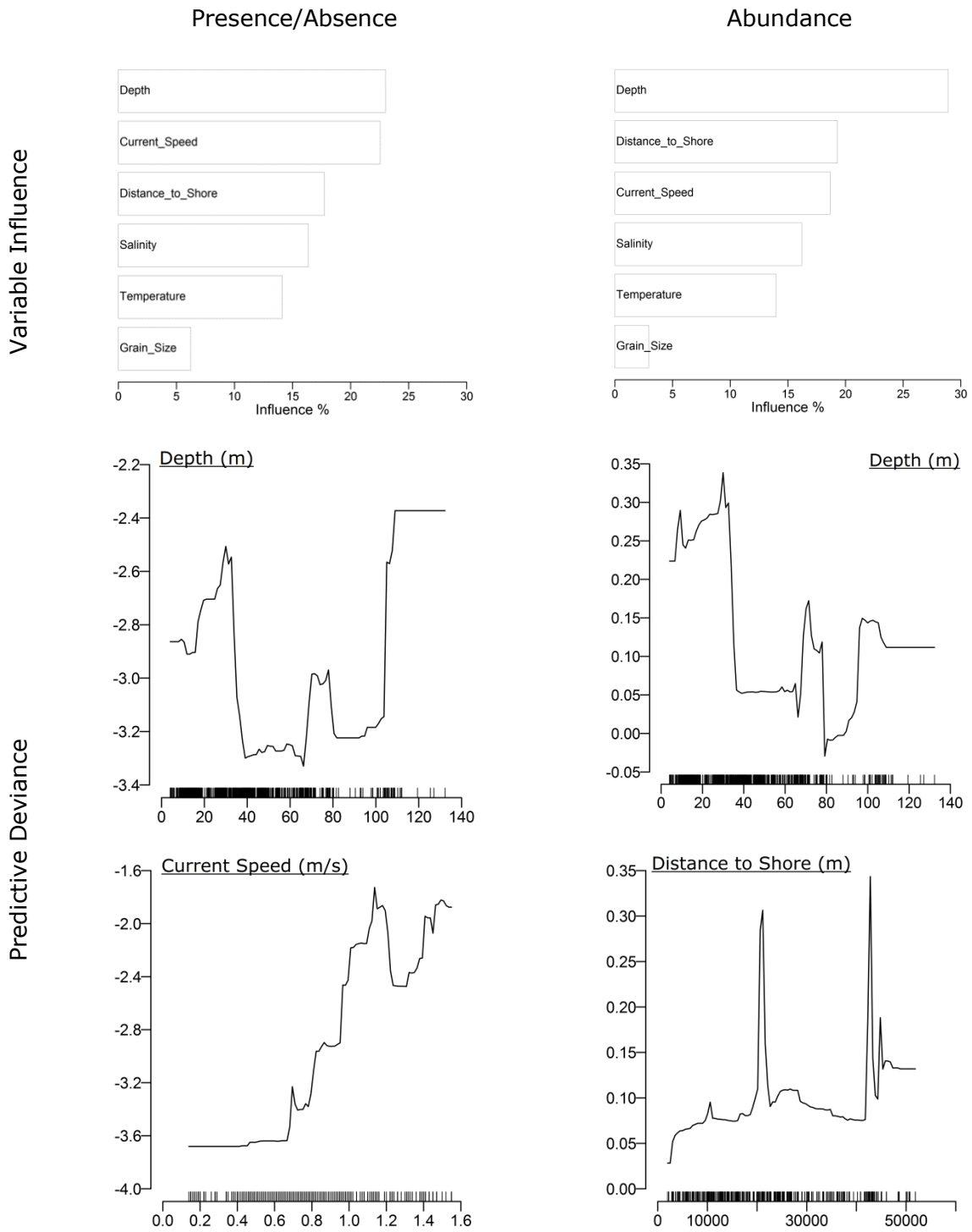


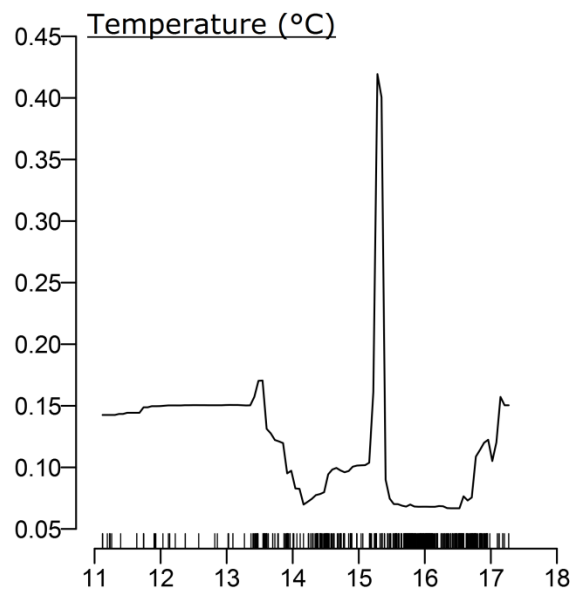
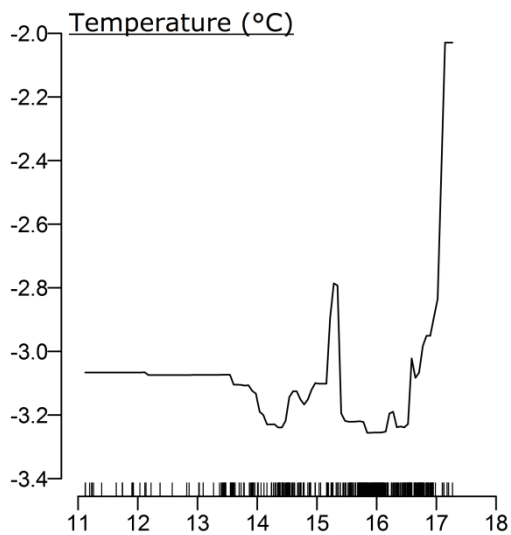
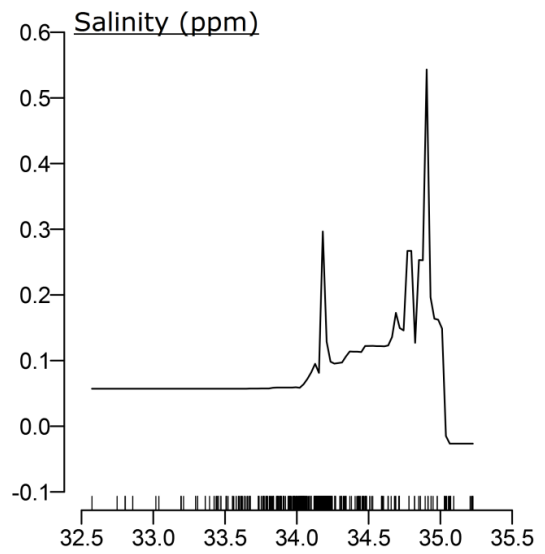
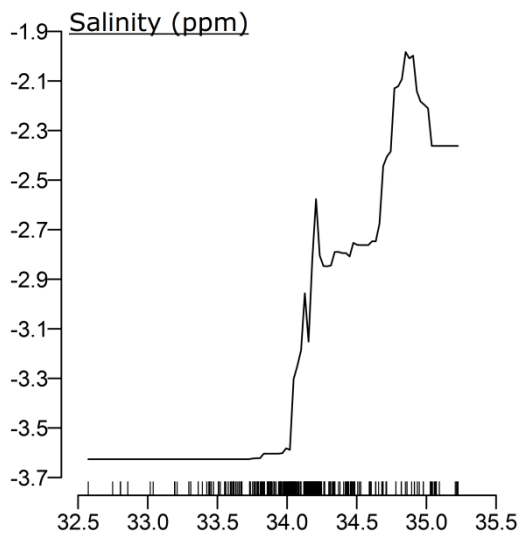
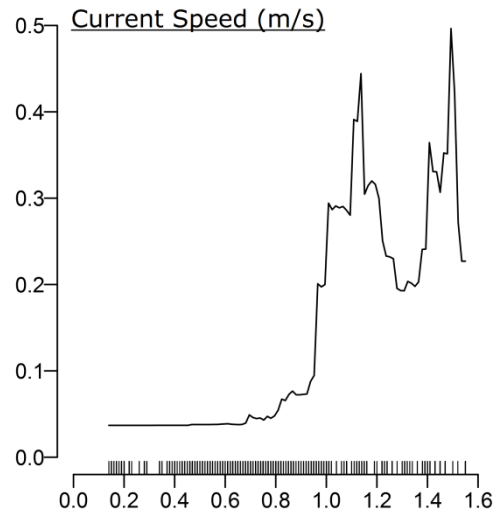
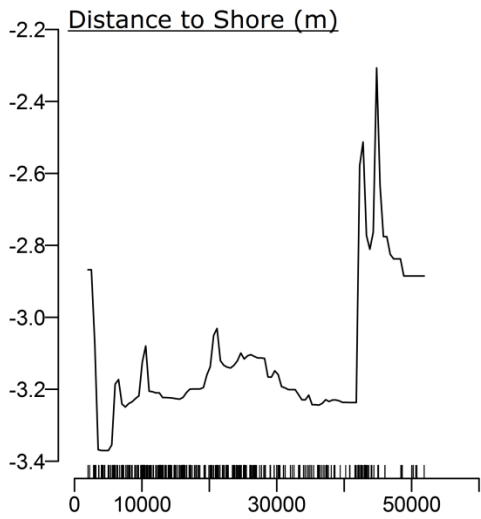


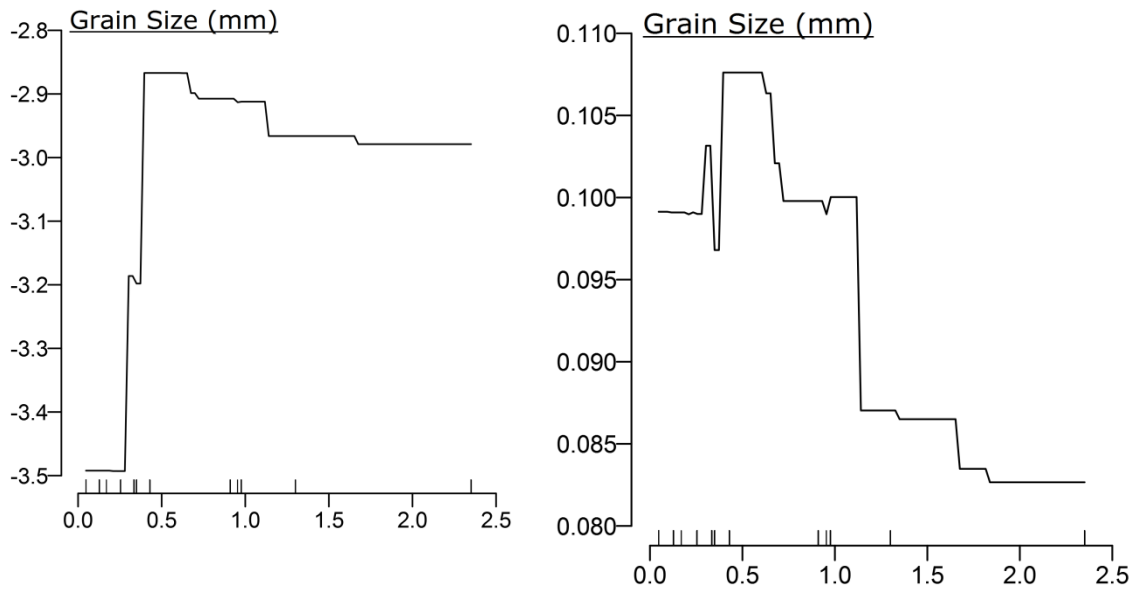


**Figure 19: Relative influence (%) of environmental variables on thornback ray BRT outputs, and BRT partial dependence plots showing relationships of environmental variables to ray presence/abundance. Tick marks indicate deciles of the distribution of the predictors.**

# Blonde Ray



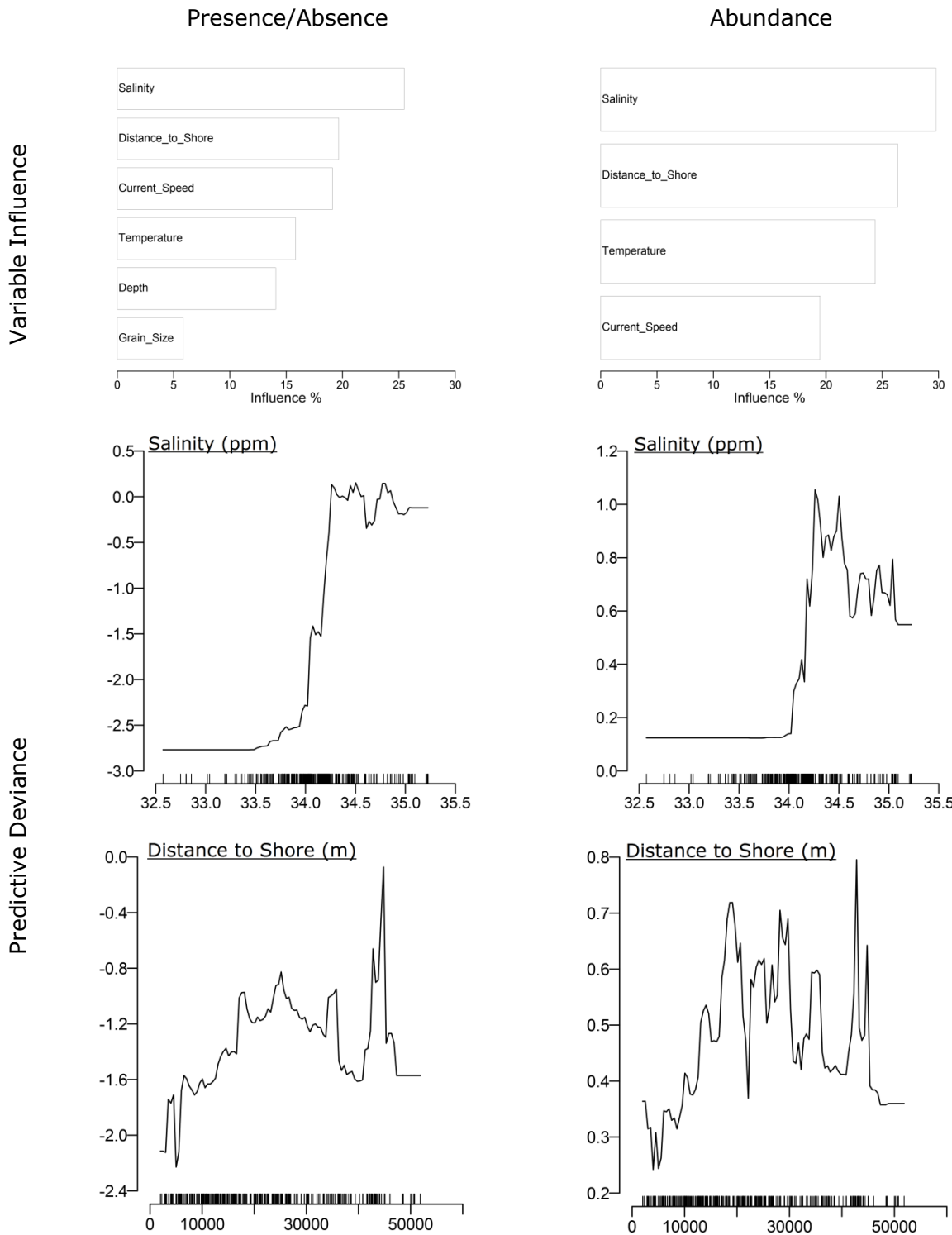


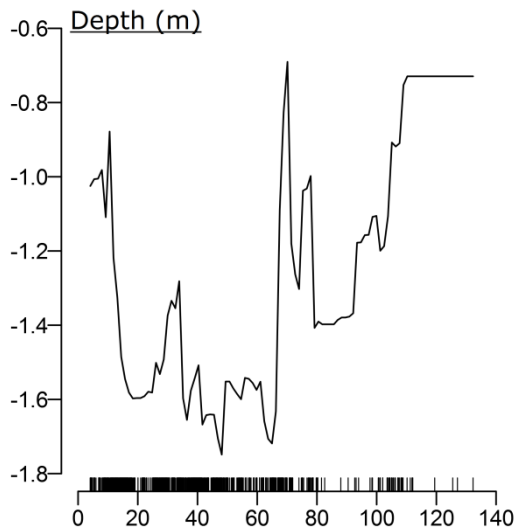
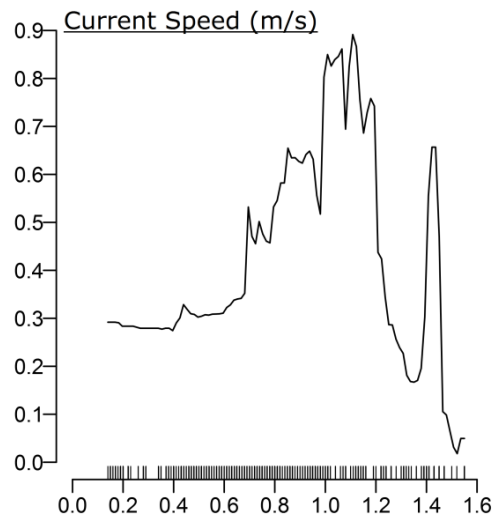
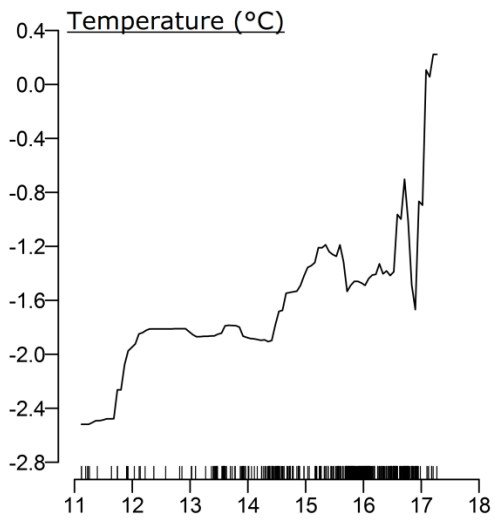
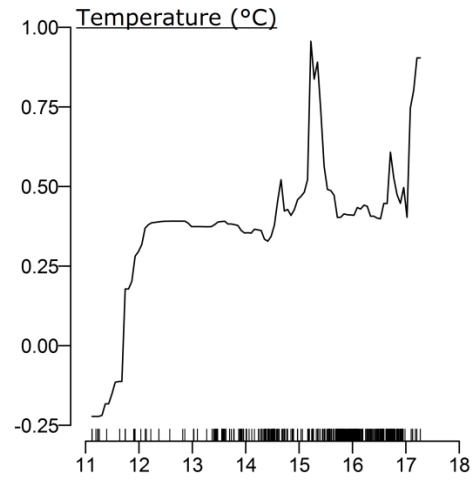
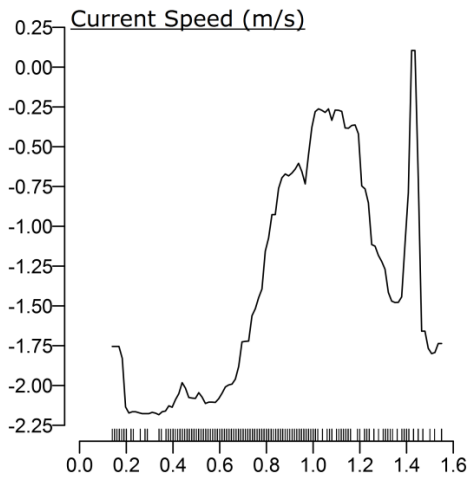


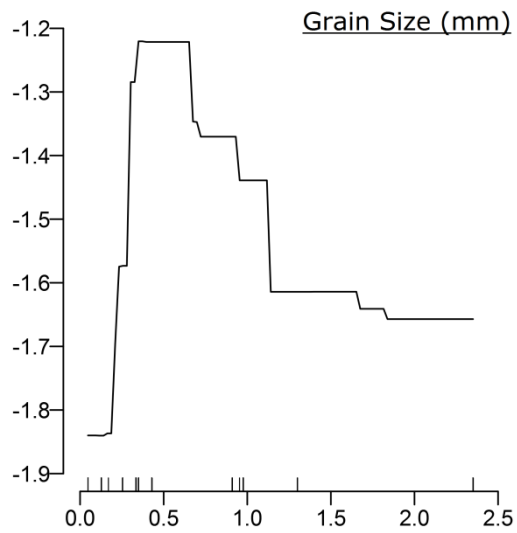
**Figure 20: Relative influence (%) of environmental variables on blonde ray BRT outputs, and BRT partial dependence plots showing relationships of environmental variables to ray presence/abundance. Tick marks indicate deciles of the distribution of the predictors.**



# Spotted Ray

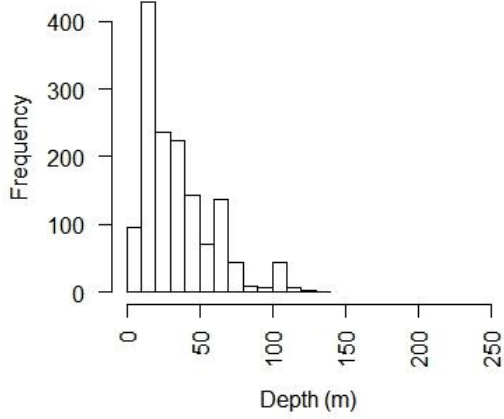




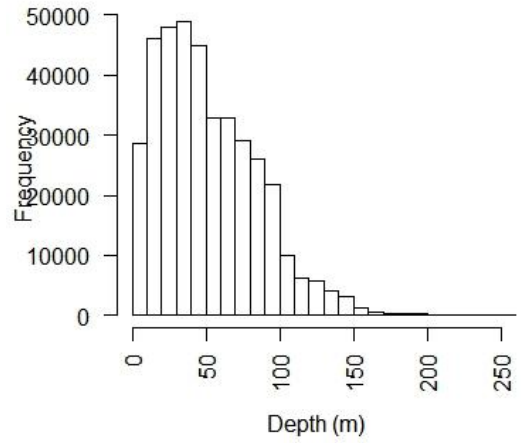


**Figure 21: Relative influence (%) of environmental variables on spotted ray BRT outputs, and BRT partial dependence plots showing relationships of environmental variables to ray presence/abundance. Tick marks indicate deciles of the distribution of the predictors.**

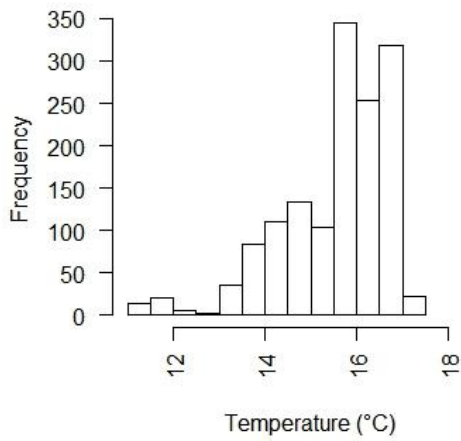
**Histogram of Depths (survey)**



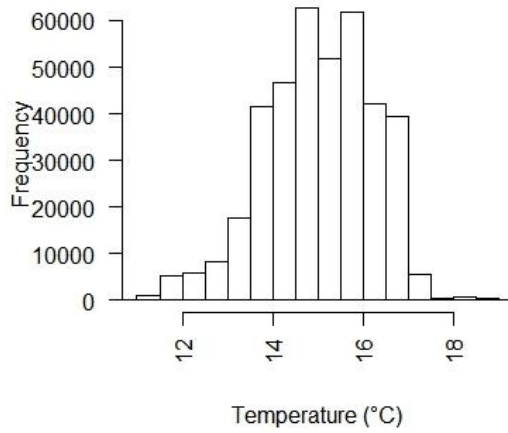
**Histogram of Depths (all Irish Sea)**



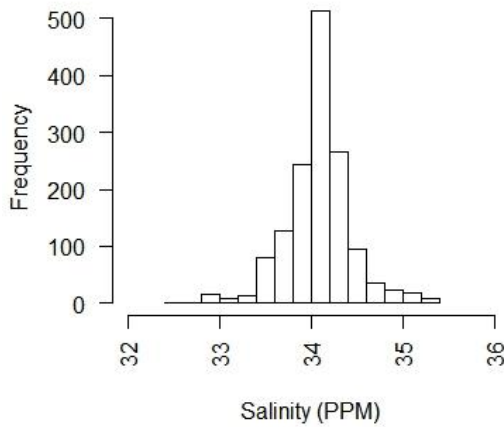
**Histogram of Temperatures (survey)**



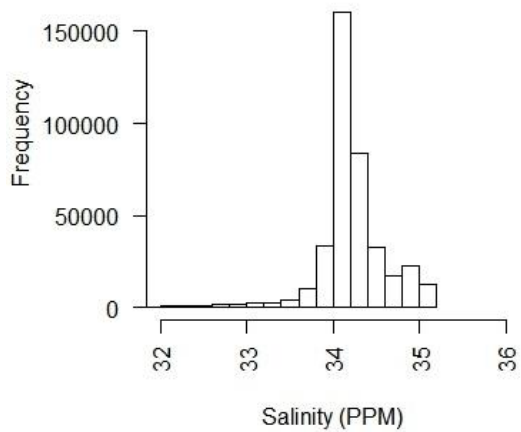
**Histogram of Temps. (all Irish Sea)**



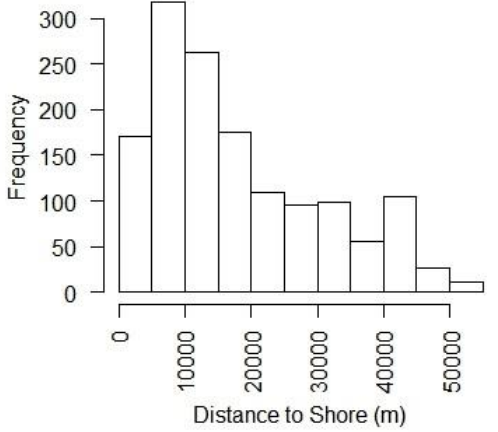
**Histogram of Salinities (survey)**



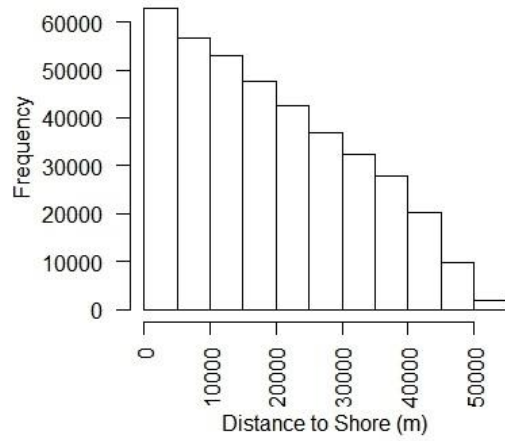
**Histogram of Salinities (all Irish Sea)**



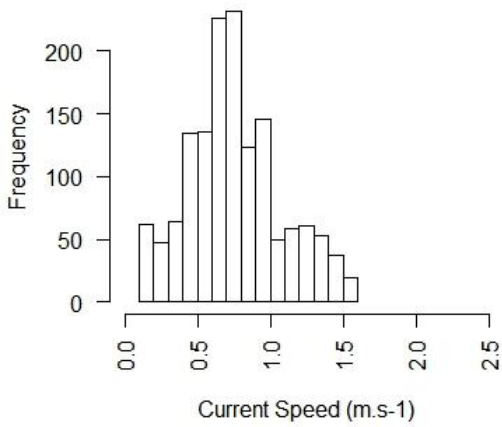
**Histogram of Dist. to Shore (survey)**



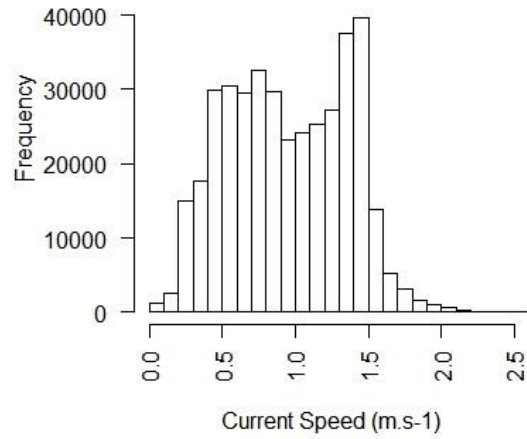
**Histogram of Dist. to Shore (all Irish Sea)**



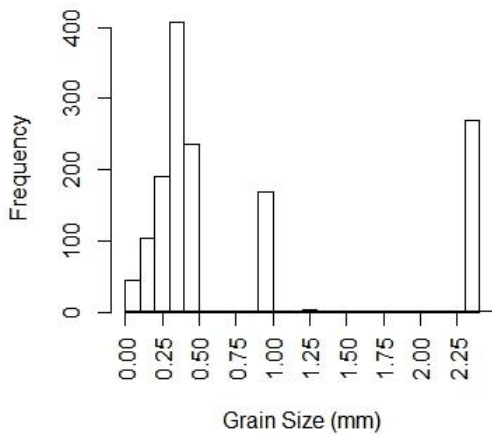
**Histogram of Current Speeds (survey)**



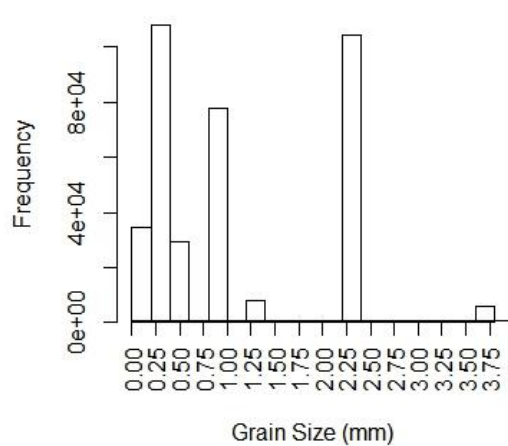
**Histogram of Cur. Speeds (all Irish Sea)**



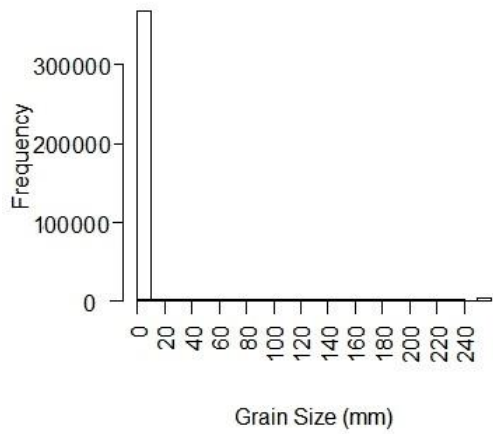
**Histogram of Sub. Grain Sizes (survey)**



**Hist. of Grain Sizes (all Irish Sea)**



**Hist. of Sub. Grain Sizes (all Irish Sea)**



**Figure 22: Histograms of environmental variables from survey (left) and environmental databases (right and final)**