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## Modelling sensitive elasmobranch habitats

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### Abstract

Basic information on the distribution and habitat preferences of ecologically important species is essential for their management and protection. In the Mediterranean Sea there is increasing concern over elasmobranch species because their biological (ecological) characteristics makes them highly vulnerable to fishing pressure. Their removal could affect the structure and function of marine ecosystems, inducing changes in trophic interactions at the community level due to the selective elimination of predators or prey species, competitors and species replacement. In this study Bayesian hierarchical spatial models are used to map the sensitive habitats of the three most caught elasmobranch species (*Galeus melastomus*, *Scyliorhinus canicula*, *Etmopterus spinax*) in the western Mediterranean Sea, based on fishery-dependent bottom trawl data. Results show that habitats associated with hard substrata and sandy beds, mainly in deep waters and with a high seabed gradient, have a greater probability registering the presence of the studied species than those associated with muddy shallow waters. Temperature and chlorophyll-*a* concentration show a negative relationship with *Scyliorhinus canicula* occurrence. Our results identify some of the sensitive habitats for elasmobranchs in the western Mediterranean Sea (GSA06 South), providing essential and easy-to-use interpretation tools, such as predictive distribution maps, with the final aim of improving management and conservation of these vulnerable species.

**Keywords:** Bayesian hierarchical spatial model, elasmobranch habitat, Mediterranean Sea, species distribution modelling.

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## 1. Introduction

There is increasing concern worldwide over elasmobranch species because their K-selection life-history traits make them susceptible to population depletion as a result of anthropogenic activity, including unsustainable fisheries, by-catch, and habitat modification [6]. Most elasmobranchs are predators at or near the top of marine food chains and thus, play an important role in marine ecosystems, potentially regulating the size and dynamics of their prey populations [42]. Their removal could affect the structure and function of marine ecosystems, inducing changes in trophic interactions at the community level due to selective removal of predators or prey species, competitors and species replacement.

In the Mediterranean Sea, this is of particular concern since sharks and rays make up an important percentage of the by-catch [5] and their mobile nature makes them potentially accessible to several fisheries at various bathymetric ranges [11]. Bottom trawling is considered responsible for a large proportion of the by-catch of elasmobranch species in the Mediterranean Sea, and throughout the world in general [27]. Evidence of changes in the number of elasmobranchs and the decrease in the abundance of several species (e.g. *Raja clavata* and *Dipturus batis*) over the last decade have been reported for the whole of the Mediterranean Sea and in particular, for the highly exploited area of the Gulf of Lions [1]. As a result cartilaginous fishes can be used as ecological indicators and their study and monitoring is considered essential for the conservation of the marine ecosystem [42].

In 2009 the European Commission adopted the first Action Plan for the conservation and management of elasmobranchs [10] with the aim of rebuilding their stocks under threat, and of setting down guidelines for the sustainable management of the fisheries concerned. Moreover, the implementation of an ecosystem approach to fisheries management (EAFM) and marine spatial planning (MSP) contemplates the protection of priority habitats, a policy of reducing by-catches and the study of current and expected impacts with a view to preparing efficient strategies for the preservation of the marine environment and in particular its living marine resources [21].

In order to achieve these purposes the prerequisites are a solid knowledge of species-environment relationships and the identification of priority areas using robust analysis of existing information and databases [30]. Habitat and

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9 species mapping is essential for conservation programmes because it provides  
10 a clear picture of the distribution and extent of these marine resources, and  
11 thus facilitates managing the marine environment [3].  
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13 Following Soberón and Peterson [40] and Soberón [39] these objectives  
14 can be achieved by either using Species Distribution Models (SDMs; models  
15 containing biotic or accessibility predictors and/or being limited in spatial  
16 extent) or Ecological Niche based Models (ENMs; for forecasting an approx-  
17 imation to the species' niche)[14, 49]. On the one hand, the theoretical  
18 framework of ENMs is based on the ecological niche concept which identifies  
19 a niche as a subdivision of the habitat containing the environmental condi-  
20 tions that enable individuals of a species to survive and reproduce, based on  
21 broad-scale variables (climate) that are not affected by species density [37].  
22 On the other hand, SMDs aim to predict quantities of interest at unsampled  
23 locations based on measured values at nearby sampled locations, within the  
24 range of environments sampled by the training data and within the same  
25 general time frame as that in which the sampling occurred.  
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30 In line with the SMD context, our study aims to identify sensitive habi-  
31 tats of elasmobranch species and develop probabilistic spatial scenarios as  
32 effective tools for supporting decision-making within the conservation frame-  
33 work. To this end we have analysed a group of georeferenced data of the  
34 presence/absence of the most common demersal cartilaginous species col-  
35 lected from fisheries-dependent bottom trawl sampling carried out along the  
36 continental shelf and slope of the Western Mediterranean Sea (GFCM Ge-  
37 ographical Sub Area 06) during a six-year period of time. In particular,  
38 we have modelled the occurrence data of the three most frequently cap-  
39 tured species: smallspotted catshark (*Scyliorhinus canicula*, Linnaeus, 1758),  
40 blackmouth catshark (*Galeus melastomus*, Rafinesque, 1810) and velvet belly  
41 (*Etmopterus spinax*, Linnaeus, 1758), which comprise more than 80% of the  
42 total demersal elasmobranch abundance caught during the period 2006-2011.  
43 Cluster Analysis (CA) and Multi Dimensional Scaling (MDS) techniques have  
44 been applied to observers' data in order to verify whether the three species  
45 studied are in fact representative of the whole elasmobranch community of  
46 this area.  
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51 To accomplish spatial prediction, ordinary kriging can be used to obtain  
52 the best linear unbiased predictor. However, accuracy is not always easy  
53 to achieve because there is often a large amount of variability surrounding  
54 the measurements of response and environmental variables, and traditional  
55 prediction methods, such as ordinary kriging, do not account for an attribute  
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9 with more than one level of uncertainty. This variability leads to uncertain  
10 predictions, and consequently to uninformed decision making. In order to  
11 solve this problem, we have chosen to use hierarchical Bayesian spatial models  
12 and Bayesian kriging have been used.

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14 In our approach, one of the additional advantages is the possibility of  
15 integrating current modelling approaches (such as GLM and GAM) and un-  
16 certainty analyses into a more general hierarchical framework. Within the  
17 Bayesian framework, full inference about uncertainty, given what we have  
18 observed (the data) and what we know or assume about the process (the  
19 model), comes *free* with the model predictions [2]. Spatial autocorrelation  
20 can be incorporated into a regression model through random effects that cap-  
21 ture spatial dependence in the data [22]. Since the random effects are model  
22 parameters, they also emerge with a full posterior distribution that allows  
23 quantification of uncertainty. Hierarchical stages can describe conceptual but  
24 unobservable latent processes that are ecologically important, as well as error  
25 in the observation process or gaps in the data [13].

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27 However, until recently, it was computationally quite expensive to cal-  
28 culate these Bayesian hierarchical models with this spatial structure. In  
29 this study we overcome this problem by using the integrated nested Laplace  
30 approximation (INLA) methodology and software (<http://www.r-inla.org>).  
31 INLA provides accurate approximations to posterior distributions of the pa-  
32 rameters, even in complex models, in a fast computational way [36]. In ad-  
33 dition, INLA can be used through R software, providing a familiar interface  
34 with the programming of the model.

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36 But, more importantly to us, this methodology allows us both to estimate  
37 the processes that drive the distribution of elasmobranchs and also to gener-  
38 ate predictive maps of the distribution of species in the study area, especially  
39 in non-observed locations.

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41 The establishment of regional marine protected areas for protecting sen-  
42 sitive habitats would benefit from an improved understanding of the spatial  
43 distribution of vulnerable species, such as elasmobranchs, and could help  
44 towards the more efficient management and control of marine resources.

## 51 2. Material and methods

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53 The study area was the Gulf of Alicante (Western Mediterranean), be-  
54 tween  $37^{\circ}15.6'$  and  $38^{\circ}30.0'$  N, and  $1^{\circ}0.0'$  W and  $0^{\circ}30.0'$  E (Figure 1).  
55 The Gulf of Alicante has a surface area of  $3,392 \text{ km}^2$  and an average shelf  
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width of approximately 32 km. The largest fleet is the bottom trawl one, with 169 vessels landing an average of 8,000 t per year. Seabed trawling usually takes place on the shelf, yielding a multispecific catch with European hake (*Merluccius merluccius*) as the main target species. The elasmobranch species most frequently caught are: *Galeus melastomus*, *Scyliorhinus canicula*, *Etmopterus spinax*, *Raja clavata*, *Raja asterias* and *Squalus acanthias*. Their distribution and abundance vary according to depth.

### 2.1. Data

The data set includes 400 hauls of 25 different trawler vessels and has been provided by the Spanish Oceanographic Institute (Instituto Español de Oceanografía, IEO). The IEO provides the national input of the European Observers Programme for collecting fishery-dependent data. In particular, they collect samples from the commercial fleet with observers on board. This sampling has been carried out since 2003, usually involving about 2-3 observer samplings every month for the trawler fleet, accounting for an average of 10 hauls monthly. From this database we have used the geographical location and occurrence of the elasmobranch species for each haul. The fisheries were multispecies and none of the elasmobranchs were target species.

Extrinsic factors influencing the spatial distribution of elasmobranch species used were depth, which is often the main gradient along which faunal changes occur when analyzing shelf and upper slope assemblages [19], type of substratum [7], slope of seabed and physical characteristics of the water masses [28].

For ocean processes, chlorophyll-*a* concentration and Sea Surface Temperature (SST) data can be used to locate thermal and productivity-enhancing fronts and marine productivity hotspots and thus determine the influence of such features on species distribution [45]. In addition, SST and Chl-*a* are also strong functional links between surface primary productivity and biological activity at the sea floor through the episodic deposition of particulate material [32, 23]. Previous studies have shown that the distributions of many demersal fish species are likely to be influenced by overall ecosystem productivity [31, 17, 23, 29].

In particular, Chl-*a* concentration can be used as an index of primary production of an ecosystem [24]. Obviously, primary production depends on a range of factors, including light, light penetration and temperature, which could not be taken into account here due to the absence of data. Nevertheless, the mean value of Chl-*a* concentration can be used as an independent index of

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9 primary production in the area of interest, since its variability could modify  
10 trophic conditions of the species' habitat from oligotrophic to mesotrophic  
11 [20].  
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13 Sea Surface Temperature (SST) is strongly related with primary produc-  
14 tivity and is thus a possible candidate to explain the distribution of the  
15 species [44]. Previous studies on elasmobranchs have implied that SST plays  
16 an important role in their distribution [31, 29] from a physiological stand-  
17 point. The majority of coastal elasmobranchs are ectothermic and changes  
18 in the environmental temperature are rapidly transferred to the body of the  
19 animal, thus impacting most physiological processes [17].  
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21 The environmental satellite (SST and chlorophyll-*a*) data has been ex-  
22 tracted as a monthly mean from the SeaWiFS ([http://oceancolor.gsfc.  
23 nasa.gov](http://oceancolor.gsfc.nasa.gov)). We have interpolated the raster surface of the SST and chlorophyll-  
24 *a* variables, using the *Spline* tool of ArcGIS 10. The *Spline* method is  
25 an interpolation method that estimates values using a mathematical func-  
26 tion that minimizes overall surface curvature, resulting in a smooth sur-  
27 face that passes exactly through the input points. In particular, we have  
28 used the *Tension* method, which controls the stiffness of the surface ac-  
29 cording to the character of the modelled phenomenon. This method cre-  
30 ates a less smooth surface with values more closely constrained by the sam-  
31 ple data range ([http://help.arcgis.com/en/arcgisdesktop/10.0/help/  
32 index.html#//009z0000006q000000.htm](http://help.arcgis.com/en/arcgisdesktop/10.0/help/index.html#//009z0000006q000000.htm)) (Figure 2a,2b).  
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34 Bathymetry and type of substratum data were obtained from the IEO  
35 geoportal, accessible through the website of the Spanish Institute of Oceanog-  
36 raphy (<http://www.ieo.es>). In order to obtain the value of depth at any  
37 precise location of the study area we have interpolated the bathymetric map,  
38 using GRASS GIS (<http://grass.fbk.eu>), first rasterizing contours with a res-  
39 olution of 500 m. and then using the function *r.surf.contour*, following guide-  
40 lines given in the website ([http://grass.osgeo.org/wiki/Contourlines\\_  
41 to\\_DEM](http://grass.osgeo.org/wiki/Contourlines_to_DEM)) (Figure 2c). Log-transformed bathymetry was included in the anal-  
42 ysis for smoothing the effect and preserving the linearity of this variable.  
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44 The slope map has been derived by the bathymetry map, using the *Slope*  
45 tool of the ArcGIS 10. Slope values reflect the maximum rate of change (in  
46 degrees) in elevation between neighboring values derived with ArcGIS Spatial  
47 Analyst extension ([http://webhelp.esri.com/arcgisdesktop/10/index.  
48 cfm?TopicName=How%20Slope%20works](http://webhelp.esri.com/arcgisdesktop/10/index.cfm?TopicName=How%20Slope%20works)) (Figure 2d).  
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50 The type of substratum polygon shapefile includes a classification of ten  
51 categories and a reduced version with four levels: Sand, Mud, Gravel and  
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Rock. In order to reduce the level of variability in the analysis, since we have no observations in all categories, we have used the simplified version (Figure 2e). Moreover, in the study area there are no areas of gravel, so the categories have been reduced to the remaining three.

In order to make it possible to work in the R framework maps have been transformed into *SpatialPolygonsDataFrame* objects using the *sp* R package.

### 2.2. Multivariate analysis

Our data set includes 23 different elasmobranch species. We used multivariate analysis techniques in order to verify whether the three most captured species (*Scyliorhinus canicula*, *Galeus melastomus* and *Etmopterus spinax*) were truly representative of the whole elasmobranch community in this area. In particular, we applied Cluster Analysis (CA) and Multidimensional Scaling (MDS) techniques to analyse the 400 bottom trawl hauls. If results show a high degree of similarity in the species assemblage of the different hauls, we can assume that sensitive habitats identified for the three species studied are shared by the remaining elasmobranch species. Consequently, the conservation of these habitats would go a long way to protecting the entire community of elasmobranchs in this area.

Both multivariate analyses were performed on a Euclidean similarity matrix with the average method, considering the occurrence of each species to identify possible differences between the habitats studied.

### 2.3. Modelling sensitive habitats

The spatial variation in the probability of occurrence of the three most captured species (*Scyliorhinus canicula*, *Galeus melastomus* and *Etmopterus spinax*) was modelled by using a hierarchical Bayesian spatial approach, specifically a point-reference spatial model. These models are highly suitable for situations (such as that of the present study) in which data are observed at continuous locations occurring within a defined spatial domain (geo-referenced Bernoulli data). Note that these models can also be considered as a spatial extension of logistic regression models because the modelling process describes the variability in the response variable as a function of the explanatory variables, with the addition of a stochastic spatial effect, which models the residual spatial autocorrelation [25].

Specifically, the response variable is a binary variable that represents the presence (1) or absence (0) of the species in each fishing location sampled:  $Z_i$  represents the occurrence. Consequently, the conditional distribution of

the data is  $Z_i \sim \text{Ber}(\pi_{ij})$ , assuming that observations are conditionally independent given  $\pi_{ij}$ , which is the probability of occurrence at location  $i$  ( $i = 1, \dots, n$ ) and year  $j$  ( $j = 1, \dots, 6$ ). At the first stage of the hierarchical model, we model the observed data (occurrence of elasmobranchs) as a GLM by using the customary (for binary data) logit link function, but incorporating a spatial and a possible temporal effect. That is,

$$\text{logit}(\pi_{ij}) = X\beta + Y_j + W_i, \quad (2.1)$$

where  $\beta$  represents the vector of the regression coefficients,  $X$  is the matrix of covariates,  $W_i$  represents the spatially structured random effect,  $Y_j$  is the component of the temporal unstructured random effect at year  $j$ , and the logit transformation is defined as  $\text{logit}(\pi_{ij}) = \log(\pi_{ij}/1 - \pi_{ij})$ .

$W_i$  is assumed to be Gaussian with a given covariance matrix  $\sigma_W^2 H(\phi)$ , depending on the distance between locations, and with hyperparameters  $\sigma_W^2$  and  $\phi$  representing respectively the variance and the range of the spatial effect:

$$W \sim N(0, \sigma_W^2 H(\phi)). \quad (2.2)$$

#### 2.4. Bayesian inference

Once the model has been determined, the next step is to estimate its parameters. Following Bayesian reasoning, the parameters are treated as random variables, and prior knowledge has to be incorporated via the corresponding prior distributions of the said parameters. In particular, for the parameters involved in the fixed effects, we use the Gaussian distribution  $\beta \sim N(0, 100)$ . In this second stage of the hierarchical model the uncertainty about the parameters used in the first level is incorporated and propagated across model stages to more accurately reflect overall inferential uncertainty.

In the third, and final, level of hierarchy, prior knowledge about the hyperparameters is expressed. For the temporal effect we assume, following Rue and Held [35], LogGamma prior distribution on the log-precision  $\lambda_y$  ( $a=1$ ,  $b= 5e -05$ ). The choice of the priors of the hyperparameters of the spatial effect will be described in the following section.

As usual in this context, the resulting hierarchical Bayesian model has no closed expression for the posterior distribution of all the parameters, and thus numerical approximations are needed. Here, due to speed of computational processing, we use the integrated nested Laplace approximation (INLA) methodology and software (<http://www.r-inla.org>) as an alternative to the Markov chain Monte Carlo (MCMC) method.

### 2.5. The INLA framework

To better understand the idea behind this modelling, the key is to think of these models as a particular case of the *Structured Additive Regression (STAR) models* called *Latent Gaussian models* [36]. In these models the mean of the response variable  $Z_i$  is linked to a structured predictor that accounts for the effects of various covariates in an additive way. Gaussian prior distributions are assigned to all the components of the additive predictor which is the latent Gaussian model.

Here, the latent models represent the elasmobranch occurrence phenomena that exists independently of whether species are observed in a given location or not. Thus, we are not building hierarchical models solely for discretely observed data, but for approximations of entire processes defined on continuous domains. Until recently, the problem was the infeasibility of fitting the particular case of continuously indexed Gaussian models, as is the case with our spatial component  $W$ .

Lindgren et al. [26] have proposed a solution to this problem: the *Stochastic Partial Differential Equation (SPDE)* approach. This alternative solution is an explicit link between Gaussian models and the Gaussian Markov Random model [35]. The benefits are that the Markov property makes the covariance matrix sparse, enabling the use of efficient (and faster) numerical algorithms and the use of the Matérn covariance function, which is a highly flexible and general family of functions in spatial statistics.

Under this perspective, the equation 2.2 changes as follows:

$$W \sim N(0, Q(\kappa, \tau)). \quad (2.3)$$

Now the spatial effect depends on two different parameters:  $\kappa$  and  $\tau$ , which determine the range of the effect and the total variance, respectively. Hyper-priors for  $\kappa$  and  $\tau$  are centered in values such that the range is about 20% of the diameter of the region and the variance is equal to 1 [26].

Here, the two major bonuses are that INLA can be used through `R`, providing a familiar interface with the model specification (see Lindgren [25] for a detailed explanation of the INLA syntax) and that inference and prediction in unsampled locations could be were performed simultaneously.

INLA provides a variety of approximation strategies for the posterior distributions. In this study we have used the default ones: the simplified Laplace approximation for marginalization, and the Central Composite Design for the numerical integration of the hyperparameters. These are the

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9 default and recommended settings providing reasonable accuracy with maximum  
10 computational efficiency (Held et al., 2010)[15].  
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## 12 *2.6. Model prediction*

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14 Once the inference has been carried out, the next step is to predict the  
15 occurrence of elasmobranchs in the rest of the area of interest, especially in  
16 unsampled locations. Here, we adopted a Bayesian kriging, which allows for  
17 the incorporation of parameter uncertainty into the prediction process by  
18 treating the parameters as random variables.  
19

20 A common method for performing prediction with a Bayesian kriging is to  
21 take observations and construct a regular lattice over them. In this study, we  
22 have considered a more computationally efficient approach. Using the INLA  
23 SPDE module we created a triangulation around the sampled points in the  
24 region of interest (Figure 3). As opposed to a regular grid, a triangulation is  
25 a partition of the region into triangles, satisfying constraints on their size and  
26 shape in order to ensure smooth transitions between large and small triangles.  
27 Initially, observations are treated as initial vertices for the triangulation, and  
28 extra vertices are added heuristically to minimize the number of triangles  
29 needed to cover the region subject to the triangulation constraints. These  
30 additional vertices are used as prediction locations.  
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32 The triangulation approach has a number of advantages over a regular  
33 grid. Firstly, the triangulation is denser in regions where there are more  
34 observations and consequently there is more information, and more detail is  
35 needed. Secondly, it saves computing time, because prediction locations are  
36 typically much lower in number than those in a regular grid. And thirdly, it  
37 is possible to take boundary effects into account by generating a mesh with  
38 small triangles in the domain of interest, and using larger triangles in the  
39 extension used to avoid boundary effects.  
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41 After obtaining the prediction in the selected location, there are additional  
42 functions that linearly interpolate the results within each triangle into  
43 a finer regular grid. As a result of the process, for each point of the area we  
44 obtain a predictive posterior distribution of elasmobranch occurrence for the  
45 whole study area. This means that for each posterior distribution, unlike the  
46 mean and confidence interval produced by classical analyses, we are able to  
47 make explicit probability statements about the estimation of elasmobranch  
48 occurrence.  
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### 2.7. Model selection

Models were compared considering two criteria: the Deviance Information Criterion, usually denoted as DIC [41], which is computed routinely by INLA as the default criterion for comparing hierarchical models; and the Conditional Predictive Ordinate (CPO), which has been used as a predictive measure (of the models). In particular, as indicated by Roos and Held [34], we computed the mean logarithmic CPO (LCPO). Lower values for both DIC and LCPO represent the best compromise between fit and parsimony.

### 2.8. Model evaluation and calibration

The dataset was randomly split into two main subsets: a training dataset including 70% of the total observations, and a validation dataset containing the remaining 30% of the data. The relationship between occurrence data and the environmental variables was modelled by using the training dataset and the quality of predictions was then assessed by using the validation dataset. We repeated validation 10 times for the best model for each species and results were averaged over the different random subsets.

We performed a validation procedure to formally evaluate overall model prediction using the area under the receiver-operating characteristic curve (AUC) [12], specificity, sensitivity and kappa.

AUC measures the ability of a model to discriminate between those sites where a species is present and those where it is absent, and has been widely used in the species distribution modelling literature [8]. AUC ranges from 0 to 1, with values below 0.6 indicating a performance no better than random, values between 0.7-0.9 considered as useful, and values  $> 0.9$  as excellent. AUC is tabulated through the confusion matrix indicating the true positive (TP), false positive (FP), false negative (FN), and true negative (TN) predictions. We can summarize that there are two types of prediction errors: false positive (FP) and false negative (FN). FP leads to an over-prediction while FN or omission error, leads to an under-prediction. From the confusion matrix we calculated the specificity, sensitivity and kappa criteria.

Specificity is the proportion of TN correctly predicted and reflects a model's ability to predict an absence given that a species in fact does not occur at a location. Sensitivity is the proportion of TP correctly predicted and reflects a model's ability to predict a presence given that a species in fact occurs at a location.

Kappa measures the proportion of correctly classified units after accounting for the probability of chance agreement. It requires a threshold to be

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9 applied to the predictions in order to convert them to presence-absence pre-  
10 dictions. Kappa provides an index that considers both FP and FN errors.  
11 In this study, a maxKappa is used for each model generated.  
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13 All the analyses described in this paper were carried out using the R 2.15  
14 software [33].  
15

### 16 17 **3. Results**

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19 The similarity dendrogram for the bottom trawl hauls revealed the exis-  
20 tence of three different assemblages for the elasmobranchs, which were con-  
21 firmed by the MDS analysis (Figure 4).  
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23 Picked dogfish (*Squalus acanthias*) and common eagle ray (*Myliobatis*  
24 *Aquila*) form a separate group, bull ray (*Pteromylaeus bovinus*) are in a  
25 group of their own, and all the other elasmobranch species are included in  
26 one single group. This latter group includes 20 out of the 23 of elasmobranch  
27 species caught in the study area, including the three most caught species  
28 which are the ones used in this study.  
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30 A total of 400 trawl fishery operations were observed during a period of  
31 six years. In the case of the smallspotted catshark (*Scyliorhinus canicula*),  
32 its presence was recorded in 204 of these hauls, that of the blackmouth cat-  
33 shark (*Galeus melastomus*) in 135 and that of the velvet belly (*Etmopterus*  
34 *spinax*) in 54. The main predictors of elasmobranch habitats in the western  
35 Mediterranean Sea were depth, slope and type of substratum.  
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37 SST and chlorophyll-*a* concentration show a negative relationship with  
38 species occurrence but affect only the distribution of *S. canicula* (Table 1).  
39 The final models with the best fit for *G. melastomus* and *E. spinax* do not  
40 include SST and chlorophyll-*a* concentration as relevant variables (Table 1).  
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42 No important yearly differences were found in this area for the occurrence  
43 of these species. All the models that include the temporal effect, show higher  
44 Deviance Information Criterion (DIC) than those without it.  
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46 The model selected for its best fit (based on the lowest DIC and LCPO)  
47 with *S. canicula* has log-transformed bathymetry, type of substratum, slope,  
48 SST and chlorophyll-*a* concentration as covariates, and a stochastic spatial  
49 component that accounts for the residual spatial autocorrelation. Table 1  
50 presents a numerical summary of the posterior distributions of the fixed ef-  
51 fects for this final model. This summary contains the mean, the standard  
52 deviation, the median and a 95% credible interval, which is a central interval  
53 containing 95% of the probability under the posterior distribution.  
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Species	predictor	mean	sd	$Q_{0.025}$	$Q_{0.5}$	$Q_{0.975}$
<i>S. canicula</i>	(Intercept)	0.23	2.14	-4.23	0.73	4.32
	Log Depth	1.06	0.63	-0.32	1.04	2.05
	Seabed(Mud)	-0.32	0.42	-1.16	-0.33	0.51
	Seabed(Rock)	-1.91	0.95	-3.87	-1.88	-0.12
	Slope	0.21	0.11	-0.51	0.22	0.74
	Chlorophyll-a	-13.96	7.83	-29.96	-13.82	1.24
<i>G. melastomus</i>	SST	-0.52	0.27	-0.22	-0.51	1.05
	(Intercept)	-1.72	2.91	7.53	-1.89	4.94
	Log Depth	0.33	-0.27	0.25	0.35	0.85
	Seabed(Mud)	0.41	-0.50	0.40	0.42	1.29
	Seabed(Rock)	-0.72	1.28	-3.36	-0.68	1.69
<i>E. spinax</i>	Slope	0.19	0.02	-0.06	0.20	0.33
	(Intercept)	-2.35	12.76	-32.34	-2.72	28.65
	Log Depth	5.45	3.63	2.70	5.35	10.39
	Seabed(Mud)	0.08	0.85	-1.61	0.09	1.73
	Seabed(Rock)	-0.73	1.28	-3.36	-0.68	1.70
	Slope	0.09	0.03	-0.06	0.08	0.10

Table 1: Numerical summary of the posterior distributions of the fixed effects for the best model of the three species studied. This summary contains the mean, the standard deviation, the median and a 95% credible interval, which is a central interval containing 95% of the probability under the posterior distribution.

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10 Results showed a positive relationship between bathymetry and the pres-  
11 ence of *S. canicula* (posterior mean = 1.06; 95% CI = [-0.32,2.05]). Con-  
12 versely, chlorophyll-a concentration showed a negative relation with respect  
13 to the presence of this species (posterior mean = -13.96; 95% CI = [-29.96,1.24]).  
14 For low SST values, the occurrence of *S. canicula* is higher (posterior mean  
15 = -0.52; 95% CI = [-0.22,1.05]). Rock substratum is the type of seabed that  
16 shows the lowest estimated probability of occurrence (posterior mean = -1.91;  
17 95% CI = [-3.87,-0.12]) with respect to the reference level (sand substratum).  
18 Muddy substrata also showed a lower estimated coefficient than the reference  
19 level (posterior mean = -0.32; 95% CI = [-1.16,0.51]), leaving sandy substrata  
20 as the kind of sediment granulometry category with the highest probability  
21 of the presence of *S. canicula*. A positive correlation is characterized by a  
22 high slope gradient and the probability of occurrence (posterior mean = 0.21;  
23 95% CI = [-0.51,0.74]) of *S. canicula*. As can be appreciated in Figure 5(a),  
24 the median posterior probability of the occurrence of *S. canicula* in the Gulf  
25 of Alicante, is greater over a high slope gradient, in deeper waters where  
26 chlorophyll-a and SST values are higher, and where there are sandy seabeds.  
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31 Habitats associated with hard substrata and sandy beds, mainly from  
32 deeper waters and with a high slope gradient, show a greater probability of  
33 the presence of *G. melastomus* than those associated with mud from shallow  
34 waters and low slope gradient (Table 1 and Figure 5(b)). Table 1 showed a  
35 positive relation between log-bathymetry and the presence of *G. melastomus*  
36 (posterior mean = 0.33; 95% CI = [0.25, 0.85]). Rock substratum is the  
37 type of seabed that shows the highest estimated probability of occurrence  
38 (posterior mean = -0.72; 95% CI = [-3.36,1.69]) with respect to the reference  
39 level (sand substratum). Muddy substrata showed a lower estimated coeffi-  
40 cient than the reference level (posterior mean = 0.41; 95% CI = [0.40,1.29]).  
41 High slope gradient positively influences the probability of occurrence of *G.*  
42 *melastomus* (posterior mean = 0.19; 95% CI = [-0.06,0.33]). Figure 4(b)  
43 shows high median posterior probability of occurrence of *G. melastomus* over  
44 steeper slopes, in deeper waters and where there are rocky and sandy seabeds.  
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50 The results for *E. spinax* are very similar to those for *G. melastomus*.  
51 The best model fit for this species included depth, slope of seabed and type  
52 of substratum as relevant covariates. Table 1 shows a positive relation be-  
53 tween log-bathymetry (posterior mean = 5.45; 95% CI = [2.70,10.39]), slope  
54 (posterior mean = 0.09; 95% CI = [-0.06,0.10]) and *E. spinax* occurrence.  
55 Habitats associated with hard substrata (posterior mean = -0.73; 95% CI  
56 = [-3.36,1.70]) show the highest estimated probability of occurrence with re-  
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spect to the reference level (sand substratum), the lowest corresponding to muddy beds (posterior mean = 0.08; 95% CI = [-1.61,1.73]).

Figure 5(c) shows a map of the median posterior probability of occurrence of *E. spinax*, with a marked influence of depth. High probabilities appear in deep water, and low probabilities in coastal waters.

Model prediction performance statistics of all models are presented in Table 2. All models have achieved AUC values greater than 0.80, which indicates an excellent degree of discrimination between those locations where a species is present and those where it is absent. All maxKappa values are between 0.55 and 0.70, which represents a good degree of similarity between the occurrence of the species and the available real evidence. Specificity and sensitivity also show high values ( $> 0.8$ ), reflecting a high ability of the model to predict true negative and true positive predictions correctly.

	AUC	maxKappa	sensitivity	specificity
<i>S. canicula</i>	0.88	0.63	0.87	0.81
<i>G. melastomus</i>	0.84	0.69	0.95	0.90
<i>E. spinax</i>	0.90	0.72	0.84	0.92

Table 2: Model prediction performance statistics for the three species studied. AUC (Area Under the receiver-operated characteristic Curve), maxKappa, sensitivity and specificity.

## 4. Discussion

### 4.1. Biological conclusions

Fishery-dependent data were used to improve our understanding of habitat utilization by elasmobranchs in the western Mediterranean Sea. In this study we used data from observers on board commercial trawlers, which represent one of the most important, but often underestimated, sources of data for the study of demersal fish. The methodology used is a Bayesian spatial hierarchical model that makes possible to assess the influence of the covariates on the presence/absence of species, as well as to predict the probability of occurrence in non-sampled areas. We have also introduced the spatial-temporal component into the study, an important effect which is commonly overlooked in most fishery studies that use traditional methods.

The estimated parameters have contributed to quantify habitat use and reveal important relationships of environmental variables with each species'

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9 habitat. With the available data, the main predictors of elasmobranch habi-  
10 tats in the western Mediterranean were found to be depth, slope of seabed  
11 and type of substrate.  
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13 Elasmobranch species from the Gulf of Alicante show different optimum  
14 depths, which may indicate certain of fine-tuned bathymetric segregation,  
15 although they were in fact found to coexist on shelf and slope bottoms.  
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17 However, the direct effect of depth on species occurrence is expected to  
18 be relatively small in relation to the indirect effects of bathymetry due to  
19 its correlation with many crucial environmental and biological parameters.  
20 Due to this, in the absence of such data (e.g. CTD data for oceanographic  
21 characteristics in the near bottom), a good knowledge of the bathymetric  
22 distribution of species could explain the spatial pattern and it is essential for  
23 fisheries management.  
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25 From our results, we can summarize that, in our study area, *E. spinax*  
26 inhabits the deepest stratum, *G. melastomus* the middle and upper slope  
27 and *S. canicula* the shelf and the middle slope. On the upper slope, maps  
28 show a habitat overlap between *G. melastomus* and *E. spinax*, and on the  
29 middle slope a slight overlap between *G. melastomus* and *S. canicula*. Habitat  
30 overlap does not necessarily imply competition, except when resources are  
31 in short supply. Otherwise, on rich shelf bottoms, species that are spatially  
32 segregated are not driven to differentiate their diets and may easily converge  
33 in the use of resources in overlapping areas.  
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35 Our spatial results are in accordance with a recent trophic study of these  
36 species in the Balearic Islands [46]. *S. canicula* and *G. melastomus* both  
37 prey mainly on euphausiids and share the habitat. However, in our study,  
38 *G. melastomus* expressed a wider and deeper distribution trend with respect  
39 to *S. canicula*. A possible explanation for this could be a phenomenon of  
40 competitive exclusion due to the exploitation of similar resources. Based on  
41 the competitive exclusion principle, other species are forced to retreat to the  
42 bathymetric and/or geographic range to which they are most highly adapted  
43 in relation to the other potential inhabitants. In this case *G. melastomus*  
44 retreat to a depth interval of between 400 m. and 700 m., usually home  
45 to the biomass peak of decapod crustaceans, which constitute an important  
46 part of the diet of this species. *E. spinax* feeds preferentially on cephalopods,  
47 while euphausiids are only a small part of the diet. This different trophic  
48 pattern with respect to *G. melastomus* would be a mechanism for reducing  
49 competition in the deepest stratum.  
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51 In general, our results show a negative relationship between all the elas-  
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mobranch species studied and depth, and high slope gradient values. In addition, for *S. canicula*, the probability of their presence is higher where SST and chlorophyll-*a* concentration values are lower. This may be explained by the fact that shallow sunlight waters above the continental shelf are usually areas of high productivity and SST mean values, while the deeper waters away from coastlines usually lack sunlight and nutrients, and present low values of chlorophyll-*a* concentration and SST.

This study confirms the importance of the type of substratum in the patterns of elasmobranch spatial distribution, as substrate type was included among the best models for all species. Our analysis shows that elasmobranchs prefer hard and sandy substrates while muddy ones affect their occurrence negatively. This preference has already been documented [38] and is probably it is partly attributable to the distribution of their preferred prey, which as mentioned earlier, are crustaceans [16].

These patterns were also consistent with those from other studies reporting on habitat utilization by various species (e.g. *R. brachyura*, *R. montagu* and *S. stellaris* in [9]; *R. clavata* in [18]; *S. canicula* in [47]).

Although the present study was limited to three species, multivariate analysis of elasmobranch assemblage show that 20 out of 23 species of elasmobranchs caught in this area are always fished jointly with one of the species examined. These results indicate that sensitive habitats identified for the three species studied are shared by the other, less frequently caught elasmobranchs. The preservation of these habitats may be useful for protecting the majority of the species of the elasmobranch community in this area. However a more thorough analysis should be done to verify with which of the species studied a given elasmobranch species is usually fished and what kind of habitat shared.

Finally, it should be noted that although the fishery-dependent data that we used were collected with a systematic sampling design, Bayesian spatial models may also aid analyses of data with geographically uneven levels of survey effort because such bias can be incorporated within the spatial random-effect term, thereby reducing its influence on estimates of the effects of environmental variables. By treating spatial effects as a variable of interest, hierarchical Bayesian spatial models can suggest the identity of additional environmental covariates that may improve model fit or the existence of area effects that may limit population viability.

However, some other data are available for elasmobranch species from online databases, such as Fishbase and the Global Biodiversity Information

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9 Facility (GBIF). These databases include presence-only data and provide  
10 probability maps on a more extensive spatial scale. Macro-scale studies al-  
11 low for a broader and more complete view of ecosystem status, but their  
12 use often leads to a compromise in the analysis, because the quality and  
13 quantity of data available for large ecosystems and long time-series are often  
14 lower. Mapping sensitive habitats of vulnerable species within a region for  
15 conservation planning requires the highest level of accuracy. Here, Bayesian  
16 interpolations are sufficiently reliable for the purpose of effective decision  
17 making and a range of evaluation criteria demonstrated the good predictive  
18 performance and properties of this approach as well as its advantages in term  
19 of ecological interpretability.  
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#### 24 *4.2. Applicability of the results for fisheries management*

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26 Improved knowledge of the spatial distribution of commercially impor-  
27 tant fish species and their relationships with the marine environment could  
28 form an integral aspect of a precautionary approach [43]. There is growing  
29 worldwide support for the argument that fisheries should be conducted in a  
30 way that is robust to environmental change, and thus that fish stocks should  
31 never be exploited to a point where they cease to be resilient to environmental  
32 change.  
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35 In order to achieve this purpose, the European Marine Strategy Frame-  
36 work Directive has specifically requested the incorporation of any existing  
37 knowledge about environmental drivers in the assessment of ecosystems and  
38 fisheries and in advice [48].  
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41 Implementing plans and control schemes that would target specific species  
42 assemblages, based on a good knowledge of the species' spatial distribution  
43 in relation to the environment, could serve as a sustainable approach to fish-  
44 eries management and also for other marine activities and uses [29]. The  
45 establishment of marine protected areas for protecting sensitive habitats, in  
46 line with the recent trends for a holistic ecosystem-based approach to man-  
47 agement and Marine Spatial Planning, would also benefit from an improved  
48 understanding of the spatial distribution of vulnerable species such as elas-  
49 mobranchs.  
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52 To achieve these objectives, predictive habitat maps, such as those gen-  
53 erated by the approach presented here, could be useful source of information  
54 in the selection of areas for improved regional management or technical mea-  
55 sures adoption.  
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10 We believe that the use of this approach for constructing maps of the  
11 spatial distribution of vulnerable species may help the design of integrated  
12 programmes for the more efficient management and control of marine re-  
13 sources.  
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## 15 **5. Conclusions**

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17 Species habitat analysis should be able to identify those areas within the  
18 distribution of a species that contribute most to sustain the long-term viabil-  
19 ity of a population. Although it may be complicated to define the boundaries  
20 of sensitive habitats, the definition of these areas, combined with an efficient  
21 fishery management that recognizes the importance of such areas, represents  
22 the first step towards facilitating an EAFM approach [45]. However, accuracy  
23 is not always easy to achieve because there is often a large amount of variabil-  
24 ity surrounding the measurements of response and environmental variables  
25 [22]. This variability leads to uncertain predictions, and consequently to un-  
26 informed decision making. It is therefore important to develop tools which  
27 account for measurements with significant variability. Here, we have shown  
28 a Bayesian spatial hierarchical model that makes it possible to identify sen-  
29 sitive habitats together with a full specification of associated uncertainty. In  
30 our study we have improved knowledge of the habitat utilisation of elasmobranchs  
31 in the Gulf of Alicante and provided practical tools for conservation  
32 planning and resource management. However, as both species and environ-  
33 mental data are sampled over a limited period of time and area of space, the  
34 models fitted can only reflect a snapshot view of the expected relationship.  
35 Future studies should compare the spatial distribution of these species from  
36 a fishery-independent scientific survey, which is often considered as being a  
37 more reliable abundance index because of its scientifically rigorous design [4].  
38 However, this first approximation could be serve to promote a greater effort  
39 in data collection and to identify the areas on which future research attempts  
40 should concentrate.  
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**Figure legends**

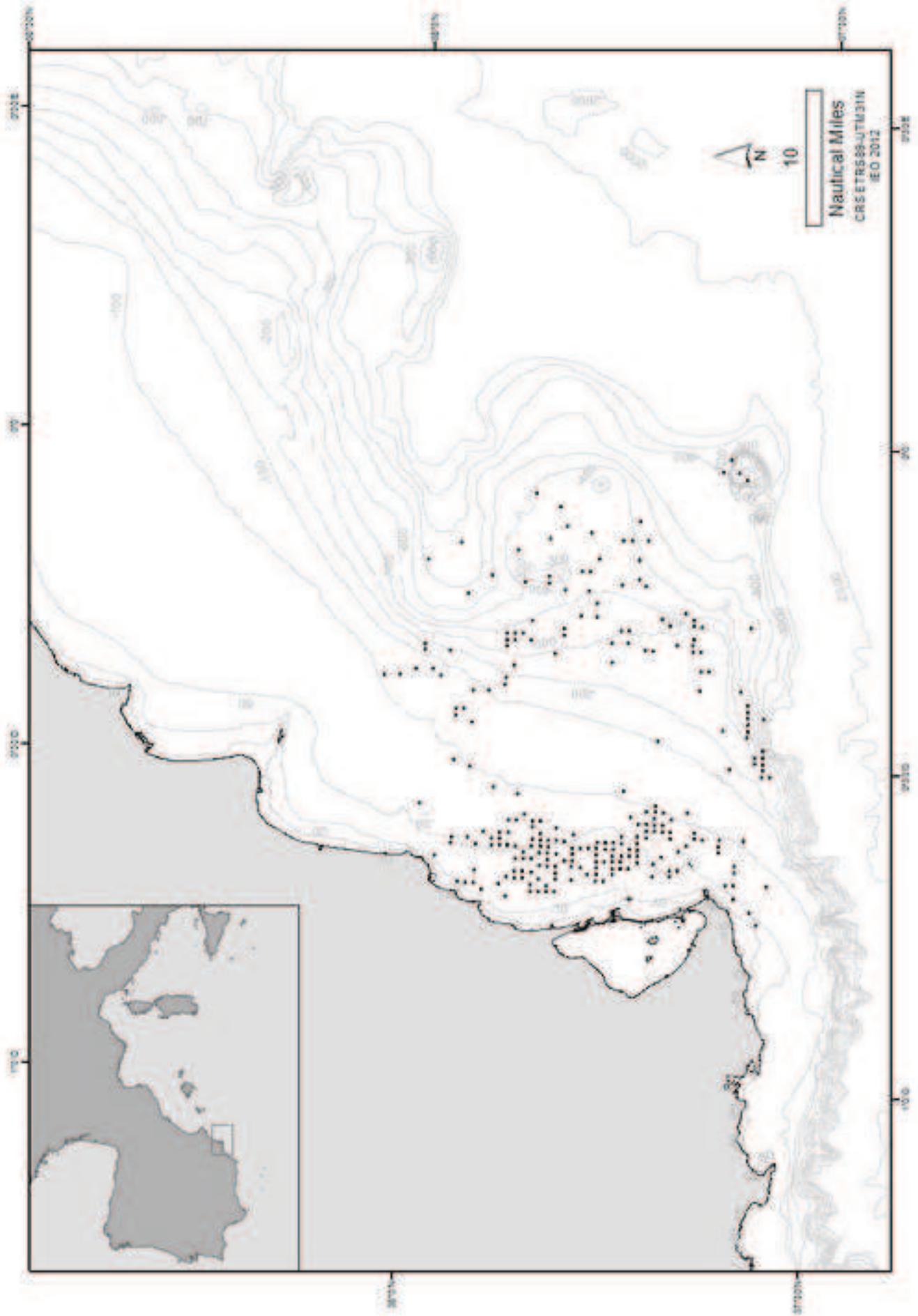
*Figure 1:* Map of the study area with the sampling locations indicated by black dots.

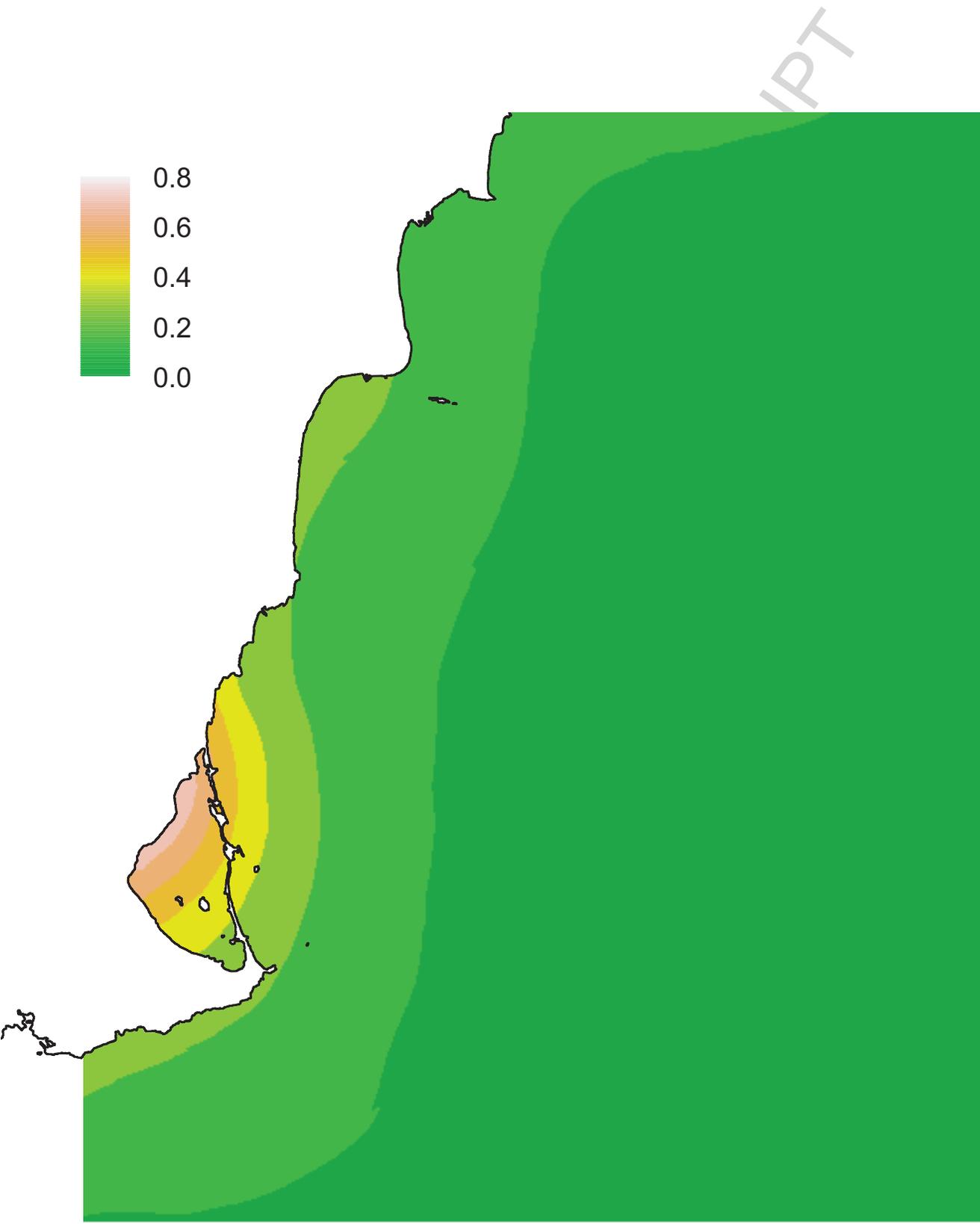
*Figure 2:* The spatial patterns of the environmental variables used to map the habitat models, including (A) satellite derived Chlorophyll-*a* mean values; (B) satellite derived sea surface temperature mean values; (C) bathymetric map; (D) slope map; (E) seabed sediment type map.

*Figure 3:* The triangulation of the Gulf of Alicante. The (●) mark the fishing locations.

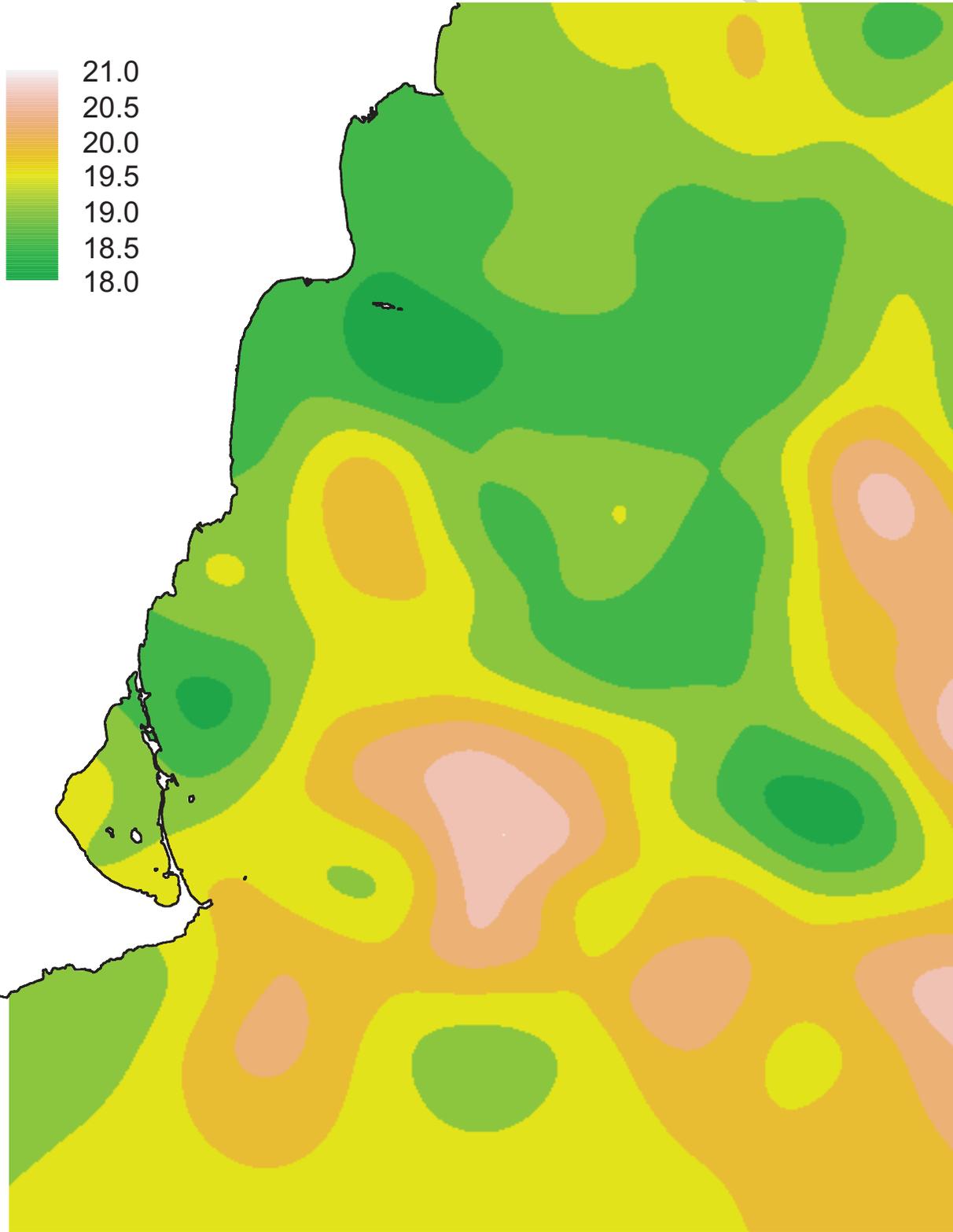
*Figure 4:* Analysis Cluster dendrogram (4a) and MDS ordination (4b) of elasmobranch species caught during bottom trawl commercial hauls carried out in the Gulf of Alicante.

*Figure 5:* Median of the posterior probability of the presence of the studied elasmobranchs: *S. canicula* (5a); *G. melastomus* (5b); *E. spinax* (5c). Sampling locations for the presence (●) and the absence (●) were plotted.

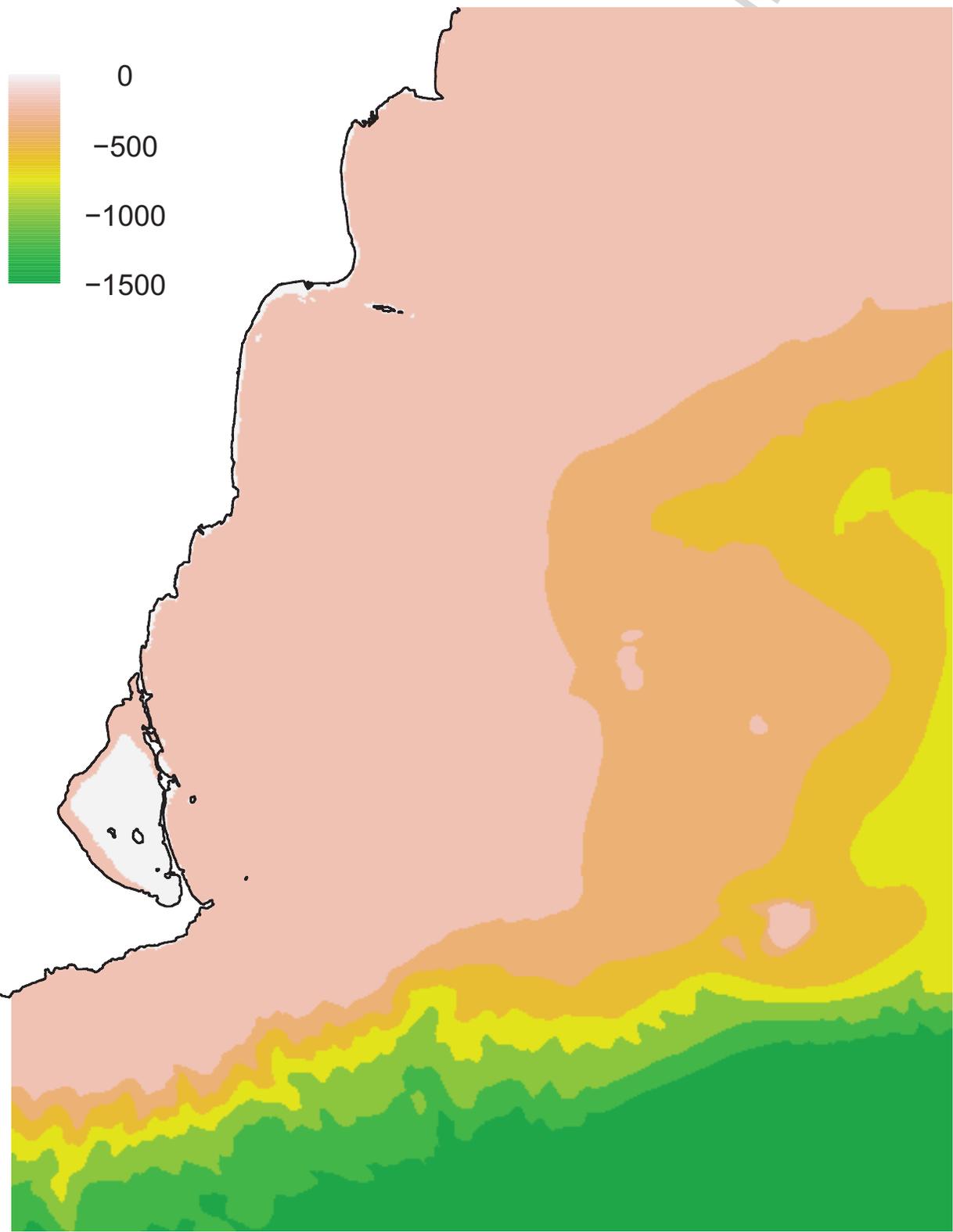


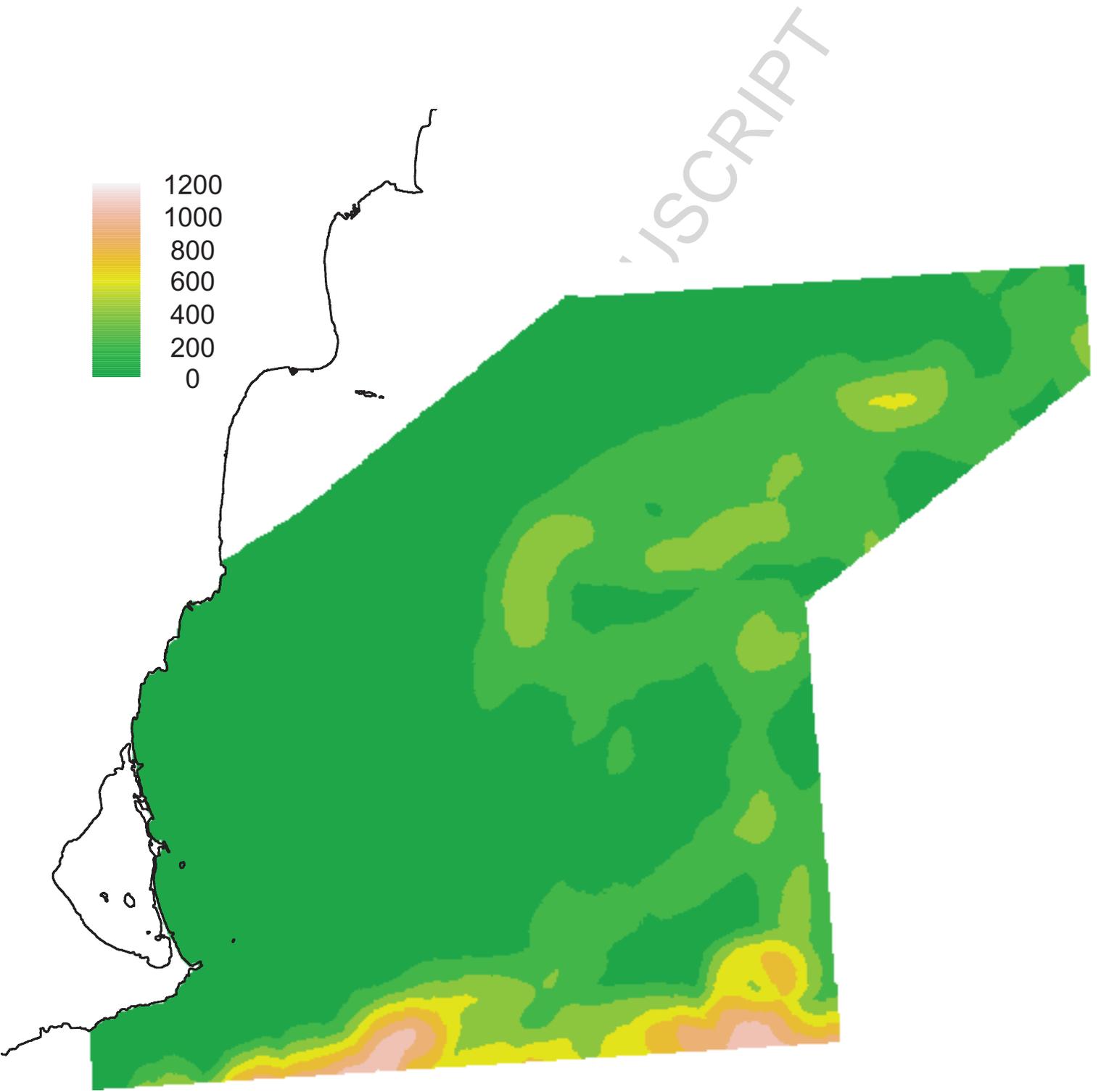


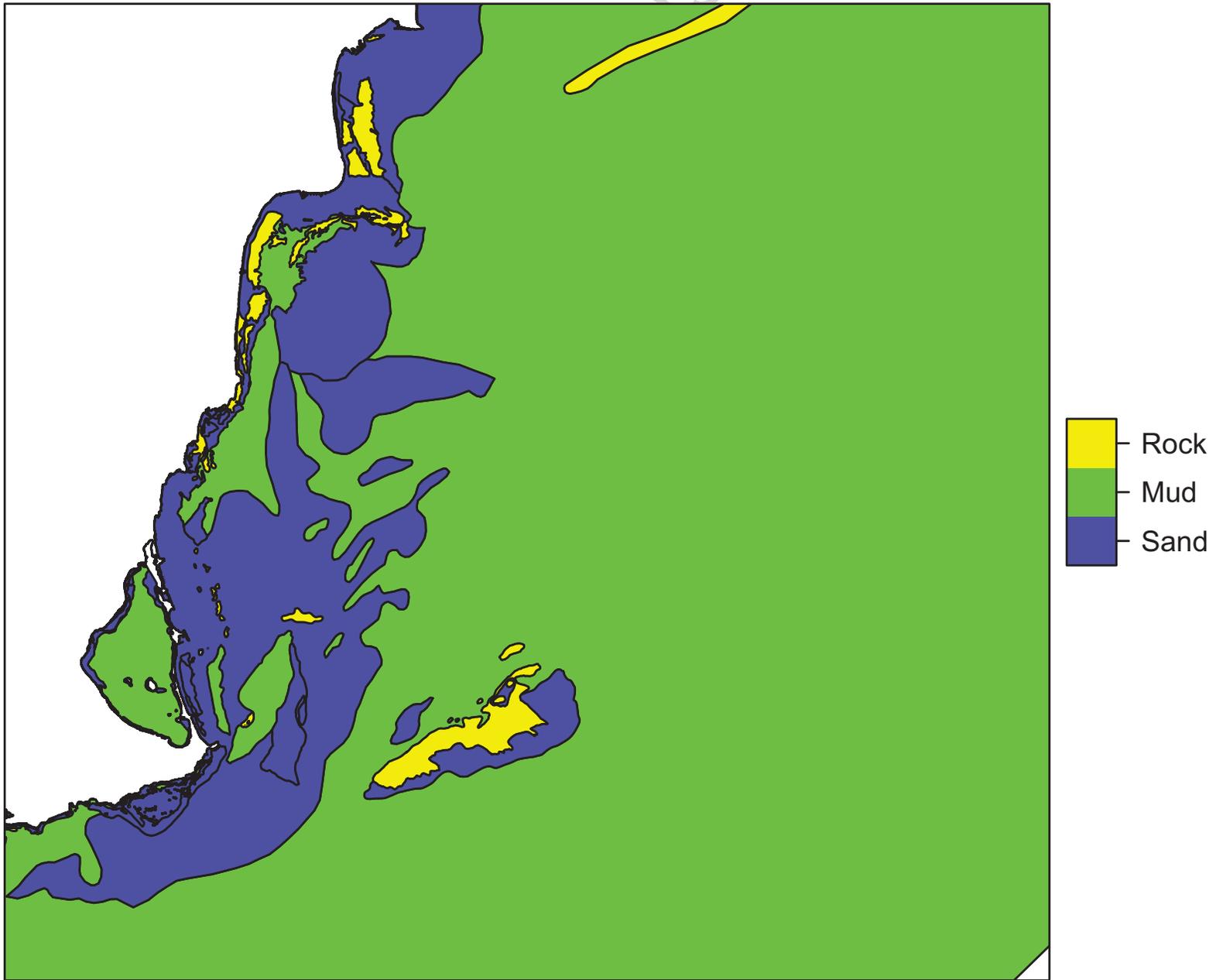
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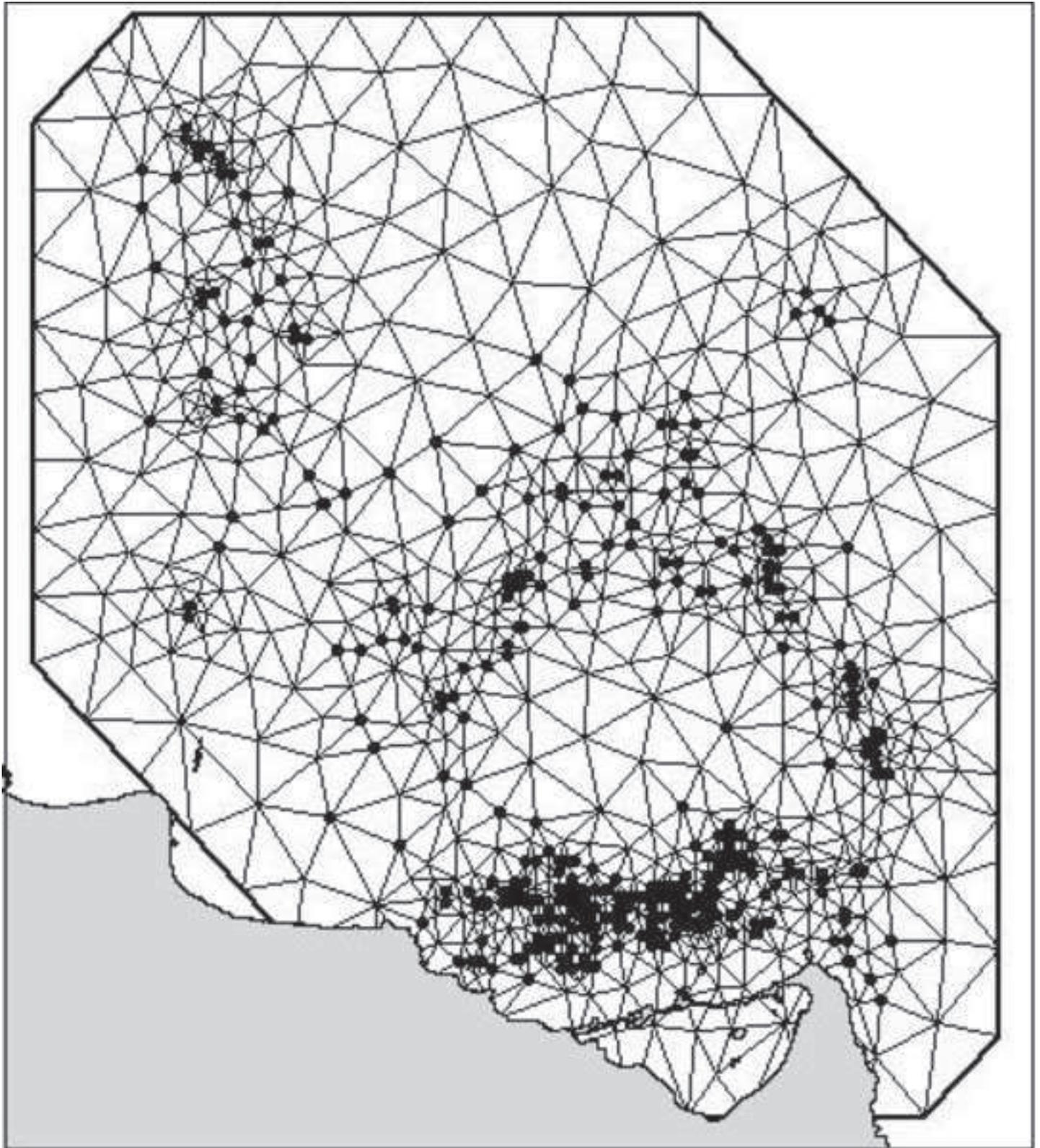


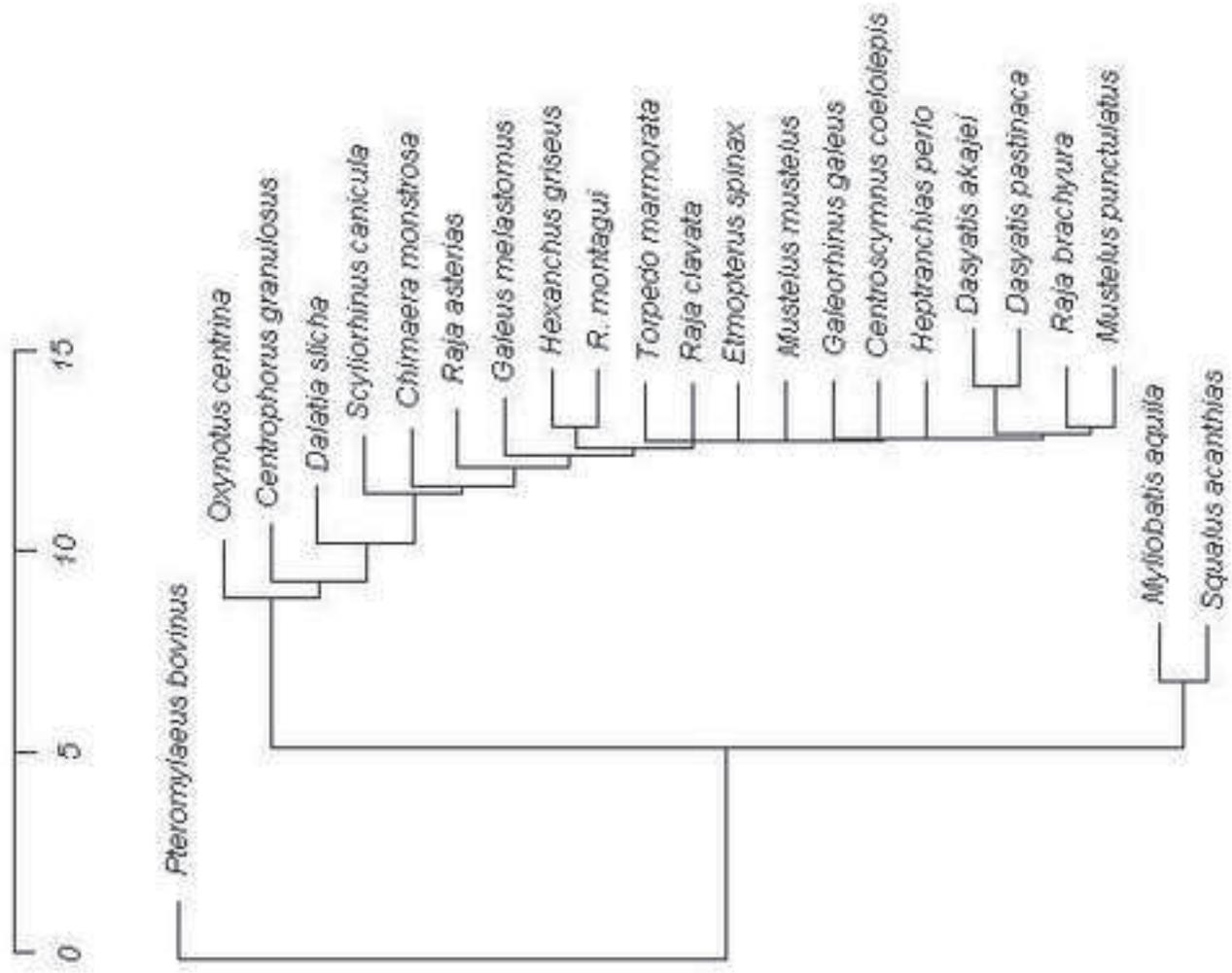
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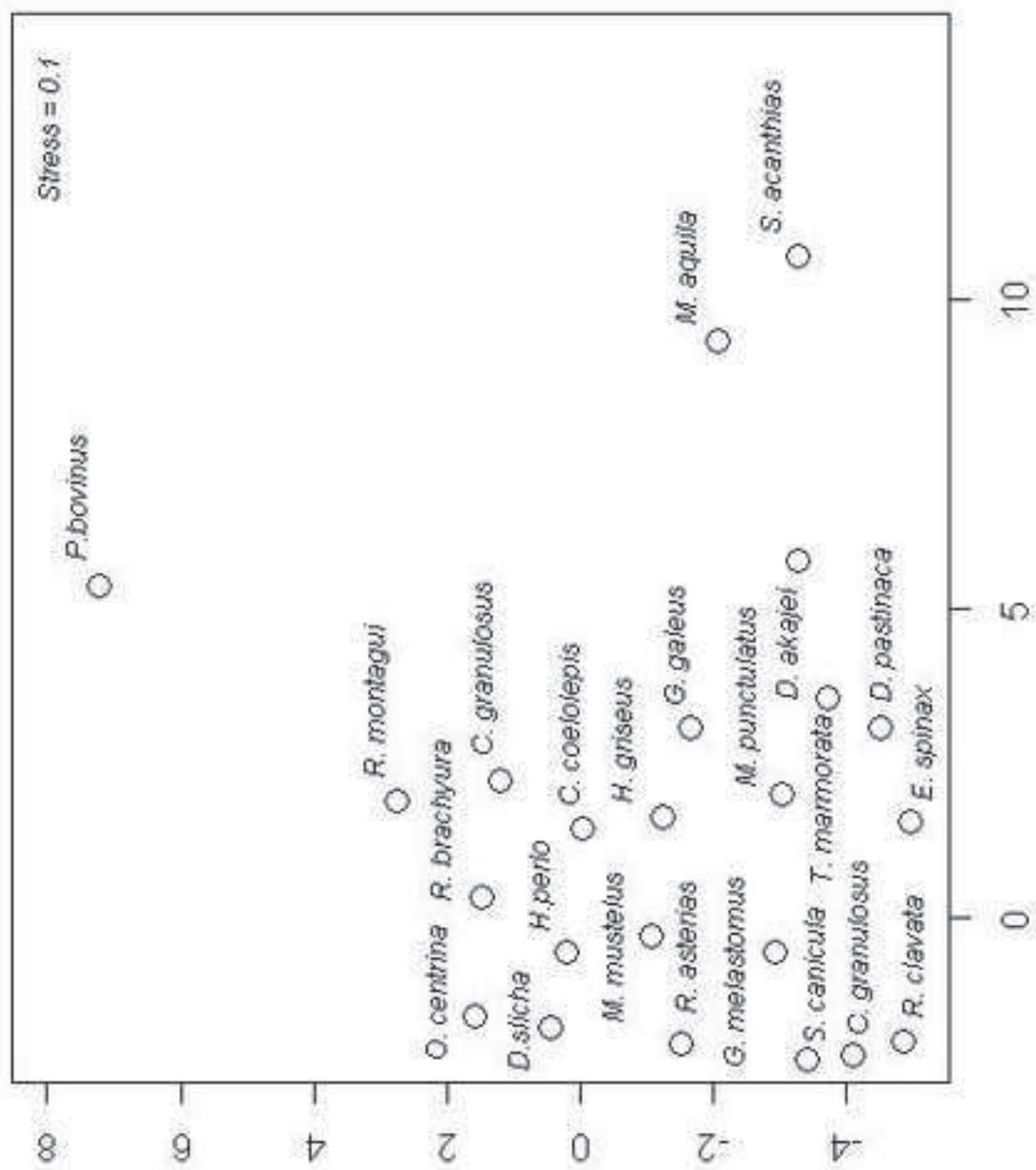


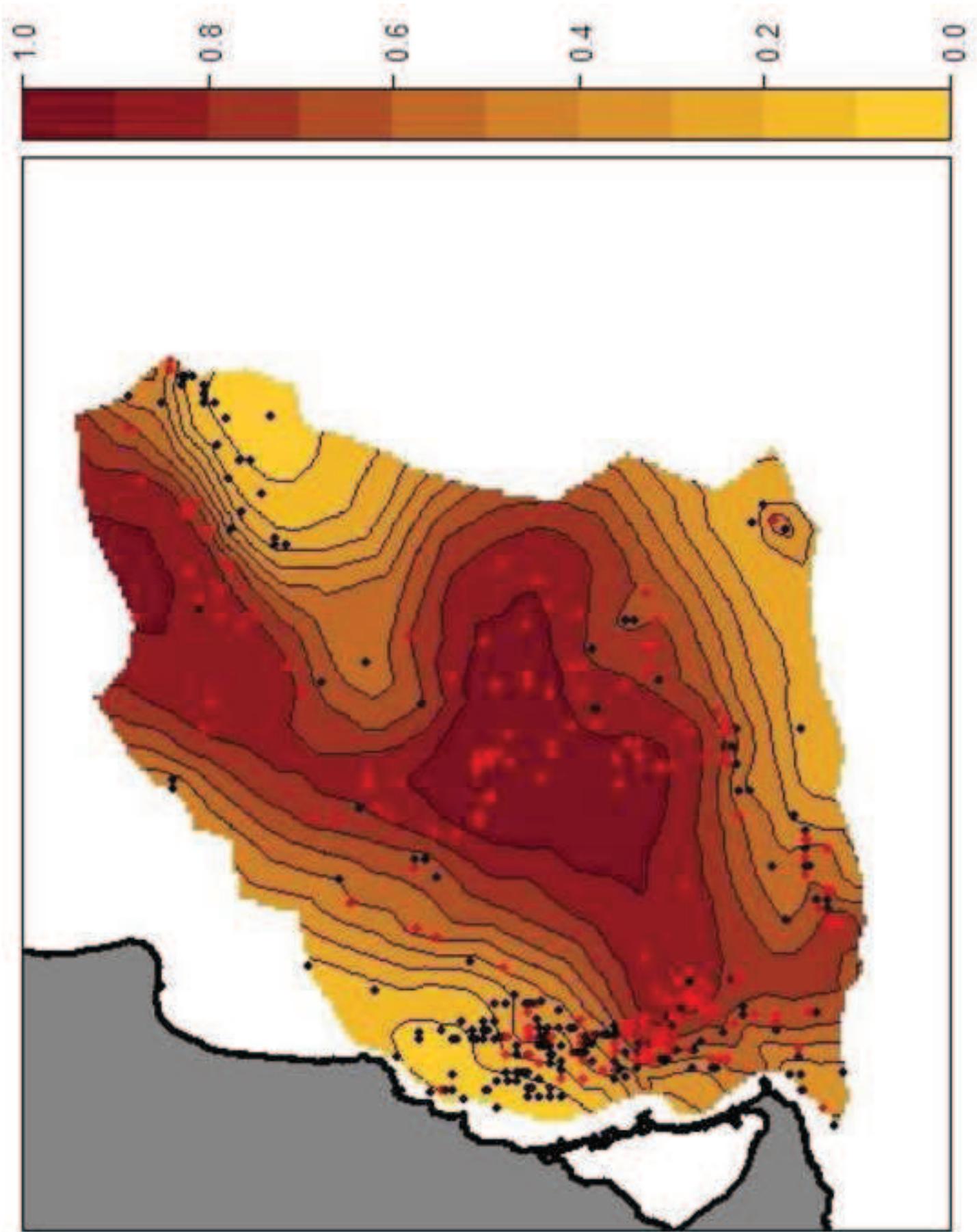


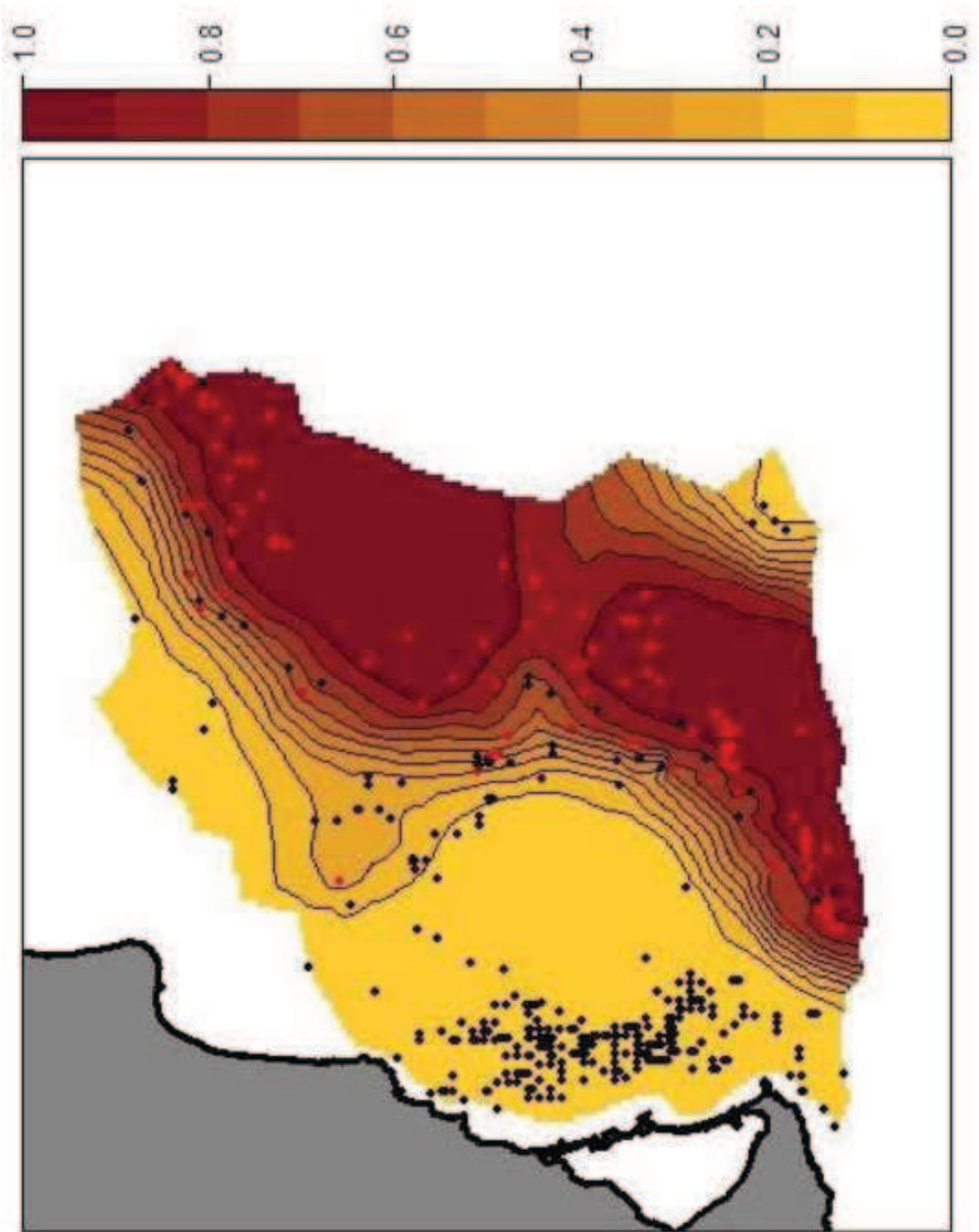


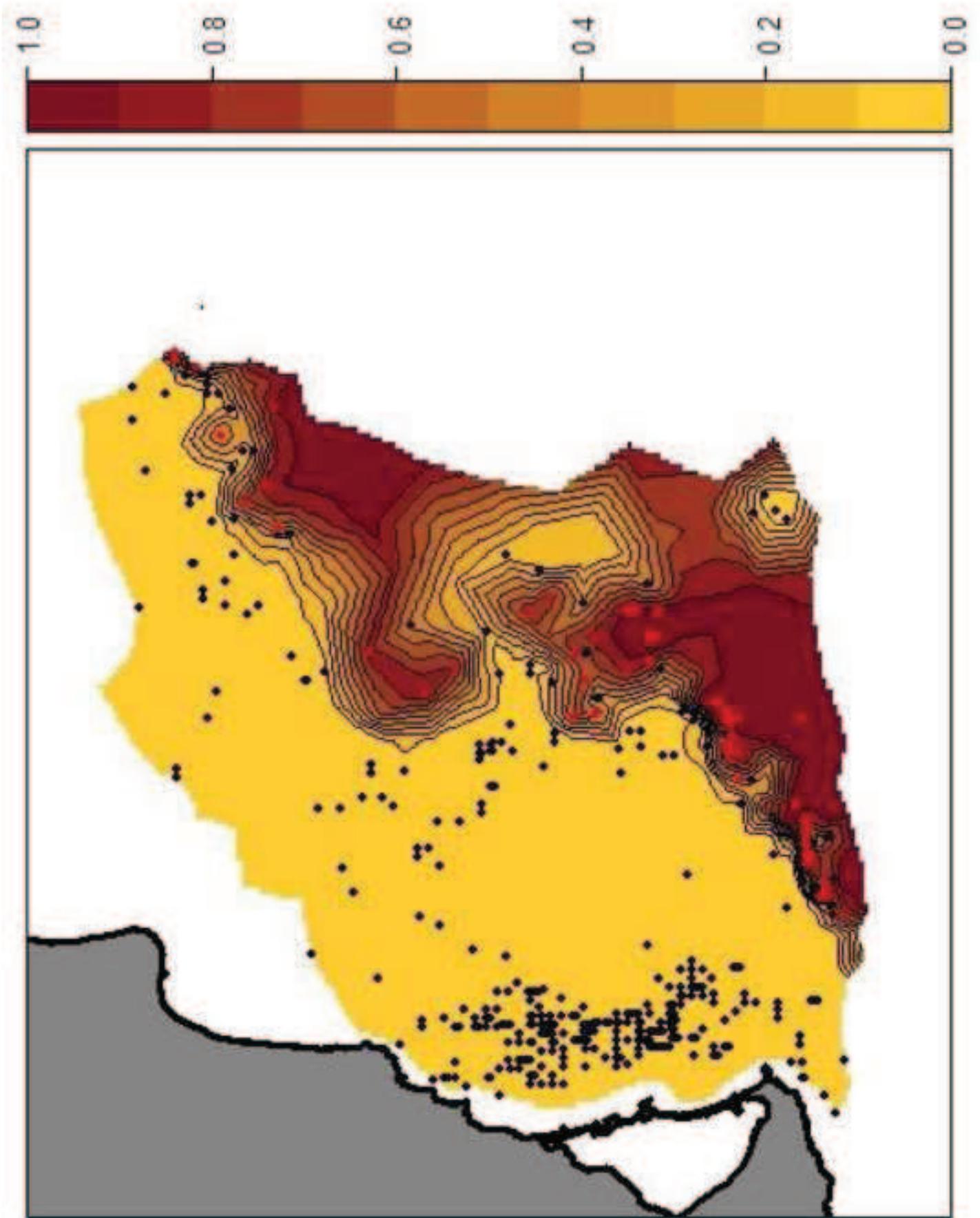












**Highlights**

Bayesian hierarchical spatial models were used to map the sensitive habitats of elasmobranchs.

Habitat associated with hard, sandy and high slope seabeds, mainly from deep waters, have a higher probability of presence.

The studied species show different optimum depths, which could indicate certain of bathymetric segregation.

Maps of predicted probability of occurrence were provided to improve fishery management