



Modelling seabirds biodiversity through Bayesian Spatial Beta regression models: A proxy to inform marine protected areas in the Mediterranean Sea

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ABSTRACT

Seabirds are bioindicators of marine ecosystems health and one of the world's most endangered avian groups. The creation of marine protected areas plays an important role in the conservation of marine environment and its biodiversity. The distributions of top predators, as seabirds, have been commonly used for the management and creation of these figures of protection.

The main objective of this study is to investigate seabirds biodiversity distribution in the Mediterranean Sea through the use of Bayesian spatial Beta regression models. We used an extensive historical database of at-sea locations of 19 different seabird species as well as geophysical, climatology variables and cumulative anthropogenic threats to model species biodiversity. We found negative associations between seabirds biodiversity and distance to the coast as well as concavity of the seabed, and positive with chlorophyll and slope. Further, a positive association was found between seabirds biodiversity and coastal impact.

In this study we define as hot spot of seabird biodiversity those areas with a posterior predictive mean over 0.50. We found potential hot spots in the Mediterranean Sea which do not overlap with the existing MPAs and marine IBAs. Specifically, our hot spots areas do not overlap with the 52.04% and 16.87% of the current MPAs and marine IBAs, respectively. Overall, our study highlights the need for the extension of spatial prioritization of conservation areas to seabirds biodiversity, addressing the challenges of establishing transboundary governance.

1. Introduction

The management of marine protected areas (MPAs hereafter) based on top predators distributions can be highly efficient, leading to higher biodiversity levels and more ecosystem benefits (Lascelles et al., 2016; Pennino et al., 2017; Davies et al., 2021). In the last decades, the creation of MPAs were recognized as an essential tool towards the conservation and management of marine biodiversity, including seabirds (Abdulla et al., 2008; Arcos et al., 2012; Cleasby et al., 2020). As an example, BirdLife International extended its Important Bird Area (IBA hereafter) Programme to the marine environment (Bird Life International, 2010) with the purpose of designating MPAs areas based on

seabirds data (Arcos et al., 2009, 2012).

Although there has been a high emphasis on the establishment of MPAs, their location and effectiveness haven been questioned (UNEP-WCMC, 2016; Zupan et al., 2018). Similarly, there are also concerns about whether MPAs can ensure the long-term persistence of species in the face of changing ocean conditions as well as whether they can help buffer marine communites against the impacts of climate change (Handley et al., 2020).

For the designation of MPAs one of the main prerequisite is a solid knowledge of species-environment relationships as well as the identification of priority areas using robust analysis of existing information (Pennino et al., 2013; Beal et al., 2021a,b). Species and biodiversity

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mapping is essential for both, management and conservation strategies, because it could provide a clear picture of the distribution and extent of wildlife populations and thus facilitates managing their environment (Davies et al., 2021).

Similarly, marine IBAs are defined according to the regular presence of threatened seabird species, as well as congregations of >1% of global populations. Although marine IBAs designation is not underpinned by legal obligation, they may be used to designate protected areas under national legislation. Currently, not all the marine IBAs hold a figure of protection, however they should be considered in spatial management plannings due to their significant contribution to the conservation of seabirds and their habitats (McGowan et al., 2018).

Seabirds comprise several different families of birds inhabiting marine ecosystems. This group of species are among the world's most endangered avian groups mainly due to their vulnerability to human activities, including climate change, bycatch, invasive species, overfishing and oil spills (Lee et al., 2008; Croxall et al., 2012; Bi et al., 2021). They are top or mesopredators and their populations tend to reflect conditions over large spatial and long-term scales, converting them in valuable bioindicators of marine ecosystems health (Croxall and Rothery, 1991; Croxall et al., 2012; Dias et al., 2019), and they are considered umbrella species (Branton and Richardson, 2011).

Seabirds breed in colonies in land. The knowledge of the distribution and size of the breeding areas (i.e. colonies) allow us to improve the management of coastal areas as well as the seaward extension of the breeding colonies (Boermann et al., 2020). In the last years, important breeding areas for seabirds have been identified through terrestrial Important Bird and Biodiversity Areas (IBAs; Donald et al., 2019). Nevertheless, seabirds are also mobile, they can move large distances for feeding or migrating, assembling at specific marine areas (hot spots). While key breeding sites for seabirds are well known and mostly managed under different levels of protection, their habits at-sea are often poorly understood (Lascelles et al., 2012; Beal et al., 2021a,b).

The designation of these marine hot spots is often challenging due to the practical difficulties of sampling open sea waters (Wood et al., 2008; Fabri et al., 2014). Despite the recent advances in biologging technology for the identification of important marine hot spots (telemetry, data-loggers, etc.), several marine regions are still poorly studied. This is the case of the Mediterranean Sea, where available data are mainly restricted to local scale areas and to a few regional hot-spots, usually encompassing only some species (Oro and Ruiz, 1997; Arcos et al., 2009; Péron et al., 2013). Therefore, the identification and conservation of relevant seabirds hot spots is crucial for the effective management of these top predators and their underlying ecosystem in order to reduce the biodiversity loss (Arcos et al., 2012; Handley et al., 2021; Davies et al., 2021; Beal et al., 2021a,b).

This study aims to investigate the seabirds biodiversity distribution at-sea using a large spatial scale: the entire Mediterranean Sea. Many threats are altering the seabird habitats in the Mediterranean such as habitat loss and degradation, pollution, overfishing and recently climate change (Coll et al., 2010, 2012; Florentino and Vitale, 2021). Assessing the consequences of human impacts is crucial both to protect and ensure the seabird biodiversity.

Similar to most of coastal ecosystems, MPAs have become one of the primary tool in the Mediterranean Sea for the protection of biodiversity, with more than 100 MPAs that cover approximately 5% of the continental shelf (Claudet et al., 2020). However, mostly of the Mediterranean MPAs network has been set up following local sociopolitical targets instead of ecological considerations (García-Charton et al., 2008) and the effectiveness of these MPAs to protect the different marine biodiversity taxas is poor (Horta e Costa et al., 2016; Claudet et al., 2020).

Within this context, in this work we used Bayesian hierarchical spatial models to (i) model the distribution of seabird biodiversity in relation to 16 physical, climatology and anthropogenic variables, and to identify their respective contribution, (ii) to map seabird's biodiversity in the Mediterranean Sea and (iii) to quantify the degree of overlap of

high biodiversity areas with present MPAs and marine IBAs to explore how current approaches are protecting this important biodiversity component.

In particular, we make use of a particular case of Bayesian hierarchical spatial models, namely Areal data Beta regression models. We implement them within the Bayesian approach, as analysing spatial models within this approach has shown several advantages over traditional methods (Banerjee et al., 2014). In particular, it provides a more realistic and accurate estimation of uncertainty while allowing the spatial component to be added as a random effect term in a natural way, reducing so its influence on estimates of the effects of geographical variables (Gelfand and Smith, 1990). The use of robust and accurate methods is essential for improving the understanding of the spatial distribution of seabird biodiversity and could help the management of regional MPAs and marine IBAs. Indeed, we show how our estimates overlap with many of the existing protected areas but more importantly, we present new marine areas susceptible of protection from a seabird point of view.

2. Material and methods

2.1. Study area

The Mediterranean Sea is the largest and deepest enclosed sea on Earth, with more than 17,000 described marine species which contribute to almost 7% of the world's marine biodiversity (Coll et al., 2010, 2012). This basin is highly heterogeneous from an environmental, ecological and socio-economic point of view. It covers approximately 2,500,000 km² (excluding the Black Sea), and it is connected through the Strait of Gibraltar to the Atlantic Ocean in the west, and through the Strait of Bosphorus to the Sea of Marmara and the Black Sea in the north-east, while in the south-east the Suez Canal links the Mediterranean to the Red Sea and the Indian Ocean (Coll et al., 2010, 2012). Two distinct basins are identified in the Mediterranean, the western (0.85 million km²) and the eastern (1.65 million km²), divided by the Strait of Sicily. Strong environmental gradients characterized these basins making the eastern basin more oligotrophic than the western one (Estrada, 1996). Additionally, local characteristics enrich coastal areas with specific conditions of wind, temporal thermoclines, river discharges and municipal sewage. The average depth of the Mediterranean is approximately of 1460 m and the maximum is 5267 m. Sea surface temperature shows a high seasonality and an important spatial gradients from west to east and north to south (Bosc et al., 2004). Overall, the Mediterranean has narrow continental shelves and a large part of its basin can be classified as deep sea with bottom temperatures that can vary from 12.8° to 15.5 °C, and high salinity of 37.5–39.5 PSU (Emig and Geistdoerfer, 2005; Danovaro et al., 2010).

2.2. Seabirds biodiversity index

An extensive historical database of at-sea locations corresponding to 19 different seabird species obtained from Sea Around Us project (www.seararoundus.org) was used. The database included information about the foraging ranges of the seabird species considered during both breeding and non-breeding season and spans over 11 years (1990–2000). As explained in Coll et al. (2012), quantitative information on the distribution of seabird species consisted of two different layers: one describing the foraging ranges during the breeding season, and a second during the non-breeding season. We created a buffer distance for each seabird foraging range using a combination of references and expert knowledge (www.birdlife.org; www.avibirds.com; Cramp and Simmons, 1977, 1983; Cramp, 1985; Monbailliu, 1986; Harrison, 1987; del Hoyo et al., 1992, 1996; Johnsgard, 1993; Handrinos and Akritis, 1997; de and Brooke, 2004; Sterry, 2004; Nelson, 2005; Louzao et al., 2006; Yésou, 2006; Bourgeois and Vidal, 2008). For seabird species foraging only in pelagic waters, foraging ranges were drawn

following available distribution maps from the literature. Table 1 depicts the names of the species included in our analysis as well as buffer distances (km) used to define the main foraging ranges during breeding and non-breeding season. Species were classified in pelagic (4) or coastal (15) based in their feeding ecology following Martínez-Abrán (2011).

Therefore, and following the methodology by Coll et al. (2010, 2012), we estimated the seabird species biodiversity index as the sum of the species co-occurring by overlapping distribution maps at fine-scale resolution ($0.1 \times 0.1^\circ$ grid cells). Then we re-computed the known occurrences in relative terms between 0 (no species present) and 1 (100% of species present). The index was measured for a total of 25,584 locations (Fig. 1).

2.3. Environmental variables

Environmental variables were extracted from the Bio-Oracle (Tyberghein et al., 2012) (<https://www.bio-oracle.org>) and the MARSPEC (Sbrocco and Barber, 2013) (<http://www.marspec.org>) databases. Ecological theory posits that many factors may determine species distributions. Bio-Oracle and MARSPEC was assembled in order to maximize different potential factors that may influence marine species distributions, including physical, chemical and biological variables. In this study, 12 climatology of geophysical, biotic and climate rasters for world oceans in a 5 arcmin spatial resolution were extracted from these databases (Tyberghein et al., 2012). These variables represent the environmental conditions of the last twenty-years and provide cumulative information about the environmental regimes of the Mediterranean. Finally, the environmental variables used are depicted in Table 2.

2.4. Cumulative anthropogenic threats

Four different direct and indirect anthropogenic threats occurring in

Table 1

Latin and common names of the seabirds species included in this study as well as buffer distances (km) during breeding and non-breeding season. Asterisks (*) indicate pelagic species. P: The ranges of pelagic foragers were defined without using a buffer; X: Species that leave the Mediterranean on a seasonal basis and thus, they do not have a range layer during that season.

Latin Name	Common Name	Buffer (Breeding Season)	Buffer (Non- Breeding Season)
<i>Calonectris diomedea</i> (*)	Cory's Shearwater	P	X
<i>Hydrobates pelagicus</i> <i>melitensis</i> (*)	European Storm Petrel	50	X
<i>Ichthyaetus audouinii</i>	Audouin's Gull	10	10
<i>Larus fuscus</i>	Lesser Black-Backed Gull	X	10
<i>Larus genei</i>	Slender-Billed Gull	10	10
<i>Larus melanocephalus</i>	Mediterranean Gull	10	10
<i>Larus michahellis</i>	Yellow-legged Gull	10	10
<i>Larus ridibundus</i>	Common Black-Headed Gull	X	10
<i>Pelecanus crispus</i>	Dalmatian Pelican	X	5
<i>Phalacrocorax aristotelis</i> <i>desmarestii</i>	European Shag	10	10
<i>Phalacrocorax carbo</i>	Great Cormorant	X	5
<i>Puffinus mauretanicus</i> (*)	Balearic Shearwater	P	P
<i>Puffinus yelkouan</i> (*)	Levantine Shearwater	P	P
<i>Sterna albifrons</i>	Little Tern	5	X
<i>Sterna bengalensis</i>	Lesser Crested Tern	5	5
<i>Sterna caspia</i>	Caspian Tern	5	5
<i>Sterna hirundo</i>	Common Tern	5	5
<i>Sterna nilotica</i>	Gull-billed Tern	5	X
<i>Sterna sandvicensis</i>	Sandwich Tern	10	10

the Mediterranean Sea were considered for this study based on previous data compilations and with a spatial resolution of $0.1 \times 0.1^\circ$ grid cells representing average conditions during 2000–2010 mainly (Coll et al., 2010, 2012). The generated variables accounted for the presence or absence of the different threats (expressed in a continuum between 0 and 1) at each grid cell. Specifically, the threats used are: (1) Coastal-based impacts: cumulative effects from inorganic and organic coastal pollution, litter, nutrient runoff and hypoxia as well as the presence of alien species and aquaculture activities. (2) Climate change: cumulative effects from changes in sea water temperature, in the intensity of ultraviolet radiation and in water acidification. (3) Maritime traffic: cumulative effects from maritime traffic due to shipping and other transport and the presence of oil rigs. (4) Trawling fishing activities: cumulative (historical to present) high disturbance on the sea floor by bottom fishing gear operations (from 1950 to 2006).

In addition a fifth variable was added to better represent the fishery footprint. Automatic Identification System (AIS) (Kroodsma et al., 2018) maps sourced online from the Global Fishing Watch website (GFW: <http://globalfishingwatch.org>) were indeed used. GFW estimates daily fishing effort by combining scores for all fishing vessels operating in the area. Fishing is defined as the period that a vessel spends away from shore in which it is not transiting to and from the fishing grounds. We focused in the fishing activity of trawlers, long liners and purse seiners from 2012 to 2017.

In order to better interpret both the direction (positive or negative) and magnitudes (effect sizes) of the parameter estimates in relation to the others, all the explanatory variables, both environmental and anthropogenic predictors, were standardized, i.e. difference from the mean divided by the corresponding standard deviation (Gelman, 2008).

Although there is a temporal mismatch between some of the explanatory variables and the seabird data, they are still the best available cumulative predictors as well as indicators that spatially represent the areas with the greatest environmental and anthropogenic impacts.

2.5. Bayesian Spatial Beta regression with INLA

Beta distributions, usually denoted by $\text{Be}(a, b)$, are commonly used to model variables that assume values in the unit interval (0,1) such as the above mentioned seabird biodiversity index. A Beta distribution depends on two scaling parameters (a, b), but can also be parametrized in terms of its mean $\mu = \frac{a}{a+b}$ and a dispersion parameter $\varphi = a+b$, being its variance $\sigma^2 = \frac{\mu(1-\mu)}{1+\varphi}$. This reparametrization supports the truncated nature of the Beta distribution, allowing also to express the fact that the variance depends on the mean, and maximum variance is observed at the centre of the distribution whereas it is minimum at the edges.

As above mentioned, Beta distributions are defined in the open interval (0, 1). Nevertheless, in practice, as it is our case with the biodiversity index, data may come from the closed interval [0, 1]. In such cases, one option to deal with zeros and ones in Beta distributions is to transform them (Smithson and Verkuilen, 2006). In particular:

$$y^* = \frac{y(N-1) + 1/2}{N}, \quad (1)$$

being N the number of observations. This transformation compresses the data symmetrically around 0.5 from a range of $m = 1$ to $(N-1)/N$, so extreme values are affected more than values lying close to 1/2. Additionally, as it is pointed out in Maier (2014), if $N \rightarrow \infty$ the compression vanishes, that is, larger data sets are less affected by this transformation. From now on, we assume that the variable biodiversity index takes values in the open interval (0, 1), as we apply to it the transformation in (1).

In this scenario the interest is to relate this index with respect to a set of covariates (environmental variables), a similar approach to the generalised linear models is used, namely the Beta regression models

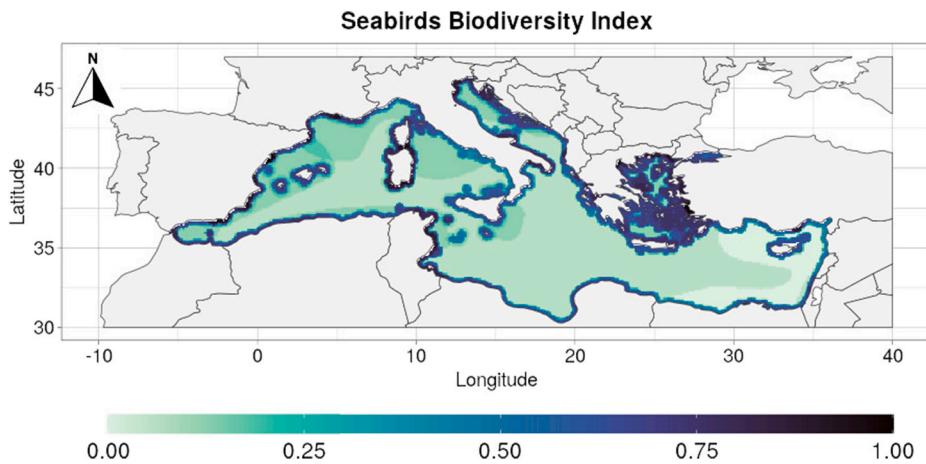


Fig. 1. Seabirds biodiversity index for the Mediterranean Sea.

Table 2
Summary of the environmental covariates used in the study.

Variables	Description	Source
Chlorophyll	Chlorophyll-a concentration (in mg.m-3)	Bio-Oracle
SSS	Sea Surface Salinity (in PSU)	Bio-Oracle
SBT	Sea Bottom Temperature (in C)	Bio-Oracle
SST	Sea Surface Temperature (in C)	Bio-Oracle
Bathymetry	Depth of the seabed (in m)	MARSPEC
AspE	East-West aspect of seabed (in radians)	MARSPEC
AspN	North-South aspect of seabed (in radians)	MARSPEC
Curvature	Curvature of the seabed	MARSPEC
Distance	Distance to the coast (in km)	MARSPEC
Slope	Slope of the seabed (in degree)	MARSPEC
Concavity	Concavity of the seabed (in degree)	MARSPEC
Rugosity	Complexity of the seabed (in degree)	MARSPEC

(Ferrari and Cribari-Neto, 2004). In particular, the mean of the biodiversity index is linked to the environmental predictors via a suitable link function (logit). But, as stated in Paradinas et al. (2018), the immeasurable complexity of ecological spatial processes often means that the spatial variability of the data exceed the variability explained by the explanatory variables. In this case, a good solution to improve model fit and prediction is to introduce spatial terms capable of improving fine scale predictions and identifying hidden spatial hot and/or cold spots that may be important for management purposes.

In particular, if Y_i denotes the value of the index in each location of the grid (denoted i), a spatial Beta regression model can be written as follows:

$$\begin{aligned} Y_i &\sim \text{Beta}(\mu_i, \varphi) \\ \text{logit}(\mu_i) &= X_i \beta + u_i, \\ \theta &= \log(\varphi), \end{aligned} \quad (2a)$$

where note that the precision φ is assumed to be not dependent on any effect and is reparametrized as $\theta = \log(\varphi)$ in order to assure that φ was a positive parameter; $\beta = \{\beta_0, \beta_1, \dots, \beta_m\}$ denotes the vector of regression coefficients regarding to the m fixed effects; X_i is the vector corresponding to the i -th row of the design matrix whose first element is 1 (the one multiplying the intercept β_0), whereas u_i corresponds to an area-specific effect, which is modeled as spatially structured. Although other structures could be specified on $u = \{u_1, \dots, u_n\}$, in this study we implement the conditional autoregressive (ICAR, Besag, 1974).

More detailed, if we consider n areas, each characterized by a set of neighbors $\mathcal{N}(i)$, u_i is assumed to be the following random variable:

$$u_i | u_j, i \neq j, \tau \sim N\left(\frac{1}{\mathcal{N}_i} \sum_{i \sim j} u_j, \frac{1}{\mathcal{N}_i \tau}\right),$$

where $i \sim j$ denotes that j is a neighbor of i , $\frac{1}{\mathcal{N}_i} \sum_{i \sim j} u_j$ is the mean for the area i which is depending of the number of neighbors of i (\mathcal{N}_i), and $\frac{1}{\mathcal{N}_i \tau}$ corresponds to the precision for the area i which is also depending on (\mathcal{N}_i) . If an area has many neighbors then its precision will be bigger (and consequently, the variance will be smaller).

Once the model is stated, the next step is to make inference and prediction. In our case, we have made use of the Bayesian approach, as it provides a good way to address the uncertainty associated with our predictions and estimates. In this respect, Bayesian hierarchical methods are becoming very popular due to the easiness which they can accommodate the complexity of the relationships involved in natural systems. Modelling these relationships often requires specifying sub-models inside the additive predictor that allow a suspected hidden or latent effect (such as the spatial effect) to be inferred that characterise these relationships. In the context of hierarchical Bayesian models, parameters are treated as random variables and so, prior knowledge (if available) can be incorporated using the corresponding prior distributions. In our case, default vague Gaussian distributions $N(\mu = 0, \tau = 0.001)$ have been imposed for the parameters involved in the fixed effects (β_j), while in order to express the prior knowledge (or the lack of it) about hyperparameters, the default prior $\text{loggamma}(1, 0.1)$ was used for θ , and penalized complexity prior (PC-prior) was established for the precision of the random effect τ according to Simpson et al. (2017). In our particular case, the PC-prior for τ was defined in terms of the square root of its inverse, the standard deviation σ , such that $P(\sigma > 5) = 0.1$.

In line with all the above exposed, the full model can be written as:

$$\begin{aligned} Y_i &\sim \text{Beta}(\mu_i, \varphi), \\ \text{logit}(\mu_i) &= X_i \beta + u_i, \\ \varphi &= \exp(\theta), \\ \beta_j &\sim N(0, \tau = 10^{-3}), \\ u_i | u_j, i \neq j, \tau &\sim N\left(\frac{1}{\mathcal{N}_i} \sum_{i \sim j} u_j, \frac{1}{\mathcal{N}_i \tau}\right), \\ \tau &\sim \text{PC-prior}(5, 0.1), \\ \theta &\sim \text{LogGamma}(1, 0.01). \end{aligned} \quad (2b)$$

As it can be observed in equation (2), the three hierarchical stages of the model can be clearly distinguished: the likelihood (on top), the Gaussian latent fields (in the middle) and the hyperparameters (on the bottom).

As it usually happens with hierarchical complex models, numerical approaches are needed to approximate the resulting posterior distributions. In this case, this approximation was performed using the integrated nested Laplace approximation (Rue et al., 2009; Gómez-Rubio,

2020), by means of R-INLA, its implementation in R (R Core Team, 2021). For reproducibility, the R code is available in the public GitHub repository: <https://github.com/sarzoblanca/Modelling-seabirds-biodiversity-through-Bayesian-Spatial-Beta-regression-models>.

2.6. Model selection

We first evaluated the correlation among variables in order to avoid collinearity in our analysis. For all variables, correlations were low (data not shown). Further, and due to the high number of covariates included in this analysis (i.e., 17), we implemented a variable selection method through the R package *subsetselect* (Orestes Cerdeira et al., 2018). This R package looks for subsets which are optimal under various criteria. In this study our criterion was the proportion of variability explained by a subset of variables, particularly we selected the subset that explained the 80% of the variability. Further, this methodology was applied considering two different scenarios. Firstly, we assumed that all the variables were equally relevant in the model, i.e. we did not coerce the inclusion of any of them. Secondly, and given the biological relevance of some of the variables considered, we forced them to be included into the model and hence, the variable selection method was applied to the remaining covariates. Specifically, in this second scenario we coerced three variables: chlorophyll, SST and distance to the coast. Once we found the best model in each scenario, we employed a leave-one-out cross-validation process via the mean logarithmic conditional predictive ordinate (LCPO, Roos and Held, 2011) to select the most appropriate model.

2.7. Overlap with MPAs and marine IBAs

The data corresponding to the Mediterranean marine IBAs were obtained by request to the BirdLife's World Bird Database (WBDB; available at www.birdlife.org/datazone/sites). For details in the establishment of marine Important Bird Areas and data protocols see Arcos et al. (2009); BirdLife International (2010) and Croxall et al. (2012).

The data of the MPAs were obtained from the World Database on Protected Areas (WDPA). This dataset contained national and regional parks, World Heritage sites (WHS) and Specially Protected Area of Mediterranean Importance (Barcelona Convention) (SPAMI).

To assess the overlap between the already established marine IBAs, MPAs and the identified areas of seabirds biodiversity presented in this study, we first need to define the areas which may be considered as hot spot of seabird biodiversity. To that end, we refer as hot spot of seabird biodiversity those areas with a posterior predictive mean value over 0.50. Percentage of overlapped areas with IBAs was computed as

$$\% \text{ overlap IBAs} = \frac{\# \text{ grid cells in the intersection of the hotspots with the IBAs}}{\# \text{ grid cells in IBAs}}, \quad (3)$$

and for MPAs as

$$\% \text{ overlap MPAs} = \frac{\# \text{ grid cells in the intersection of the hotspots with the MPAs}}{\# \text{ grid cells in MPAs}} \quad (4)$$

Finally, and for the sake of comparison, we also present those areas with a posterior predictive mean value over 0.75.

3. Results

The final number of selected variables through the variable selection method performed were eight for each scenario considered (i.e., (1) without coercing any variable and (2) coercing variables on their biological relevance), although the type of variables differed. Nevertheless, based on the LCPO value, the best model selected was that where we coerced three variables (LCPO values being -34.63 and -37.06 for models 1 and 2, respectively). The final model retained as relevant

covariates: chlorophyll, sea surface temperature (SST), distance to the coast, slope, concavity, East-West aspect component of the seabed (AspE), coastal impact and the marine traffic, jointly with the spatial effect. Table 3 presents the posterior mean, standard deviation and 95% symmetric credible intervals for the parameters corresponding to the fixed effects. Furthermore, in Fig. 2 we depict the relevant covariates for the spatial model presented.

Among the variables selected, all the variables were relevant (i.e. the zero is not included in their credible intervals) except for SST, AspE, and marine traffic. In particular, distance to the coast is the most relevant one, reflecting that seabird biodiversity is higher in coastal waters. Another relevant environmental predictor for seabird biodiversity is chlorophyll concentration. Our results show a positive association between this variable and seabird biodiversity, suggesting that seabirds are likely to concentrate in more productive areas. Moreover, seabird biodiversity seems also to be lower in areas where the seabed is more concave and with bigger slope (Table 3).

Among the anthropogenic threats, coastal impact seems to have a relevant impact in the seabirds spatial distribution. The relationship with our response variable is positive, i.e. the most coastal impact the higher value of the seabirds biodiversity index. This result may also be related with the lack of information for deep areas in our database as well as for the fact that coastal impact is more present in coastal areas.

With respect spatial effect, Fig. 3 displays the posterior spatial mean along with its standard deviation.

Fig. 3 displays the posterior distribution of the spatial effect, i.e. it mainly shows the correlated structure that covariates can not explain based on geographical coordinates. As it can be observed, posterior spatial effects compensate the effect of covariates, reflecting the spatial posterior mean a similar pattern to the variable distance to the coast with the exception of the Easter Mediterranean. This area compressed the lowest mean, and mainly reflects the balancing of the spatial effects for the existing high contrast in the Seabirds biodiversity index between the coast and nearest areas. This is also reflected in the spatial posterior standard deviation, where highest values are located in the Easter Mediterranean reflecting a greater uncertainty.

Finally, in Fig. 4 we present the overlap between the areas with a posterior predictive mean over 0.50 and 0.75 as well as the MPAs and marine IBAs already established in the Mediterranean Sea. Furthermore, in Table 4 we depict the percentage of overlap between our predictive means and MPAs and marine IBAs, respectively while Fig. 5 presents the non-overlapped areas obtained in our study which may be susceptible of protection.

4. Discussion

Seabirds are sentinels of the sea. They are considered bioindicators of marine ecosystems due to their populations tend to reflect changes in habitat quality, reduction of fish abundance (overfishing), changes in weather (climate change), as well as many other large-scale anthropogenic threats (Rajpar et al., 2018; Handley et al., 2021). Human impacts predicted for the next future on marine ecosystems will increase mainly

Table 3

Posterior mean, standard deviation and 95% symmetric credible intervals. Note that distance to the coast is the most relevant variable on the selected model.

	Mean	Sd	95% CI
Intercept	-15.252	0.392	[-16.022, -14.482]
Chlorophyll	0.222	0.038	[0.147, 0.297]
SST	-0.597	0.683	[-1.938, 0.743]
AspE	-0.002	0.005	[-0.013, 0.008]
Distance to the coast	-13.338	0.189	[-13.709, -12.968]
Slope	0.047	0.005	[0.038, 0.056]
Concavity	-0.022	0.003	[-0.028, -0.016]
Coastal impact	0.290	0.008	[0.275, 0.305]
Marine traffic	-0.003	0.010	[-0.022, 0.017]

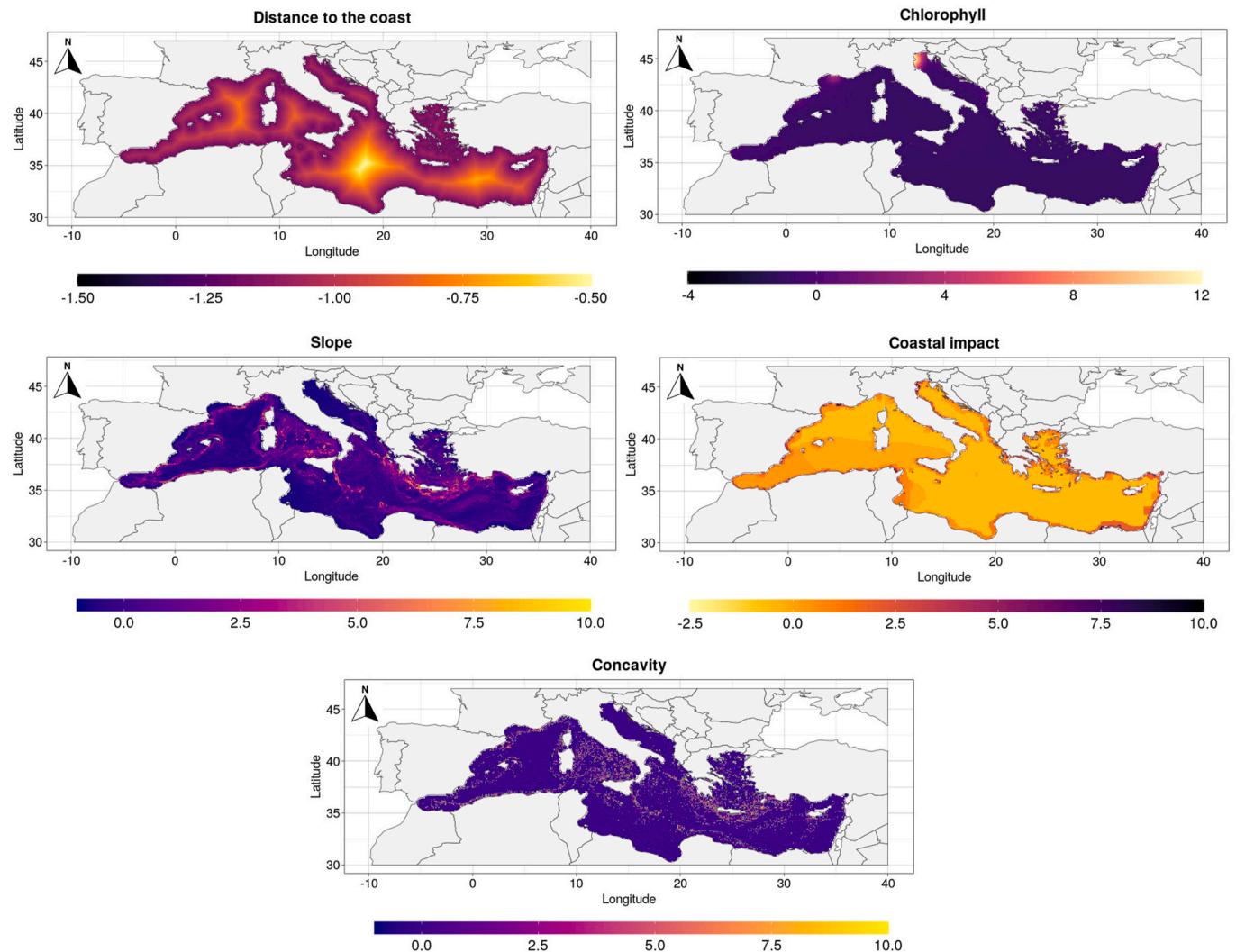


Fig. 2. Geographical representation of the relevant covariates included in the final model. It can be noted the high productivity areas in the coasts of France and North of the Adriatic Sea; the high slope and concavity areas delineating the continental shelf; the higher coastal impact mainly in the East coast of Spain, South coast of France, North coast of Adriatic Sea, coast of Greece and Tunisia.

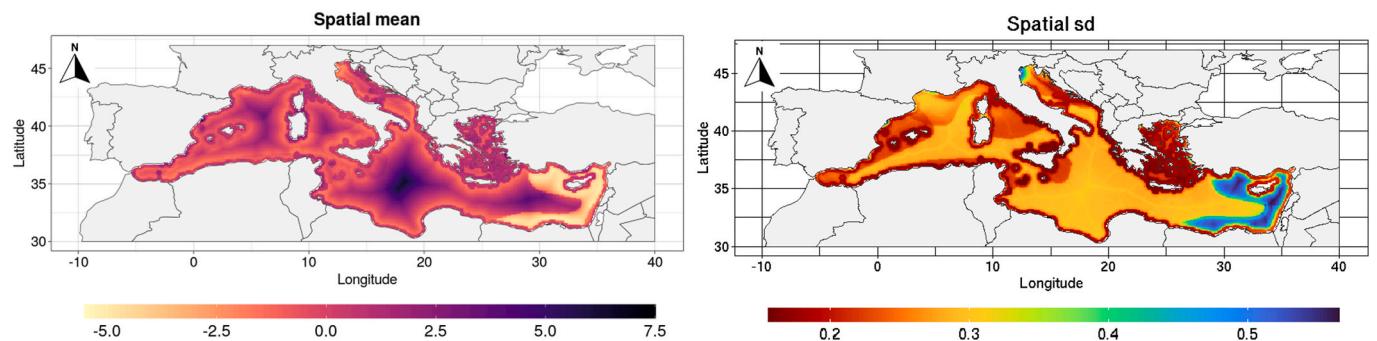


Fig. 3. Mean (on the left) and standard deviation (on the right) of the posterior distribution of the spatial effect. Eastern Mediterranean coast compressed the lowest mean, showing the compensation of the spatial effects for the existing high contrast in the Seabirds biodiversity index between the coast and nearest areas. This high contrast is also reflected in the posterior spatial standard deviation.

due to cumulative impacts (Coll et al., 2010, 2012; Halpern et al., 2019). Assessing the consequences of anthropogenic pressures is therefore crucial both to predict and prevent changes of habitats and species. In this context, seabirds arise as a fundamental tool to assess the current and future effects of these changes in marine ecosystems.

Marine protected areas play a key role in the conservation of marine

species and habitats. In this study we consider not only the already established MPAs, but also the marine IBAs as they have been reported as important tools for spatial conservation (McGowan et al., 2018). We use an extensive database of at-sea locations corresponding to 19 different seabird species to investigate the seabirds biodiversity distribution in the Mediterranean Sea through a Bayesian Spatial Beta

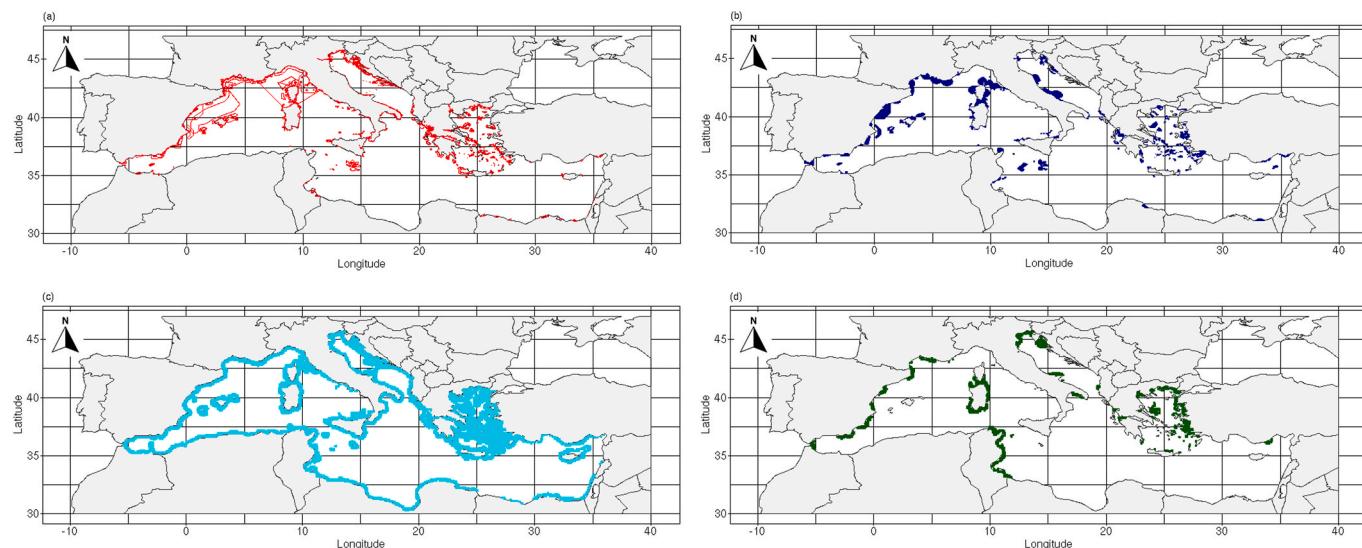


Fig. 4. Figures (a) and (b) present MPAs (red) and marine IBAs (blue), respectively; while Figures (c) and (d) depict posterior predictive mean values over 0.50 (cyan) and 0.75 (green), respectively. Posterior predictive mean over 0.50 (cyan) cover almost all the Mediterranean coast while posterior predictive mean over 0.75 (green) is mainly located in the East coast of Spain, Tunisia, and Greece; South coast of France, Sardinia and West coast of Turkey.

Table 4

Overlap between our predictive hot spots (predictive mean over 0.5 and 0.75) and the current marine protected areas (MPAs and marine IBAs).

Predictive mean > 0.5	Overlapped areas (%)	Non overlapped areas (%)
MPAs	47.96	52.04
Marine IBAs	83.13	16.87
Predictive mean > 0.75	Overlapped areas (%)	Non overlapped areas (%)
MPAs	22.78	77.21
Marine IBAs	10.97	89.01

regression model. Our results, in line with Coll et al. (2012), show that the abundance of species in the Mediterranean Sea seems to be greater in coastal areas, mainly along the central and north shores. However, it is worth to note that there is a big gap in data in the SE part of the Mediterranean Sea, likely due to data availability (Coll et al., 2010). Moreover, we modeled seabirds biodiversity according to several environmental and anthropogenic variables. From the 17 initial variables proposed, we implemented a variable selection method and only eight of them were finally selected and used in the modelling. We found a negative association between distance to the coast and seabirds biodiversity. This may be related to the lack of information in deep-sea areas reported in previous studies (Wood et al., 2008; Fabri et al., 2014), despite the fact that four of the included seabird species were pelagic. Nevertheless, another possible explanation is that most of our data correspond to reproductive distributions. Along breeding season seabirds act as foragers flying back and forth from central locations (i.e. colonies) and therefore, there is a range of limit on the distance they can travel before flying back to attend to their breeding duties.

Furthermore, we found a positive association between seabirds biodiversity, chlorophyll and slope of the seabed. On the contrary, concavity was negatively associated with seabirds biodiversity. These results may be indirectly related to areas that represent feeding hot spots, especially for seabird pelagic species. Specifically, areas with less concave seabeds in the study area correspond to productive areas where many seabird preys are concentrated, creating the preferred feeding areas (Pennino et al., 2020). Interestingly, a suggestion of a negative relationship was found between the cumulative historical mean of the sea surface temperature and the seabird biodiversity. These results could be due to the high association of higher seabird biodiversity value with productive areas, normally related to colder masses of water, or could be

a signal that seabirds are more sensitive to higher temperature. As in our mesoscale study we considered aggregated historical means of the oceanographic variables and no temporal correlations were included in the model, this result need to be interpreted cautiously. However, many specific species and area-specific studies already highlighted that highly productive coastal systems are predicted to experience substantial effects from climate change (Goyert et al., 2018; Riddick et al., 2018; Mitchell et al., 2020). Climate change therefore could pose a longer-term threat to seabirds, and as this could be mediated via availability of key prey species, other marine predators could also face similar threats (Carroll et al., 2015). Nevertheless, more detailed studies are need to confirm this hypothesis.

Regarding anthropogenic threats, our study suggests that the coastal impact could affects positively the seabirds biodiversity (i.e. the bigger coastal impact the higher seabirds biodiversity). We consider that the underneath reason is triple: (i) the lack of available information in deep areas (and as a result, the higher index is related to coastal areas); (ii) the increased use in the last decades of anthropized areas by seabirds to feed and breed (Real et al., 2017; Gamble et al., 2019; Battisti, 2020); (3) bias due to the mismatch in the biodiversity and anthropogenic data temporal resolutions.

In this study we define potential marine hot spots for seabirds those areas with a posterior predictive mean over 0.50 and 0.75, i.e. areas where biodiversity index is greater than 0.50 or 0.75, respectively. Using the value 0.75 we will be less precautionary in terms of protection, as areas are smaller due to the fact that we protect only hot spots where the biodiversity index is greater than 0.75. Studies have shown that protected areas may need to cover at least 20–30% of the area of concern to be an effective tool in management (Roberts and Hawking, 2000; Pennino et al., 2018). Therefore, this second scenario, could represent the best compromise between ecological and management benefits as it implies the lowest losses for human activities while still encompassed areas of high species biodiversity.

According to our results, MPAs and marine IBAs seem to partially cover some of the presented hot spots. Concretely, the 47.96% and the 83.13% of the MPAs and marine IBAs, respectively (considering posterior predictive mean values over 0.50); and 22.78% and 10.97% of the MPAs and marine IBAs, respectively (considering posterior predictive mean values over 0.75), overlap with the hot spots found in our study. This is the case for the East coast of Spain, Balearic Islands, north coast of Sardinia, Tyrrhenian Sea, Ionian Sea, Adriatic Sea and Aegean Sea. It is

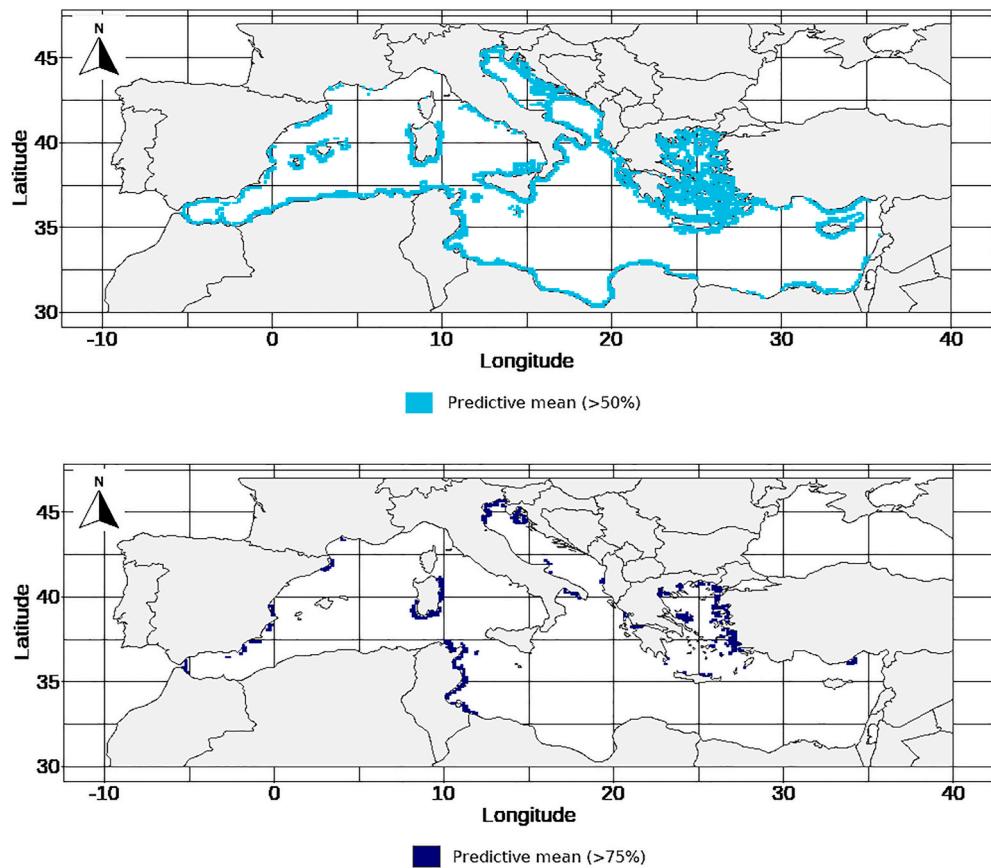


Fig. 5. Potential marine hot spots currently non protected by MPAs or marine IBAs that showed a posterior mean value over 0.50 (on top, cyan) or over 0.75 (on the bottom, dark blue). It is worth to note potential marine protected areas in the east coast of Spain, Sardinia, Adriatic Sea, west coast of Turkey and east coast of Tunisia.

worth to note the higher percentage of overlap obtained for marine IBAs. This may be due to the fact that (i) our potential hot spots are mainly coastal areas such as the marine IBAs (in contrast to MPAs which also cover deeper areas); and (ii) marine IBAs were designed based on seabird data. Nevertheless, some of our potential hot spots fall outside the current protected areas which, if they were properly protected may help mitigate current and future threats facing seabird species in the Mediterranean.

It is however important to highlight that MPAs and marine IBAs are not only based on species biodiversity criteria, but also on species conservation status and other social, economic and political criteria related with the feasibility of MPAs real implementation (Arcos et al., 2012). Therefore more studies will be needed to integrate, in addition to the biodiversity index, all the ecosystem components required to improve the identification and implementation of new MPAs. In particular, as already highlighted by other studies on the Mediterranean biodiversity (e.g., Micheli et al., 2013), despite the conservation effort initiatives, major challenges face the biodiversity of seabirds in the Mediterranean. These include the need for the extension of spatial prioritization of conservation areas, and the acquisition of additional information from data-poor areas and species, addressing the challenges of establishing transboundary governance and complex conditions. A collective prioritised action is needed for the south, eastern and high seas of the Mediterranean Sea, where little information is available. Transboundary governance is essential for the protection of marine ecosystems and highly mobile species that span international borders (Tuda et al., 2019). However, transboundary marine resource management often faces many challenges, because transboundary ecosystems are complex with multiple problems at many different scales. The challenge in managing transboundary marine systems is therefore to devise

governance mechanisms to maintain ecosystem function while enabling sustainable use at appropriate scales.

5. Conclusions

In this study we analyse seabirds biodiversity in the Mediterranean Sea through Bayesian Spatial Beta regression models. We have found some hot spots areas susceptible of protection and we compare them with the already established MPAs and marine IBAs in the Mediterranean Sea. In overall, marine IBAs seems to be well placed to seabird conservation. We have found that some of our new areas are an extension of the current MPAs and marine IBAs. However, our results also highlight other regions which do not have any figure of protection. This is the case for the north coast of Africa (Algeria and Tunisian waters, east of Gulf of Gabès and south part of the Levant Sea), the south and west coasts of Turkey (Marmara and Aegean regions, and north of the Levant Sea), Sardinia, north of Adriatic Sea and west coast of Spain (south of Valencia, Alicante and Murcia regions). Our results are especially relevant to elaborate spatially explicit management plan (e.g., Marine Spatial Planning, MPA, etc.) factoring seabird species. Indeed, they show that despite the high mobility of these species, some areas consistently offer favorable habitats and should be prioritize for conservation measures.

It is important to bear in mind that this study does not consider the temporality of the data, but aims to make a mesoscale spatial approximation of the seabird distribution in the Mediterranean Sea. Further analysis are needed to explore complementary databases in order to investigate the possible seasonal and annual trends related with the species and habitat dynamics.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

The code is available in the github repository of the first author as stated in the manuscript

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