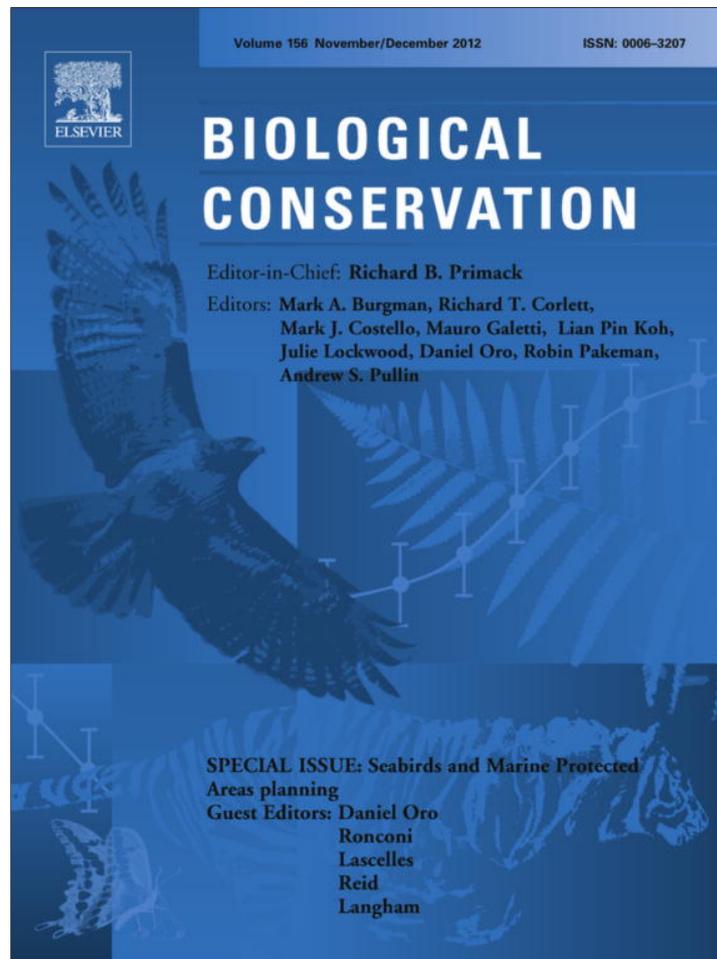


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Biological Conservation

journal homepage: www.elsevier.com/locate/biocon

Assessing the location and stability of foraging hotspots for pelagic seabirds: An approach to identify marine Important Bird Areas (IBAs) in Spain

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ARTICLE INFO

Article history:

Available online 9 January 2012

Keywords:

Habitat model
Marine protected area
MAXENT
Mediterranean
Shearwater
Storm-petrel

ABSTRACT

Protected areas play a key role in the preservation of biodiversity, but their implementation at sea is lagged behind terrestrial environments, especially in offshore areas. Here we describe the identification of foraging hotspots off the Mediterranean Iberian coast using three Procellariiform species as examples, and assess the stability of these sites. Then, we show how these foraging hotspots contributed to the delimitation of marine Important Bird Areas (IBAs). The whole process consisted of: (1) seabird data collection (extensive boat-based surveys and seabird tracking, conducted in 1999–2010) and compilation of relevant spatial descriptors of the marine environment; (2) species distribution modeling (SDM) aimed at identifying areas with high habitat quality for the different seabird species (3); identification and delimitation of the main seabird hotspots, based on models, supported by direct seabird data, and mediated by expert opinion; (4) application of BirdLife International IBA criteria for hotspot validation; and (5) combination of hotspots from different species to set the final limits of the marine IBAs. This approach allowed to identify a series of hotspots for pelagic species in the study area, and provided nice examples of stability assessment, which slightly differed in performance between seabird species. They contributed to the Spanish marine IBA inventory, which is in the process of receiving legal protection. Future work should be directed at confirming the stability of the marine IBAs in the long term, and to address the development of management plans to make effective the protection of these sites.

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1. Introduction

Protected areas are recognized as key tools for biodiversity conservation (Lovejoy, 2006). However, the marine environment has received little attention relative to terrestrial areas, and less than 1% of the ocean's surface is included in marine protected areas (MPAs) (Wood et al., 2008). Moreover, most MPAs are small, coastal sites, focusing on benthic habitats (e.g. coral reefs, sea-grass prairies), whereas the dynamic open sea and its related biota have been largely neglected (Game et al., 2009).

In line with this general pattern, seabirds have received protection in many of their breeding colonies, but few sites have been protected at sea for these top predators (Grémillet and Boulinier, 2009). Moreover, the few MPA initiatives regarding seabirds have been primarily directed at protecting the marine areas surrounding seabird colonies (e.g. Airmé et al., 2003; McSorley et al., 2003; Yorio, 2009) and, to a lesser extent, distinct coastal and/or shallow areas hosting non-breeding congregations of highly gregarious species such as sea-duck (McSorley et al., 2005; O'Brien et al., this

issue; Skov et al., 2007). Far less attention has been placed on offshore areas, although these include key foraging sites for several seabird species (Hyrenbach et al., 2006; Harris et al., 2007; Louzao et al., 2006; Nur et al., 2011). The dynamic nature of the marine environment, the lack of obvious boundaries and the requirement of large extensions for effective protection of wide ranging megafauna have been among the major concerns regarding the identification of such areas (Alpine and Hobday, 2007; Game et al., 2009; Hyrenbach et al., 2000). In addition, the difficulties to carry out studies at sea have contributed to the scarcity of MPA proposals in offshore areas (Lascelles et al., this issue).

New efforts are directed at addressing this gap, brought about by the increasing awareness of the threats facing the marine environment worldwide, including seabirds (BirdLife International, 2011; Butchart et al., 2004), and also the increasing facilities to study and monitor seabirds at sea (extensive long-term surveys and the upsurge of tracking technologies and analytical tools; e.g. Camphuysen et al., this issue; Le Corre et al., this issue; Louzao et al., 2009, 2011; Montevecchi et al., this issue; Opper et al., this issue). These efforts are supported by increasing political willingness and commitment, backed by the Convention on Biological Diversity (CBD) target of protecting at least 10% of the World

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ocean's surface by 2020 (Lascelles et al., this issue). In accordance, BirdLife International has set among its priorities the extension of its Important Bird Area (IBA) Programme to the marine environment, with the aim of guiding the designation of MPAs for seabirds worldwide (BirdLife International, 2004, 2010a).

Within this frame, one of the first comprehensive initiatives to identify marine IBAs at national level was conducted in Spain (Arcos et al., 2009). Based on this initiative, we report here on the most novel contribution of the Spanish marine IBA inventory, the identification of hotspots for pelagic species in the open sea, which primarily represent important foraging grounds. The main aims of this paper are to: (1) depict the process to identify, assess the stability and delimit seabird foraging hotspots for pelagic species; and (2) describe the remaining steps from hotspot identification to IBA delimitation.

2. Material and methods

2.1. Study area

The present study is framed within the initiative of marine IBAs identification in Spain (Arcos et al., 2009). Here we focus on the

Iberian Mediterranean shelf and the adjacent pelagic waters, from Almeria in the SW to the Spanish–French border in the NE (Fig. 1). Previous work in this region (Abelló et al., 2003; Arcos and Oro, 2002; Louzao et al., 2006) allowed to use longer datasets here than elsewhere in Spain, thus providing the best conditions to exemplify both the identification of seabird foraging hotspots and the assessment of their stability. The continental shelf is very narrow (ca. 3 km) in the south (Vera Gulf) and widens towards the centre of the region, reaching a width of up to 70 km off the Ebro Delta area; in the northernmost area the shelf becomes relatively narrow again, and is indented by submarine canyons (Salat, 1996). Ocean productivity is notoriously heterogeneous in the region, being influenced by marine currents (Atlantic waters flowing northwards in the SW and Mediterranean waters flowing southwards in the NE) and the input of freshwater run-off, which deliver large amounts of nutrients and fertilize the coastal waters (Arnau et al., 2004).

The Iberian Mediterranean marine region is of particular seabird conservation concern, as several sensitive species regularly occur there in high numbers, including Mediterranean endemic taxa: Cory's (Scopoli's) shearwater *Calonectris diomedea diomedea*, Balearic shearwater *Puffinus mauretanicus*, yelkouan shearwater *Puffinus*

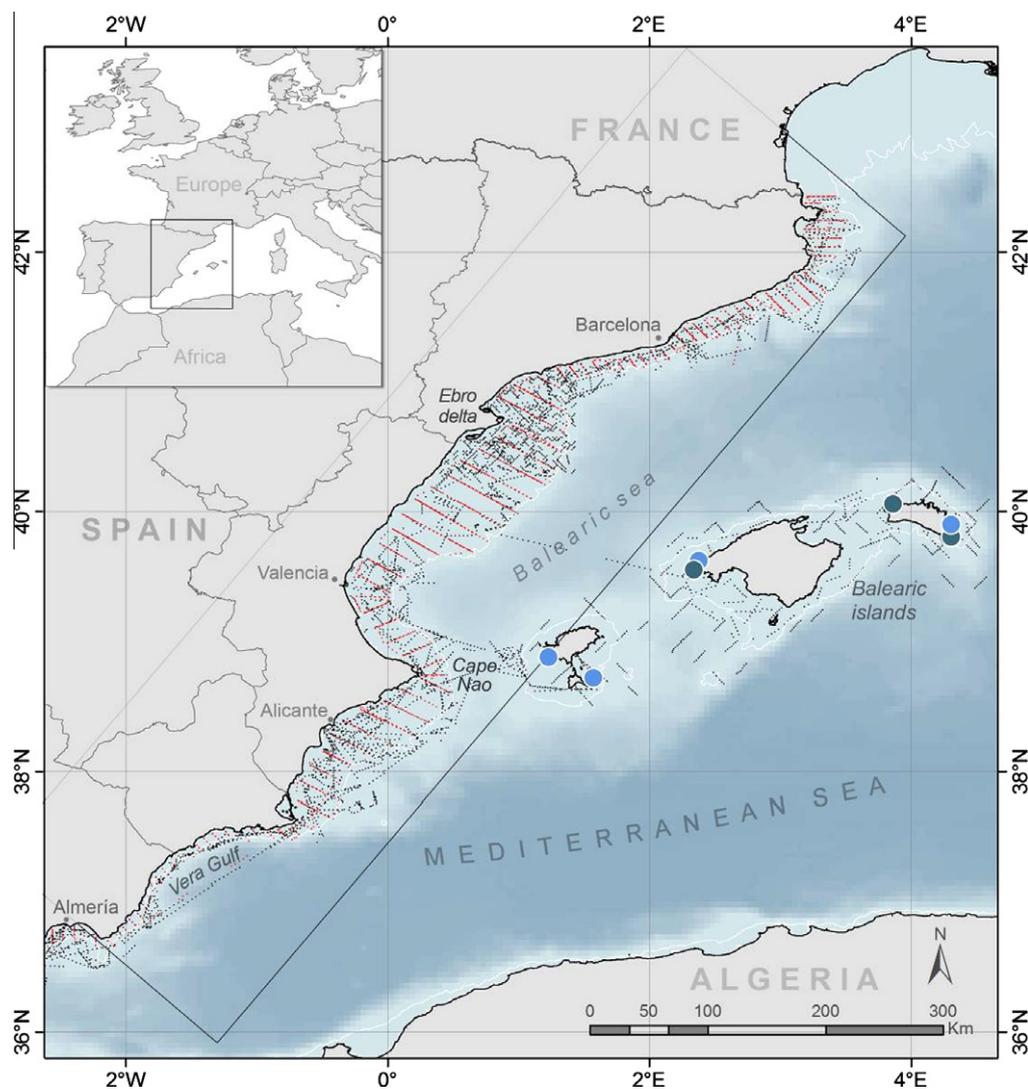


Fig. 1. Map of the study area (diagonal rectangle) and adjacent waters in the western Mediterranean. Boat-based transect locations (mid-position for the 10-min count units) are represented by small dots (black for the breeding and red for the non-breeding seasons), and the circles correspond to shearwater colonies where tracking was conducted (light for Balearic shearwaters, dark for Cory's shearwaters). Finally, the 200-m isobaths is also shown (white line). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

yelkouan, European (Mediterranean) storm-petrel *Hydrobates pelagicus melitensis*, European (Mediterranean) shag *Phalacrocorax aristotelis desmarestii*, and Audouin's gull *Larus audouinii* (BirdLife International, 2011; Zotier et al., 1999). Here we selected as examples three species of Procellariiforms, as representatives of the seabird "pelagic" community: Cory's and the Balearic shearwaters, and the European storm-petrel. Cory's shearwater and the European storm-petrel are summer visitors (March–October, breeding May–October), whereas the Balearic shearwater is present most of the year, mainly from October to June (breeding March–June).

2.2. Overview of the marine IBA identification process

For the identification of marine IBAs, four types of sites were considered, depending on the ecological reason for seabirds to use them (BirdLife International, 2010a): (1) non-breeding (coastal) concentrations; (2) areas for pelagic species; (3) seaward extensions to breeding colonies; and (4) migration bottlenecks. These sites could be eventually combined into a single IBA (see Section 2.7), but followed slightly different approaches to their identification. For the foraging hotspots for pelagic species (type 2), which are the focus of this paper, the process is described in full length in the following Sections 2.3–2.7, and is also outlined in Fig. 2.

2.3. Data collection

Fieldwork was focused on two main approaches, boat-based seabird counts and remote tracking of tagged individuals. The compilation of remote sensing data was also key to produce habitat species distribution models (SDMs hereafter; see Section 2.4).

2.3.1. Boat-based surveys

Within the study area we relied on information from two annual oceanographic surveys organized by the Spanish Institute of Oceanography (IEO), the MEDITS bottom trawl survey (late Spring, 4 years) and the ECOMED acoustic survey (late Autumn, 5 years), as well as a specific seabird survey around the Ebro Delta in Spring–Summer (3 years), within the period 2000–2007 (Table 1). Additional data from another 5 MEDITS cruises within the period 1999–2010 were also compiled and included in the validation of SDMs (Section 2.4), and as supporting information for hotspot delimitation (Section 2.5).

Seabird surveys followed the methodology proposed by Tasker et al. (1984): birds were counted within a 300 m strip transect band, at one or two sides ahead of the vessel depending on census conditions; snap-shot counts were used to count flying birds. Seabird observations were summed up into 10 min survey units, for which species density values were estimated (birds/km²). Birds outside the transect band were also considered for presence/absence information. During the oceanographic surveys, stern counts of seabirds attending the vessel in experimental trawling operations were also recorded following Abelló et al. (2003), to complement transect data.

2.3.2. Individual remote tracking

Individual remote tracking relevant to the study area included breeding Cory's shearwaters from three colonies of the Balearic islands, using either Platform Terminal Transmitters (PTTs, 2005–2006) or Global Positioning System loggers (GPS, 2007), attached to the back feathers with TESA tape (Arcos et al., 2009; Louzao et al., 2009). PTT tracking data of Balearic shearwaters were also

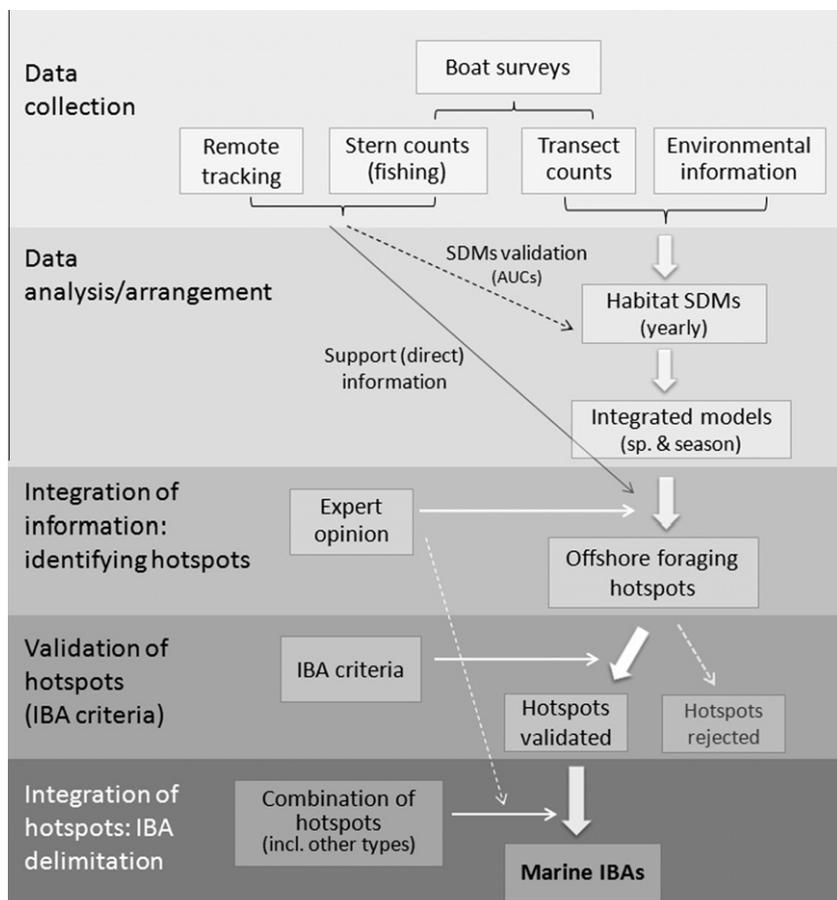


Fig. 2. Outline of the process of IBA identification, focusing on the foraging hotspots. See text for more details (Sections 2.3 through 2.7).

Table 1

Boat surveys effort for the three cruises conducted within the study area: number of transect units (10-min counts), number of experimental trawling operations for which stern seabird counts were conducted (for IEO cruises), and distance and area surveyed (during transects). For the MEDITS cruise, information from years for which species distribution models (SDMs) were not built (i.e. supporting/validating data) is presented separately.

Cruise	10-min counts	stern counts	Distance (km)	Area (km ²)	Period	
					Month	Years
ECOMED (IEO)	2256	30	7003.3	2897.8	Nov–Dec	2003–2007
MEDITS (IEO) – core years	1792	432	5167.9	2619.2	May–Jun	2000, 2002, 2006–2007
MEDITS (IEO) – support years	1341	278	3772.0	1885.2	May–Jun	1999, 2004–2005, 2008, 2010
Ebro Delta surveys	708	–	1186.7	629.3	May–Jun	2005–2007
TOTAL	6097	740	17 129.9	8031.4		1999–2010

used, taking advantage of previous work in the region by SEO/Bird-Life (1999–2001; Ruiz and Martí, 2004). These tracking data are summarized in Table 2.

2.3.3. Environmental variables

Information on habitat features was compiled and used to build SDMs (see Section 2.4). Habitat variables were selected on the basis of data availability and potential biological relevance, after bibliographical revision and preliminary modeling trials. The selected variables included both static and dynamic features (Table 3), the latter being behind the variability that characterizes the marine environment.

Static features consisted of a set of measures related both to the topography of the marine environment (depth, slope, distance to coast and distance to shelf-break) and to the location of breeding colonies. These variables were calculated from ETOPOv2 bathymetric data (NGDC and NOAA, 2006) and GSHHS shoreline (Wessel and Smith, 1996) (Table 3).

Dynamic features were derived from time series of remote sensing data, in particular seasonal and monthly Terra MODIS SST (Sea Surface Temperature 11 μ daytime) and Aqua MODIS Chl-a (Chlorophyll-a concentration) imagery from Ocean Color Web (Feldman and McClain, 2007) (Table 3). We also introduced the distance to oceanic fronts as a surrogate of food availability (Louzao et al., 2006; Valavanis et al., 2005). Oceanic fronts were computed on the basis of monthly Terra MODIS SST imagery using a Sobel edge detection filter (Praca and Gannier, 2008). From the resulting temperature gradients, oceanic fronts were identified as the areas with more pronounced gradients, here defined as areas above the 95 percentile values. Once identified, distance to the fronts was calculated by means of Cost Distance methodology implemented in ESRI Spatial Analyst. The temporal definition of this set of variables was necessarily linked to the timing of the oceanographic surveys. Thus, we selected (1) eight seasonal variables, related to SST and Chl-a for the four (3-month) seasons previous to the surveys, assuming that the overall productivity of the environment is conditioned by SST and Chl-a values during the previous year; and (2) three monthly variables related to SST, Chl-a and distance to oceanic fronts which coincided with the month with the highest frequency of surveys, assuming that areas where food is concentrated are related to productivity phenomena that determine species' short-term distributions.

Table 2

Remote tracking survey effort for Cory's *Calonectris diomedea* and Balearic shearwaters *Puffinus mauretanicus*. These birds were tagged in their breeding colonies at the Balearic Islands, but foraged extensively within the study area. See Section 2.3.2 for details.

Species	Device	Colonies (n)	Birds tracked (n)	Tagging locations (n)	Period	
					Month	Years
<i>Calonectris diomedea</i>	PTT	2	18	196	Aug–Sep	2005–2006
	GPS	3	29	22 422	Aug–Sep	2007
<i>Puffinus mauretanicus</i>	PTT	4	18	573	Jun–Jul	1999–2001
Total		7	65	23 191	Jun–Sep	1999–2007

2.4. Data analysis

This step of the process was focused on the production of SDMs, as they allowed capturing the relationship between seabirds and their habitat and to assess the temporal variability of such habitat. This reduced the biases related to direct seabird data, which represent snap-shots in time and space. However, boat-based and remote tracking data were also arranged to help their visualization and support the identification of seabird foraging hotspots.

2.4.1. Model construction

SDMs were based on transect count data, and were built for each species, for the two most ecologically relevant seasons (breeding and/or non-breeding) on a yearly basis, according to the availability of oceanographic surveys (Table 1). The modeled area included the Balearic Islands, though here we report on the results for the study area as defined in Fig. 1. We used a modeling method based on maximum entropy implemented in the software MAXENT (Phillips et al., 2006), because of its flexibility when handling different kind of species data and responses. The basic principle of the statistical approach implemented in MAXENT is the estimation of the probability of a distribution with maximum entropy (that is, the most spread out or the most uniform distribution) given a set of conditions (the environmental characteristics of the site where the species is detected) that shows our incomplete information regarding the distribution of the species (Phillips et al., 2006). This approach based on presence but not absence data seems particularly appropriate in the seascape, where a low encounter probability for many species is to be expected and consequently many false negatives occur (Péron et al., 2010).

The general approach of MAXENT also offers great adaptability and allows incorporating information related to observed seabird numbers to give greater importance to areas where a species is more abundant (Herrando et al., 2011). Preliminary tests showed that abundance improved the predictive strength of the SDMs. Hence, models were developed from quantitative data in which relative abundance categories were used leading to an increasing number of presences. Six abundance categories were defined: 1 for a single individual and for observations from outside the transect band, 2 for 2–5 individuals, 3 for 6–10 individuals, 4 for 11–25 individuals, 5 for 26–100 individuals, and 6 for more than 100 individuals. These intervals were defined considering the existing

Table 3
Habitat variables used to produce species distribution models. To build the models, all data sources were adjusted to a resolution of 2.5' (≈ 4.5 km) pixels, which was the standard format for most variables. See Section 2.3.3 for details.

Variable	Spatial resolution	Temporal resolution	Source
Sea depth	2'	Constant	ETOPO (http://www.ngdc.noaa.gov)
Slope	2'	Constant	Derived from ETOPO
Distance to coast	2.5'	Constant	Derived from GHSS <i>shoreline</i> (http://www.ngdc.noaa.gov)
Distance to shelf-break	2.5'	Constant	Derived from ETOPO
Distance to breeding colonies	2.5'	Constant	Method CostDistance (GIS). Data from Martí and Del Moral (2003)
Sea surface temperature (SST)	2.5'	Monthly & Seasonal	SST (Terra MODIS; http://oceancolor.gsfc.nasa.gov/)
Chlorophyll concentration (Chl-a)	2.5'	Monthly & Seasonal	Chlorophyll (Aqua Modis; http://oceancolor.gsfc.nasa.gov/)
Distance to productivity fronts	2.5'	Monthly	Derived from monthly Terra MODIS SST, using Sobel filter and Cost Distance

dataset (with a high proportion of the observations including few birds, and a few counts accounting for large groups), and taking into account expert opinion.

SDMs were run on the 100% of training data taking advantage of relative abundance data to provide the best estimates of the species potential distribution. Outputs were projected to the resolution fixed by environmental information, which usually was 2.5 minutes of arc ('), i.e. about 4.5 km pixels (Table 3). Default parameterization of MAXENT was used to develop the SDMs, limiting the response to environmental variables to linear and quadratic functions. All available environmental variables (5 static + 11 dynamic) were included, except distance to colonies, which was only considered for the breeding season, when these sites exert their main influence on seabird distribution patterns (Orlans and Pearson, 1979). Seasonal and monthly Chl-a and seasonal SST were not available for 2000 and 2002, hence the corresponding breeding season SDMs included only two dynamic variables (i.e. monthly SST and distance to oceanic fronts). For 1999 only static variables were available, and models have not been included here. Finally, MEDITS data for 2004 and 2005 were not modeled as were provided by an external observer for complementation, and only stern counts were available for MEDITS 2008 and 2010.

2.4.2. Model evaluation

The predictive reliability of the models was assessed in two ways. First, model performance was estimated with the AUC (Area Under the Curve) generated between the SDMs predictions and presence/absence data from surveys used for model building. The AUC of the ROC curve (Receiver Operating Characteristics) provides a measure of the models predictive capability ranging between 0.5 (no predictive power) and 1 (a perfect model) (Boyce et al., 2002). This metrics was complemented measuring the strength of linear dependence between predictions and relative abundance categories (1–6) based on the Pearson product-moment correlation coefficient (PCC) (Phillips et al., 2009). Second, we used the AUC to test to what extent predictions produced by SDMs matched with data derived from surveys available from other years, as a measure of hotspot stability over time. Thus, seasonal SDMs from a given year were assessed with presence/absence data derived from transect and stern counts (breeding season) conducted on surveys from other years, including years for which models were not available (Table 1). Computations were made with "PresenceAbsence" and "Hmisc" libraries implemented in R software.

2.4.3. Models integration

Hierarchically prioritized maps were created from SDMs to highlight the best seabird areas (for each species, season and year), using two simple and effective approaches with strong ecological components. Firstly, we defined as presence areas (in terms of prevalence of the data used in the model development) those with habitat suitability values above the lowest 10% percentile. Secondly, within the presence areas three scores of habitat suitability were

used (1, 2, and 3, from low to high quality), defined by the following thresholds: (1) the average mean of the suitable values within the areas of presence; and (2) the average mean of the values above the previous threshold (Herrando et al., 2011).

For each species and season we combined the models of different years, by averaging the scores defined above. We then defined three categories of habitat quality over time: (1) moderate (averaged score from >1.5 to 2); good (>2–2.5); and (3) optimal (>2.5–3). This way we combined habitat suitability and stability, as any area above score 2 (which was used as a guiding baseline for the identification of hotspots, see Section 2.5) would be the result of repeated years of moderate to high annual scores.

2.4.4. Arrangement of direct seabird information

Direct information on seabird distribution patterns, as obtained from boat surveys and remote tracking, were arranged in a way that helped their visualization, thus optimizing their contribution to the integration of data sources (Section 2.5). *BirdLife International* (2010a) recommendations were taken into account. Boat-based data were represented selecting the upper 95% percentile of the positive values (i.e. presence data), as well as values above the mean of positive values, to reduce the confusion created by a large number of observations (Table 1) when plotted in a map. This way the areas of highest densities were highlighted. For tracking data, 25%, 50% and 75% kernels were used to highlight the most used areas. As the aim was to use this information just for support, the smoothing factor was selected arbitrarily at $h = 0.1$ for PTTs and $h = 0.05$ for GPSs, taking in consideration the adequacy of the results to the raw data. Kernels were produced independently for every year, colony and species.

2.5. Integration of data sources (intra-specific): identification of hotspots

Once all available spatial information had been arranged, hotspots for each seabird species (and relevant season) were identified and delimited. This process was primarily guided by the integrated SDMs, for which optimal areas were almost always selected and good areas most often helped to delimit the hotspots (i.e. averaged scores above 2 were prioritized). However, direct seabird information (i.e. boat-based and tracking data) did also play a role, so that: (1) hotspots revealed by SDMs were only considered if direct data supported their relevance and (2) direct data independent of the SDMs (i.e. not used for modeling) were also used to set the limits, allowing for deviations from the models when obvious hotspots were highlighted and appeared relevant. Moreover, exceptionally a hotspot was identified based on the overlap of two or more independent layers clearly highlighting the site, even if SDMs did not provide relevant support. Thus the identification and delimitation of hotspots was partly subjective. To maximize the rigor of this process, however, it was guided by expert opinion. This culminated in a small workshop with over 10 people with experience on

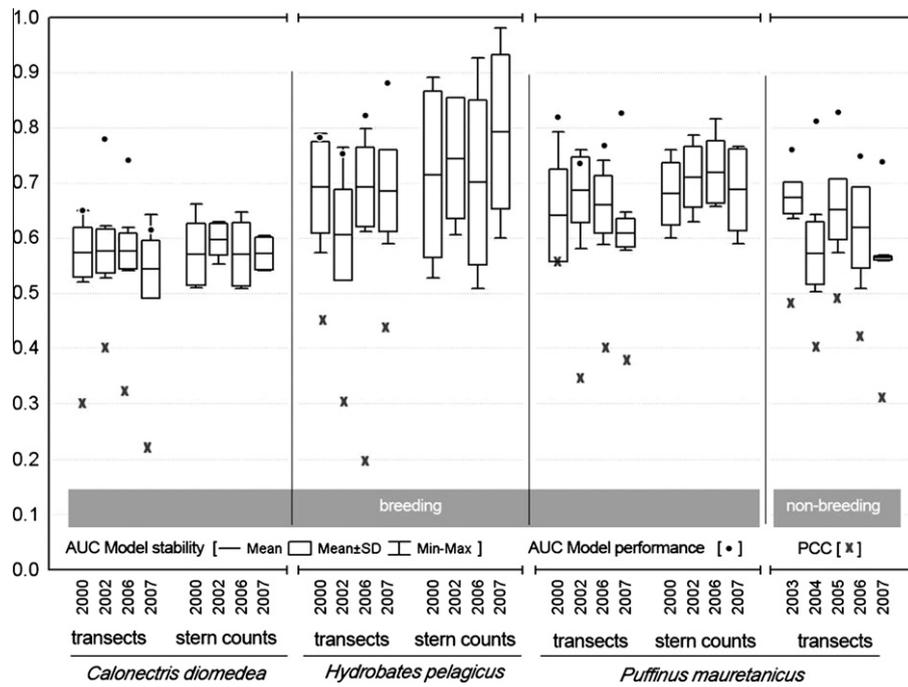


Fig. 3. Habitat species distribution models (SDMs) validation for Cory's shearwater and the European storm-petrel (breeding period), and the Balearic shearwater (breeding and non-breeding periods), on a year basis. Dots correspond to the AUC values resulting of validating models with the data used to build them (i.e. transect data for the same year), and are used to determine model performance. Box plots correspond to the AUC values obtained when validating models with independent data (transect counts from other years, and stern counts during trawling operations), which provide a measure of model stability across years. Finally, Pearson correlation coefficient (PCC) values indicate the relationship between predictions and relative abundance (range: -1 to 1). See Section 2.4.2 for details.

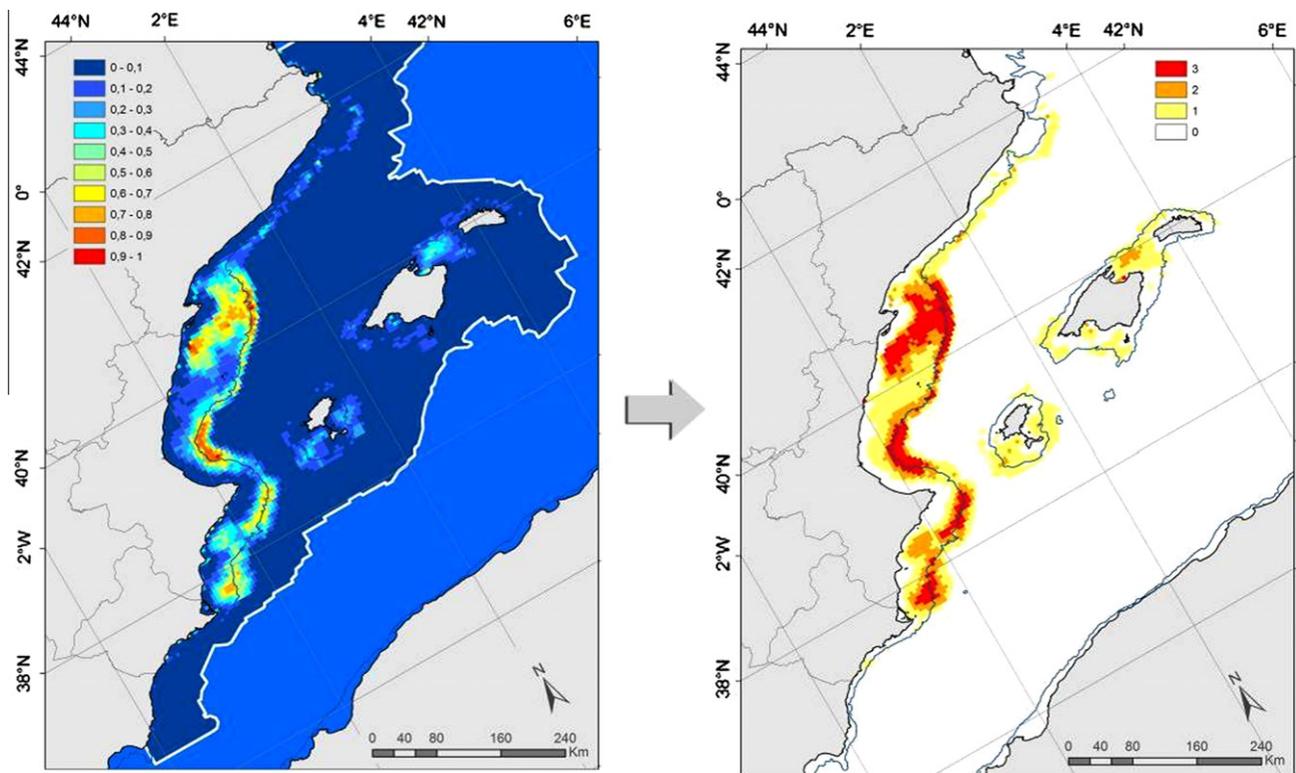


Fig. 4. Categorization of an annual model, taking as example the European storm-petrel (breeding season, 2007). The left figure shows habitat suitability values on a continuum from 0 (low) to 1 (optimal). On the right figure these values have been converted into in four categories, from 0 ("no presence") to 3 (highly suitable areas). Only categories 1 (yellow), 2 (orange), and 3 (red) are represented. See Section 2.4.3 for details. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

diverse relevant issues: the local seabird community and marine environment, habitat modeling, IBA criteria, BirdLife International strategy, and similar projects in other parts of the world.

2.6. Application of BirdLife International IBA criteria to validate the seabird hotspots

To qualify as an IBA, a given area requires meeting one or more of a series of objective, numerical criteria established by BirdLife International (Heath and Evans, 2000). These criteria allow assessing the ornithological importance of the area in an international context, thus ensuring that sites are comparable throughout the globe. In simple terms, a site meets IBA criteria if it regularly holds over 1% of the global (A), regional (B, Europe) or sub-regional (C, European Union) population of a given species. Species of special conservation concern can also validate IBAs with lower numbers.

The IBA criteria were used to validate or reject the hotspots identified following the previous steps. If a hotspot regularly held a significant number of individuals of a given seabird species (according to the thresholds set by the corresponding IBA criteria), it was validated as meriting IBA consideration. Otherwise, the hotspot was disregarded.

To assess seabird numbers in a hotspot, density values were averaged from all boat transect-counts within the hotspot (per species and season) and these estimates were projected to the whole hotspot area, provided that these counts were representative in number and coverage. Bootstrap resampling was used to assess confidence intervals (Quinn and Keough, 2002). This provided a figure of total birds using the area 'simultaneously'. These figures should be regarded as conservative, as turnover rates were not considered.

2.7. Integration of seabird hotspots (inter-species) and final delimitation of marine IBAs

Once all foraging hotspots had been identified and validated for each species and season, we set the final boundaries of the marine IBAs. This process incorporated other types of seabird hotspots (e.g. seaward extensions to breeding colonies), and all the species

for which relevant sites had been identified and validated. If different seabird hotspots partly overlapped, they were combined to form a single IBA, provided that it made biological sense (i.e. the relevant habitat features were continuous, as well as the overall seabird distribution pattern observed). The final boundaries of marine IBAs consisted of straight lines to facilitate their recognition by marine stakeholders, key to their effective management once protected. When different hotspots were combined to form a larger IBA, seabird numbers occurring there were re-estimated taking into account the new area coverage, and IBA criteria were re-assessed accordingly.

3. Results

The identification of seabird foraging hotspots within the study area was based on a relatively large dataset of boat-based counts and tracking studies over a period of 11 years, including the data used for validation. In total we used boat data from 6097 transect units (10 min counts) and 740 stern-counts along 17 cruises, counting across 17,130 km and covering over 8000 km² (Table 1). Of these, 12 cruises contributed to build the SDMs. Tracking data were obtained for Cory's shearwaters (three colonies, 47 individuals including PTTs and GPSs), and PTT data from another 18 Balearic shearwaters were also used (Table 2). Habitat variables were compiled for 2000–2007 (Table 3).

For each of the three study species 4 annual SDMs were generated for the breeding season, whereas a further 5 annual SDMs were built for the Balearic shearwater in the non-breeding season (Table 1). SMD performance (i.e. evaluation based on data used to build the models) was reasonably good, with all SMDs achieving AUC values above 0.7 (i.e. reasonable discrimination power), with the exception of Cory's shearwater in 2000 and 2007 (Fig. 3). As for SMD stability (i.e. evaluation from independent data), AUC values were slightly lower, as expected, but still quite good (Fig. 3). In both cases AUCs were consistent between years and sources of validating information, but showed slight differences between species, with Cory's shearwaters displaying the lowest values and European storm-petrels the highest (Fig. 3). Regarding the strength

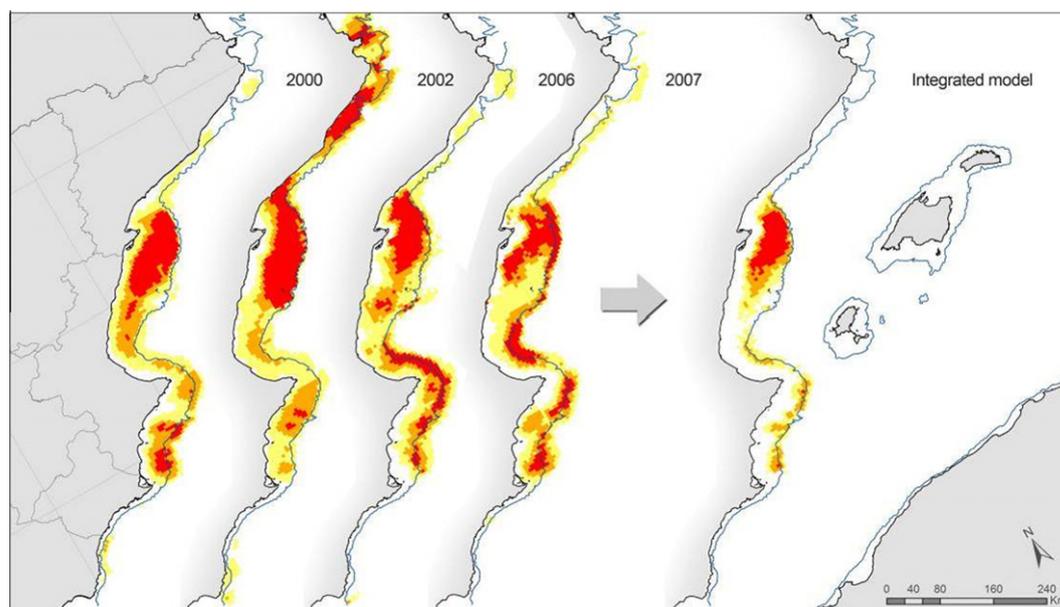


Fig. 5. Integration of models across different years, taking as example the European storm-petrel (breeding season). Categorized models for different years were averaged, and resulted in an integrated model that showed moderate areas (yellow, averaged score from >1.5 to 2); good (orange, >2–2.5); and optimal (red, >2.5–3). Note that this is a conservative approach that only enhances those areas that are good or optimal on a regular basis (i.e. stable); for instance, optimal areas in an unusual year such as 2002 are not reflected in the final map. See Section 2.4.3 for details. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

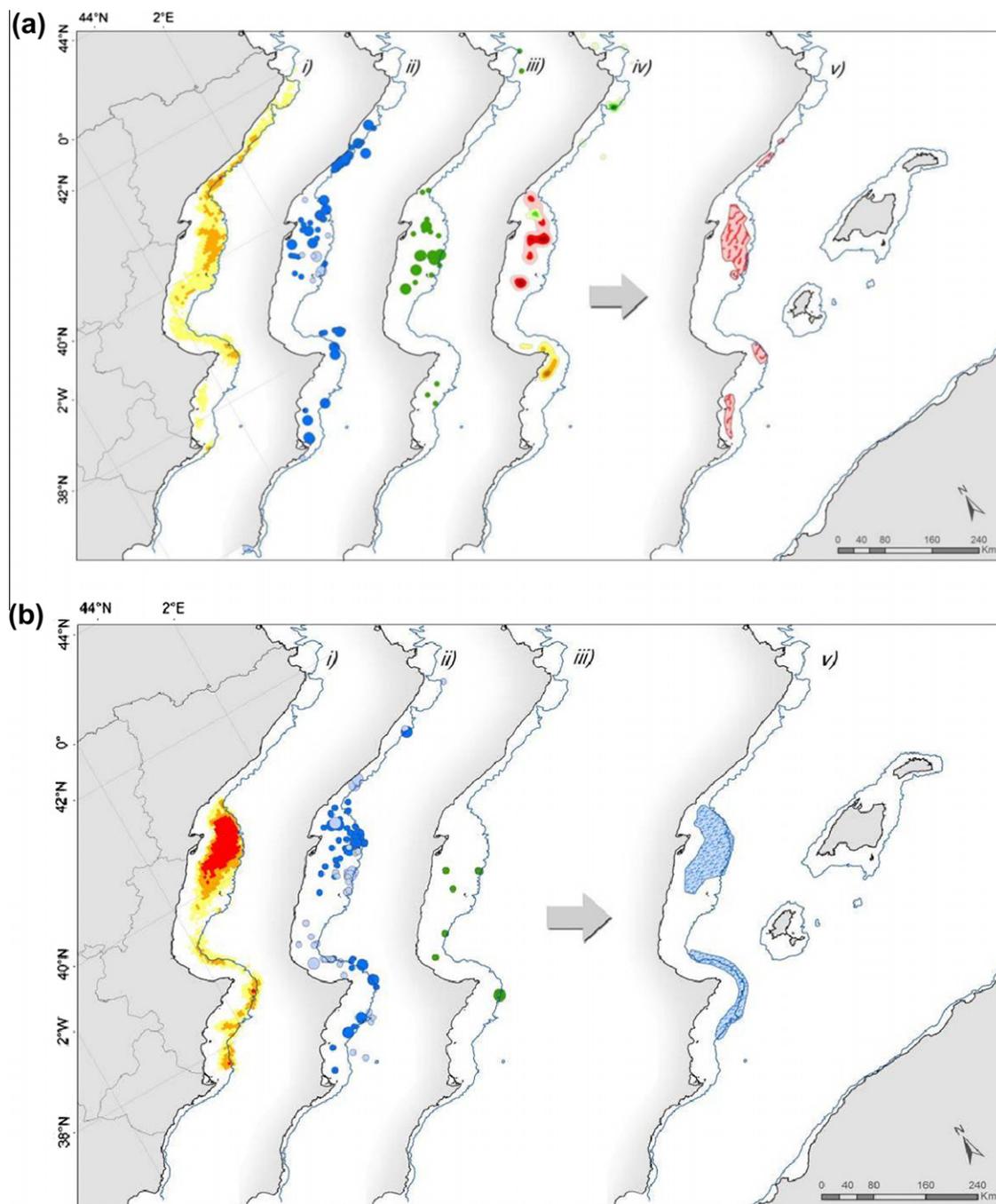


Fig. 6. Integration of information to identify and delimitate foraging hotspots for the three study species: (a) Cory's shearwater, breeding; (b) European storm-petrel, breeding; (c) Balearic shearwater, breeding; and (d) Balearic shearwater, non-breeding. The process starts with the integrated habitat models ("i"), and incorporates any available direct data to refine the identification and delimitation of the final hotspots ("v"), being mediated by expert opinion. Circles ("ii" and "iii") correspond to boat-based count data, and represent the density/abundance values above the 95% percentile (large circles) and above the mean (small circles) of positive values; "ii" correspond to transect data (dark dots, data used to build the models; light dots, data from years not used for modeling), and "iii" to stern counts during trawling operations. Tracking data is represented by kernels ("iv"; dark color, 25%; medium, 50%; light 75%). See Section 2.5 for details. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

of relation between predictions and relative abundance, for all models there was a moderate linear dependence as measured by the PCC (Fig. 3), with a high level of statistical significance in all cases ($p < 0.001$).

The categorization of SDMs and the subsequent integration of different years are shown taking as example the European storm-petrel (Figs. 4 and 5, respectively). Once integrated, models usually showed consistency with both related data (i.e. transects used to

build the models) and independent data (non-related boat counts, tracking locations), allowing to easily identify and delimit the key foraging hotspots (Fig. 6). Some sites, however, were not so obvious and expert opinion had a major role on their delimitation (see Section 2.5; Fig. 6).

In total 13 foraging hotspots were identified for the three study species (Table 4, Figs. 6 and 7). These hotspots ranged from strictly coastal areas (for Balearic shearwaters in Autumn–Winter) to outer

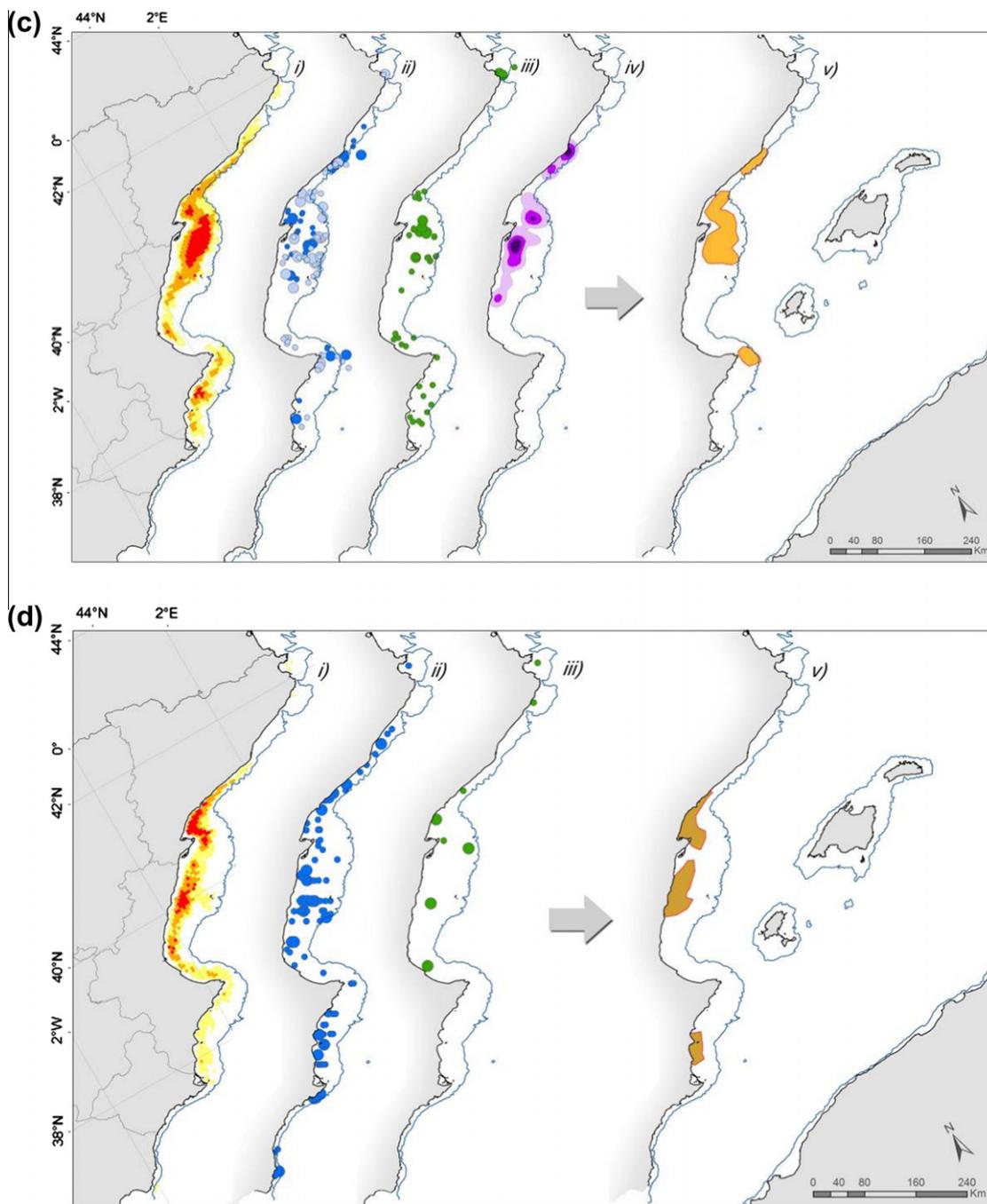


Fig. 6 (continued)

shelf and continental slope areas (especially for the European storm-petrel). Three hotspots were disregarded following IBA criteria, all of them corresponding to Cory's shearwater (Table 4). The remaining 10 sites were combined with seaward extensions for Cory's shearwater and the European storm-petrel, as well as with hotspots of any type (see Section 2.2) for other eight seabird species, and altogether contributed to set the limits of four out of eight marine IBAs identified in the study area, representing over 90% of them in terms of surface (Fig. 7). Only one of these IBAs, once all the hotspots were integrated, was disconnected from the coastline. The remaining four IBAs were primarily identified as seaward extensions to colonies, except one that included a foraging hotspot for the yelkouan shearwater.

4. Discussion

4.1. Location and stability of offshore seabird hotspots

The establishment of MPAs for pelagic seabirds faces several difficulties including the wide-ranging nature of these organisms (that makes necessary protecting relatively large areas to be effective), the dynamic nature of the marine environment (which poses a challenge regarding the stability of the protected sites), the lack of obvious boundaries to set MPA limits, and the difficulties to carry out extensive studies in the open sea (Alpine and Hobday, 2007; Game et al., 2009; Hyrenbach et al., 2000; Lascelles et al., this issue). These constraints have often led to suggest that the

offshore MPA approach is not appropriate to ensure seabird conservation (Boersma and Parrish, 1999). However, this view has started to change in recent years, due to the increasing perception of the threats that seabirds face in the open oceans, and also the increasing facilities to address the identification of offshore hotspots, as well as to assess their stability over time (Game et al., 2009; Lascelles et al., this issue). For instance, areas that could

merit MPA designation in the Southern Ocean have been proposed using long-term datasets of boat-based seabird counts (Harris et al., 2007), and the compilation of tracking data has helped to identify seabird hotspots in the open seas (BirdLife International, 2004). Boat-count and tracking data are subject to potentially strong biases, as they just represent snap-shots in time and space, but they can be regarded as complementary, and their combined

Table 4

Hotspots identified for the breeding (all three study specie) and non-breeding seasons (Balearic shearwater). For each hotspot the area and the mean number of birds estimated to be present “simultaneously” are presented, as well as the corresponding 95% Confidence Intervals, within brackets. The necessary thresholds to meet IBA criteria are also shown (both global, A, and regional, B). Finally, last column shows if hotspots were validated or not by IBA criteria, also indicating if their value was global or regional.

Species	Season	Hotspot location	Area (km ²)	Averaged bird numbers	IBA threshold	Validated by IBA criteria
Cory's shearwater	Breeding	Barcelona-N	52.0	111 (34–190)	A: 8700	No
		Barcelona-S	1474.8	1189 (542–2068)	B: 1090	Yes (B)
		Ebro Delta	2883.7	1600 (897–2439)		Yes (B)
		Cape Nao	456.5	458 (107–1008)		No
		Alicante-S	665.4	257 (43–589)		No
European storm-petrel	Breeding	Ebro Delta	4375.8	3783 (2574–5330)	A: 15,000	Yes (B)
		Cape Nao	2271.3	1899 (1185–2691)	B: 300	Yes (B)
Balearic shearwater	Breeding	Barcelona	551.3	2230 (691–4161)	A & B: 66	Yes (A)
		Ebro Delta	3872.9	4940 (3219–7174)		Yes (A)
		Cape Nao	643.4	896 (289–1904)		Yes (A)
	Non-breeding	Ebro Delta-N	1355.7	6682 (2064–12 807)		Yes (A)
		Ebro Delta-S	1865.8	5307 (3151–8083)		Yes (A)
		Alicante-S	666.2	1926 (927–3180)		Yes (A)

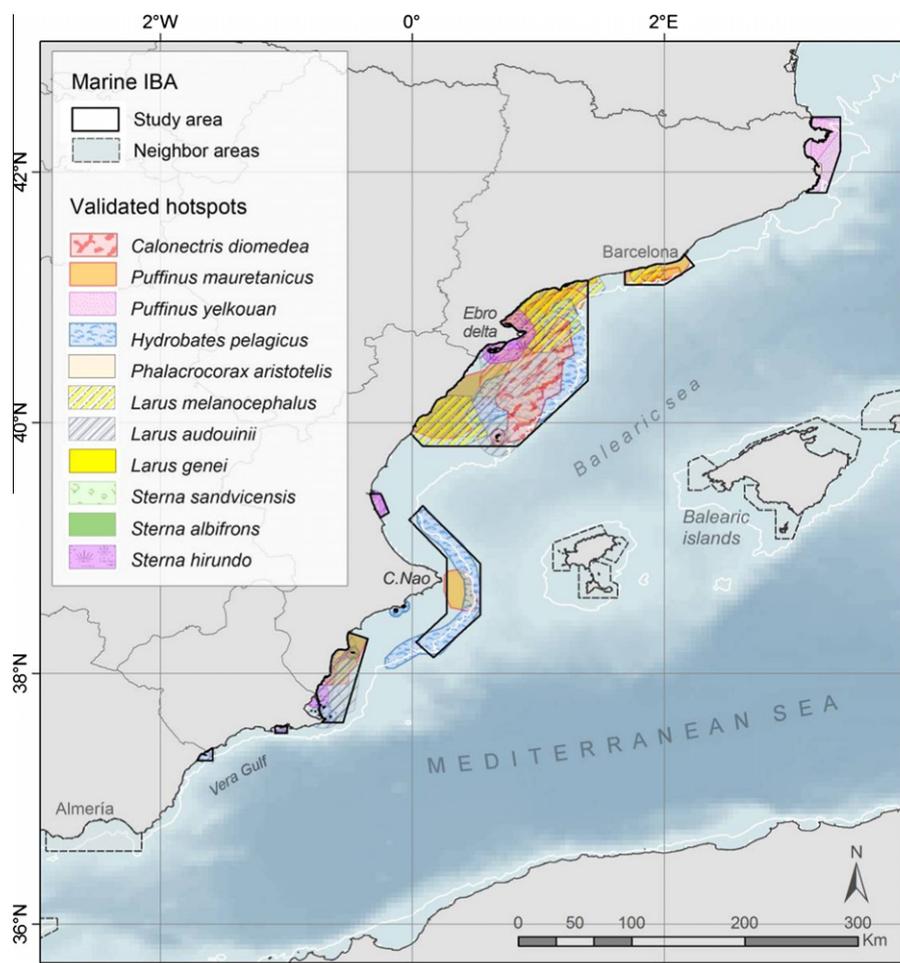


Fig. 7. Marine IBA delimitation process. Validated foraging hotspots for the three study species were combined with other types of hotspots (seaward extensions to colonies), as well as hotspots identified for other species (both foraging areas and colony extensions). The limits of the marine IBAs were set to encompass the hotspots the best possible way using straight lines to simplify future management. All the hotspots shown in the figure accomplished the required IBA criteria. See Section 2.7 for details.

use has been a step forward for the identification of offshore MPAs (e.g. Hyrenbach et al., 2006). A further and significant step has been the development of species distribution modeling techniques incorporating habitat descriptors, which allow capturing the relationship between seabirds and their habitat and to assess the temporal variability of such habitat, thus contributing to reduce data bias and provide more accurate MPA proposals (e.g. Le Corre et al., this issue; Louzao et al., 2006, 2011; Oppel et al., this issue; Nur et al., 2011).

The present study integrates all these approaches and represents a sound example of hotspot identification for pelagic seabirds. Indeed, the study is based on reasonably large datasets of both boat-based counts and tracking information over a wide area, thus allowing combining complementary data to identify hotspots and, to some degree, assess their stability at relatively large spatial and temporal scales. The process was objectively structured so that objective, reproducible information could be generated through the use of innovative methodologies. SDMs played a fundamental role here, largely contributing to the identification and delimitation of seabird foraging hotspots. The SDMs integration process was a particularly good example of how models allow assessing hotspot stability, and to disregard areas that are subject to strong inter-year variability, a process supported by the direct seabird information (i.e. boat-count and tracking data). Expert opinion was also a key piece, allowing supervising the process of hotspot delimitation, which necessarily had to incorporate a subjective component when combining several data sources to set limits in a dynamic and roughly continuous habitat. Finally, for hotspots to be considered as meriting IBA consideration, they had to meet BirdLife International IBA criteria, as a last validation step. It is worth to note that this study was integrated into a larger project that ended up with an inventory of marine IBAs for the whole of Spanish waters, now firmly proposed to become MPAs (see Section 4.2).

In spite of these achievements, the study had also some limitations worth to be mentioned. Firstly, all the hotspots highlighted here were located over the continental shelf and slope, coinciding with areas of high productivity and high prey availability (Arnau et al., 2004; Bellido et al., 2008; Salat, 1996). These areas are related to features direct or indirectly influenced by topography, such as river plumes and oceanic fronts, which explains their value for seabirds (Ballance, 2007; Louzao et al., 2006; Nur et al., 2011). Therefore, the identification of truly oceanic areas, unrelated to obvious topographical features, still poses a challenge to the identification of seabird foraging hotspots. This is particularly so for the most unpredictable tropical and sub-tropical areas (Weimerskirch, 2007), which might require flexible approaches to MPAs (Hyrenbach et al., 2000; Game et al., 2009; Lascelles et al., this issue). Secondly, even in the case of sites coinciding with topographical features, we cannot guarantee their stability in the long term under the current scenario of rapid environmental change, though this could also apply to protected sites inland (Hannah et al., 2007). Thirdly, behavioral information from boat observations was collected but not analyzed, and tracking devices did not include additional recorders of activity, and therefore there is no sound proof that the hotspots identified were actually foraging areas. However, behavioral information derived from GPS movements (Louzao et al., 2009) and expert opinion input (including experience from the boat observers) were consistent at pointing the identified hotspots as foraging areas. Fourthly, the usefulness of the MPA approach could differ between species, as suggested by the different performance of the models presented here (AUC values), probably linked to the particular ecological requirements of each species (McPherson and Jetz, 2007). Cory's shearwater presented the most ubiquitous distribution, and is also the most widespread of the three study species (BirdLife International, 2011), suggesting that

MPA designation for this Procellariiform would not be so effective as for the Balearic shearwater and the European storm-petrel, which showed higher predictability. Other species for which foraging hotspots were identified within the study area are the yellouan shearwater, the Mediterranean gull *Larus melanocephalus* and Audouin's gull. Finally, when considering the whole inventory of Spanish marine IBAs, other areas and/or species counted with more limited datasets, and it was not always possible to count with robust SDMs to guide the process of hotspot identification.

4.2. Implications for conservation

The present study was part of a more ambitious project to identify marine IBAs in Spain, which was conducted in parallel to a sister project in Portugal (Ramírez et al., 2008). There was strong feed-back between both projects, which jointly contributed substantially to the "marine IBA toolkit" (BirdLife International, 2010a), a living document that is intended to provide guidance to any new initiative on marine IBA identification worldwide.

The Spanish marine IBA inventory produced a total of 44 marine IBAs, covering altogether over 50,000 km² (i.e. more than 5% of the Spanish waters). These areas have been recently acknowledged and proposed as Special Protection Areas (SPAs) by the Spanish Government, within the Natura 2000 network framework (BirdLife International, 2010b; European Commission, 2007), and once approved will represent the first complete national inventory of SPAs/MPAs for seabirds worldwide. These sites, along with the colonies that already enjoy some degree of protection, will provide a coherent network of protected areas combining the needs of seabirds throughout their life cycle, provided that these are undertaken within Spanish waters. International cooperation will be essential to extend the protection needs of these birds to other countries and international waters, given the large-scale movements of many seabird species (Croxall, 2008).

Along with the designation of MPAs/SPAs, it will be necessary to develop and implement appropriate management plans to gain effective protection for the seabirds and their habitats (Hooker and Gerber, 2004; Norse et al., 2005). This will require a detailed diagnosis of the threats to seabirds on a site by site basis, and the development of management tools that mitigate them. Of the serious threats that seabirds face in the marine environment (Boersma et al., 2002), some will likely be difficult to address on a site-by-site basis, such as diffuse pollution and climate change. But other serious threats can be handled more easily, particularly seabird bycatch (Anderson et al., 2011; Karpouzi et al., 2007). MPAs placed near the coast, as those proposed here, could also address issues related with pollution (especially point-source events), recreational activities, and industrial development (e.g. windfarms) (Pedersen et al., 2009; Pichegru et al., 2010; Ronconi et al., 2002; Velando and Munilla, 2011). Finally, it is also very important to complement these site-based conservation efforts with other regulations at the wider scale, an issue for which Marine Spatial Planning brings new opportunities (Ehler and Douvère, 2009).

Acknowledgements

We are indebted to many people for their help and support, for which a full list cannot be given here. BirdLife International provided valuable support throughout the process of marine IBA identification, particularly via the Global Seabird Programme, the IBA Programme and the European Division, and national partners such as SPEA. Special thanks go to the Spanish Institute of Oceanography (IEO), which allowed the presence of seabird observers in oceanographic surveys. Pere Abelló and Maite Louzao kindly contributed with valuable datasets that were used for model validation, and Magda Pla greatly helped with the compilation of remote sensing

data. Ben Lascelles, Maite Louzao, Kees Camphuysen and two anonymous referees provided valuable input on earlier versions of this manuscript. This piece of work includes results of three EC-funded LIFE Projects conducted by SEO/BirdLife: LIFE97 NAT/E/004147 (Recovery plan of the Balearic shearwater; 1998–2001), LIFE04NAT/ES/000049 (Marine IBAs in Spain; 2004–2009) and LIFE07NAT/E/000732 (INDEMARES; 2009–2013), which also received funds and support of the Spanish Ministry of Environment and Rural and Marine Affairs (MARM) and the Autonomous Governments. This was also supported by the BirdLife Preventing Extinctions Programme–Species Guardians (Balearic shearwater).

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