






Article

# The Big Five: Species Distribution Models from Citizen Science Data as Tool for Preserving the Largest Protected Saproxylic Beetles in Italy

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**Abstract: Background.** Volunteers’ participation in scientific research has increased in recent decades. Citizen science (CS) data have been used in quantitative ecology to analyse species ranges by means of species distribution models. We investigated the Italian distribution of five large saproxylic beetles (*big five*), to describe their niche space, paramount areas for their conservation, and conservation gaps. **Methods.** CS data from two projects, climate and environmental variables were used to produce Habitat suitability (HS) maps for each species and averaged HS maps. The *big five*’s conservation status was assessed interpolating HS maps with the distribution of protected areas, concomitantly identifying conservation gaps. **Results.** The pre-alpine and Apennines arcs, north-eastern Sicily and eastern Sardinia, were identified as conservation’s hotspots. Ranking HS levels from minimum to optimal, the extent of conservation gaps decreases as environmental suitability for the *big five* increases. **Conclusions.** For the first time in Italy, CS data have been used to investigate niche space of the largest protected saproxylic beetles and analyse the distribution of their suitable habitat. The resulting HS raster maps and vector layers, reporting HS value in all Italian protected areas (n° 3771), were provided and discussed, reporting an application example for conservation purposes.

**Keywords:** Cerambycidae; conservation biology; gap analysis; Lucanidae; protected areas; remote sensing; satellite imagery; Scarabaeidae; species distribution model

## 1. Introduction

The participation of non-scientist volunteers in scientific research, referred to as citizen science (CS), has consistently increased in recent decades [1]. Following a period of rapid growth and a process of professionalisation, the non-expert contribution to global research can now be considered fundamental in many disciplines [2–5]. Particularly, CS has proved to be a powerful tool for facing conservation challenges, from public awareness-raising

regarding environmental issues to building scientific knowledge [6]. In recent years, CS data have been increasingly used in quantitative ecology to predict current species range by means of species distribution models (SDM) [5,7,8]. SDM, besides being useful in theoretical research on species ecology and distribution, represents a powerful tool in nature conservation and management [9]. Developing robust SDMs needs a large dataset, but collecting occurrence data over a large spatial scale poses a severe challenge to researchers; CS projects offer an effective alternative to tackle this issue [1,4]. The distribution of a species can change in response to a large number of interrelated natural and anthropogenic processes. Climate and land use changes, urbanisation, deforestation, increasing extent of lands earmarked for agriculture and invasive species introduction are the main factors driving the Anthropocene's biodiversity loss [10–13]. Even though the processes contributing to the decline of many organisms are well known, many endangered species still have poorly studied geographic distributions [14]. Unfortunately, collecting occurrence data on invertebrates, particularly on endangered insect species, can be difficult, due to their short adult activity period, hidden life cycle, low detection probability, the great sampling effort needed and, in many cases, the engagement of expert entomologists for species identification. In this regard, citizens' involvement in entomological studies has recently become a pillar of conservation-oriented research [15,16]. In Italy, several CS projects focusing on insects have been recently carried out: Farfalle in ToUr (2013–present), Life MIPP (2012–2017), InNat (2017–2022), Life ESC360 (2018–2022) and X-Polli:Nation (2021–present), just to cite a few. Some of these projects focused on endangered saproxylic species, mainly dealing with the conservation of saproxylic beetles (order Coleoptera). Saproxylic beetles depend upon dead or dying wood during some part of their life-cycle and represent one of the largest taxa contributing to forest saproxylic biodiversity [17,18]. Playing a remarkable role in the trophic web of the forest ecosystem [19,20], they are considered good indicators of forest health [21]. Indeed, saproxylic beetles have been the subject of CS and research projects, which demonstrated their relevance as flagship and umbrella species, whose conservation leads to the preservation of many other forest-dwelling species [22–26].

We selected data on saproxylic beetle occurrence from two CS projects carried out in Italy. Five saproxylic beetle taxonomic units (TU) were chosen: *Morimus* Brullé, 1832, *Lucanus cervus* (Linnaeus, 1758), *Cerambyx cerdo* Linnaeus, 1758, *Rosalia alpina* (Linnaeus, 1758) and *Osmoderma* Serville, 1828. These five TUs (hereafter the *big five*) are easily recognizable by the citizen due to their relatively large size (from 15 mm of the smallest *R. alpina* to ~90 mm of the largest *L. cervus*) [27] and thanks to in-depth sheets for each target TU provided in the project-related apps and websites.

For the TU *Morimus* (Cerambycidae), we considered two taxa occurring in Italy as subspecies of *Morimus asper* (Sulzer 1776) (hereafter *M. asper asper/funereus*), as asserted by many authors [28–30], omitting the formerly *Morimus asper ganglbaueri* Reitter, 1894. *M. asper asper/funereus* adults measure 15–40 mm in length [31], have an elongated oval body and can be chromatically and morphologically distinguished from similar longhorn beetles of the Italian fauna [32]. The European stag beetle *L. cervus* (Lucanidae) is one of the best-known coleopteran species and the largest stag beetle species in Europe, characterized by a pronounced sexual dimorphism in adults [33]. The species is widely distributed in northern and central regions, whereas only the congeneric *Lucanus tetraodon* Thunberg, 1806 occurs in the central and southern portion of the Italian peninsula and Sicily [34,35]. Differences in the morphology of the male mandibles make the species easily identifiable from the closely related *L. tetraodon* [33,36]. Adults of the great Capricorn beetle *C. cerdo* (Cerambycidae), can be distinguished from other similar (and co-occurring) congeneric species, such as *C. welensii* (Küster, 1845), by expert entomologists thanks to their heavy sculptured pronotum, blackish body and reddish elytral apex [31,37,38]. Adults of the Rosalia longicorn *R. alpina* (Cerambycidae) are easily identifiable thanks to their peculiar colour and the black spots on the elytra [31,39,40]. Due to the difficulties in morphological identification of the European *Osmoderma* spp. (Scarabaeidae), species assignment remains

a task for specialists. Hence, for the TU *Osmoderma*, we considered the species of this genus occurring in Italy, which share the same micro-habitat, inhabiting mature and hallow broad-leaved trees: *O. eremita* (Scopoli, 1763), *O. cristinae* Sparacio 1994 and the putative Italian subspecies *O. eremita italicum* Sparacio, 2000 [41].

Although distributed across Europe in old-growth forests, populations of the *big five* have been, in the past centuries threatened by forest practices, such as the removal of dead wood, which dramatically reduced their larval habitat [32,42]. The conservation of these species is enforced by the European Habitats Directive 92/43/EC, which lists all TUs in the Annexes II (together with the subspecies *M. asper funereus*), and three TUs (*C. cerdo*, *R. alpina* and *Osmoderma* spp.) in Annexes IV, with *R. alpina* and *O. eremita* as priority species. Additionally, they are classified as Least Concern (*C. cerdo*, *L. cervus*, *M. asper asper*), Near Threatened (*R. alpina*), Vulnerable (*M. asper funereus*, *O. eremita*) and Endangered (*O. cristinae*) in the Italian IUCN Red List [43].

In view of their relevance as flagship and umbrella species, for the protection of the local saproxylic communities, and considering their conservation status, SDMs of the *big five* were developed to provide a useful tool to concentrate conservation efforts [22,43].

The present study aims to: (i) identify suitable areas and explore the ecological niches of the TUs; (ii) analyse TU habitat suitability maps in order to highlight hotspots areas for their conservation; (iii) match the identified suitable areas with the Italian protected areas to develop a useful tool for conservation purpose, providing a case of practical application.

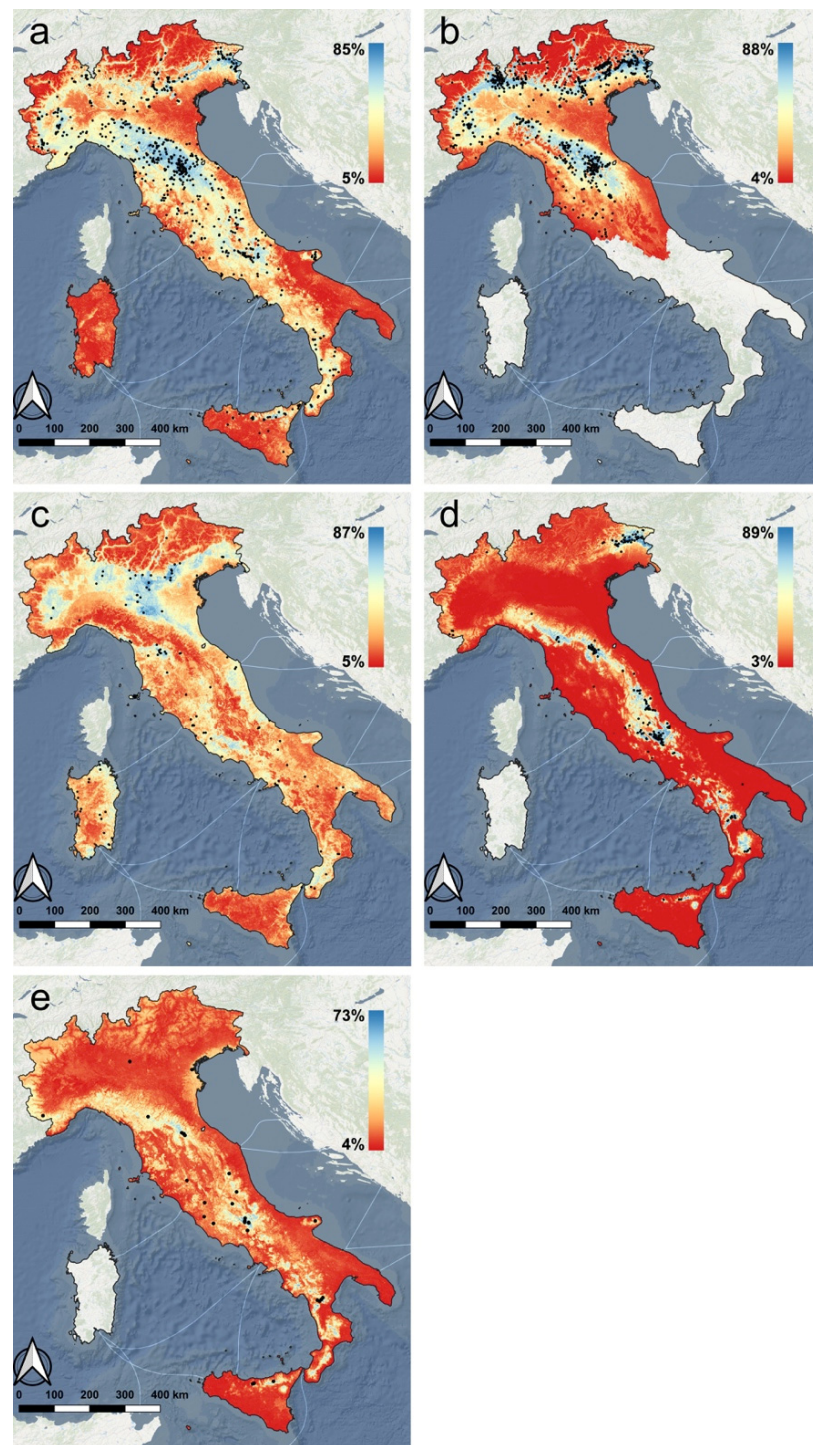
## 2. Materials and Methods

SDMs for the *big five* were developed using a comprehensive modelling and simulation framework technique based on the R package ‘sdm’ [44]. The generated models’ ensemble was used to predict species potential distribution and highlight any possible gap in their conservation status by comparison with current extent and distribution of protected areas in Italy. Predicted *big five* distributions were obtained combining remote sensing data on climate and vegetation indices, with a high resolution (~1 km), with species occurrence data (presence and pseudo-absence). Details regarding the specific attributes of occurrence data, environmental variables and modelling are outlined henceforth.

### 2.1. Occurrence Data

Occurrence data came from two CS projects: a European project financed by the EU Life programme, *Monitoring Insects with Public Participation* (Life 11/NAT/IT 000252) and a national project financed by the Ministry of the Ecological Transition (InNat). The data came from non-expert participants that used the websites and mobile apps of the CS projects to send records of the target species, accompanied by photographs to allow the validation by experts. Pictures were uploaded on the project websites or through the mobile apps, identified and validated by expert entomologists. The raw dataset consisted of 3538 reports from 865 people, uploaded from 2014 to 2020 (accession data: January 2021), even though some records ( $n = 125$ ) date back to the early 2000s and have been uploaded later. A data cleaning procedure was performed to increase the quality of occurrence data and the model’s performance [45,46]. Data preparation consisted in removing occurrence data lying outside Italian borders and in eliminating duplicate records. Furthermore, a grid with the same resolution (~1 km), extent and origin of environmental variables was created to select a single occurrence record in each occupied cell, avoiding multiple records which would lead to resampling the same environmental predictors. This procedure led to the following occurrence data per TU: 696 for *M. asper asper/funereus*, 894 for *L. cervus*, 124 for *C. cerdo*, 243 for *R. alpina* and 32 for *Osmoderma* spp. (Figure 1).





**Figure 1.** Maps of the suitable habitat for each TU, where the colour scale represents the habitat suitability (HS) from minimum (red) to optimal HS (blue). Black points represent the distribution of the *big five* occurrence data used in the SMD framework. Reports from the Life MIPP and InNat citizen science projects were selected excluding duplicate occurrences and doubletons within the same  $\sim 1 \text{ km}^2$  cell. In (a), the HS map of *Morimus asper asper* / *funereus*; in (b), *Lucanus cervus*; in (c), *Cerambyx cerdo*; in (d), *Rosalia alpina*; in (e), *Osmoderma* spp. The *L. cervus* HS map was clipped in central Italy according to its known occurrence data and considering that only *L. tetraodon* is present in southern Italy.

## 2.2. Environmental Variables Selection

Given the fundamental role of climate, soil properties, vegetation indices, forest structure and land use for the saproxylic beetle fauna [42,47–49], we compiled a dataset consisting of 47 biotic and abiotic variables (Table 1). The set of predictors for the SDMs consisted in 19 bioclimatic variables, 6 seasonal variables ( $6 \times 4 = 24$  in total), among which were vegetation and soil water indices, 3 geomorphological variables (altitude, slope and aspect) and the human modification of terrestrial systems index. Climate data were obtained from WorldClim website (<https://www.worldclim.org/data/index.html>) (accessed on 22 March 2021), recently updated to the 2.1 version (January 2020), which provides 19 bioclimatic variables at very high spatial resolution (~1 km at the equator). These bioclimatic variables represent historical climate data (1970–2000) on annual trends, seasonality and extreme or limiting environmental factors [50]. Elevation above sea level was obtained from WorldClim; slope and aspect were computed using the terrain function of the R package ‘raster’ [51]. Seasonal wind speed, water vapour pressure and solar radiation were calculated from the available monthly variables on WorldClim, dividing seasons according to meteorological breakdown into four three-month periods (i.e., winter starts in December to end in February) [52]. As soil properties represent fundamental factors for the larval stage of saproxylic beetles [53], the soil water index (SWI) from Copernicus Global Land Service database [54] was used as a predictor variable. Daily SWI data were downloaded for a six years period (2015–2020) and averaged to obtain seasonal SWI using the Geostatistical Analyst module of ESRI ArcGis<sup>TM</sup>. The SWI quantifies the moisture condition at various depths in the soil, providing a 1 km resolution product covering Europe (Version 1) [55], which has been demonstrated to yield high agreement with ground observations [56]. The normalised difference vegetation index (NDVI) and the enhanced vegetation index (EVI) were chosen as independent variables, being correlated to vegetation biomass and canopy biophysical parameters such as photosynthetic activity [57–59]. NDVI and EVI were downloaded through the online Data Pool at the NASA Land Processes Distributed Active Archive Center (LP DAAC, <https://lpdaac.usgs.gov>) (accessed on 22 March 2021), provided by the MODIS 6 collection products. A monthly temporal aggregation over a ten years period (2000–2010) at a spatial resolution of 1 km provided the chosen features for the data acquisition. Seasonal averages of SWI, NDVI and EVI were then computed. To account for the human impact on the environment, data on global human modification of terrestrial systems (HMTS) were downloaded from the NASA data centre of Earth Observing System Data and Information System (EOSDIS). HMTS index quantifies human modification of lands, at a spatial resolution of 1 km, modelling 13 anthropogenic stressors within five major categories: human settlement, agriculture, transportation, mining and energy production, and electrical infrastructure [60]. The HMTS index output is a continuous 0–1 metric that reflects the proportion of modified landscape.

**Table 1.** Variables used to model habitat suitability of the *big five* saproxylic beetle species. The results of the variance inflation factor (VIF) stepwise procedure indicate the BIO variables used in the SDM framework for each TU (VIF < 10).

Source (Time Interval)	Code	Description	VIF Results
WorldClim (1970–2000)	BIO 1	Annual mean temperature	Maf, Lc, Ra
	BIO 2	Mean diurnal range: mean of monthly (max temp.-min temp.)	Cc
	BIO 3	Isothermality (BIO 2/BIO 7) ( $\times 100$ )	Maf, Lc, Cc, Ra, Os
	BIO 4	Temperature seasonality (standard deviation $\times 100$ )	Maf, Lc, Ra, Os
	BIO 5	Max temperature of warmest month	
	BIO 6	Min temperature of coldest month	Os

Table 1. Cont.

Source (Time Interval)	Code	Description	VIF Results
Computed with R software	BIO 7	Temperature annual range (BIO 5–BIO 6)	
	BIO 8	Mean temperature of wettest quarter	Maf, Lc, Cc, Ra, Os
	BIO 9	Mean temperature of driest quarter	Maf, Lc, Cc, Ra, Os
	BIO 10	Mean temperature of warmest quarter	Cc
	BIO 11	Mean temperature of coldest quarter	
	BIO 12	Annual precipitation	
	BIO 13	Precipitation of wettest month	Maf, Lc, Cc, Ra, Os
	BIO 14	Precipitation of driest month	
	BIO 15	Precipitation seasonality (coefficient of variation)	Maf, Lc, Cc, Ra, Os
	BIO 16	Precipitation of wettest quarter	
	BIO 17	Precipitation of driest quarter	
	BIO 18	Precipitation of warmest quarter	Maf
	BIO 19	Precipitation of coldest quarter	Maf, Lc, Cc, Ra, Os
	Altitude	Digital elevation model (DEM)	
	SR <sub>seasonal</sub>	Solar radiation	
	WS <sub>seasonal</sub>	Wind speed	
	WVP <sub>seasonal</sub>	Water vapour pressure	
	Slope	Slope of the cell from WorldClim altitude	
	Aspect	Orientation of the cell from WorldClim altitude	
Copernicus Land Service (2015–2020)	SWI <sub>seasonal</sub>	Soil water index	
MODIS Vegetation index products (2000–2010)	NDVI <sub>seasonal</sub>	Normalized difference vegetation index	
NASA-EOSDIS (2016)	EVI <sub>seasonal</sub>	Enhanced vegetation index	
	HMTS	Human modification of terrestrial systems index	

Maf: *Morimus asper asper/funereus*; Lc: *Lucanus cervus*; Cc: *Cerambyx cerdo*; Ra: *Rosalia alpina*; Os: *Osmoderma* spp.

### 2.3. Species Distribution Model

As it is likely that the 19 bioclimatic variables from WorldClim are subject to multicollinearity issue [61], to check the overall correlation a variance inflation factor (VIF) stepwise procedure was performed using the `vifstep` function in the ‘`usdm`’ R package [62]. The spatial coordinates of occurrence data of each TU (separately) were used to extract values of the 19 bioclimatic variables, then the VIF analysis was performed. `Vifstep`, calculates VIF for all variables, excludes the one with highest VIF (threshold = 10), then repeats the procedure until no variable with VIF greater than threshold remains [62]. Only variables that had VIF > 10 were excluded from subsequent analyses [63,64]. Four among the most commonly used modelling methods were used in the SDM framework: generalised linear model (GLM), boosted regression tree (BRT), random forest (RF) and maximum entropy (MaxEnt) [65,66]. Pseudo-absence data were generated for each TU, obtaining more than twice the amount of occurrence data, in order to yield the most reliable distribution models [67]. For this purpose, a random method in geographic space was used, which removes points located in presence cells. Two data-splitting procedures, subsampling and bootstrapping, were used to produce partitions of the data. For the subsampling procedure, 30% of the initial data was used. Partitions were then used to train the models, whilst the remaining data were used for models’ evaluation. Both procedures were applied to each modelling method and repeated three times, leading to a total of 24 model outcomes for each TU, considering the whole SDM framework (4 modelling methods × 2 data-splitting procedures × 3 replications). Model outcomes were selected according to their Area Under Curve value (AUC), effective in summarizing the overall accuracy [68], choosing those with an AUC greater than 0.8, i.e., with an excellent discriminating ability [69]. The chosen model outcomes were then combined using a weighted averaging based on true skill statistic (TSS) and a threshold optimization criterion to maximise sensitivity and specificity [44,70]. The result of the best model outcomes’ combination was used: (i) to build five habitat suitability (HS) maps, (ii) to calculate the relative importance of environmental variables for each

TU (based on Pearson correlation test) and (iii) to draw niche-space plots, characterising the *big five*'s ecological requirements. Finally, to provide useful tools for saproxylic beetle conservation, two HS maps were produced summarising the *big five*'s HS maps. The first HS map ( $HS_{mean}$ ), resulting from averaging the HS for each TU, highlighted those areas suitable for *big five* conservation as a whole. To generate the second HS map ( $HS_{max}$ ), the maximum HS value of each 1 km<sup>2</sup> cell was used, regardless of the TU. The  $HS_{max}$  map can be useful to pinpoint meaningless areas for *big five* conservation, together with areas where protection's actions should target few Tus. The HS range (max-min value) of both maps has been divided into five equal ranks (hereafter HS levels), defined as follows: minimum, low, medium, high and optimal HS. Then, the raster layer unique value tool in QGIS [71] was applied to the projected  $HS_{mean}$  and  $HS_{max}$  maps (EPSG: 6875, RDN2008/Italy zone) to calculate the extent (km<sup>2</sup>) of each HS level. Considering that *L. cervus*, *Osmoderma* spp. and *R. alpina* do not occur in Sardinia [28] and *L. cervus* does not occur in part of central and in southern Italy [33,72], their HS maps were clipped according to the known distributions, to avoid over/under estimation in calculating the  $HS_{mean}$  and  $HS_{max}$  maps.

#### 2.4. Gap Analysis

Boundaries of 3948 Italian reserves and national parks were downloaded, as three shapefile layers, from the world database on protected areas [73]. The protected areas predominantly or entirely marine were excluded, leading to a subset of 3771 protected areas. Portions of these protected areas on the sea were excluded by clipping the vector layers with the mainland boundary of Italy. The zonal statistic tool in QGIS was used to calculate basic statistics (mean, median and maximum value) for each protected area, based on  $HS_{mean}$  and  $HS_{max}$  raster layers. Then, the resulting statistics were stored in the attribute table of the shapefiles containing the 3771 protected areas (provided in Supplementary Materials). Finally,  $HS_{mean}$  and  $HS_{max}$  raster layers were clipped according to the maximum extent of protected areas, merging the three shapefiles.

The output raster layers were reprojected as above described to calculate HS levels' extent (km<sup>2</sup>) within protected areas and, by subtraction, the conservation's gaps. In order to show how our results can contribute to conservation action, we provided a concrete example at a smaller scale. We chose to use the SDM results to identify a conservation gap within a recognized hotspot area, by overlaying the  $HS_{mean}$  map (raster file) with the borders of protected areas (shape file).

### 3. Results

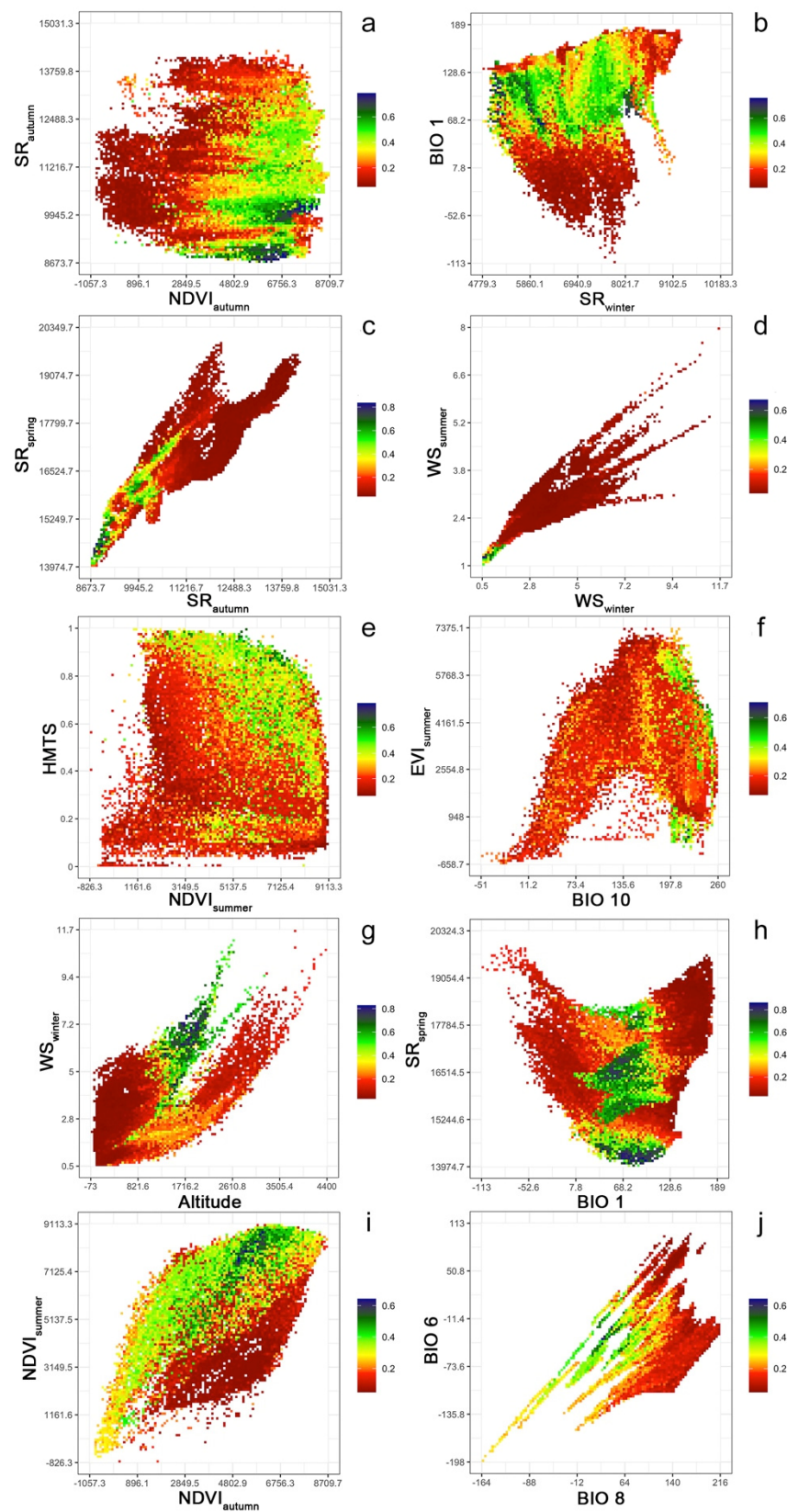
#### 3.1. Species Distribution Model

According to the VIF results, 7 out of 19 bioclimatic variables were excluded from all SDMs due to collinearity problems ( $VIF > 10$ ). Among the 12 remaining bioclimatic variables, those showing a  $VIF < 10$  for each TU were used as predictors together with the remaining 28 environmental variables (Table 1). Considering the whole SDMs, the RF modelling method reported the best performances, i.e., highest AUC, TSS values and lowest deviance ( $AUC = 0.90$ ,  $TSS = 0.71$ ,  $deviance = 0.67$ ) (Table 2). Details on the 24 model outcomes, for each TU, are reported in Table S1. The outcomes with an excellent discriminating ability, chosen to be combined, were 17 for *M. asper asper/funereus*, 24 for *L. cervus*, 9 for *C. cerdo*, 24 for *R. alpina* and 13 for *Osmoderma* spp. The *big five* HS maps, resulting from the model ensemble, were provided as geoTIFF raster layers (Supplementary Materials and illustrated in Figure 1). Environmental variables' importance, assessed by the model ensemble of each TU, are reported in Figure S1 (Supplementary Materials). Two niche space plots for each TU were reported to illustrate the role of the more relevant environmental variables (according to the Pearson correlation results) in predicting the occurrence of suitable habitat (Figure 2 and Figure S1). *Morimus asper asper/funereus* shows the widest distribution among the *big five*, with the highest HS values in northeast Italy and along the northern Apennines (Emilia-Romagna and Tuscany regions). Suitable habitat of this TU is distributed along the whole pre-alpine arc, within the northern and central



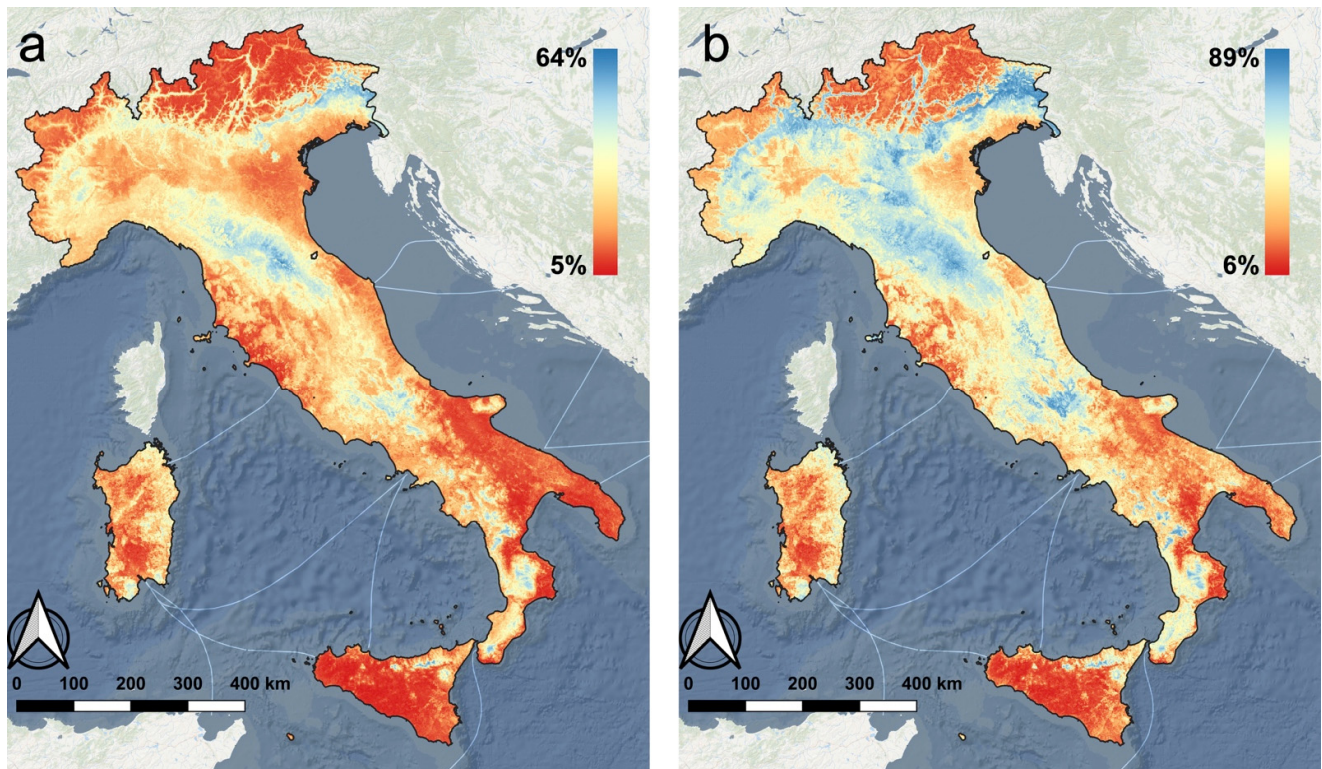
Apennines, in southwestern Italy (Lucan and Calabrian Apennines) and along the mountain ranges of northeast Sicily (Figure 1a). Suitable habitat occurs at high autumn NDVI, low autumn SR and where annual mean temperature (BIO1) is in the range 7–13 °C (Figure 2a,b). The highest *L. cervus* HS values were predicted in the eastern portion of the pre-alpine arc and in the west/north-west Po plain (Piedmont and western Lombardian Prealps). Predicted HS slowly decreases along the northern Apennines till the southern border of the Umbria-Marche Apennines (central Apennines) (Figure 1b). Low values of spring and autumn SR and summer and winter WS positively correlate with high *L. cervus* HS (Figure 2c,d). The *C. cerdo* HS map shows an optimum in the central and western Po plain (Figure 1c). The distribution of suitable habitat for this species is positively correlated with HMTS, summer NDVI and summer mean temperature (BIO10) (Figure 2e,f). Although reporting the highest HS value (89%), *R. alpina* shows the narrowest extent of suitable habitat, limited to those localities in the altitude range 800–2000 m asl, characterised by moderate winter wind speed (4–9 m/s) and an annual mean temperature from 1 to 13 °C (Figure 2g,h). Hotspots for this species overlap the mountain ranges of northern and central Apennines, northeast Prealps, peaks of the southern Apennines (Samnite, Lucan and Calabrian Apennines) and mountain ranges of northeast Sicily (Figure 1d). The suitable habitat for *Osmoderma* spp., although distributed all over plain, hilly and mountainous areas of Italy, shows the lowest maximum HS value (73%) reported among the *big five*. The lowest HS values are predicted in the Po plain, along the Murge plateau (southeast Italy) and in the south, central and western part of Sicily (Figure 1e). Summer and autumn NDVI positively correlate with this TU's presence (Figure 2i). Minimum temperature of the coldest month (BIO 6) within the range −7 °C and 2 °C positively correlates with *Osmoderma* spp. occurrence, as well as mean temperature of the wettest quarter (BIO 8) within the range −8 °C and 14 °C (Figure 2j). To better identify the conservation's hotspots for each TU please refer to the raster layers provided in Supplementary Materials (HS\_maps\_raster\_layers.zip). The HS<sub>mean</sub> map illustrates the distribution of the hotspots paramount for the *big five*'s conservation (Figure 3a). The Sulcis subregion and the eastern portion of Sardinia are added to the above-mentioned zones, due to the presence of suitable habitat for *C. cerdo* and *M. asper asper/funereus*. The HS<sub>max</sub> map highlights that the central and northernmost portion of the Alps, the coastal area of Tuscany (the Maremma), the plain in northern Apulia region, the plains along the Italian shores of the Ionian sea, the south-central and western Sicily and the south-central Sardinia present the lowest HS for the *big five* (Figure 3b).





**Figure 2.** Graphical representation of the niche space for the *big five*: (a,b) *Morimus asper asper/funereus*, (c,d) *Lucanus cervus*, (e,f) *Cerambyx cerdo*, (g,h) *Rosalia alpina* and (i,j) *Osmoderma* spp. The colour scale indicates habitat suitability (HS) according to a two-dimensional environmental space, based on the selected predictors, from low HS (dark red) to high HS (dark blue). Environmental variables are reported

in the following units: solar radiation (SR) ( $\text{kJ}/(\text{m}^2 \times \text{day})$ ); wind speed (WS) [ $\text{m}/\text{s}$ ]; BIO1, BIO6, BIO8 and BIO10 ( $^{\circ}\text{C} \times 10$ ), altitude (m asl). Human modification of terrestrial systems (HMTS) is a continuous 0–1 metric. The valid range and scale factor for NDVI and EVI are, respectively,  $-2000$ – $10,000$  and  $0.0001$ .



**Figure 3.** Maps of the suitable habitat for the *big five*, where the colour scale represents the habitat suitability (HS) from minimum (red) to optimal HS (green). In (a), the  $\text{HS}_{\text{mean}}$  map indicates the hot spots for the *big five* conservation as a whole, derived from the raster layer produced by averaging the HS of each TU. In (b), the  $\text{HS}_{\text{max}}$  map, produced by selecting the maximum value of each cell among the TUs' HS maps, shows those relevant areas for the conservation of at least one TU (green) and meaningless areas for *big five* conservation (red). For the HS maps of each TU and the raster layers of  $\text{HS}_{\text{mean}}$  and  $\text{HS}_{\text{max}}$  please refer to the Supplementary Materials (HS\_maps\_raster\_layers.zip).

**Table 2.** Summary of the SDM framework results, reporting the actual number of occurrence data, the generated pseudo-absence for each taxonomic unit (TU), together with the means of each calculated metric per modelling method. Metrics' means were calculated from the model outcomes ( $n^{\circ} 24$ ) for each TU (reported in Supplementary Materials Table S1).

Taxonomic Unit ( $n^{\circ}$ Occurrence/Pseudo-Absence)	Method	AUC	COR	TSS	Deviance
<i>Morimus asper/funereus</i> (696/1400)	GLM	0.79	0.47	0.47	1.04
	BRT	0.80	0.50	0.48	1.10
	RF	0.88	0.66	0.62	0.80
	MaxEnt	0.82	0.53	0.52	1.02
<i>Lucanus cervus</i> (894/1800)	GLM	0.91	0.70	0.69	0.71
	BRT	0.91	0.70	0.69	0.88
	RF	0.95	0.80	0.78	0.54
	MaxEnt	0.93	0.72	0.72	0.69
<i>Cerambyx cerdo</i> (124/300)	GLM	0.77	0.44	0.46	1.15
	BRT	0.78	0.50	0.48	1.06

Table 2. Cont.

Taxonomic Unit (n° Occurrence/Pseudo-Absence)	Method	AUC	COR	TSS	Deviance
<i>Rosalia alpina</i> (243/600)	RF	0.84	0.61	0.57	0.86
	MaxEnt	0.77	0.44	0.50	1.11
	GLM	0.96	0.82	0.85	0.48
	BRT	0.96	0.80	0.82	0.68
	RF	0.98	0.86	0.89	0.38
<i>Osmoderma</i> spp. (32/120)	MaxEnt	0.97	0.84	0.87	0.47
	GLM	0.64	0.24	0.38	16.5
	BRT	0.84	0.57	0.68	0.82
	RF	0.85	0.58	0.67	0.76
	MaxEnt	0.84	0.54	0.67	0.86

AUC: area under the ROC function; COR: correlation; TSS: true skill statistic; GLM: generalized linear model; BRT: boosted regression tree; RF: random forest; MaxEnt: maximum entropy.

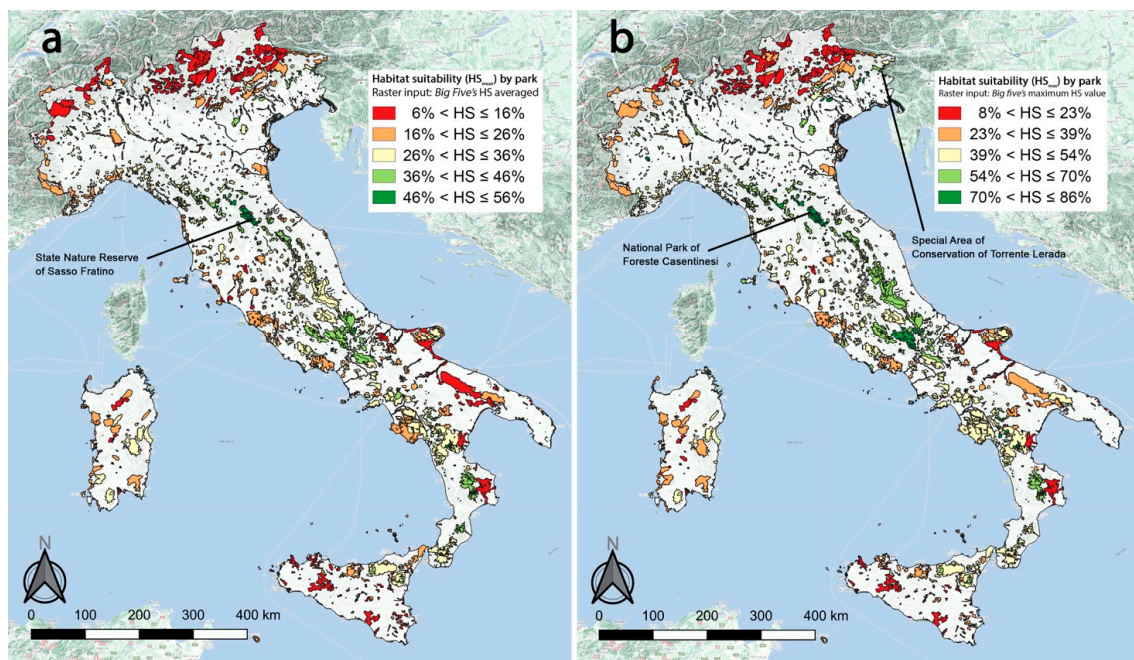
### 3.2. Gap Analysis

The overall result of the zonal statistic tool applied to the shapefiles of protected areas was reported as Supplementary Materials (Protected\_areas\_ITA\_vector\_layers.zip) and graphically represented showing the differences among protected areas in mean value of  $HS_{mean}$  and  $HS_{max}$  maps (Figure 4a,b). The protected areas reporting high value of suitable habitat for the *big five* as a whole ( $HS_{mean}$ ) are located in the north-east, in the southern portion of the northern Apennine, in the central Apennines and in the southern Apennine (Calabria region) (Figure 4a). Considering the zonal statistic result for  $HS_{mean}$  raster layer, the protected area reporting the highest mean, median and maximum value is the state nature reserve of Sasso Fratino (Emilia-Romagna region). Conversely, the lowest values were recorded in the regional nature reserve Monte Conca (Sicily region). As regards the  $HS_{max}$  map raster layer, the special area of conservation of Torrente Lerada (Friuli-Venezia Giulia region) reported the highest mean and median values, whereas the National Park of Foreste Casentinesi showed the highest maximum value (Emilia-Romagna and Tuscany regions) (Figure 4b). The amount of conservation gaps decreases at increasing HS level, from ~80% of the minimum to ~57% of the optimal HS level, considering the suitable habitat for the *big five* as a whole ( $HS_{mean}$ ) (Table 3). On the other hand, the extent of conservation gaps concerning  $HS_{max}$  does not show any decreasing trend (Table 3). A practical example of how protected area shapefiles can overlay  $HS_{mean}$  map to highlight conservation gaps and possibly plan targeted actions is illustrated in Figure 5. A relevant area for the *big five* conservation (marked by red squares in Figure 5) is located in the northern Apennines (central Italy), between SACs (Special Areas of Conservation-Habitat Directive 92/43/CE). This area, consisting of approximately 100 km<sup>2</sup>, holds a wide territory characterized by high  $HS_{mean}$  values (range 43–57%), deserving of being placed under environmental protection.

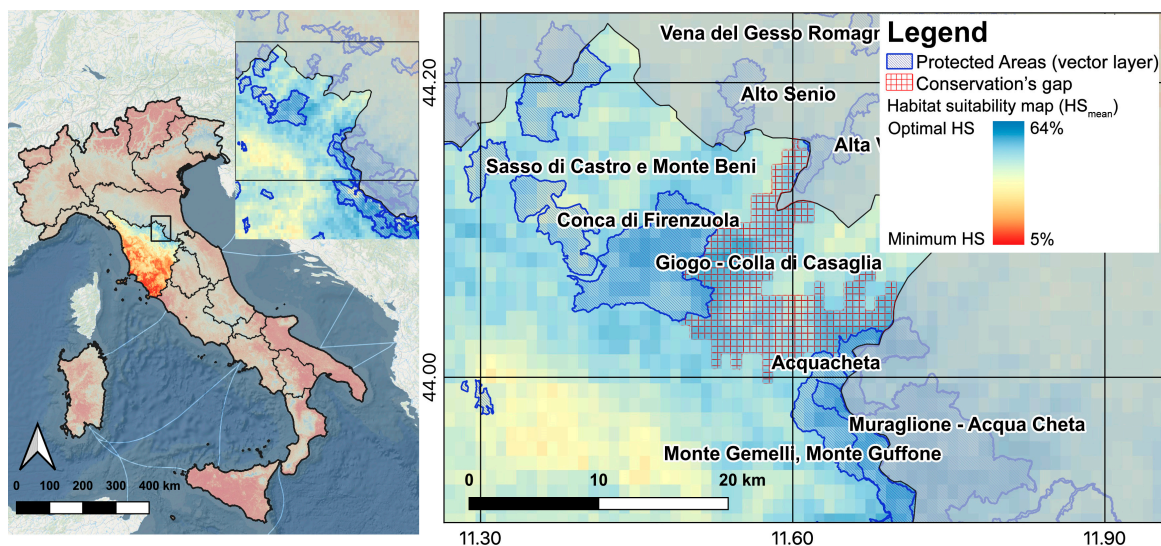
**Table 3.** Results of the raster layer unique value tool applied to the habitat suitability (HS) maps. The extent of the five HS levels was reported for the Italian mainland and for the protected areas (considering their maximum extent). The conservation gaps were reported as the percentage of non-protected areas for each HS level over the Italian mainland.

HS Level	$HS_{mean}$ Map HS Range (%)	Italian Mainland (km <sup>2</sup> )	Protected Areas (km <sup>2</sup> )	Gaps (%)	$HS_{max}$ Map HS Range (%)	Italian Mainland (km <sup>2</sup> )	Protected Areas (km <sup>2</sup> )	Gaps (%)
Minimum	5.13–16.73	107,885.44	21,899.15	79.70	5.92–22.56	58,542.79	11,938.42	79.61
Low	16.74–28.33	108,664.60	22,049.60	79.71	22.57–39.19	86,013.58	19,559.92	77.26
Medium	28.34–39.94	65,765.25	14,611.82	77.78	39.20–55.83	91,029.87	18,971.21	79.16
High	39.95–51.54	16,074.49	5244.24	67.38	55.84–72.46	52,795.37	10,128.74	80.82
Optimal	51.55–63.14	1531.39	665.86	56.52	72.47–89.09	11,450.40	3181.22	72.22





**Figure 4.** Maps showing the distribution of the Italian protected areas and their relevance for the conservation of *big five's* suitable habitat. In (a), each protected area was coloured according to the average  $HS_{mean}$  value, dividing the range (min–max) in five HS levels: red = minimum, orange = low, yellow = medium, light green = high and dark green = optimal HS. In (b), the shape of each protected area was coloured according to the average  $HS_{max}$  value, following the same ranking procedure. Average, together with median and maximum value, of both HS maps by protected areas were stored in Supplementary Materials (Protected\_areas\_ITA\_vector\_layers.zip).



**Figure 5.** Map showing the habitat suitability hotspot in northern Apennines of the Tuscany region. The area marked by red squares indicates the conservation gap highlighted by overlaying the national protected area boundaries to the  $HS_{mean}$  map of the *big five*.

#### 4. Discussion

This is the first study modelling the distribution of protected saproxylic beetles in Italy using CS data. Our findings confirmed that citizens' participation in conservation projects, as long as their contributions are validated by experts, can play a crucial role in studying the distribution and habitat preferences of endangered insect species. Involvement of



the citizen already proved to be a useful tool in monitoring saproxylic beetle species [74]. Besides, as previously suggested, CS projects can improve knowledge about saproxylic beetle distribution, accelerating the process of gathering occurrence data [16]. In particular, our results pinpointed that suitable habitat has a greater extent for some TUs (i.e., *M. asper asper/funereus* and *L. cervus*), while it might be restricted for some others (i.e., *R. alpina* and *Osmoderma* spp.). Indeed, *M. asper asper/funereus* and *L. cervus* are among the most widespread protected saproxylic beetle species in Italy [16]. A wide area, covering the Pre-alpine arc and the northern Apennines, reported the highest values of suitable habitat either for *M. asper asper/funereus* and *L. cervus*. This result is in line with the preferences of these species for mature and well-structured deciduous forests, especially for lowland and medium-altitude oak woodlands [33,43,75]. Conversely, the habitat of *Osmoderma* spp. and *R. alpina* can be considered so narrow to be properly described as a series of suitable woodland “islands” that remain in a “sea” of unsuitable land. According to previous findings [76], the suitable habitat for *R. alpina* occurs mainly in the mountainous altitudinal zone (Figures 2g and 1d), following almost entirely the distribution of beech forest (*Fagus sylvatica*) [77]. Indeed, even if *R. alpina* can colonise plenty of deciduous tree species, from the coastline to about 2000 m asl, it is considered a montane species, associated with beech forests [23,78]. The preference of *R. alpina* for cold climates is supported by the niche space results which indicate that sites with an annual mean temperature within the range 1–13 °C and a low to medium spring solar radiation are suitable for this species. Contrastingly, other TUs, such as *C. cerdo*, prefer high summer temperatures and present high HS values in the lowland of the Po valley, characterised by medium-high values of HMTS owing to the intensive agricultural activity. These findings corroborate previous considerations about habitat openness and isolated trees as important parameters for predicting the presence of this species [79]. In Italy *C. cerdo* generally occurs in semi-open wood stands and viable populations can also be found in tree-lined avenues [37,43]. It has to be remarked that, our predicted HS maps are based on remote sensing data, which did not take into account some fine-scale habitat features, such as presence of hallow or dead trees, stands and logs, crucial for saproxylic beetles’ life-cycle. Nevertheless, the highlighted hotspots might facilitate the process of fine-scale assessment of suitable habitat, targeting field surveys where the HS index reported the highest values. In addition, it might be interesting to conduct surveys in those areas where high HS values have been predicted and no data on *big five*’s occurrence have been reported. This would help both to validate the proposed model and to add new data on the presence of the *big five*.

To summarise, as it is evident by comparing the HS maps of each TU (Figure 1), the *big five* showed some differences in the extent and geographical location of suitable habitat, a direct consequence of dissimilarities in their niche space. Nevertheless, the considerations made regarding HS values for each TU might also be applied to some congeneric species, as in the case of *Osmoderma* spp. For instance, *Cerambyx welensii*, which is not protected by Habitat Directive, shares the same ecological niche with *C. cerdo*.

As a consequence of the differences in niche space between TUs, the area of the highlighted hotspots (HS<sub>mean</sub> map in Figure 3a) has a reduced extent and is marked by lower HS values if compared to the HS maps of single TUs. However, we believe it is critical to focus conservation actions on the highlighted hotspots. Primarily because it might be a way to make the most of the frequently scarce resources earmarked for conservation; secondly, as an umbrella effect, the conservation status of many other species sharing the *big five*’s habitat, may also be improved. Furthermore, the provided HS maps of each TU (Supplementary Materials: HS\_maps\_raster\_layers.zip) could be useful for conservation managers to highlight more accurately TU-specific sites, within the boundaries of the protected area under their own jurisdiction, crucial for conservation purposes.

Alongside their contribution to conservation management, the provided HS maps for the *big five* fill the gaps in their distribution and provide insights about their habitat preferences. Besides, HS maps can be considered a baseline for further research aiming at studying the range contraction of these endangered species (extinction risk) under future

scenarios [80–82]. Monitoring changes in species distribution may indeed be considered an early warning signal for habitat and species loss.

As regards levels of suitable habitat within the network of protected areas, the results of the zonal statistic tool can be compared to highlight the difference between mean value of  $HS_{mean}$  and  $HS_{max}$  within each reserve. This match highlights: those protected areas that represent hot spots for the conservation of the *big five* as a whole, those reserves holding relevant sites for just some target species and the protected areas less valuable for the *big five* protection (Figure 4a,b). In particular, some protected areas of the central Po plain and the central Apennines (Umbria-Marche Apennine), while being less pivotal for the *big five* (low  $HS_{mean}$  value), own critical sites for the conservation of certain target species (high  $HS_{max}$  value). For instance, the Po plain contains protected areas that show marked improvements in the HS level—from low  $HS_{mean}$  to high  $HS_{max}$ —such as the Special Protection Areas of Valli di Novellara and Valli di Gruppo (Emilia Romagna Region). This finding entails that, even an area characterised by a high level of human landscape modification (logging, farming and agriculture activities), might contain suitable sites for species such as *C. cerdo* or *O. eremita*, which benefit from individual old growth trees, albeit placed in an anthropized context. The same reasoning could be applied to some protected areas of central Italy, which have suitable sites for *M. asper asper/funereus*, *L. cervus* and *R. alpina*, turning from medium  $HS_{mean}$  to high  $HS_{max}$  level (e.g., Gran Sasso e Monti della Laga National Park) (Figure 4a,b).

Finally, as regards the gap analysis results, conservation measures are focused on the *big five*'s hot spots ( $HS_{mean}$ ), since nearly the 50% of optimal HS level falls within the protected areas network. Considering  $HS_{max}$ , the absence of a decreasing trend in conservation gaps might be the result of the habitat preferences of some TUs for anthropized landscape, where protected areas are mainly small and far apart (e.g., the presence of suitable habitat for *C. cerdo* in the Po plain). In this regard, the creation of ecological corridors, to connect protected areas, could be a priority to prevent the risk of local extinction.

From a research point of view, CS data inherently present some biases, e.g., due to the different detection probability of the species in relation to their abundance and behaviours. Among the five TUs, *Osmoderma* spp. is probably the less suited for CS monitoring in Italy, due to its low detectability by non-expert entomologists. Furthermore, the difference in the number of visitors among protected areas (attractiveness, accessibility, etc.), should be taken into account to remove spatial autocorrelation among occurrence data [83]. By contrast, it should be mentioned that museum data—frequently used in SDM—could suffer from biases too, e.g., spatial and temporal problems due to old records, which require careful examination to avoid introducing error in distribution models [84,85]. On the other hand, we would like to remark that public participation represents a pivotal way to educate new generations and increase their awareness on nature conservation issues [86–88]. Indeed, even citizens, though to a lesser extent with respect to researchers, might notice changes in abundance and distribution of target species through a continuative participation in CS projects. Finally, the provided practical example in the northern Apennines allowed us to highlight the process to identify conservation gaps and to target managing actions. Hence, we demonstrated how CS data, once validated and analysed by researchers, could contribute to increase knowledge on species ecology and highlight those areas where conservation actions should be focused. Consequently, the final task of national and local authorities, together with park managers, should be to concentrate their efforts on expanding/establishing protected areas located in the highlighted hotspots.

**Supplementary Materials:** The following supporting information can be downloaded at: <https://doi.org/10.5281/zenodo.7523948>:  $HS_{mean}$ ,  $HS_{max}$  and HS maps of each TU (raster layers); shape files of protected areas with their mean, median and maximum values of  $HS_{mean}$  and  $HS_{max}$  raster layers (vector layers); Table S1 and Figure S1.

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