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National-scale estimates of mammal species abundance in Italy for the Habitat Directive reporting

Technical Report

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Summary

This report describes the methodological frameworks developed in collaboration with ATIt ETS (https://www.mammiferi.org) to estimate the abundance of mammal populations at the scale of Italy for the species listed under Annexes II, IV, and V of the Habitats Directive. For each species, the estimation methodology was defined based on the availability and quality of data supplied by the individual Italian regions. The report provides, for every species and biogeographical region (Alpine, Continental and Mediterranean), population abundance estimates with 95% confidence intervals, estimates of the extent of habitat area, and, where possible, estimates of temporal trends in population abundance.

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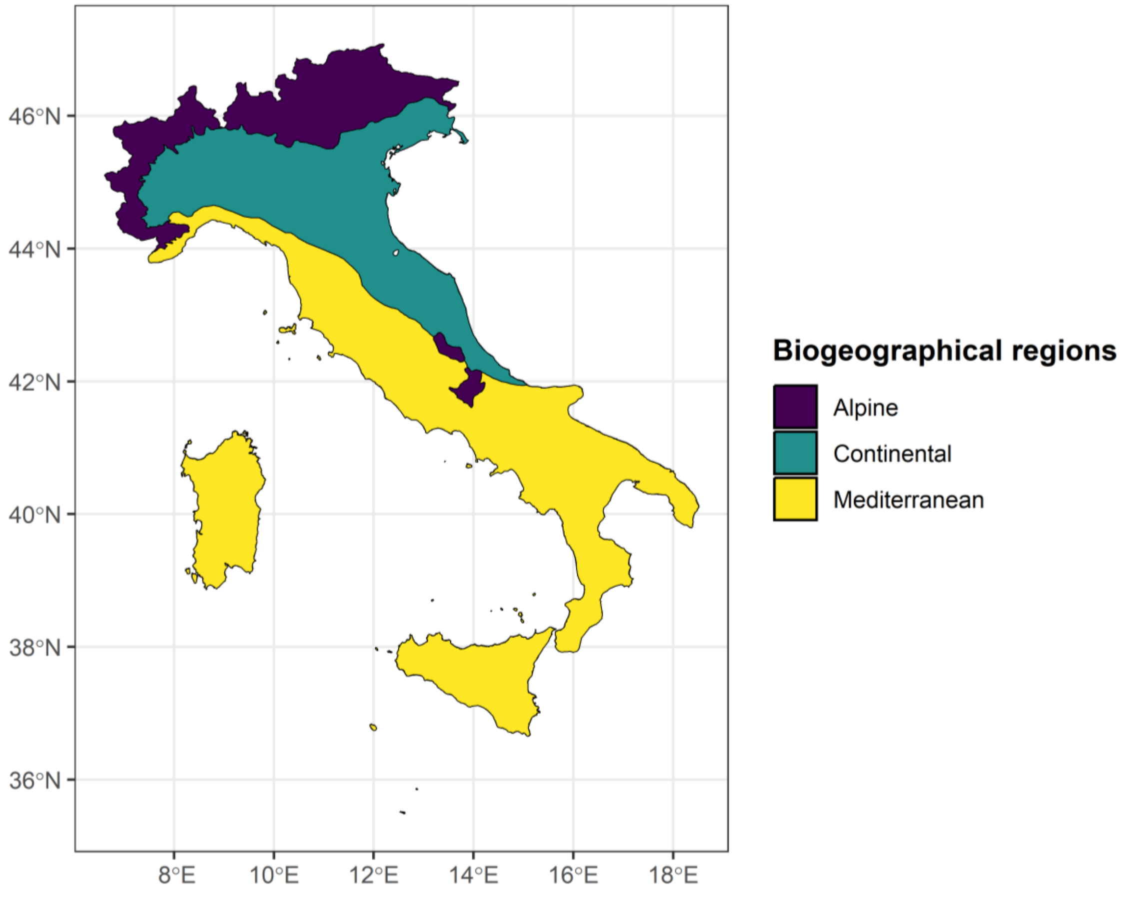
1. INTRODUCTION

The 5th Report of the Habitats Directive requires a quantitative assessment of mammal population sizes for the species listed under Annexes II, IV, and V for the Mediterranean, Continental, and Alpine biogeographical regions in Italy (Fig. 1). However, with the exception of large carnivore and ungulate species (e.g., Lapini et al. 2022; La Morgia et al. 2022), such population estimates are lacking at this spatial scale. To address this gap, it is necessary to either compile quantitative data collected by the administrative regions or use locally published estimates, and to develop methods for extrapolating these estimates across the species' full distribution within the three biogeographical regions.

This report describes the activities carried out in collaboration with ATIt ETS (https://www.mammiferi.org) to obtain these estimates. In particular, it illustrates the methodological framework developed, the results obtained, and the limitations of the work..

Fig. 1. Subdivision of Italian national territory based on biogeographical regions.



The following species in Italy are listed in Annexes II, IV, and V:

Order Soricomorpha: *Crocidura sicula.*

Order Lagomorpha: *Lepus timidus.*

Order Rodentia: *Dryomys nitedula, Muscardinus avellanarius, Hystrix cristata.*

Order Chiroptera: *Barbastella barbastellus, Eptesicus nilssonii, Eptesicus serotinus, Hypsugo savii, Miniopterus schreibersii, Myotis alcathoe, Myotis bechsteini, Myotis blythi, Myotis brandtii, Myotis capaccinii, Myotis daubentonii, Myotis emarginatus, Myotis myotis, Myotis mystacinus, Myotis nattereri, Myotis punicus, Nyctalus lasiopterus, Nyctalus leisleri, Nyctalus noctula, Pipistrellus kuhlii, Pipistrellus nathusii, Pipistrellus pipistrellus, Pipistrellus pygmaeus, Pipistrellus auritus, Pipistrellus austriacus, Pipistrellus macrobullaris, Pipistrellus sardus, Rhinolophus blasii, Rhinolophus euryale, Rhinolophus ferrumequinum, Rhinolophus hipposideros, Rhinolophus mehelyi, Tadarida teniotis, Vespertilio murinus.*

Order Carnivora: *Canis aureus, Canis lupus, Felis sylvestris, Lutra lutra, Lynx lynx, Martes martes, Mustela putorius, Ursus arctos.*

Order Cetartiodactyla: *Capra aegagrus, Capra ibex, Cervus elaphus, Ovis ammon musimon, Rupicapra pyrenaica ornata, Rupicapra rupicapra.*

The species for which population estimates already exist are *Canis lupus*, *C. aureus*, *Lynx lynx*, *Ursus arctos*, and all the ungulate species.

2. DISTRIBUTION DATA

To extrapolate abundance estimates at the regional scale, it is necessary to have species distribution data, which can substantially influence the final abundance estimates. For all analyses in this report, we combined two types of distribution data: national scale atlases and Area of Habitat (AoH) maps. We obtained the atlases at 10x10 km resolution from the Italian Institute for Environmental Protection and Research (ISPRA, https://www.isprambiente.gov.it/it). We generated the AoH maps following the methodology described in Rondinini et al. (2011), using the most recent (year = 2022) 300-m resolution land-cover layer from the ESA Climate Change Initiative (ESA 2017, https://www.esa-landcover-cci.org). We obtained habitat-preference data from the IUCN Red List database (IUCN, 2025), and then converted them into ESA CCI categories using the cross-walk presented in Santini et al. (2019). We then masked the national-scale atlases by the AoH maps to estimate the available habitat area per atlas cell.

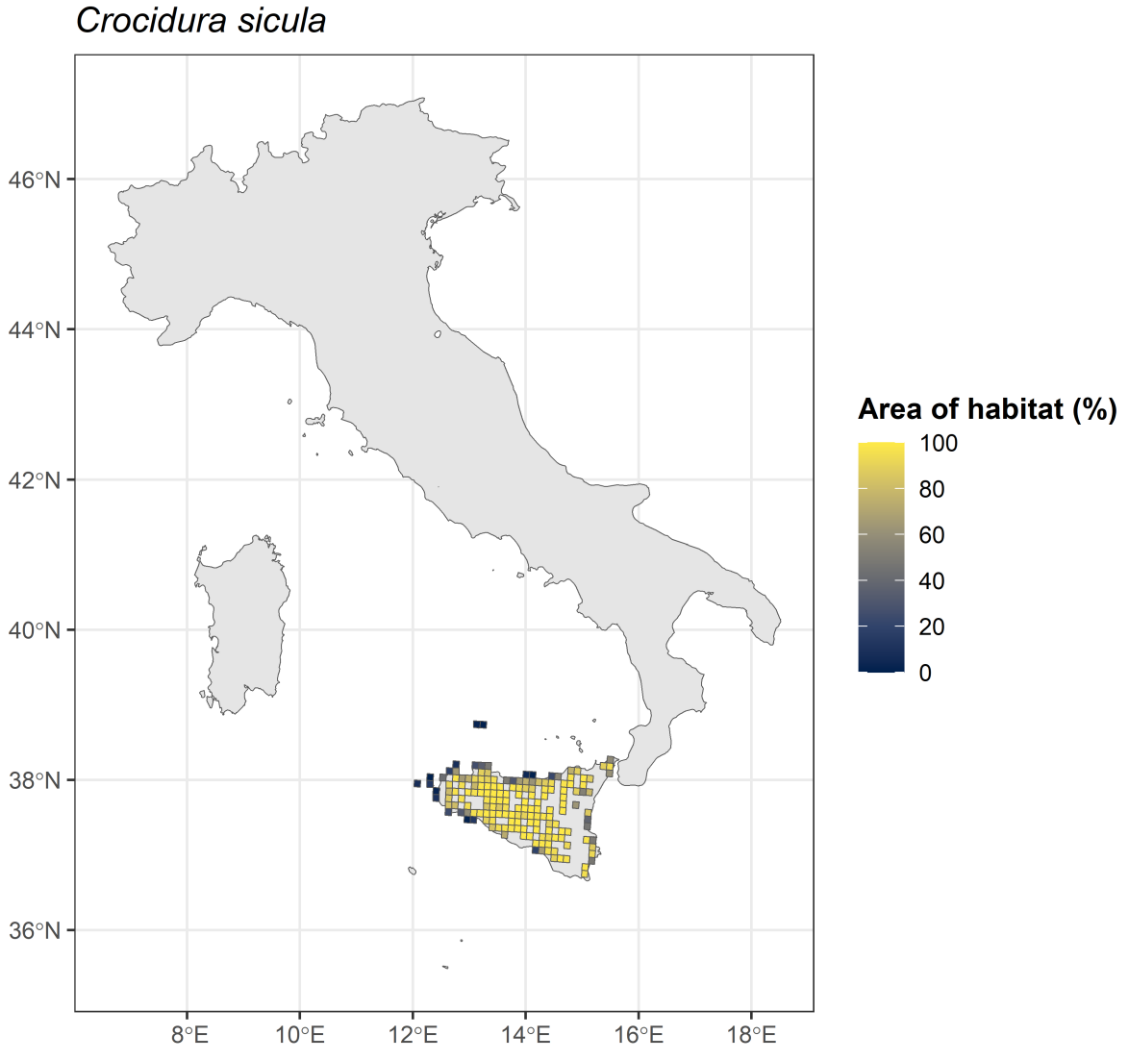
Lumbierres et al. (2021) recently published AoH maps for all mammals using a slightly different methodology, however after inspective their models for our target species, we concluded they were unsuitable for our purposes. This is because Lumbierres et al.'s models were masked using the IUCN Red List range maps, which do not align well with national atlases, potentially causing substantial over- or underestimation.

2.1 Species with insufficient data

Sicilian shrew (*Crocidura sicula*)

We found no abundance estimates or data from which regional-scale estimates could be derived for the Sicilian shrew. Based on the AoH maps, we estimated the extent of habitat area in the Mediterranean region to be 12,831.7 km² (Fig. 2).

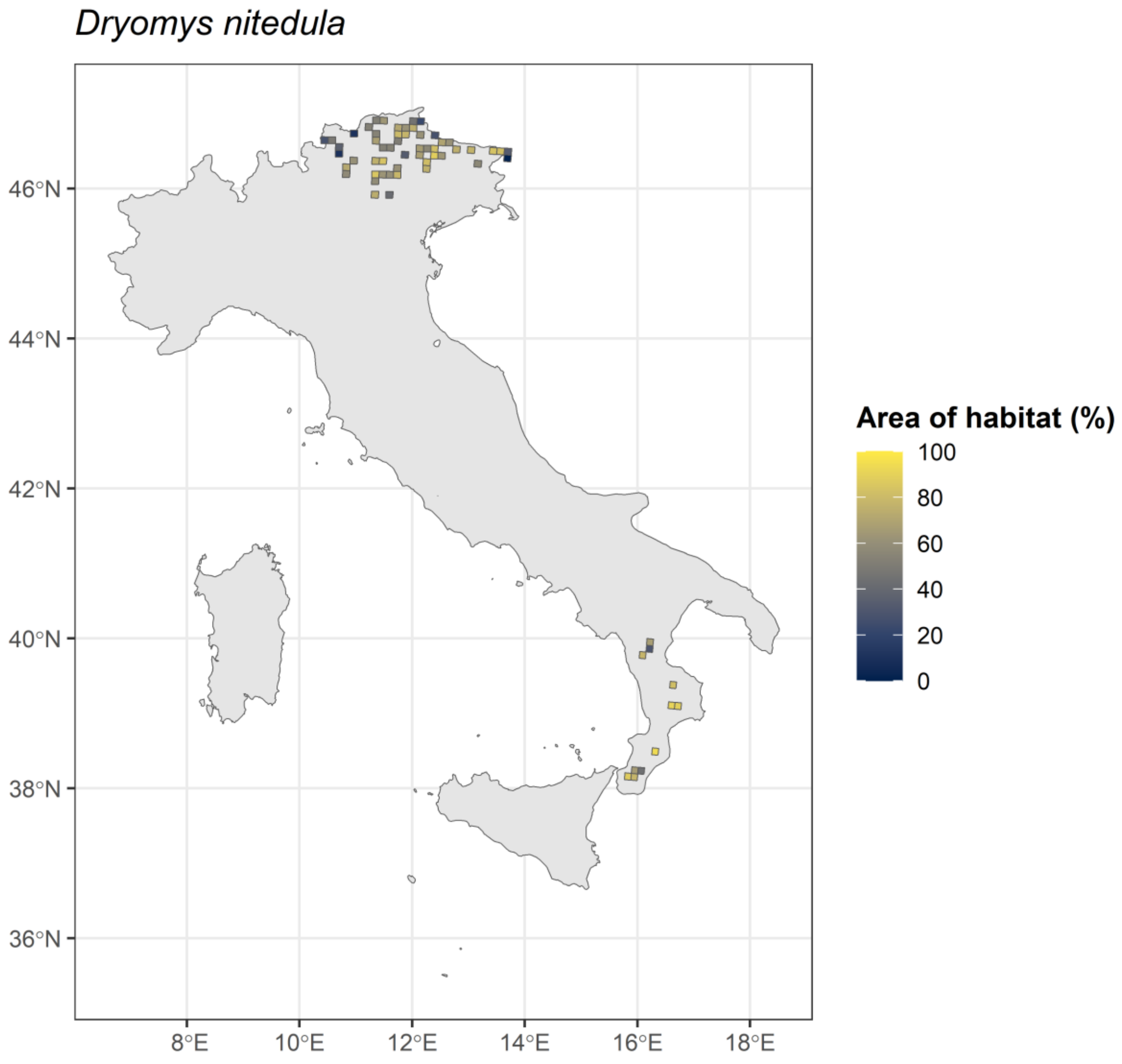
Fig. 2. Distribution of *Crocidura sicula* in Italy. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).



Forest dormouse (*Dryomys nitedula*)

We found no abundance estimates or data from which regional-scale estimates could be derived for the forest dormouse in Italy. Nest-box data were collected in the Aspromonte region (Calabria), but only two individuals were captured. To the best of our knowledge, only two studies in Europe estimated the population density of this species. The first was conducted in the Białowieża Forest in Poland between 2001 and 2004, and reported densities ranging from 0.14 individuals/ha to 1.90 individuals/ha (Borowski & Ściński 2013). The second study was based on a long-term monitoring program in central Lithuania's forest between 1999 and 2013, and reported "minimum number alive" estimates of 0.45 ± 0.15 individuals/ha before hibernation and 0.67 ± 0.21 individuals/ha after hibernation (Juškaitis 2014). Based on the AoH maps, we estimated the extent of habitat area to be 3,308.8 km² in the Alpine region and 806.3 km² in the Mediterranean region (Fig. 3).

Fig. 3. Distribution of *Dryomys nitedula* in Italy. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).



2.2 Home range-based estimates

European polecat (*Mustela putorius*)

We found no abundance estimates for the European polecat in Italy. We are aware of one single study in Sweden that estimated polecat population density in Europe (Hofmeester et al. 2024), which reported densities between 0.084 and 0.270 individuals/km². However, Rondinini et al. (2006) estimated the home-range areas and pairwise home range overlap for eight male and two female European polecats in Italy via minimum convex polygons. We started from these home range estimates to derive a preliminary abundance estimate. We first estimated the male population using male home range data, and subsequently derived the female population applying documented population sex ratios. For each 10 × 10 km cell, we randomly drew 1,000 male home-range sizes (646 ha – 1,696 ha) from which we subtracted a randomly drawn total overlap area with neighbouring males (9.8 ha – 64.1 ha). This yielded a distribution of exclusive home-range sizes per cell, which we converted to densities as:

$$density = \frac{1}{exclusive\ home\ range}$$

We obtained a median male density of 0.09 ind/km², which falls within the range reported by Hofmeester et al. (2024). We then multiplied the distribution of simulated male densities for each cell by the available habitat area, and summed the results across all cells. We obtained a national male-only abundance distribution, yielding a total of 7,189 males (95% CI: 6,889–7,475). To estimate the total population size, we accounted for documented male-biased sex ratios (Barrientos 2015; Zalewski et al. 2022). Because this bias is more pronounced in areas where the American mink (*Neovison vison*) is absent, we only used estimates of polecat populations in mink-free regions (studies reported sex bias as the percentage of male with respect to females, ranging from 18.67% to 38.65%). We obtained the final population estimate as:

$$Total\ population = male\ population + (male\ population - sex\ bias)$$

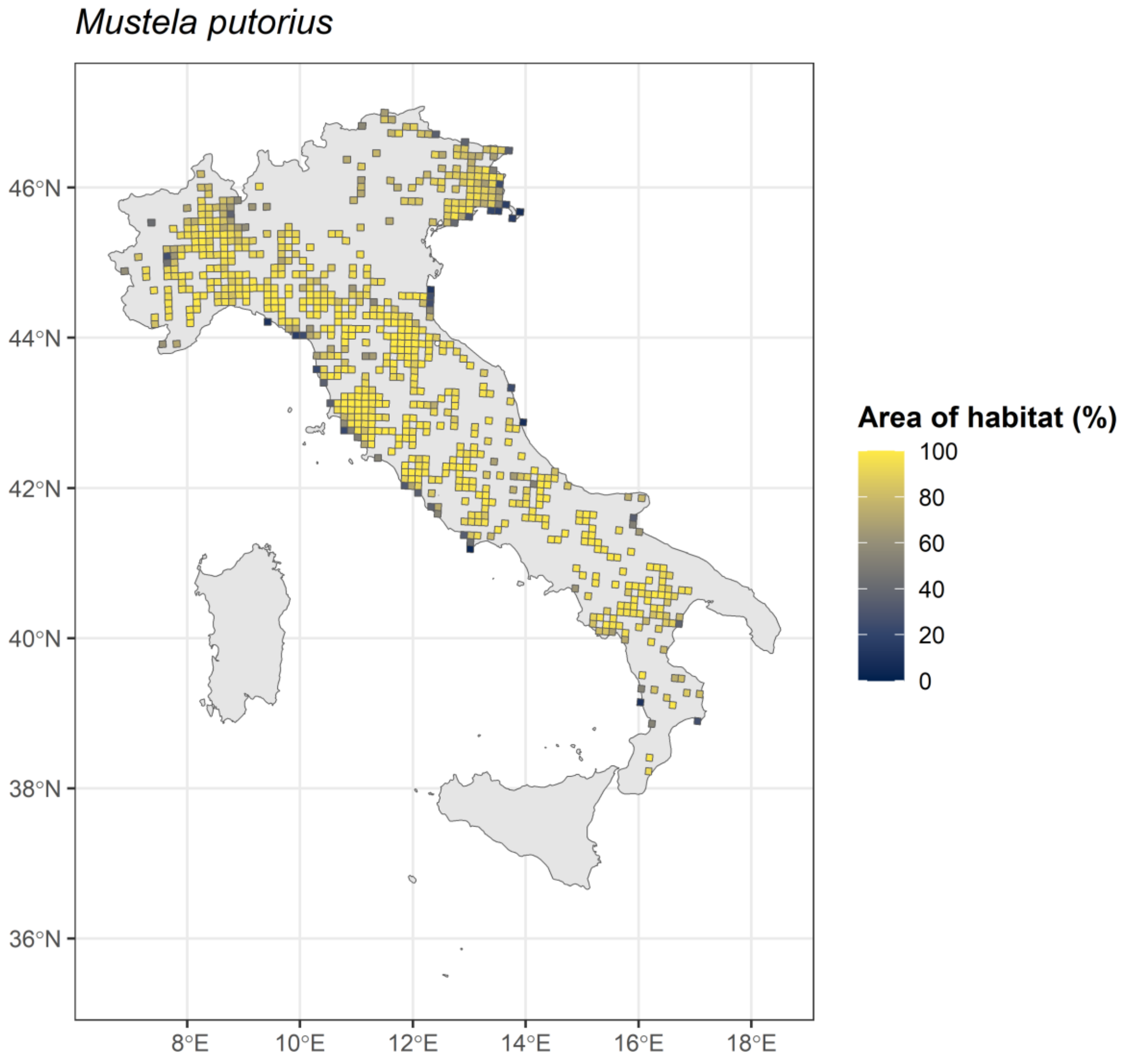
Where:

$$Sex\ bias = male\ population\ \times (\frac{\%\ more\ males}{100})$$

We randomly sampled the proportion of males from a uniform distribution using the 18.67– 38.65% interval. We estimated a total of 11,582 individuals (95% CI: 10,713–12,381) across the entire habitat area in Italy (65,183.5 km²). At the regional level, we estimated 1,193 individuals (95% CI: 1,078–

1,289) in the Alpine region (6,703.5 km²), 5,324 (95% CI: 4,902–5,680) in the Continental region (29,905.2 km²), and 5,090 (95% CI: 4,662–5,445) in the Mediterranean region (28,574.8 km²).

Fig. 4. Distribution of *Mustela putorius* in Italy. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).

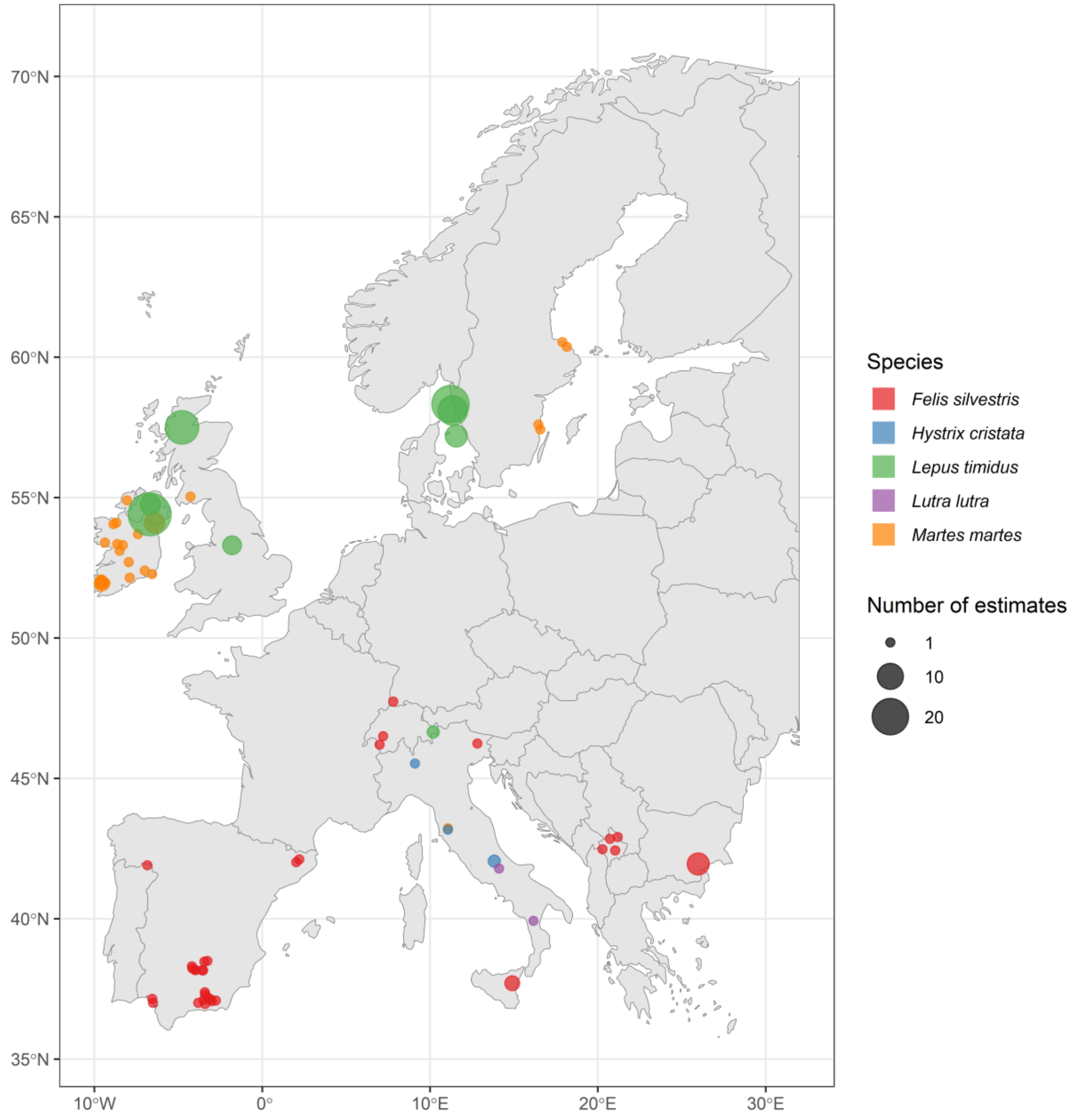


2.3 Estimates obtained through extrapolation of local data

For species such as the mountain hare, crested porcupine and pine marten, only a limited number of local population density estimates were available (Fig. 5), which does not allow for the development of robust modelling approaches. In these cases, we adopted a highly simplistic assumption, which is that the densities estimated at the sampled locations were representative of the entire species range in

Italy. To account for uncertainty, we considered both the variability among available estimates and from the statistical uncertainty of the estimates themselves. Therefore, these should be regarded as preliminary, coarse estimates, and should be interpreted with caution. To generate these estimates, we sampled 1,000 values from a log-normal distribution (parametrized using the local estimates' mean and standard deviation) for each atlas cell where the species was recorded as present. We then multiplied each sampled density value by the area of habitat within that cell, therefore obtaining a distribution of population abundances.

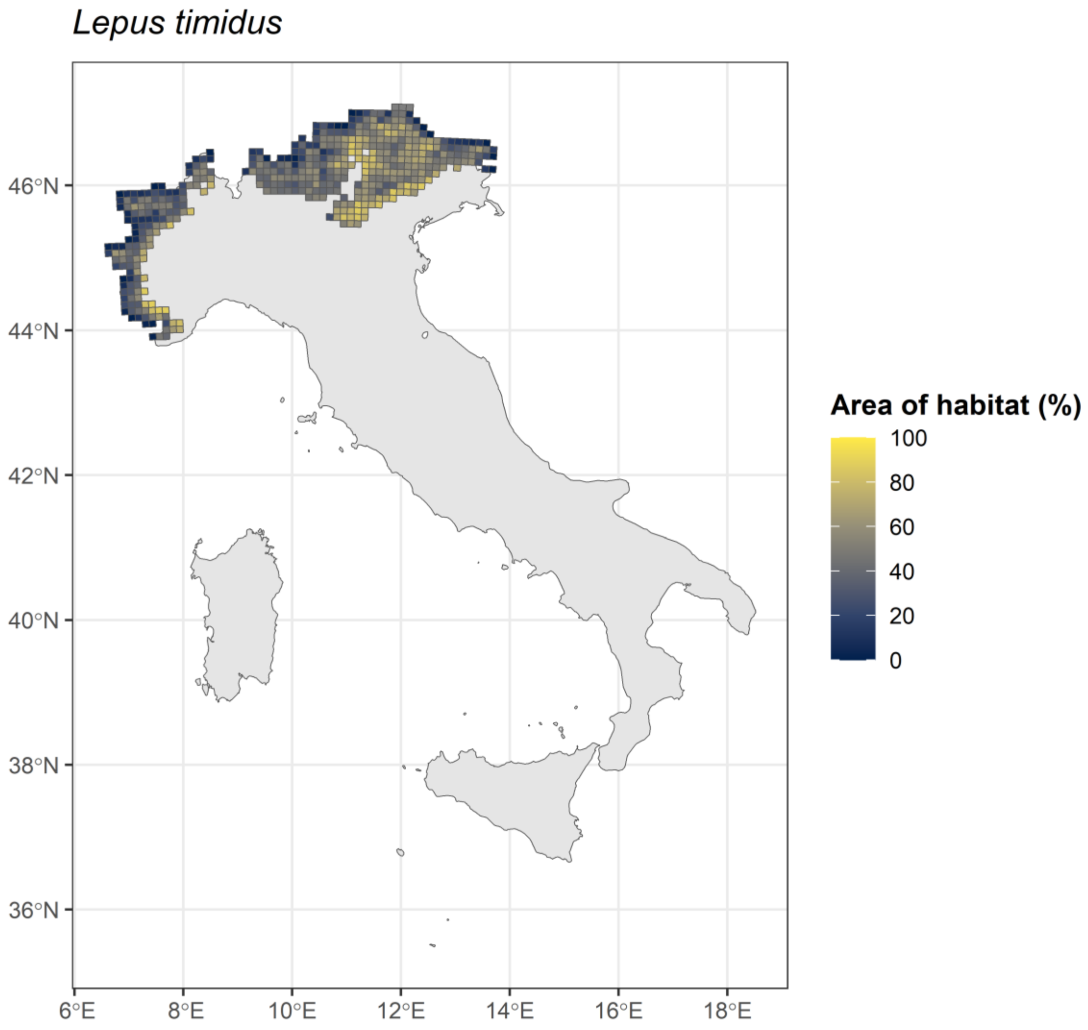
Fig. 5. Spatial distribution of density estimates currently available in Europe for *Felis silvestris*, *Hystrix cristata*, *Lepus timidus*, *Lutra lutra*, and *Martes martes*. Point size is proportional to the number of estimates at each site, using a 1 km aggregation threshold.



Mountain hare (*Lepus timidus*)

We found around 100 population density estimates for the mountain hare in the literature, but from only nine sites across Europe: 8 in Scandinavia and the United Kingdom, and a single site in the Swiss Alps. The estimates are extremely variable, ranging from 0.7 individuals per km² (Northern Ireland; Reid & Montgomery 2010) to 419 individuals per km² (Sweden; Angerbjörn 1986). The study conducted in the Swiss Alps by Renhus & Bollmann (2016) reported a density of 3.2 ± 0.7 individuals per km². Using this density estimate and following the methodology outlined above, we estimated a population of 91,688 individuals (95% CI: 85,392–97,196) in the Alpine region, for a total habitat area of 22,517.1 km² (Fig. 6).

Fig. 6. Distribution of *Lepus timidus* in Italy. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).

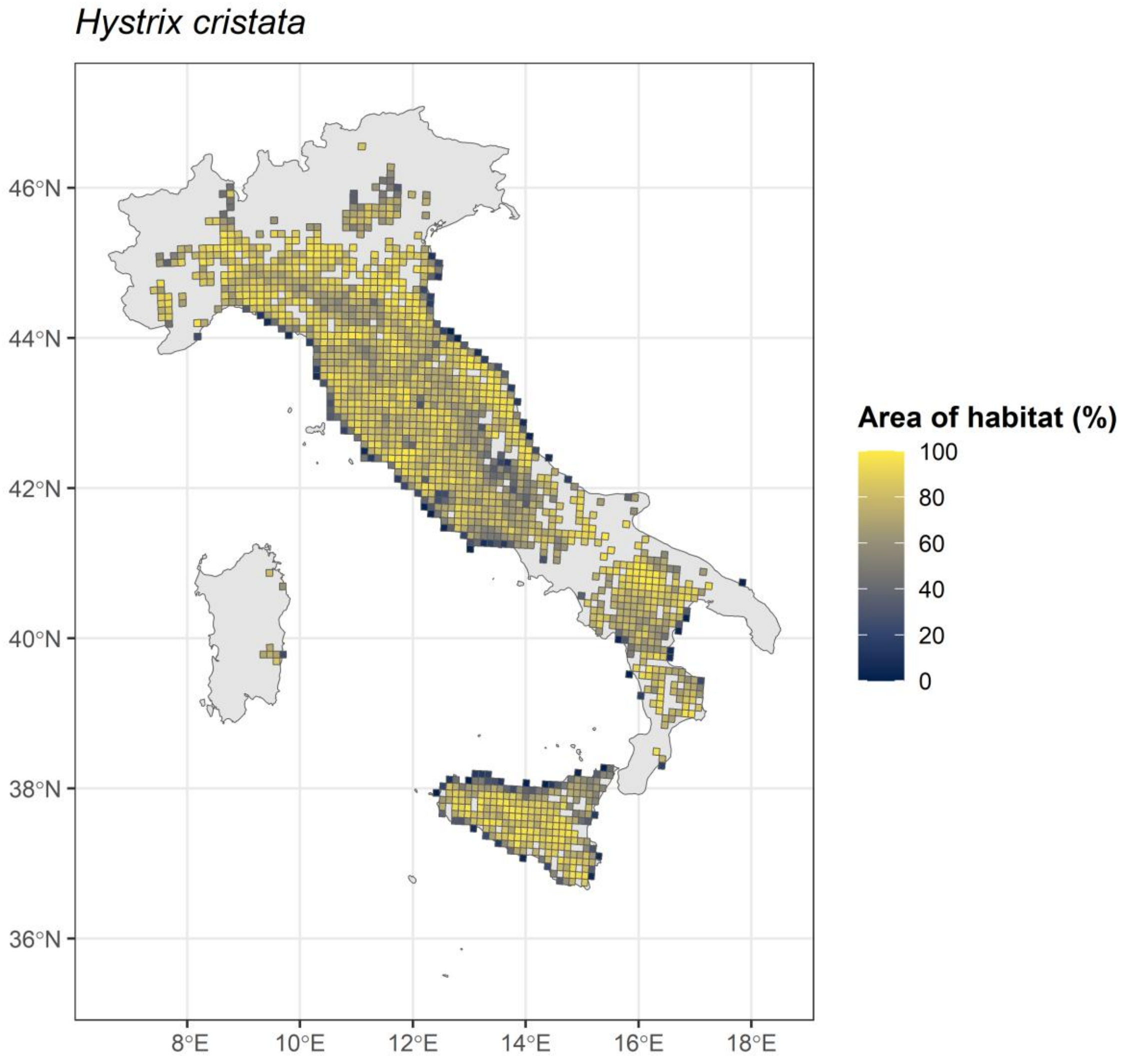


Crested porcupine (*Hystrix cristata*)

We are aware of only four published density estimates for the crested porcupine in Italy. The first was produced by Franchini et al. (2022) and reported a density of 0.10 ± 0.001 individuals per km² in Tuscany, which is an unusually low value given the species ecological traits (Santini et al. 2021). This low estimate likely reflects the use of a presence-only method that did not account for detectability. The second estimate was produced by Palencia et al. (2024) using the Random Encounter Model in Lombardy, at the northern margin of the porcupine's range, yielding 0.49 ± 0.33 individuals per km². The third estimate comes from a preprint (Dragonetti et al. 2025; currently under review, personal communication from the first author) that applied the Random Encounter Model in two areas of the Abruzzo National Park, producing densities of 1.84 ± 0.68 and 1.08 ± 0.67 individuals per km². The fourth estimate comes from an unpublished technical report of an assessment conducted in Umbria (Alfina area; Ceci et al. 2024), also using a Random Encounter Model, which yielded a density of 6.02 ± 1.47 individuals per km².

Using the density reported by Palencia et al. and the AoH in the Alpine (4,501.2 km²) and Continental (45,145.0 km²) regions, we derived regional population estimates of 2,326 individuals (95% CI: 2,127–2,481) and 23,333 individuals (95% CI: 22,700–23,850), respectively (Fig. 7). Based on the higher density estimates from Dragonetti et al. (2025) and Ceci et al. (2024), we estimated 179,811 individuals (95% CI: 101,151–1,452,901) in the Mediterranean region (habitat area = 77,517.0 km²; Fig. 7). We did not use the estimate by Franchini et al. (2022) for the Mediterranean region as it is unrealistically low, leading to only 12,716 porcupines across all of Italy. Additionally, the extremely low small standard deviation would result in an extrapolation uncertainty of zero.

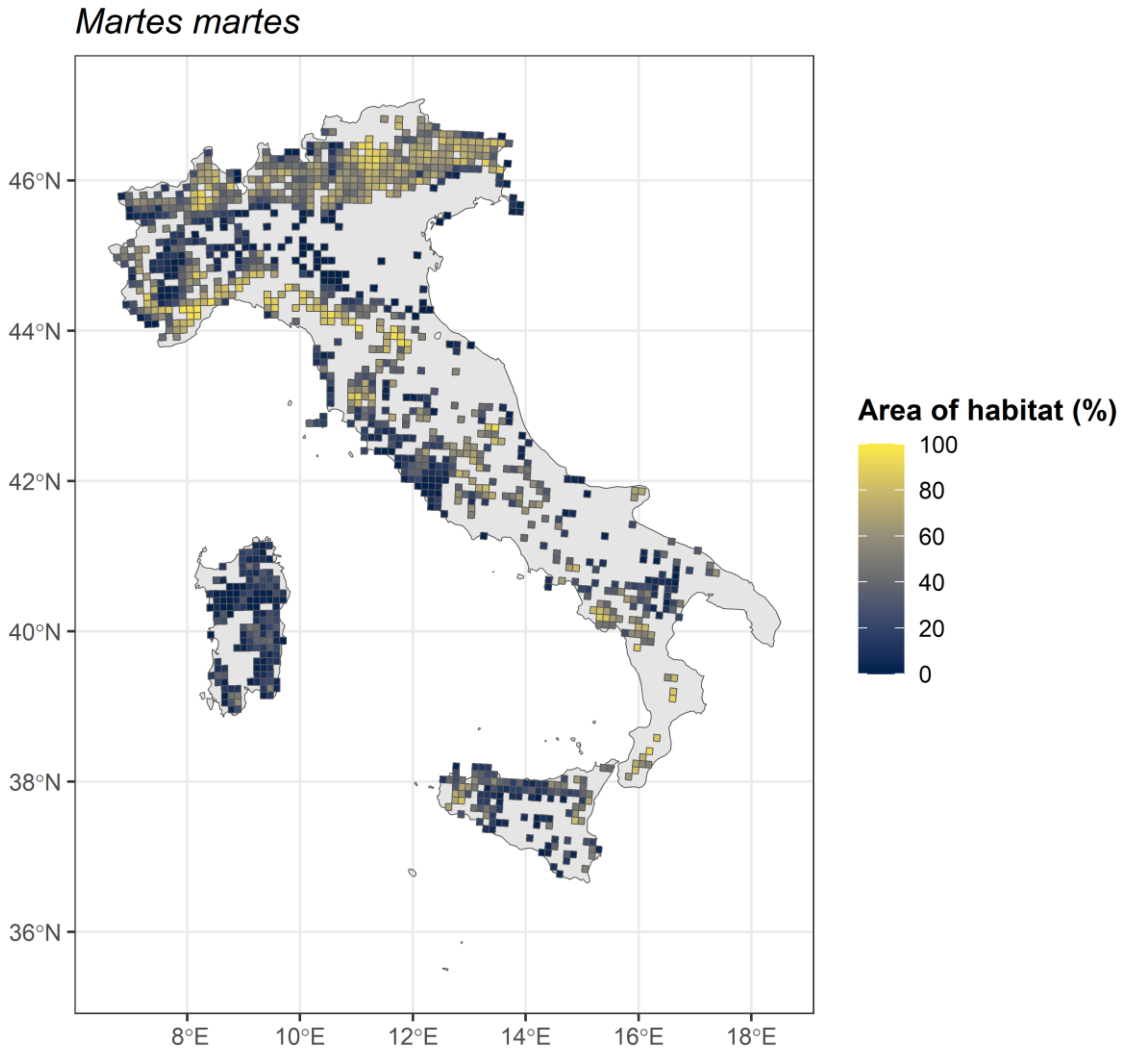
Fig. 7. Distribution of *Hystrix cristata* in Italy. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).



Pine marten (*Martes martes*)

Due to the difficulty in distinguishing the pine marten from the stone marten in camera-trap studies, many reports provide combined densities for the genus *Martes*, whereas very few provide separate estimates for the two species. We found 33 pine marten density estimates in Europe: 21 from Ireland, 7 from the United Kingdom, 4 from Sweden, and only one from Italy, ranging from 0.05 to 2.6 individuals per km². The Italian estimate, produced by Manzo et al. (2012) in Tuscany, reported a density of 0.34 individuals per km² (95% CI: 0.21–0.47). Assuming that density is constant across the entire Italian territory where the species is present, and following the methodology described above, we obtained a total estimate of 15,905 pine martens (95% CI: 15,834–15,959) over 46 426.5 km² of habitat area (Fig. 8). At the regional scale, we estimated 6,995 individuals (95% CI: 6,946–7,032) across the Alpine region (20,532.2 km²), 2,720 individuals (95 % CI: 2,692–2,743) across the Continental region (7,984.1 km²), and 6,103 individuals (95% CI: 6,061–6,133) across the Mediterranean region (17,910.1 km²).

Fig. 8. Distribution of *Martes martes* in Italy. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).



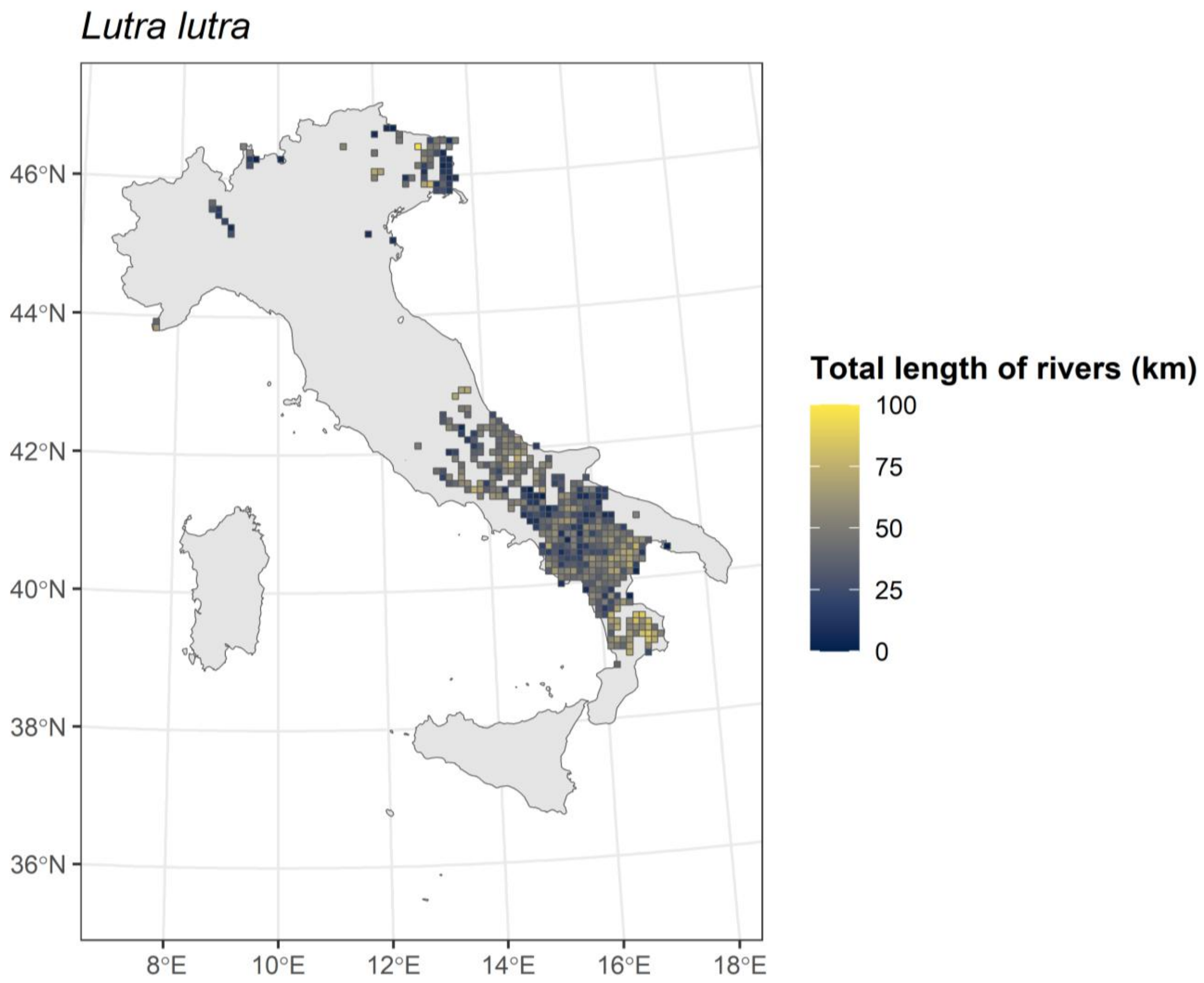
Eurasian otter (*Lutra lutra*)

For the Eurasian otter, we used two available density estimates: one by Prigioni et al. (2006), reporting a linear density of 0.18–0.20 individuals per km (only the 95% confidence interval is provided) in the Pollino National Park, and one by Lerone et al. (2022), reporting 0.152 individuals per km (95% CI: 0.139–0.177) along the Sangro river. To obtain an overall population estimate, we used the national hydrographic network provided by ISPRA up to the third order intersecting the atlas grid cells, and multiplied the length of each linear segment by a randomly sampled density value. Since the standard error (SE) was not available, we derived it from the 95% confidence interval as:

$$SE = \frac{upper\ limit\ of\ 95\%\ CI - lower\ limit\ of\ 95\%\ CI}{3.92}$$

and we then sampled randomly from the two resulting log-normal distributions. In the absence of a mean estimate from Prigioni et al. (2006), we assumed a mean of 0.19 for that distribution. We then summed the estimates across all atlas cells and repeated the operation 1,000 times, thus generating a distribution of 1,000 abundance estimates. Overall, we estimated a total population of 3,158 otters (95% CI: 3,150–3,165) distributed across 18,470.4 km of linear habitat (Fig. 9), with 225 individuals (95% CI: 223–227) in the Alpine region (1,316.1 km), 368 (95% CI: 365–371) in the Continental region (2,152.7 km), and 2,565 (95% CI: 2,558–2,571) in the Mediterranean region (15,001.6 km).

Fig. 9. Distribution of *Lutra lutra* in Italy. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).



2.4 Modelling approaches

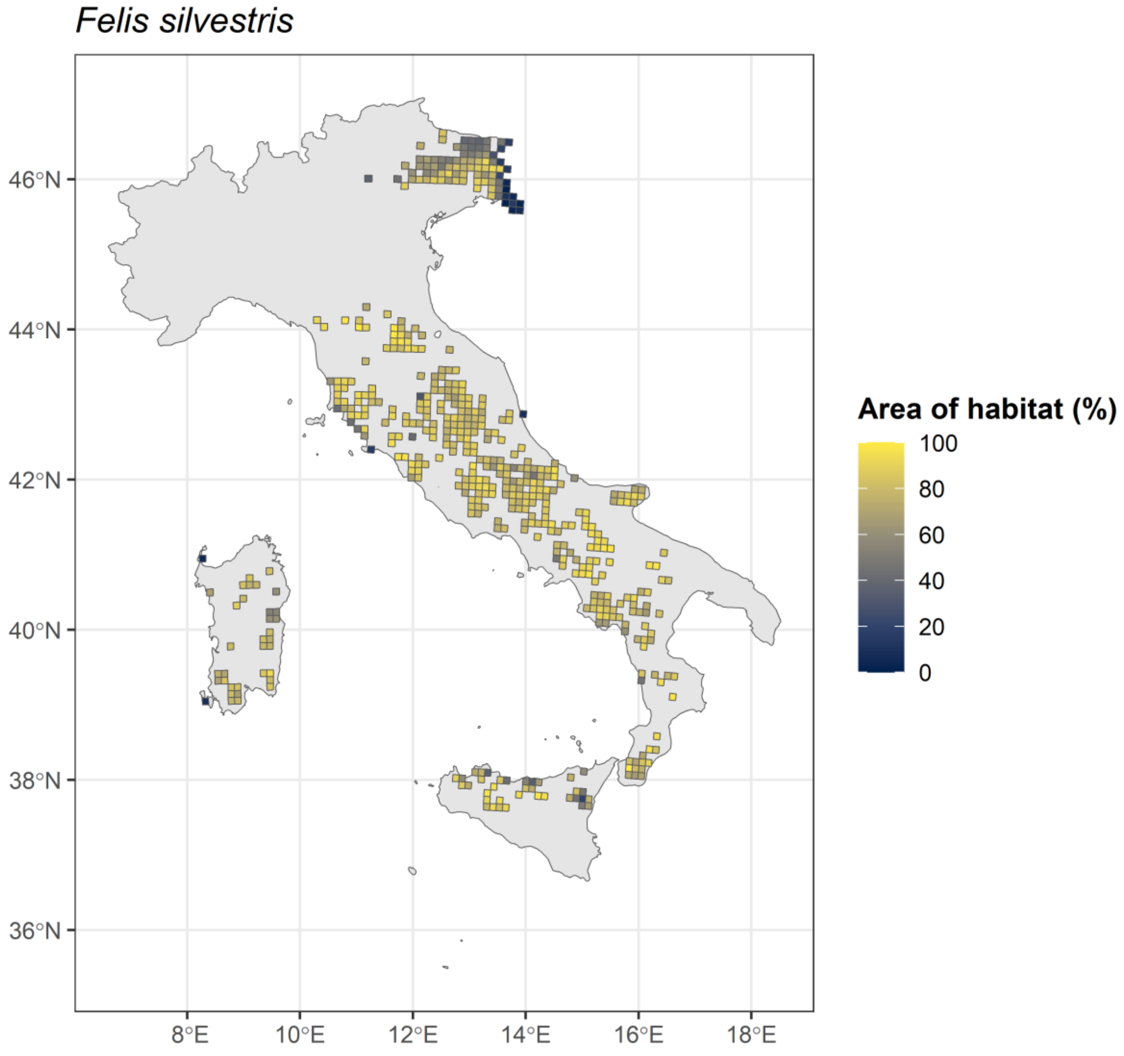
Wildcat (*Felis silvestris*)

The wildcat presents a different situation compared to the previous cases. Numerous density estimates exist across Europe (Fig. 5), but in Italy they are available only at the two extremes of the environmental gradient. Specifically, we found 42 density estimates from 33 sites located in several countries (Bulgaria, Italy, Kosovo, Portugal, Spain, Switzerland, and Turkey), of which only 5 estimates are from Italy: one in the Carnic Alps and four in the Etna Park in Sicily (Fig. 5). We therefore opted for a modelling approach that could capture the effect of one or more environmental gradients on the species' average density, thus relaxing the assumption of homogeneous density across the species range.

We considered all density estimates and evaluated their relationship with the following environmental variables: proportion of agricultural land, accessibility (travel time from cities with at least 50,000 inhabitants; Nelson et al. 2008), human population density (CIESIN – Columbia University 2018), and the Normalized Difference Vegetation Index (NDVI; NASA LP DAAC, https://doi.org/10.5067/MODIS/MOD13C1.061). Given the average size of study areas used for estimating density, and the uncertainty in the coordinates associated with individual studies, we used environmental variables at a spatial resolution of 0.1 decimal degrees (~10 km). We then applied a linear mixed-effects model, allowing us to control for sampling method and sampling site as random effects. Given the limited sample size and the need to control for confounding factors, we constrained the model's complexity to linear terms only. As an initial exploratory analysis, we performed model selection using a frequentist inference framework, testing all combinations of the four environmental predictors. The best model according to AIC (AIC weight = 0.7) included only NDVI, which showed a positive effect on density (2.26 ± 0.71). To obtain predictions for the entire national territory, we followed the methodology described in Pranzini et al. (2022). We generated a distribution of predictions for all atlas grid cells using a similar model but under a Bayesian inference framework. We employed weakly informative priors following Lemoine (2019) (N: mean = 0, SD = 0.5^2). These predictions were then multiplied by the habitat area within each cell and summed to obtain a total abundance estimate. From the resulting distribution, we excluded biologically implausible estimates with densities < 0.01 or > 1.1 ind./km² (based on literature values ranging from 0.02 to 1.01 ind./km²). These outliers reflect statistical uncertainty due to the small sample size, but we deemed them as biologically unrealistic. This exclusion (~5 % of the total) allowed us to reduce the prediction interval. From the remaining distribution, we extracted the median and the 2.5th and 97.5th percentiles (95% of the distribution).

The result for the entire peninsula, based on an available habitat area of 20,633.0 km² (Fig. 10), was 4,076 individuals (95% CI: 608–11,054) distributed as follows: 746 (95% CI: 110–2,289) in the Alpine region (4,203.7 km²), 716 (95% CI: 111–2,068) in the Continental region (3,803.0 km²), and 2,494 (95% CI: 340–7,154) in the Mediterranean region (13,272.9 km²).

Fig. 10. Distribution of *Felis silvestris* in Italy. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).



2.5 Resampling approaches

For bat species and the hazel dormouse that lacked density estimates but for which other type of data were available, it was possible to employ a resampling approach (bootstrapping), previously used to estimate the population size of the wolf in Italy (Boitani & Salvatore 2017). This method enables working with limited data while still providing an estimate of uncertainty. However, such estimates and the associated uncertainties must be interpreted in light of the assumptions they are based on, which differ between the two cases discussed below.

In the case of bats, data were in the form of roost mapping and roost counts. The underlying assumption is that in the atlas cells where roosts were recorded, all existing roosts were detected.

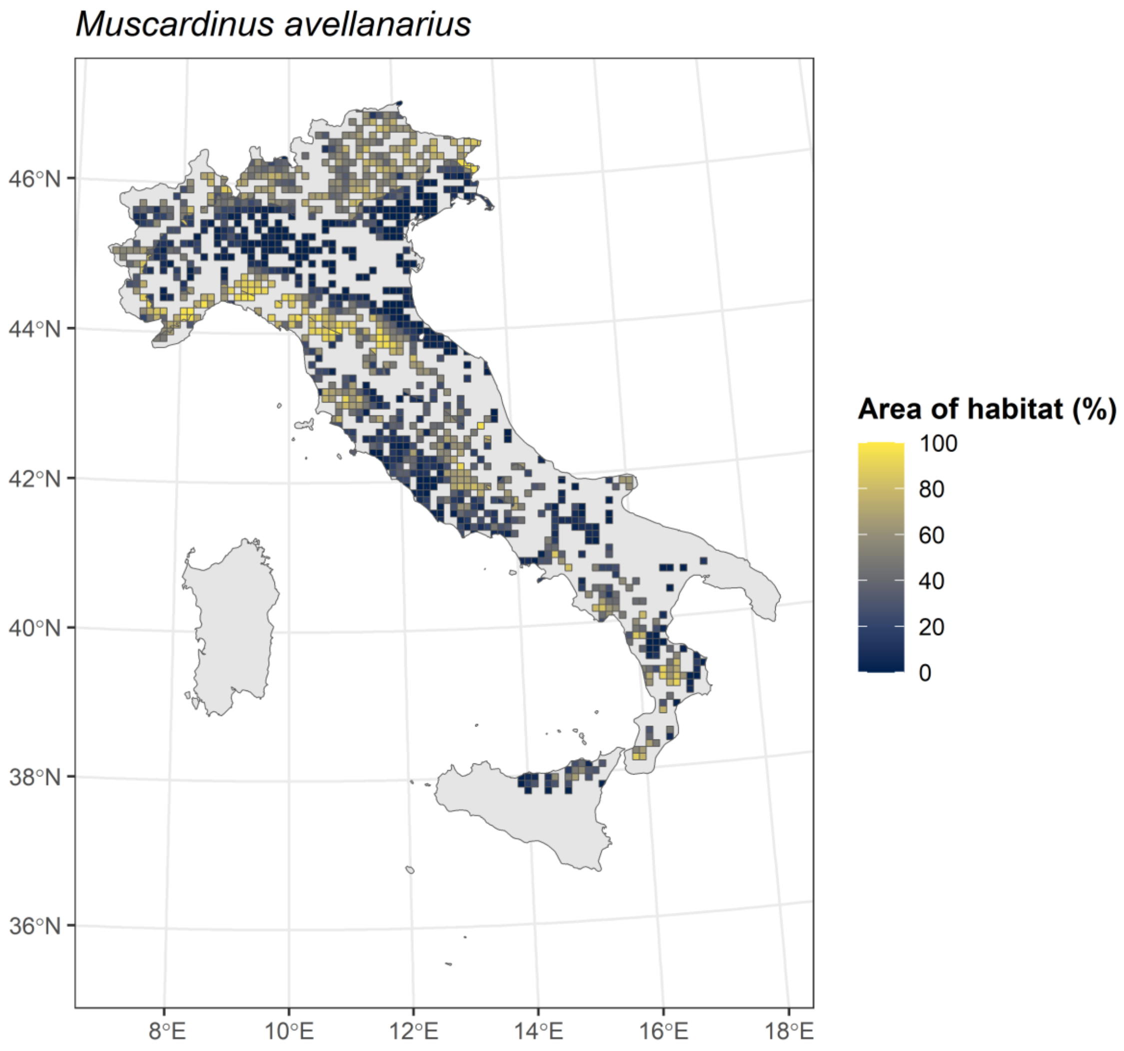
Since this is unlikely to be true, the resulting estimates should be interpreted as minimum population estimates. In the case of the hazel dormouse, data were in the form of nest box counts. We had capture data but no way to estimate detectability, so we used the maximum density observed during recaptures. Here as well, the resulting estimate should be regarded as a minimum population estimate.

Hazel dormouse (*Muscardinus avellanarius*)

For the hazel dormouse, population abundance extrapolation was based on field counts obtained via nest-boxes. These data were available for the regions Valle d'Aosta (n = 6 sites), Lombardy (n = 118 sites), Emilia-Romagna (n = 42 sites), and Lazio (n = 39 sites). We therefore partitioned the raw data by biogeographical region and produced independent abundance estimates for each. From the nest-box counts we derived density estimates for each site. Given the heterogeneity of sampling protocols, the reference area for density calculation was defined as the area covered by that grid when traps where deployed following this design, while when traps were deployed along linear transects, a 100 m buffer (50 m each side) around the transect line was adopted to obtain the area of the corresponding strip transects. The buffer width was selected based on documented home range sizes in this species, which also dictates the ideal spacing within traps in a grid (Juškaitis 1997). We filtered data temporally to include only records from 2019 onward. At sites with multiple monthly replicates per year, we selected the maximum density estimate for each sampling season. These seasonally maximum values represent Minimum Number Alive (MNA) estimates for each site, from which we derived density distributions for each biogeographical region. To extrapolate national abundance, we used the distribution atlas refined it by habitat area (see section 2). For each biogeographical region, the corresponding density distribution was used to extrapolate abundance across its atlas cells via bootstrap resampling with replacement (n = 1,000), adjusting each cell's density by its proportion of habitat area. The point estimate of abundance is the median of the bootstrap distribution, and the 95% confidence interval is delimited by its 2.5th and 97.5th percentiles.

The nest-box–derived density distributions ranged from 0.06 to 2.93 individuals/ha, which we deemed plausible based on comparisons with published literature for this species (Sozio et al. 2016) and trait-based expectations (Santini et al. 2024). We predicted an abundance of 560,477 individuals (95% CI: 499,752–623,909) for the Alpine region (14,243.55 km²; Fig. 11), 355,456 individuals (95% CI: 327,312–384,302) for the Continental region (8,903.30 km²) and 962,070 individuals (95% CI: 855,825–1,072,272) for the Mediterranean region (15,554.08 km²).

Fig. 11. Distribution of *Muscardinus avellanarius* in Italy. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).



Chiroptera

For all bat species we applied the same methodology, except for *Myotis crypticus*, for which no distribution atlas was available (Fig. 12). We obtained data from seven regions: Campania, Sardinia, Lazio, Emilia-Romagna, Piedmont, Lombardy, and Friuli-Venezia Giulia. Data was extremely heterogeneous, both in the types of information reported and in the categories used for roost type. From these data we retained only counts at reproductive roosts (nurseries) or winter roosts (hibernacula) with at least five individuals, and excluded counts conducted earlier than 2010. When roost category was not explicitly reported, we used survey date to classify records: roosts surveyed between March and August were classified as reproductive roosts, while those between December and February were classified as winter roosts. Applying these criteria led to the exclusion of seven additional species for which no usable data remained: *Eptesicus nilssonii*, *Myotis alcathoe*, *M. bechsteinii*, *M. brandtii*, *Plecotus austriacus*, and *P. macrobullaris*. Then, for each biogeographical region, and separately for winter and reproductive roosts, we counted the number of roosts per 10 × 10 km atlas cell and recorded the corresponding roost sizes. We then converted roost counts to density by dividing by the estimated habitat area per cell (Table 1). We did not consider cells with no roost reported for the calculation of roost density. We could not know if those cells were surveyed or not, so we assumed that only cells within a maximum daily movement range from the nearest recorded roost were surveyed. Maximum nightly movement distances reported by Froidevaux et al. (2023) for the Italian species range from over 700 m up to a maximum of under 19 km (with 75% of the species moving less than 10km). Since atlas cells measure 10 × 10 km, we assumed that cells without records had not been surveyed.

To generate abundance estimates, we used bootstrap resampling of the distribution of roost counts and roost sizes, assuming that densities and roost sizes in surveyed cells were representative of all presence cells. We resampled 1,000 times from these distribution for each cell of the atlas, and calculated the product of roost count, mean roost size, and the cell's AoH. This yielded 1,000 population estimates per cell, which we summed across cells to obtain 1,000 total population estimates. From this distribution we extracted the median and the 2.5th and 97.5th percentiles (encompassing 95% of the distribution). Because reproductive roost counts only include females, we multiplied reproductive estimates by two. This procedure yielded population estimates per species and region based on reproductive (Table 2) and winter roosts (Table 3), where data were available.

Since this method assumes complete census coverage in surveyed cells, these values must be regarded as minimum estimates. Therefore, for each species and biogeographical region the final estimate should be the larger of the two values obtained from reproductive and winter roosts. At the same time, not all estimates are based on equal sampling effort, so estimates derived from a greater number of cells (Tables 2 and 3) may be more reliable. Expert judgment is required to determine the most appropriate estimate on a species-by-species basis.

Fig. 12.1. Distribution of 12 bat species in Italy, in alphabetical order from *Barbastella barbastellus* to *Myotis emarginatus*. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).

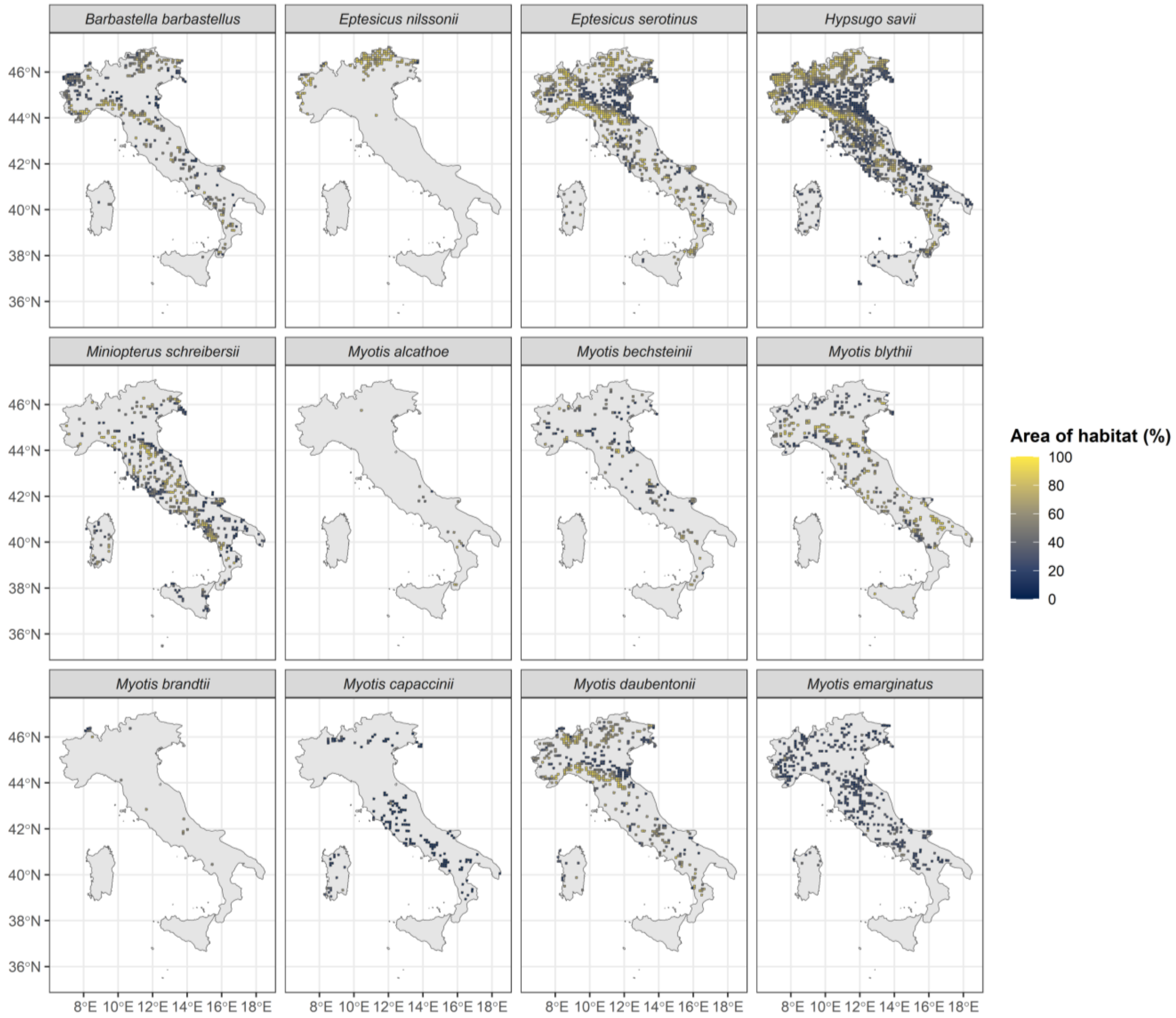


Fig. 12.2. Distribution of 12 bat species in Italy, in alphabetical order from *Myotis myotis* to *Plecotus austriacus*. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).

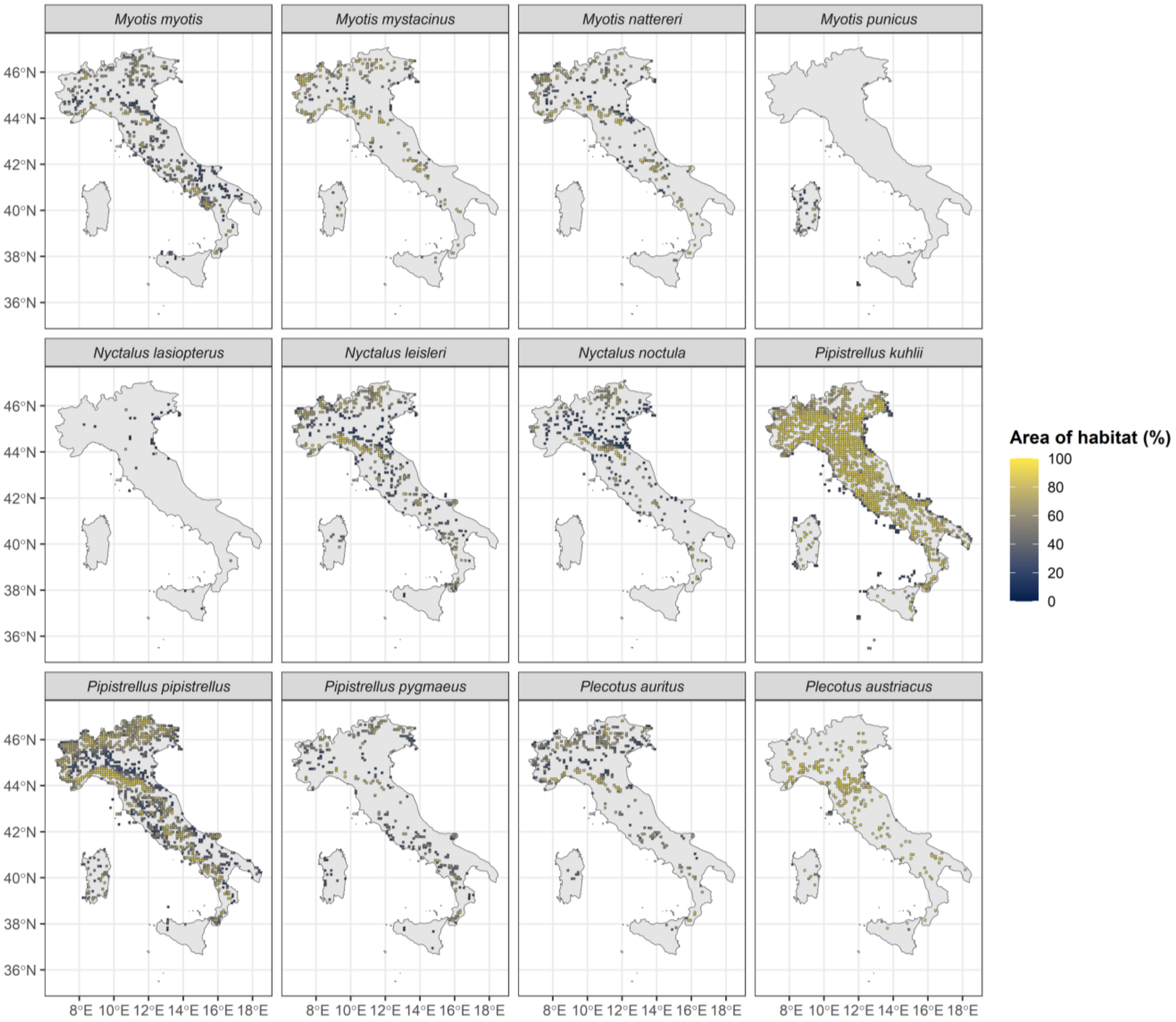


Fig. 12.3. Distribution of 12 bat species in Italy, in alphabetical order from *Plecotus macrobullaris* to *Tadarida teniotis*. For each 10 × 10 km cell, the percentage of habitat area is shown, calculated from the IUCN Red List land-cover classes for the species and reclassified following Santini et al. (2019).

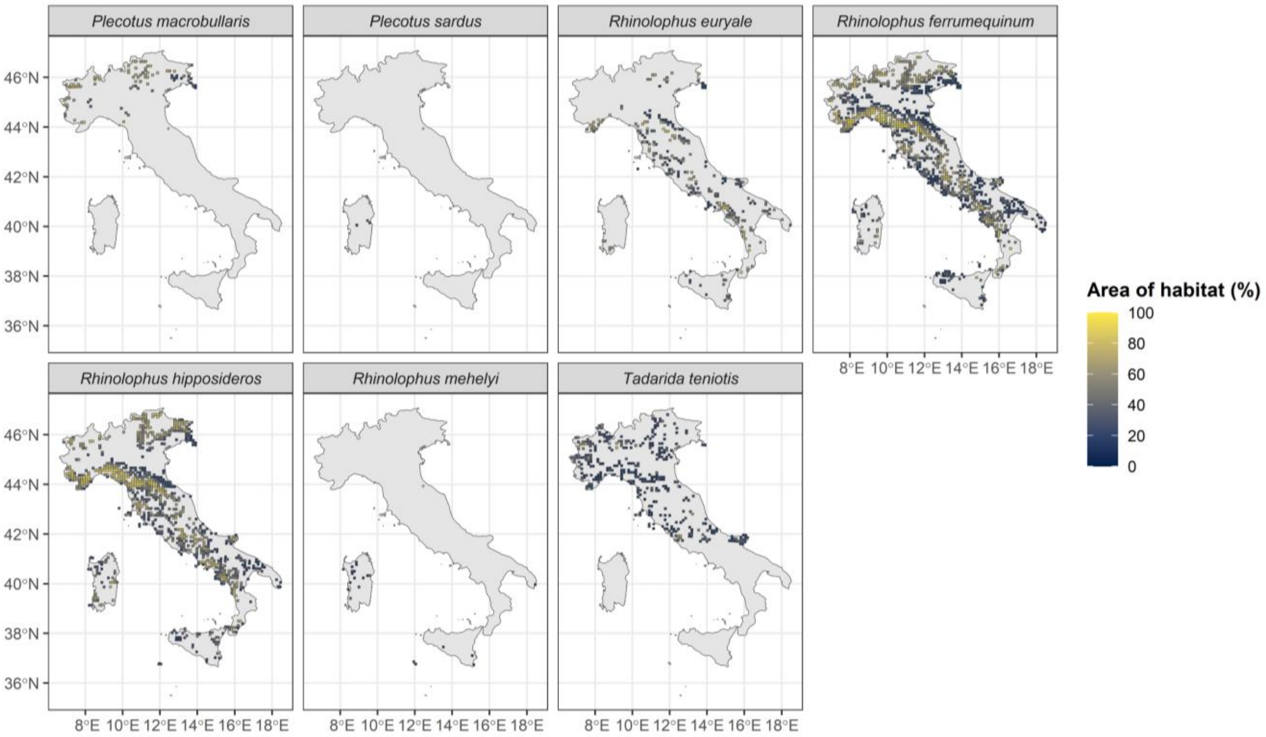


Table 1. Area of habitat (km²) for each bat species across the three biogeographical regions. These values were obtained by intersecting the atlas distribution data with Area of Habitat layers and regional boundaries.

Species	Alpine	Continental	Mediterranean
Barbastella barbastellus	8,052.50	4,979.50	5,680.40
Eptesicus nilssonii	10,220.39	186.86	—
Eptesicus serotinus	12,0935.20	17,369.10	14,062.40
Hypsugo savii	21,891.20	18,707.40	20,839.10
Miniopterus schreibersii	3,156.10	6,110.60	14,487.10
Myotis alcathoe	172.7	66.10	633.40
Myotis bechsteinii	1,884.70	2,122.30	2,513.74
Myotis blythii	1,704.30	7,503.20	9,802.40
Myotis brandtii	479.00	70.80	182.80
Myotis capaccinii	267.10	25.50	543.30

Species	Alpine	Continental	Mediterranean
Myotis daubentonii	9,144.80	8,657.80	5,391.70
Myotis emarginatus	1,495.10	3,492.80	3,177.60
Myotis myotis	6,799.10	5,421.20	10,419.30
Myotis mystacinus	9,814.90	4,785.68	4,100.48
Myotis nattereri	8,253.20	5,100.10	4,362.30
Myotis punicus	—	—	1,274.73
Nyctalus lasiopterus	69.80	207.20	253.50
Nyctalus leisleri	11,658.90	6,589.20	7,235.10
Nyctalus noctula	4,881.40	4,828.20	3,071.10
Pipistrellus kuhlii	17,370.20	53,698.90	52,707.00
Pipistrellus pipistrellus	26,253.60	19,089.30	25,248.00
Pipistrellus pygmaeus	4,606.70	2,448.80	6,101.50
Plecotus auritus	9,256.50	5,223.50	4,165.00
Plecotus austriacus	1,588.70	11,527.40	9,025.10
Plecotus macrobullaris	4,601.00	844.20	88.40
Plecotus sardus	—	—	55.90
Rhinolophus euryale	758.40	1,794.70	8,318.00
Rhinolophus ferrumequinum	12,604.90	10,375.90	21,152.00
Rhinolophus hipposideros	11’251.40	11’454.80	22’871.50
Rhinolophus mehelyi	—	—	135.70
Tadarida teniotis	2’617.00	2’079.00	2’057.50

Table 2. Estimates obtained using reproductive roosts (nurseries), where *n* indicates the number of atlas cells for which a roost-density estimate was available and subsequently extrapolated to the region.

Species	**Alpine**		**Continental**		**Mediterranean**	
	Median (CI95%)	**n**	**Median (CI95%)**	**n**	**Median (CI95%)**	**n**
Barbastella barbastellus	—	—	5,424 (4,504—6,279)	1	—	—
Eptesicus serotinus	—	—	27,176 (24,742—29,656)	4	—	—
Hypsugo savii	—	—	12,579 (12,048—13,146)	2	88,495 (76,014—102,345)	6
Miniopterus schreibersii	4,210 (3,108—5,324)	2	10,322,338 (6,763,884—14,564,250)	8	6,032,354 (3,261,105—10,442,195)	13
Myotis blythii	—	—	589 (535—645)	1	2,334,681 (2,049,287—2,622,794)	2
Myotis capaccinii	—	—	—	—	423,324 (103,725—1,524,701)	5
Myotis daubentonii	9,005 (8,108—9,931)	1	246,744 (185,588—327,100)	5	—	—
Myotis emarginatus	98,444 (73,245—131,617)	3	4,667,933 (1,977,999—8,947,304)	9	1,596,896 (1,596,896—2,032,612)	4
Myotis myotis	—	—	1,520 (1,348—1,691)	1	—	—
Myotis mystacinus	12,341 (12,341—12,341)	1	—	—	—	—
Myotis nattereri	1,489 (1,340—1,630)	1	—	—	—	—
Myotis punicus	—	—	—	—	214,779 (122,341—380,219)	5
Nyctalus noctula	—	—	3,963,383 (2,820,335—5,089,463)	2	—	—
Pipistrellus kuhlii	—	—	23,522 (22,511—24,499)	4	366,336 (293,500—454,447)	4
Pipistrellus pipistrellus	3,615 (3,422—3,816)	1	—	—	148,748 (122,612—178,945)	6
Pipistrellus pygmaeus	—	—	—	—	1,458 (1,307—1,595)	1
Plecotus auritus	—	—	—	—	15,079 (14,913—15,240)	1
Plecotus sardus	—	—	—	—	429 (133—713)	1
Rhinolophus euryale	—	—	893,141 (510,668—1,477,123)	3	1,287,023 (609,276—2,301,677)	14
Rhinolophus ferrumequinum	43,679 (35,011—53,712)	4	3,065,324 (460,232—19,353,903)	17	335,070 (274,873—408,049)	14

Rhinolophus hipposideros	20,819 (18,470—23,675)	8	55,814 (41,334—90,317)	24	514,702 (214,487—1,282,616)	13
Rhinolophus mehelyi	—	—	—	—	120,745 (27,093—310,711)	2
Tadarida teniotis	—	—	—	—	110,060 (71,425—155,516)	1

Table 3. Estimates obtained using winter roosts (hybernacula), where *n* indicates the number of atlas cells for which a roost-density estimate was available and subsequently extrapolated to the region.

Species	**Alpine**		**Continental**		**Mediterranean**	
	Median (CI95%)	**n**	**Median (CI95%)**	**n**	**Median (CI95%)**	**n**
Barbastella barbastellus	4,149 (4,031—4,271)	1	—	—	—	—
Eptesicus serotinus	—	—	2,054 (1,918—2,188)	1	—	—
Miniopterus schreibersii	—	—	11,512,834 (6,276,078—18,935,122)	8	555,146 (319,308—896,388)	12
Myotis blythii	—	—	598 (543—651)	1	—	—
Myotis capaccinii	10,139 (7,275—13,225)	2	—	—	49 (36—61)	—
Myotis emarginatus	—	—	—	—	15,193 (12,007—18,692)	2
Myotis myotis	—	—	25,311 (22,182—28,376)	1	—	—
Myotis punicus	—	—	—	—	4,283 (2,598—6,084)	2
Plecotus auritus	—	—	2,956 (2,580—3,322)	1	—	—
Plecotus sardus	—	—	—	—	90 (33—153)	1
Rhinolophus euryale	—	—	1,158,470 (314,860—2,574,895)	3	689,525 (434,623—1,005,276)	12
Rhinolophus ferrumequinum	24,567 (19,657—30,537)	2	9,236,530 (4,305,289—18,145,137)	17	392,026 (255,407—695,086)	23
Rhinolophus hipposideros	—	—	1,037,521 (538,745—1,861,290)	19	444,021 (314,910—616,203)	12
Rhinolophus mehelyi	—	—	—	—	68,884 (8,086—418,863)	3

3. TEMPORAL POPULATION TRENDS

Within the reporting framework, it is also required to assess observed population trends between the two reporting periods (2013–2018 and 2023–2024), classify each trend as ‘stable’, ‘increasing’, ‘decreasing’, ‘uncertain’, or ‘unknown’, and assign a percentage change range (0–12%, 13–25%, 26–50%, 51–100%, >100 %). We were able to estimate trends, albeit incompletely, only for the hazel dormouse and bats, for which usable data existed in both time periods.

Hazel dormouse (*Muscardinus avellanarius*)

For the hazel dormouse, the only sites with comparable temporal replicates on the same transects during 2015–2018 and 2019–2020 were sixteen sites in Lazio. For each transect, we calculated the mean density estimate in each period and then computed the relative percentage change as:

$$\Delta Change\% = 100 \times \frac{\left(Density_{t_2} - Density_{t_1}\right)}{Density_{t_1}}$$

where $Density_{t_1}$ and $Density_{t_2}$ are the density estimates at times 1 and 2, respectively. We then derived the overall relative percentage change and its 95% CI via bootstrapping. The general trend resulted positive, with an estimated change of 93.6 % (95% CI: -30.8 % – 316.7 %). We emphasize, however, that this estimate pertains to a single region and therefore cannot be considered representative of the species’ entire peninsular distribution.

Chiroptera

For bats, we retained only those roosts that had been censused in both reporting periods (2013–2018 and 2023–2024) for each species and region. Because the regional data do not assign unique identifiers to roosts, we assumed that any two roosts with coordinates less than 100 m apart represented the same site. For each such matched roost, we calculated the percentage change in roost size as:

$$\Delta Change\% = 100 \times \frac{\left(RoostSize_{t_2} - RoostSize_{t_1}\right)}{RoostSize_{t_1}}$$

where $RoostSize_{t_1}$ and $RoostSize_{t_2}$ are the counts of bats in the roost at times 1 and 2, respectively. We then averaged these percentages and computed the standard error, from which we derived the 95% confidence interval. Because relatively few roosts were censused in both periods, we also report the sample size underlying each estimate as a measure of its representativeness. This analysis was only feasible for a small, non-representative subset of roosts across the three regions (see Tables 4 and 5). Only for *R. hipposideros* and *R. euryale* in the Continental region the number of winter roosts was >10 (Table 5), and in both cases the overall trend was positive.

Table 4. Temporal trend estimates obtained using the nursery roost temporal replicates.

Species	**Alpine**		**Continental**		**Mediterranean**	
	Trend% (CI95%)	**n**	**Trend% (CI95%)**	**n**	**Trend% (CI95%)**	**n**
Myotis emarginatus	-73,1	1	41 (5,3–76,8)	2	-27.4 (-49,2–-5,6)	2
Rhinolophus ferrumequinum	-23,6	1	131,2 (106,5–156)	2	-7,2	1
Miniopterus schreibersii	—	—	43,5 (22,9–64,2)	2	—	
Rhinolophus euryale	—	—	103,8 (96,4–111,2)	2	-22,8	1
Myotis capaccinii	—	—	—	—	115,7	1
Pipistrellus pipistrellus	—	—	—	—	689,5	1
Rhinolophus hipposideros	—	—	—	—	-46,2 (-95,6–3,3)	2

Table 5. Temporal trend estimates obtained using the winter roost temporal replicates.

Species	**Alpine**		**Continental**		**Mediterranean**	
	Trend% (CI95%)	**n**	**Trend% (CI95%)**	**n**	**Trend% (CI95%)**	**n**
Miniopterus schreibersii	—	—	305,9 (-252,8–864,7)	5	—	—
Rhinolophus ferrumequinum	—	—	49,5 (8–90,9)	12	293,1 (-264,9–851,1)	2
Rhinolophus hipposideros	—	—	131,5 (46,5–216,5)	16	136,6 (-196,6–469,9)	2
Rhinolophus euryale	—	—	—	—	-33,4	1

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