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RESEARCH ARTICLE

A modelling approach to infer the effects of wind farms on landscape connectivity for bats

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Abstract Little is known about the potentially disrupting effects of wind farms on the habitat connectivity of flying vertebrates at the landscape scale. We developed a regional-scale model to assess the wind farm impact on bat migration and commuting routes. The model was implemented for the bat *Nyctalus leisleri* in a region of central Italy currently undergoing considerable wind farm development. A Species Distribution Model (SDM) for *N. leisleri* was generated using the MaxEnt algorithm based on 47 presence records (reduced to 19 after the autocorrelation procedure) and 10 environmental variables derived from topographic and land cover maps. We used the SDM to create a map of connectivity using the software UNICOR to identify potential commuting corridors (PCCs). The incidence of each wind farm on bat flight corridors was assessed by overlaying the existing (380) and planned (195) turbine locations onto the PCCs. The SDM was statistically robust (AUC > 0.8). Most of the corridors were concentrated in the western part of the region, which hosts the largest suitable areas for the species; most of the existing (54 %) and planned (72 %) wind farms interfered with important corridors connecting the western and the eastern parts of the region. Our results provide key information on the impact of the wind farm industry on biodiversity on a regional scale. The novel approach adopted, based on SDM and connectivity analysis, could be easily extended to other flying vertebrates and landscapes and constitutes a promising planning tool necessary for harmonizing the development of renewable energy infrastructures with issues of biodiversity conservation.

Keywords Connectivity analysis · *Nyctalus leisleri* · Renewable energy impact · Species distribution models · Wind farms

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Introduction

Preserving and restoring connectivity has become a major conservation priority, with conservation organisations investing considerable resources to achieve these goals (Beier et al. 2006; McRae et al. 2008). Indeed, connectivity among habitats and populations is considered a critical factor that determines a wide range of ecological phenomena, including gene flow, metapopulation dynamics, demographic rescue, seed dispersal, infectious disease spread, range expansion, exotic invasions, population persistence, and biodiversity maintenance (Calabrese and Fagan 2004; Crooks and Sanjayan 2006; Carranza et al. 2012). Landscape connectivity may greatly influence the distribution of animals when it alters their movements and their ability to reach foraging grounds (Henry et al. 2007), and the extent to which a certain landscape facilitates the movements of organisms and their genes faces critical threat due to both fragmentation and habitat loss (Henry et al. 2007). Understanding the ecological processes that depend on connectivity and making effective conservation planning decisions to conserve them requires the quantification of how connectivity is affected by landscape features (McRae et al. 2008). Thus, to conserve and manage species effectively, it is necessary to increase the link between empirical data and predictive models (Walpole et al. 2012). An important application of such efforts involves predicting the impacts of anthropogenic activities and environmental changes on animal populations and their habitats (e.g., Hoegh-Guldberg 1999; McRae et al. 2008), and identifying areas or species with conservation priority (e.g., Carroll et al. 2001).

The emission of greenhouse gases and the use of carbon-based resources for energy production are changing the structure and dynamics of ecosystems at an unprecedented rate (Hooper et al. 2005; Jones et al. 2009a). Indeed, as human populations continue to expand in size and become increasingly urban in nature, such environmental problems undoubtedly will become even more exacerbated (Thomas et al. 2004; Kareiva et al. 2007). Climate change may threaten the long-term persistence of many species of plants and animals, alter distributional patterns at global and regional levels, and result in local assemblages of species that are quite different from those that currently constitute coevolved communities (Parmesan 2006; Jones et al. 2009a).

The need to halt this trend has created a very positive attitude of many scientists and environmentalists towards the development of sustainable ways to meet the ever-growing energetic demands of humankind (Rodrigues et al. 2008). The wind farm industry represents one valuable response to mitigate the detrimental effects of carbon emission-related global warming on biodiversity (Arnett 2005; Harbusch and Bach 2005). However, there is accumulating evidence of the adverse effects of this industry on wildlife, particularly flying vertebrates (Johnson and Erickson 2008; Telleria 2009). For several years, wind farm impact assessments have mostly targeted birds (Rodrigues et al. 2008) and, to a lesser extent, bats (Rodrigues et al. 2008; Jones et al. 2009b). Bats are sensitive to human-induced changes to ecosystems (Moreno and Halffter 2001; Kunz et al. 2007; Jones et al. 2009a); thus, wind farm effects are currently regarded as an additional threat to the long-term persistence of at least several bat species in a progressively human-altered environment (Kunz et al. 2007: Rodrigues et al. 2008: Parsons and Battley 2013; Hayes 2013).

The presence and location of wind turbines can affect flying vertebrate populations in different ways, from direct mortality associated with the action of rotary blades (Arnett et al. 2008; Horn et al. 2008; Rodrigues et al. 2008; Rydell et al. 2012; Hayes 2013), to the disturbance or severing of migration or commuting routes (Rodrigues et al. 2008; Jones et al. 2009b; Cryan 2011) and the disturbance or loss of foraging habitat (Rodrigues et al. 2008; Roscioni et al. 2013) or roosts (Arnett 2005; Harbusch and Bach 2005; Rodrigues et al. 2008).

Although collision impacts have been analysed in detail for many species (Arnett 2005; Rodrigues et al. 2008; Telleria 2009; Rydell et al. 2010), little is known about the large-scale impact and more specifically on the interference of the large-scale movement (e.g., migration, commuting routes) of flying vertebrates (Hötker et al. 2006; Cryan and Brown 2007; Baerwald et al. 2009; Rodrigues et al. 2008; Jones et al. 2009b; Roscioni et al. 2013; Santos et al. 2013).

A large portion of the bats killed by turbines is considered to be migrants that travel in autumn from their breeding to wintering grounds (Rodrigues et al. 2008; Jones et al. 2009b; Cryan, 2011). Indeed, if wind turbines kill migratory in addition to sedentary bats, they may potentially cause the decline of bat populations on a large geographical scale (Voigt et al. 2012), a consideration that highlights the need to develop and implement species and scale-specific conservation and monitoring approaches.

The interference of wind farms on bat movements, such as the loss or shifting of flying paths, which could interfere with migration and commuting routes and access to roosts (Harbusch and Bach 2005; Hötker et al. 2006), and the related collision risk is relatively unknown (Cryan and Brown 2007; Rodrigues et al. 2008, Baerwald et al. 2009; Jones et al. 2009b). The loss of habitat structures has a detrimental effect on biodiversity and affects bat species that depend on those features for foraging and commuting (Ehrenbold et al. 2013). Furthermore, the risk of disrupting connectivity for bats is higher along such linear landscape features as mountain ridges or rivers because these features provide feeding resources, navigational references, protection from wind and predators, and roosting sites (Verboom and Huitema 1997; Estrada and Coates-Estrada 2001; Hein et al. 2009). Regardless, organisms may or may not adapt to anthropogenic changes in landscape connectivity and may eventually undergo local extinctions (Henry et al. 2007). Although a broad spatial view is needed for the large-scale planning of wind farms, there is a lack of appropriate methods that can enable landscape planners to locate turbines in a way that minimises the disruption of connectivity, particularly with regard to susceptible species (Rodrigues et al. 2008; Jones et al. 2009b; Santos et al. 2013; Roscioni et al. 2013).

The purpose of this paper is to propose a scientifically sound and practical method for the assessment of the interference of wind turbines on habitat connectivity of flying vertebrates at a regional scale. Specifically, we developed a method to assess the large-scale impact of planned and existing wind turbines on bats based on Species Distribution Models (SDMs) and connectivity analyses. The model was tested on the bat *Nyctalus leisleri* Kuhl 1817 in an area of central Italy currently undergoing the considerable development of wind farms. We selected *N. leisleri* because of its migrant behaviour and its vulnerability to wind farm development, in accordance with EUROBATS conservation protocols (Rodrigues et al. 2008; Jones et al. 2009b, Battersby (comp.) 2010). The integration of these two approaches provides the sound planning tools that are necessary for harmonising the development of renewable energy infrastructures with the conservation of threatened/endangered species.

We implemented our protocol according to the following objectives: (a) identification of the most suitable areas for the targeted species; (b) identification of corridors between suitable areas; (c) identification of the most impacting wind turbines that interfere with major connectivity routes; and (d) provision of mitigation measures for connectivity disruption.

Methods

Study area

The protocol was implemented in a district of central Italy (Molise) covering an area of 4,460 km^2, characterised by a large-scale development of wind farms. A total 380 wind turbines on 28 wind farms are already operating in the region, and another 195 turbines (11 wind farms) are planned (Fig. 1). We deliberately selected a regional rather than a national scale, as this is the geographical (and administrative) scale at which wind farm development is planned and mitigation or compensation actions would be carried out (Roscioni et al. 2013). Moreover, considering a fine-scale analysis, which allows an accurate description of the local conditions, has been proven to be very effective for regional conservation planning (Grantham et al. 2009; Mills et al. 2010).

The method for the impact assessment of wind farms on bat commuting corridors at the regional scale is schematically illustrated (Fig. 2). The first step of the procedure was to build a SDM for *N. leisleri* derived from geo-referenced presence data and environmental variable maps. Secondly, we performed a connectivity analysis using a landscape resistance surface map that synthesised the critical factors that might influence the commuting movements of *N. leisleri*. Lastly, the existing and planned wind turbines were overlapped onto the species commuting corridors to identify areas to be preserved (no new wind turbines), curtailment areas (where a cut in the wind turbine speed should be considered), and areas where the expansion of wind farms did not interfere with this species.

Species distribution model and identification of most suitable areas

We developed our SDM using the maximum entropy algorithm MaxEnt 3.3.3k (Phillips et al. 2004, 2006) because of its good performance with small datasets and presence data only (Elith et al. 2006; Phillips and Dudík 2008). Additionally, the

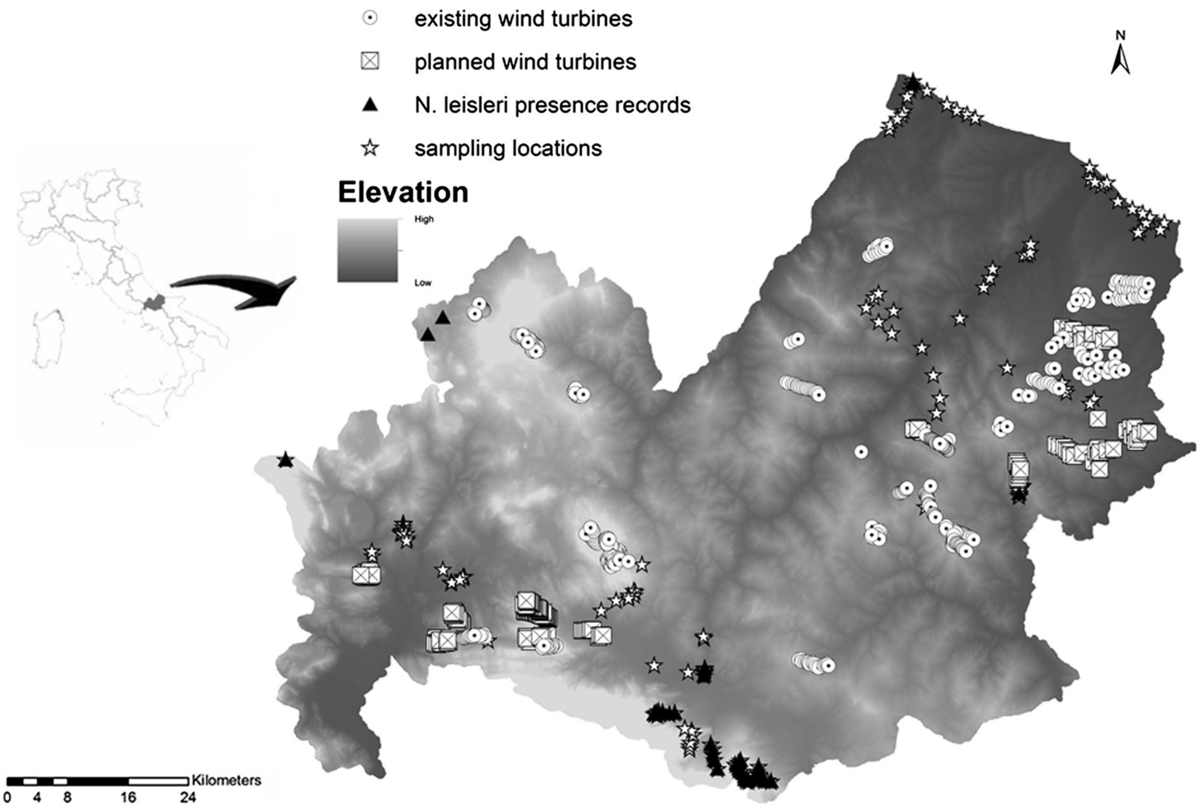
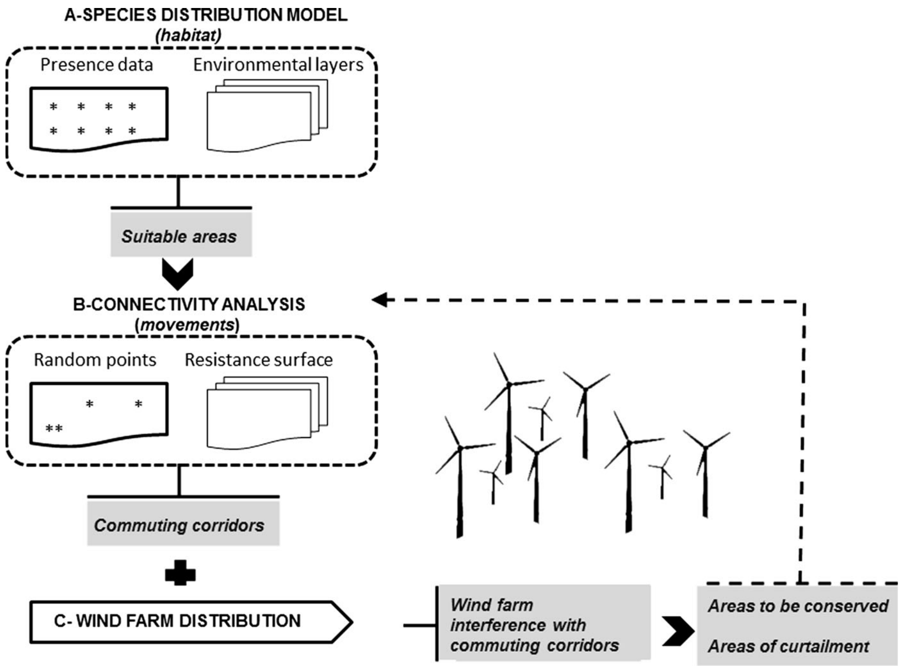


Fig. 1 Sample locations, *Nyctalus leisleri* presence records in the Molise region (central Italy) used for the MaxEnt model and location of the existing and planned wind turbines in the area (data provided by the Environmental Department of Molise district)

Fig. 2 Flowchart summarizing the procedure used to assess the interference of wind farms and wind turbines with commuting corridors of *N. leisleri* in central Italy



nocturnal and elusive behaviour of bats makes this group prone to the existence of false absences, which impairs the use of presence/absence models (Rebelo and Jones 2010).

Presence data During 2010–2011, we collected 47 presence data for *N. leisleri* based on an opportunistic survey of 165 locations at wind farm areas and control areas in different sectors of the region (Fig. 1). We applied a transect analysis (Rebelo and Jones 2010) to check whether our sampling locations were representative of the regional environmental heterogeneity (ESM1). The data were collected using bat detectors either in the time expansion mode or by direct ultrasound sampling (D240X and D1000X Pettersson bat detectors, respectively, Pettersson Elektronik AB, Uppsala, Sweden). We recorded bat occurrence at point locations for approx. 60 min/site starting at 30 min after sunset, i.e., when *N. leisleri* is typically active (Waters et al. 1999); as this species broadcasts intense echolocation calls, it can be easily detected and recorded with bat detectors. For species recognition, we used the programme BatSound 4.1. (Pettersson Elektronik AB, Uppsala, Sweden) to generate oscillograms, spectrograms, and power spectra, selecting one to three echolocation calls per sequence. For sound analysis we used a 512-pt. FFT with a Hamming window. Echolocation calls were identified by applying the classification functions described by Russo and Jones (2002), and social calls were identified according to Russo and Jones (2000) and Russ (1999). To avoid the existence of spatial auto-correlation in the presence dataset, we used average nearest neighbour analyses to remove clusters in the data (Merckx et al. 2011; Santos et al. 2013), obtaining 19 presence records used in the SDM. The analyses were performed in a GIS environment (ArcGis 10.0–ESRI, Redlands, CA, USA).

Environmental variables We selected a set of eco-geographical variables (EGVs), taking into account the ecological requirements of the species (Waters et al. 1999; Russo and Jones 2003, Rainho and Palmeirim, 2011). The variables were derived from Corine Land Cover (1:100.000), Digital Terrain Model (40 m), and hydrographic maps (1:50.000) (ESM2). We selected 10 out of a set of 15 original variables providing the highest gain in 100 MaxEnt univariate models (see below). Because a detailed description of the species distribution modelling procedure is beyond the scope of this paper, we present only the 10 variables that best explained the distribution of the species in the study area (ESM2).

We reclassified the Corine Land Cover (CLC) into 16 categories that are ecologically meaningful for this species (see ESM3 for the CLC map and legend).

As proxies of bat movements and exposure to winds, a map of steep areas (slope $> 40°$) and a "north–south facing" map, respectively, were derived from the Digital Terrain Model (Santos et al. 2013). We then created maps of the Euclidean distances from water courses, steep areas, and some selected land cover categories (ESM2). These landscape elements are related to bat foraging and roosting (Rainho and Palmeirim, 2011; Roscioni et al. 2013; Santos et al. 2013). All EGVs had a 40-m resolution and were implemented and managed in a GIS environment (ArcGis 10.0–ESRI, Redlands, CA, USA).

Modelling procedure We built the SDM using the default MaxEnt settings, with the exception of "β regularization multiplier", "number of replicates", "default prevalence", and "maximum iterations". Different β values were assayed and evaluated to assess which models were the most informative using the corrected Akaike information criterion (AICc), as proposed by Warren et al. (2010) for the ENMTOOLS software. We then set the software to randomly split the occurrence data into two subsets, with 70 % of the records used to train the model and the remaining 30 % used to evaluate its predictive power. This step was replicated 50 times using a bootstrapping approach each time randomly selecting different 70–30 % portions of the occurrence data. The predictive power of the model was evaluated by calculating the area under the receiver operating characteristic curve (AUC) (Swets 1988; Phillips et al. 2006). The value of the default prevalence was set to 0.6 instead of 0.5 (default option) because this species is easy to detect in typical presence sites (Elith et al. 2011). We set 1000 maximum iterations to build a model with a high predictive power (Phillips et al. 2006).

The MaxEnt output was converted into a binary map (1 = suitable areas; 0 = unsuitable areas), choosing the 10th percentile of the distribution of probability of occurrence as the threshold (Phillips and Dudík 2008; Ficetola et al. 2007, 2009). The 10th percentile threshold offers a highly conservative estimate of the species' tolerance to each predictor in a complex environment and for the small datasets of species occurrences (less than 25) available for calibration (Pearson et al. 2007; Svenning et al. 2008; Ficetola et al. 2009; Rebelo and Jones 2010; Santos et al. 2013; Bosso et al. 2013; Roscioni et al. 2013).

Connectivity analyses and identification of commuting corridors

For the connectivity analyses, we used UNICOR (Landguth et al. 2012), a recently developed software that integrates kernel density estimations with a least-cost path prediction to produce smooth probability density predictions for movement patterns across complex landscapes (i.e., using probability density functions to smooth output paths). The nonparametric resistant kernel approach implemented in UNICOR (Landguth et al. 2012) uses the modified Dijkstra's algorithm that builds a least-cost dispersal around each source cell (Cushman et al. 2006; Landguth et al. 2012; Wasserman et al. 2012).

First, we produced an expert-based resistance surface to describe the movement of the species through the landscape (Compton et al. 2007; Landguth et al. 2012) by taking into account suitable and unsuitable areas and three proxies of linear features important for commuting and migration routes (Waters et al. 1999; Russo and Jones 2003; Morris et al. 2010): slopes, forest edges, and hydrographic networks. In the resistance surface, each cell value (pixel) represents the unit cost of crossing each location (Landguth et al. 2012), and the pixel 'resistance values' reflect the influence of each variable on species movements (Cushman et al. 2006, Spear et al. 2010). In particular, we assigned a resistant value of 1 (low resistance) to the suitable areas (Fig. 3), whereas we assigned a resistant value of 3 (medium) to steep areas (>40° of slope) or to areas containing forest edges or water courses. Lastly, we assigned a resistant value of 8 (high resistance) to the other pixels not included in the categories mentioned above (Landguth et al. 2012) (the map of resistance surface is provided in ESM4).

To identify commuting corridors, 50 point locations (source cells) were randomly sampled from the suitable areas for *N. leisleri* (Fig. 3). We repeated the extraction 10 times and used UNICOR to produce 10 maps, reporting for every pixel the expected movement rates between the selected 50 random points; we then summed the outputs in a new synthetic connectivity map. Lastly, potential commuting corridor maps (hereafter called PCCs) were produced by extracting from the synthetic connectivity map only the pixels that scored above the map median (Cianfrani et al. 2013). Although *N. leisleri* is known to be a migrant species (Rodrigues et al. 2008; Jones et al. 2009b; Voigt et al. 2012), due to lack of information on the migratory behaviour of this species in the study area, we assumed that the corridors represent commuting rather than migratory routes. Unlike migration, commuting constitutes the nightly movement between foraging sites or between the latter and the roost (Verboom and Huitema 1997; Kunz et al. 2007; Cryan and Brown 2007; Cryan and Barclay 2009).

Wind farm interference with commuting routes

The potential impact caused by wind farms on *N. leisleri* was assessed by projecting a map of 150-m circular buffers centred on existing and planned turbine onto the PCCs applying the zonal statistics function of ArcMap10. The buffer size was defined considering the area at risk of collision and habitat loss around each turbine (Arnett 2005; Rodrigues et al. 2008; Roscioni et al. 2013). We considered as impacting all the turbines whose buffer included at least one of the PCCs identified in the model.

Results

Species distribution model and identification of most suitable foraging areas

The distribution model for *N. leisleri* achieved a very good predictive ability (AUC = 0.87 ± 0.05 c.f. Swets 1988; Phillips et al. 2006; Bosso et al.2013). The map showed that the most suitable areas for *N. leisleri* were concentrated in the western part of the region (73.24 % of the total suitable areas) (Fig. 3, ESM5).

Connectivity analyses and identification of commuting corridors

The PCCs map for *N. leisleri* (Fig. 4) showed that the corridors were concentrated in the western sector of

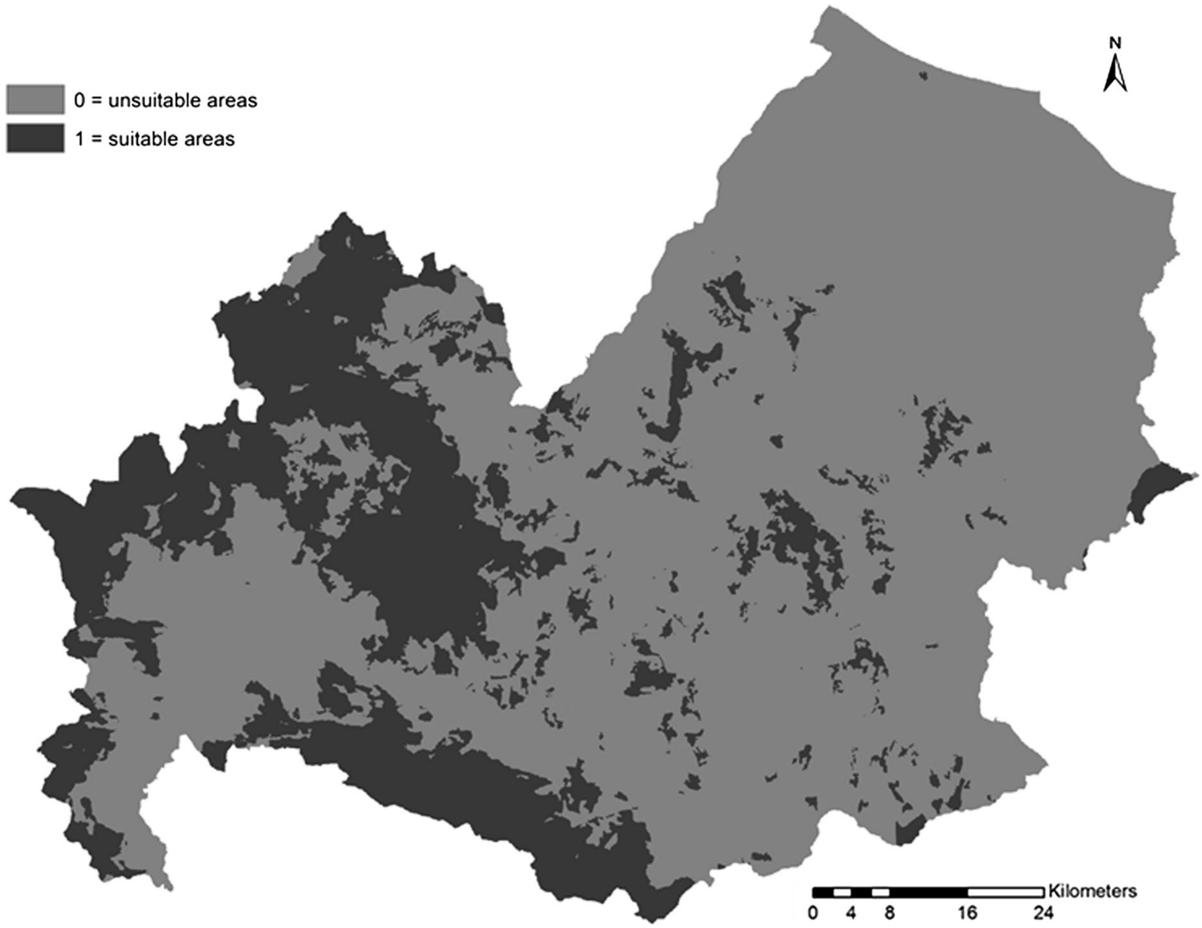


Fig. 3 Most suitable areas for *N. leisleri* in the Molise region (central Italy) obtained by converting the MaxEnt outputs into binary map using the 10th percentile threshold

the Molise district. Furthermore, many corridors connected the western sector with the south-eastern sector, though only one corridor connected the northern-coastal areas.

Wind farm interference with commuting routes

We found that 34 of the planned turbines in 8 planned wind farms and 88 of the existing turbines in 15 operating wind farms were potentially harmful to *N. leisleri* because of the overlap with the bat commuting routes (Fig. 5, ESM6). Specifically, seven wind farms had the highest impact because over 50 % of their turbines encountered connectivity routes (ESM6). The areas of major risk were concentrated in the western part of the region (Fig. 5, ESM6), in the corridor that allowed the species to reach the coastal areas (Fig. 5a, ESM6), and in the south-eastern area (Fig. 5b, ESM6).

Discussion

The most suitable areas for *N. leisleri* identified by SDM were mostly concentrated in the western part of the region where forests are widespread and dominate the landscape, confirming the strict relationship of *N. leisleri* with forests (Waters et al. 1999; Russo and Jones 2003; Ruczynsky and Bogdanowicz, 2005; Roscioni et al. 2013). According to our predictions, this is also the area of the highest concentration of PCCs. Therefore, the western part of the study area deserves careful attention both in terms of species protection and the potential detrimental impact of

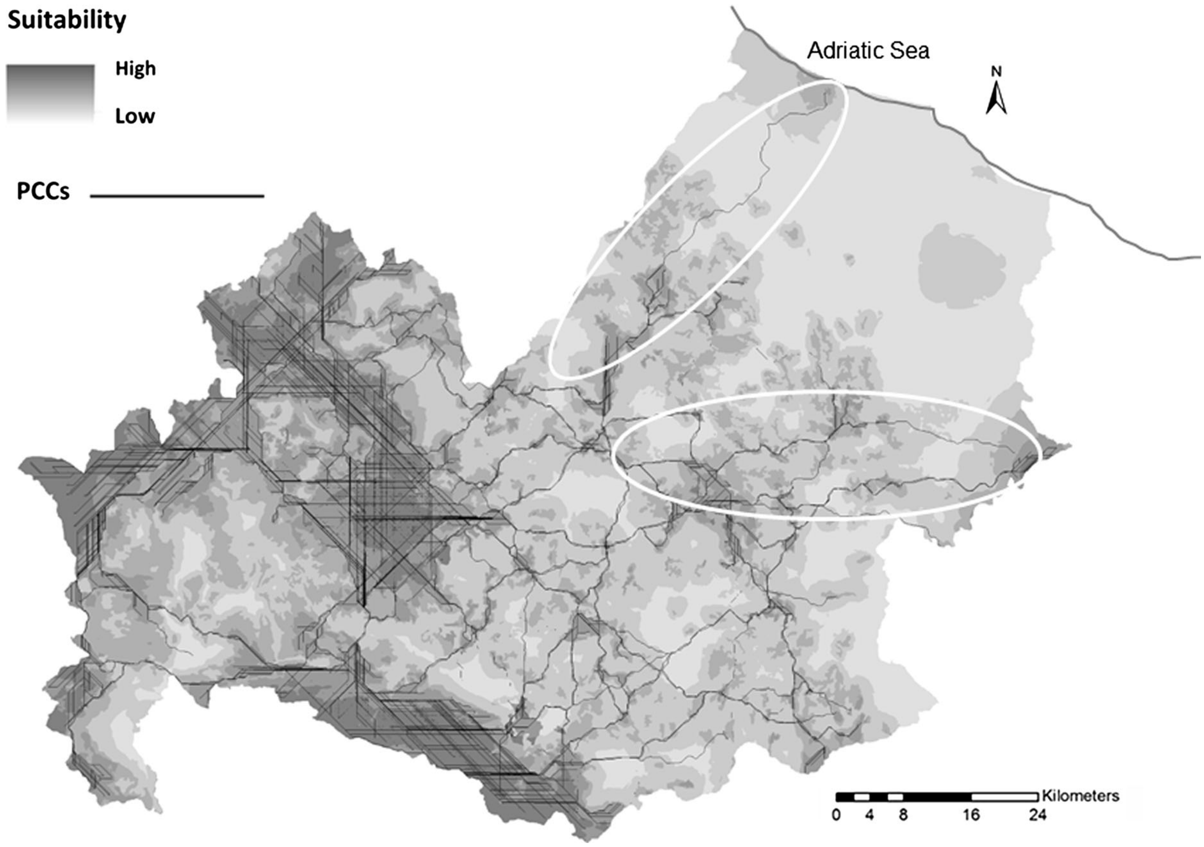


Fig. 4 Potential Commuting Corridors (PCCs) for *N. leisleri* in the Molise region (central Italy). Suitability is referred to the results obtained by MaxEnt procedure. *White ellipses* highlight the corridors towards the south eastern sector and to the coast

wind farms on the corridors connecting foraging areas. When evaluating the impact of wind turbines on bats, consideration should be given to the local movements to and from foraging sites, to long-distance movements between summer and hibernation sites, and to autumnal swarming (Rodrigues et al. 2008; Jones et al. 2009b; Cryan 2011; Voigt et al. 2012). Negative impacts on corridors involve the interruption of commuting routes and gene flow (Landguth et al. 2012; Wasserman et al. 2012; Cianfrani et al. 2013). We also detected other areas of concern in the region, including several PCCs for *N. leisleri* that link the western to the south-eastern sectors of the region. In addition, two existing wind facilities intersect the only corridor that allows *N. leisleri* to reach the coastal area. This area deserves careful attention and mitigation actions, as attention should also be paid to migration routes for wind turbine located close to prominent landscape features, such as river valleys, upland ridges, upland passes, and coastlines (Rodrigues et al. 2008; Jones et al. 2009b).

As predicted, both the number of turbines and their location in the landscape were crucial to determining different intensities of the predicted impact (Erickson et al. 2004; Rodrigues et al. 2008). Species exploring wind farm-impacted areas are exposed to collision risk and the disruption of flight paths and population connectivity (Horn et al. 2008; Jones et al. 2009b; Cryan 2011).

Caveats and limitations of the model

Our approach can potentially be applied to other geographical contexts and taxa, allowing the identification of wind facilities located at critical sites for flying vertebrates.

The impacts of wind farms on flying vertebrates include reduction in size and quality of the available habitat, loss of connectivity, as well as impediment or disruption of movement (as well as dispersal) to new

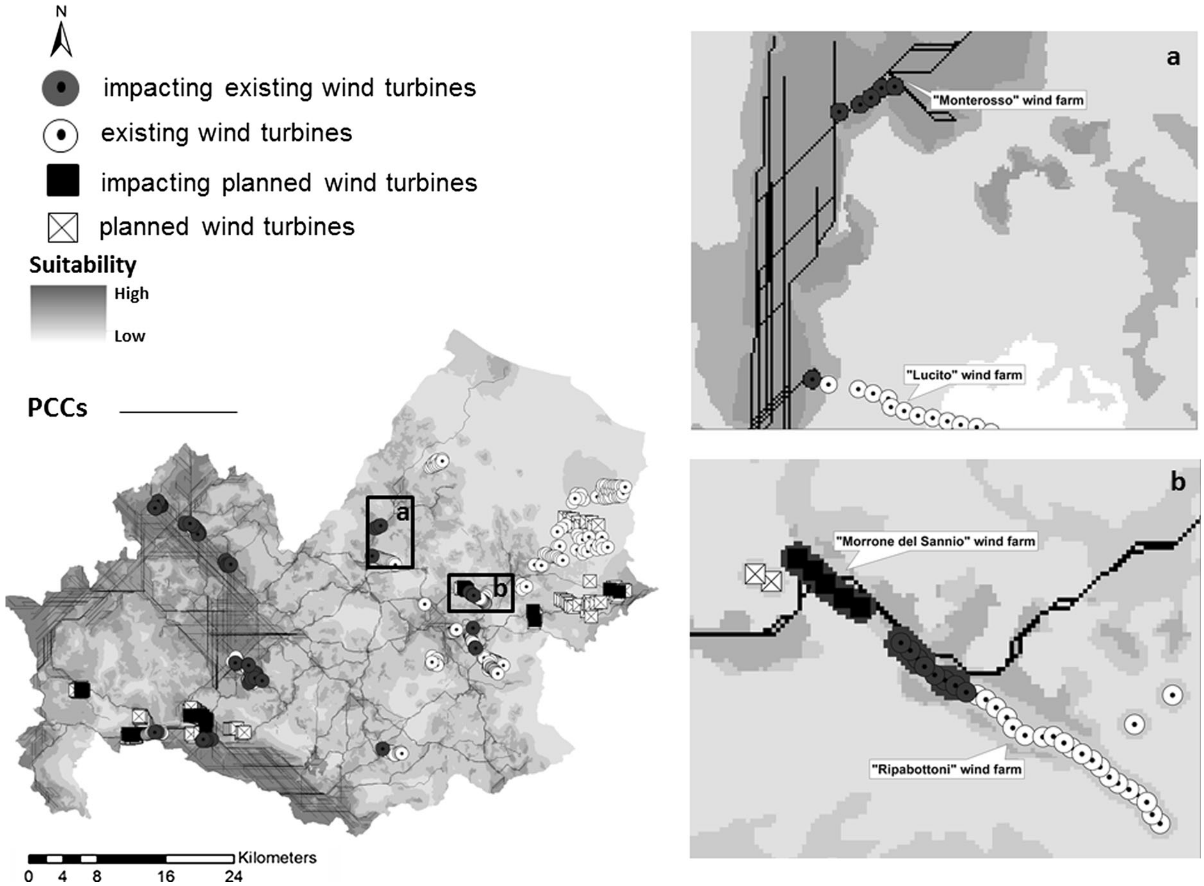


Fig. 5 Wind farm impact on *N. leisleri* commuting routes. The impact was determined by tracing a 150-m radius around each wind turbine buffer and by overlaying buffers to *N. leisleri* Potential Commuting Corridors (PCCs). We considered as impacting all the turbines whose buffer included at least one of the PCCs identified in the model. To the right, two examples are zoomed: **a** the existing "Lucito" and "Monterosso" wind farms placed in the corridor that connects the western part of the region to the coastal area; **b** the existing "Ripabottoni" and the planned "Morrone del Sannio" wind farms intercepting the corridor that connects the western area to the south-eastern area

habitats, thereby affecting seasonal migration patterns (Rudnick et al. 2012; Roscioni et al. 2013). Specifically, wind farm disruption could affect the foraging behaviour of species that may not be able to adapt to anthropogenic-induced changes in landscape connectivity and may eventually undergo local extinction (Henry et al. 2007).

One limitation to our model is the scarce knowledge of bat dispersal abilities and of the characteristics of migratory routes (Fleming and Eby 2003, Kunz et al. 2007). Thus, the variables considered in the resistance surface might not cover all the ecological factors influencing species dispersal. Most bat species fly along linear landscape elements instead of crossing open areas (Hein et al. 2009) as they rely on such elements as a reference for navigation (Serra-Cobo et al. 2000; Baerwald et al. 2009). The three ecological variables entered in the resistance surface are effective proxies of linear features that are known, at present, to be important for bat movements and foraging behaviour (Waters et al. 1999; Russo and Jones 2003; Morris et al. 2010).

Conservation measures

Our modelling results showed that the entire western part of the Molise region should be considered critical for the survival of this species (Roscioni et al. 2013). To avoid connectivity disruption of the commuting routes for *N. leisleri*, new turbines should be strictly limited in this part of the region. More specifically, based on our model results, we recommend avoiding the construction of the 34 turbines in the 8 planned wind farms that interfere with connectivity routes or that operation be governed by adequate restrictions, such as curtailment or even cessation during critical bat seasons (Rodrigues et al. 2008; Arnett et al. 2011). In addition, the 88 operating turbines that already threaten *N. leisleri* in the 15 existing risky wind farms should be subject to operational rules. Specifically, wind farm curtailment when wind speeds <7 km/h is an effective mitigation measure (Arnett 2005; Horn et al. 2008), as relatively small changes in wind turbine operation result in a meaningful reduction in bat mortality (Baerwald et al. 2009; Arnett et al. 2011). Although recent studies have shown that curtailment is also effective at wind speeds <5 km/h (e.g., Arnett et al. 2011), there is no consensus on the exact wind speed value; thus, further studies are needed to clarify this issue.

Particular attention must also be given to the corridor that connect the northern-coastal areas to the other commuting routes of *N. leisleri*. Indeed, Voigt et al. (2012) proved that wind farms not only influence populations in nearby areas but that they also have effects at distances of several hundreds to one thousand kilometres.

Final remarks

Through our modelling approach, we were able to investigate the very important issue of the potential impact of wind turbines on habitat and connectivity disruption for bats at a regional scale, crucial aspects that have been highlighted as a research priority in national and international documents regarding the consideration of bats (Cryan and Barclay 2009; Arnett et al. 2011; Cryan 2011; Roscioni et al. 2013), including the EUROBATS guidelines (Rodrigues et al. 2008) and the Bat Conservation Trust report for Britain (Jones et al. 2009b). The outcomes obtained through our study and those of Santos et al. (2013) and Roscioni et al. (2013) highlight the value of a cumulative landscape approach to identify the most important areas for bats to provide key recommendations for the further development of the wind farm industry. Many of the insights and conclusions obtained in this study were facilitated by the proposed analytical framework based on species distribution models and connectivity analyses, (1) offering a better understanding of the distribution of *N. leisleri* in relation to environmental factors, (2) providing valuable information concerning the influence of habitat quality in shaping the distribution of this species in the region, (3) identifying potential linkages in the landscape matrix that are able to promote the fluxes between habitats, and (4) completing the set of planning tools necessary to achieve the sustainable development of renewable energy infrastructures.

Such an approach may be easily extended to other flying vertebrate species assemblages as well as to other taxa and conservation issues that take into account any other infrastructure which may cause a barrier effect. Nonetheless, to make this approach realistic and practically useful the ecological and behavioural characteristics required for movements by a given species must be well known.

Additionally, the final model could be used to plan proper surveys for the monitoring of wildlife fatalities, concentrating field efforts on the wind farms that affect species, both in terms of habitat alteration and connectivity disruption.

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