



Indicator species for avian biodiversity hotspots: Combination of specialists and generalists is necessary in less natural environments



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ABSTRACT

In this work, I tested the premise that the distribution of a group of few common bird species can be used to predict bird species hotspots in Central Italy. The data on bird observations were collected on 530 sampled sites (150 in cultivated, 150 in forest, 150 in grassland and 80 in urban and peri-urban environments). In each environment, sampled sites with values of bird species richness in the upper than third quartile were classified as high species richness spots (HSRS), while sites with lower bird species richness were classified as non-HSRS (binary classification system).

Generalized Linear Models (GLM) were applied using HSRS or non-HSRS as binomial response variable and bird species occurrence was used as the predictor variable. All selected models showed “fair” or “good” capacities to predict the avian hotspots, using only few common birds (4–6) species. However, bird species selected as predictors were different on each environment. In more natural environments (grassland, forest), specialist species were selected, while in most disturbed environments (cultivated and urban) both generalist and specialist species were selected. The results are in agreement with other studies which show how homogenization of bird communities is strongly correlated to landscape disturbance. The findings supports the hypothesis that indicators have to incorporate both specialists and generalist's species simultaneously. Furthermore, the groups of birds selected as surrogates are easy to detect and this makes it possible to involve citizen-science programmes in obtain data. This approach can be a cheap and efficient and can help to significantly speed up the process of assessing ecosystems that might be under threat.

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1. Introduction

Species richness (number of species present in a given area) is often used as an operational variable reflecting the state of biological diversity (Jiguet, Renault, & Petiau, 2005) constituting one of the most useful measures of biodiversity, also in birds (Gotelli & Colwell, 2001; Morelli, 2013; Ricklefs, 2012; Young et al., 2013). Since the study of biodiversity is very intensive in terms of time, effort, cost and difficult, the development of surrogates of biodiversity or species richness is considered analogous to a sort of ‘holy grail of conservation’ (Lindenmayer et al., 2014). One way to increase the knowledge-base on biodiversity is to identify measurable attributes or indicators of biodiversity for use in environmental inventories, monitoring, and assessment programs

(Caro & O'Doherty, 1999; Loss, Ruiz, & Brawn, 2009; Noss, 1990). During the last twenty years several studies have been performed to determine a set of suitable parameters useful to identifying biodiversity hotspots (Myers, Mittermeier, Mittermeier, da Fonseca, & Kent, 2000; Prendergast, Quinn, Lawton, Eversham, & Gibbons, 1993; Stuart-Smith et al., 2013). Some land-cover metrics could be considered as good surrogates of species diversity, because the habitat diversity is associated with an increase of niche availability for the species (Kisel, McInnes, Toomey, & Orme, 2011); this is supported by a number of studies (Goetz, Steinberg, Dubayah, & Blair, 2007; Morelli et al., 2013; Schindler et al., 2015; Schindler, von Wehrden, Poirazidis, Wrba, & Kati, 2013).

The taxonomic surrogates, instead, are predominantly based on biological data, for example, groups of species such as birds (Grantham, Pressey, Wells, & Beattie, 2010). Among the numerous “surrogate” candidates developed in the last decades, bird distribution is potentially one of the most useful for several reasons: birds are widely distributed and breeding bird records are among the easiest species distribution data sets to obtain thanks

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to the presence of birding all around the world (Carrascal, Cayuela, Palomino, & Seoane, 2012; Kissling, Böhning-Gaese, & Jetz, 2009; Kissling, Sekercioglu, & Jetz, 2012; Padoa-Schioppa, Baietto, Massa, & Bottoni, 2006). Among the taxonomic surrogates, we can cite the top predators, flagship species, umbrella species or focal species (Caro & O'Doherty, 1999; Lambeck, 1997; Roberge & Angelstam, 2004; Sergio, Newton, & Marchesi, 2005; Sergio, Newton, Marchesi, & Pedrini, 2006). Many examples exist about the relationships between the distribution of a single species, or group of species, and biodiversity patterns: the Hooded Crow *Corvus cornix* has been used as a surrogate for wetland bird species richness (Kosicki & Chylarecki, 2014); the occurrence of Cuckoo *Cuculus canorus* appear greater on sites with higher avian biodiversity because these areas are characterized by higher diversity of host species (Saino et al., 2009; Tryjanowski & Morelli, 2015). Similarly, the occurrence of raptors highest positioned in the trophic chain, indicates areas occupied by numerous species lower in the food chain (Sergio et al., 2005). The study of complex biotic and abiotic interactions focusses on the study of “bioindicators” that can be used by a wide range of scientists, managers and governmental agencies, interested in assessing the health and well-being of species, populations, and ecosystems (Burger, 2006). However, the “niche theory” predicts differences on the community composition among different environments (Clavero, Brotons, & Herrando, 2011; Ricklefs, 2012), the key-species used as surrogate of biodiversity should be different among different environments. Then, different species should be expected as surrogate of biodiversity in different landscape, characterized by dissimilar structure and land use composition.

In this work, I evaluated the occurrence of bird species as a potential surrogate of avian biodiversity hotspots by considering the differences in bird community composition and the dependency of surrogates to different types of environments. Furthermore, I identified the species surrogate shared among these environments (cultivated, forest, grassland and urban).

2. Methods

2.1. Study area and bird data collection

The field data were collected in the Marche region, Central Italy (centroid: 43°43'34.63"N, 12°38'32.56"E) at altitudes that ranged from 0 to 1200 m a.s.l. The climate in this region is temperate (Pesaresi, Galdenzi, Biondi, & Casavecchia, 2014; Tomaselli, Balduzzi, & Filipello, 1972) and characterized by high spring and summer temperatures and a marked summer drought. The land cover composition in the study area consists mainly of cultivated fields (50%), forest (22%), grasslands (10%), urban and semi urban (10%) and other typologies (8%).

During this study a total of 530 sampled sites were surveyed. Sites were selected according to accessibility, considering also representativeness of different landscapes present in the region. When due to problems of accessibility a site was not visited, was replaced by other sampled sites, in the proximity. Environmental data was derived from a land cover map of the Marche region (1:10.000) (AA.VV., 2010). Descriptions of the 200 m radius area around the sampled-point were made in order to quantify the land-use composition and structural characteristics of sampled sites. The selection of 200 m radius was driven by the results of previous studies performed in the same region (Morelli, 2012; Morelli et al., 2013). The ecological reasons are related to two different concerns: (a) work to small spatial scale, for example using 50 or 100 m radius, can be inadequate to include the entire home range of some bird species (mainly species with big sized home range, as the Eurasian golden oriole, *Oriolus oriolus* or the European turtle dove, *Streptopelia turtur* (Baumann, 1999; Browne & Aebischer, 2005; Browne, 2003)

and (b) the land-use information extracted from the regional maps or Corine Land Cover can be inaccurate at small spatial resolution (Morelli et al., 2013).

The percentages of land used within the buffer was calculated through ArcGIS 10 analysis, summarized as following: (a) the creation of a series of 200-m radius buffer areas around each sampled point; (b) the “intersect operator” between buffer areas and regional land cover map (AA. VV., 2010); and (c) the use of matrix crosstab to quantify the relative coverage of each land use classes. Land-use categories were taken from the map of land-use in the Marche region and were reclassified in larger groups to obtain 8 land-use typologies and were renamed as: built (e.g., residential building, production facility, built with infrastructure and processing areas), cultivated (e.g., cultivated and farmland categories), forest, reforest, grassland (e.g., pastures and meadows), shrubs, riparian and roads (e.g., paved, unpaved and railways). Sampled sites were classified as cultivated (arable fields), forest or grassland when the main land use was >50% (Morelli et al., 2013). Sample sites with mixed composition, where none of land-uses had at least than 50%, but an important composition of the use was urbanization (building, roads, etc.) (more than 20%), were classified as urban/semi urban environments. Finally, sample sites with mixed compositions, but with low composition of urbanization, were excluded from the analysis because they were not common enough to be modelled (less than 3% cases, $n = 14$). As result, a total of 150 sites were classified as cultivated landscape, 150 sites as forest landscape, 150 sites as grassland landscape and 80 sites as urban or peri-urban environment.

The survey of birds was conducted between mid-April and the end of July 2012. The point counts (Bibby, Burgess, & Hill, 1992) were spaced relatively uniformly in each environment, separated by an average 300 m from each other. The minimal value of separation between neighbour points was 200 m. The potential issue of non-independence of data was avoided because overlapping between buffer areas in the sampled sites was less than 5%. All points were visited at least two times, between 0600 and 1000 h for 10 min in sunny conditions. All birds detected visually and acoustically within a 100-m radius around the observer were recorded. At each sampled site, bird species richness was calculated as the sum of different bird species recorded during all visits. Average bird species richness was calculated for each environment, using all sampled sites belonging to each environment.

2.2. Data analysis and model performance

The sampled sites were classified using a binary classifier system: the sites with values of bird species richness greater than the average per each belonging environment and falling upper the quartile Q3, were classified as high species richness spot (HSRS) (value 1) and the sites with lower values, were classified as non-HSRS (value 0) (Fig. 1). The limit value of quartiles was estimated for the species richness per each environment type.

The Bartlett test of homogeneity of variances among groups was significant, so differences of bird species richness among environments were verified by mean of the Kruskal–Wallis rank sum test. Consequently, a detailed comparison between environments was performed applying the multiple comparison test “kruskalmc”, from the ‘pgirmess’ package for R (Siegel & Castellan, 1988).

The diversity for each environment was also calculated by utilizing the Shannon–Weaver diversity index (H) using the formula $H = -\sum p_i \ln p_i$, where p_i is the frequency of the different bird species in each environment (Shannon, 1949). Along with these values, the Shannon's equitability index (E_H) (Magurran, 2004) was calculated using the formula $E_H = H/H_{\max} = H/\ln S$ that assumes a value between 0 and 1 with 1 being complete evenness. H_{\max} is the maximum values of H . S is the total number of species.

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