Efficiency of birds as bioindicators for other taxa in mountain farmlands

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A B S T R A C T

Biodiversity loss is a global issue, particularly in mountain regions, where land-use/land-cover and climate change dramatically impact on species and communities. Sound ecological research and up-to-date information on biodiversity are needed to support conservation efforts. However, this information is often difficult and costly to obtain. Therefore, bioindicators serve as surrogates to provide information on the entire biocenosis. Birds are considered excellent bioindicators as they occupy different ecological niches and trait spaces.

We present a study about the efficiency of birds as bioindicators for the diversity of other taxa in a mountain region in the Central Alps. We surveyed bird communities at 115 sites across a gradient of different grasslands and crops and compared them with the diversity of other taxa (bats, butterflies, grasshoppers, arachnids, and vascular plants). We aimed to identify indicator bird species for grasslands and crops, to assess cross-community concordance between birds and other taxa, and to model the efficiency of bird indices and indicator species as bioindicators of the diversity across habitat types and taxa.

We identified indicator bird species for different grassland and crop types and found that efficiency of bird indices and single species varied for habitat types and taxa. We highlight the importance of using carefully selected bioindicators in biodiversity monitoring and conservation planning, and the need for an integrated and interdisciplinary approach for biodiversity research. Moreover, by looking at a combination of different indices we can gain a more comprehensive understanding of ecosystem functioning. We also provide a framework for the use of bird-based monitoring programs and bird-derived indices to guide biodiversity conservation, and emphasise the importance of incorporating different bioindicators into biodiversity research and monitoring to provide a more comprehensive understanding of ecological biodiversity patterns and trends.

1. Introduction

In recent decades, biodiversity has undergone a historically unprecedented crisis, resulting in rapid declines worldwide (Turvey and Crees, 2019). This trend is particularly concerning in many mountain areas, where biodiversity is under severe threat due to global change (Huber et al., 2005). Indeed, the intensification of agriculture and the sealing of valley floors, the abandonment of less profitable agricultural areas and rising temperatures, especially at higher elevation, are causing major declines in biodiversity in mountain farmland ecosystems (Jamwal et al., 2022; Tasser et al., 2023). Conserving biodiversity in the face of land use and climate change is therefore one of the most important challenges facing society today (Balmford and Bond, 2005). Robust ecological knowledge is key to conservation strategies, which should be underpinned by the availability of accurate and up-to-date biodiversity information (Tittensor et al., 2014). However, in many cases, the inventory of large taxonomic groups (e.g., arthropods) is costly and often difficult, as data are difficult to collect and assess directly (Yong et al., 2018). It is therefore often necessary to adopt surrogate approaches (Rodrigues et al., 2007), using more easily collected taxon-based bioindicators, which can act as proxies for poorly known taxonomic groups, to considerably reduce the time and resources

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required (Lindenmayer et al., 2015). Taxon-based bioindicators (i.e. a single taxonomic group as bioindicator for other taxa) are more likely to represent a broader range of biological patterns and processes than habitat-based bioindicators (i.e. habitat characteristics as bioindicator for taxa), even though the latter are generally considered to be cost-effective (Lindenmayer et al., 2014). Furthermore, bioindicators are routinely used in biodiversity monitoring and conservation planning to assess environmental conditions (Lindenmayer et al., 2015).

Diversity indices (e.g., species richness, Shannon diversity, guild specific richness) or community weighted mean indices (based on functional traits; Moretti et al., 2017) of relatively well-known and easily surveyed taxa may be effectively used to obtain information on otherwise overlooked and difficult-to-detect organisms (Burrascano et al., 2018). In addition, indices based on functional traits or different guilds are strongly influenced by the environment, and therefore seem to show stronger and clearer effects than bioindicators based on tax-onomical diversity (e.g., Brunbjerg et al., 2018). Moreover, the use of indicator species as bioindicators can be considered a robust and cost-effective approach (e.g., Morelli et al., 2021; Souza and Vianna, 2022). Indicator species are defined as species that are closely tied to a particular habitat type and, as such, are particularly sensitive to changes in environmental conditions (Simamora et al., 2021). Examples for such indicator species are the Water pipit *Anthus spinoletta* as bioindicator for other high-elevation specialist species (Ceresa et al., 2023), the Rock partridge *Alectoris graeca* for high mountain slopes and rocky grasslands, the Eurasian nightjar *Caprimulgus europaeus* for forest edges, the Collared flycatcher *Ficedula albicollis* for beech forests, and the Red-backed shrike *Lanius collurio* for shrublands (Valerio et al., 2016). Several studies have demonstrated the efficiency of using single species as bioindicators of different ecological processes and characteristics in diverse environments (e.g., global change; Terrigeol et al., 2022), but far fewer have tested their efficiency also as potential bioindicators of multiple taxa (e.g., Pearman and Weber, 2007). The ideal bioindicator co-occurs with many species belonging to different taxa, and responds to variations in environmental conditions to which the other species are also sensitive (Simamora et al., 2021). There is evidence that bio-indicators are context-dependent, with often ambiguous efficiency, especially as ecological patterns become more complex, as is the case in mountain areas (Hess et al., 2006).

Birds are generally considered as excellent bioindicators, and they have been widely used for a long time (Furness and Greenwood, 1993). They are a well-known and easily counted group, occupying most habitat types and different ecological niches, and are usually highly sensitive to environmental change (climate and land-use changes; Gaston et al., 2003; Li et al., 2022). Additionally, they provide important ecosystem services (e.g., pollination, pest control, recreational interest; Sekercioglu et al., 2016). Thus, bird-based monitoring programs and bird-derived indices remain a common practice, at local, national, and supranational levels for biodiversity and environmental monitoring, with important implications for conservation strategies. For example, the EU Bird Directive (old 79/409/EEC and now 2009/147/EC) is the oldest EU legislation on the environment that aims to protect all European wild birds and their habitats; the Farmland Bird Index (Gregory et al., 2005) has been officially adopted by the EU as a proxy for assessing the more general status of biodiversity in agricultural landscapes in Europe. Italy adopted the Mountain Grassland Bird Index (Rete Rurale Nazionale and LIPU, 2020) as bioindicator for the quality of mountain ecosystems and their biodiversity.

The use of birds as bioindicators has been widely applied in mountain areas (Scridel et al., 2018) and the validity of birds as bioindicators for other taxa has been studied and proven worldwide (e.g., Eglington et al., 2012a). To the best of our knowledge, this is the first study to assess their bioindicator efficiency, i.e., their ability to reflect indices of other taxa, in mountain farmland landscapes.

We surveyed bird communities at 115 sites across a broad gradient of grasslands and crops in the Central Alps and compared them with a range of diversity indices of other taxa sampled at the same sites and in the same years, including vascular plants, bats, grasshoppers, butter-flies, and arachnids. We focused on farmland landscapes ranging from valley floors to mountain peaks, to capture the agricultural landscapes most threatened by land use and climate change (Scridel et al., 2018). We had three objectives for the study: (1) to assess cross-community concordance between bird communities and other taxa communities within mountain farmlands, as quantifying cross-taxonomic congruence is a critical step in identifying bioindicators (Gioria et al., 2011); (2) to identify indicator species from the bird communities for different habitat types; (3) to test the efficiency of bird indices (both taxonomic and functional) and of single indicator species in predicting diversity in other taxa. Particularly for the last objective, we aim to understand the additive value that different bird indices or indicator species could provide in predicting biodiversity when modelled using such information from the avian community in addition to the 'traditional' environmental factors. We also aim to identify the 'best' indicator bird species and/or index for each taxon of mountain landscapes, thereby contributing to the identification of overall biodiversity, its trends, and patterns.

This innovative approach has the potential to identify key bird indices or species that, together with ecological aspects, contribute to the identification of the overall biodiversity patterns, intercepting possible environmental drivers not already explained by the traditional environmental variables alone.

2. Materials and methods

2.1. Study area

This study was carried out in the Central Alps, over the entire Autonomous Province of South Tyrol (north-eastern Italy). South Tyrol lies between 194 and 3,905 m above sea level (asl) and covers an area of around 7,400 km^2, resulting in significant local climate variations. Valley floors typically have warmer temperatures than mountainous areas. Precipitation is influenced by orography, with the highest values in the mountainous areas. Precipitation in the southern part of South Tyrol is mainly concentrated in autumn and spring, while the northern part shows maximum precipitation in summer (Crespi et al., 2021). We used data from three years of the Biodiversity Monitoring South Tyrol (Hilpold et al., 2023) and selected sites occurring in farmed environments, encompassing the variety of agricultural areas typical of the Alpine region, i.e. grasslands, annual (arable lands) and permanent crops (vineyards and apple orchards), from valley floors to the alpine belt (207–2,534 m asl), totalling in 115 sites (Fig. 1). Following this stratification, sites were randomly selected within the framework of the South Tyrol Biodiversity Monitoring (Hilpold et al., 2023). Permanent crops were mostly located in valley floors, whereas grasslands (meadows, pastures) were found from the montane to the subalpine and alpine belts. The sub-montane area (i.e., the lower part of the montane belt between 600 and 1000 m asl) is the most diverse, alternating between annual crops and meadows. Grasslands were divided into two subcategories depending on the elevation: grasslands above 1,800 m asl (alpine and subalpine grasslands) and below that elevational threshold (hilly and montane grasslands, hereafter montane grasslands).

2.2. Biodiversity variables

2.2.1. Bird survey methods

Bird communities were surveyed using 10-minute point-counts during the breeding season from mid-April to mid-July within a 100 m-radius of the site centroids in 2019, 2020 and 2021. Sites were visited three times in the same year between sunrise and 11 a.m. by a single ornithologist (M.A.), with at least two weeks between visits, and changing the order of sites between subsequent surveys. For subalpine and alpine sites, we performed only two visits, because of the much
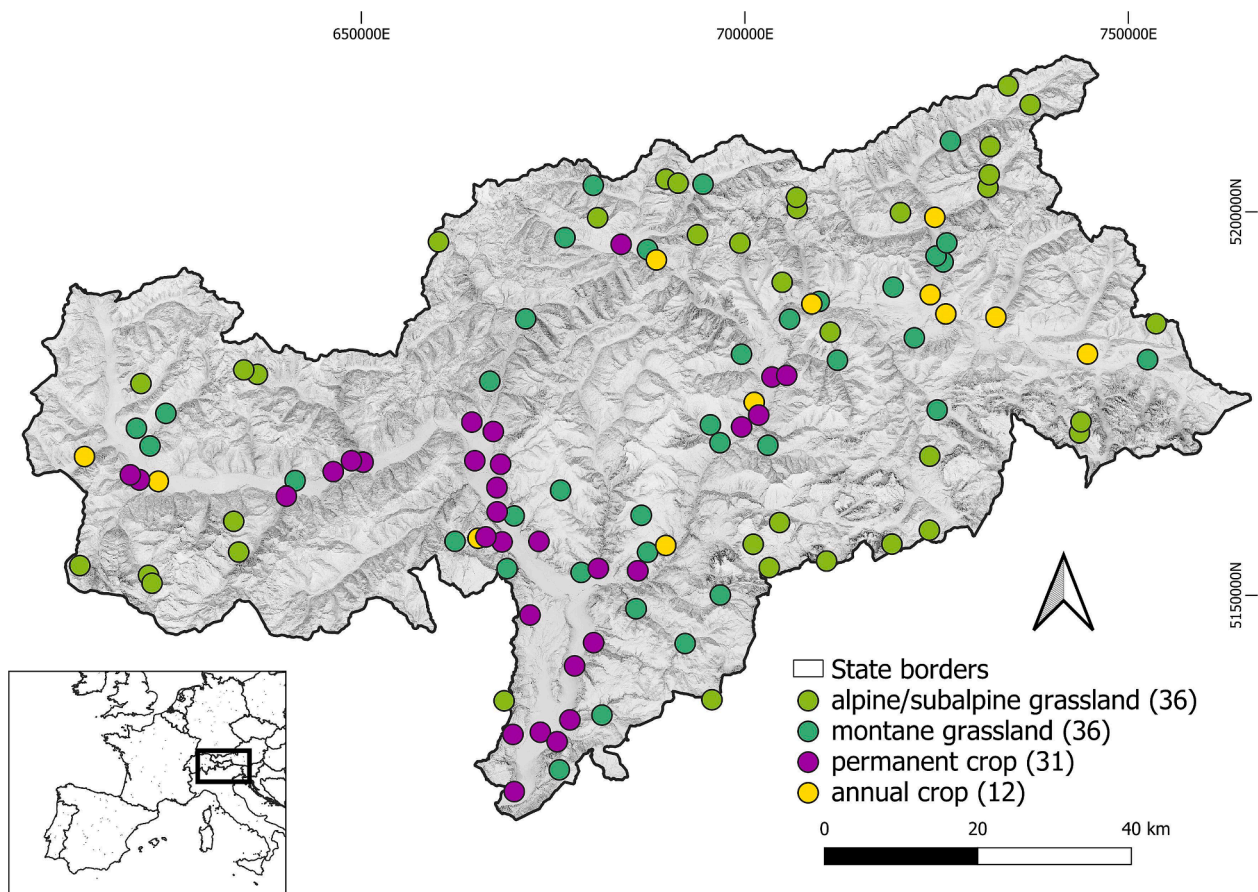
Fig. 1. Representation, distribution, and number of sites within the study area located in South Tyrol (Northeastern Italy).

shorter breeding season at higher elevation. We excluded birds only flying over the sites and species occurring exclusively as migrants within the region. Surveys under moderate/strong wind or heavy rain/snow were avoided.

At each site the species richness (total number of species observed at a site) and the Shannon diversity index (using the maximum number of individuals recorded per species from the total visits) were estimated using the function 'estimatedD' in 'iNEXT' R package (Hsieh et al., 2016); both indices were calculated setting the sampling coverage at 98 % (Chiu, 2023; Roswell et al., 2021). We decided to use a uniform sampling coverage for all diversity indices and taxa in this study. This approach helps to account both for different abundances and variations in detectability that can arise due to differences in landscapes, number of site per habitat type, species, and taxa (Hsieh et al., 2016).

We also selected functional traits that characterise the birds' habitat requirements, and might affect their ability to respond to land-use/land-cover and climate changes (Anderle et al., 2022). The traits considered were diet, foraging substrate, body mass, broods per year, nest type, habitat use during breeding season, territoriality, migration strategy, and overall specialisation (normalising the mean values of diet, foraging behaviour, foraging substrate, habitat, and nesting site specialisms). Starting from these traits, at each site a Rao's functional entropy index was calculated using the 'FD' package in R (Laliberté et al., 2014) to evaluate the overall functional diversity of each community.

Additionally, we used specific community weighted mean (CWM) indices for threatened species (near threatened, vulnerable, endangered, critically endangered; derived from Ceresa and Kranebitter, 2020), omnivorous species, invertebrates eaters, vertebrates, fish and carrion eaters, plant and seed eaters (Wilman et al., 2014), and farmland birds, based on the list of species used to assess the Common farmland bird indicator for Europe (https://pecbms.info/trends-and-indicators/indi

cators/indicators/E_C_Fa/) and the Montane Grassland Bird index for the Italian Rural Network (Rete Rurale Nazionale and LIPU, 2020). CWM indices were calculated for each site using 'FD' package in R (Laliberté et al., 2014).

See Table S1 for all indices description.

2.2.2. Environmental variables

We derived elevation, slope, and potential solar radiation from the Digital Terrain Model based on Airborne Laser Scanning campaign carried out in 2006 by the Province of South Tyrol (http://geocatalogo.retecivica.bz.it/geokatalog/) with a spatial resolution of 2.5 m. In addition, we derived three temperature maps (for the years 2019, 2020, and 2021) with a spatial resolution of 250 m by using data from Crespi et al. (2021). Each map was obtained computing the mean temperature value for the period from 15 April to 15 July consistent with the year when all taxa were surveyed and selecting for the values at the centroid of each site.

2.2.3. Survey methods for other taxa

We selected different taxa exhibiting distinct eco-functional traits (e. g., different physiology, morphology, trophic position, and taxonomic relatedness as well as responding to different spatial scales and providing different ecosystem services): bats, butterflies (Lepidoptera: Rhopalocera), grasshoppers (Orthoptera and Mantodea), arachnids (Arachnida), and vascular plants. They were surveyed according to standardized methods described in the handbook of the long-term project Monitoring Biodiversity South Tyrol (Hilpold et al., 2023). At each site, all taxa (including birds) were surveyed in the same year. Bats were sampled by Elekon Batloggers A + detectors programmed to autonomously record echolocation calls (following Barataud, 2020) throughout the night for at least three consecutive nights (from sunset to

sunrise) per site, with good weather conditions, and placed at a height of 1.5 m above ground. We analysed the recorded calls manually using BatExplorer to automatically calculated call measures (Elkon AG, 2023), and using the rhythms of activity as proxies for abundance.

Butterfly surveys (adults only) were performed with a combination of transect sampling and a time area count (Guariento et al., 2023). We performed four (in alpine sites three) replicated counts per site from May to August to cover both seasonal and weather-related changes.

For grasshoppers, the survey included grasshoppers and locusts (Caelifera), bush crickets and related groups (Ensifera); we also included mantids (Mantodea) together with orthopterans because of similarities in their habits and in the survey methods that can be adopted (Hilpold et al., 2020). The method consisted in an exhaustive search within a plot of 100 m^2 for a maximum of 30 min in late summer (Hilpold et al., 2023).

Arachnida (Araneae, Opiliones and Scorpiones) were retrieved from pitfall traps, beating, and sweeping samples as described in Hilpold et al. (2023). Combining different collection techniques for this diverse group has the advantage to capture better the arachnid community, form ground dwelling to tree crown specialists.

The botanical survey was performed within plots of 100 m^2 squares established parallel to the slope. For all vascular plant species, a percentage coverage for the corresponding layer (herb, shrub, tree) was estimated as abundance proxy (Dengler et al., 2016).

2.2.4. Biodiversity cumulative indices

For each site, a cumulative species richness and a Shannon diversity index were calculated by summing the single index values of each taxon (not considering birds, as they were used as explanatory variables), each divided by the corresponding maximum value (Buckland et al., 2011).

2.3. Statistical analysis

2.3.1. Indicator bird species

In this study, we used the term 'indicator species' to refer to bird species that are associated with a particular habitat type and are thus sensitive to environmental changes occurring in that habitat (Simamora et al., 2021), in our case represented by a gradient of different grasslands and crops. The main purpose of identifying an indicator bird species for a particular habitat type was to assess whether the indicator species could also serve as bioindicator for other taxa present in the same habitat. To identify potential indicator species for grasslands and crops, we investigated the relationship between the occurrence of individual species and the available habitat within the area. Specifically, we searched for species associated with montane grasslands, subalpine/ alpine grasslands, permanent and annual crops, the combination of grasslands (montane and subalpine/alpine together) and crops (permanent and annual together), and with the combination montane grasslands - annual crops (representing the diverse landscape of the submontane zone). Indicator species were identified using the species-level analysis, i.e., the indicator value (IndVal) analysis using the 'indicspecies' package for R (De Cáceres et al., 2020). We excluded combination with no ecological sense (e.g., permanent crop and subalpine/alpine grassland cannot coexist).

The 'IndVal' analysis is based on "specificity", which estimate the probability of a given species to be associated to a target habitat (species specific of a particular habitat), and "fidelity", which is the probability of a species to be found in a newly surveyed site within the same habitat (Dufrene and Legendre, 1997). The combination of "specificity" and "fidelity" produce a percentage indicator value (IndVal) for each species. In this study, bird species with a IndVal > 30% and significative p-value (<0.05) were considered as indicator species (De Cáceres et al., 2012). To better characterise specific indicator species and relate them to farmland landscapes, we also included in this analysis bird data collected in other habitats within the same monitoring scheme (Anderle et al., 2023, 2022; Hilpold et al., 2023). This included bird surveys in 19

deciduous forests, 12 coniferous forests, 12 wetlands, and 20 settlements, conducted between 2019 and 2021. By incorporating data from these additional habitat types, we aimed to gain a more robust and nuanced understanding of the distribution and habitat preferences of farmland indicator bird species, by considering a wider set of farmland landscapes potentially available to birds in the region.

2.3.2. Compositional dissimilarity of different communities

We firstly standardised all taxonomic community matrices with a Hellinger standardization to minimise effects of vastly different sample total abundances (Roberts, 2019). We then calculated compositional dissimilarity within the entire bird community, within only the bird species selected as bioindicators, and within each community of other taxa, respectively, across all 115 sites using the Bray-Curtis similarity index. This index ranges between 0 and 1, where 0 means that two sites have the same species composition, and 1 means that two sites are completely different in species composition, i.e., they do not share any species. Finally, we applied a Mantel's test to assess the strength of concordance among bird and other taxa communities (Rooney and Bayley, 2012), within grasslands and crops. With this test we evaluated the null hypothesis of no relationship between two community matrices (e.g., Rooney and Bayley, 2012). The significance of each Mantel test was assessed using 999 permutations. If a single community (here birds) is representative for other taxa, then the patterns of community similarity between sites and taxa should be correlated (SU et al., 2004). The concordance was also tested between the whole bird community and the indicator species only, to test if the indicator species alone could serve as bioindicator for the entire bird community. See Fig. S1 for a schematic summary of this analysis.

2.3.3. Multi factor models

To assess the efficiency of birds as bioindicators for the richness and diversity of other taxa (i.e. bats, butterflies, grasshoppers, arachnids, and vascular plants), we analysed species richness, Shannon diversity of single taxa and of all taxa together (using cumulative indices; Buckland et al., 2011), using multivariate regression models (Zuur et al., 2013). These models tested the predictive value of bird indices and the abundance of indicator species together with the environmental co-variates (elevation, slope, potential solar radiation, and mean spring temperature). To avoid presenting too many parameters to the modelling approach, we only entered in the models the bird indexes that showed a significant correlation (P-value < 0.05) with a specific other taxa index (Table S2 and S3). If no variable exhibited a correlation, the model was not developed. Before running the models we standardised data by scaling all the indices (Zuur et al., 2010), and we evaluated the model variance inflation factors (VIFs) accounting for multicollinearity and excluding the most problematic variables (VIF > 3; Zuur et al., 2010). We also assessed the uniformity of residuals, examined the occurrence of outliers, compared simulated and observed dispersion, and checked for potential zero-inflation using the 'DHARMa' R package (Hartig, 2020). All models underwent statistical validation based on these tests before the subsequent approaches.

We then ran two types of models for each individual index of other taxa used as response variables. The first type of model, called the bird indices model, included bird diversity indices along with environmental variables. The second type of model, called the indicator species model, included individual indicator bird species and environmental variables. Here, single bird indicator species were also modelled with bird species richness and Shannon diversity index as response variables. We ran the two approaches separately to find the best bird index and indicator species respectively for each taxon and within different habitat types, and to avoid dependency between indices. We then built all possible models for each one of the other taxa indices with the 'dredge' function in the R package 'MuMIn' (Barton, 2020). Adopting an information-theoretic approach, we performed a model selection based on the Akaike's information criterion (Burnham and Anderson, 2004)

corrected for small sample size (AICc). The most supported models were selected (ΔAICc < 2), after excluding uninformative parameters (i.e., indices or environment variables that were included only in models that comprised more parsimonious and simpler models as nested ones; Arnold, 2010). Modelling other taxa indices with environmental variables across all habitat types, we finally obtained 75 averaged (most supported) indicator species models and 75 bird indices models. See Fig. S2 for a schematic summary of this analysis.

3. Results

In terms of compositional dissimilarity of different communities, as expected, bird communities changed consistently with the composition of indicator species in all habitat types, except in montane grasslands. The vascular plant community showed the most consistent changes with the bird communities in the different habitat types (Fig. 2). In terms of models, bird communities were unsurprisingly best represented by the bird indicator species, with a total of 15 models, while bat communities the least represented with 4 models. The single species most frequently selected as bioindicators were European serin *Serinus serinus* (19 models), Alpine accentor *Prunella collaris* (12 models) and Alpine chough *Pyrrhocorax graculus* (10 models). Biodiversity cumulative indices (encompassing all taxa except birds) were the best represented by the bird indices, with a total of 16 models, and bat indices the less with 8 models. The indices that were most frequently retained in the models were threatened birds (in 17 models), bird species richness and farmland birds (in 16 models; Table S4 and S5).

3.1. Indicator bird species

The IndVal analysis identified a total of 14 indicator bird species (Table 1). In particular, one species for montane grasslands, five for alpine/subalpine grasslands, four for annual crops, one for permanent crops, one for crops (annual and permanent crops combined), and two for montane grasslands and annual crops combined were identified.

3.2. Compositional dissimilarity of different communities

Dissimilarities revealed significant correlations between bird communities and other communities, including bats, butterflies, grasshoppers, vascular plants, and arachnids. These correlations demonstrated how different communities are linked in different farmlands.

Specifically, the whole bird community changed significantly based on the composition of indicator species across different habitat types, except within montane grasslands.

Bat communities showed significant correlations with bird communities in most habitat types, except for annual crops and montane grasslands.

Butterfly communities changed significantly in correlation with bird communities in most habitat types, except for annual crops. Correlations with bird indicator species were also evident in most habitat types.

Grasshopper communities displayed significant correlations with bird communities in all habitat types. The strongest correlations occurred when considering all indicator species across different habitat types.

Arachnid communities showed significant correlations with bird communities in several habitat types. The strongest correlation, considering all indicator species, occurred across all habitat types and Alpine/subalpine grasslands.

Vascular plant communities also changed significantly in correlation with bird communities across various habitat types, except for annual crops. There were notable correlations in most habitat types when only bird indicator species were considered. For complete results see Fig. 2.

3.3. Multi factor models

Goodness of fit (by means of adjusted-R^2 according to 'MuMIn' R package) for bird indices models (Table S4) ranged between 0.081 and 0.908, and for indicator species models (Table S5) between 0.040 and 0.809.

The models showed that both bird species richness and Shannon diversity were negatively associated with Water pipit abundance in all habitat types. Bird species richness was positively associated with Yellowhammer *Emberiza citrinella* in all farmlands considered together and within annual crops, while it was negatively associated with Northern wheatear *Oenanthe oenanthe* in all farmlands considered together (Fig. 4).

No significant associations were found between bird and bat indices (Fig. 3). However, Alpine accentor was negatively associated with bats in all farmlands together and in grasslands, and European serin in all farmlands together (Fig. 4).

Both butterfly indices were positively associated with the Shannon bird index in crops (Fig. 3), and negatively with European serin across all farmlands together (Fig. 4). Both species richness and Shannon diversity of birds and butterflies were positively associated in all farmlands and grasslands (Fig. 3). Butterfly species richness was negatively
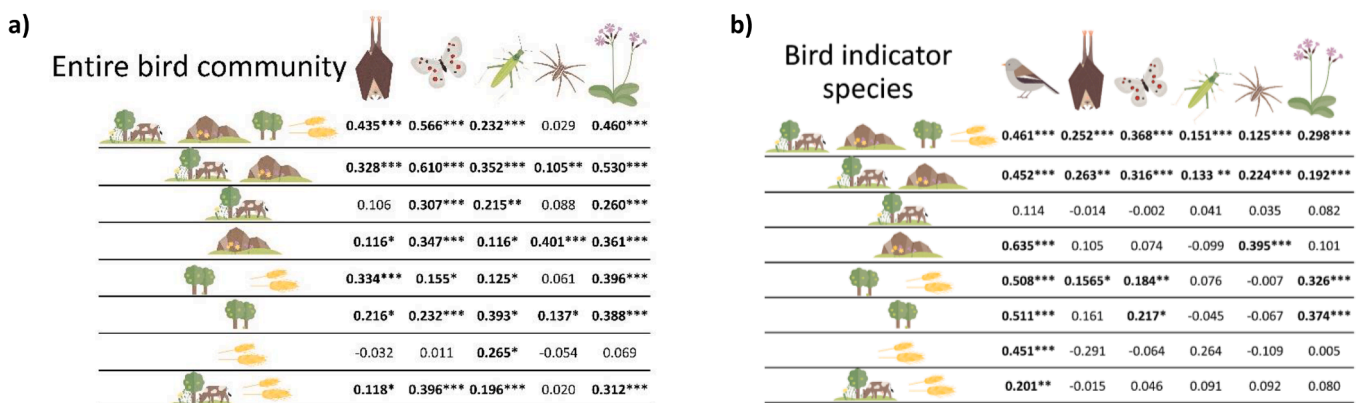

Fig. 2. Dissimilarity results for all taxa referring to (a) bird community composed by all species, and (b) by indicator species only. Taxa icons represent different taxa, while 🐄 represents montane grasslands, 🏔️ alpine/subalpine grasslands, 🌳 permanent crops, and 🌾 annual crops. Combination of icons represent all habitat types, grasslands (montane - alpine/subalpine), crops (permanent - annual crops), and montane zone (montane grasslands - annual crops). Bold numbers represent significant coefficients based on Mantel test assessing the strength of cross-taxonomic congruence in compositional dissimilarity. * < 0.05, **< 0.01, and *** < 0.001.

Table 1

IndVal analysis results on bird species indicators of different habitat types. Habitat types not shown in the tables had no resulted indicator bird species. IndVal is the combination of specificity and fidelity (%). * < 0.05, **< 0.01, and *** < 0.001.

Habitat type	Indicator species	Specificity	Fidelity	IndVal	P-value
Montane grasslands	Rock bunting	0.8902	0.1622	0.38	0.019*
Alpine/subalpine grasslands	Water pipit	0.8182	0.6944	0.754	0.001***
	Northern wheatear	0.9118	0.4722	0.656	0.001***
	Alpine accentor	1	0.25	0.5	0.001***
	Alpine chough	1	0.2222	0.471	0.002**
	Common linnet	0.6718	0.25	0.41	0.015*
Annual crops	Carrion crow	0.5603	0.8333	0.683	0.002**
	Eurasian tree sparrow	0.6258	0.4167	0.511	0.003**
	Eurasian skylark	0.75	0.25	0.433	0.006**
	Grey wagtail	1	0.1667	0.408	0.017*
Permanent crops	European serin	0.6591	0.7	0.679	0.001***
Crops (permanent - annual crops)	Eurasian wryneck	0.9129	0.3571	0.571	0.001***
Montane grasslands - annual crops	Red-backed shrike	0.8799	0.3265	0.536	0.001***
	Yellowhammer	0.9727	0.2245	0.467	0.001***

associated with threatened birds across all farmlands, with plant- and seed-eating birds within crops (Fig. 3), and with European serin in permanent crops, while it was positively associated with Rock bunting *Emberiza cia* across all farmlands together (Fig. 4).

Grasshopper and bird species richness were positively associated across all farmlands together, with omnivorous birds within annual crops (Fig. 3), and negatively with Alpine accentor across all farmlands together (Fig. 4). Shannon diversity was negatively associated with European serin within permanent crops (Fig. 4). However, both grasshopper indices were negatively associated with threatened birds within grasslands (Fig. 3) and with European serin across all farmlands together, and crops (Fig. 4).

Positive associations were found between arachnid and bird species richness within permanent crops, while a negative association was noted with farmland birds across most farmlands (Fig. 3).

Vascular plant Shannon diversity was positively associated with bird species richness within grasslands and with bird Shannon diversity within montane grasslands (Fig. 3). However, plant species richness was negatively associated with bird Rao's functional index (Fig. 3) and European serin within montane grasslands (Fig. 4). Both plant indices were negatively associated with Eurasian tree sparrow *Passer montanus* across all farmlands together (Fig. 4).

Both biodiversity cumulative indices were positively associated with bird species richness across all farmlands together, but they were negatively associated with threatened birds within grasslands (Fig. 3), with Alpine chough within grasslands and with European serin within permanent crops (Fig. 4). Cumulative species richness was negatively associated with farmland birds (Fig. 3) and European serin across all farmlands together (Fig. 4), while cumulative Shannon diversity was negatively associated with threatened birds across all farmlands together (Fig. 3), with Alpine chough within all farmlands together and alpine/subalpine grasslands (Fig. 4), while positively with omnivorous birds within annual crops (Fig. 3). See Fig. 3 and 4 for the complete model results, and Table S4 and S5 for standardised parameters, standard errors, p-values, and goodness of fit for the most supported models.

4. Discussion

To the best of our knowledge, this is the first work assessing the efficiency of birds as bioindicators for farmland biodiversity in an Alpine region. Furthermore, this is the first time that the efficiency has been tested not only for bird taxonomic indices, but also for bird functional indices and indicator species.

Similar works have mostly focused on tropical forests or human modified ecosystem of temperate areas (Chiatante et al., 2021; Sauberer et al., 2004). In this study, we examined birds as bioindicators in agriculture-dominated landscapes ranging from the valley floor to the alpine belt, encompassing the most threatened habitat types in the Alps

(Tasser et al., 2007). Furthermore, previous work has mainly focused either on the global scale, where the efficiency of birds as taxon-based bioindicators is very high but of little use for many practical conservation measures, or on the field-scale, where environmental variables and microclimates are so specific that responses can vary from year to year, and results are site-specific (Eglington et al., 2012b; Martin et al., 2015). Here, we focused on the regional scale, as it has been extensively demonstrated that such a scale plays a significant role in predicting the efficiency of bioindicators (e.g., Turtureanu et al., 2014). The regional scale (i.e. sub-national in Italy) is often the 'reference' level where management and conservation strategies are mostly planned and implemented, and where local governments have potential influence on environmental and landscape changes (Hinojosa et al., 2019). Given the speed at which global change is occurring, regional and local governments need fast and cost-effective ecological bioindicators that provide clear indications of socio-economic and climate change impacts on biodiversity and help to quantify the effects of implemented or proposed conservation measures. Our results confirmed that, at the regional scale, birds work well as bioindicator for other taxa, but their efficiency varies between habitat types. It changes according to the specific bird index considered and the strength of responses varies within taxa.

Most importantly, our work has highlighted the importance of using multi-taxon survey schemes to gain a more comprehensive understanding of the regional biodiversity. Arachnids, birds, and bats tend to respond to environmental drivers at a larger scale, whereas others, such as butterflies and grasshoppers, or vascular plants, at a more local or field scale (Hess et al., 2006). Birds are highly responsive to habitat composition/configuration and structural heterogeneity of vegetation (Anderle et al., 2023, 2022; Chiatante et al., 2021), while many vascular plants occupy more specific niches characterised by a particular microclimate, soil and management type, as do herbivorous insects that depend on them (Korell et al., 2021). Furthermore, common or divergent ecological and physiological traits, such as diet and trophic level, home range size or dispersal ability, may condition taxon-specific responses to the same ecological gradient and to different bird indices (Yong et al., 2018).

Our results stressed the need to go beyond species richness or taxonomic indices in ecological studies, since other indices may provide complementary answers. Instead, we encourage the inclusion of functional indices in ecological bioindicator models, and including threatened species and single indicator species. Incorporating all these indices provides a more comprehensive view of the efficiency of a group (here, birds) as a bioindicator of broader biodiversity patterns and leads to a better representation of biodiversity patterns and ecological functioning. For example, in our results, butterflies respond to bird species richness and Shannon diversity, but bats respond only to the threatened bird index and to plant- and seed-eating birds. Using only one category of the indices could result in a partial view of community structure
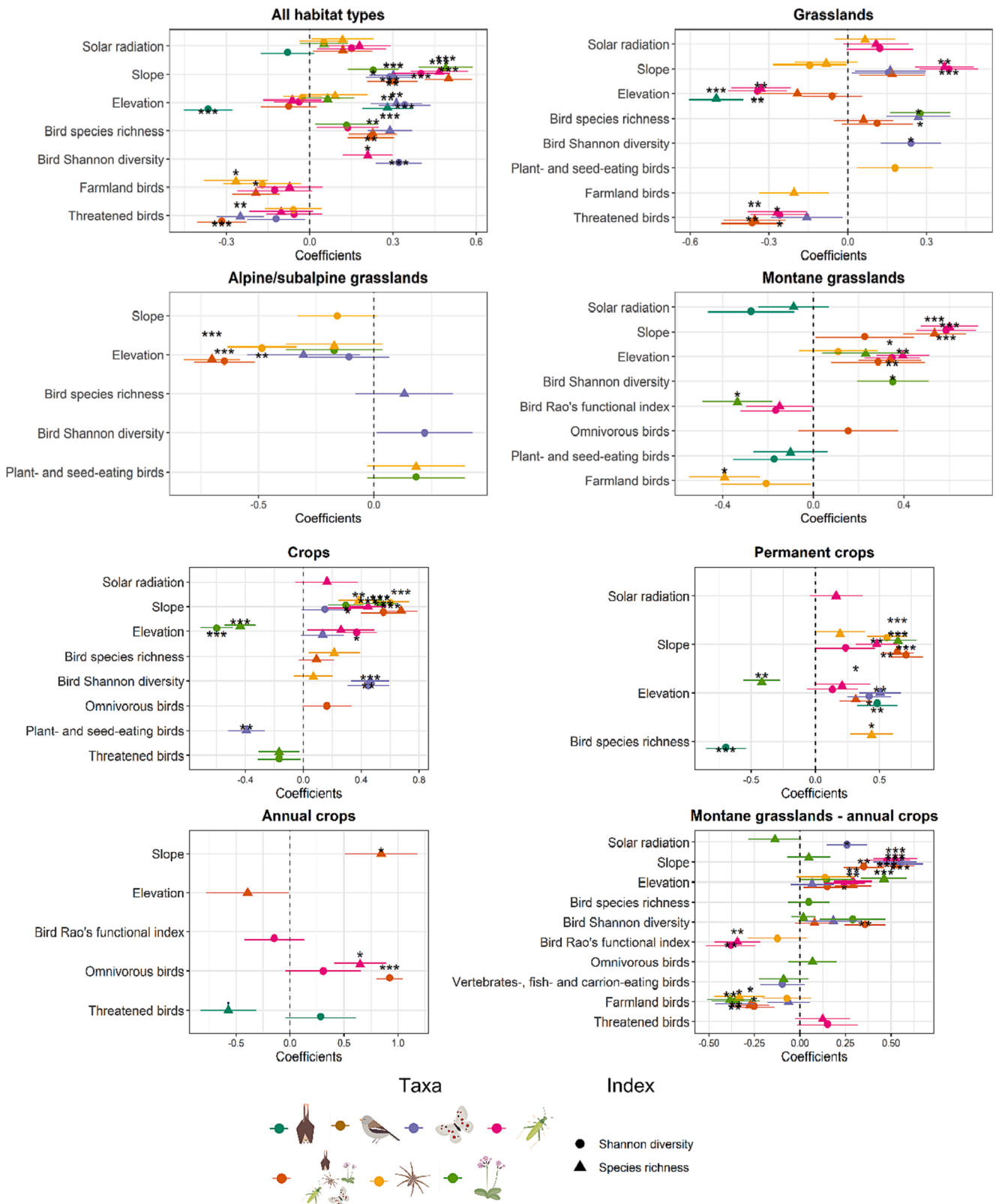
Fig. 3. Bird indices model averaging results, divided per habitat type. Different colours indicate the estimated coefficient of different taxa. * < 0.05, **< 0.01, and *** < 0.001.

within ecosystems (Martin et al., 2015).

An often underestimated aspect is the impact of the sampling scheme on the correlation patterns and efficiency of the bioindicators. The strength of our results is that they are derived from a consistent

collection of data at the same sample sites during the same field season for all taxa surveyed. Given that many taxa may show strong interannual variation, such as insects that are highly dependent on warmer or less rainy years, vascular plants on dry seasons and birds on adverse weather
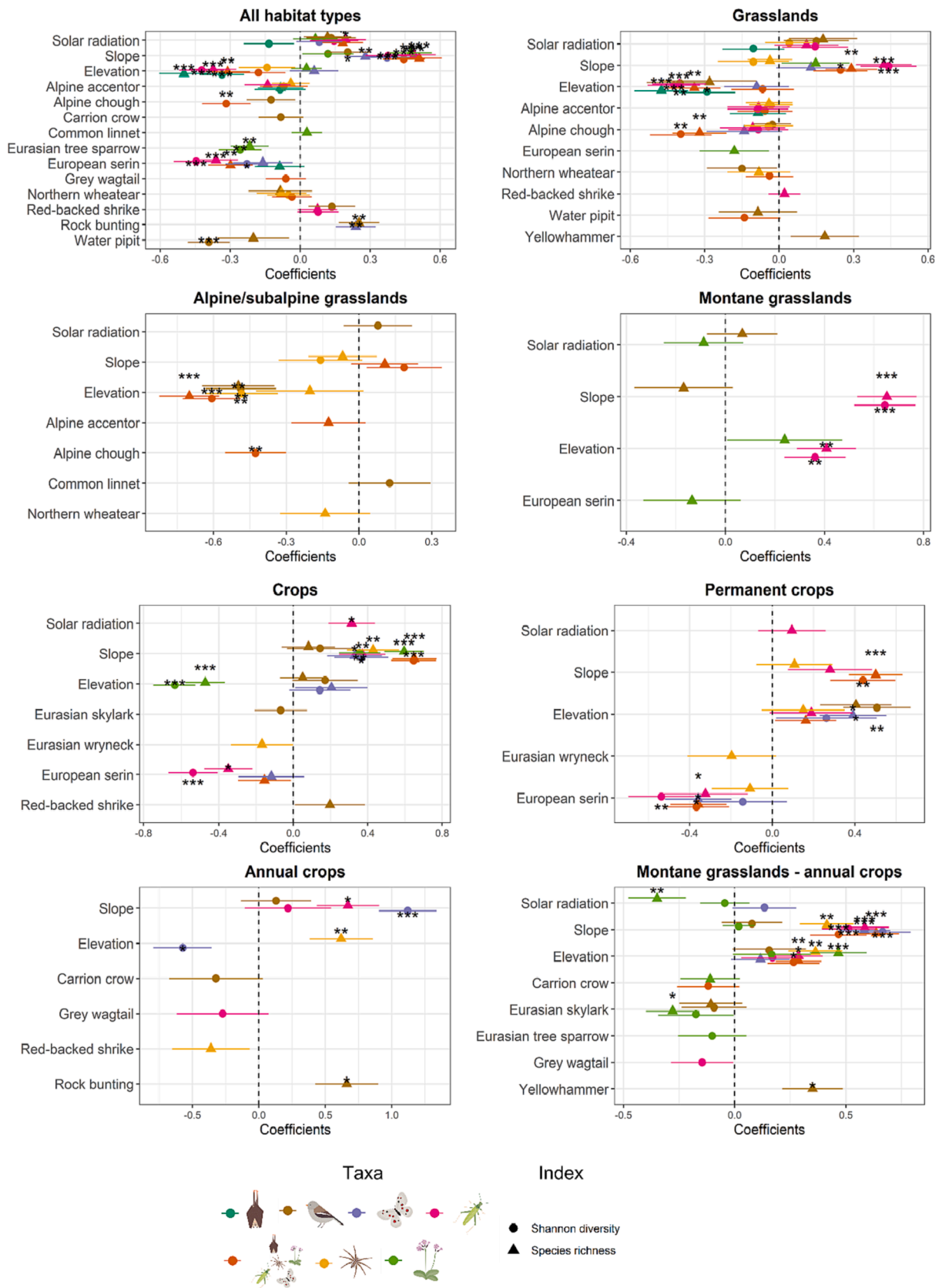
Fig. 4. Indicator species model averaging results, divided per habitat type. Different colours indicate the estimated coefficient of different taxa. * < 0.05, **< 0.01, and *** < 0.001.

years, e.g., at wintering sites (Fischer et al., 2020; Haest et al., 2020; Hu et al., 2021), the simultaneous surveys over several years represent a real added value of our approach.

4.1. Compositional dissimilarity of different communities

Some authors (e.g., Rooney and Bayley, 2012; Su et al., 2004) have argued that, in the context of conservation strategies, investigations of cross-taxon congruence should prioritise the analysis of congruence patterns in beta diversity. Beta diversity allows to assess the community similarity between two sites. Assessing changes in the composition of different communities in a given landscape or habitat may prove crucial to understanding why populations or taxa are responding in the same or different ways in the face of environmental changes. Indeed, ecological and environmental factors may affect different communities of different taxa, suggesting the need for diverse and targeted conservation efforts (Kühl et al., 2020).

Our results showed that the total bird community often changed consistently with other taxa communities, particularly for grasshoppers, which exhibited consistent compositional dissimilarity across all habitat types. For annual crops we found less concordance among different taxa community compositions, probably because birds are more sensitive to the environmental diversity of the surrounding landscape (Anderle et al., 2023). Other taxa are more sensitive to the site management itself. In addition, in this region, annual crops are mostly surrounded by other farmlands (Tasser et al., 2007).

Contrary to Bucher et al. (2019), in our study system arachnids showed good concordance with bird communities only in alpine/sub-alpine grasslands, which represent the most homogeneous landscape among the sampled ones. Alpine and subalpine bird and arachnid communities have similar ecological needs, e.g., they share high dispersal abilities, they have similar requirements for landscape heterogeneity, and both are predators of arthropods (Bonte et al., 2012; Bucher et al., 2019). Also, arachnids, together with other ground-dwelling invertebrates, are themselves an important resource for typical alpine birds (Rolando et al., 2006).

The composition of the bird indicator species changed consistently with all taxa communities in most habitat types. This result is very relevant because it allows the evaluation of community changes within grasslands and within the region, using only a few indicator species (14 in our case). In addition, where there is a lack of funding or specialist taxonomists for different taxa - an increasingly common situation - targeted monitoring using bird indicator species could provide a comprehensive understanding of grassland and regional biodiversity as a whole.

The strongest concordance observed in the dissimilarity matrices was between butterfly and total bird grassland communities. Given the increasing threats to extensively managed mountain grasslands and the large number of threatened species that depend on these habitats (Scholtz and Twidwell, 2022), it is noteworthy that there are relatively few monitoring schemes that focus on both taxa simultaneously (Kühl et al., 2020). Furthermore, the inclusion of a third taxon that is less consistent with the trends of these two (e.g., arachnids), could provide complementary information and thus improve our understanding of the overall biodiversity dependent on grasslands (Oberprieler et al., 2020).

4.2. Multi factor models

We modeled bird diversity indices alongside environmental variables to determine their efficiency in more complex scenarios. Our models revealed that the most efficient index depends on the taxon and the habitat type in question. Indeed, certain taxa were found to be associated with numerous indices, both taxonomic and functional, as was particularly the case for butterflies, vascular plants, grasshoppers, and arachnids. Furthermore, the best model always had more than one type of index (taxonomical or functional), proving that a single category

alone cannot best represent a particular taxon. Contrary to our expectations, bats (the only vertebrate in the response variables) responded in only a few models, primarily with indices related to threatened, and plant- and seed-eating birds. One possible explanation is that the two taxa exhibit different habitat uses. Bats use farmland primarily for feeding, leading to frequent commuting between their roosts (which can be quite distant) and their foraging areas. This dynamic behaviour results in a significant diversity of bat species and an abundance of passages within these habitat types (Mendes et al., 2017). In contrast, farmland landscapes tend to be relatively unique for specific farmland birds or less suitable for nesting passerine birds due to their high management intensity and landscape homogenisation, resulting in lower bird richness and diversity (Anderle et al., 2023).

Our models showed that butterflies and birds were significantly and positively associated, not only for community similarity, but also for species richness and Shannon diversity in all habitat types together, in grasslands and in crops, demonstrating that the diversity of the two taxa follows similar patterns along mountain farmlands. From this evidence, we conclude that both birds and butterflies seem to respond similarly to the present habitat types, and that conservation actions for one taxon are likely to have a positive impact on the other one. However, this evidence is based on the current state of knowledge, and future changes in both land-use and climate may lead to different responses, particularly as butterflies are highly dependent on extensive grasslands (Guariento et al., 2023) and their persistence, whereas birds are more responsive to landscape variables (Anderle et al., 2022).

Interestingly, for arachnids the most significant index was the farmland bird index, where high values for farmland species indicate lower arachnid species richness and Shannon diversity. This could be due to the very specific habitat types found in farmland, with fewer but more specialised arachnid species, but also most likely to different scales of response to environmental drivers. Another explanation could be related to the structure of farmland, e.g., permanent crops are more structured (grass, shrub, and tree layers) and offer more niches for arachnids (Theron et al., 2020), however, these habitats are not particularly suitable for farmland birds (community is mainly composed of common and generalist species; Reif et al., 2008). In the case of grasshoppers, functional diversity, and certain traits such as omnivore or the threat level of birds emerged as most significant factors. Once again, this highlights the importance of not relying solely on bird taxonomic indices. For vascular plants, it is interesting to note that there were no bird variables included in the models across different farmland. Very likely, the two taxa respond to different landscape scales. Vascular plants often respond to factors acting at the local scale, such as fine-grained land-use type, farming intensity, soil and microclimate, whereas birds tend to be more sensitive to factors operating at the landscape scale, thus being more affected by land-use composition and configuration (Anderle et al., 2022).

Cumulative indices (of all taxa together), were in general largely predicted by both bird taxonomic and functional indices. Specifically, bird species richness and threatened species seem to convey important insights into the taxonomic richness and diversity of the entire biodiversity present in all habitat types and within grasslands. Similarly, omnivorous birds can provide valuable information on the richness of the total biocenosis in crops, annual crops, and montane grasslands. In our models, we also evaluated indicator bird species to test if habitat-specific species can be used as a proxy for biodiversity in a particular landscape or at a regional scale. This is the first work to test this in a mountain region.

Our models showed that, unlike taxonomic and functional indices, species act as proxies for environmental variables by reflecting the intrinsic ecological characteristics of the species' own ecology. For example, Rock bunting appeared to be a good proxy for high environmental diversity by showing positive associations with butterflies. In contrast, European serin represented extremely intensive and homogeneous landscapes, leading to a negative association with other taxa. Red-

backed shrike showed negative associations with butterflies in montane landscapes and with arachnids in annual crops, and conversely positive associations with bird richness. This reflects the number of near-natural elements or patchy habitats present in croplands. These are important characteristics for birds (Anderle et al., 2022), but conversely, the fragmentation of grasslands has a negative impact on butterfly communities especially in croplands (Kormann et al., 2019). Alpine accentor and Alpine chough, species that rely on mountain rocks, were negatively associated with other habitat types, with bats, butterflies, grasshoppers, arachnids, and with cumulative biodiversity indices, a pattern that probably represents the negative effects of rocky areas on these taxa.

The results of the indicator bird species models are very important because they show how individual common species can be not only good ecological bioindicators (as it has been widely demonstrated, e.g., Morelli et al., 2021), but also good taxon-based bioindicators for the biodiversity present at regional scales. This implies that a pool of indicator species can be used to represent alpine biodiversity in Alpine farmlands. The interpretation of these patterns and a good knowledge of the ecology of the indicator species used can help define conservation measures and management practices to improve biodiversity. Finally, we believe that the use of individual indicator species is more promising when focusing on a specific habitat type rather than combining different ones. For instance, the case of Alpine accentor, a high-elevation specialist, highlights that using a specialist species in an Alpine ecological gradient could lead to trivial results due to the typically lower species richness of animal communities at higher elevations.

5. Conclusion

Our models showed that birds are efficient bioindicators of the diversity and composition of other taxa, and that incorporating different indices (taxonomic, functional, and single species) provides a more holistic view of their efficiency as bioindicators for broader biodiversity patterns and for the complexity of ecological interactions. The most efficient bird index varied by taxon and habitat type. This highlights the importance of selecting appropriate indices for specific research objectives. For example, we recommend the use of certain common species (European serin in permanent crops, Alpine accentor in alpine grasslands, and Red-backed shrike in montane landscapes) that can serve as valuable taxon-based bioindicators for specific habitat types or taxa. The ecological characteristics of these indicator species provide insights into the overall biodiversity and can inform conservation strategies.

The study emphasises the importance of regional-scale investigations, as regional policies often play a crucial role in biodiversity management and conservation strategies. The regional (or sub-national) scale is a practical level for implementing conservation measures in response to global change.

We emphasise the importance of multi-taxon monitoring schemes to gain a comprehensive understanding of regional biodiversity. Our study reveals that different taxa, such as birds, arachnids, and bats, respond differently to environmental factors at different scales but can be partially predicted/explained by specific bird indices.

In conclusion, we recommend that in ecological and conservation studies, in addition to indices of species richness and functional diversity, an index of threatened species and an index of farmland species (or specialist species of the habitat type being monitored) should be included in the models. In addition, including single indicator species can further improve the models, providing a more comprehensive representation of overall biodiversity and ecological patterns.

CRediT authorship contribution statement

Matteo Anderle: Conceptualization, Writing – review & editing, Writing – original draft, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Mattia Brambilla:** Conceptualization, Writing – review & editing, Validation, Supervision, Conceptualization. **Lisa Angelini:** Writing – review & editing, Investigation, Data curation. **Elia Guariento:** Writing – review & editing, Investigation, Data curation. **Chiara Paniccia:** Writing – review & editing, Investigation, Data curation. **Julia Plunger:** Writing – review & editing, Supervision. **Julia Seeber:** Writing – review & editing, Supervision. **Simon Stifter:** Writing – review & editing, Investigation. **Ulrike Tappeiner:** Writing – review & editing, Funding acquisition. **Erich Tasser:** Writing – review & editing, Supervision. **Andreas Hilpold:** Conceptualization, Writing – review & editing, Supervision, Project administration, Investigation, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ecolind.2024.111569.

References

Anderle, M., Brambilla, M., Hilpold, A., Matabishi, J.G., Paniccia, C., Rocchini, D., Rossin, J., Tasser, E., Torresani, M., Tappeiner, U., Seeber, J., 2023. Habitat heterogeneity promotes bird diversity in agricultural landscapes: Insights from remote sensing data. Basic Appl. Ecol. 70, 38–49. https://doi.org/10.1016/j.baae.2023.04.006.

Anderle, M., Paniccia, C., Mattia Brambilla, ·, Hilpold, A., Volani, S., Tasser, E., Seeber, J., Tappeiner, U., 2022. The contribution of landscape features, climate and topography in shaping taxonomical and functional diversity of avian communities in a heterogeneous Alpine region. Oecologia 199, 499–512. https://doi.org/10.1007/s00442-022-05134-7.

Arnold, T.W., 2010. Uninformative parameters and model selection Using Akaike's information criterion. J. Wildl. Manage. 74, 1175–1178. https://doi.org/10.2193/2009-367.

Balmford, A., Bond, W., 2005. Trends in the state of nature and their implications for human well-being. Ecol. Lett. 8, 1218–1234. https://doi.org/0.1111/j.1461-0248.2005.00814.x.

Barataud, M., 2020. Acoustic Ecology of European bats: Species Identification, Study of their Habitats and Foraging Behaviour, 2nd ed., BIOTOPE, Mèze. ed.

Barton, K., 2020. Package ' MuMIn'. Multi-Model Inference R Package Version 1.43.17.

Bonte, D., Van Dyck, H., Bullock, J.M., Coulon, A., Delgado, M., Gibbs, M., Lehouck, V., Matthysen, E., Mustin, K., Saastamoinen, M., Schtickzelle, N., Stevens, V.M., Vandewoestijne, S., Baguette, M., Barton, K., Benton, T.G., Chaput-Bardy, A., Clobert, J., Dytham, C., Hovestadt, T., Meier, C.M., Palmer, S.C.F., Turlure, C., Travis, J.M.J., 2012. Costs of dispersal. Biol. Rev. 87, 290–312. https://doi.org/10.1111/j.1469-185X.2011.00201.x.

Brunbjerg, A.K., Bruun, H.H., Dalby, L., Fløjgaard, C., Frøslev, T.G., Høye, T.T., Goldberg, I., Læssøe, T., Hansen, M.D.D., Brøndum, L., Skipper, L., Fog, K., Ejrnæs, R., 2018. Vascular plant species richness and bioindication predict multi-taxon species richness. Methods Ecol. Evol. 9, 2372–2382. https://doi.org/10.1111/2041-210X.13087.

Bucher, R., Nickel, H., Kaib, S., Will, M., Carchi, J., Farwig, N., Schabo, D.G., 2019. Birds and plants as indicators of arthropod species richness in temperate farmland. Ecol. Indic. 103, 272–279. https://doi.org/10.1016/j.ecolind.2019.04.011.

Buckland, S.T., Studeny, A.C., Magurran, A.E., Illian, J.B., Newson, S.E., 2011. The geometric mean of relative abundance indices: a biodiversity measure with a difference. Ecosphere 2, art100. https://doi.org/10.1890/ES11-00186.1.

Burnham, K.P., Anderson, D.R., 2004. Model Selection and Multimodel Inference, Model Selection and Multimodel Inference. https://doi.org/10.1007/b97636.

Burrascano, S., de Andrade, R.B., Paillet, Y., Ódor, P., Antonini, G., Bouget, C., Campagnaro, T., Gosselin, F., Janssen, P., Persiani, A.M., Nascimbene, J., Sabatini, F. M., Sitzia, C., Blasi, C., 2018. Congruence across taxa and spatial scales: Are we asking too much of species data? Glob. Ecol. Biogeogr. 27, 980–990. https://doi.org/10.1111/geb.12766.

Ceresa, F., Brambilla, M., Kvist, L., Vitulano, S., Pes, M., Tomasi, L., Pedrini, P., Hilpold, A., Kranebitter, P., 2023. Landscape characteristics influence regional dispersal in a high-elevation specialist migratory bird, the water pipit Anthus spinoletta. Mol. Ecol. 32, 1875–1892. https://doi.org/10.1111/mec.16853.

Ceresa, F., Kranebitter, P., 2020. Lista Rossa 2020 degli uccelli nidificanti in Alto Adige. Gredleriana. https://doi.org/10.5281/ZENODO.4245030.

Chiatante, G., Pellitteri-Rosa, D., Torretta, E., Nonnis Marzano, F., Meriggi, A., 2021. Indicators of biodiversity in an intensively cultivated and heavily human modified landscape. Ecol. Indic. 130, 108060 https://doi.org/10.1016/j.ecolind.2021.108060.

Chiu, C., 2023. Sample coverage estimation, rarefaction, and extrapolation based on sample-based abundance data. Ecology 104. https://doi.org/10.1002/ecy.4099.

Crespi, A., Matiu, M., Bertoldi, G., Petitta, M., Zebisch, M., 2021. A high-resolution gridded dataset of daily temperature and precipitation records (1980–2018) for Trentino-South Tyrol (north-eastern Italian Alps). Earth Syst. Sci. Data 13, 2801–2818. https://doi.org/10.5194/essd-13-2801-2021.

De Cáceres, M., Jansen, F., Dell, N., 2020. 'indicspecies' R Package - Relationship Between Species and Groups of Sites.

De Cáceres, M., Legendre, P., Wiser, S.K., Brotons, L., 2012. Using species combinations in indicator value analyses. Methods Ecol. Evol. 3, 973–982. https://doi.org/10.1111/j.2041-210X.2012.00246.x.

Dengler, J., Boch, S., Filibeck, G., Chiarucci, A., Dembicz, I., Guarino, R., Henneberg, B., Janišová, M., Marcenò, C., Naqinezhad, A., Polchaninova, N.Y., Vassilev, K., Biurrun, I., 2016. Assessing plant diversity and composition in grass- lands across spatial scales: the standardised EDGG sampling methodology. Bull. Eurasian Dry Grassl. Gr. 13–30.

Dufrene, M., Legendre, P., 1997. Species Assemblages and Indicator Species: The Need for a Flexible Asymmetrical Approach. Ecol. Monogr. 67, 345. https://doi.org/10.2307/2963459.

Eglington, S.M., Noble, D.G., Fuller, R.J., 2012a. A meta-analysis of spatial relationships in species richness across taxa: Birds as indicators of wider biodiversity in temperate regions. J. Nat. Conserv. https://doi.org/10.1016/j.jnc.2012.07.002.

Eglington, S.M., Noble, D.G., Fuller, R.J., 2012b. A meta-analysis of spatial relationships in species richness across taxa: Birds as indicators of wider biodiversity in temperate regions. J. Nat. Conserv. 20, 301–309. https://doi.org/10.1016/j.jnc.2012.07.002.

Elkon AG, 2023. BatExplorer 2.2 User Guide.

Fischer, F.M., Chytrý, K., Těšitel, J., Danihelka, J., Chytrý, M., 2020. Weather fluctuations drive short-term dynamics and long-term stability in plant communities: A 25-year study in a Central European dry grassland. J. Veg. Sci. 31, 711–721. https://doi.org/10.1111/jvs.12895.

Furness, R.W., Greenwood, J.J.D., 1993. Birds as Monitors of Environmental Change. Springer Netherlands, Dordrecht. https://doi.org/10.1007/978-94-015-1322-7.

Gaston, K.J., Blackburn, T.M., Goldewijk, K.K., 2003. Habitat conversion and global avian biodiversity loss. Proc. R Soc. London. Ser. B Biol. Sci. 270, 1293–1300. https://doi.org/10.1098/rspb.2002.2303.

Gioria, M., Bacaro, G., Feehan, J., 2011. Evaluating and interpreting cross-taxon congruence: Potential pitfalls and solutions. Acta Oecol. 37, 187–194. https://doi.org/10.1016/j.actao.2011.02.001.

Gregory, R.D., van Strien, A., Vorisek, P., Gmelig Meyling, A.W., Noble, D.G., Foppen, R. P., Gibbons, D.W., 2005. Developing indicators for European birds. Philos. Trans. R. Soc. B Biol. Sci. 360, 269–288. https://doi.org/10.1098/rstb.2004.1602.

Guariento, E., Rüdisser, J., Fiedler, K., Paniccia, C., Stifter, S., Tappeiner, U., Seeber, J., Hilpold, A., 2023. From diverse to simple: butterfly communities erode from extensive grasslands to intensively used farmland and urban areas. Biodivers. Conserv. 32, 867–882. https://doi.org/10.1007/s10531-022-02498-3.

Haest, B., Hüppop, O., Bairlein, F., 2020. Weather at the winter and stopover areas determines spring migration onset, progress, and advancements in Afro-Palearctic migrant birds. Proc. Natl. Acad. Sci. 117, 17056–17062. https://doi.org/10.1073/pnas.1920448117.

Hartig, F., 2020. DHARMa: residual diagnostics for hierarchical (multi-level/mixed) regression models.

Hess, G.R., Bartel, R.A., Leidner, A.K., Rosenfeld, K.M., Rubino, M.J., Snider, S.B., Ricketts, T.H., 2006. Effectiveness of biodiversity indicators varies with extent, grain, and region. Biol. Conserv. 132, 448–457. https://doi.org/10.1016/j.biocon.2006.04.037.

Hilpold, A., Anderle, M., Guariento, E., Marsoner, T., Mina, M., Paniccia, C., Plunger, J., Rigo, F., Rüdisser, J., Scotti, A., Seeber, J., Steinwandter, M., Stifter, S., Strobl, J., Suarez-Muñoz, M., Vanek, M., Bottarin, R., Tappeiner, U., 2023. Handbook Biodiversity Monitoring South Tyrol, Eurac Research. https://doi.org/10.57749/2qm9-fq40.

Hilpold, A., Kirschner, P., Dengler, J., 2020. Scientific Report - Proposal of a standardized EDGG surveying methodology for orthopteroid insects. Palaearct. Grasslands - J. Eurasian Dry Grassl. Gr, 52–57. https://doi.org/10.21570/EDGG.PG.46.52-57.

Hinojosa, L., Tasser, E., Rüdisser, J., Leitinger, G., Schermer, M., Lambin, E.F., Tappeiner, U., 2019. Geographical heterogeneity in mountain grasslands dynamics in the Austrian-Italian Tyrol region. Appl. Geogr. 106, 50–59. https://doi.org/10.1016/j.apgeog.2019.03.006.

Hsieh, T.C., Ma, K.H., Chao, A., 2016. iNEXT: an R package for rarefaction and extrapolation of species diversity (<scp>H</scp> ill numbers). Methods Ecol. Evol. 7, 1451–1456. https://doi.org/10.1111/2041-210X.12613.

Hu, G., Stefanescu, C., Oliver, T.H., Roy, D.B., Brereton, T., Van Swaay, C., Reynolds, D. R., Chapman, J.W., 2021. Environmental drivers of annual population fluctuations in a trans-Saharan insect migrant. Proc. Natl. Acad. Sci. 118 https://doi.org/10.1073/pnas.2102762118.

Huber, U.M., Bugmann, H.K., Reasoner, M.A., 2005. Global Change and Mountain Regions. Springer, Netherlands, Dordrecht. https://doi.org/10.1007/1-4020-3508-X.

Jamwal, P.S., Di Febbraro, M., Carranza, M.L., Savage, M., Loy, A., 2022. Global change on the roof of the world: Vulnerability of Himalayan otter species to land use and climate alterations. Divers. Distrib. 28, 1635–1649. https://doi.org/10.1111/ddi.13377.

Korell, L., Auge, H., Chase, J.M., Harpole, W.S., Knight, T.M., 2021. Responses of plant diversity to precipitation change are strongest at local spatial scales and in drylands. Nat. Commun. 12, 2489. https://doi.org/10.1038/s41467-021-22766-0.

Kormann, U.G., Scherber, C., Tscharntke, T., Batáry, P., Rösch, V., 2019. Connectedness of habitat fragments boosts conservation benefits for butterflies, but only in landscapes with little cropland. Landsc. Ecol. 34, 1045–1056. https://doi.org/10.1007/s10980-019-00835-6.

Kühl, H.S., Bowler, D.E., Bösch, L., Bruelheide, H., Dauber, J., Eichenberg, D., Eisenhauer, N., Fernández, N., Guerra, C.A., Henle, K., Herbinger, I., Isaac, N.J.B., Jansen, F., König-Ries, B., Kühn, I., Nilsen, E.B., Pe'er, G., Richter, A., Schulte, R., Settele, J., van Dam, N.M., Voigt, M., Wägele, W.J., Wirth, C., Bonn, A., 2020. Effective Biodiversity Monitoring Needs a Culture of Integration. One Earth 3, 462–474. https://doi.org/10.1016/j.oneear.2020.09.010.

Laliberté, Etienne, Legendre, P., Shipley, B., 2014. FD: Measuring Functional Diversity (FD) from Multiple Traits, and Other Tools for Functional Ecology. R package version 1.0-12.1.

Li, L., Tietze, D.T., Fritz, A., Basile, M., Lü, Z., Storch, I., 2022. Beta diversities of grassland birds indicate the importance of pastoralism for nature conservation of the Qinghai-Tibetan plateau. Front. Conserv. Sci. 3 https://doi.org/10.3389/fcosc.2022.902887.

Lindenmayer, D.B., Barton, P.S., Lane, P.W., Westgate, M.J., Mcburney, L., 2014. An Empirical Assessment and Comparison of Species-Based and Habitat-Based Surrogates: A Case Study of Forest Vertebrates and Large Old Trees. PLoS One 9, 89807. https://doi.org/10.1371/journal.pone.0089807.

Lindenmayer, D., Pierson, J., Barton, P., Beger, M., Branquinho, C., Calhoun, A., Caro, T., Greig, H., Gross, J., Heino, J., Hunter, M., Lane, P., Longo, C., Martin, K., McDowell, W.H., Mellin, C., Salo, H., Tulloch, A., Westgate, M., 2015. A new framework for selecting environmental surrogates. Sci. Total Environ. https://doi.org/10.1016/j.scitotenv.2015.08.056.

Martin, K., José, T.I., Mark, D., 2015. Avian surrogates in terrestrial ecosystems: theory and practice. In: Lindenmayer, D., Barton, P., Pierson, J. (Eds.), Indicators and Surrogates of Biodiversity and Environmental Change. CSIRO Publishing, Melbourne Australia, pp. 33–44.

Mendes, E.S., Fonseca, C., Marques, S.F., Maia, D., Ramos Pereira, M.J., 2017. Bat richness and activity in heterogeneous landscapes: guild-specific and scale-dependent? Landsc. Ecol. 32, 295–311. https://doi.org/10.1007/s10980-016-0444-0.

Morelli, F., Reif, J., Díaz, M., Tryjanowski, P., Ibáñez-Álamo, J.D., Suhonen, J., Jokimäki, J., Kaisanlahti-Jokimäki, M.-L., Pape Møller, A., Bussière, R., Mägi, M., Kominos, T., Galanaki, A., Bukas, N., Markó, G., Pruscini, F., Jerzak, L., Ciebiera, O., Benedetti, Y., 2021. Top ten birds indicators of high environmental quality in European cities. Ecol. Indic. 133, 108397 https://doi.org/10.1016/j.ecolind.2021.108397.

Moretti, M., Dias, A.T.C., de Bello, F., Altermatt, F., Chown, S.L., Azcárate, F.M., Bell, J. R., Fournier, B., Hedde, M., Hortal, J., Ibanez, S., Öckinger, E., Sousa, J.P., Ellers, J., Berg, M.P., 2017. Handbook of protocols for standardized measurement of terrestrial invertebrate functional traits. Funct. Ecol. 31, 558–567. https://doi.org/10.1111/1365-2435.12776.

Rete Rurale Nazionale, LIPU, 2020. Common breeding farmland birds in Italy. Update of population trends and Farmland Bird Indicator for National Rural Network 2000-2015.

Oberprieler, S.K., Andersen, A.N., Yeates, D.K., 2020. Selecting complementary target taxa for representing terrestrial invertebrate diversity in the Australian seasonal tropics. Ecol. Indic. 109, 105836 https://doi.org/10.1016/j.ecolind.2019.105836.

Pearman, P.B., Weber, D., 2007. Common species determine richness patterns in biodiversity indicator taxa. Biol. Conserv. 138, 109–119. https://doi.org/10.1016/j.biocon.2007.04.005.

Reif, J., Voříšek, P., Šťastný, K., Bejček, V., Petr, J., 2008. Agricultural intensification and farmland birds: new insights from a central European country. Ibis (Lond. 1859). 150, 596–605. https://doi.org/10.1111/j.1474-919X.2008.00829.x.

Roberts, D.W., 2019. "labdsv" R Package - Ordination and Multivariate Analysis for Ecology.

Rodrigues, A.S.L., Brooks, T.M., Rodrigues', A.S.L., Brooks2', T.M., 2007. Shortcuts for Biodiversity Conservation Planning: The Effectiveness of Surrogates. Source Annu. Rev. Ecol. 38, 713–737. https://doi.org/10.1.

Rolando, A., Caprio, E., Rinaldi, E., Ellena, I., 2006. The impact of high-altitude ski-runs on alpine grassland bird communities. J. Appl. Ecol. 44, 210–219. https://doi.org/10.1111/j.1365-2664.2006.01253.x.

Rooney, R.C., Bayley, S.E., 2012. Community congruence of plants, invertebrates and birds in natural and constructed shallow open-water wetlands: Do we need to monitor multiple assemblages? Ecol. Indic. 20, 42–50. https://doi.org/10.1016/j.ecolind.2011.11.029.

Roswell, M., Dushoff, J., Winfree, R., 2021. A conceptual guide to measuring species diversity. Oikos 130, 321–338. https://doi.org/10.1111/oik.07202.

Sauberer, N., Zulka, K.P., Abensperg-Traun, M., Berg, H.-M., Bieringer, G., Milasowszky, N., Moser, D., Plutzar, C., Pollheimer, M., Storch, C., Tröstl, R., Zechmeister, H., Grabherr, G., 2004. Surrogate taxa for biodiversity in agricultural landscapes of eastern Austria. Biol. Conserv. 117, 181–190. https://doi.org/10.1016/S0006-3207(03)00291-X.

Scholtz, R., Twidwell, D., 2022. The last continuous grasslands on Earth: Identification and conservation importance. Conserv. Sci. Pract. 4 https://doi.org/10.1111/csp2.626.

Scridel, D., Brambilla, M., Martin, K., Lehikoinen, A., Iemma, A., Matteo, A., Jähnig, S., Caprio, E., Bogliani, G., Pedrini, P., Rolando, A., Arlettaz, R., Chamberlain, D., 2018. A review and meta-analysis of the effects of climate change on Holarctic mountain and upland bird populations. Ibis (Lond. 1859). 160, 489–515. https://doi.org/10.1111/ibi.12585.

Sekercioglu, Ç.H., Wenny, D.G., Whelan, C.J., 2016. Why birds matter: avian ecological function and ecosystem services., Eds. ed.

Simamora, T.I., Purbowo, S.D., Laumonier, Y., 2021. Looking for indicator bird species in the context of forest fragmentation and isolation in West Kalimantan. Indonesia. Glob. Ecol. Conserv. 27, e01610.

Souza, G.B.G., Vianna, M., 2022. Challenges in identifying indicator fish species in highly dynamic systems such as estuaries. Estuar. Coast. Shelf Sci. 276 https://doi.org/10.1016/j.ecss.2022.108019.

Su, J.C., Debinski, D.M., Jakubauskas, M.E., Kindscher, K., 2004. Beyond Species Richness: Community Similarity as a Measure of Cross-Taxon Congruence for Coarse-Filter Conservation. Conserv. Biol. 18, 167–173. https://doi.org/10.1111/j.1523-1739.2004.00337.x.

Tasser, E., Walde, J., Tappeiner, U., Teutsch, A., Noggler, W., 2007. Land-use changes and natural reforestation in the Eastern Central Alps. Agric. Ecosyst. Environ. 118, 115–129. https://doi.org/10.1016/j.agee.2006.05.004.

Tasser, E., Unterthurner, B., Agreiter, A., Aukenthaler, H., Gerstgrasser, L., Giardino, M., Tappeiner, U., Rüdisser, J., 2023. Long-term game species dynamic as indicator for changing landscape quality. Sci. Total Environ. 874, 162375 https://doi.org/10.1016/j.scitotenv.2023.162375.

Terrigeol, A., Ewane Ebouele, S., Darveau, M., Hébert, C., Rivest, L.P., Fortin, D., 2022. On the efficiency of indicator species for broad-scale monitoring of bird diversity across climate conditions. Ecol. Indic. 137 https://doi.org/10.1016/j.ecolind.2022.108773.

Theron, K.J., Gaigher, R., Pryke, J.S., Samways, M.J., 2020. High quality remnant patches in a complex agricultural landscape sustain high spider diversity. Biol. Conserv. 243, 108480 https://doi.org/10.1016/j.biocon.2020.108480.

Tittensor, D.P., Walpole, M., Hill, S.L.L., Boyce, D.G., Britten, G.L., Burgess, N.D., Butchart, S.H.M., Leadley, P.W., Regan, E.C., Alkemade, R., Baumung, R., Bellard, C., Bouwman, L., Bowles-Newark, N.J., Chenery, A.M., Cheung, W.W.L., Christensen, V., Cooper, H.D., Crowther, A.R., Dixon, M.J.R., Galli, A., Gaveau, V., Gregory, R.D., Gutierrez, N.L., Hirsch, T.L., Höft, R., Januchowski-Hartley, S.R., Karmann, M., Krug, C.B., Leverington, F.J., Loh, J., Lojenga, R.K., Malsch, K., Marques, A., Morgan, D.H.W., Mumby, P.J., Newbold, T., Noonan-Mooney, K., Pagad, S.N., Parks, B.C., Pereira, H.M., Robertson, T., Rondinini, C., Santini, L., Scharlemann, J.P.W., Schindler, S., Sumaila, U.R., Teh, L.S.L., Van Kolck, J., Visconti, P., Ye, Y., 2014. A mid-term analysis of progress toward international biodiversity targets. Science (80-.). 346, 241–244. https://doi.org/10.1126/science.1257484.

Turtureanu, P.D., Palpurina, S., Becker, T., Dolnik, C., Ruprecht, E., Sutcliffe, L.M.E., Szabó, A., Dengler, J., 2014. Scale- and taxon-dependent biodiversity patterns of dry grassland vegetation in Transylvania. Agric. Ecosyst. Environ. 182, 15–24. https://doi.org/10.1016/j.agee.2013.10.028.

Turvey, S.T., Crees, J.J., 2019. Extinction in the Anthropocene. Curr. Biol. 29, R982–R986.

Valerio, F., Basile, M., Balestrieri, R., Posillico, M., Di Donato, S., Altea, T., Matteucci, G., 2016. The reliability of a composite biodiversity indicator in predicting bird species richness at different spatial scales. Ecol. Indic. 71, 627–635. https://doi.org/10.1016/j.ecolind.2016.07.043.

Wilman, H., Belmaker, J., Simpson, J., de la Rosa, C., Rivadeneira, M.M., Jetz, W., 2014. EltonTraits 1.0: Species-level foraging attributes of the world's birds and mammals. Ecology 95, 2027. https://doi.org/10.1890/13-1917.1.

Yong, D.L., Barton, P.S., Ikin, K., Evans, M.J., Crane, M., Okada, S., Cunningham, S.A., Lindenmayer, D.B., 2018. Cross-taxonomic surrogates for biodiversity conservation in human-modified landscapes – A multi-taxa approach. Biol. Conserv. 224, 336–346. https://doi.org/10.1016/j.biocon.2018.06.008.

Zuur, A.F., Ieno, E.N., Elphick, C.S., 2010. A protocol for data exploration to avoid common statistical problems. Methods Ecol. Evol. 1, 3–14. https://doi.org/10.1111/j.2041-210X.2009.00001.x.

Zuur, A.F., Hilbe, J.M., Ieno, E.N., 2013. A Beginner's Guide to GLM and GLMM with R. Beginner's Guide Series.