



Original Articles

Cuckoo density as a predictor of functional and phylogenetic species richness in the predictive modelling approach: Extension of Tryjanowski and Morelli (2015) paradigm in the analytical context

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ABSTRACT

The Common Cuckoo *Cuculus canorus* is a well known brood parasite bird species whose density is presumed to be correlated with taxonomic, functional and phylogenetic bird species richness. However, due to the complex interplay between environmental estimates and co-evolutionary processes, the power of this relationship is still debatable. Various attempts to create statistical models have not been conclusive, because multilevel interactions between Cuckoo density, environmental conditions, and host species richness measurements have not been addressed so far. Therefore, we extended the concept of the Cuckoo as an independent bird biodiversity surrogate, and instead of simply using its occurrence, we incorporated an index of its density as an additional predictor in the modelling procedure of avian biodiversity. We applied six different indices of biodiversity as bird species richness measures, i.e. the number of bird individuals, the number of host species richness, functional richness, functional evenness, functional divergence, and evolutionary distinctiveness. We generated two sets of Species Distribution Models (SDM) for each group of biodiversity measures. One set included Cuckoo density as an additional predictor, while the other did not. Having evaluated these models in the Random Forest approach, it turned out that Cuckoo density improved model performance in each case. Species density was positively associated with taxonomic diversity (total species richness and host species richness), functional richness and evolutionary distinctiveness, and at the same time it was negatively correlated with functional evenness and functional divergence of bird communities. Thus, we suggest that through co-evolution of relationships, the Cuckoo prefers habitats attractive to numerous bird species, especially phylogenetically unique host. From the applied ecology perspective, Cuckoo density can be considered as a quantitative measure of functional interaction processes in the SDM approach, leading to the identification of avian diversity surrogates.

1. Introduction

Identifying and describing mechanisms of species distribution is a central topic in conservation biology and biogeographical studies (Shabani et al., 2016; Fink et al., 2017; Parker and Abatzoglou, 2017; Villero et al., 2017). Usually linked with a complex interplay between environmental estimates and landscape heterogeneity, it has spawned a large body of research on possible drivers of the observed distribution of organisms (Guisan and Zimmermann, 2000; Ay, et al., 2017; Sheehan et al., 2017). As a side issue, it also promoted further research on interactions between species, because coexisting biotic elements as well as processes of co-evolution also play an important role in species distribution patterns (Poulin and Morand, 2005; Thompson, 2005; Wisz

et al., 2013; Gavish et al., 2017; Morelli and Tryjanowski, 2014; Morelli et al., 2015; Godsoe et al., 2017). Co-evolution is a process in which evolutionary changes of one species result from interactions with other species (Møller et al., 2011a,b). Therefore, it is not surprising that a lot of charismatic co-occurring organisms, especially predators (Kosicki et al., 2016) and brood parasites (Tryjanowski and Morelli, 2015), as well as the effect of their mutual interactions (Kosicki and Chylarecki, 2014; Morelli and Tryjanowski, 2014), were suggested to be suitable independent predictors in analyses aimed at explaining species distribution.

From the applied ecology viewpoint, these coexisting, easy to detect species, which are chosen on the basis of biological/evolutionary processes, are also often used as surrogates of elusive ecological processes

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(Lindenmayer et al., 2015). However, due to complex multilevel interactions between environmental components, biotic interactions and species richness, the effectiveness of surrogates is still a subject of debate, especially in the context of a functional and phylogenetic community (Grantham et al., 2010; Marfil-Daza et al., 2013; Lindenmayer et al., 2015; Tolvanen et al., 2017; Cernansky, 2017).

Species coexistence processes and functions that species play in the ecosystem can be revealed using different biodiversity measures (Petchey and Gaston, 2006). Functional diversity is probably one of the most important components of biodiversity, where species occurrence and their density are linked with the ecosystem's functioning and environmental components (Hillebrand and Matthiessen, 2009; Cernansky, 2017). On the other hand, phylogenetic diversity measures evolutionary relationships between species in a landscape, thus helping to evaluate diversity in a community not only at the functional, but also evolutionary level (Tucker et al., 2016). Thus, the most informative surrogate of biodiversity should reflect both the number of species in a given community (as literature usually demonstrates, e.g. Calladine et al., 2017; Yong et al., 2016) and functional and phylogenetic interactions between them (Lindenmayer et al., 2015; Morelli et al., 2017).

One of the species suggested to effectively reflect higher avian species richness at phylogenetic and functional levels is the Common Cuckoo *Cululus canorus* Linnaeus, 1758 (e.g. Morelli et al., 2017). However, due to ecological constraints that can potentially limit the application of this species as a bird diversity surrogate, the concept is still debated (*sensu* Caro and O'Doherty, 1999). Apart from many attributes, an ideal indicator (surrogate) should be the most important predictor on a large scale in the predictive mapping approach, regardless of the method used (Caro and O'Doherty, 1999; Sebek et al., 2012; Kosicki et al., 2016). The most recent research in this field (Morelli et al., 2017) has not addressed the issue, because predictive models with and without Cuckoo density as an additional predictor have not been evaluated yet. So far, only Cuckoo occurrence was used as a predictor, while the influence of its index of density on species richness has been broadly neglected (e.g. Tryjanowski and Morelli, 2015; Morelli et al., 2017).

For this reason, we decided to extend the paradigm of Tryjanowski and Morelli's (2015) and Morelli's et al. (2017), and use Cuckoo density as an additional independent variable for six biodiversity measures in the predictive modelling approach. Nevertheless, the most common problem of such models is optimisation, because species distribution modelling employs a number of predictors that may affect species diversity in many ways (Seppelt and Voinov, 2002; Hof, et al., 2012; Carrasco et al., 2014; Kosicki, 2017). As a result, various models often have contrasting results (Gottfried et al., 1999; Guisán and Theurillat, 2000; Elith and Graham, 2009; Mattsson et al., 2013; Kosicki, 2017). The best solution to the problem is probably to use machine learning methods. From a wide range of methods, the Random Forest is considered to be the most suitable (Ismail and Mutanga, 2010; Vincenzi et al., 2011). It is a non-parametric regression which has a potential to deal with complex relationships between predictors that result from noise and a large amount of data, influenced in many ways by dependent variables (Breiman, 2001; Ismail and Mutanga, 2010; Vincenzi et al., 2011). Importantly, instead of constructing the "best model", the RF tool creates a lot of specific models based on randomly perturbed data that improve prediction efficiency (Prasad et al., 2006; Virkkala et al., 2010; Mutanga et al., 2012), and simultaneously provides model evaluation based on the out-of-bag error. However, apart from the construction of many trees and random evaluation, a cross-validation test of model quality is also necessary. Therefore, in our study we used an independent dataset to evaluate the obtained results to see if they reflected the real situation in the environment (Fourcade, 2016).

Considering the above-mentioned, we tested the usefulness of the Common Cuckoo as a predictor of taxonomic, functional, and phylogenetic species richness. The species is common in Poland (Sikora et al., 2007) and widely recognised. The mean density is ~ 0.28 pair/km²

(Kuczyński and Chylarecki, 2012; Kosicki and Chylarecki, 2014) and the gradient of its occurrence increases from northern to southern parts of the country (Sikora et al., 2007). It should be also noted that it is easy to detect during the breeding season due to its loud and generally known vocalisation (Tomiałojć and Stawarczyk, 2003). The Cuckoo is an obligatory brood parasite that exploits reproductive behaviour of numerous insectivorous passerines to fulfil its reproductive needs (Soler et al., 1999; Stokke et al., 2007; Davies, 2011; Wesołowski and Mokwa, 2013; Tolvanen et al., 2017), an interaction that proves its tight co-evolution (Krüger et al., 2009). For this reason, we suspected that Cuckoo density should correlate with species richness. However, brood parasite density and species diversity are also expected to vary, depending on different habitat types and/or other environmental aspects, e.g. climate, topography and vegetation (Tolvanen et al., 2017). Thus, the first step was to develop a species distribution model of Cuckoo density, and then two kinds of models for each measure of bird biodiversity, i.e. with and without Cuckoo density as an additional predictor. By comparing effectiveness of models with and without the Cuckoo, potential surrogates could be evaluated.

The aim of our study is to extend the paradigm of Morelli et al. (2017) and Tryjanowski and Morelli (2015), and use Cuckoo density as an additional independent variable for six biodiversity measures in the predictive modelling approach. For this purpose, we developed and evaluated predictive mechanistic models for taxonomic, functional and phylogenetic species richness with and without Cuckoo density as an additional predictor in the SDM approach.

2. Material and methods

2.1. Bird data

Cuckoo density, number of bird species and their density were derived from the Common Breeding Birds Monitoring Scheme (Chylarecki and Jawinska, 2007), and collected in Poland in years 2000–2013 in 970 1 km² grid cells (see Appendix A, Fig. S1). Each square was chosen randomly out of 311,664 1 km² squares covering all Poland. In particular breeding seasons each grid cell was surveyed twice (first between 10 April and 15 May; second between 16 May and 30 June). Each survey started between the dawn and 9 am and lasted about 90 min. Birds were noted perpendicular to two parallel 1 km transects along an east-west or north-south axis, and recorded in three distance categories (< 25 m, 25–100 m, > 100 m). The surveys were carried out by ornithologists-volunteers. Observers noted all birds seen or heard in the field; in the case of the Common Cuckoo recorded calling males prevailed, as visual contact with non-vocalising individuals of this species was rather scarce during the survey (see: Bibby et al., 2000).

2.2. Environmental data source

As predictors we used various environmental data coming from different GIS databases. All data were converted into GRASS GIS (GRASS Development Team, 2015) with the grid size of 1 km², and re-projected to the coordinate system EPSG4284 projection (<http://spatialreference.org/ref/epsg/4284/>).

Topographic metrics data were derived from the SRTM database (Jarvis et al., 2008). We used four topographic metrics related to each grid square, such as elevation (mean altitude in the square); aspect (0° means the slope faces the North, 90° – the East, 180° – the South, and 270° – the West); roughness (largest inter-cell difference of a central pixel and its surrounding cell); and slope (the average slope in the square expressed as percentage).

Climate data were acquired from the WorldClim database (www.worldclim.org), which is a set of global climate layers (climate grids) with spatial resolution of 1 km². Six climatic variables were obtained for each grid square: Annual Mean Temperature (AMT), Mean Temperature of the Warmest Quarter (MTWAQ), Mean Temperature of

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