



Cuckoos: The holy grail of avian biodiversity conservation?

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ABSTRACT

The ongoing rapid loss of biodiversity is urging conservationist to develop biodiversity monitoring methods that are both effective and inexpensive. The identification of areas that are rich in biodiversity is an essential prerequisite to guide further conservation actions. Next to several data-intensive and more complex modelling approaches to identify biodiversity 'hotspots', there are also many conservation scientists and practitioners that are looking for approaches based on surrogate species or taxa. In certain cases, single-species surrogates have been proposed to represent a certain aspect of a broader set of species, but their effectiveness is a highly debated issue. A number of recent studies have suggested the common cuckoo (*Cuculus canorus*) to be an extremely effective, yet inexpensive, single-species surrogate to map and monitor avian biodiversity across continents and at different spatial scales. If this would indeed be the case, the implications towards conservation planning would be tremendous, which raises the question: Has the holy grail of avian biodiversity conservation been found? In this paper, the methodology and significance of the results of these studies are questioned and, hence, the use of the common cuckoo as a single-species surrogate for avian biodiversity. The studies all heavily rely on the AUC value to assess model accuracy of estimating common cuckoo occurrence using species richness (and not vice versa). Using simulations of different scenarios of relative species commonness and evenness, I show that the underlying statistical dependency between species richness and occurrence of a species results in highly inflated and volatile AUC values for the majority of the 300 simulated species, depending on their commonness and the overall species evenness. As such, I hope to be able to discourage conservation scientists and practitioners from investing time, effort, and money in using the common cuckoo as a single-species surrogate for avian biodiversity conservation.

1. Introduction

Conservation organizations and practitioners are typically faced with limited funding and knowledge, and identifying priorities to be able to support the most species at the least cost, hence, becomes of utmost importance (Mac Nally and Fleishman, 2002; Myers et al., 2000; Rodrigues and Brooks, 2007). Knowledge on where areas rich in biodiversity are located is an essential prerequisite to be able to set these priorities (Pearman and Weber, 2007). Although there are many definitions of biodiversity (Jacobs et al., 2013), in practice it often centers on species richness, i.e., the number of species present, in an area (Caro, 2010; Chao and Chiu, 2016).

Methods for species richness estimation have been a research topic for several decades (Fleishman et al., 2018). Despite the familiarity of species richness, it is surprisingly difficult to measure accurately (Gotelli and Colwell, 2011). Several more recent methods to estimate species richness, such as stacked and joint species distribution models, try to take advantage of increased computing power, but many of these still need to be tested for transferability and repeatability (Fleishman

et al., 2018). Because of the limitations in funding and knowledge, conservation organizations, practitioners, and scientists, have also been looking for shortcuts in the form of surrogate species or taxa (Roberge and Angelstam, 2004). Surrogate species are individual species that are used to represent a broader set of species in order to simplify conservation and management planning and communication (Wiens et al., 2008). The effectiveness of various surrogate groups and approaches for biodiversity conservation in general, however, remains a highly debated issue (Cabeza et al., 2008; Kosicki and Hromada, 2018; Wiens et al., 2008). The search for taxonomic surrogates of species richness has yielded mixed results, with studies reporting from no over tentative to great promise for the approach (Jyväsjärvi et al., 2018).

Recently, a number of studies have suggested the common cuckoo (*Cuculus canorus*) to be an excellent single-species surrogate for avian species richness, from the local and regional (Møller et al., 2017; Morelli et al., 2017b, 2015; Tryjanowski and Morelli, 2015), to the national and (inter-)continental scale (Morelli et al., 2017a, 2015). The common cuckoo is a charismatic species that is easy to monitor, widespread both geographically and across the main types of

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landscapes, and also adequate for citizen science approaches as it is easy to detect from its familiar song (Morelli et al., 2017b; Tryjanowski and Morelli, 2015). The first study on the common cuckoo as a surrogate for species richness (Tryjanowski and Morelli, 2015), suggested that the common cuckoo was a better predictor of avian species richness than a group of “top predators”, consisting of Buzzard (*Buteo buteo*), Goshawk (*Accipiter gentilis*), Sparrowhawk (*Accipiter nisus*), and Kestrel (*Falco tinnunculus*), in an agricultural area in Poland at a local level with a study site covering 141 km². Morelli et al. (2015) subsequently proposed that the utility of the common cuckoo as a surrogate species could be extended to larger scales (e.g. France at a national scale) across Europe, and to additional indices of taxonomic bird diversity, such as Shannon-Weaver bird diversity, host species richness, and host species richness rank. They also suggested that cuckoo occurrence outperforms two landscape heterogeneity indices, i.e., land-use diversity and weighted edge density. Morelli et al. (2017b) then suggested that the common cuckoo, apart from being an excellent surrogate of taxonomic avian diversity, is also a good surrogate for other avian biodiversity components, such as functional richness and functional evenness. Møller et al. (2017) used, amongst other things, the link between cuckoo occurrence and bird species richness to propose that the folklore about the link between the longevity of farmers and the syllables of cuckoos is indeed likely to be true. Morelli et al. (2017a) put forward that the multi-scale expediency of the common cuckoo as a surrogate for avian species richness can be extended to an even wider geographic range by demonstrating links between cuckoo occurrence and bird species richness in ten European and two Asian countries. They conclude that the common cuckoo is a suitable intercontinental bio-indicator for bird richness hotspots, including under climate change scenarios and in areas where other cuckoo species co-occur. These studies altogether suggest that the common cuckoo is an extremely effective but also inexpensive tool to map and monitor avian biodiversity across continents at different spatial scales. As such, this could have tremendous implications in terms of avian conservation efforts and success, which raises the question: Has the holy grail of avian biodiversity conservation been found?

In this paper, the methodology and the validity of the results that have led to the suggestion of the common cuckoo as a surrogate species for avian species richness are questioned. All of the publications have in common that they use bird species richness as an independent variable to predict cuckoo occurrence, and not vice versa. Moreover, they all heavily rely on the Area Under the Curve (AUC) from Receiver Operating Characteristic (ROC) analysis to demonstrate the accuracy of these predictions of cuckoo occurrence. I use the data from Morelli et al. (2017a) to first show the large uncertainty in the estimates of the AUC of their model. I then use simulations to estimate the AUC value distributions of 300 simulated species, from very common to rare, for the model of Morelli et al. (2017a) as a function of different plausible relative species commonness distributions and species evenness, based on data from Tryjanowski and Morelli (2015). This allowed to more appropriately assess the significance of the AUC values obtained by Morelli et al. (2017a). I hypothesized that the underlying statistical dependency between species richness and occurrence of a species as a function of the relative commonness and evenness may result in highly inflated AUC values.

2. Material and methods

2.1. Data

Data on bird species richness (i.e., the number of species) and cuckoo occurrence (detected/not detected) at each sample site in ten European and two Asian countries, including the type of survey and dominant environment, have been published as supplementary material by Morelli et al. (2017a). Details on the number of sites per country and other summary statistics can be found in Morelli et al. (2017a) and are

not reproduced here. I first used this dataset to repeat the analysis of Morelli et al. (2017a), but now appropriately assess the uncertainty in the reported AUC values (see Section 2.2). I also used this dataset as a baseline for the simulations to estimate the distributions of expected AUC values for all species from different plausible relative species commonness and evenness distributions.

Unfortunately, the dataset from Morelli et al. (2017a) does not include data on relative frequency of occurrence for each species in the samples, i.e. species commonness and evenness data. As such, to obtain representative reference values for a typical relative species commonness distribution, I fit an exponential function to the relative species commonness data from Tryjanowski and Morelli (2015) using nonlinear least squares. The intercept a and slope b for the function $y = e^{a+bx}$ with $x = 1$ to 157 (i.e., the number of species in Tryjanowski and Morelli (2015) and $y =$ the occurrence frequency of each species, were 4.22 and -0.05 , respectively. The R script (R Core Team, 2018) to estimate the coefficients of the exponential function can be accessed at Haest (2018). I used these estimated coefficients as a baseline for the relative species commonness distributions in the simulations of the AUC value distributions under different species evenness scenarios (see Section 2.3).

2.2. AUC uncertainty estimation

Important distinctions exist between inferential (or explanatory) and predictive model assessment. In inferential modelling the emphasis of model performance lies in assessing explanatory power, i.e. measuring the strength of relationships for example through R^2 -type statistics or predictor statistical significance. In predictive modelling, the emphasis of model assessment lies in predictive power, referring to the performance of the model on new or unseen data (Shmueli, 2010). AUC is a measure to assess predictive accuracy (Elith et al., 2006), and AUC estimation, just as other predictive performance measures, should be performed on data that has not been used to train the model to avoid overestimation of model accuracy (Congalton and Green, 2009). Several methods exist to approach splitting a dataset into training and test (and possibly also validation) data. The most important difference, however, lies in whether a single split of some given proportion is used, or the split is repeated several times through some sort of resampling. Using a resampling method allows the estimation of confidence intervals around the accuracy measure, and as such provides information on model uncertainty (Lyons et al., 2018).

The studies that have proposed the common cuckoo as a surrogate species of avian species richness all calculated AUC values on the model that uses the full dataset. I repeated the modelling of common cuckoo occurrence using avian species richness as in Morelli et al. (2017a), but instead of using the full dataset to calculate only one AUC value (per country), I more appropriately used resampling to estimate the uncertainty in the AUC estimations. I repeated a 5-fold cross-validation a 1000 times, resulting in 5000 AUC estimates based on different subsets of the full dataset. In each 5-fold cross-validation, the dataset is randomly split into 5 groups, of which 4 are then used as training data for the cuckoo occurrence model and 1 to calculate AUC, iterated 5 times so each group functions as the test set once. The R script to perform this uncertainty analysis can be accessed at Haest (2018).

2.3. Simulations of AUC value distributions as a function of relative species commonness and evenness

I hypothesized that AUC values for models that estimate occurrence of a species using species richness may be highly inflated due to the intrinsic underlying increased probability of occurrence of any species when species richness increases. To test this hypothesis, I estimated the distributions of AUC values for all species under different scenarios of relative species evenness, i.e. species commonness distributions with different exponential slopes, given the species richness data from

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