



# Birds as surrogates for mammals and reptiles: Are patterns of cross-taxonomic associations stable over time in a human-modified landscape?



Ding Li Yong\*, Philip S. Barton, Sachiko Okada, Mason Crane, David B. Lindenmayer

Fenner School of Environment and Society, The Australian National University, Canberra, ACT 2601, Australia

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## ABSTRACT

Cross-taxonomic surrogates can be feasible alternatives to direct measurements of biodiversity in conservation if validated with robust data and used with explicit goals. However, few studies of cross-taxonomic surrogates have examined how temporal changes in composition or richness in one taxon can drive variation in concordant patterns of diversity in another taxon, particularly in a dynamic and heavily modified landscape. We examined this problem by assessing changes in cross-taxonomic associations over time between the surrogate (birds) and target vertebrate taxa (mammals, reptiles) that demand high sampling effort, in a heterogeneous mosaic landscape comprising pine monoculture, eucalypt woodland remnants and agricultural land. Focussing on four study years (1999, 2001, 2011, 2013) from a dataset collected over 15 years, we: (1) investigated temporal changes in cross-taxonomic congruency among three animal taxa (2) explored how temporal variation in composition and species richness of each taxon might account for variation in cross-taxonomic congruency, and (3) identified habitat structural variables that are strongly correlated with species composition of each taxon. We found the strength of cross-taxonomic congruency varied between taxa in response to both landscape context and over time. Among the three taxa, overall correlations were weak but were consistently positive and strongest between birds and mammals, while correlations involving reptiles were usually weak and negative. We also found that stronger species richness and composition correlations between birds and mammals were not only more prevalent in woodland remnants in the agricultural matrix, but they also increased in strength over time. Temporal shifts in species composition differed in rate and extent among the taxa even though these shifts were significant over time, while important habitat structural correlates were seldom shared across taxa. Our study highlights the role of the landscape matrix and time in shaping animal communities and the resulting cross-taxonomic associations in the woodland remnants, especially after a major perturbation event (i.e. plantation establishment). In such dynamic landscapes, differing and taxon-specific shifts in species diversity over time can influence the strength, direction and consistency of cross-taxonomic correlations, therefore posing a 'temporal' problem for the use of surrogates like birds in monitoring and assessment of biodiversity, and conservation management practices in general.

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## 1. Introduction

Land-use change increasingly threatens biodiversity globally by driving habitat loss and degradation (Sala et al., 2000; Reidsma et al., 2006; Sayer et al., 2013). As a result, there is an urgent need to understand how diverse groups of biota respond to land-use modification across various scales (e.g. Mattison and Norris, 2005; Haines-Young, 2009). Such knowledge is integral to informing deci-

sions on how sites should be conserved and managed (Meir et al., 2004; Vandewalle et al., 2010). However, resource and taxonomic limitations impose enormous difficulties on sampling large suites of taxonomic groups (Lawton et al., 1998; Schulze et al., 2004; Gardner et al., 2008) to understand broad changes in biodiversity patterns. This has resulted in multiple surrogate approaches being developed to act as proxies for components of biodiversity not able to be directly measured (Prendergast and Eversham, 1997; Caro, 2010; Lindenmayer et al., 2015), or biota that are costly or logistically difficult to survey within time frames available for decision-making (Favreau et al., 2006).

\* Corresponding author.

E-mail address: [ding.li@anu.edu.au](mailto:ding.li@anu.edu.au) (D.L. Yong).

Species-based surrogates of biodiversity are a common type of surrogate (e.g. Caro, 2010), and are based on the hypothesis that the occurrence or diversity of a surrogate or indicator taxon reflects the occurrence (i.e. co-occurrence) or diversity (i.e. species richness, composition) of other sets of target taxa (Rohr et al., 2007; Rondinini et al., 2006; Gaspar et al., 2010). The best examples of these species-based surrogates include cross-taxonomic surrogates (e.g. Kati et al., 2004; Gallardo et al., 2011; Gaspar et al., 2010; Fattorini et al., 2012), biodiversity indicator species or species groups (e.g. Nally and Fleishman, 2002; Roberge and Angelstam, 2004; Branton and Richardson, 2011), and higher-taxonomic groups (e.g. Báldi, 2003; Heino and Soinen, 2007).

Species surrogates of diversity in conservation have several empirical and conceptual shortcomings (e.g. Andelman and Fagan, 2000; Heink and Kowarik, 2010). First, studies of cross-taxonomic relationships have yielded mixed results in terms of the strength and direction of congruency across different taxa, often varying with the analytical approaches used (Gioria et al., 2011), even when landscape contexts and scales are broadly similar (Wolters et al., 2006; Lewandowski et al., 2010). At small to intermediate spatial scales of study, cross-taxonomic congruency of species richness was found to be weak in some studies (e.g. Kati et al., 2004; Lovell et al., 2007; Santi et al., 2010) but strong in others (e.g. Negi and Gadgil, 2002). Such divergent findings are further exacerbated by the fact that these surrogates are often used to predict occurrence and diversity of target taxa with different ecological attributes (e.g. dispersal ability, habitat requirements, life histories) (e.g. Ricketts et al., 1999). Second, many studies testing surrogacy relationships with respect to a biodiversity target are not clearly defined within a theoretical framework, thus weakening the ecological basis for using a surrogate (Belovsky et al., 2004; Lindenmayer and Likens, 2011). Many studies emphasise the identification of cross-taxonomic surrogate associations, but fail to define the surrogate relationships clearly, or under a robust framework that incorporate cause-effect relationships and predictive strength (Barton et al., 2015). Others such as Hunter et al. (2016) have pointed out controversies arising from surrogate concept as a result of differing goals of surrogate application in conservation. Third, many studies of surrogates are ‘snapshot’ investigations and fail to tackle the problem of how species surrogates perform over time, or with respect to temporal variability in ecological processes (Anderson, 2001; Favreau et al., 2006; Magurran et al., 2010). For any biodiversity surrogate to function as a useful tool for conservation, it should consistently predict diversity patterns or responses of other species over time (Rodrigues et al., 2000). Understanding of how biodiversity surrogates perform over time (Favreau et al., 2006) is constrained by the paucity of long-term datasets, with the result that few studies (e.g. Thomson et al., 2007) have examined how long-term shifts in the composition of animal communities associated with landscape modification may affect cross-taxonomic congruency (see Table 1 for definitions).

Biodiversity patterns in general, and individual species in particular, respond to the extent of landscape modification in different and diverse ways (Fischer and Lindenmayer, 2007). Typically, modification of the landscape leads to changes in habitat spatial configuration and structure (e.g. patch size, matrix quality, edge effects), which impact animal communities differently, depending on individual species’ ecological needs and their ability to disperse across the wider landscape (Dormann et al., 2007; Driscoll et al., 2013). Over time, species composition in a biotic community can be affected by dynamic changes in landscape configuration and vegetation structure or habitat recovery post-disturbance (e.g. Guedo and Lamb, 2013). While it remains unclear how shifts in community composition of one taxon change relative to other taxa, a taxonomic group can act as a good surrogate for others if it undergoes turnover (see Table 1 for definition) in species richness or compo-

sitional patterns that are consistent and congruent with other taxa over space and time. For instance, strong patterns of congruency between turnover of invertebrate and macroalgal diversity highlight the potential of macroalgae assemblages to act as biodiversity surrogates for fish and invertebrates (Thomson et al., 2014).

In this study, we investigated temporal variation in cross-taxonomic congruency (see Table 1 for definitions) of diversity between pairs of three taxa, and explored how (a) temporal shifts in diversity and (b) habitat correlates specific to each animal taxon can drive variation in the extent of cross-taxonomic congruency. We used a large dataset that has been collected over a period of 15 years in a dynamic, human-modified landscape that has undergone rapid transformation from a woodland-agriculture mosaic to large tracts of pine monoculture (Lindenmayer et al., 2001; Lindenmayer et al., 2008a,b). We focussed on birds, mammals and reptiles as these taxa are not only frequently used in conservation assessments (e.g. Westgate et al., 2014), but are also species-rich in our study landscape (see Supplementary Tables A6–A8 for list of species). In addition, sampling these three taxa demands very different amounts of effort and resources given the nature of field surveys. For instance, birds can be easily surveyed and have found to be popular and cost-effective surrogates in inventories of biodiversity (e.g. Lawton et al., 1998; Gardner et al., 2008) whereas sampling reptile diversity not only involves a very different methodology, but also demands specialist knowledge (e.g. McDiarmid et al., 2011). For mammals, the nocturnal habits and cryptic behaviour of many species (e.g. Suter et al., 2000) means effort-intensive night surveys and baited traps are needed to survey them. Differences in natural history across taxa, and disparate sampling effort to be invested in different taxonomic groups underscores the need for viable biodiversity surrogates, which could facilitate more optimal use of resources in inventorying biodiversity.

The aim of our study was to evaluate congruence in diversity and species composition measures between birds, mammals and reptiles over time, and thus uncover evidence for consistent cross-taxonomic surrogacy (Table 1 for definitions), as the quantification of cross-taxonomic congruency is a critical step in identifying surrogates (Gioria et al., 2011). To quantify cross-taxonomic congruency, we used metrics of correlation between species richness and species composition, given that both measures are frequently adopted in studies of cross-taxon surrogates (e.g. Kati et al., 2004; Sauberer et al., 2004; Gaspar et al., 2010; Cabra-García et al., 2012) and collectively can offer a comprehensive evaluation of cross-taxonomic congruency (Su et al., 2004; Gioria et al., 2011). To address our study aims, we posed three questions:

- (1) based on the strength and direction of associations between pairs of taxa, what is the extent of variation in cross-taxonomic congruence patterns at the species richness and composition levels over 15 years?

Given the limited vagility of reptiles, smaller spatial requirements (Stow et al., 2014) and the limited effect posed by habitat fragmentation on lizard communities (e.g. Jellinek et al., 2004) compared to birds or mammals, we predicted that reptiles were likely to show low congruency in diversity patterns with either mammals or birds.

Cross-taxonomic congruency patterns are often derived from measures of diversity and are thus determined by temporal shifts in the diversity of different taxonomic groups relative to each other. To (a) explore the extent of temporal variation in diversity across the taxonomic groups and (b) determine how different habitat structural variables in remnant woodlands can influence each taxon in our study, we asked:

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