Cross-taxonomic surrogates for biodiversity conservation in human-modified landscapes – A multi-taxa approach

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ABSTRACT

Cross-taxonomic surrogates are often used in conservation planning because inventorying large suites of taxa is either not feasible or too costly. However, cross-taxonomic surrogates are seldom tested rigorously using both correlational and representation-based approaches at the spatial scales at which conservation management occurs. Here, we evaluated the effectiveness of five ecologically contrasting taxa (birds, herpetofauna, wild bees, beetles, trees) as cross-taxonomic surrogates in native woodland patches within a heavily modified, farming and plantation-dominated landscape. We first compared species richness and compositional heterogeneity across taxa before testing for cross-taxonomic congruence using a correlative approach. We then quantified how well each taxon incidentally represented other taxa in their best patch sets, and the costs of doing so using a complementarity-based approach. We found significant pairwise associations between some taxa (birds, bees), but no single taxon was strongly correlated with all other taxa. Woodland patch sets prioritised for beetles represented other taxa best, followed by birds, but were the costliest and required the largest amount of woodland. This contrasted with patch sets prioritised for wild bees or herpetofauna, which achieved higher representation of other taxa at lower costs. Our study highlighted the influence of taxon-specific patterns of diversity and heterogeneity on how remnant vegetation patches should be prioritised for conservation, a consideration not immediately obvious in correlative analyses of surrogacy. Second, taxa that are not the most speciose (e.g. wild bees) can be efficient surrogates, achieving higher incidental representation for other taxa at lower costs. Thus, while species-rich taxa are ideal as surrogates for prioritising conservation, conservation planners should not overlook the potential of less speciose taxa such as bees, while considering the cost-effectiveness of surveying multiple different taxa.

1. Introduction

Land use change driven by agricultural expansion and intensification is among the leading drivers of biodiversity loss worldwide (Foley et al., 2011; Alexander et al., 2015). Presently, a large proportion of the world's agricultural land is already used for grazing livestock, with permanent pastures covering nearly a quarter of the world's land surface (Wirsenius et al., 2010; FAOSTAT, 2014). Intensification of agricultural production in existing farming landscapes is expected to exacerbate biodiversity declines (Benton et al., 2003; Donald et al., 2006; Cunningham et al., 2013). Therefore, effective conservation of biodiversity will necessitate conservation initiatives in agricultural systems that are underpinned by robust ecological research (Tscharntke et al., 2005; Norris, 2008; Ranganathan et al., 2008; Kay et al., 2016).

Knowledge of biodiversity patterns is essential for understanding the consequences of land use change and guiding subsequent conservation decisions (Margules and Pressey, 2000; Ferrier, 2002; Phalan et al., 2011; Guisan et al., 2013). Given that it is neither cost-effective nor practical to inventory large groups of taxa, there is a need to adopt surrogate approaches drawing on more easily gathered data to guide biodiversity conservation (Rodrigues and Brooks, 2007; Caro, 2010; Lindenmayer et al., 2015). Surrogate approaches are usually grounded on the presumption that a measured subset of biodiversity components in the landscape can provide useful information on broader biodiversity patterns, therefore allowing variation in other aspects of biodiversity to be predicted (Heino, 2010; Larsen et al., 2012; Barton et al., 2015). Many surrogate approaches adopted in conservation management and monitoring employ species data (e.g. cross-taxonomic surrogates), often in combination with vegetation and environmental data (e.g. Grantham et al., 2010; Barton et al., 2014; Lindenmayer et al., 2014). Over time,

the interest in using surrogates to guide conservation management has fuelled a large amount of research to evaluate their utility.

Because cross-taxonomic surrogates offer expedient means to evaluate biodiversity for conservation planning, easily surveyed taxa such as birds have been widely proposed as surrogates (e.g. Eglington et al., 2012; Carrascal et al., 2012; Di Minin and Moilanen, 2014). However, while some studies endorse the use of cross-taxonomic surrogates (e.g. Larsen et al., 2012), others have highlighted problems (e.g. Andelman and Fagan, 2000; Paavola et al., 2006). First, there is increasing evidence of how spatial scale, grain and resolution can shape the extent of correlation between different taxa, thus compromising their effectiveness as surrogates for other groups (e.g. Hess et al., 2006; Paavola et al., 2006; Westgate et al., 2014). Second, differences in ecology and responses to environmental variables among taxa can be expected to drive taxon-specific turnover patterns (e.g. Turtureanu et al., 2014), weakening the strong cross-taxonomic congruence expected of a good surrogate (Yong et al., 2016). Third, the diversity of criteria, concepts and approaches used to evaluate the effectiveness of biodiversity surrogates across different studies has rendered it challenging to draw a consensus on what constitutes a good surrogate (Favreau et al., 2006; Hunter et al., 2016). Put together, these problems highlight the need to identify better biodiversity surrogates, and cross-validate their effectiveness through different analytical approaches (e.g. Favreau et al., 2006; Grantham et al., 2010).

In this study, we tested the effectiveness of a cross-taxonomic surrogate approach to guide conserving planning for woodland biodiversity in a human-modified landscape. The conceptual framework for our study was guided by three questions, and grounded systematically on field inventorying, initial identification of surrogate taxa, and cross-validation of these surrogate groups in a systematic conservation planning approach. First, we asked: (1) Which pairs of taxa show strong cross-taxonomic congruence? To do this, we inventoried two vertebrate groups (birds, herpetofauna), two insect groups (wild bees, beetles) and one plant group (trees). We then applied a correlative approach to assess the degree of pairwise cross-taxonomic association (i.e. cross-taxonomic congruence) in species richness and composition (Sauberer et al., 2004; Su et al., 2004; Rooney and Azeria, 2015). As with many studies, we hypothesized that taxa showing high cross-taxonomic congruency could perform better as species surrogates for other taxa.

Second, we asked: (2) How effective are surrogate taxa in incidentally representing the occurrences of other taxa in sets of woodland patches prioritised for the surrogate? This question is important because it allows initially identified surrogate taxa to be validated in realistic conservation planning scenarios. Ideally, an effective surrogate taxon should be expected to capture a high proportion of the representation targets for other taxa (Larsen et al., 2012; Di Minin and Moilanen, 2014), without being excessively costly itself – i.e. requiring the conservation of a large amount of woodland patches. To do this, we adopted a complementarity-based, site-selection approach (see Table 1 for definitions of terms) to identify near-optimal sets of remnant woodland patches in our landscape using a priori representation targets set for each taxon. We then determined how well other taxa were incidentally represented in the patch sets selected for the (surrogate) taxon (e.g. Sætersdal et al., 2004; Albuquerque and Beier, 2016). Additionally, determining the total area of woodland patches in patch sets selected for each taxon at a given representation target provided a proxy of relative cost, and allowed us to compare the cost-effectiveness of multiple scenarios using different focal taxa as surrogates.

Finally, we asked: (3) How similar are these best sets of habitat patches selected for each taxon, and at each defined representation target. We therefore compared the sets of woodland patches selected for each taxon at each representation target by assessing the degree of overlap (as measured with dissimilarity, distance metrics) in patch set solutions between taxa following Ikin et al. (2016). Since many species in human-modified landscapes can be expected to be wide-ranging generalists rather than habitat specialists given the effects of biotic homogenisation (e.g. Ekroos et al., 2010), we expected differences between sets of woodland patches selected for each taxon to be low because many of these taxa are likely occur in a large proportion of woodland patches.

2. Methods and materials

2.1. Study area and design

The highly modified Nanangroe landscape (34°58′S, 148°28′E) consists of approximately 30,000 ha of agricultural (i.e. grazing) land and exotic Monterey pine *Pinus radiata* plantations (Fig. 1). Much of the original cover of box-gum grassy woodlands, an ecological community now listed as critically endangered (Rawlings et al., 2010), has been extensively cleared in the past two centuries for agriculture. This has left numerous scattered remnant patches across the landscape (Lindenmayer et al., 2008). In 1998, the landscape matrix surrounding many of these remnants was transformed by the establishment of extensive plantations of pine (Lindenmayer et al., 2008). As a result, these remnant woodland patches became embedded within either a matrix of grassy pasture actively grazed by livestock or pine plantations. Permanent transects were marked and established at all study patches prior to the commencement of the study. In woodland patches exceeding 1 ha, a 200-m long transect was established while 100-m long transects were established for patches smaller than 1 ha. For this study, a total of 42 remnant woodland patches in both kinds of matrix were identified to represent the full range of patch area classes (See Supplementary Table 1 for full list of woodland patches and their attributes) for biodiversity sampling.

Table 1
Glossary of key terms (in text) and definitions.

Term	Definition
Biodiversity surrogate	A defined taxonomic group (e.g. birds) or group(s) of species whose occurrence or diversity predicts that of another, usually less well-known group(s) of species.
Cross-taxonomic congruence	Degree of association or co-variation in the diversity pattern of a defined group of species with respect to another group. Common metrics include measures of correlation strength such as Spearman's ρ and Pearson's r.
Compositional turnover	Variation in the composition of species across space; an approach to quantify beta diversity in a landscape.
Conservation feature	A unit to be represented in a solution of reserve sites in systematic conservation planning scenarios. Usually quantified as the presence of a species in a defined site.
Incidental representation	Representation of taxa in a set of identified sites/reserves that was not targeted *a priori*, usually in a systematic conservation planning scenario.
Representation target	Defined numerical thresholds in the representation of selected conservation features (e.g. occurrence and distribution of a surrogate taxon) in a systematic conservation planning context.
Complementarity	A principle in designing networks of reserve sites in conservation whereby the selection of sites iteratively adds sites that complement those already selected (Vane-Wright et al., 1991; Justus and Sarkar, 2002).
Simulated annealing	An algorithm implemented in Marxan to identify near-optimal solutions in selecting networks of reserve sites in conservation (Game and Grantham, 2008).