# Higher-taxon and functional group responses of ant and bird assemblages to livestock grazing: a test of an explicit surrogate concept

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**ABSTRACT**

Biodiversity monitoring programs are routinely established to quantify changes in biotic communities in response to land management. Surrogacy is implicitly used in many such monitoring programs whereby the measurement of a component of biodiversity is used to infer responses of broader biodiversity. Yet rarely is this surrogacy validated by demonstrating that measured variables and the target variable of interest have matching responses to management treatments. Here we examined the responses of higher-taxon and functional groupings of ants and birds (our surrogate variables) two years after the implementation of experimental livestock grazing treatments, and compared these with the responses of total ant and bird species richness (our target variables) to the same treatments. We found significant and strong correlations between surrogate and target variables, but this did not predict corresponding similar response to treatments. For ants, we found that the genus *Monomorium* had a negative response to the grazing exclusion treatment, but there was no matching response of species richness, and so no surrogacy was identified. For birds, total species richness had a weak positive response to spring/summer grazing exclusion, and the abundance of honeyeaters (Meliphagidae) showed a similar positive response, suggesting surrogacy. Our study highlights that correlations among variables do not necessarily lead to surrogacy, and indeed that different sub-components of biotic assemblages can respond in ways that contrast with overall species richness. Careful assessment of the matched responses of surrogate and target variables to management can provide a simple and robust way to critically assess biodiversity surrogacy.

**Keywords**: biodiversity conservation, grazing, insect, indicator, modified landscape, monitoring

## INTRODUCTION

Biodiversity monitoring programs are routinely established to quantify changes in biotic communities in response to different land management practices (Lindenmayer and Likens 2010; Vackar et al. 2012). Acquiring and analysing monitoring data requires considerable time and effort. Using surrogate variables to make inferences about other unmeasured variables of interest is one approach to reducing monitoring costs (Caro 2010; Lindenmayer and Likens 2011). This can be, for example, in the form of higher-taxon surrogacy, where patterns occurring at a higher taxonomic level, such as family or genus, are used to infer patterns of species-level responses (Williams and Gaston 1994; Brennan et al. 2006; Driessen and Kirkpatrick 2017). Functional surrogacy can also be used, whereby individuals are grouped by their shared ecological attributes, such as diet or body size, and used to infer broader assemblage responses to the environment (Gollan et al. 2010; Bhusal et al. 2014; Barton and Moir 2015). Each of these approaches can offer potentially simple, cheap, and ecologically meaningful ways to quantify broader biotic patterns, but nevertheless require proper evaluation before surrogacy can be attributed.

Biodiversity surrogates can be used to provide information about the response of biota to management interventions aimed at conserving broader biodiversity (Lindenmayer et al. 2002; Gonzalez et al. 2013; Barton and Moir 2015). For example, increased abundance of a particular species following altered land management might be used to infer a broader community response to management intervention (Gollan et al. 2010; Barton and Moir 2015). However, it is important to distinguish between studies that identify a simple correlation between a target and its surrogate from those that show matched responses of these variables to a shared treatment. This difference is essential to moving beyond establishing an association and towards establishing surrogacy within a particular context (Barton et al. 2015; Pierson et al. 2016). The additional step of identifying matched responses is needed because

target and surrogate variables may not necessarily respond to an intervention in the same way, despite themselves being correlated, yet few studies acknowledge or empirically test this (Pierson et al. 2016).

In this study, we used an explicit surrogate concept to guide our evaluation of surrogates of biodiversity responses to livestock grazing treatments (Fig. 1). This concept is adapted from the medical sciences (Atkinson et al. 2001; Barton et al. 2015) and shows how a surrogate variable is placed between a treatment and its target, while accounting for covariates. Monitoring of different taxa was subsequently undertaken to assess the effects of grazing treatments on biodiversity, and this provides the basis of our current study. We examined the responses of a suite of higher-taxon and functional groupings of ants and birds (our surrogate variables) and see if any match the response of overall species richness (our target variables) to the livestock grazing treatments. Our questions were: (1) Which surrogate and target variables respond to the grazing treatments? (2) Which surrogate and target variables are correlated? (3) Which variables are both strongly correlated *and* show similar responses to the grazing treatments? These analyses provide the basis for an objective assessment of matched responses of surrogate and target variables to a common treatment and are hence a simple, but important, test of surrogate validity.

## METHODS

### Study area and design

Our study was conducted in south-eastern Australia, with sites spanning an area approximately 100 km east to west, and 150 km north to south (Figure S1). Within this area, we established 78 sites, each of 40 x 200 m (0.8 ha), across 29 different farms from mid-2010. All sites were located in temperate grassy woodland, which is characterised by a patchy distribution of *Eucalyptus* trees in grassland largely dominated by native perennials

95 (Lindenmayer et al. 2012; Barton et al. 2016). Grassy woodland was once widespread in
96 south-eastern Australia, but has been subject to large-scale clearing or modification due to
97 agricultural practices including grazing (McIntyre et al. 2014).
98 We grouped the 29 farms into three blocks, each representing a historical 'business as
99 usual' grazing practice of either continuous grazing, short-term rotational grazing (conversion
100 to rotational grazing practice within the last five years), or long-term rotational grazing
101 (conversion to rotational grazing practice for greater than 10 years). Farms with continuous
102 grazing allowed livestock access to sites all year round, whereas farms with rotational
103 grazing typically rotate higher numbers of livestock through sites, but for a limited duration.
104 Sites were assigned within in each farm to one of three different treatments: (i) all-year
105 exclusion, (ii) spring/summer exclusion, and (iii) 'business as usual'. All-year exclusion sites
106 had little or no grazing by livestock in the year prior to our study. Spring/summer exclusion
107 sites were not grazed during the six month period of spring and summer prior to our study.
108 The 'business as usual' sites continued grazing in line with the usual grazing practices of the
109 farm (*viz*. continuous, short-term rotational, long-term rotational). We documented data on
110 livestock numbers and duration of grazing events for each site as reported by landholders in
111 the 12 months prior to this study, and provide grazing summary statistics in Table S1.
112
113 **Soil and vegetation covariates**
114 Soil and vegetation surveys were conducted on every site during January and February 2012,
115 approximately two years after the grazing treatments commenced. We established two 20 x
116 50 m quadrats at 0-50 m and 150-200 m along the centre line of each site (Figure S1). Within
117 each quadrat, we recorded the number of tree stems > 10 cm in diameter. A 50m transect was
118 located down the centre of each plot with biometric step-count measurements (Gibbons et al.
119 2008) taken every metre to assess percentage cover of ground layer native and exotic grass

cover, and leaf litter cover. In addition, ground-layer plant biomass was assessed using a rising plate pasture meter to determine average height of ground cover present (Filip's Manual Folding Plate Meter, Jenquip, New Zealand (Correll et al. 2003). Vegetation measures were averaged across the two quadrats to give one measure per site. We also collected soil cores of 10 cm diameter x 5 cm depth every 16.5 m (n = 12) along the 200-m centre transect of each site, following the careful removal of any surface plant and litter biomass present. We then pooled soil samples 1-4, 5-8, and 9-12 for each site to provide three bulked samples per site (see Figure S1). We air dried samples at 35°C for 48 h prior to processing, then crushed the dried samples and passed each through a 2-mm sieve. We quantified total carbon and nitrogen (%) in each sample using Dumas combustion analysis (Vario Max, Elementar, Germany) (Matejovic 1997), and expressed results as a C:N ratio. We determined total phosphorus (%) using the Kjeldahl method (Diamond 2006). All soil measures were averaged to give one value per site.

**Ant sampling**

We sampled ground-active ants using pitfall traps (250 ml plastic jars) dug in flush with the ground surface and half-filled with a 50% polyethylene glycol solution. Three pitfall traps were deployed in each site for a two-week period in December 2011 (Figure S1), with ants removed and pooled to give one sample per site. Our sampling approach deliberately prioritised spatial replication across many sites over sampling intensity within sites, resulting in standardised bias towards the more active species of the ant community.

Specimens were sorted and identified to subfamily, genus, and species (or morphospecies) by a taxonomic specialist and assigned a functional group based on their genus membership using the classification scheme described by Andersen (1995a, 1997) (see Table S3). We used only the four most abundant functional groups in further analysis: the

145 Dominant Dolichoderinae, Generalist Myrmecinae, Opportunists, and Hot Climate
146 Specialists. Ant functional groups were first described as a way to improve prediction and
147 generalisation of ant species responses to disturbance, and have been used previously to
148 examine responses to livestock grazing (Hoffmann 2010; Barton et al. 2016). The list of ant
149 species and their functional groupings is given in Table S3.
150
151 **Bird surveys**
152 Birds were surveyed during spring of 2011 within a 25m radius at both ends of every site.
153 Surveys consisted of five-minute point counts with two repeat visits by highly skilled field
154 staff. All bird species seen or heard during the four counts were pooled to give one sample
155 per site. There were sufficient data for two families of birds (Acanthizidae and Meliphagidae)
156 (> 100 individuals) to allow for separate analysis as higher-taxon surrogates. Bird species
157 also were assigned to their dominant foraging stratum (ground, canopy/shrub, aerial) (Kutt
158 and Martin 2010), and these were used as our functional group surrogates. The list of bird
159 species and their functional groupings is given in Table S4.
160
161 **Statistical analysis**
162 We first used principal components analysis (PCA) to identify collinearity among the nine
163 soil and vegetation measures. PCA generated three new variables (notation of PC1, PC2,
164 PC3) that each represented an environmental gradient among our sites (Table S2). These
165 variables accounted for a combined 67% of variation in our environmental data. The first
166 component represented a gradient from under trees out to improved pasture/grassland sites.
167 The second component represented a gradient of exotic perennial to native annual grass
168 cover. The third component represented a gradient of increasing native perennial grass cover.

We selected species richness of each taxon as the target variable of interest, with this variable being the most commonly used measure of diversity in applied ecology and conservation (Fleishman et al. 2006; Magurran and McGill 2011). We next considered overall abundance of each taxon, richness of families or genera, abundance of individuals within key families or genera, and abundance of individuals within functional groups as our surrogate variables. We focused on abundance within higher taxonomic or functional groups because it is often correlated with species richness (Bock et al. 2007; Magurran and McGill 2011), but much easier to measure than species-level richness.

To address **Question 1** (Which surrogate and target variables respond to the grazing treatments?), we designed a statistical model that could be used to test for the effects of grazing treatments on our suite of target and surrogate variables for each taxon. We used a generalised linear mixed model (Bolker et al. 2009) to test for the main effects of farm grazing history (three levels: continuous, short rotational, long rotational), and the nested interaction of the applied grazing treatments (three levels: all-year exclusion, spring/summer exclusion, business as usual) within their associated historical grazing practice. To account for potential correlation among sites within an individual farm, we used farm as a random effect and structured our models as follows:

(a) *response variable ~ grazing history + grazing history:grazing treatment + random(farm)*

Next, we ran a second set of models testing for the effects of the three environmental covariates derived from our PCA (PC1, PC2, PC3). This was so we could compare the effects of the grazing treatments *per se* where environmental variation is accounted for in the experimental design, with the effects of environmental variation where the grazing treatments and experimental design are ignored. We again used farm as a random effect, and structured our models as follows:

194 (b) *response variable ~ PC1 + PC2 + PC3 + random(farm).*

195 The full list of response variables examined with our models are given in Table 1. We
196 used a negative binomial error distribution due to overdispersion of the data. We ran our
197 models with the 'glmmTMB' function in glmmTMB (Magnusson et al. 2017) using R
198 statistical software (R Development Core Team 2017). We wanted to compare the direction
199 and magnitude of grazing effects on both target and surrogate variables to visually identify
200 matched responses of variables to each treatment. Effect estimates were therefore plotted of
201 each nested grazing treatment on each surrogate and target variable. Effect estimates of
202 spring/summer exclusion and all-year exclusion were calculated relative to the 'business as
203 usual' grazing treatment. Effects plots provide a quantitate estimate of the difference between
204 two groups. We used 95% confidence intervals to indicate important effects – i.e. if an effect
205 confidence interval crossed the zero-effect line, then the effect size was not considered to be
206 significant.

207 To answer **Question 2 (**Which surrogate and target variables are correlated?), we
208 calculated Pearson correlation coefficients between species richness (the target) and all
209 higher-taxon and functional surrogate variables listed in Table 1. Both ant and bird target and
210 surrogate variables were different measures of the broader assemblage, so some correlations
211 were expected. However, we wanted to know if the strength of correlation (r) between target
212 and surrogate variables was a useful predictor of the correspondence between surrogate and
213 target responses to the grazing treatments and environmental covariates. To answer **Question**
214 **3** (Which variables are both strongly correlated *and* show similar responses to the grazing
215 treatments?), we ranked surrogate variables in order of correlation strength, and noted against
216 each one the direction and significance of the effect of the grazing treatments and
217 environmental covariates.

218

## RESULTS

*Effects of grazing treatments on ants and birds*

No significant effects of historical grazing context was found for any of our ant or bird assemblage measures, and we therefore focused on the grazing treatments. For ants, we found no significant effect of any grazing treatment on ant species richness (our target variable) (Fig. 2). However, we did find a significant negative effect of grazing exclusion on the ant genus *Monomorium* from farms with a short-term rotational grazing history (Fig. 2). Notably, we found that, for birds, the spring/summer exclusion treatment had a near-significant (0.06, see Table S6) positive effect on species richness on farms with a history of continuous grazing, and this corresponded with a significant positive effect on the abundance of canopy and shrub foraging birds (Fig. 3). A significant negative effect of spring/summer grazing exclusion was found for bird species richness on farms with a history of long-term rotational grazing, and this corresponded with a similar response of birds in the family Meliphagidae (Fig. 3). There were no effects of grazing exclusion on any measure of the bird community.

*Effects of environmental covariates on ants and birds*

Several significant effects of the environmental covariates on ant and bird assemblages were found. For ants, PC1 (tree- to grassland-dominated) had a significant positive effect on ants in the genus *Rhytidoponera* and Opportunists (Fig. 4), and a negative effect on the genus *Monomorium* and the Generalist Myrmecines (Fig. 4). Only PC2 (gradient from exotic perennials to native annuals) had a significant positive effect on species richness, which corresponded with a positive effect on genus richness and the abundance of the genus *Pheidole* (Fig. 4). For birds, none of the covariates had an effect on species richness. However, PC1 had a negative effect on the abundance of Acanthizidae and Meliphagidae, as well as the abundance of aerial and canopy/shrub foragers (Fig. 4). PC2 had a significant

positive effect on the abundance of Acanthizidae. PC3 (gradient of increasing native perennials) had a significant positive effect on the abundance of Meliphagidae.

*Correlations between surrogates and targets*

Genus richness of ants and family richness of birds were most strongly correlated ($r > 0.8$) with their target variable of species richness (Table 2, Table 3). Abundance of key families (birds), genera (ants), or functional groups had weaker (but often still significant) correlations with species richness (Table 2, Table 3). We found only two instances of a significant correlation being matched by a similar response, both for birds. This included a positive response of bird species richness and abundance of canopy and shrub foragers to spring/summer exclusion grazing in farms with historical continuous grazing, and a matched negative effect of spring/summer exclusion grazing on species richness and abundance of Meliphagidae in farms with long-term rotational grazing (Table 3). Interestingly, we found an instance of no correlation but matched positive response to environmental covariate PC2 for abundance of the ant genus *Pheidole* and total species richness (Table 2). There were also some strong correlations between surrogate and target variables (e.g. total abundance and family richness of birds) and a matched *absence* of response to grazing and environment (Table 3).

## DISCUSSION

We examined the responses of different measures of ant and bird assemblages to livestock grazing treatments and environmental covariates to demonstrate a way to identify and validate biodiversity surrogate responses to environmental change. We approached the problem by using a clear conceptualisation of treatment–surrogate–target relationships (Barton et al. 2015). We found that few surrogate responses matched those of the target

(overall species richness), thus invalidating their surrogacy in terms of indicating an effect of grazing or the environment on ant or bird assemblages. Although there were several strong correlations between target and surrogate variables, this did not provide additional insight into whether they had matched responses to the grazing treatments or environment. The correlations between some surrogate and target variables and their matched lack of response to grazing might also suggest potential surrogacy for ineffective treatments. Our approach demonstrates the value of using a clear surrogacy concept for straight-forward validation of biodiversity surrogates.

*Corresponding effect sizes as a way to validate surrogacy*

Testing the hypothesis of no correspondence between target and surrogate provided a starting point for the validation of a surrogate variable, and is routinely used in the medical sciences (NIH Definitions Working Group 2000; Atkinson et al. 2001). For ants, we found no response of species richness to the grazing treatments, and therefore no surrogacy for treatment effects was identified. The abundance of the genus *Monomorium*, however, showed a strong negative response to grazing exclusion, but was surprisingly the only ant response to grazing. However, we did find that abundance of the genus *Pheidole* corresponded with species richness in their positive response to environmental covariate PC2, which represented an environmental gradient from exotic-dominated to native-dominated grassland. Higher-taxon abundance, therefore, appears to be a plausible surrogate for species richness responses to environment gradients. This is consistent with other studies showing higher-taxon approaches to surrogacy in insects (Cardoso et al. 2004; Rosser and Eggleton 2012; Driessen and Kirkpatrick 2017), and the prominent role of environmental gradients in structuring insect communities by acting on key species groups (Bernadou et al. 2015; Gutierrez-Canovas et al. 2015). This has been shown repeatedly for ants, where different genera are

known to respond quite differently to the environment (Andersen 1995a; Bestelmeyer and Wiens 2001; Barton et al. 2016).

In contrast with ants, bird species richness responded to the grazing treatments. Specifically, there was a modest decrease in bird species richness in spring/summer grazing exclusion sites on farms with a history of long-term rotational grazing, and this was matched by a decrease in the abundance of Meliphagidae (honeyeaters). There also was a near-significant increase in species richness on sites with the recent application of a spring/summer grazing exclusion regime. This was matched by an increase in canopy and shrub foraging birds. From an ecological perspective, continuous grazing can negatively affect bird diversity (Eldridge et al. 2016), and it is a good outcome to find that spring/summer grazing exclusion practices led to a small increase in overall richness. It is intriguing, then, to find that spring/summer grazing exclusion had a negative effect on farms that already practice restricted grazing. Other studies of rotational grazing have shown no effect on birds (Dorrough et al. 2012) or negative effects on birds (Ranellucci et al. 2012) relative to continuous grazing. Changes to grazing regimes will alter seed, nectar and insect resources for birds, and even within the short time-frame of our study appear to have had effects on components of the bird community. From a surrogacy perspective, our results show there are two plausible surrogate bird variables for the assessment of grazing treatments in our study region. Identifying both Meliphagidae and canopy/shrub foragers as surrogates of total species richness, albeit in different grazing contexts, is an important finding. Long-term monitoring of biodiversity in our study sites (i.e. >10 years), including canopy/shrub foragers in spring/summer grazing exclusion sites and honeyeaters in exclusion sites, will be critical totesting of the temporal robustness of these surrogates further, and their ability to detect biotic changes over time (Barton et al. 2014).

We also found that one ant surrogate variable (abundance of *Monomorium*) responded negatively to grazing exclusion but total ant species richness did not. Ecologically, it is unclear why this genus responded in this way, but could be due to a preference for more disturbed sites. Identifying this response to the grazing treatment does not translate to *Monomorium* being a surrogate for that intervention. In the absence of a target response, the response of a variable is just a different kind of direct measure and does not perform the function of guiding inference of the effect of a treatment on a target (Lindenmayer and Likens 2011; Barton et al. 2015). We suggest that scenarios that demonstrate associations between variables in the absence of a target cannot be called surrogacy, in the explicit sense (*sensu* Fig. 1), unless the hypothesis of correspondence is tested in some way.

*Does surrogate-target correlation predict treatment effect?*

Higher-taxon richness was the measure most strongly correlated with species richness for each taxon. This might be expected as it considered the diversity of organisms, whereas all other measures considered counts of individuals within groups. For ants, the strongest correlation was for genus richness, yet this variable did not match the positive response of species richness to the PC2 environmental covariate. Previous work has shown higher-taxon richness to be an unreliable surrogate for species richness in Australian ants (Andersen 1995b), so it is interesting that we showed a strong correlation, but no matched response, to an environmental gradient. Other significantly correlated measures (e.g. overall abundance, abundance of *Melophorus*) also did not show a similar response as species richness to the PC2 environmental gradient, with only the abundance of *Pheidole* matching the response of species richness despite not being correlated. For ants, then, raw correlation between a surrogate variable (either genus richness or group abundance) and overall species richness is a poor predictor of surrogacy potential.

For birds, total abundance and family richness were the most strongly correlated measures with bird species richness, and showed a similar lack of response to grazing exclusion as overall richness relative to all three business as usual contexts. However, even when our target of species richness did show a response to spring/summer grazing exclusion, overall bird abundance and family richness did not. This should be troubling, as abundance can often be a good surrogate for species richness (Bock et al. 2007; Magurran and McGill 2011), and a great deal of emphasis is often placed on correlation as a pre-requisite to surrogacy (Westgate et al. 2014; Yong et al. 2016). Yet, both these assumptions were to shown to be false in our study of livestock grazing.

*Conclusions*

We have shown that a recently applied ecological intervention (i.e. altered livestock grazing) induced changes in species richness of the bird community, but not the ant community. Some components of the bird community responded in a similar way, and thus could be plausible surrogates. In contrast, only a single genus in the ant community responded to grazing but cannot be regarded as a surrogate for our target. Instead, our candidate surrogate variables that had a response to grazing or the environment, but did not match the target response, provide different kinds of information useful to understanding biotic responses to environmental change more broadly. Our study also highlights that coarse measures such as community species richness can be a poor target measure for different sub-components of a community to act as biodiversity surrogates. Our choice of surrogate variables was loosely based on requiring less effort to measure than the target of species richness, whilst being informative. It could be argued that richness of species within key genera, families, or functional groups rather than abundance, might be more informative. But this negates the intrinsic purpose of a surrogate variable being easier to measure, and species level

identification of ants, in particular, is time and expertise intensive. If this were to be done then simple direct measurement of the target (i.e. species richness of ants and birds) could have been performed, and surrogacy not required (Lindenmayer and Likens 2011). Nevertheless, we have demonstrated how an explicit approach to surrogate validation can provide a robust way to critically assess surrogacy for biodiversity responses to environmental change.

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517 **Table 1.** List of surrogate variables for each taxon, grouped into higher-taxon and functional

518 surrogates.

| Surrogate variable | Ants | Birds |
|---|---|---|
| Higher-taxon richness | Genus richness | Family richness |
| General abundance | Overall abundance | Overall abundance |
| Higher-taxon abundance | Abundance of *Iridomyrmex* | Abundance of Acanthizidae |
| | Abundance of *Melophorus* | Abundance of Meliphagidae |
| | Abundance of *Monomorium* | |
| | Abundance of *Nylanderia* | |
| | Abundance of *Pheidole* | |
| | Abundance of *Rhytidoponera* | |
| Functional abundance | Abundance of hot climate specialists | Abundance of Ground foragers |
| | Abundance of generalist myrmecines | Abundance of Canopy and Shrub foragers |
| | Abundance of dominant Dolichoderinae | Abundance of Aerial foragers |
| | Abundance of opportunists | |
| Target | Species richness | Species richness |

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522 **Table 2.** Surrogate ant variables ranked in order of correlation strength with their target of

523 ant species richness, and the corresponding effects of grazing treatments.

| Ant variables | Correlation with species richness | P | Effect of all-year exclusion | Effect of spring/summer exclusion | PC1 | PC2 | PC3 |
|---|---|---|---|---|---|---|---|
| Total species richness | n/a | | - | - | - | +ve | - |
| Genus richness | 0.822 | *** | - | - | - | - | - |
| Abundance of hot climate specialists | 0.391 | *** | - | - | - | - | - |
| Abundance of *Melophorus* | 0.385 | *** | - | - | - | - | - |
| Abundance of generalist myrmecines | 0.263 | * | - | - | -ve | - | - |
| Total abundance | 0.252 | * | - | - | -ve | | - |
| Abundance of *Pheidole* | 0.202 | n.s. | - | - | - | +ve | - |
| Abundance of *Monomorium* | 0.188 | n.s. | -ve | - | -ve | - | - |
| Abundance of opportunists | 0.131 | n.s. | - | - | +ve | - | - |
| Abundance of *Nylanderia* | 0.112 | n.s. | - | - | - | - | - |
| Abundance of dominant Dolichoderinae | 0.085 | n.s. | - | - | - | - | - |
| Abundance of *Iridomyrmex* | 0.084 | n.s. | - | - | - | - | - |
| Abundance of *Rhytidoponera* | -0.008 | n.s. | - | - | +ve | - | - |

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526 **Table 3.** Surrogate bird variables ranked in order of correlation strength with their target of
527 bird species richness, and the corresponding effects of grazing treatments. Direction of effect
528 and grazing context are given.

| Bird variables | Correlation with species richness | P | Effect of all-year exclusion | Effect of spring/summer exclusion | PC1 | PC2 | PC3 |
|---|---|---|---|---|---|---|---|
| Total species richness | n/a | | - | +ve CG, -ve LH | - | - | - |
| Family richness | 0.899 | *** | - | - | - | - | - |
| Total abundance | 0.802 | *** | - | - | - | - | - |
| Abundance of Canopy and Shrub foragers | 0.764 | *** | - | +ve CG | -ve | - | - |
| Abundance of Aerial foragers | 0.587 | *** | - | - | -ve | - | - |
| Abundance of Meliphagidae | 0.531 | *** | - | -ve LH | -ve | - | +ve |
| Abundance of Acanthizidae | 0.433 | *** | - | - | -ve | +ve | - |
| Abundance of Ground foragers | 0.305 | n.s. | - | - | - | - | - |

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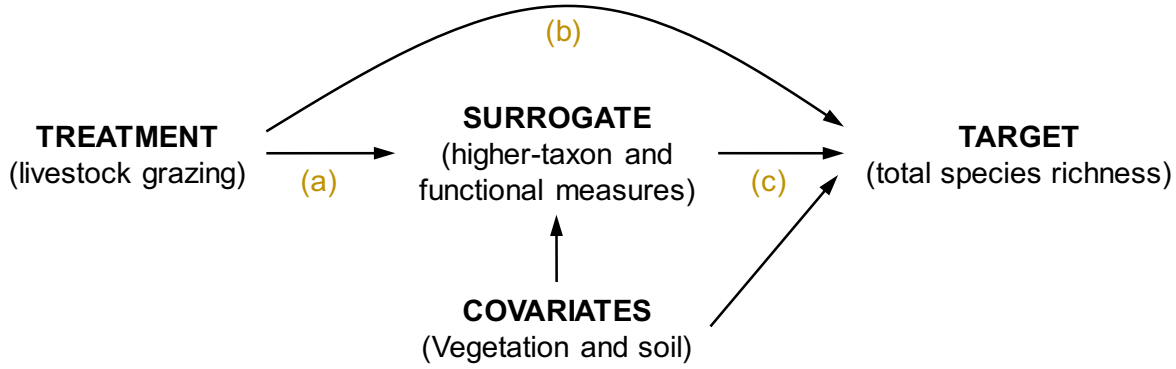


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533 **Figure 1.** A surrogate concept that incorporates the relationships between treatment,
534 surrogate, and target, as well as covariates. (a) We quantified the effects of the grazing
535 treatments on a range of candidate surrogate variables, as well as (b) treatment effects of the
536 target for both bird and ant assemblages. Environmental covariates were also considered in
537 separate models. (c) We then examined the correlations between surrogate and target
538 variables to see if this gave any insight into which surrogate and target responses to the
539 treatment were similar.

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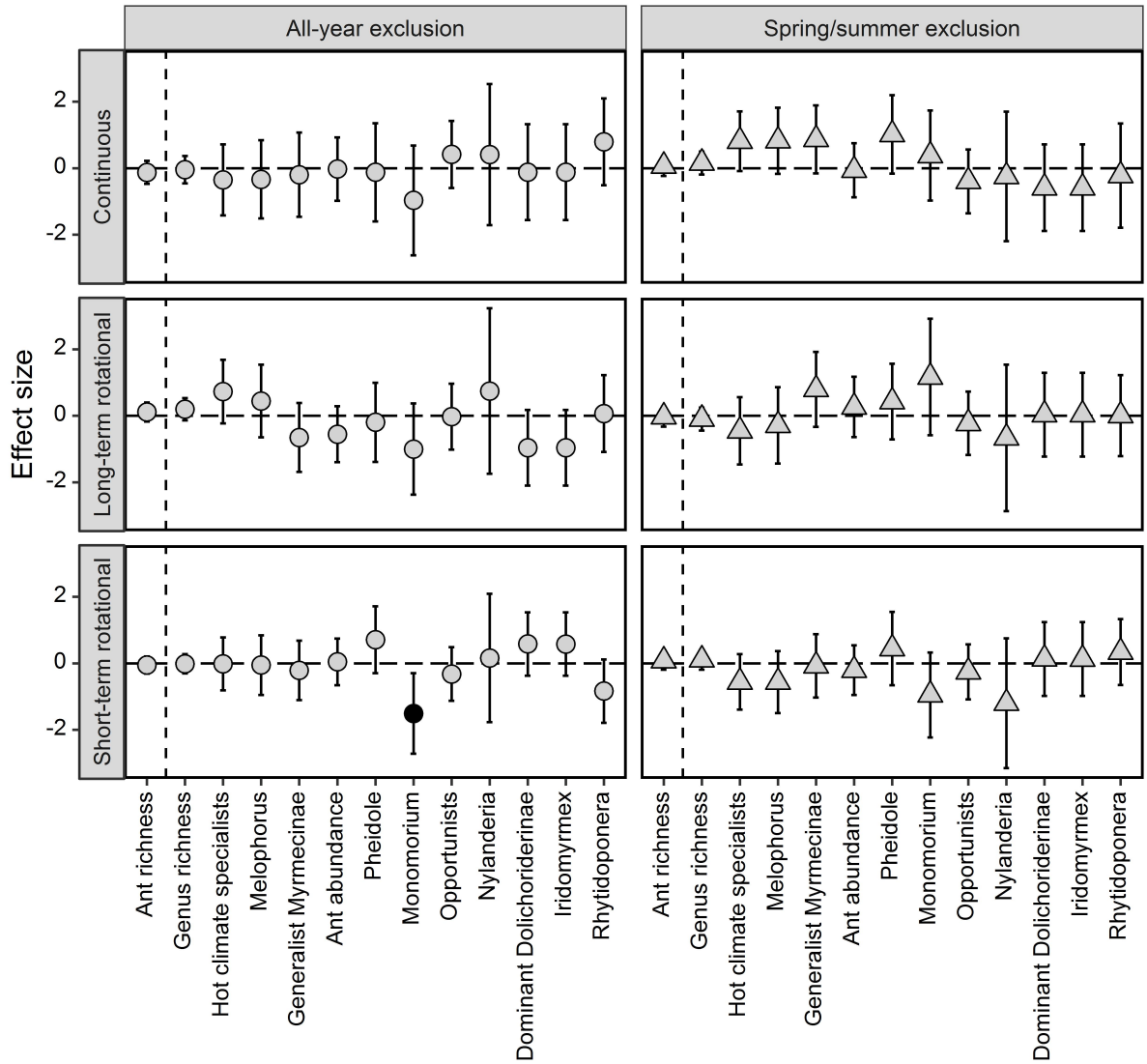


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545 **Figure 2.** Effects of grazing treatments on ant species richness (the target) and various ant

546 surrogate variables relative to sites with business-as-usual grazing. Mean effect sizes and

547 their 95% confidence intervals are given.

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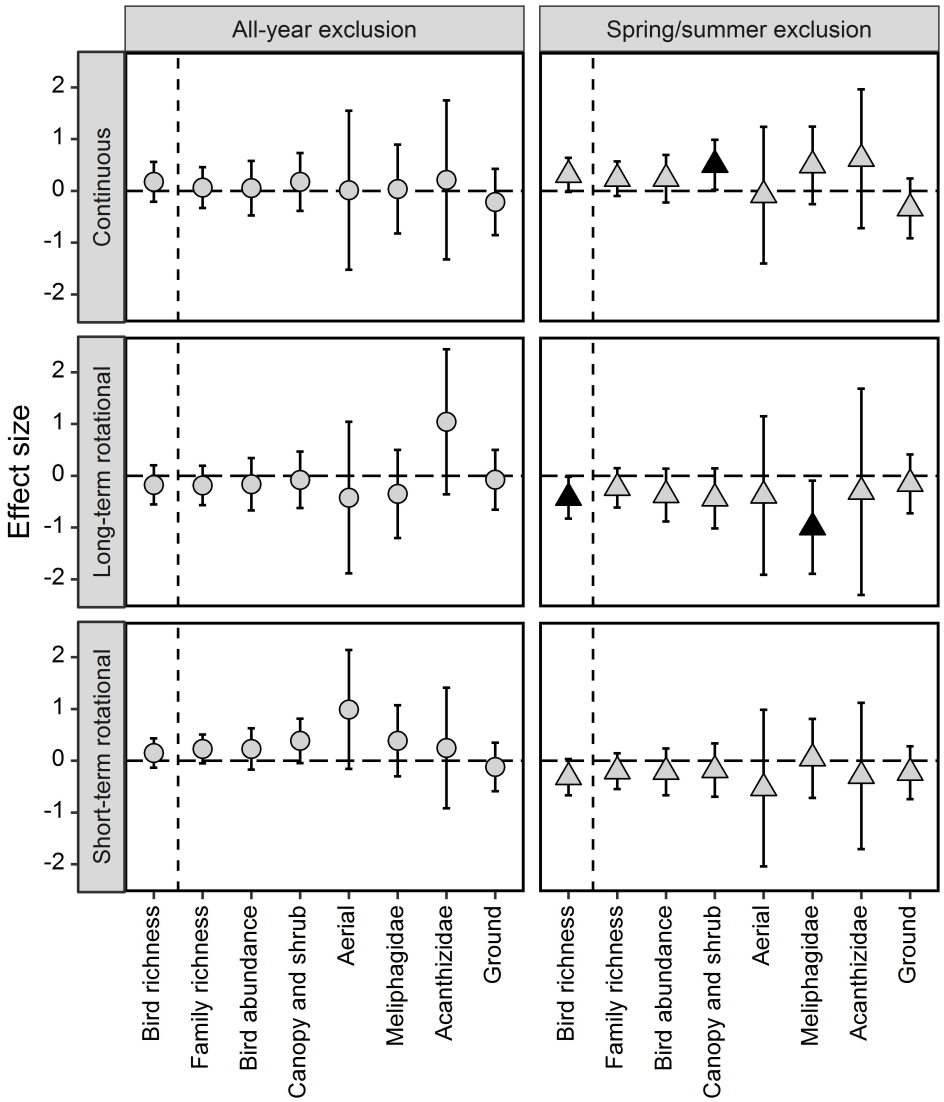


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550 **Figure 3.** Effects of grazing treatments on bird species richness (the target) and various

551 surrogate variables relative to sites with business-as-usual grazing. Mean effect sizes and

552 their 95% confidence intervals are given.

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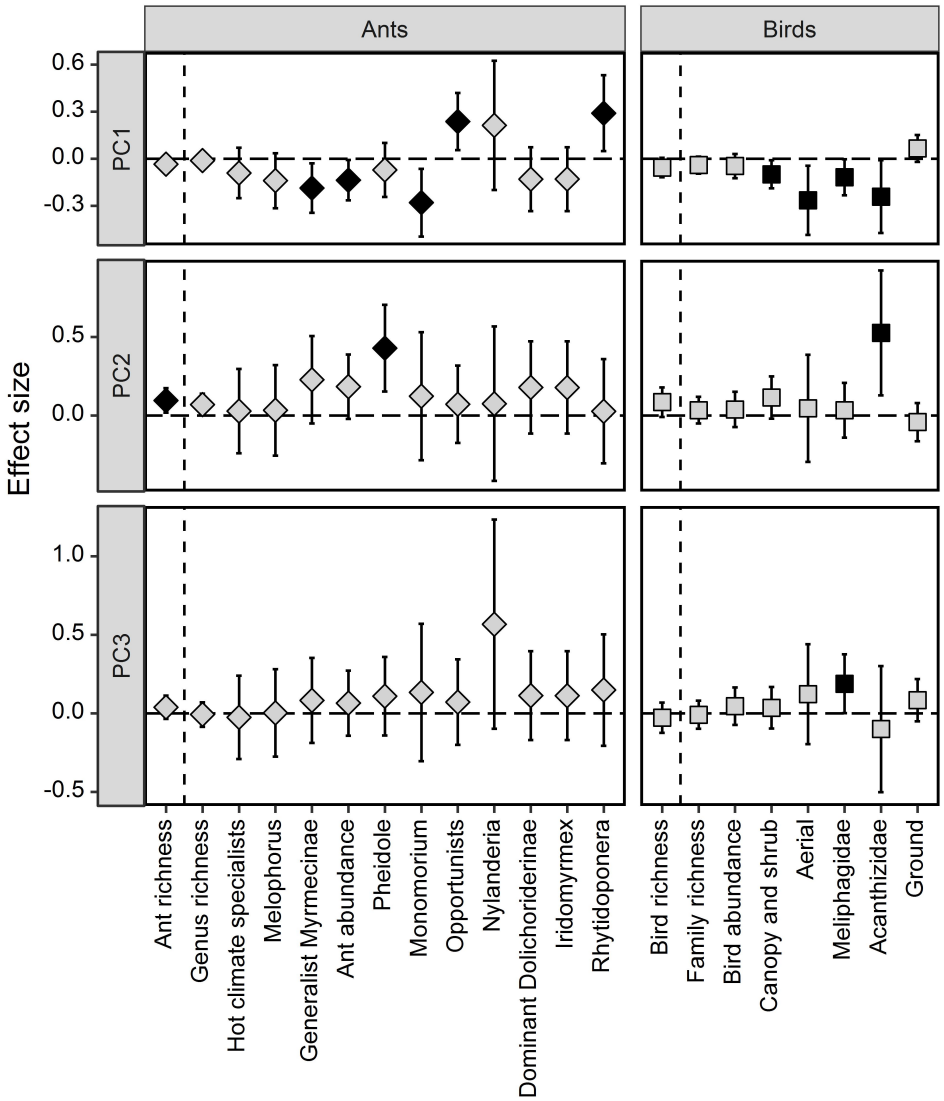


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556 **Figure 4.** Effects of environmental covariates on ant and bird surrogate variables.

557 Environmental effects are relative to the intercept, with mean effect sizes and their 95%

558 confidence intervals given. PC1 represents a gradient from under trees out to improved

559 pasture/grassland sites. PC2 represents a gradient of exotic perennial to native annual grass

560 cover. PC3 represents a gradient of increasing native perennial grass cover (see Table S2).