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Abstract

Habitat loss is widely acknowledged as a key driver of global biodiversity decline. However, whether biodiversity loss occurs in response to reductions in habitat amount versus reductions in connectivity in fragmented landscapes is debated. A challenge in resolving this issue is that measures of the amount of native woody vegetation cover and those calculated for structural connectivity are often highly correlated. Using multi-season detection-occupancy models we address the question: After accounting for the effects of native woody vegetation cover, what is the contribution of structural connectivity to site occupancy, site persistence and site colonization by birds? In this context, structural connectivity corresponded to the configuration of vegetation cover in the landscape surrounding our sites. We constructed multi-season detection-occupancy models for 44 individual bird species based on long-term field surveys in the temperate woodlands of eastern Australia. We found responses to vegetation amount were far more prevalent than responses to structural connectivity (35 vs 6 species). The range of responses by different species to vegetation amount, to structural connectivity, or to both, suggests that these elements have different effects on the processes of occupancy, persistence and colonization. The predominance of vegetation amount effects in our study, particularly the positive effects for a range of species of conservation concern, suggests the critical importance of both conserving existing areas of native vegetation cover and increasing the amount of that cover. At least for birds, efforts to physically connect particular patches may have relatively less benefit compared to programs to boost overall vegetation cover.

Keywords	Temperate woodland, restoration, south-eastern Australia, endangered ecological communities, circuit theory
Taxonomy	Environmental Science, Biological Sciences
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Highlights

- Biodiversity loss can result from changes in habitat loss and connectivity
- We tested their relative effect on birds in a 13 year study
- Habitat amount was a more prevalent variable in occupancy models than connectivity
- Responses to total vegetation cover and to connectivity were not always positive
- Land managers should identify species targeted by vegetation restoration actions

Habitat amount versus connectivity: an empirical study of bird responses

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Running Head: Bird responses to vegetation cover and connectivity

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Abstract

Habitat loss is widely acknowledged as a key driver of global biodiversity decline. However, whether biodiversity loss occurs in response to reductions in habitat amount versus reductions in connectivity in fragmented landscapes is debated. A challenge in resolving this issue is that measures of the amount of native woody vegetation cover and those calculated for structural connectivity are often highly correlated. Using multi-season detection-occupancy models we address the question: *After accounting for the effects of native woody vegetation cover, what is the contribution of structural connectivity to site occupancy, site persistence and site colonization by birds?* In this context, structural connectivity corresponded to the configuration of vegetation cover in the landscape surrounding our sites. We constructed multi-season detection-occupancy models for 44 individual bird species based on long-term field surveys in the temperate woodlands of eastern Australia. We found responses to vegetation amount were far more prevalent than responses to structural connectivity (35 vs 6 species). The range of responses by different species to vegetation amount, to structural connectivity, or to both, suggests that these elements have different effects on the processes of occupancy, persistence and colonization. The predominance of vegetation amount effects in our study, particularly the positive effects for a range of species of conservation concern, suggests the critical importance of both conserving existing areas of native vegetation cover and increasing the amount of that cover. At least for birds, efforts to physically connect particular patches may have relatively less benefit compared to programs to boost overall vegetation cover.

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1 Introduction

More than 60% of the earth's terrestrial natural vegetation has been cleared or significantly modified by human activities (Gibbs and Salmon, 2015; SERA, 2016), particularly for agriculture and grazing of domestic livestock (FAO, 2009; Williams and Price, 2011; Tilman et al., 2017). These changes have had profound effects on ecological processes and on biodiversity (Maxwell et al., 2016; Ceballos et al., 2017; IPBES, 2018).

The transformation of landscapes typically leads to a loss of native vegetation cover and can result in the sub-division or fragmentation of remaining vegetation cover (Forman, 1995). The results of these two processes is both a change in the amount of native vegetation remaining and the structural connectivity or spatial configuration of that remaining habitat. The spatial configuration of vegetation can have major impacts on the ability of organisms to move between areas of habitat (Driscoll et al., 2013; Pinaud et al., 2018), leading to changes in structural connectivity for those organisms (Soulé et al., 2004; Lindenmayer and Fischer, 2006; Dickson et al., 2018).

It is widely acknowledged that habitat loss is a primary driver of biodiversity loss worldwide (Fischer and Lindenmayer, 2007; Haddad et al., 2015). In major reviews, Fahrig (2003, 2017) suggested that the total amount of vegetation cover was the key driver of biodiversity (such as species richness) in human-modified landscapes. In contrast, the spatial configuration of that cover (i.e. structural connectivity) – independent of the amount of habitat – was found to have limited influence on biota, and such effects (when detected) were positive (Fahrig, 2017). This finding has proved contentious, as others have argued that fragmentation is important and the potentially negative effects on biota resulting from

reduced structural connectivity should not be discounted (Haddad et al., 2015; Fletcher et al., 2016; Dickson et al., 2018; Fletcher et al., 2018a). Debates about the relative influence of habitat amount versus habitat configuration are ongoing and unresolved (Fahrig, 2017; Fletcher et al., 2018a). In this context, it is important to quantify the relative contribution of vegetation amount and structural connectivity (or vegetation configuration) to biodiversity persistence in human-modified landscapes. This is because such studies can influence the kinds of land management strategies undertaken to achieve conservation outcomes. As an example, they can affect actions taken to restore landscapes by influencing decisions either to expand the total amount of native vegetation cover in a landscape or to focus on physical connections between existing remnant vegetation patches (see Falcy and Estades, 2010).

Here we sought to explore the importance of the amount of vegetation cover and the structural connectivity (i.e. spatial configuration) of that vegetation for birds in a large-scale (1.8 m ha), long-term (13 year) study in the temperate woodlands of south-eastern New South Wales, Australia. Our study encompassed 156 sites, each of 2 ha, on 46 farms in which the amount of native woodland tree cover varied from 3% to 34% of the area of 2 km in radius surrounding our sites (which were themselves wooded). In addition, the amount and spatial pattern of vegetation cover around these long-term field sites has been dynamic as a consequence of natural regeneration as well as extensive revegetation projects (Lindenmayer et al., 2016a). At the same time, changes in legislation in New South Wales have resulted in land clearing (i.e. a net loss in vegetation cover) in some areas, including in the areas surrounding our long-term sites in parts of our study region (NSW OEH, 2018).

In our target study environment, extensive land clearing in the past (see Benson, 2008) has resulted in agricultural landscapes dominated by pastures with only small remaining patches of temperate woodland (Gibbons and Boak, 2002). This is common in many formerly wooded agricultural landscapes globally (IPBES, 2018). Extensive landscape modification, together with the fact that structural connectivity measures are sometimes calculated from estimates of woody vegetation cover (see McRae et al., 2008; McGarigal, 2015), means that native vegetation cover and native vegetation configuration can be correlated (Lindenmayer and Hobbs, 2007). This creates a major challenge for quantifying the relative contribution of the amount of native woody vegetation cover versus vegetation configuration to the occurrence of biodiversity in agricultural landscapes. We sought to tackle this challenge by addressing the overarching question: *After accounting for the effects of the total amount of native woody vegetation cover in the landscape, what is the contribution of structural connectivity to site occupancy, site persistence and site colonization by birds?* Due to the dependence of many species in our study region on trees for foraging or nesting (Fischer et al., 2010; Lindenmayer et al., 2015), we predicted a positive relationship between the amount of native vegetation cover and site occupancy, site persistence, and site colonization. Patterns of spatial configuration in vegetation cover characterized by large gaps in tree cover (and hence low levels of connectivity) may impair the movement of birds through cleared or semi-cleared agricultural landscapes (e.g. Cooper and Walters, 2002). Thus, we predicted there would be negative responses to low levels of structural connectivity for some species (Soulé et al., 2004; Morrison et al., 2006; McRae et al., 2008; Fahrig, 2017; Dickson et al., 2018).

2. Methods

2.1 Study area

Our study encompassed a 1.8 million ha agricultural area (and spanning 150 km north-south and 120 km east-west) within the South West Slopes region of New South Wales, south-

eastern Australia (Fig. 1). The region was formerly dominated by temperate woodland (Lindenmayer et al., 2010), but has been cleared of an estimated 85% of its original cover to facilitate livestock grazing and cereal cropping. It is one of the most heavily modified agricultural regions worldwide (Fischer et al., 2009) and is characterised by a range of land degradation problems (Lindenmayer et al., 2016b). In an effort to tackle these problems, major restoration programs have been undertaken (Lindenmayer et al., 2016a). There also has been substantial natural regeneration of temperate woodlands, particularly over the past 15 years (Geddes et al., 2011; Lindenmayer et al., 2012), often as a result of changes in livestock grazing pressure (Fischer et al., 2009). Thus, woody vegetation in the South West Slopes region can be grouped in three broad categories: actively replanted woodland (restoration plantings), naturally regenerated woodland (regrowth woodland), and old-growth woodland (Lindenmayer et al., 2016b). Importantly, these different broad types of native vegetation cover typically support different assemblages of birds (Lindenmayer et al., 2012) and hence it was appropriate to use this site-type classification for the study reported here.

2.2 Study design

Our investigation was based on 156 long-term field sites, each of 2 ha in size and comprising a 200 m long and 100 m wide transect with permanent steel post markers established at the 0, 50, 100, 150 and 200m points along the transect (Fig 2). The size of our sites was broadly matched to the typical size of woodland patches that characterize the heavily modified agricultural areas of south-eastern Australia (Gibbons and Boak, 2002). Our 156 sites were located on 39 farms (Fig. 1), and comprised 33 restoration planting sites, 57 regrowth woodland sites, and 66 old-growth woodland sites. Restoration plantings were areas of planted understory and overstory native vegetation with a mix of native and exotic ground cover. Woody plants were typically spaced 2 m apart, but there was not a standard set of spacing and plant species composition protocols applied in revegetation efforts. All restoration plantings were at least seven years old at the start of this investigation (2002) and many were 10-20 years old. Most restoration plantings had been established to mitigate problems associated with soil erosion and/or secondary salinity. Regrowth woodland refers to existing living trees recovering after disturbance by fire, clearing or both, or regeneration of trees from seeds germinating after being dropped by overstory trees. Areas of regrowth woodland were generally of similar age to the replanted woodlands in our study. Old-growth woodland stands were typically dominated by large scattered trees that were 200 or more years old.

2.3 Field surveys of birds

Our study area supports more than 166 species of native birds including a range of species of conservation concern (Montague-Drake et al., 2009). We conducted surveys in 2002, 2004, 2006, 2008, 2009, 2011, 2013 and 2015. We completed 1248 site x year survey combinations over the 13-year period of our study. We conducted all surveys in late October, which is the breeding season for the majority of species and when summer migrants have arrived. Our standardized protocol entailed 5-minute point interval counts (*sensu* Pyke and Recher, 1983) at the 0 m, 100 m and 200 m points along the 200 m transect at each site, with birds recorded when within 100 m of an observer. We did not record birds outside of our 2 ha sites. In each year of our surveys, each site was surveyed twice by two different, highly experienced ornithologists, on different days to account for observer heterogeneity and day effects (Cunningham et al., 1999; Field et al., 2002; Lindenmayer et al., 2009). We did not treat individual point counts as independent samples, but rather pooled counts across the 0 m, 100 m and 200 m plots within each site to give the presence/absence of each species at that site on

any given survey day. Repeat surveys at a site within a year were included as repeats to allow estimation of detection rates.

2.4 Measures of vegetation cover and structural connectivity

We calculated the proportion of 25 m x 25 m pixels that supported native vegetation cover within a square with a side length of 2 km centred at each of our 156 long-term sites, we term this variable ‘vegetation cover’. This was done from satellite data for each year from 2002 to 2015 (the duration of our study). Notably, the vegetation cover at our sites has remained intact, but the amount of native woody vegetation cover in the surrounding landscape has changed, with both increases and decreases over the 13-year duration of the study.

We used the software package Circuitscape (McRae et al., 2008) to calculate a measure of structural connectivity (i.e. native vegetation configuration) in the landscape surrounding each site between the years 2002 and 2015. We used the same squares used to compute vegetation cover. Specifically, we used conductance to measure structural connectivity, which corresponds to landscape permeability and hence the potential exchange of individuals between populations (see McRae et al., 2008; Dickson et al., 2018). For computational reasons, due to the large number of Circuitscape runs (156 sites x 8 years of surveys), we decided to aggregate the satellite data into 50 m x 50 m grids with a score for vegetation cover ranging from 0 to 4, counting the number of 25 m x 25 m grids that were vegetated.

Let v denote the number of 25 m x 25 m grid cells in the 100 m x 100 m “super” grid cell that are vegetated, that is, v ranges from 0 to 4. The resistance of each super grid cell is, $r = (5 - v)^2$, and note, we are assuming that no cell has infinite resistance to birds moving across it. We applied a quadratic transformation to this score, which gave the difference between 1 and 2 vegetated cells greater weight than the difference between 3 and 4 vegetated cells, and provided an intuitively interpretable measure of resistance from simulated grids.

Now consider the raster grid for one site and one year, we denote the grid by

$$\mathbf{R} = r_{ij}, i = 1, \dots, 41 \text{ and } j = 1, \dots, 41$$

With the centre grid cell presenting the site. The resistance raster, $\mathbf{R}$, served as our input to Circuitscape to arrive at effective resistances (resistance distance), denoted by $\hat{R}_{kC}$, $k = 1, 1680$, the effective resistance between each point on the grid and the centre point. We then convert the effective resistances to effective conductances, via $\hat{G}_{kC} = 1/\hat{R}_{kC}$. Our measure of conductance for a given site and year is then the average of the effective conductances, $\hat{G}_{kC}$, measured from the centre point of the grid to each of the other grid cells (see McRae et al., 2008, specifically Table 1, for more details).

We calculated measures of the amount of native woody vegetation cover and structural connectivity in the landscapes surrounding each of our study sites in each year of our investigation. Hence our study was an investigation of spatio-temporal landscape context effects and was not a patch-level study. Spatial and temporal changes in the amount of vegetation cover and structural connectivity occurred during the study period because of vegetation restoration (i.e. restoration plantings and natural regeneration) but also land clearing.

3. Statistical analyses

We used a dynamic multi-species occupancy model to quantify the initial occupancy status in 2002 and the subsequent colonization and persistence of unoccupied and occupied sites, respectively. In employing a multi-species occupancy model framework, we acknowledge that our inference was associated with the probability of use of sites rather than strict site occupancy. We followed the notation of Royle and Kéry (2007) with appropriate modifications based on Maphisa et al. (2019) (Appendix A Eq. A.1).

Let I represent the number of species, J be the number of sites, K be the number of repeat surveys and T be the number of primary sampling periods (in our case years). Let the binary variable $y_{i,j,k,t}$ denote whether or not species i was detected at site j during sampling occasion k in year t . We denote the true occupancy status of site j of species I during the initial sampling period t by the binary variable: $z_{i,j,t}$. We denote the probability of occupancy by $\psi_{i,j,t} = \Pr(z_{i,j,t} = 1)$, which we allowed to vary due to site-level characteristics (see below for more details). Royle and Kéry (2007) define the survival/persistence probability $\phi_{i,j,t} = \Pr(z_{i,j,t+1} = 1 \mid z_{i,j,t} = 1)$ and the colonization probability $\gamma_{i,j,t} = \Pr(z_{i,j,t+1} = 1 \mid z_{i,j,t} = 0)$.

Royle and Kéry (2007) used the state-space representation of the occupancy-detection model as follows. The state models for initial occupancy, persistence and colonization are given by the following logistic regression models. Initial Occupancy for species i at site j :

$$z_{i,j,1} \sim \text{Bernoulli}(\Psi_{i,j,1}), i = 1, \dots, I, \text{ and } j = 1, \dots, J$$

where we allowed the initial occupancy probability to depend on the following covariates via a logit link function:

$$\text{logit}(\Psi_{i,j,1}) = \theta_i^0 + \theta_i^1 \text{Planting}_{j,1} + \theta_i^2 \text{Regrowth}_{j,1} + \theta_i^3 \text{VegCover}_{j,1} + \theta_i^4 \text{ResConn}_{j,1}$$

where: $\text{Planting}_{j,1}$ is an indicator variable for planting (note that the reference level is old growth) at site j and time period 1, $\text{Regrowth}_{j,1}$ is an indicator for regrowth sites, $\text{VegCover}_{j,1}$ is the total amount of vegetation cover and $\text{ResConn}_{j,1}$ is the residual amount of connectivity. The species specific parameters: $\theta_i^0, \theta_i^1, \theta_i^2, \theta_i^3, \theta_i^4$ were assumed to follow normal distributions. For subsequent years, we have the following relationships:

$$z_{i,j,t} \mid z_{i,j,t-1} \sim \text{Bernoulli}(z_{i,j,t-1} \phi_{i,j,t-1} + [1 - z_{i,j,t-1}] \gamma_{i,j,t-1})$$

and

$$\Psi_{i,j,t} = \Psi_{i,j,t-1} \phi_{i,j,t-1} + (1 - \Psi_{i,j,t-1}) \gamma_{i,j,t-1}$$

with the following logistic models for persistence and colonization:

$$\text{logit}(\phi_{i,j,t}) = \eta_i^0 + \eta_i^1 \text{Planting}_{j,t} + \eta_i^2 \text{Regrowth}_{j,t} + \eta_i^3 \text{VegCover}_{j,t} + \eta_i^4 \text{ResConn}_{j,t}$$

and

$$\text{logit}(\gamma_{i,j,t}) = \lambda_i^0 + \lambda_i^1 \text{Planting}_{j,t} + \lambda_i^2 \text{Regrowth}_{j,t} + \lambda_i^3 \text{VegCover}_{j,t} + \lambda_i^4 \text{ResConn}_{j,t}$$

where the terms η_i^l and λ_i^l , $l = 0, \dots, 4$ are the species-specific parameters for persistence and colonization which are assumed to follow a normal distribution.

The observation equation, for $y_{i,j,k,t}$, is given by:

$$y_{i,j,k,t} \sim \text{Bernoulli}(z_{i,j,t} p_{i,j,k,t})$$

where $p_{i,j,k,t}$ is the probability of detecting and was modelled as follows:

$$\text{logit}(p_{i,j,k,t}) = \delta_i^0 + \delta_i^1 \text{Wind}_{j,k,t} + \delta_i^2 \text{Planting}_{j,k,t} + \delta_i^3 \text{Regrowth}_{j,k,t} + \delta_i^4 \text{TimeOfDay}_{j,k,t}$$

where δ_i^l , $l = 0, \dots, 4$ are species specific parameters for the detection process and $\text{Wind}_{j,k,t}$, $\text{Planting}_{j,k,t}$, $\text{Regrowth}_{j,k,t}$ and $\text{TimeOfDay}_{j,k,t}$ are the amount of wind (with four categories from 1 [no wind] to 4 [very windy] planting indicator, regrowth indicator and time of day the survey commenced, respectively for the repeat surveys in the same primary sampling unit at t , and site j .

We ran the model using the runjags (Denwood, 2016) package in R (R Core Team, 2018) which provides an interface to the JAGS (Just Another Gibbs Sampler) (see Appendix A). We ran four chains with a burn-in of 20 000 iterations followed by 50 000 samples which were thinned by a factor of ten, leaving 4000 (4 chains by 1000) for posterior inference. Convergence of the chains was assessed via the Gelman-Rubin statistic ($\hat{R}$) (Gelman and Rubin, 1992). All model parameters had $\hat{R}$ statistics less than 1.01, indicating adequate mixing of the chains. We assessed the residuals of both the detection and occupancy parts of the model using Dunn-Smyth residuals (Warton et al., 2017) and the Bayesian p-value (Royle et al., 2007). We constructed norm quantile-quantile plots, residuals vs fitted values and each of the model parameters. In general, there were no obvious patterns across the 44 species and eight time periods with one or two exceptions when a species was not detected very frequently in a given year. The Bayesian p-value was 0.5395 indicating no issues with model fit. We present posterior medians and 95% credible intervals.

Given high levels of correlation between vegetation amount and structural connectivity (see Results), we employed the methods of Graham (2003) and Dormann et al. (2013). Specifically, we regressed structural connectivity (response variable) on vegetation amount (predictor variable) and called the resulting residuals “residual structural connectivity”. Residual structural connectivity is orthogonal to vegetation amount and we can examine what additional effects connectivity has above and beyond vegetation amount.

4. Results

4.1 Correlation between vegetation amount and structural connectivity

We found evidence of strong correlation between native woody vegetation cover and structural connectivity with values varying from 0.733 to 0.760 in any given year. This is illustrated by the extensive clustering of sites in the bottom left corner of a vegetation cover x structural connectivity plot, indicating that our data were dominated by low values for both measures (Appendix C Fig. C.1).

4.2 Responses to native woody vegetation cover and structural connectivity

Of the 166 birds species recorded in our 13-year study, we recorded sufficient detections (> 100) of 44 to facilitate individual species analysis (Appendix B Table B.1). Eight of these were bird species of conservation concern (Montague-Drake et al., 2009). These were the Crested Shrike-tit (*Falcunculus frontatus*), Diamond Firetail (*Stagonopleura guttata*), Dusky Woodswallow (*Artamus cyanopterus*), Jacky Winter (*Microeca fascinans*), Restless Flycatcher (*Myiagra inquieta*), Rufous Whistler (*Pachycephala rufiventris*), Superb Parrot (*Polytelis swainsonii*), and White-browed Woodswallow (*Artamus superciliosus*).

4.2.1 Detection

We identified strong effects of wind on detection, with 37 of the 44 individual species less likely to be detected under increasingly windy conditions (Figs. C.5, C.8). There was a less pronounced time of day effect, with three species more likely to be detected early in a survey period, whereas another three species were more often recorded later in the day (Fig. C.5). We found strong effects of vegetation type on detection. Relative to old growth, eight species were more likely and 18 species were less likely to be detected in restoration plantings. Five species were more likely and three species were less likely to be detected in regrowth woodland relative to old growth woodland (Fig. C.6).

4.2.2 Occupancy

We found evidence that initial site occupancy (i.e. occupancy at the start of our investigation) was influenced by vegetation type with five species more likely and one species less likely to occupy restoration plantings relative to old growth woodland (Figs. C.2, C.7). There were no such individual species effects for site occupancy in regrowth woodland relative versus old growth woodland. Effects of the amount of vegetation cover on occupancy were prevalent; 12 species responded positively and five negatively to an increasing amount of native vegetation in the landscape surrounding our sites (Fig. 3). Six species of conservation concern (Brown Treecreeper, Crested Shrike-tit, Dusky Woodswallow, Jacky Winter, Restless Flycatcher, and Rufous Whistler); responded positively to an increasing amount of vegetation cover (Fig. 3). Negative relationships between site occupancy and the amount of vegetation cover were typically identified for taxa associated with open-country environments (e.g. Brown Songlark (*Megalurus cruralis*), Galah (*Eolophus roseicapilla*) and the exotic Common Starling (*Sturnus vulgaris*)). Site occupancy was not related to structural connectivity for any species (Fig. 3).

4.2.3 Persistence

Few species exhibited differences in site persistence among vegetation types; one species was more likely to persist in restoration plantings versus old growth and three species in regrowth relative to old growth (Figs. C.3, C.7). The persistence of seven species was negatively related and one species positively related to the amount of native vegetation cover surrounding our sites (Fig. 4). One of the species that was negatively associated with the amount of native vegetation cover was of conservation concern (the Superb Parrot). The persistence at a site of only one species (the Rufous Whistler, which is a bird of conservation concern) was related to high levels of structural connectivity whereas two species were more likely to persist at sites with low levels of structural connectivity (the exotic Common Starling and the Rainbow Bee-eater, *Merops ornatus*) (Fig. 4).

4.2.4 Colonization

We found that three species were more likely and two species less likely to colonize restoration plantings relative to old growth (Figs. C.4, C.8). Seven species were more likely (and no species less likely) to colonize sites where the amount of surrounding native vegetation was high. Of these, two species (the Restless Flycatcher, White-browed Woodswallow) were of conservation concern (Fig. 5). Three species (Grey Fantail (*Rhipidura albiscapa*), Peaceful Dove (*Geopelia striata*) and Weebill (*Smicrornis brevirostris*) were more likely (and no species less likely) to colonize sites where there high levels of structural connectivity. (Fig. 5)

In summary, our analyses revealed marked inter-specific differences in occupancy, persistence and colonization responses to total vegetation amount and structural connectivity. Moreover, few species exhibited broadly similar occupancy, persistence or colonization responses to vegetation amount, to connectivity, or both. For example, colonization of sites by only one species (the Grey Fantail) exhibited the same (positive) association with both the total amount of vegetation cover and structural connectivity (Fig. 5). Site occupancy and site colonization but not site persistence of the Restless Flycatcher was positively related to the amount of cover. In the case of the Rufous Whistler, the species exhibited a positive site occupancy response to increasing vegetation cover (Fig. 3) and a positive colonization response to increasing levels of structural connectivity (Fig. 5). The Common Starling was more likely to persist at sites with low levels of vegetation cover and low levels of structural connectivity (Fig. 4). A similar pattern for this species was found for site occupancy and vegetation cover but not for structural connectivity. The White-plumed Honeyeater (*Ptilotula penicillata*) was characterized by positive site occupancy and positive site persistence relationships with vegetation amount (Figs. 3, 4) but there was no evidence of a colonization response to vegetation cover (Fig. 5). There also were no structural connectivity relationships for this species for any of measures (i.e. site occupancy, site persistence nor site colonization) (Figs. 3-5).

5. Discussion

We sought to quantify relationships between vegetation amount and the spatial configuration of vegetation (as reflected by widely employed measures of structural connectivity (reviewed by Dickson et al., 2018)) and three key aspects of species response: site occupancy at the outset of the study, species persistence at a site over the duration of our investigation, and colonization of sites. We found that responses to vegetation amount were almost six times more prevalent than responses to structural connectivity with the majority of vegetation amount relationships being positive. After accounting for the effects of the total amount of vegetation in the landscape, we found that vegetation configuration (i.e. structural connectivity) did not affect site occupancy and only influenced site persistence or site colonization for six of the 41 species analysed. Few species exhibited similar occupancy, persistence or colonization responses to vegetation amount or structural connectivity. There were broad vegetation type effects for site occupancy, site persistence and site colonization for a wide range of species with the most prevalent effects being for the contrast between restoration plantings and old growth woodland. We further discuss these and other key findings in the remainder of this section and conclude with some commentary on the implications for vegetation management.

5.1 Vegetation amount versus structural connectivity effects

We found that, after accounting for the effects of vegetation amount, there were comparatively few effects of vegetation configuration (i.e. structural connectivity) (6 vs 35 for vegetation amount; Figs. 3-5). Our findings are concordant with earlier investigations indicating that the amount of vegetation cover is important for many species in extensively modified agricultural landscapes (e.g. Fahrig, 2003, 2017), but that for some species, structural connectivity also can have important effects (Fletcher et al., 2018a, 2018b).

We found that responses to vegetation amount were more common for site occupancy (17 responses; 12 positive, five negative) than for site persistence (eight responses; seven positive, one negative) and site colonization (seven responses; all positive, including three species of conservation concern). Positive relationships between an increasing amount of vegetation cover and site occupancy included those for six bird species of conservation concern. In contrast, negative relationships between site occupancy and vegetation cover were for taxa typically associated with open-country environments. One explanation for the prevalence of site occupancy responses relative to those for site persistence and site colonization is that site persistence and colonization are comparatively long-term processes and prolonged periods of monitoring may be required to quantify them in the type of detection-occupancy framework employed in this study. Species-specific investigations such as those completed by Zanette et al. (2000) and Cooper and Walters (2002) may be required to empirically document patterns of long-term site persistence and/or site colonization.

We detected negative relationships between site persistence and the amount of vegetation cover for seven species of birds (Fig. 5). The vast majority of these species are open-country taxa for which cleared areas are often suitable, or partially suitable, habitat. Examples include the Australian Magpie (*Cracticus tibicen*), Common Starling, and Pied Butcherbird (*Cracticus nigrogularis*). The dominance of such extensively modified and cleared environments in agricultural landscapes is likely to have facilitated their long-term persistence at our monitoring sites.

We detected surprisingly few species responses to structural connectivity (none for occupancy, three for site persistence and three for site colonization) (Fig. 3-5). Five of these structural connectivity relationships were positive, indicating higher levels of persistence or colonization were associated with higher levels of structural connectivity, with one of these species being of conservation concern (site persistence by the Rufous Whistler; Fig. 5). It is possible that most species of birds we examined are relatively mobile and their ability to occupy, persist or colonize sites may not be strongly affected by the configuration of vegetation cover in the surrounding landscape, as long as an adequate amount of habitat is available (at least at the scale and in the way it was measured in this study; see below). An additional, or alternative explanation for the paucity of colonization relationships with structural connectivity may be that a longer period of study than the 13 years of this investigation may be required to quantify patterns of site colonization for some species. This is especially important given the relatively low rates of breeding success (and hence potentially few dispersing offspring) among many Australian birds (Belder et al., 2018).

We suggest there are at least two key explanations for our results for the differences in the prevalence of responses to amount of native vegetation cover versus structural connectivity. First, our target group in this investigation was birds, many of which have high levels of mobility. Hence, whether and how much vegetation is present rather than the spatial arrangement of that vegetation may be the most important factor governing observed patterns of site occupancy, site persistence and site colonization. Second, there are very high levels of correlation between vegetation amount and vegetation configuration (the average value

across years was $R = 0.73$; see Fig. C.1). This was not surprising given that structural connectivity is largely derived from how much and where native woody vegetation cover occurs in a landscape (McRae et al., 2008). Numerous other measures of structural connectivity (see McGarigal, 2015) have similar problems of being derived from vegetation amount. We attempted to address this problem by using sequential regression (Graham, 2003; Dormann et al., 2013) and exploring the effects of residuals for structural connectivity after accounting for the amount of vegetation cover. A further but related issue was that the vast majority of landscapes in our study were characterized by both low levels of native vegetation cover and low values of structural connectivity (Fig. C.1). This was unavoidable because Australian temperate woodlands are among the most heavily modified biomes worldwide, with some woodland types 95-99% cleared (Lindenmayer et al., 2010). Such low levels of cover and low levels of structural connectivity can reduce the power of statistical analyses, and may include less variation than what would be necessary to produce detectable responses in some bird species. Further tests of vegetation cover and structural connectivity would require studies targeting areas with greater levels of cover and higher and more variable spatial patterns of that cover leading to higher values of structural connectivity. However, such conditions in temperate woodland landscapes simply do not exist (Gibbons and Boak, 2002). This is because of past and present land use practices (especially land clearing) (Benson, 2008) – an outcome not dissimilar to many other intensively used agricultural environments around the world (Gibbs and Salmon, 2015; IPBES, 2018). An alternative approach to solving the problems associated with the high levels of correlation between native woody vegetation cover and structural connectivity would be to conduct experiments in artificial landscapes where different spatial patterns could be created for equivalent levels of vegetation amount. These may be appropriate at a micro- or mesoscale, but such artificially created conditions will be far from realistic in the vast majority of highly modified agricultural environments globally. Nor would they be ecologically acceptable in the already very highly modified landscapes such as the ones examined in this study where remaining patches of native vegetation cover often belong to vegetation communities such as Box Gum Grassy Woodland that have been formally classified as being Critically Endangered.

We found that the range of responses to native vegetation cover and structural connectivity were typically species-specific, even among relatively functionally similar taxa such as congeneric bird species. Moreover, even within species, there were marked differences in site occupancy, site persistence and site colonization responses to vegetation amount, to structural connectivity, or both. This suggests that vegetation cover and structural connectivity have different effects on the different processes of occupancy, persistence and colonization. Such species-specific site occupancy, site persistence, and site colonization responses that characterized our analyses may well be attributed to the notion that habitat is a species-level concept (see Hall et al., 1997) and similarly for structural connectivity (Lindenmayer and Fischer, 2006; Worboys et al., 2015). On this basis, relatively simple measures of total vegetation cover or generalized estimates of structural connectivity derived from widely employed computer packages (as in this investigation) may not reflect what actually constitutes functional habitat or functional connectivity for a given species (Lindenmayer and Fischer, 2007; Prevedello and Vieira, 2010; Pulsford et al., 2017) or for a given key process (e.g. long-term persistence at sites versus colonization of sites). As an illustration from our study, species such as the Brown Songlark and the Australasian Pipit (*Anthus novaeseelandiae*) are strongly associated with cultivated paddocks and croplands that are not well represented by measures of woody native vegetation cover (e.g. temperate woodland) nor for structural connectivity metrics derived from that cover. A related issue is

that of the fixed scale of species-specific responses to vegetation cover and structural connectivity. Our measures of vegetation cover and structural connectivity were calculated at a fixed scale (in a 2 x 2 km grid cell surrounding each long-term site). However, what constitutes important differences in habitat and levels of structural connectivity will likely be at different scales for different species. For example, small-bodied bird species typically have smaller territory sizes relative to larger species (Schoener, 1968) and hence the spatial scale of suitable habitat will typically be different for each bird species as a consequence of their size.

5.2 Broad vegetation type effects

We found evidence of vegetation type effects in many of the models we constructed for site occupancy, site persistence, and site colonization. The most prevalent effects were for the contrast between restoration plantings and old growth woodland. There were mixed positive versus negative responses to the three broad types of vegetation that featured in our study. Site occupancy of species such as the Noisy Miner (*Manorina melanocephala*) was low in restoration plantings whereas for others like the Crested Shrike-tit (*Falcunculus frontatus*) and White-plumed Honeyeater it was higher in such vegetation types. Patterns of site occupancy, site persistence, and site colonization for these and all other species were markedly different in regrowth and old growth woodland. These results suggest that different broad vegetation types have contrasting effects on the different processes of site occupancy, site persistence, and site colonization. These findings corroborate the results of earlier work that demonstrated that restoration plantings, regrowth woodland and old growth woodland support different assemblages of species (Lindenmayer et al., 2012).

Finally, our findings for the effects of vegetation type, the amount of native vegetation cover and structural connectivity in the surrounding landscape highlight that, for many species of animals, multiple factors at multiple scales have an important influence on the different processes of site occupancy, site persistence, and site colonization. This illustrates the potential limitations of simple measures such as coarse-scale, satellite-based estimates of woody vegetation cover as a proxy for animal occurrence.

5.3 Implications for management

The outcomes of our work are valuable from a practical on-the-ground management perspective. In this investigation, the predominance of vegetation cover effects, and particularly positive effects for a range of species of conservation concern, suggest the critical importance of not only conserving existing areas of native vegetation cover but increasing the amount of that cover. Options for increasing the amount of habitat include investing in revegetation programs or facilitating the natural regeneration of temperate woodlands, both of which can have positive biodiversity outcomes. Our results also suggest that, at least for birds, efforts to physically connect particular patches (thereby enhancing structural connectivity) may have relatively less benefit compared to programs to boost overall vegetation cover. A further recommendation would be for land managers to be cognizant of the type of vegetation (e.g. old growth versus restoration plantings) they are conserving, not simply vegetation amount. This is because our analyses revealed that site-level factors matter for some species (e.g. site occupancy by the hyper-aggressive Noisy Miner was reduced in restoration plantings). Site-level occupancy, including for a range of birds of conservation concern, was also influenced by landscape-level vegetation cover.

Supplementary materials

Appendix A. Equation A.1. Prior specification for Dynamic multi-species occupancy modelling.

Appendix B. Table B.1. Numbers of detections of each bird species in a given year of field survey.

Appendix C. Fig. C.1. Scatter plots of the amount of native vegetation cover and connectivity, with their corresponding marginal histograms.

Fig. C.2. Forest plot showing relationships between planting (panel A) and regrowth (panel B) sites compared to old growth sites and initial site occupancy at 156 long-term field sites in south-eastern Australia.

Fig. C.3. Forest plot showing relationships between planting (panel A) and regrowth (panel B) sites compared to old growth sites and the probability of persistence at 156 long-term field sites in south-eastern Australia.

Fig. C.4. Forest plot showing relationships between planting (panel A) and regrowth (panel B) sites compared to old growth sites and the probability of colonization at 156 long-term field sites in south-eastern Australia.

Fig. C.5. Forest plot showing relationships between wind (panel A) and time of day (panel B) sites and the detection probability at 156 long-term field sites in south-eastern Australia.

Fig. C.6. Forest plot showing relationships between planting (panel A) and regrowth (panel B) sites compared to old growth sites and the detection probability at 156 long-term field sites in south-eastern Australia.

Fig. C.7. Forest plot showing the intercepts for initial occupancy (panel A) and persistence (panel B) at 156 long-term field sites in south-eastern Australia.

Fig. C.8. Forest plot showing the intercepts for colonization (panel A) and detection (panel B) at 156 long-term field sites in south-eastern Australia.

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Figure legends

Fig. 1. Location of the study area and long-term field sites in the South West Slopes of south-eastern Australia.

Fig. 2. Location of a study site showing a 200 metre bird-survey transect (yellow line) in a stand of temperate woodland. The total amount of woody native vegetation cover and the spatial configuration of cover in the landscape surrounding a site (including the one shown in the image) was calculated and used in statistical analyses (see text).

Fig. 3. Forest plot showing relationships between vegetation amount (panel A) and residual connectivity (panel B) and initial site occupancy at 156 long-term field sites in south-eastern Australia.

Fig. 4. Forest plot showing relationships between vegetation amount (panel A) and residual connectivity (panel B) and persistence at 156 long-term field sites in south-eastern Australia.

Fig. 5. Forest plot showing relationships between vegetation amount (panel A) and residual connectivity (panel B) and colonization at 156 long-term field sites in south-eastern Australia.

Author statement

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Appendix A.

Equation A.1: Prior specification for Dynamic multi-species occupancy modelling

Model: initial occupancy:

$$\text{logit}(\Psi_{i,j,1}) = \theta_i^0 + \theta_i^1 \text{Planting}_{j,1} + \theta_i^2 \text{Regrowth}_{j,1} + \theta_i^3 \text{VegCover}_{j,1} + \theta_i^4 \text{ResConn}_{j,1}$$

The intercept:

$$\theta_i^0 \sim N(\mu_\psi^0, \tau_\psi^0)$$

A normal distribution with mean μ_ψ^0 and precision τ_ψ^0 with hyper-parameters

$$\pi_\psi^0 \sim U(0,1)$$

$$\mu_\psi^0 = \log(\pi_\psi^0 / (1 - \pi_\psi^0))$$

$$\sigma_\psi^0 \sim U(0,10)$$

$$\tau_\psi^0 = \frac{1}{\sigma_\psi^0}$$

The θ_i^0 are denoted by $u.psi[i]$, $i = 1, \dots, 44$.

The remaining regression parameters:

$$\theta_i^l \sim N(\mu_\psi^l, \tau_\psi^l), l = 1, \dots, 4$$

A normal distribution with mean μ_ψ^l and precision τ_ψ^l with hyper-parameters

$$\mu_\psi^l \sim N(0, 0.37), l = 1, \dots, 4$$

$$\sigma_\psi^l \sim U(0,10), l = 1, \dots, 4$$

$$\tau_\psi^l = \frac{1}{\sigma_\psi^l}, l = 1, \dots, 4$$

The precision of 0.37 was taken from Goijman et al. (2015). In the JAGS code, the θ_i^l are denoted by , a1.psi[i], $i = 1, \dots, 44$, , a2.psi[i], $i = 1, \dots, 44$, , a3.psi[i], $i = 1, \dots, 44$ and , a4.psi[i], $i = 1, \dots, 44$

We used similar prior specifications for the other intercepts and regression parameters for the persistence, colonization and detection processes.

The η_i^l , the regression parameters for the persistence process, $\phi_{i,j,t}$, are denoted by a1.phi[i], a2.phi[i], a3.phi[i] and a4.phi[i] and the intercept η_i^0 denoted by $u.psi[i]$ in the JAGS code.

The λ_i^l , the regression parameters for the persistence process, $\gamma_{i,j,t}$, are denoted by a1.gam[i], a2.gam[i], a3.gam[i] and a4.gam[i] and the intercept λ_i^0 denoted by $u.gam[i]$ in the JAGS code.

Finally, the δ_i^l , the regression parameters for the detection process, $p_{i,j,k,t}$, are denoted by $b1[i]$, $b2[i]$, $b3[i]$ and $b3[i]$ and the intercept δ_i^0 denoted by $v.gam[i]$ in the JAGS code.

JAGS CODE:

```
sink("global2.jags")
cat("

#JAGS code starts
model
{

## Prior distributions
mean.mu.psi.u~ dunif(0, 1)
mean.psi.u <- log(mean.mu.psi.u)- log(1-mean.mu.psi.u)

mean.mu.phi.u~ dunif(0, 1)
mean.phi.u <- log(mean.mu.phi.u)- log(1-mean.mu.phi.u)

mean.mu.gam.u~ dunif(0, 1)
mean.gam.u <- log(mean.mu.gam.u)- log(1-mean.mu.gam.u)

mean.mu.v ~ dunif(0, 1)
mean.v <- log(mean.mu.v)- log(1-mean.mu.v)

mu.psi.a1 ~ dnorm(0, 0.37)
mu.psi.a2 ~ dnorm(0, 0.37)
mu.psi.a3 ~ dnorm(0, 0.37)
mu.psi.a4 ~ dnorm(0, 0.37)

mu.phi.a1 ~ dnorm(0, 0.37)
mu.phi.a2 ~ dnorm(0, 0.37)
mu.phi.a3 ~ dnorm(0, 0.37)
mu.phi.a4 ~ dnorm(0, 0.37)

mu.gam.a1 ~ dnorm(0, 0.37)
mu.gam.a2 ~ dnorm(0, 0.37)
mu.gam.a3 ~ dnorm(0, 0.37)
mu.gam.a4 ~ dnorm(0, 0.37)

mu.b1 ~ dnorm(0, 0.37)
mu.b2 ~ dnorm(0, 0.37)
mu.b3 ~ dnorm(0, 0.37)
mu.b4 ~ dnorm(0, 0.37)

sd.psi.a1~dunif(0,10)
tau.psi.a1<-pow(sd.psi.a1,-2)

sd.psi.a2~dunif(0,10)
tau.psi.a2<-pow(sd.psi.a2,-2)

sd.psi.a3~dunif(0,10)
tau.psi.a3<-pow(sd.psi.a3,-2)

sd.psi.a4~dunif(0,10)
tau.psi.a4<-pow(sd.psi.a4,-2)

sd.phi.a1~dunif(0,10)
tau.phi.a1<-pow(sd.phi.a1,-2)

sd.phi.a2~dunif(0,10)
```



```

tau.phi.a2<-pow(sd.phi.a2,-2)

sd.phi.a3~dunif(0,10)
tau.phi.a3<-pow(sd.phi.a3,-2)

sd.phi.a4~dunif(0,10)
tau.phi.a4<-pow(sd.phi.a4,-2)


sd.gam.a1~dunif(0,10)
tau.gam.a1<-pow(sd.gam.a1,-2)

sd.gam.a2~dunif(0,10)
tau.gam.a2<-pow(sd.gam.a2,-2)

sd.gam.a3~dunif(0,10)
tau.gam.a3<-pow(sd.gam.a3,-2)

sd.gam.a4~dunif(0,10)
tau.gam.a4<-pow(sd.gam.a4,-2)


sd.b1~dunif(0,10)
tau.b1<-pow(sd.b1,-2)

sd.b2~dunif(0,10)
tau.b2<-pow(sd.b2,-2)

sd.b3~dunif(0,10)
tau.b3<-pow(sd.b3,-2)

sd.b4~dunif(0,10)
tau.b4<-pow(sd.b4,-2)

sd.mu.u~dunif(0,10)
tau.mu.u<-pow(sd.mu.u,-2)

sd.mu.v~dunif(0,10)
tau.mu.v<-pow(sd.mu.v,-2)


sd.psi.u~dunif(0,10)
sd.phi.u~dunif(0,10)
sd.gam.u~dunif(0,10)
sd.v~dunif(0,10)

tau.psi.u<-pow(sd.psi.u,-2)
tau.phi.u<-pow(sd.phi.u,-2)
tau.gam.u<-pow(sd.gam.u,-2)

tau.v<-pow(sd.v,-2)

for (i in 1:nspec){

a1.psi[i] ~ dnorm (mu.psi.a1, tau.psi.a1)
a2.psi[i] ~ dnorm (mu.psi.a2, tau.psi.a2)
a3.psi[i] ~ dnorm (mu.psi.a3, tau.psi.a3)
a4.psi[i] ~ dnorm (mu.psi.a4, tau.psi.a4)

a1.phi[i] ~ dnorm (mu.phi.a1, tau.phi.a1)
a2.phi[i] ~ dnorm (mu.phi.a2, tau.phi.a2)
a3.phi[i] ~ dnorm (mu.phi.a3, tau.phi.a3)
a4.phi[i] ~ dnorm (mu.phi.a4, tau.phi.a4)

a1.gam[i] ~ dnorm (mu.gam.a1, tau.gam.a1)
a2.gam[i] ~ dnorm (mu.gam.a2, tau.gam.a2)
a3.gam[i] ~ dnorm (mu.gam.a3, tau.gam.a3)
a4.gam[i] ~ dnorm (mu.gam.a4, tau.gam.a4)

```

```

b1[i]~dnorm(mu.b1,tau.b1)
b2[i]~dnorm(mu.b2,tau.b2)
b3[i]~dnorm(mu.b3,tau.b3)
b4[i]~dnorm(mu.b4,tau.b4)

u.psi[i] ~ dnorm(mean.psi.u, tau.psi.u)
u.phi[i] ~ dnorm(mean.phi.u, tau.phi.u)
u.gam[i] ~ dnorm(mean.gam.u, tau.gam.u)

v[i] ~ dnorm(mean.mu.v, tau.v)

## Process model
for (j in 1:nsite) {

logit(psi[i,j,1]) <-u.psi[i] + a1.psi[i]*PlantingO[j,1] + a2.psi[i]*RegrowthO[j,1] + a3.psi[i]*TotVeg[j,1] + a4.psi[i]*ConnRes[j,1]
z[i,j,1]~dbern(psi[i,j,1])

for (t in 2:nyear){
psi[i,j,t]<- phi[i,j,t] * z[i,j,t-1] + gam[i,j,t]*(1-z[i,j,t-1])
z[i,j,t]~dbern(phi[i,j,t] * z[i,j,t-1] + gam[i,j,t]*(1-z[i,j,t-1]))
logit(phi[i,j,t]) <- u.phi[i] + a1.phi[i]*PlantingO[j,t] + a2.phi[i]*RegrowthO[j,t] + a3.phi[i]*TotVeg[j,t] + a4.phi[i]*ConnRes[j,t]
logit(gam[i,j,t]) <- u.gam[i] + a1.gam[i]*PlantingO[j,t] + a2.gam[i]*RegrowthO[j,t] + a3.gam[i]*TotVeg[j,t] + a4.gam[i]*ConnRes[j,t]
} # year for process model

for (t in 1:nyear) {
## Observation model
for (k in 1:nrep) {
y[i,j,k,t] ~ dbern(mu.y[i,j,k,t])
mu.y[i,j,k,t] <- p[i,j,k,t]*z[i,j,t]
logit(p[i,j,k,t]) <- v[i] + b1[i]*Wind[j,k,t] + b2[i]*PlantingD[j,k,t] + b3[i]*RegrowthD[j,k,t] + b4[i]*TimeOfDay[j,k,t]

## Observed deviance
dev[i,j,k,t]<-y[i,j,k,t]*log(mu.y[i,j,k,t])+(1-y[i,j,k,t])*log(1-mu.y[i,j,k,t])

### Predict new observation and compute deviance
y.new[i,j,k,t] ~ dbern(mu.y[i,j,k,t])
dev.sim[i,j,k,t]<- y.new[i,j,k,t]*log(mu.y[i,j,k,t])+(1-y.new[i,j,k,t])*log(1-mu.y[i,j,k,t])

} #rep
}#year observation model
}#site
}#species

sum.dev<-sum(dev[,,,])
sum.dev.sim<-sum(dev.sim[,,,])

test<-step(sum.dev.sim - sum.dev)
bpvalue<-mean(test)

} #model
",fill=TRUE)
sink()

```

R Code to call jags

```

sp.data = list(y=y, nrep=nrep, nsite=nsite, nspec=nspec, nyear=nyear, Wind=Wind, PlantingD=PlantingD, PlantingO=PlantingO,
RegrowthD=RegrowthD, RegrowthO = RegrowthO,
TotVeg=TotVeg, ConnRes=ConnRes, TimeOfDay=TimeOfDay)

```

```

## Initialize z to be sites where at least 1 detection
zst<-array(0,dim=c(nspec,nsite,nyear))

```

```

for (i in 1:nspec) {
for (j in 1:nsite) {
for (t in 1:nyear) {
zst[i,j,t]<-(sum(y[i,j,,t])>0)*1
}}}
zst[is.na(zst)]<-1

```

```

inits1<- list(z=zst,mean.mu.psi.u=runif(1,0,1),mean.mu.phi.u=runif(1,0,1), mean.mu.gam.u=runif(1,0,1),
mean.mu.v=runif(1,0,1),sd.mu.u=runif(1,0.1,5), sd.mu.v=runif(1,0.1,5),sd.psi.u=runif(1,0.1,5),sd.phi.u=runif(1,0.1,5),
sd.gam.u=runif(1,0.1,5),sd.v=runif(1,0.1,5), mu.b1=runif(1,-2,2),mu.b2=runif(1,-2,2)
,mu.b3=runif(1,-2,2),mu.b4=runif(1,-2,2), sd.b1=runif(1,0.1,5),sd.b2=runif(1,0.1,5),
sd.b3=runif(1,0.1,5),sd.b4=runif(1,0.1,5), mu.psi.a1=runif(1,-2,2),
mu.psi.a2=runif(1,-2,2),mu.psi.a3=runif(1,-2,2),mu.psi.a4=runif(1,-2,2),
sd.psi.a1=runif(1,0.1,5),sd.psi.a2=runif(1,0.1,5),sd.psi.a3=runif(1,0.1,5),
sd.psi.a4=runif(1,0.1,5), mu.phi.a1=runif(1,-2,2),mu.phi.a2=runif(1,-2,2),
mu.phi.a3=runif(1,-2,2),mu.phi.a4=runif(1,-2,2), sd.phi.a1=runif(1,0.1,5),sd.phi.a2=runif(1,0.1,5),sd.phi.a3=runif(1,0.1,5),
sd.phi.a4=runif(1,0.1,5), mu.gam.a1=runif(1,-2,2),mu.gam.a2=runif(1,-2,2),
mu.gam.a3=runif(1,-2,2),mu.gam.a4=runif(1,-2,2), sd.gam.a1=runif(1,0.1,5),sd.gam.a2=runif(1,0.1,5),sd.gam.a3=runif(1,0.1,5),
sd.gam.a4=runif(1,0.1,5))

```

```

inits2<- list(z=zst,mean.mu.psi.u=runif(1,0,1),mean.mu.phi.u=runif(1,0,1), mean.mu.gam.u=runif(1,0,1),
mean.mu.v=runif(1,0,1),sd.mu.u=runif(1,0.1,5), sd.mu.v=runif(1,0.1,5),sd.psi.u=runif(1,0.1,5),sd.phi.u=runif(1,0.1,5),
sd.gam.u=runif(1,0.1,5),sd.v=runif(1,0.1,5), mu.b1=runif(1,-2,2),mu.b2=runif(1,-2,2)
,mu.b3=runif(1,-2,2),mu.b4=runif(1,-2,2), sd.b1=runif(1,0.1,5),sd.b2=runif(1,0.1,5),
sd.b3=runif(1,0.1,5),sd.b4=runif(1,0.1,5), mu.psi.a1=runif(1,-2,2),
mu.psi.a2=runif(1,-2,2),mu.psi.a3=runif(1,-2,2),mu.psi.a4=runif(1,-2,2),
sd.psi.a1=runif(1,0.1,5),sd.psi.a2=runif(1,0.1,5),sd.psi.a3=runif(1,0.1,5),
sd.psi.a4=runif(1,0.1,5), mu.phi.a1=runif(1,-2,2),mu.phi.a2=runif(1,-2,2),
mu.phi.a3=runif(1,-2,2),mu.phi.a4=runif(1,-2,2), sd.phi.a1=runif(1,0.1,5),sd.phi.a2=runif(1,0.1,5),sd.phi.a3=runif(1,0.1,5),
sd.phi.a4=runif(1,0.1,5), mu.gam.a1=runif(1,-2,2),mu.gam.a2=runif(1,-2,2),
mu.gam.a3=runif(1,-2,2),mu.gam.a4=runif(1,-2,2), sd.gam.a1=runif(1,0.1,5),sd.gam.a2=runif(1,0.1,5),sd.gam.a3=runif(1,0.1,5),
sd.gam.a4=runif(1,0.1,5))

```

```

inits3<- list(z=zst,mean.mu.psi.u=runif(1,0,1),mean.mu.phi.u=runif(1,0,1), mean.mu.gam.u=runif(1,0,1),
mean.mu.v=runif(1,0,1),sd.mu.u=runif(1,0.1,5), sd.mu.v=runif(1,0.1,5),sd.psi.u=runif(1,0.1,5),sd.phi.u=runif(1,0.1,5),
sd.gam.u=runif(1,0.1,5),sd.v=runif(1,0.1,5), mu.b1=runif(1,-2,2),mu.b2=runif(1,-2,2)
,mu.b3=runif(1,-2,2),mu.b4=runif(1,-2,2), sd.b1=runif(1,0.1,5),sd.b2=runif(1,0.1,5),
sd.b3=runif(1,0.1,5),sd.b4=runif(1,0.1,5), mu.psi.a1=runif(1,-2,2),
mu.psi.a2=runif(1,-2,2),mu.psi.a3=runif(1,-2,2),mu.psi.a4=runif(1,-2,2),
sd.psi.a1=runif(1,0.1,5),sd.psi.a2=runif(1,0.1,5),sd.psi.a3=runif(1,0.1,5),
sd.psi.a4=runif(1,0.1,5), mu.phi.a1=runif(1,-2,2),mu.phi.a2=runif(1,-2,2),
mu.phi.a3=runif(1,-2,2),mu.phi.a4=runif(1,-2,2), sd.phi.a1=runif(1,0.1,5),sd.phi.a2=runif(1,0.1,5),sd.phi.a3=runif(1,0.1,5),
sd.phi.a4=runif(1,0.1,5), mu.gam.a1=runif(1,-2,2),mu.gam.a2=runif(1,-2,2),
mu.gam.a3=runif(1,-2,2),mu.gam.a4=runif(1,-2,2), sd.gam.a1=runif(1,0.1,5),sd.gam.a2=runif(1,0.1,5),sd.gam.a3=runif(1,0.1,5),
sd.gam.a4=runif(1,0.1,5))

```

```

inits4<- list(z=zst,mean.mu.psi.u=runif(1,0,1),mean.mu.phi.u=runif(1,0,1), mean.mu.gam.u=runif(1,0,1),
mean.mu.v=runif(1,0,1),sd.mu.u=runif(1,0.1,5), sd.mu.v=runif(1,0.1,5),sd.psi.u=runif(1,0.1,5),sd.phi.u=runif(1,0.1,5),
sd.gam.u=runif(1,0.1,5),sd.v=runif(1,0.1,5), mu.b1=runif(1,-2,2),mu.b2=runif(1,-2,2)
,mu.b3=runif(1,-2,2),mu.b4=runif(1,-2,2), sd.b1=runif(1,0.1,5),sd.b2=runif(1,0.1,5),
sd.b3=runif(1,0.1,5),sd.b4=runif(1,0.1,5), mu.psi.a1=runif(1,-2,2),
mu.psi.a2=runif(1,-2,2),mu.psi.a3=runif(1,-2,2),mu.psi.a4=runif(1,-2,2),
sd.psi.a1=runif(1,0.1,5),sd.psi.a2=runif(1,0.1,5),sd.psi.a3=runif(1,0.1,5),
sd.psi.a4=runif(1,0.1,5), mu.phi.a1=runif(1,-2,2),mu.phi.a2=runif(1,-2,2),
mu.phi.a3=runif(1,-2,2),mu.phi.a4=runif(1,-2,2), sd.phi.a1=runif(1,0.1,5),sd.phi.a2=runif(1,0.1,5),sd.phi.a3=runif(1,0.1,5),
sd.phi.a4=runif(1,0.1,5), mu.gam.a1=runif(1,-2,2),mu.gam.a2=runif(1,-2,2),
mu.gam.a3=runif(1,-2,2),mu.gam.a4=runif(1,-2,2), sd.gam.a1=runif(1,0.1,5),sd.gam.a2=runif(1,0.1,5),sd.gam.a3=runif(1,0.1,5),
sd.gam.a4=runif(1,0.1,5))

```

```

inits<-list(inits1,inits2,inits3,inits4)

```

```

## Specify the parameters to be monitored

```

```

sp.params <- c("mean.mu.psi.u","mean.mu.phi.u","mean.mu.gam.u","mean.mu.v", "sd.mu.u", "sd.psi.u", "sd.phi.u", "sd.gam.u",
"sd.v","u.psi","u.phi","u.gam","v", "mu.b1","sd.b1","b1","mu.b2","sd.b2","b2","mu.b3","sd.b3","b3","mu.b4","sd.b4","b4",
"mu.psi.a1","sd.psi.a1","a1.psi","mu.psi.a2","sd.psi.a2","a2.psi","mu.psi.a3","sd.psi.a3","a3.psi","mu.psi.a4","sd.psi.a4","a4.psi",
"mu.phi.a1","sd.phi.a1","a1.phi","mu.phi.a2","sd.phi.a2","a2.phi","mu.phi.a3","sd.phi.a3","a3.phi","mu.phi.a4","sd.phi.a4","a4.phi",
"mu.gam.a1","sd.gam.a1","a1.gam","mu.gam.a2","sd.gam.a2","a2.gam","mu.gam.a3","sd.gam.a3","a3.gam","mu.gam.a4","sd.gam.a4","a4.gam",
"z","psi","test","bpvalue")

```

```

fit.runjags44sp.dynamic<-run.jags("X:/SWSCConnectivity/Circuitscape/MultiSeasonOcc/global2.jags",
n.chains=4,data=sp.data,inits=inits,method="parallel", monitor=sp.params, adapt=4000, burnin = 20000,
sample=1000,thin=50)

```

Reference

Goijsman, A.P., Conroy, M.J., Bernardos, J.N., Zaccagnini, E. 2015. Multi-season regional analysis of multi-species occupancy: Implications for bird conservation in agricultural lands in east-central Argentina, PLoS One, 10(6): e0130874. doi:10.1371/journal.pone.0130874.

Appendix B.

Table B.1. Numbers of detections of each bird species in a given year of field survey. Species for which there were sufficient numbers of detections to facilitate detailed statistical analysis are shown in bold. Species of conservation concern are marked with a star.

SpeciesName	ScientificName	2002	2004	2006	2008	2009	2011	2013	2015	Total
Apostlebird	Struthidea cinerea	2	2	1	1	4	4	2	2	18
Australasian Grebe	Tachybaptus novaehollandiae	1	1	5	2	0	2	5	2	18
Australasian Pipit	Anthus novaeseelandiae	9	5	6	18	19	10	16	5	88
Australian Hobby	Falco longipennis	1	1	1	2	1	2	0	1	9
Australian King-Parrot	Alisterus scapularis	0	0	1	0	0	0	1	1	3
Australian Magpie	Cracticus tibicen	192	184	194	203	199	198	166	169	1505
Australian Owlet-nightjar	Aegotheles cristatus	0	0	0	1	0	2	0	0	3
Australian Pelican	Pelecanus conspicillatus	0	0	0	0	0	0	1	0	1
Australian Raven	Corvus coronoides	43	32	23	19	28	16	20	19	200
Australian Reed-Warbler	Acrocephalus australis	6	3	5	3	4	6	4	3	34
Australian Shelduck	Tadorna tadornoides	0	1	0	0	0	0	0	1	2
Australian White Ibis	Threskiornis molucca	0	2	0	1	0	0	0	0	3
Australian Wood Duck	Chenonetta jubata	2	8	6	3	4	6	7	11	47
*Black-chinned Honeyeater	Melithreptus gularis	11	4	20	4	5	2	6	2	54
Black-faced Cuckoo-shrike	Coracina novaehollandiae	47	44	50	56	52	52	58	38	397
*Black-faced Woodswallow	Artamus cinereus	0	1	0	2	0	0	0	0	3
Black-fronted Dotterel	Elsyornis melanops	0	0	0	1	0	0	0	0	1
Black-shouldered Kite	Elanus axillaris	1	0	0	0	1	3	2	0	7
Black-tailed Native-hen	Tribonyx ventralis	0	0	0	0	1	0	0	0	1
Black Falcon	Falco subniger	0	0	0	0	0	1	0	0	1
Blue-billed Duck	Oxyura australis	0	0	0	0	0	1	0	0	1
Blue-faced Honeyeater	Entomyzon cyanotis	5	7	8	9	6	7	6	7	55
Blue Bonnet	Northiella haematogaster	0	0	0	0	1	0	0	0	1
Brown-headed Honeyeater	Melithreptus brevirostris	3	1	3	3	4	7	7	6	34
Brown Falcon	Falco berigora	3	0	2	0	3	3	0	2	13
Brown Goshawk	Accipiter fasciatus	3	2	4	2	0	2	2	0	15
Brown Quail	Coturnix ypsilophora	0	1	0	0	0	3	1	0	5
Brown Songlark	Cincloramphus cruralis	9	29	2	37	25	18	5	31	156
Brown Thornbill	Acanthiza pusilla	1	0	0	0	3	4	1	2	11
*Brown Treecreeper	Climacteris picumnus	50	55	60	61	60	55	37	40	418
Brush Cuckoo	Cacomantis variolosus	0	1	0	0	0	0	0	0	1
Budgerigar	Melopsittacus undulatus	2	0	0	5	1	6	0	2	16
Buff-rumped Thornbill	Acanthiza reguloides	4	5	7	9	6	11	11	4	57
Cockatiel	Nymphicus hollandicus	9	22	0	38	30	3	8	6	116
Collared Sparrowhawk	Accipiter cirrocephalus	0	0	2	2	1	1	1	2	9
Common Blackbird	Turdus merula	8	8	5	5	1	2	4	2	35
Common Bronzewing	Phaps chalcoptera	19	30	24	16	19	9	8	8	133
Common Starling	Sturnus vulgaris	99	104	77	109	116	106	84	93	788
Crested Pigeon	Ocyphaps lophotes	69	78	104	114	87	61	51	50	614
*Crested Shrike-tit	Falcunculus frontatus	35	18	27	28	22	14	28	22	194
Crimson Chat	Epthianura tricolor	0	0	0	2	0	0	1	0	3
Crimson Rosella	Platycercus elegans	19	25	25	20	25	18	11	14	157
Diamond Dove	Geopelia cuneata	0	0	1	0	0	0	0	0	1
*Diamond Firetail	Stagonopleura guttata	8	6	3	8	10	12	17	18	82
Dollarbird	Eurystomus orientalis	8	0	4	4	3	2	1	1	23
Double-barred Finch	Taeniopygia bichenovii	0	0	0	0	0	1	1	0	2
*Dusky Woodswallow	Artamus cyanopterus	43	31	28	31	33	22	22	26	236
Eastern Great Egret	Ardea alba	0	1	0	0	0	0	0	0	1
Eastern Rosella	Platycercus eximius	157	185	174	187	176	166	153	160	1358
*Eastern Yellow Robin	Eopsaltria australis	7	4	3	2	4	3	1	2	26
Eurasian Skylark	Alauda arvensis	0	0	0	0	0	0	0	1	1
European Goldfinch	Carduelis carduelis	4	0	2	0	0	0	0	1	7

Fairy Martin	Petrochelidon ariel	4	3	4	0	4	6	5	2	28
Fan-tailed Cuckoo	Cacomantis flabelliformis	0	3	1	0	1	0	0	1	6
Fuscous Honeyeater	Ptilotula fuscus	1	0	8	3	5	2	3	1	23
Galah	Eolophus roseicapillus	105	119	134	124	128	95	106	84	895
Gang-gang Cockatoo	Callocephalon fimbriatum	0	2	0	0	0	0	0	0	2
Golden-headed Cisticola	Cisticola exilis	0	1	1	0	0	0	0	0	2
Golden Whistler	Pachycephala pectoralis	1	2	0	0	2	0	1	2	8
Great Cormorant	Phalacrocorax carbo	0	0	0	0	0	1	0	0	1
*Grey-crowned Babbler	Pomatostomus temporalis	1	8	3	6	9	15	7	7	56
Grey Butcherbird	Cracticus torquatus	19	13	24	19	21	26	21	25	168
Grey Currawong	Strepera versicolor	1	0	0	0	1	0	0	0	2
Grey Fantail	Rhipidura albiscapa	12	17	5	5	15	30	29	29	142
Grey Shrike-thrush	Colluricincla harmonica	91	75	80	72	75	81	57	65	596
Grey Teal	Anas gracilis	0	1	0	0	2	4	4	2	13
Hardhead	Aythya australis	0	1	0	0	0	1	0	1	3
*Hooded Robin	Melanodryas cucullata	8	5	3	5	6	6	0	4	37
Horsfield's Bronze-Cuckoo	Chalcites basalis	15	6	1	4	9	2	5	4	46
Horsfield's Bushlark	Mirafra javanica	2	0	0	1	4	1	0	0	8
House Sparrow	Passer domesticus	20	5	9	7	9	2	4	2	58
*Jacky Winter	Microeca fascians	24	20	20	19	28	16	17	17	161
Laughing Kookaburra	Dacelo novaeguineae	32	30	35	31	30	32	24	19	233
Leaden Flycatcher	Myiagra rubecula	4	1	1	4	1	0	3	3	17
Little Black Cormorant	Phalacrocorax sulcirostris	0	0	0	0	0	0	1	0	1
Little Corella	Cacatua sanguinea	1	6	5	9	1	4	6	4	36
Little Eagle	Hieraetus morphnoides	0	0	1	2	0	0	0	0	3
Little Friarbird	Philemon citreogularis	26	15	36	25	16	25	9	6	158
Little Lorikeet	Glossopsitta pusilla	3	4	7	7	0	0	0	0	21
Little Pied Cormorant	Microcarbo melanoleucos	0	0	1	1	0	1	0	0	3
Little Raven	Corvus mellori	0	2	2	6	15	8	15	3	51
Long-billed Corella	Cacatua tenuirostris	0	0	0	1	0	2	0	4	7
Magpie-lark	Grallina cyanoleuca	99	83	86	92	82	77	63	64	646
Masked Lapwing	Vanellus miles	1	2	1	4	1	1	2	1	13
Masked Woodswallow	Artamus personatus	33	7	1	5	3	0	8	0	57
Mistletoebird	Dicaeum hirundinaceum	6	10	5	11	19	18	14	16	99
Nankeen Kestrel	Falco cenchroides	0	0	3	2	2	5	3	4	19
Noisy Friarbird	Philemon corniculatus	46	23	24	6	7	16	8	15	145
Noisy Miner	Manorina melanoccephala	170	177	177	150	129	132	133	146	1214
Olive-backed Oriole	Oriolus sagittatus	5	6	2	2	1	1	3	2	22
Pacific Black Duck	Anas superciliosa	1	2	1	2	1	5	5	3	20
Painted Button-quail	Turnix varius	0	0	1	0	0	1	0	0	2
*Painted Honeyeater	Grantiella picta	1	1	0	0	1	0	0	0	3
Pallid Cuckoo	Cacomantis pallidus	0	3	0	2	9	3	0	4	21
Peaceful Dove	Geopelia striata	27	23	40	20	12	3	8	14	147
Peregrine Falcon	Falco peregrinus	3	5	0	0	2	1	0	0	11
Pied Butcherbird	Cracticus nigrogularis	20	23	20	26	24	23	21	19	176
Pied Currawong	Strepera graculina	3	2	6	5	3	3	3	4	29
Plumed Whistling-Duck	Dendrocygna eytoni	0	0	0	0	0	0	0	1	1
Purple-crowned Lorikeet	Glossopsitta porphyrocephala	0	0	0	0	0	1	0	0	1
Rainbow Bee-eater	Merops ornatus	21	12	15	13	12	10	14	12	109
Red-backed Kingfisher	Todiramphus pyrrhopygius	1	0	0	0	0	0	0	0	1
Red-browed Finch	Neochmia temporalis	2	4	3	2	0	5	2	6	24
Red-capped Robin	Petroica goodenovii	7	1	3	11	11	4	9	5	51
Red-rumped Parrot	Psephotus haematonotus	112	104	155	139	136	98	84	74	902
Red Wattlebird	Anthochaera carunculata	33	75	52	70	25	63	39	42	399
Restless Flycatcher	Myiagra inquieta	24	14	18	11	18	28	21	25	159
Rufous Songlark	Cincloramphus mathewsi	60	170	38	86	135	138	105	119	851
Rufous Whistler	Pachycephala rufiventris	33	31	35	21	52	48	53	62	335
Sacred Kingfisher	Todiramphus sanctus	18	16	20	25	14	25	19	19	156
Satin Flycatcher	Myiagra cyanoleuca	0	0	0	0	0	1	0	0	1

*Scarlet Robin	Petroica boodang	0	1	0	1	0	0	0	0	2
Shining Bronze-Cuckoo	Chalcites lucidus	0	1	0	0	0	3	3	2	9
Silvereye	Zosterops lateralis	3	4	1	5	2	3	6	5	29
Southern Boobook	Ninox novaeseelandiae	0	0	3	0	0	1	0	0	4
*Southern Whiteface	Aphelocephala leucopsis	0	3	1	3	7	1	0	0	15
*Speckled Warbler	Chthonicola sagittata	1	4	3	0	3	3	6	0	20
Spotted Dove	Streptopelia chinensis	0	0	1	0	0	0	0	0	1
Spotted Harrier	Circus assimilis	1	0	1	0	3	1	1	1	8
Spotted Pardalote	Pardalotus punctatus	5	2	3	3	3	2	8	0	26
Straw-necked Ibis	Threskiornis spinicollis	1	1	1	1	5	3	0	0	12
Striated Pardalote	Pardalotus striatus	158	146	139	148	185	145	121	89	1131
Striated Thornbill	Acanthiza lineata	0	3	3	1	3	2	5	3	20
Striped Honeyeater	Plectorhyncha lanceolata	0	0	1	1	0	0	0	0	2
Stubble Quail	Coturnix pectoralis	0	5	3	6	10	12	1	9	46
Sulphur-crested Cockatoo	Cacatua galerita	17	17	18	18	12	14	12	15	123
Superb Fairy-wren	Malurus cyaneus	46	48	39	34	48	78	78	80	451
*Superb Parrot	Polytelis swainsonii	15	14	18	38	20	18	20	23	166
Tawny Frogmouth	Podargus strigoides	1	0	0	1	1	1	0	0	4
Tree Martin	Petrochelidon nigricans	6	7	9	9	10	11	8	6	66
Turquoise Parrot	Neophema pulchella	0	0	0	0	0	0	2	0	2
*Varied Sittella	Daphoenositta chrysoptera	1	0	0	0	5	2	0	3	11
Wedge-tailed Eagle	Aquila audax	2	0	0	2	1	1	3	4	13
Weebill	Smicrornis brevirostris	11	14	17	19	24	29	39	41	194
Welcome Swallow	Hirundo neoxena	24	19	33	14	28	14	23	15	170
Western Gerygone	Gerygone fusca	12	9	4	3	6	13	9	17	73
Whistling Kite	Haliastur spheurnus	0	0	0	0	1	0	1	0	2
White-bellied Cuckoo-shrike	Coracina papuensis	0	0	0	0	2	0	0	0	2
White-browed Babbler	Pomatostomus superciliosus	5	6	5	9	13	7	2	4	51
White-browed Scrubwren	Sericornis frontalis	4	3	4	3	1	4	4	4	27
*White-browed Woodswallow	Artamus superciliosus	84	17	25	95	20	1	106	4	352
White-eared Honeyeater	Nesoptilotis leucotis	1	0	0	0	0	0	0	0	1
White-faced Heron	Egretta novaehollandiae	2	1	1	4	4	7	4	2	25
White-fronted Chat	Ephianura albifrons	0	0	1	1	1	0	0	0	3
White-naped Honeyeater	Melithreptus lunatus	3	2	3	0	1	0	1	2	12
White-necked Heron	Ardea pacifica	0	1	1	1	0	4	1	3	11
White-plumed Honeyeater	Ptilotula penicillatus	175	175	186	162	144	150	142	143	1277
White-throated Gerygone	Gerygone olivacea	0	2	0	3	2	6	8	8	29
White-throated Treecreeper	Cormobates leucophaea	11	8	6	9	3	8	7	5	57
White-winged Chough	Corcorax melanorhamphos	45	61	49	67	68	64	58	56	468
White-winged Triller	Lalage sueurii	9	20	6	29	84	26	62	34	270
Willie Wagtail	Rhipidura leucophrys	184	156	153	155	160	172	146	146	1272
Yellow-billed Spoonbill	Platalea flavipes	0	1	0	0	0	1	0	0	2
Yellow-faced Honeyeater	Caligavis chrysops	2	2	2	3	1	3	1	2	16
Yellow-rumped Thornbill	Acanthiza chrysorrhoa	20	21	16	29	55	50	34	62	287
Yellow-tailed Black-Cockatoo	Calyptrorhynchus funereus	0	1	0	0	0	0	0	0	1
Yellow-tufted Honeyeater	Lichenostomus melanops	0	0	2	2	1	2	0	0	7
Yellow Thornbill	Acanthiza nana	2	8	6	12	7	19	20	22	96
Zebra Finch	Taeniopygia guttata	0	0	0	1	0	0	0	0	1

Appendix C.

Fig. C.1. Scatter plots of the amount of native vegetation cover and connectivity, with their corresponding marginal histograms.

Fig. C.2. Forest plot showing relationships between planting (panel A) and regrowth (panel B) sites compared to old growth sites and initial site occupancy at 156 long-term field sites in south-eastern Australia.

Fig. C.3. Forest plot showing relationships between planting (panel A) and regrowth (panel B) sites compared to old growth sites and the probability of persistence at 156 long-term field sites in south-eastern Australia.

Fig. C.4. Forest plot showing relationships between planting (panel A) and regrowth (panel B) sites compared to old growth sites and the probability of colonization at 156 long-term field sites in south-eastern Australia.

Fig. C.5. Forest plot showing relationships between wind (panel A) and time of day (panel B) sites and the detection probability at 156 long-term field sites in south-eastern Australia.

Fig. C.6. Forest plot showing relationships between planting (panel A) and regrowth (panel B) sites compared to old growth sites and the detection probability at 156 long-term field sites in south-eastern Australia.

Fig. C.7. Forest plot showing the intercepts for initial occupancy (panel A) and persistence (panel B) at 156 long-term field sites in south-eastern Australia.

Fig. C.8. Forest plot showing the intercepts for colonization (panel A) and detection (panel B) at 156 long-term field sites in south-eastern Australia.