Direct and indirect effects of agricultural land cover on bird species richness

by

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ABSTRACT

Agriculture is one of the largest threats to global biodiversity including to birds. But we know little about whether the effects of agriculture on birds are mainly direct through farming operations, or indirect through effects on natural habitats. We sampled birds at 127 sites in eastern Ontario Canada. We used structural equation modelling (SEM) to evaluate the direct and indirect effects of agriculture on species richness of three bird guilds: forest birds, shrub-edge birds, and grassland birds. We found that forest bird richness was driven by the negative indirect effect of cropland via habitat loss. Shrub-edge and grassland bird richness increased with the amount of agriculture, despite negative indirect effects. Management efforts for bird diversity in agricultural landscapes should focus on preserving grassland and forest habitat including forest edges, while managing agricultural land, for instance, by selecting perennial crops and low impact agricultural activities.

ACKNOWLEDGEMENTS

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relationships are represented as arrows originating from the predictor and terminating at the response. The predicted relationship is either positive shown as +, or negative shown as −.

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INTRODUCTION

Agriculture is one of the largest threats to global biodiversity, mainly due to conversion of natural habitats to agricultural land covers (Dirzo and Raven 2003; Tilman et al. 2017). Such agriculturally-driven habitat loss and degradation result in both lower species abundances (Tilman et al. 2017) and lower species richness (Devictor and Jiguet 2006). Chemical inputs such as fertilizers and pesticides further reduce habitat quality for many species (Tilman 1999; Stoate et al. 2009; Jeliazkov et al. 2016; Stanton et al. 2018; Martin et al. 2020).

Birds that have similar habitat requirements likely respond in similar ways to landscape changes resulting from agriculture. Some agriculture covers can mimic native grassland habitat, which grassland birds benefit from, especially in landscapes lacking native grasslands (Santana et al. 2017; Frei et al. 2018). On the other hand, field edges and hedgerows (i.e., shrubby field margins) can provide nesting and roosting habitat and connectivity among habitat patches for open-country shrub-forest edge birds (Benton et al. 2003; Fonderflick et al. 2013; Wilson et al. 2017). These species benefit from the openness of agriculture as long as suitable shrub and edge habitat are present in the landscape (Wilson et al. 2017). For forest birds, the openness created by agricultural expansion into forested areas results in a loss of habitat and a decline in species diversity (Endenburg et al. 2019).

While there has been considerable research on the impacts of agriculture on birds, we know little about whether these impacts are direct or indirect. An understanding of direct and indirect effects is also necessary for understanding the total effects (the summation of direct and indirect effects) of a given variable on the response variable of interest. Direct effects imply a direct relationship between the agricultural activity and the bird response and could either be a response to the agricultural land cover or to agricultural operations within agricultural land (e.g., chemical application, tilling, mowing crops). Indirect effects of agriculture in contrast refer to a response to how the activity of agriculture transforms the landscape, beyond the insertion of agricultural land cover. In this case, birds are not responding to the agricultural cover types or operations *per se,* but instead, to the way that agriculture influences the extent and configuration of different types of natural land cover in the landscape.

Whether agriculture influences birds directly or indirectly has implications for how we might manage agricultural landscapes for birds. If agriculture itself is directly influencing birds then our efforts should target the agricultural component of the landscape, by manipulating the agricultural cover types or the activities on agricultural land (e.g., chemical application, tilling). On the other hand, if agriculture is indirectly influencing birds through habitat loss or creation then our efforts should focus on how best to manage the composition and configuration of the natural landscape within the agroecosystem. In many cases both direct and indirect effects will likely influence species but by understanding their relative impacts we can determine how management strategies might be best directed.

Structural equation modeling (SEM) is a way to jointly evaluate the direct and indirect effects of landscape change on biodiversity (Lefcheck 2019). SEM combines multiple relationships among variables in a single model. Recent examples include the use of SEM to determine the indirect effects of habitat loss on biodiversity through its effect on habitat fragmentation (Püttker et al. 2020), and the indirect effects of agricultural landscape pattern on aquatic invertebrate diversity through its effects on water chemistry (Collins et al. 2019). Here we use SEM to evaluate the direct and indirect effects of agriculture on bird species richness in a naturally forested ecosystem in eastern Canada.

Overall, we expect the direct effect of agriculture to influence bird richness but, because agriculture takes up land that would otherwise be natural habitat, we also expect that agriculture will indirectly affect most species by reducing the availability of natural habitats. We tested our predictions in a rural agricultural region in Eastern Ontario, Canada where we measured bird richness of three habitat-defined bird guilds: forest birds, shrub-forest edge birds (hereafter 'shrub-edge birds'), and grassland birds. In the landscape surrounding each site, we measured agriculture variables (cropland, perennial forages and grassland, and mean field size) and habitat variables (forest, shrubland, hedgerows, and forest edge). Based on our hypotheses we made predictions about relationships between landscape variables and bird richness (Table 2). We then created three SEM diagrams, one for each bird guild, based on predicted relationships between variables to estimate the direct and indirect effects of agriculture on bird guild richness (Figure 11 – 13).

METHODS

We sampled birds using autonomous recording units at 127 sites along roads in Eastern Ontario during the 2016 breeding season (Figure 1). We sampled at three time periods in the morning (30 minutes before sunrise, 30 minutes after sunrise, and 90 minutes after sunrise) on 2 days per site to determine bird richness (number of species) in each of the three habitat-based guilds: forest guild, shrub-edge guild, and grassland guild. In the landscape around each site, we measured mean field size, the length of forest edge and the proportion of the landscape in cropland, perennial forages and grassland, forest, shrubland, and hedgerows. We created three structural equation modelling (SEM) diagrams representing our predictions (Figure 11 – 13), one for each bird species guild. We tested the relationships among the agricultural variables (upper row of the SEM diagram), the habitat variables (middle row), and bird richness (lowest row) using confirmatory path analysis. We then calculated the direct, indirect via habitat, and total effects of the agriculture variables on bird richness.

Site Selection

We used a GIS road layer (Esri Inc. 2016) to randomly place potential bird sampling sites on accessible roads, except for primary highways. This resulted in 205 potential sites, of which we identified 127 that represented gradients along two land cover axes within 1 km of the sites: 1) a high proportion agriculture to a high proportion forest and 2) within the agricultural land cover class, a high proportion of cropland to a high proportion of pasture land and forage crops. Land cover types were identified using the Agriculture and Agri-Food Canada annual crop inventory (Fisette et al. 2013).

Bird sampling methods

We conducted surveys of the bird communities during the 2016 breeding season (6 June to 19 July 2016) at 127 sites (Figure 1). We used SM2+ autonomous acoustic recording units (Wildlife Acoustics Inc.) placed at approximate breast height on a fence post or a tree along the roadside, with the microphones facing away from and perpendicular to the road. The units were programmed to conduct daily surveys over 7 days. We programmed the units to record for 10 minutes every half hour from 60 minutes before sunrise until 4 hours after sunrise. We selected a systematic subsample of these recordings for interpretation, using the first and last clear (i.e., no heavy rain or wind) recording dates (generally 5-7 days apart) at each site. Within selected dates, a single skilled observer interpreted the first 3 minutes of each 10-minute recording for three time periods: 30 minutes before sunrise, 30 minutes after sunrise, and 90 minutes after sunrise. The observer recorded the minute within the 3-minute acoustic file during which each species was first detected.

Bird Guilds

We assigned each species to one of four guilds based on its breeding habitat associations provided in the Birds of North America Online (Rodewald 2015): forest guild, shrub-edge guild, grassland guild, and wetland guild. Forest species are associated with forest habitat. Shrub-edge species are associated with shrub, scrub, early successional habitats, and forest edges. Grassland species are associated with grassland and/or open field habitats. Guild richness at each site was the number of species present for each guild (Table S2). We did not include wetland species in this analysis given the lack of natural wetland habitat in our study area.

Landscape variables

We calculated the amount of cropland, perennial forages and grassland, mean field size, the amount of forest, shrubland, hedgerows, and forest edge length within a 1 km^2 square around each site using the 2016 Agriculture and Agri-Food Canada annual crop inventory (AAFC 2016; Fisette et al. 2013). In Eastern Ontario most landowners, particularly farmers, own 100-hectare properties that total an area of 1 km^2. Additionally, this scale is comparable to previous studies in the region that are based on an empirical scale of effect analysis for birds (Vala et al. 2020). Therefore, for this analysis 1 km^2 is the most relevant scale for farmland management applications. The annual crop inventory accurately maps land cover types in Ontario at a 30-m resolution and includes 66 land cover classes (Fisette et al. 2013).

We grouped land cover types to create forest, cropland, and perennial forages land covers. The forest land cover combined mixed-wood, broadleaf, and coniferous forest. For cropland we combined 20 classes of annual row crops, primarily corn, soy and wheat, and vegetables and fruits. Perennial forages included pasture and hay (Statistics Canada, 2011). Because native grassland was uncommon in our study region, we combined grassland with perennial forages, as perennial forages functionally mimic grassland habitat (Santana et al. 2017; Frei et al. 2018). Shrubland was a unique land cover. In addition to the landscape variables, we considered measuring local habitat within 150 m of the sample sites to represent the habitat where detected species were calling from. However, local and landscape (1 km^2) habitat were highly correlated (Appendix I: Figure S15 and S16). Therefore, we only used the landscape variables in our statistical analyses.

We calculated mean field size, forest edge, and proportion of hedgerows in each landscape using ESRI ArcMap (Esri Inc. 2020a) and aerial imagery (Esri Inc. 2020b). We used Patch Analyst 5 extension (Rempel et al. 2012) to calculate mean field size and total forest edge. Mean field size was calculated using the mean patch size metric for all agricultural land covers. We excluded field fragments by removing all fields that were less than 10,000 m^2. Forest edge was calculated using the total edge metric for the forest land cover. To calculate the proportion of a landscape in hedgerows we digitized woody hedgerows using the 2020 World Imagery Basemap in ESRI ArcMap (Esri 2020b), which provides one meter or better satellite and aerial imagery. Based on other landscape research in the study area, we defined hedgerows as woody linear strips around agricultural fields, that were less than 30m wide and had no gaps in the canopy greater than 12m (i.e., average tree canopy size). The minimum hedgerow length was 24m (i.e., two average tree canopy widths). To include hedgerows that were removed between the year of our field study (2016) and the year of the basemap (2020), we compared hedgerows in the 2020 basemap to 2016 Google imagery (Google Earth Pro 2016).

Statistical analysis

We tested our predictions (Figure 11 – 13) using confirmatory path analysis to calculate the direct and indirect relationships between the agricultural variables (SEM diagram upper row), habitat variables (middle row), and bird richness (lower row). We created three structural equation modeling (SEM) diagrams, one for forest birds, shrub-edge birds, and grassland birds (Shipley 2000, 2009). The SEM diagram unifies all the variables in a single causal network to test all the hypotheses simultaneously. A variable can be both a predictor and response, however, our modelling approach does not permit latent variables or cyclic variables whereby one variable can indirectly influence itself via a feedback loop. We used confirmatory path analysis because it can accommodate small to moderate sample sizes and count data (i.e., richness; Lefcheck 2019). We standardized all landscape variables before conducting the analysis using the mean and standard deviation. Bird richness variables were not standardized. We tested for spatial autocorrelation in species richness for each guild using Moran's I and found species richness was not spatially correlated for all three guilds.

We conducted the confirmatory path analysis in R using the piecewiseSEM package (R Core Team 2020; Appendix II). We began the confirmatory path analysis by conducting the directional separation test (Shipley 2000; Gonzalez-Voyer and von Hardenberg 2014), which evaluates the assumption that the SEM diagram structure reflects the data, by testing the implied independence between every pair of variables that are not directly linked. We used linear and generalized linear models to determine the probability that each unlinked pair was statistically independent (Figure 11 – 13; Appendix I: Table S6 – S8). We added links between variables that were not statistically independent. We then combined all of these probabilities using Fisher's C statistic:

$$C = -2\sum_{i=1}^{k}(ln(p_i))$$

where k is the number of independence claims and p_i is the null probability of the independence test associated with the *i*th independence claim (Shipley 2009). We compared the C value to a chi-square distribution with 2k degrees of freedom (Shipley 2000).

We then fit a series of linear and generalized linear models for each response variable, including those that were both predictors and responses (Figure 11 – 13), to determine the coefficients of all hypothesized paths leading to each response variable in the SEM diagrams. Bird richness was modeled as count data using a generalized linear model with a Poisson distribution and log-link function. All other variables were modeled using linear models with one exception: forest was modelled as a quadratic where forest edge was the predictor. The quadratic forest estimate was calculated by summing the linear and quadratic estimates. For each model we used a model selection approach (Burnham and Anderson 2002) to evaluate the statistical support for individual hypothesized paths within the model. The candidate model sets included the global model containing all predictors hypothesized to directly influence the response, an intercept-only (null) model, and all sub-models derived from the global model. The predictors in the top model with the lowest AICc were considered to have strong support. The predictors in models within 2 AICc units from the top model, but not included in the top model, were considered to have weak support. We tested model fit of the top model using the fitted and predicted values.

We used the parameterized SEM diagrams to determine the direct, indirect, and total effects of the agriculture variables on bird richness. The direct effect is the arrow directly linking the agriculture variable to bird richness (Figures 2 – 4). The indirect effect is the sum of all pathways leading from the agriculture variable to bird richness, excluding the direct arrow. Each indirect pathway was calculated by multiplying the estimates of all arrows in the pathway. The total effect of an agriculture variable was calculated by adding its direct and indirect effects.

RESULTS

Bird Community

We identified 100 bird species in total: 48 forest species, 26 shrub-edge species, and 12 grassland species (Appendix I: Figure S14). The average number of species observed per site was 17 (range 1 – 28) (Appendix I: Table S2). There were on average 7 shrub-edge bird species per site (range: 0 – 14), 7 forest bird species (range: 0 – 18) and 1 grassland bird species (range: 0 – 5; Appendix I: Table S2). All of the most commonly found species were shrub-edge species; American Crow (*Corvus brachyrhynchos*), American Goldfinch (*Spinus tristis*), American Robin (*Turdus migratorius*), and Song Sparrow (*Melospiza melodia*) were found at more than 100 sites (Appendix I: Table S1). We found four species listed as threatened on Canada's Species-at-Risk list (SARA 2002): Barn Swallow (*Hirundo rustica*) at 9 sites, Bobolink (*Dolichonyx oryzivorus*) at 29 sites, Eastern Meadowlark (*Sturnella magna*) at 20 sites, and Wood Thrush (*Hylocichla mustelina*) at 20 sites. We also found two species listed as special concern: Common Nighthawk (*Chordeiles minor*) at 2 sites, and Eastern Wood Pewee (*Contopus virens*) at 28 sites (Appendix: Table S1). Of the 6 species-at-risk, 4 species were grassland birds (3 threatened, 1 special concern) and 2 were forest birds (1 threatened, 1 special concern; Appendix I: Table S1).

Landscape Composition

In the 1 km^2 landscapes surrounding the sites, forest was the most common land cover (average proportion: 0.35, range: 0.03 – 0.90), followed by the amount of cropland (avg: 0.26, range: 0 – 0.88), perennial forages and grassland (avg: 0.19, range: 0 – 0.79), shrubland (avg: 0.07, range: 0 – 0.41), and hedgerow (avg: 0.01, range: 0 – 0.07). Mean field size was 12.8 ha (range: 0 – 88.2 ha; note, 7 landscapes had no agricultural fields) and the average total length of forest edge was 8344.9 m (range: 352.4 – 16839.3 m; Appendix I: Table S3). Forest edge length was strongly correlated with the proportion cropland (-0.74), and the proportion forest (0.72; Appendix I Table S4).

Structural Equation Modelling (SEM)

Following the independence test for our three focal avian guilds, we added arrows between: 1) cropland and hedgerow, forest edge, and bird richness for all guilds; 2) perennial forages/grassland and hedgerow, forest edge, and shrub-edge bird richness; 3) forest and shrubland; and 4) shrubland and forest edge (Figure 2 – 4). With these arrows added, the p-value of the Fisher's C statistic for the forest bird SEM diagram (Figure 2) was 0.61, for the shrub-edge SEM diagram (Figure 3) was 0.27, and for the grassland bird SEM diagram (Figure 4) was 0.59. These p-values indicate that the correlation structure in the data did not differ from the correlational structure proposed in our path models for each guild.

Generally, we correctly predicted the direction of effect for the links in our hypothesized SEM diagrams (Figure 2 – 4; Figure 11 – 13; Table 2). As we expected, the amount of agriculture (cropland and perennial forages and grassland) reduced all woody and shrubby habitat variables (i.e. forest, shrubland, and forest edge) except hedgerow amount. Also consistent with our predictions, cropland was positively related to mean field size and mean field size was negatively related to hedgerow amount. In most cases, richness of bird guilds responded positively to the habitat variables in the predicted directions, with one exception: grassland bird richness responded slightly positively to hedgerow cover, although the size of the effect was very small.

We plotted the direct relationship of bird richness with select habitat and agricultural variables. Forest bird richness increased with proportion of forest (Figure 5). Shrub-edge bird richness increased with proportion cropland (Figure 6) and perennial forages and grassland (Figure 7). Additionally, more shrub-edge birds were present in landscapes with more forest edge (Figure 8). Finally, more grassland birds were present in landscapes with higher proportions of cropland (Figure 9) and perennial forages and grassland (Figure 10).

Direct and indirect effects of the agriculture variables varied based on bird guild. The direct effect of cropland on forest bird richness was weak, while its indirect effect was strongly negative, driven by a strong negative effect of cropland on forest amount (Table 1; Figure 2). The indirect effects of agriculture were predominantly negative as expected, except for the positive indirect effect of cropland on shrub-edge birds via forest, forest edge, and shrubland amount (Table 1; Figure 3). While the indirect effect of cropland on grassland bird richness was negative, the direct effect was positive, resulting in an overall positive effect. Mean field size unexpectedly had a weak, negative total effect on grassland bird richness (Table 1; Figure 4).

DISCUSSION

Our results suggest that the negative effect of cropland on forest bird richness is not driven by cropland itself, but rather by the negative relationship between cropland and forest. In other words, it is an effect of habitat loss for forest bird species. Our study region was previously a forested landscape (Butt et al. 2005) and the transformation of the landscape with agricultural expansion largely comes at the expense of forest habitat. Thus, forest birds are not interacting directly with cropland, but rather adjusting to the loss of forest habitat. A previous study in the region showed that agricultural expansion results in a homogenization of the forest bird community mainly due to the decline of Neotropical migrant foliage-gleaning insectivores (Endenburg et al. 2019).

Unexpectedly, we found that the richness of shrub-edge birds increases with the amount of agriculture for both cropland and perennial forages. This is surprising because both cropland and perennial forages are negatively related to the types of natural woody habitats used by this guild for nesting, such as forest edge and shrubland. This finding suggests that shrub-edge nesting species benefit from agriculture, most likely for feeding or possibly through a reduction in predator abundance, despite the associated loss of breeding habitats. It is also likely that the openness created by agriculture in a forested landscape provides benefits for shrub-edge birds since they typically do not use forest interior habitat. However, habitats such as forest edges are beneficial for shrub-edge birds (Figure 8). Shrub-edge bird abundance in agricultural landscapes would be enhanced with a mix of forest edges to provide breeding habitat. While overall, if woody and open habitats maximize richness of this species group, future research should consider whether the loss of natural edge and shrubby habitats is resulting in individuals packing into remaining edge habitats. If this is occurring, it could be resulting in density dependent effects, that could affect breeding productivity for example.

We found an overall positive effect of cropland on grassland bird richness. Our results show that, even if grassland birds rarely nest within agricultural covers (e.g. corn, soy), they will benefit when agriculture takes its place within a forested ecosystem (Sekercioğlu et al. 2007; Frei et al. 2018; Wilson et al. 2020), likely because of the transformation to a more open landscape and a possible increase in food availability. Cropland may functionally mimic open habitat especially when native grassland is rare, by providing complementary habitat and supplemental resources for foraging grassland birds (Dunning et al. 1992; Da Silva et al. 2015). However, some natural grassland or pasture habitat needs to be conserved to maintain species that are more directly dependent on grassland habitats, such as Bobolinks and Eastern Meadowlarks, in agricultural landscapes (Figure 10; Da Silva et al. 2015; Wilson et al. 2017).

Opposite to our prediction, we found that the overall effect of mean field size on grassland bird richness is weak and slightly negative. This result is surprising because grassland birds are thought to benefit from larger fields because of higher nest predation closer to field edges, resulting in higher predation in smaller fields (see predictions in Table 2; Herkert et al. 2003). One explanation for this result may be that grassland birds nest at sites regardless of the predation risk associated with field size. Additionally, the weak effect suggests that landscape composition (amount of grassland) may be a stronger driver of grassland bird richness than landscape configuration (field size) in our region. Our study region was previously forested with little native grasslands, and so the limiting factor for grassland birds may be the amount of grassland. In contrast, in a natural grassland ecosystem such as the Prairies, edge habitat is a stronger driver than the amount of grassland cover (Lockhart and Koper 2018), possibly because the amount of habitat is not limiting.

By separating the direct and indirect effects of agriculture we can more accurately interpret how to manage agricultural landscapes for birds. For example, the negative effect of agriculture on forest birds was driven by the indirect effect of habitat loss. Therefore, to manage agricultural landscapes for forest birds we should manage the natural habitat rather than the agricultural component of the landscape. By only measuring the overall effect of agriculture we may overlook the significance of habitat loss and make recommendations to manage agriculture instead. For grassland birds, habitat loss reduced the overall positive effect of cropland. By not separating the direct and indirect effects we would have overlooked the importance of the natural habitat for grassland birds and made recommendations to manage agriculture only. Thus, disentangling the direct and indirect effects of agriculture allows us to focus management strategies appropriately.

We acknowledge caveats that should be considered with respect to our study design and future applications of our SEM framework. Because our surveys were conducted along roads there may be biases in the species identified if some species are less likely to select habitats near roads (Harris and Haskell 2007). However, this bias should not affect our results as it would be true for all of our sites. We also did not test all landscape or habitat variables in each model, due to sample size limitations. Other variables might improve the model fit, but the variables selected for each model are those for which we had both data and a priori hypotheses linking them to each bird guild. Future SEM studies could include agriculture practices (e.g. tilling, pesticide usage, timing of cutting, etc.) because they are known to affect bird diversity and biodiversity in general (Frei et al. 2018; Martin et al. 2020). In our models we assumed that more agriculture, particularly cropland, leads to higher intensity practices and chemical inputs because, globally, agriculture productivity has been increasing and more agriculture requires higher intensity practices and chemical inputs to achieve higher productivity (Tilman 1999; Tuninetti et al. 2020). Future studies combining the confirmatory path analysis with agricultural practices could validate this assumption.

CONCLUSIONS

Based on whether agriculture influenced birds directly or indirectly, we can make recommendations in agricultural landscapes for how to focus management efforts. As forest birds were indirectly influenced by agriculture, management efforts should focus on preserving the amount of forest in the landscape by retaining existing forest patches and allowing forest recovery, for example on abandoned agricultural sites. Because shrub-edge and grassland birds were directly influenced by agriculture, management efforts should focus on strategies to improve agricultural land for both guilds by managing the type of crop or agricultural activities. Examples include supporting perennial crops, decreasing tillage, and reducing chemical inputs (Wilson et al. 2017; Martin et al. 2020). However, because both guilds were negatively influenced by agriculturally driven habitat loss, some natural habitat such as grassland or forest edges must be preserved in the landscape. Therefore, management efforts to preserve birds in agricultural landscapes should focus on preserving grassland and forest habitat including forest edges, while managing agricultural land, for instance, by selecting perennial crops and low impact agricultural activities.

TABLES

Table 1 – Summary of the direct, indirect, and total effects of agriculture variables (cropland, perennial forages and grassland, and mean field size) on bird richness (forest, grassland, and shrub-edge bird richness). Direct effects are derived from the direct relationship (i.e. arrow) between the agricultural variable and bird richness. Indirect effects were derived from the sum of all indirect pathways leading to bird richness from the agricultural variable, where each pathway is the product of the estimates for all relationships (i.e. arrows) in the pathway (see Table S5).

Bird Richness Guild	**Agriculture Variable**	**Indirect Pathways (number)**	**Direct Effect**	**Indirect Effect**	**Total Effect**
Forest birds	Cropland	5	-0.04	-0.207	-0.247
Shrub-Edge birds	Cropland	15	0.20	0.065	0.265
Shrub-Edge birds	Perennial Forages and Grassland	7	0.10	-0.044	0.056
Grassland birds	Cropland	5	0.34	-0.100	0.240
Grassland birds	Mean Field Size	1	-0.004	-0.004	-0.008

Table 2 – Hypotheses for predicted relationships in forest, grassland and shrub-edge bird SEM diagrams (Figure 11-13). Positive predicted relationships are represented by +, negative predicted relationships are represented by –, and peaked predicted relationships are represented by ∩.

Relationship	**Direction**	**Hypothesis**	**References**
Cropland → Mean Field Size	+	As cropland increases, mean field size increases because agricultural (i.e. cropland) expansion and intensification frequently include the amalgamation of smaller fields to larger fields.	Benton et al. 2003; Wilson et al. 2017
Cropland → Perennial Forages and Grassland	–	As cropland increases, perennial forages and grassland decrease because perennial forages and grassland may be converted to cropland to increase agriculture productivity.	Barretto et al. 2013; Stanton et al. 2018
Cropland → Forest AND Cropland → Shrubland	–	As cropland increases, other natural covers such as forest and shrubland decrease because the expansion of	Wilson et al. 2017; Endenburg et al. 2019; Santana et al. 2017; Frei et al.

		cropland comes at the expense of other landcovers.	2018; Stanton et al. 2018
Perennial Forages and Grassland → Forest AND Perennial Forages and Grassland → Shrubland	–	As perennial forages and grassland increases, other natural covers such as forest and shrubland decrease because the expansion of perennial forages comes at the expense of other natural landcovers.	Wilson et al. 2017; Endenburg et al. 2019; Santana et al. 2017; Stanton et al. 2018
Mean Field Size → Hedgerow	–	As mean field size increases, hedgerow amount decreases because field edges are lost between fields.	Benton et al. 2003; Šálek et al. 2018
Mean Field Size → Grassland Bird Richness	+	As mean field size increases, grassland bird richness increases because nest predation is highest at field edges. Large fields have a lower edge-to-area ratio, reducing overall nest predation on grassland birds.	Herkert et al. 2003
Perennial Forages and Grassland → Grassland Bird Richness	+	As perennial forages and grassland increase, grassland bird richness increases because perennial forages provides nesting habitat mimicking native grassland.	Herkert et al. 2003; Frei et al. 2018
Forest → Forest Bird Richness	+	As forest increases, forest bird richness increases because forest provides nesting habitat.	Rodewald and Yahner 2001; Endenburg et al. 2019
Shrubland → Shrub-Edge Bird Richness	+	As shrubland increases, shrub-edge bird richness increases because shrubland provides nesting habitat.	Nikolov et al. 2011; Shake et al. 2011
Hedgerow → Forest Bird Richness	+	As hedgerows increase, forest bird richness increases because hedgerows provide nesting and roosting habitat, and connectivity among forest patches.	Benton et al. 2003; Wilson et al. 2017
Hedgerow → Grassland Bird Richness	–	As hedgerows increase, grassland bird richness decreases because birds nesting	Herkert et al. 2003; Wilson et al. 2017; Stanton et al. 2018

		near hedgerows suffer high predation rates.	
Hedgerow → Shrub-Edge Bird Richness	+	As hedgerows increase, shrub-edge bird richness increases because hedgerows provide nesting and roosting habitat.	Benton et al. 2003; Wilson et al. 2017
Forest → Forest Edge	∩	Forest edge amount is highest at moderate amounts of forest because low amounts of forest have less perimeter or edge and high amounts of forest amalgamate into fewer patches that result in less forest perimeter or edge.	
Forest Edge → Shrub-Edge Bird Richness	+	As forest edge increases, shrub-edge bird richness increases because forest edge provides nesting habitat.	Fonderflick et al. 2013

FIGURES

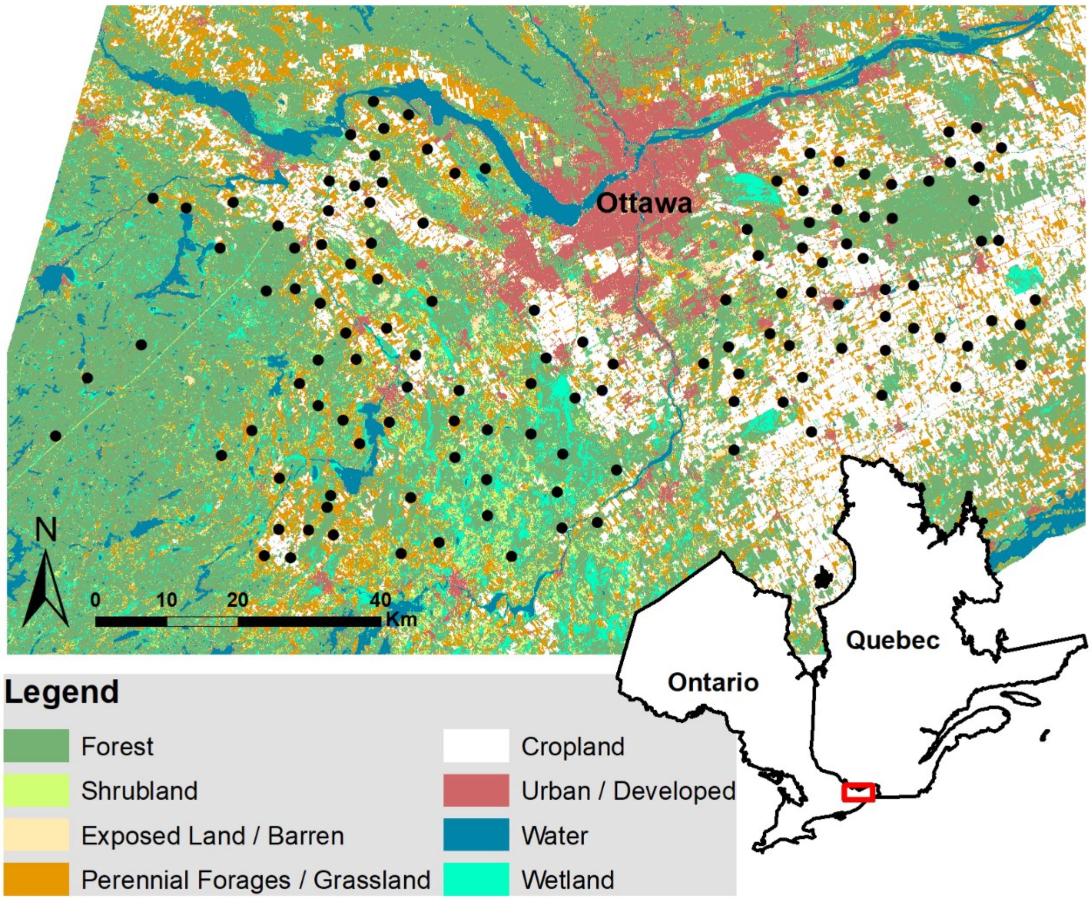

Figure 1 – Map showing the locations of 127 bird survey sites near Ottawa, Ontario, Canada with land cover types from the 2016 Agriculture and Agri-Food Canada annual crop inventory.

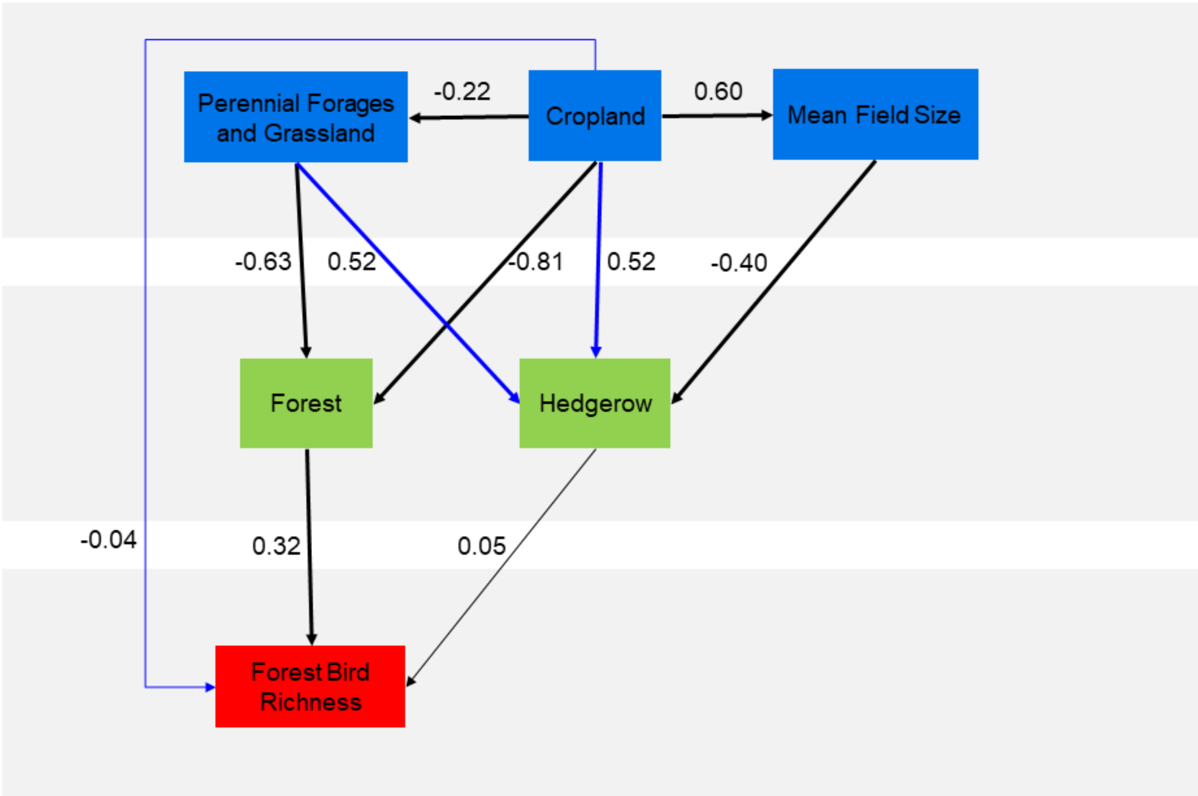

Figure 2 – Forest bird structural equation modelling (SEM) diagram with estimates for relationships among agricultural predictors (upper row), habitat variables (middle row), and forest bird richness (lower row). Agricultural predictors (proportion of perennial forages and grassland, cropland, and mean field size) and habitat variables (proportion of forest and hedgerow) were measured in 1-km^2 square landscapes surrounding each site (see Figure 1). Paths with strong statistical support are represented by thick solid arrows and paths with weak support are represented by thin solid arrows. All paths had statistical support. Standardized path coefficients were derived from the global model for each response. Blue lines represent relationships not predicted a priori in figure 11.

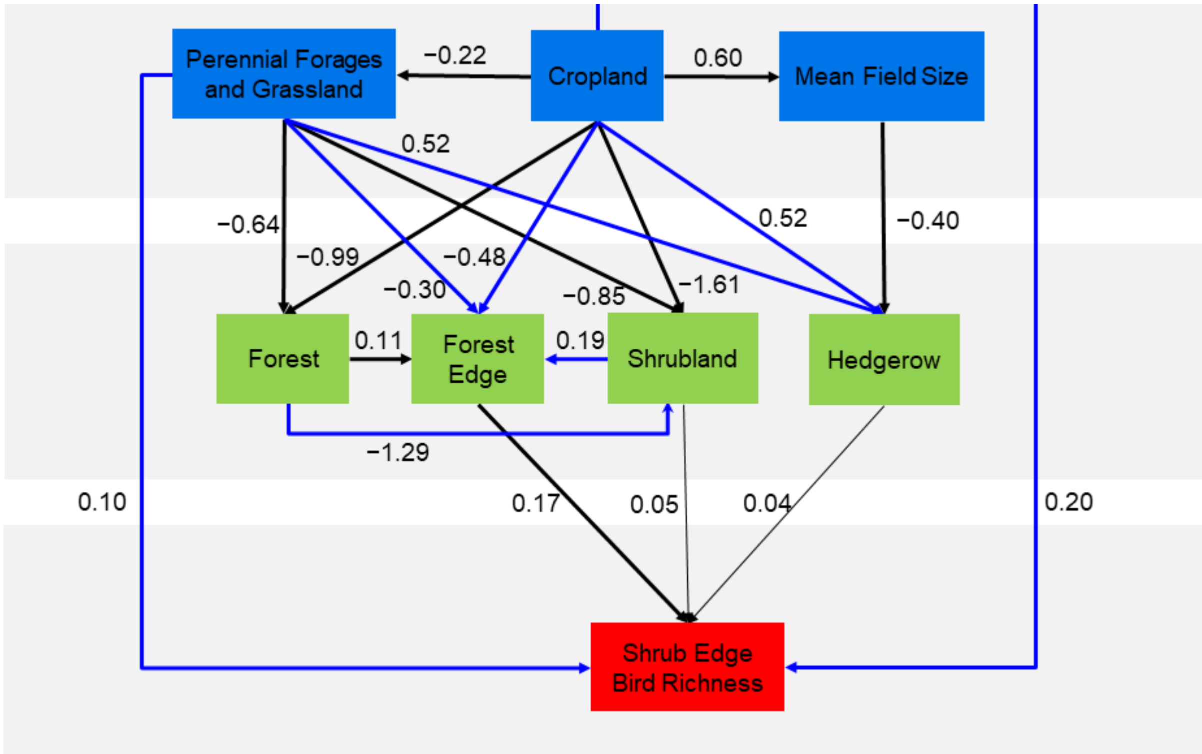

Figure 3 – Shrub-edge bird structural equation modelling (SEM) diagram with estimates for relationships among agricultural predictors (upper row), habitat variables (middle row), and shrub-edge bird richness (lower row). Agricultural predictors (proportion of perennial forages and grassland, cropland, and mean field size) and habitat variables (proportion of forest, forest edge, shrubland, and hedgerow) were measured in 1-km^2 square landscapes surrounding each site (see Figure 1). Paths with strong statistical support are represented by thick solid arrows and paths with weak support are represented by thin solid arrows. All paths had statistical support. Standardized path coefficients were derived from the global model for each response. Blue lines represent relationships not predicted a priori in Figure 12.

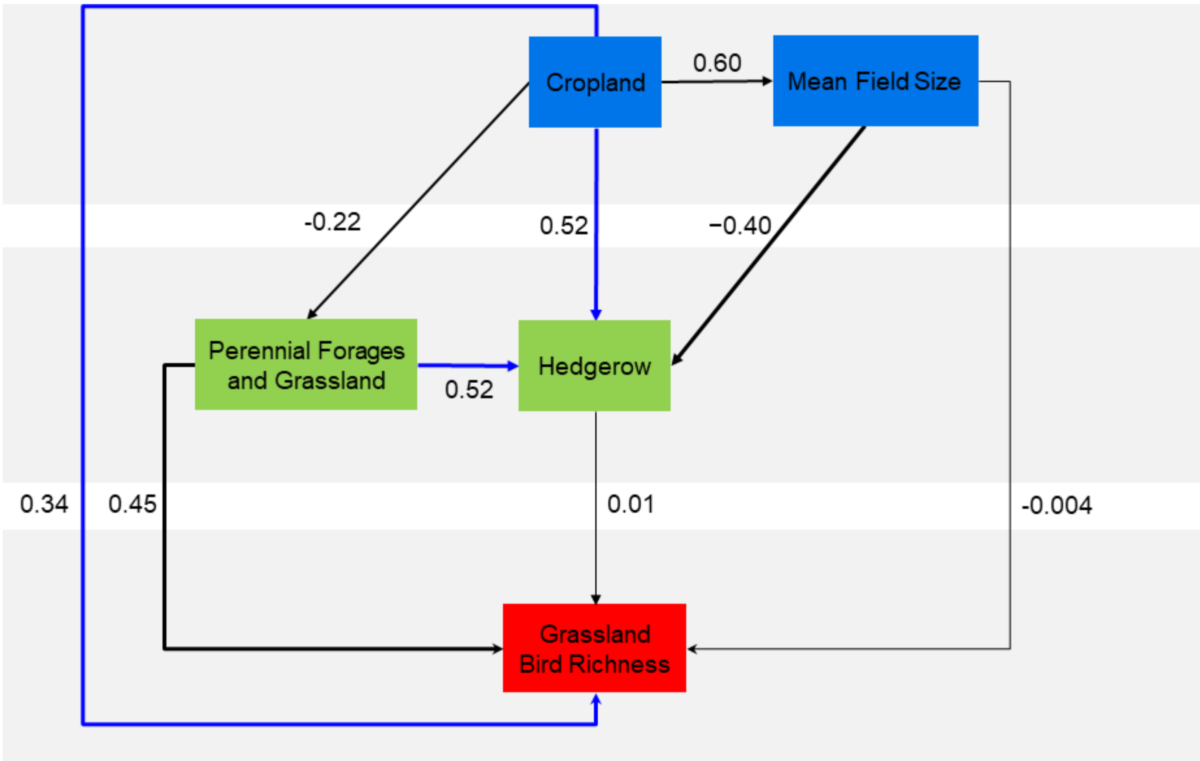

Figure 4 – Grassland bird structural equation modelling (SEM) diagram with estimates for relationships among agricultural predictors (upper row), habitat variables (middle row), and grassland bird richness (lower row). Agricultural predictors (proportion of cropland and mean field size) and habitat variables (proportion of perennial forages and grassland, and hedgerow) were measured in 1-km^2 square landscapes surrounding each site (see Figure 1). Paths with strong statistical support are represented by thick solid arrows and paths with weak support are represented by thin solid arrows. All paths had statistical support. Standardized path coefficients were derived from the global model for each response. Blue lines represent relationships not predicted a priori in Figure 13.

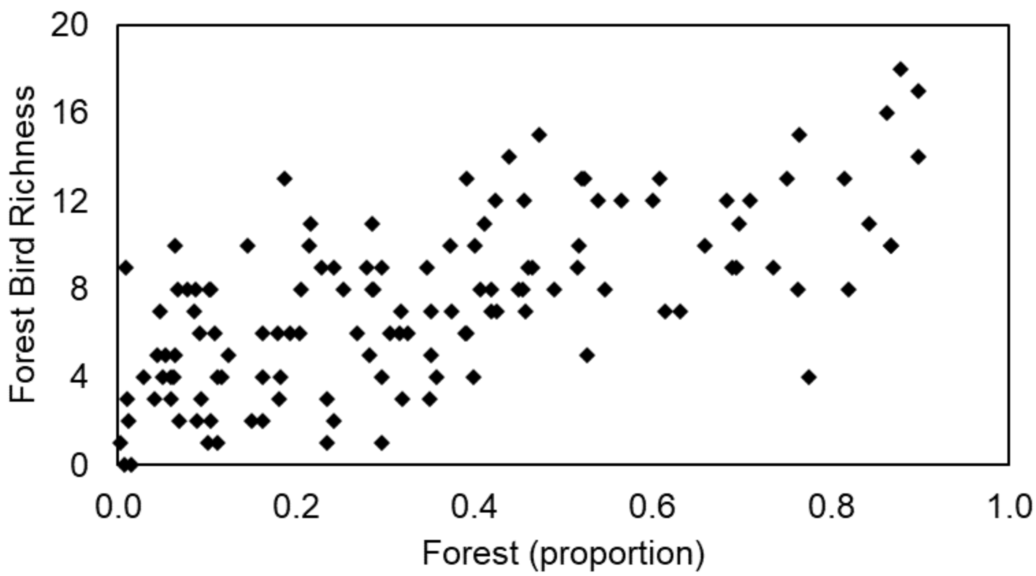

Figure 5 – Forest bird richness vs. proportion forest in the 1 km^2 square landscapes surrounding 127 bird survey sites in eastern Ontario, Canada (see Figure 1).

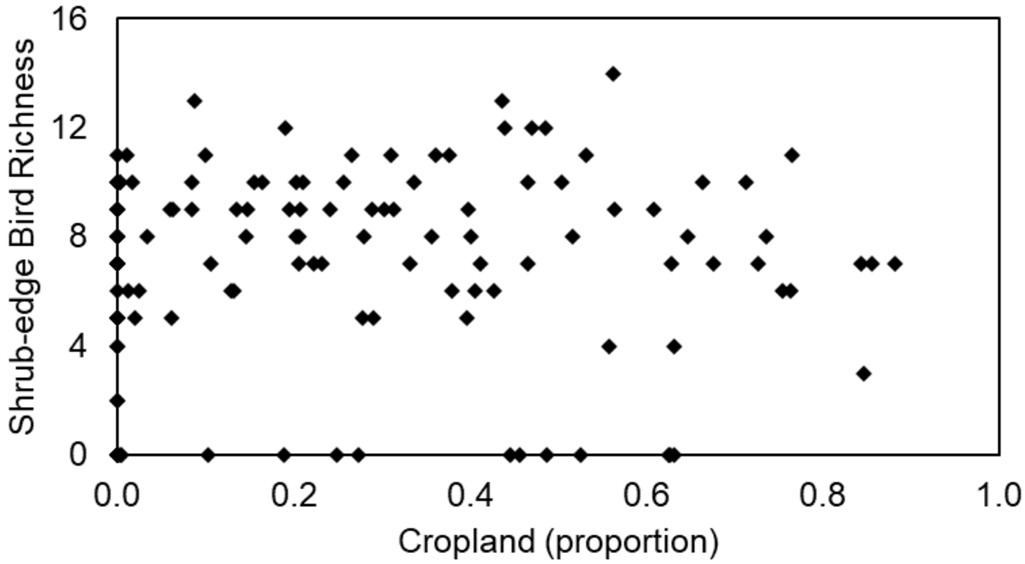

Figure 6 – Shrub-edge bird richness vs. proportion cropland in the 1 km^2 square landscapes surrounding 127 bird survey sites in eastern Ontario, Canada (see Figure 1).

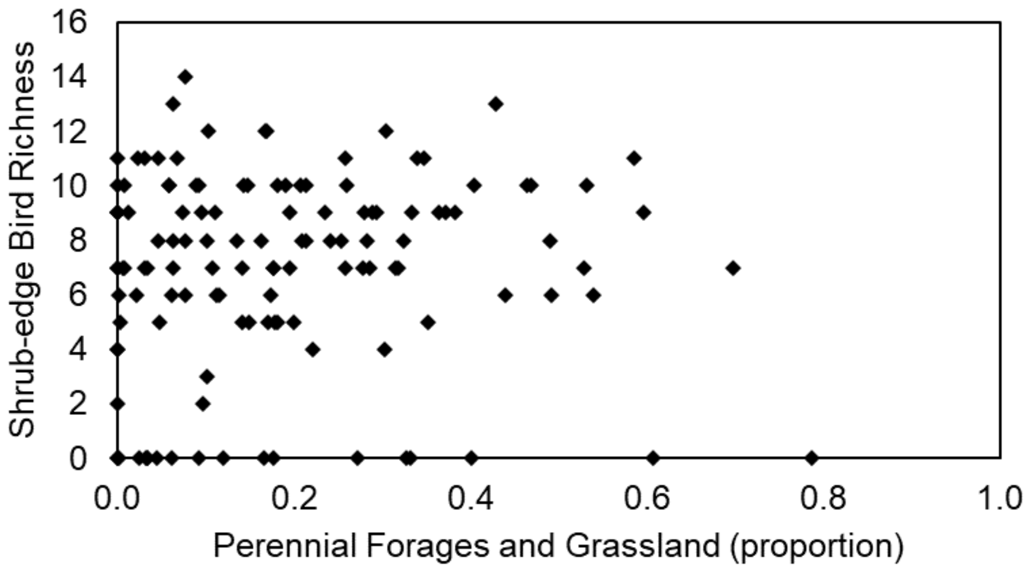

Figure 7 – Shrub-edge bird richness vs. proportion perennial forages and grassland in the 1 km^2 square landscapes surrounding 127 bird survey sites in eastern Ontario, Canada (see Figure 1).

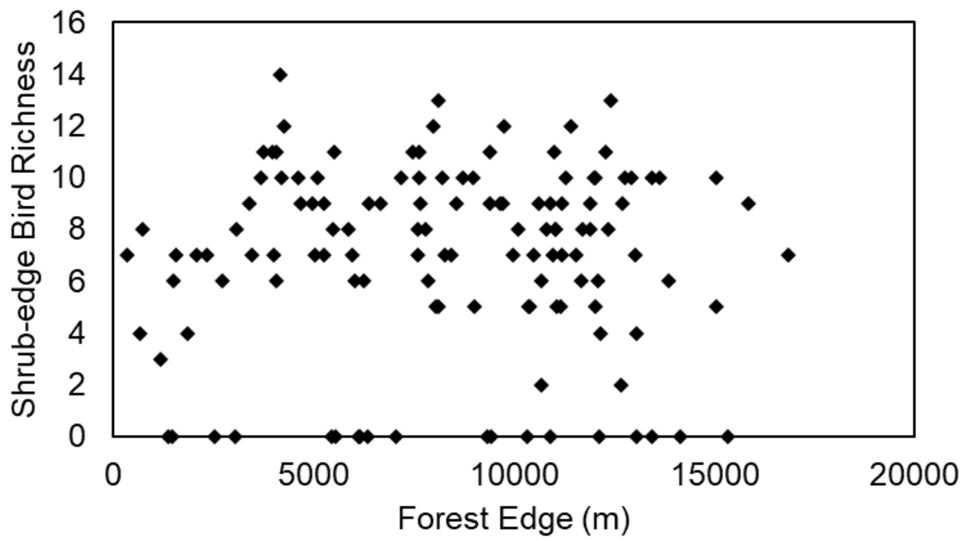

Figure 8 – Shrub-edge bird richness vs. total forest edge (m) in the 1 km^2 square landscapes surrounding 127 bird survey sites in eastern Ontario, Canada (see Figure 1).

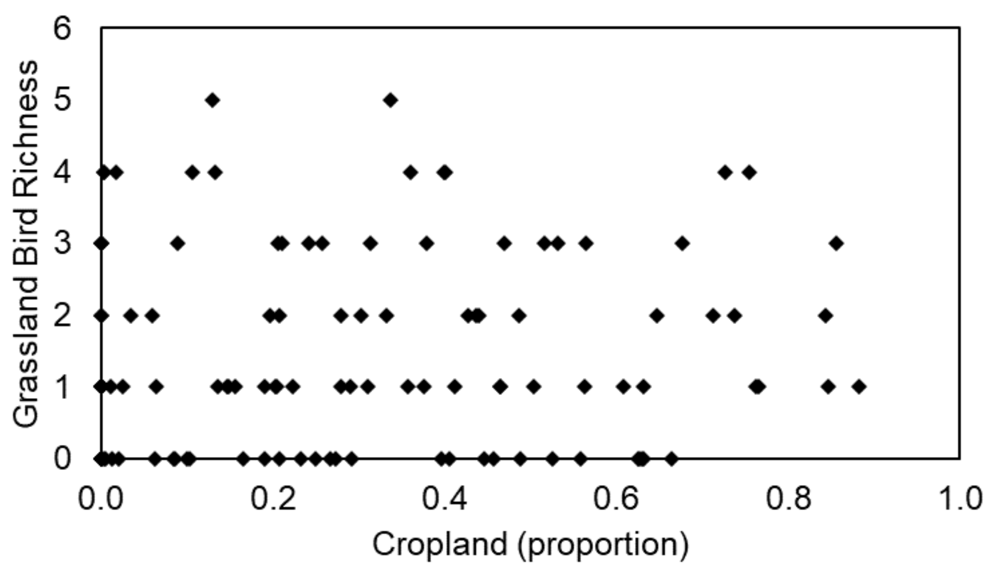

Figure 92 – Grassland bird richness vs. proportion cropland in the 1 km^2 square landscapes surrounding 127 bird survey sites in eastern Ontario, Canada (see Figure 1).

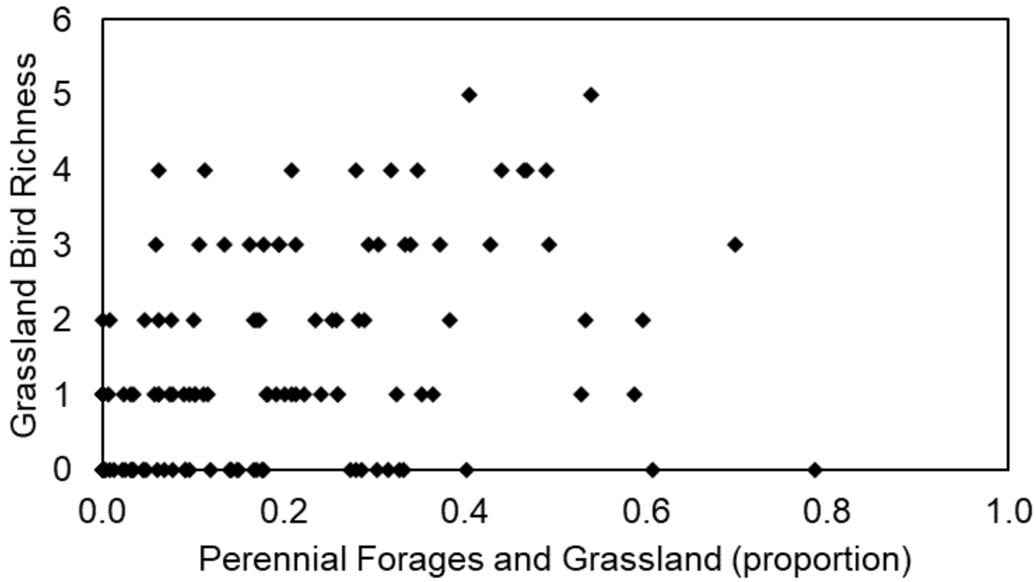

Figure 10 – Grassland bird richness vs. proportion perennial forages and grassland in the 1 km^2 square landscapes surrounding 127 bird survey sites in eastern Ontario, Canada (see Figure 1).

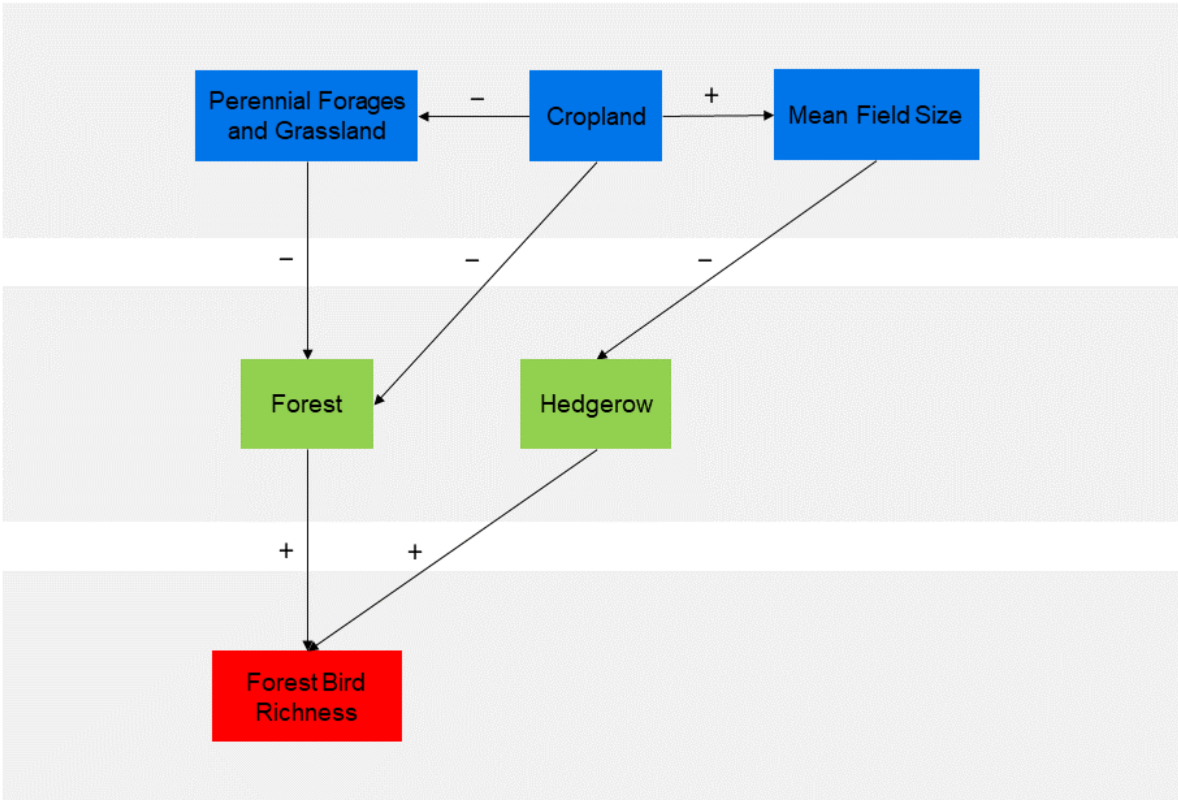

Figure 11 – Predicted forest bird structural equation modelling (SEM) diagram. A priori predicted relationships between agricultural predictors (proportion of perennial forages and grassland, cropland, and mean field size), habitat variables (proportion of forest, and hedgerow) measured in 1-km^2 square landscapes surrounding each bird survey site, and forest bird richness. Predicted relationships are represented as arrows originating from the predictor and terminating at the response. The predicted relationship is either positive shown as +, or negative shown as −.

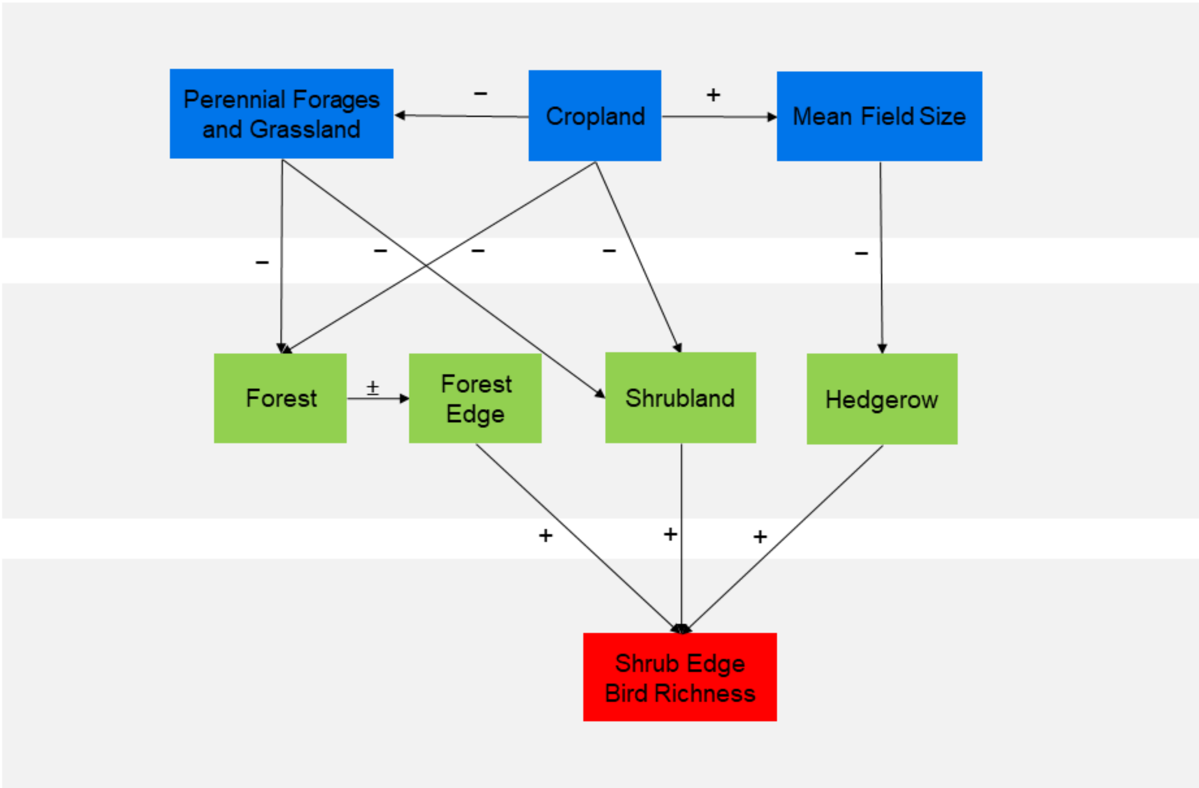

Figure 12 – Predicted shrub-edge bird structural equation modelling (SEM) diagram. Predicted relationships between agricultural predictors (proportion of perennial forages and grassland, cropland, and mean field size), habitat variables (proportion of forest, forest edge, shrubland, and hedgerow) measured in 1-km^2 square landscapes surrounding each bird survey site, and shrub-edge bird richness. Predicted relationships are represented as arrows originating from the predictor and terminating at the response. The predicted relationship is positive shown as +, negative shown as −, or peaked non-linear shown as ±.

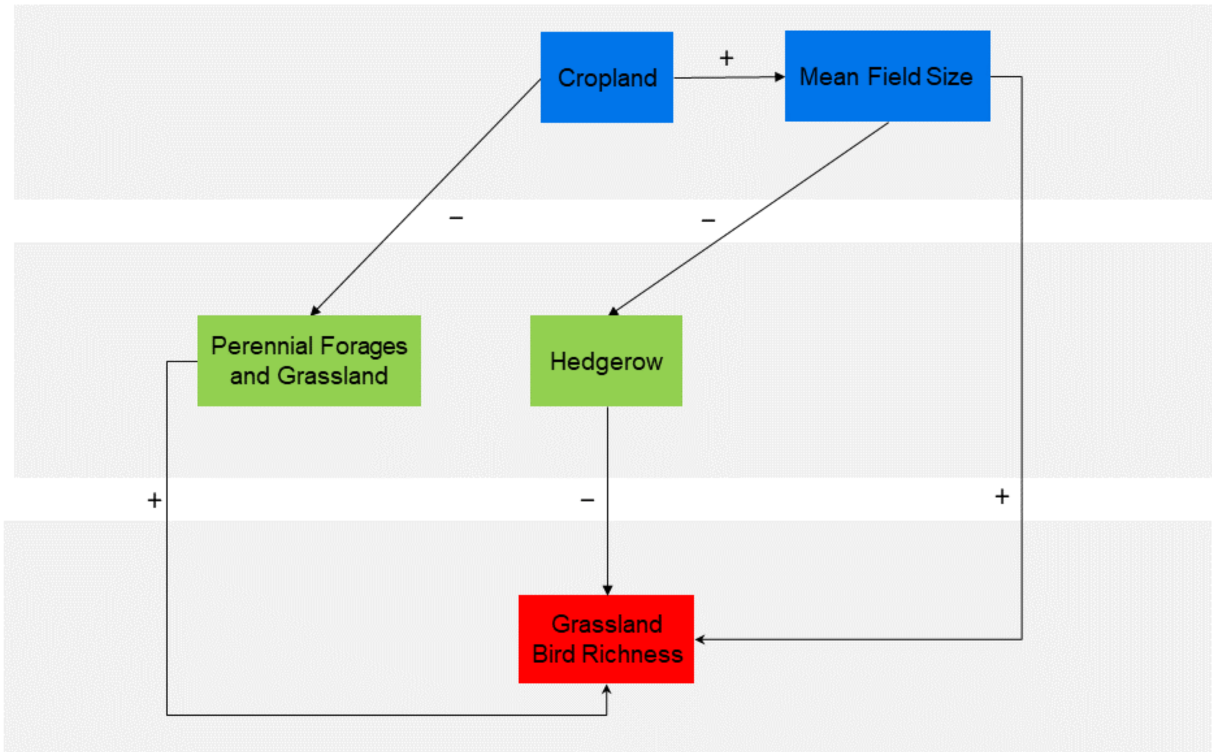

Figure 13 – Predicted grassland bird structural equation modelling (SEM) diagram. Predicted relationships between agricultural predictors (proportion of cropland, and mean field size), habitat variables (proportion of perennial forages and grassland, and hedgerow) measured in 1-km^2 square landscapes surrounding each bird survey site, and grassland bird richness. Predicted relationships are represented as arrows originating from the predictor and terminating at the response. The predicted relationship is either positive shown as +, or negative shown as −.

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APPENDIX I - SUPPLEMENTAL MATERIAL

Table S1 – List of bird species identified in the bird surveys including the scientific name, common name, assigned habitat guild (forest, grassland, shrub-edge, and wetland) based on the habitat associations provided in the Birds of North America Online, and the number of sites (of 127) where each species was identified.

Common Name	**Scientific Name**	**Habitat Guild**	**Sites Identified**
Alder Flycatcher	*Empidonax alnorum*	Shrub-edge	23
American Bittern	*Botaurus lentiginosus*	Wetland	6
American Crow	*Corvus brachyrhynchos*	Shrub-edge	122
American Goldfinch	*Spinus tristis*	Shrub-edge	101
American Redstart	*Setophaga ruticilla*	Forest	27
American Robin	*Turdus migratorius*	Shrub-edge	125
Baltimore Oriole	*Icterus galbula*	Forest	15
Barn Swallow	*Hirundo rustica*	Grassland	9
Belted Kingfisher	*Megaceryle alcyon*	Wetland	2
Black-and-white Warbler	*Mniotilta varia*	Forest	28
Blackburnian Warbler	*Setophaga fusca*	Forest	6
Black-capped Chickadee	*Poecile atricapillus*	Forest	81
Black-crowned Night-Heron	*Nycticorax nycticorax*	Wetland	1
Black-throated Blue Warbler	*Setophaga caerulescens*	Forest	1
Black-throated Green Warbler	*Setophaga virens*	Forest	11
Blue Jay	*Cyanocitta cristata*	Forest	55
Blue-headed Vireo	*Vireo solitarius*	Forest	6
Bobolink	*Dolichonyx oryzivorus*	Grassland	29
Broad-winged Hawk	*Buteo platypterus*	Forest	1
Brown Creeper	*Certhia americana*	Forest	3
Brown Thrasher	*Toxostoma rufum*	Shrub-edge	29
Brown-headed Cowbird	*Molothrus ater*	Grassland	18
Canada Goose	*Branta canadensis*	Wetland	2
Cedar Waxwing	*Bombycilla cedrorum*	Shrub-edge	48
Chestnut-sided Warbler	*Setophaga pensylvanica*	Shrub-edge	11
Chipping Sparrow	*Spizella passerina*	Forest	70
Common Grackle	*Quiscalus quiscula*	Shrub-edge	44
Common Loon	*Gavia immer*	Wetland	4
Common Nighthawk	*Chordeiles minor*	Grassland	2
Common Raven	*Corvus corax*	Forest	26
Common Yellowthroat	*Geothlypis trichas*	Wetland	97
Dark-eyed Junco	*Junco hyemalis*	Forest	5
Downy Woodpecker	*Dryobates pubescens*	Forest	15
Eastern Bluebird	*Sialia sialis*	Grassland	6

Eastern Kingbird	*Tyrannus tyrannus*	Grassland	35
Eastern Meadowlark	*Sturnella magna*	Grassland	20
Eastern Phoebe	*Sayornis phoebe*	Shrub-edge	43
Eastern Towhee	*Pipilo erythrophthalmus*	Shrub-edge	2
Eastern Wood Pewee	*Contopus virens*	Forest	28
European Starling	*Sturnus vulgaris*	Shrub-edge	26
Field Sparrow	*Spizella pusilla*	Shrub-edge	9
Golden-crowned Kinglet	*Regulus satrapa*	Forest	3
Gray Catbird	*Dumetella carolinensis*	Shrub-edge	30
Great Blue Heron	*Ardea herodias*	Wetland	3
Great Crested Flycatcher	*Myiarchus crinitus*	Forest	48
Hairy Woodpecker	*Dryobates villosus*	Forest	28
Hermit Thrush	*Catharus guttatus*	Forest	6
Horned Lark	*Eremophila alpestris*	Grassland	1
House Finch	*Haemorhous mexicanus*	Shrub-edge	4
House Sparrow	*Passer domesticus*	Shrub-edge	4
House Wren	*Troglodytes aedon*	Shrub-edge	51
Indigo Bunting	*Passerina cyanea*	Shrub-edge	1
Killdeer	*Charadrius vociferus*	Grassland	9
Least Flycatcher	*Empidonax minimus*	Forest	5
Magnolia Warbler	*Setophaga magnolia*	Forest	6
Mallard	*Anas platyrhynchos*	Wetland	1
Marsh Wren	*Cistothorus palustris*	Wetland	2
Mourning Dove	*Zenaida macroura*	Shrub-edge	99
Mourning Warbler	*Geothlypis philadelphia*	Shrub-edge	9
Nashville Warbler	*Leiothlypis ruficapilla*	Shrub-edge	5
Northern Cardinal	*Cardinalis cardinalis*	Shrub-edge	52
Northern Flicker	*Colaptes auratus*	Forest	39
Northern Mockingbird	*Mimus polyglottos*	Shrub-edge	3
Northern Parula	*Setophaga americana*	Forest	1
Northern Saw-whet Owl	*Aegolius acadicus*	Forest	1
Northern Waterthrush	*Parkesia noveboracensis*	Forest	7
Ovenbird	*Seiurus aurocapilla*	Forest	41
Philadelphia Vireo	*Vireo philadelphicus*	Forest	3
Pileated Woodpecker	*Dryocopus pileatus*	Forest	8
Pine Siskin	*Spinus pinus*	Shrub-edge	4
Pine Warbler	*Setophaga pinus*	Forest	7
Purple Finch	*Haemorhous purpureus*	Forest	12
Red-breasted Nuthatch	*Sitta canadensis*	Forest	13
Red-eyed Vireo	*Vireo olivaceus*	Forest	79
Red-winged Blackbird	*Agelaius phoeniceus*	Wetland	93

Ring-billed Gull	*Larus delawarensis*	Wetland	5
Rose-breasted Grosbeak	*Pheucticus ludovicianus*	Forest	33
Ruby-crowned Kinglet	*Regulus calendula*	Forest	1
Ruby-throated Hummingbird	*Archilochus colubris*	Forest	1
Savannah Sparrow	*Passerculus sandwichensis*	Grassland	44
Scarlet Tanager	*Piranga olivacea*	Forest	7
Song Sparrow	*Melospiza melodia*	Shrub-edge	115
Spotted Sandpiper	*Actitis macularius*	Wetland	2
Swamp Sparrow	*Melospiza georgiana*	Wetland	13
Upland Sandpiper	*Bartramia longicauda*	Grassland	2
Veery	*Catharus fuscescens*	Forest	38
Vesper Sparrow	*Pooecetes gramineus*	Grassland	16
Warbling Vireo	*Vireo gilvus*	Forest	46
White-breasted Nuthatch	*Sitta carolinensis*	Forest	25
White-throated Sparrow	*Zonotrichia albicollis*	Forest	32
Wild Turkey	*Meleagris gallopavo*	Forest	14
Wilson's Snipe	*Gallinago delicata*	Wetland	2
Wilson's Warbler	*Cardellina pusilla*	Shrub-edge	1
Winter Wren	*Troglodytes hiemalis*	Forest	3
Wood Thrush	*Hylocichla mustelina*	Forest	20
Yellow Warbler	*Setophaga petechia*	Shrub-edge	48
Yellow-bellied Sapsucker	*Sphyrapicus varius*	Forest	25
Yellow-billed Cuckoo	*Coccyzus americanus*	Forest	4
Yellow-rumped Warbler	*Setophaga coronata*	Forest	4
Yellow-throated Vireo	*Vireo flavifrons*	Forest	1

Table S2 – Bird richness by site for each bird guild (forest, grassland, shrub-edge and wetland birds) and for all birds (total richness). Includes the average bird richness, and maximum bird richness.

Site ID	Forest Bird Richness	Grassland Bird Richness	Shrub-Edge Bird Richness	Wetland Bird Richness	Total Richness
A102	8	4	6	2	20
A103	11	1	9	3	24
A104	4	2	8	3	17
A108	9	0	11	2	22
A109	8	3	13	3	27
A110	5	5	10	1	21
A12	14	2	8	2	26
A121	2	5	6	1	14
A125	6	2	8	3	19
A134	8	1	10	3	22
A137	8	3	12	3	26
A144	4	3	7	3	17
A149	2	2	9	1	14
A150	8	1	10	2	21
A152A	4	0	0	0	4
A157	2	4	8	1	15
A158	3	3	7	3	16
A159	13	3	9	2	27
A169	16	0	7	2	25
A177	0	0	4	2	6
A186	4	1	4	0	9
A187	12	3	9	2	26
A193	9	3	8	3	23
A197A	14	0	0	0	14
A202A	13	0	0	0	13
A204	10	0	6	0	16
A206A	4	0	0	0	4
A211	12	0	7	2	21
A212	13	0	2	0	15
A218	12	0	5	2	19
A29	8	2	13	3	26
A32A	11	0	0	0	11
A39	5	2	10	2	19
A42	6	2	9	2	19
A43	5	1	8	2	16
A47	4	4	6	2	16

A48	8	1	8	2	19
A49	4	1	14	2	21
A5	10	0	6	1	17
A54	7	0	10	2	19
A56	10	1	10	3	24
A62A	3	0	0	0	3
A69	9	4	10	2	25
A7	7	1	10	3	21
A72	2	2	7	1	12
A73	12	1	8	3	24
A74	13	1	8	1	23
A75	4	1	11	2	18
A76	10	0	7	1	18
A78	6	1	7	3	17
A80	2	4	11	2	19
A85	8	1	7	2	18
A86A	6	0	0	0	6
A89	3	2	10	3	18
A90	7	1	7	3	18
B10	8	0	7	2	17
B100	18	0	5	1	24
B104	7	0	10	2	19
B106A	8	0	0	0	8
B107	7	0	6	1	14
B108	8	1	9	2	20
B109	0	1	3	3	7
B110	1	3	7	1	12
B111	5	1	8	2	16
B114	10	3	11	2	26
B116	6	2	12	3	23
B117	6	1	7	1	15
B118	12	1	12	2	27
B11A	1	0	0	0	1
B12	11	0	5	1	17
B120	4	1	6	2	13
B124	5	3	7	2	17
B127	6	3	9	2	20
B13	3	2	6	2	13
B17	9	1	5	0	15
B1A	10	0	0	0	10
B2	9	0	5	2	16

B26	9	4	10	2	25
B28	8	1	9	2	20
B35	13	0	5	1	19
B37	7	0	10	2	19
B38A	6	0	0	0	6
B39	3	4	10	2	19
B4	2	2	8	3	15
B40	10	1	9	2	22
B41	6	1	7	3	17
B42	6	4	9	2	21
B44	6	0	7	1	14
B45	10	1	10	2	23
B46	5	2	7	2	16
B48	8	3	10	3	24
B49	15	0	11	1	27
B50	5	3	6	1	15
B51	10	1	11	4	26
B52A	9	0	0	0	9
B53	1	3	8	1	13
B56	3	3	9	2	17
B58A	7	0	0	0	7
B59	2	1	11	1	15
B5A	13	0	0	0	13
B6	13	0	5	0	18
B61	3	4	7	2	16
B64A	7	0	0	0	7
B68	1	1	6	2	10
B69	11	0	9	1	21
B71	12	1	5	2	20
B72A	4	0	0	0	4
B73	3	2	8	1	14
B74	8	1	9	0	18
B79	17	0	9	2	28
B81	4	4	7	3	18
B82	9	2	12	2	25
B83	4	3	10	2	19
B84	9	2	9	2	22
B85	15	1	11	1	28
B86	11	2	9	2	24
B87	9	0	11	2	22
B9	6	0	7	0	13

B93A	8	0	0	0	8
C1A	7	0	0	0	7
C2A	9	0	0	0	9
C3	12	0	4	0	16
C4	8	0	2	0	10
C5	8	1	4	0	13
C6	9	1	9	2	21
C7	7	1	10	2	20
C9	1	1	5	2	9
AVERAGE	**7**	**1**	**7**	**2**	**17**
MAX	**18**	**5**	**14**	**4**	**28**

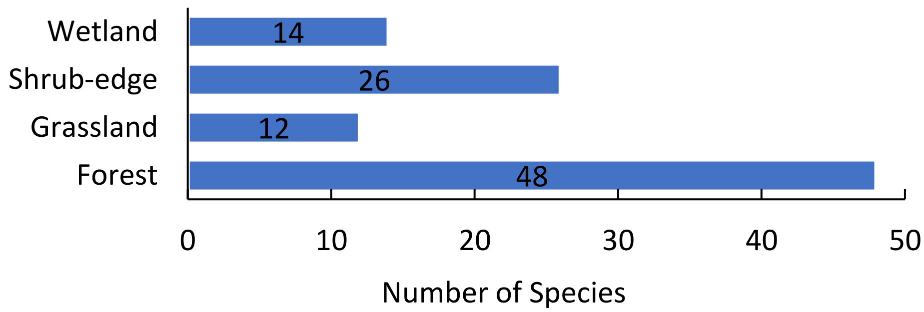

Figure S3 – Total number of species identified, grouped by bird guild (wetland, shrub-edge, grassland and forest birds).

Table S3 – Summary statistics of landscape variables (proportion forest, cropland, shrubland, wetland, hedgerows, perennial forages and grassland, and mean field size in hectares and total forest edge in meters) measured in 1 km^2 landscapes around each bird survey site, including the average and the range of each landscape variable. Note: mean field size range starts at 0 because 7 sites had no agricultural fields.

Landscape Variable	**Average**	**Range**
Proportion Forest	0.346	0.03 - 0.9
Proportion Cropland	0.263	0 - 0.88
Proportion Shrubland	0.068	0.001 - 0.41
Proportion Wetland	0.031	0 - 0.3
Proportion Hedgerows	0.014	0 - 0.07
Proportion Perennial Forages and Grassland	0.192	0 - 0.79
Mean Field Size (ha)	12.764	0 - 88.2
Forest edge (m)	8344.9	352.4 - 16839.3

Table S4 – Pearson correlation matrix for the landscape variables measured within 1 km^2 landscapes surrounding each bird survey site. Correlations > 0.5 or < -0.5 are highlighted in bold. MFS = mean field size, Edge = forest edge, Forest = proportion forest, Shrubland = proportion shrubland, Cropland = proportion cropland, Forages Grassland = proportion perennial forages and grassland, and HR = proportion hedgerows.

	MFS	**Edge**	**Forest**	**Shrubland**	**Cropland**	**Forages Grassland**	**HR**
MFS	1						
Edge	**-0.52**	1					
Forest	-0.39	**0.72**	1				
Shrubland	-0.36	**0.60**	0.17	1			
Cropland	**0.60**	**-0.74**	**-0.67**	**-0.55**	1		
Forages Grassland	-0.06	-0.24	-0.45	0.09	-0.22	1	
HR	-0.12	-0.31	-0.50	-0.03	0.17	0.42	1

Table S5 – Equations used to calculate the indirect effect of agriculture variables (cropland, perennial forages and grassland, and mean field size) on richness of bird guilds (forest, grassland, and shrub-edge bird richness) from links in Figure 3. Indirect effects were derived from the sum of all indirect pathways leading to bird richness from the agricultural variable through a habitat variable, where each pathway is the product of the estimates for all relationships (i.e. arrows) in the pathway.

Guild	**Agriculture Variable**	**Indirect Pathways (number)**	**Indirect Effect Equation**	**Indirect Effect**
Forest birds	Cropland	5	(-0.81*0.32)+(0.52*0.05)+(0.6*-0.4*0.05)+(-0.22*-0.63*0.32)+(-0.22*0.52*0.05)	-0.207
Shrub-Edge birds	Cropland	15	(0.6*-0.4*0.04)+(0.52*0.04)+(-1.61*0.05)+(-0.48*0.17)+(-0.99*0.11*0.17)+(-0.99*-1.29*0.05)+(-0.99*-1.29*0.19*0.17)+(-0.22*0.1)+(-0.22*-0.64*0.11*0.17)+(-0.22*-0.64*-1.29*0.05)+(-0.22*-0.64*-1.29*0.19+0.17)+(-0.22*-0.3*0.17)+(-0.22*-0.85*0.05)+(-0.22*-0.85*0.19*0.17)+(-0.22*0.52*0.04)	0.065
Shrub-Edge birds	Perennial Forages and Grassland	7	(-0.64*0.11*0.17)+(-0.64*-1.29*0.05)+(-0.64*-1.29*0.19*0.17)+(-0.3*0.17)+(-0.85*0.05)+(-0.85*0.19*0.17)+(0.52*0.04)	-0.044
Grassland birds	Cropland	5	(0.52*0.01)+(0.6*-0.4*0.01)+(0.6*-0.004)+(-0.22*0.52*0.01)+(-0.22*0.45)	-0.100
Grassland birds	Perennial Forages and Grassland	1	(0.52*0.01)	0.005
Grassland birds	Mean Field Size	1	(-0.4*0.01)	-0.004

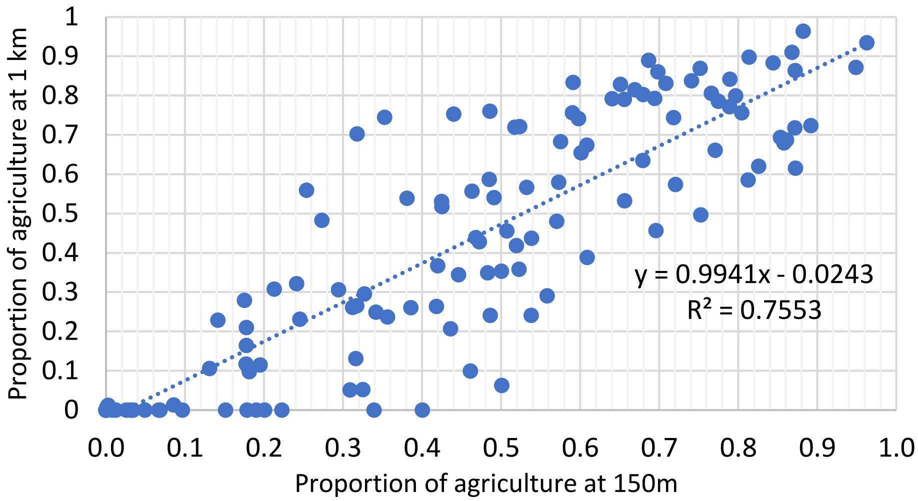

Figure S4 – The proportion of agriculture (cropland and perennial forages and grassland) in the local habitat measured within a 150m radius around each site vs. the proportion of agriculture measured in 1 km^2 landscapes surrounding each bird survey site.

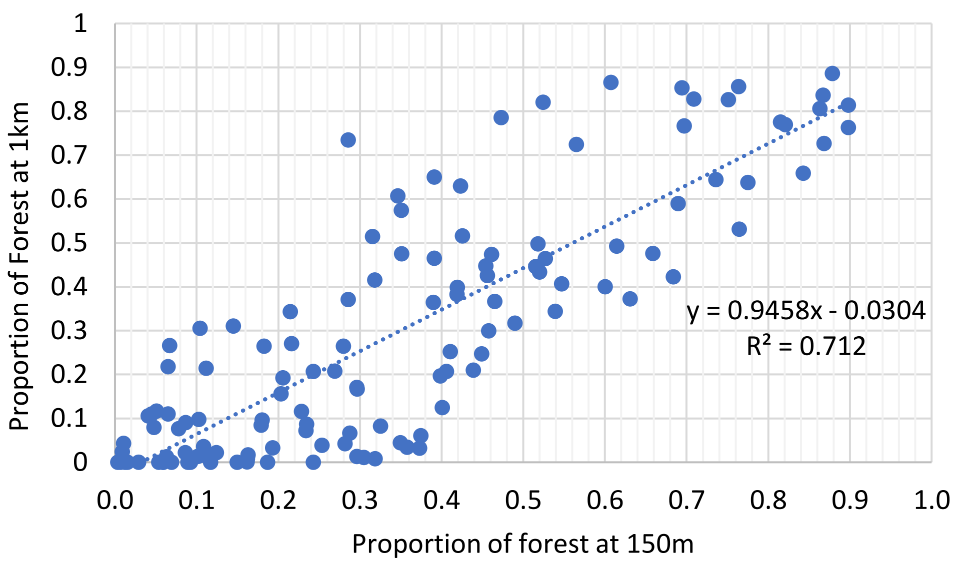

Figure S5 – The proportion of forest in the local habitat measured within a 150m radius around each site vs. the proportion of forest measured in 1 km^2 landscapes surrounding each bird survey site.

Table S6 – All conditionally independent pairs of variables from Figure 2, structured as independence claims, implied by the path model of the predicted relationships between landscape predictors and forest bird richness, and the associated models constructed to test the independence claims. Also shown are the null probabilities (p-values) used to calculate Fisher's C statistic to test the correlational structure of the full path model. The independence claim notation identifies the tested pair of variables in parentheses, followed by the variables that were statistically controlled for while testing the independence between the pair, in curled brackets.

Independence Claim	**Model**[a]	**p-value**
(MFS, ForageGrass)|{Crop}	MFS ~ Crop + ForageGrass	0.30058
(ForestRich, ForageGrass)|{Crop, Forest}	ForestRich ~ Crop + Forest + ForageGrass	0.486681
(Forest, MFS)|{Crop, ForageGrass}	Forest ~ Crop + ForageGrass + MFS	0.0485
(ForestRich, MFS)|{Crop, Forest, HR}	ForestRich ~ Crop + Forest + HR + MFS	0.763
(Forest, HR)|{Crop, ForageGrass, MFS}	Forest ~ Crop + ForageGrass + MFS + HR	0.0151

Notes: MFS = mean field size, ForageGrass = perennial forages and grassland, Crop = cropland, ForestRich = forest bird richness, HR = Hedgerow. [a] Relationships with the ForestRich response variable were tested using generalized linear models with a Poisson distribution. Relationships between all other variables were tested using linear models.

Table S7 – All conditionally independent pairs of variables from Figure 4, structured as independence claims, implied by the path model of the predicted relationships between landscape predictors and grassland bird richness, and the associated models constructed to test the independence claims. Also shown are the null probabilities (p-values) used to calculate Fisher's C statistic to test the correlational structure of the full path model. The independence claim notation identifies the tested pair of variables in parentheses, followed by the variables that were statistically controlled for while testing the independence between the pair, in curled brackets.

Independence Claim	**Model**[a]	**p-value**
(MFS, ForageGrass)|{Crop}	MFS ~ Crop + ForageGrass	0.30058

Notes: MFS = mean field size, ForageGrass = perennial forages and grassland, Crop = cropland, [a] Relationships were tested using linear models.

Table S8 – All conditionally independent pairs of variables from Figure 3, structured as independence claims, implied by the path model of the predicted relationships between landscape predictors and shrub-edge bird richness, and the associated models constructed to test the independence claims. Also shown are the null probabilities (p-values) used to calculate Fisher's C statistic to test the correlational structure of the full path model. The independence claim notation identifies the tested pair of variables in parentheses, followed by the variables that were statistically controlled for while testing the independence between the pair, in curled brackets.

Independence Claim	**Model[a]**	**p-value**
(MFS, ForageGrass)|{Crop}	MFS ~ Crop + ForageGrass	0.30058
(Forest, MFS)|{Crop, ForageGrass, Shrub}	Forest ~ Crop + ForageGrass + Shrub + MFS	0.0241
(Edge, MFS)|{Crop, Forest, ForageGrass, Shrub}	Edge ~ Crop + Forest + ForageGrass + Shrub + MFS	0.20233
(Shrub, MFS)|{Crop, ForageGrass, Forest}	Shrub ~ Crop + ForageGrass + Forest + MFS	0.24
(RichShrub, MFS)|{Crop, Edge, Shrub, HR}	RichShrub ~ Crop + Edge + Shrub + HR + MFS	0.9774
(HR, Forest)|{Crop, ForageGrass, MFS, Shrub}	HR ~ Crop + ForageGrass + MFS + Shrub + Forest	0.031856
(RichShrub, Forest)|{Crop, ForageGrass, Edge, Shrub, HR}	RichShrub ~ Crop + ForageGrass + Edge + Shrub + HR + Forest	0.5673
(Edge, HR)|{Forest, Crop, ForageGrass, MFS, Shrub}	Edge ~ Forest + Crop + ForageGrass + MFS + Shrub + HR	0.73213
(Shrub, HR)|{Crop, ForageGrass, MFS, Forest}	Shrub ~ Crop + ForageGrass + MFS + Forest + HR	0.632

Notes: MFS = mean field size, ForageGrass = perennial forages and grassland, Crop = cropland, Shrub = shrubland, Edge = forest edge, RichShrub = shrub-edge bird richness, HR = Hedgerow. [a] Relationships with the RichShrub response variable were tested using generalized linear models with a Poisson distribution. Relationships between all other variables were tested using linear models.

Table S9 – Coefficient estimates, AICc, and ΔAICc values for perennial forages and grassland (Figure 2 – 4) modelled on its candidate set of standardized predictors measured in 1 km^2 landscapes surrounding bird survey sites. The bolded model represents the top model.

Model	Crop Estimate	AICc	ΔAIC
Crop	**-0.22**	**359.95**	0
null		364.41	4.46

Table S10 – Coefficient estimates, AICc, and ΔAICc values for mean field size (Figure 2 – 4) modelled on its candidate set of standardized predictors measured in 1 km^2 landscapes surrounding bird survey sites. The bolded model represents the top model.

Model	Crop Estimate	AICc	ΔAIC
Crop	**0.60**	**309.57**	0
null		364.41	54.84

Table S11 – Forest bird model coefficient estimates, AICc, and ΔAICc values for the amount of forest (Figure 2 - 3) modelled on its candidate set of standardized predictors measured in 1 km^2 landscapes surrounding bird survey sites. The bolded model represents the top model.

Model	Crop Estimate	ForageGrass Estimate	AICc	ΔAIC
Crop + ForageGrass	**-0.81**	**-0.63**	**146.87**	0
ForageGrass			338.16	191.29
Crop			290.21	143.33
null			364.41	217.54

Table S12 – Coefficient estimates, AICc, and ΔAICc values for the proportion of hedgerows (Figure 2 – 4) modelled on its candidate set of standardized predictors measured in 1 km^2 landscapes surrounding bird survey sites. The bolded model represents the top model.

Model	Crop Estimate	ForageGrass Estimate	MFS Estimate	AICc	ΔAIC
GLOBAL	**0.52**	**0.52**	**-0.40**	**315.14**	**0**
Crop + ForageGrass				331.69	16.55
ForageGrass				341.36	26.22
MFS + ForageGrass				342.03	26.89
MFS + Crop				354.61	39.47
Crop				362.80	47.66
MFS				364.62	49.49
null				364.41	49.27

Table S13 – Forest bird model coefficient estimates, AICc, and ΔAICc values for forest bird richness (Figure 2) modelled on its candidate set of standardized predictors measured in 1 km^2 landscapes surrounding bird survey sites. The bolded model represents the top model.

Model	Crop Estimate	Forest Estimate	HR Estimate	AICc	ΔAIC
Forest		**0.32**		**644.81**	0
Forest + HR				645.44	0.63
Forest + Crop				646.16	1.36
GLOBAL				647.13	2.32
HR + Crop				686.93	42.12
Crop				694.89	50.08
HR				730.94	86.13
null				748.65	103.84

Table S14 – Grassland bird model Coefficient estimates, AICc, and ΔAICc values for grassland bird richness (Figure 4) modelled on its candidate set of standardized predictors measured in 1 km^2 landscapes surround bird survey sites. The bolded model represents the top model.

Model	Crop Estimate	ForageGrass Estimate	HR Estimate	MFS Estimate	AICc	ΔAIC
proCrop + proForageGrass	**0.34**	**0.45**			**370.56**	0
proForageGrass + proCrop + proHR					372.52	1.96
proCrop + proForageGrass + sdMPS					372.55	1.99
GLOBAL					374.52	3.96
ForageGrass + MFS					381.63	11.07
ForageGrass + MFS + HR					381.88	11.32
ForageGrass					384.50	13.94
ForageGrass + HR					385.58	15.01
MFS + HR					397.52	26.96
Crop + MFS + HR					399.11	28.55
Crop + HR					399.20	28.64
HR					400.47	29.91
Crop					404.45	33.89
Crop + MFS					406.14	35.58
MFS					406.48	35.92
null					407.61	37.05

Table S15 – Shrub-edge bird model coefficient estimates, AICc, and ΔAICc values for proportion of forest (Figure 3) modelled on its candidate set of standardized predictors measured in 1 km^2 landscapes surrounding bird survey sites. The bolded model represents the top model.

Model	**Crop Estimate**	**ForageGrass Estimate**	**Shrub Estimate**	**AICc**	**ΔAIC**
GLOBAL	**-0.99**	**-0.64**	**-0.33**	**79.18**	0
Crop + ForageGrass				146.87	67.69
Crop + Shrub				277.49	198.31
Crop				290.21	211.02
ForageGrass + Shrub				333.13	253.95
ForageGrass				338.16	258.97
Shrub				362.80	283.62
Null				364.41	285.23

Table S16 – Shrub-edge bird model coefficient estimates, AICc, and ΔAICc values for the amount of shrubland (Figure 3) modelled on its candidate set of standardized predictors measured in 1 km^2 landscapes surrounding bird survey sites. The bolded model represents the top model.

Model	**Crop Estimate**	**ForageGrass Estimate**	**Forest Estimate**	**AICc**	**ΔAIC**
GLOBAL	**-1.61**	**-0.85**	**-1.29**	**254.11**	**0**
Crop + Forest				307.32	53.21
Crop				320.04	65.92
Crop + ForageGrass				321.80	67.69
Forest + ForageGrass				360.39	106.28
Forest				362.80	108.69
null				364.41	110.30
ForageGrass				365.42	111.31

Table S17 – Shrub-edge bird model coefficient estimates, AICc, and ΔAICc values for the amount of forest edge (Figure 3) modelled on its candidate set of standardized predictors measured in 1 km^2 landscapes surrounding bird survey sites. The bolded model represents the top model.

Model	Crop Estimate	ForageGrass Estimate	Forest Estimate*	Shrub Estimate	AIC	ΔAIC
GLOBAL	**-0.48**	**-0.30**	**0.39**	**0.19**	**142.84**	**0.00**
Crop + ForageGrass + Forest					151.31	8.47
Crop + Forest + Shrub					153.89	11.05
Forest + Shrub					154.31	11.48
ForageGrass + Forest + Shrub					156.13	13.30
Crop + Forest					186.14	43.30
Crop + ForageGrass					204.36	61.53
Forest					208.40	65.56
Forest + ForageGrass					210.03	67.19
Crop + Shrub					250.55	107.71
Crop					264.25	121.41
ForageGrass + Shrub					293.05	150.21
Shrub					309.45	166.61
ForageGrass					358.92	216.08
null					364.41	221.57

*Forest was modelled as a quadratic, the estimate is calculated by added the linear and quadratic estimates.

Table S18 – Shrub-edge model coefficient estimates, AICc, and ΔAICc values for shrub-edge bird richness (Figure 3) modelled on its candidate set of standardized predictors measured in 1 km^2 landscapes surrounding bird survey sites. The bolded model represents the top model.

Model	Crop Estimate	ForageGrass Estimate	Edge Estimate	Shrub Estimate	HR Estimate	AIC	ΔAIC
Crop + ForageGrass + Edge	**0.21**	**0.13**	**0.20**			**781.69**	**0.00**
ForageGrass + Crop + Edge + Shrub						782.25	0.56
ForageGrass + Crop + Edge + HR						782.36	0.67
GLOBAL	0.20	0.10	0.17	0.05	0.04	783.19	1.50
Crop + Edge + HR						785.28	3.59
Crop + Edge + Shrub +HR						785.45	3.76
Crop + Shrub + HR						785.82	4.13
Crop + ForageGrass + Shrub						786.27	4.58
Crop + Shrub						786.32	4.63
HR						786.53	4.84
Shrub + HR						786.72	5.03
Crop + ForageGrass + Shrub + HR						787.22	5.53
Crop + Edge + Shrub						787.34	5.65
Edge + HR						787.50	5.81
null						787.99	6.30
Crop + HR						788.10	6.41
Crop + Edge						788.28	6.59
Shrub						788.34	6.65
ForageGrass + HR						788.47	6.78
Edge + Shrub + HR						788.67	6.98
ForageGrass + Shrub + HR						788.71	7.02
ForageGrass						788.97	7.28
Crop						789.07	7.38
ForageGrass + Edge + HR						789.34	7.65
Crop + ForageGrass						789.45	7.76
ForageGrass + Shrub						789.50	7.81
Crop + ForageGrass + HR						789.82	8.13
Edge						789.84	8.15
Edge + Shrub						790.12	8.43
ForageGrass + Edge						790.53	8.84
ForageGrass + Edge + Shrub + HR						790.64	8.95

ForageGrass + Edge + Shrub						791.48	9.79

APPENDIX II – PATH ANALYSIS R CODE

```
#
#Working directory
getwd()

#Load Package
library(piecewiseSEM)

#Import data
pathAnalysisData <- read.csv("PathAnalysis_Data_FinalSub.csv")

proForest <- pathAnalysisData$sdForest
proShrub <- pathAnalysisData$sdShrub
proCrop <- pathAnalysisData$sdCrop
proForageGrass <- pathAnalysisData$sdForageGrass
proWet <- pathAnalysisData$sdWet
proHR <- pathAnalysisData$sdHR
sdMPS <- pathAnalysisData$sdMPS2

#You can find out how many independence claims the model should have with this
#calculation:
#
# (#variables in model(!)/(2*2-#variables(!)))-#arrows

######################### Forest Model #########################
# 6 variables and 7 arrows

#1 <- Perennial Forages / Grassland -> proForageGrass
#2 <- Cropland -> proCrop
#3 <- Mean Field Size (standardized) -> sdMPS
#5 <- Forest -> proForest
#8 <- Hedgerow -> proHR
#9 <- Forest Guild Richness -> richForest

(factorial(6)/(2*factorial(4)))-10
= 5

## Downstream variables are the response (or dependent) and upstream variables are the
predictors (or independent).
## If A->B->C, then (A,C)|{B}, then C~B+A

# (proForageGrass, sdMPS)|{proCrop}
F1.1 <- lm(sdMPS ~ proCrop + proForageGrass, pathAnalysisData)
F1.2 <- lm(proForageGrass ~ proCrop + sdMPS, pathAnalysisData)
```

```
# (proForageGrass, richForest)|{proCrop, proForest, proHR}
F3 <- glm(richForest ~ proCrop + proForest + proForageGrass, family = "poisson",
pathAnalysisData)
# (sdMPS, proForest)|{proCrop, proForageGrass}
F6 <- lm(proForest ~ proCrop + proForageGrass + sdMPS, pathAnalysisData)
# (sdMPS, richForest)|{proCrop, proForest, proHR}
F7 <- glm(richForest ~ proCrop + proForest + proHR + sdMPS, family = "poisson",
pathAnalysisData)
# (proForest, proHR)|{proCrop, proForageGrass, sdMPS}
F8.1 <- lm(proHR ~ proCrop + proForageGrass + sdMPS + proForest, pathAnalysisData)
F8.2 <- lm(proForest ~ proCrop + proForageGrass + sdMPS + proHR, pathAnalysisData)

summary(F1.1)
summary(F1.2)
summary(F3)
summary(F6)
summary(F7)
summary(F8.1)
summary(F8.2)

# Next calculate independence claim (C) statistic - the sum of all the log(p values) * -2.
C = 8.175104609

# Calculate the degrees of freedom, df=k2, where k = the number of claims
df=5*2=10

# Use the chi square distribution to see if test statistic and df are significant/non significance.
In R, p-value = 1-pchisq(test statistic, df)
1-pchisq(8.175104609,df=10)

[1] 0.6117375

# model each response with every arrow leading to it as a predictor (using lm, glm, glmm).
#The model coefficients are the path coefficients.
#To determine the strength/coefficients of the indirect effects, you multiply the path
coefficients to the response

#### Parameterized forest bird model estimates ####

f1 <- lm(proForageGrass ~ 1, pathAnalysisData)
f2 <- lm(proForageGrass ~ proCrop, pathAnalysisData)
summary(f2)
AIC(f1, f2)
```

```
par(mfrow = c(2, 2))
plot(f2)

f3 <- lm(sdMPS ~ 1, pathAnalysisData)
f4 <- lm(sdMPS ~ proCrop, pathAnalysisData)
summary(f4)
AIC(f3, f4)

par(mfrow = c(2, 2))
plot(f4)

f5 <- lm(proForest ~ 1, pathAnalysisData)
f6 <- lm(proForest ~ proCrop, pathAnalysisData)
f7 <- lm(proForest ~ proForageGrass, pathAnalysisData)
f8 <- lm(proForest ~ proCrop + proForageGrass, pathAnalysisData)
summary(f8)
AIC(f5, f6, f7, f8)

par(mfrow = c(2, 2))
plot(f8)

f9 <- lm(proHR ~ 1, pathAnalysisData)
f10 <- lm(proHR ~ proCrop, pathAnalysisData)
f11 <- lm(proHR ~ proForageGrass, pathAnalysisData)
f12 <- lm(proHR ~ proCrop + proForageGrass, pathAnalysisData)
f13 <- lm(proHR ~ sdMPS, pathAnalysisData)
f14 <- lm(proHR ~ sdMPS + proCrop, pathAnalysisData)
f15 <- lm(proHR ~ sdMPS + proForageGrass, pathAnalysisData)
f16 <- lm(proHR ~ sdMPS + proCrop + proForageGrass, pathAnalysisData)
AIC(f9, f10,f11,f12,f13,f14,f15,f16)
summary(f16)

par(mfrow = c(2, 2))
plot(f16) ###

f17 <- glm(richForest ~ 1, family = "poisson", pathAnalysisData)
f18 <- glm(richForest ~ proForest, family = "poisson", pathAnalysisData)
f19 <- glm(richForest ~ proForest + proHR, family = "poisson", pathAnalysisData)
f20 <- glm(richForest ~ proForest + proHR + proCrop, family = "poisson", pathAnalysisData)
f21 <- glm(richForest ~ proHR, family = "poisson", pathAnalysisData)
f22 <- glm(richForest ~ proHR + proCrop, family = "poisson", pathAnalysisData)
f23 <- glm(richForest ~ proCrop, family = "poisson", pathAnalysisData)
f24 <- glm(richForest ~ proForest + proCrop, family = "poisson", pathAnalysisData)
AIC(f17, f18, f19,f20,f21,f22,f23,f24)
```

```
summary(f18)
summary(f20)

par(mfrow = c(2, 2))
plot(f18)

########################### Grassland Model ###########################

# 5 variables and 6 arrows

#1 <- Perennial Forages / Grassland -> proForageGrass
#2 <- Cropland -> proCrop
#3 <- Mean Field Size (standardized) -> sdMPS
#8 <- Hedgerow -> proHR
#10 <- Grassland Guild Richness -> richGrass

(factorial(5)/(2*factorial(3)))-9
= 1

#(proForageGrass, sdMPS)|{proCrop}
G1.1 <- lm(sdMPS ~ proCrop + proForageGrass, pathAnalysisData)
G1.2 <- lm(proForageGrass ~ proCrop + sdMPS, pathAnalysisData)
#(proForageGrass, proHR)|{proCrop, sdMPS}
#G2 <- lm(proHR ~ proCrop + sdMPS + proForageGrass, pathAnalysisData)
#(proCrop, proHR)|{sdMPS}
#G3 <- lm(proHR ~ sdMPS + proCrop, pathAnalysisData)
#(proCrop, richGrass)|{sdMPS, proForageGrass, proHR}
#G4 <- glm(richGrass ~ sdMPS + proForageGrass + proCrop, family = "poisson",
pathAnalysisData)

summary(G1.1)
summary(G1.2)

# Next calculate independence claim (C) statistic - the sum of all the log(p values) * -2.
C =  1.04407984

# Calculate the degrees of freedom, df=k2, where k = the number of claims
df=1*2=2

# Use the chi square distribution to see if test statistic and df are significant/non significance.
In R, p-value = 1-pchisq(test statistic, df)
1-pchisq( 1.04407984,df=2)

0.593309
```

```
#### Parameterized grassland bird model estimates ####

#The models in the top part of the SEM diagram have the same estimates and significance as
the forest bird model#

g1 <- glm(richGrass ~ proCrop + proForageGrass + sdMPS + proHR, family = "poisson",
pathAnalysisData)

g2 <- glm(richGrass ~ proCrop, family = "poisson", pathAnalysisData)
g10 <- glm(richGrass ~ proHR, family = "poisson", pathAnalysisData)
g8 <- glm(richGrass ~ sdMPS, family = "poisson", pathAnalysisData)
g5 <- glm(richGrass ~ proForageGrass, family = "poisson", pathAnalysisData)

g3 <- glm(richGrass ~ proCrop + proForageGrass, family = "poisson", pathAnalysisData)
g6 <- glm(richGrass ~ proForageGrass + sdMPS, family = "poisson", pathAnalysisData)
g9 <- glm(richGrass ~ sdMPS + proHR, family = "poisson", pathAnalysisData)
g11 <- glm(richGrass ~ proCrop + sdMPS, family = "poisson", pathAnalysisData)
g12 <- glm(richGrass ~ proCrop + proHR, family = "poisson", pathAnalysisData)
g13 <- glm(richGrass ~ proForageGrass + proHR, family = "poisson", pathAnalysisData)

g7 <- glm(richGrass ~ proForageGrass + sdMPS + proHR, family = "poisson", pathAnalysisData)
g7.2 <- glm(richGrass ~ proForageGrass + proCrop + proHR, family = "poisson",
pathAnalysisData)
g7.3 <- glm(richGrass ~ proCrop + sdMPS + proHR, family = "poisson", pathAnalysisData)
g4 <- glm(richGrass ~ proCrop + proForageGrass + sdMPS, family = "poisson", pathAnalysisData)

g14 <- glm(richGrass ~ 1, family = "poisson", pathAnalysisData)
AIC(g1,g2,g3,g4,g5,g6,g7,g8,g9,g10,g11,g12,g13,g14,g7.2,g7.3)
summary(g3)
summary(g7.2)
summary(g4)
summary(g1)

par(mfrow = c(2, 2))
plot(g3)
############################ Shrub/Edge Model ##################################
# 8 variables and 13 arrows

#1 <- Perennial Forages / Grassland -> proForageGrass
#2 <- Cropland -> proCrop
#3 <- Mean Field Size (standardized) -> sdMPS
#5 <- Forest -> proForest
#6 <- Shrubland -> proShrub
```

```
#8 <- Hedgerow -> proHR
#11 <- Shrub/edge Guild Richness -> richShrub
#13 <- Forest Edge (standardized) -> sdEdge

(factorial(8)/(2*factorial(6)))-19
=9


#(proForageGrass, sdMPS)|{proCrop}
S1.1 <- lm(sdMPS ~ proCrop + proForageGrass, pathAnalysisData)
S1.2 <- lm(proForageGrass ~ proCrop + sdMPS, pathAnalysisData)
#(sdMPS, proForest)|{proCrop, proForageGrass, proShrub}
S6 <- lm(proForest ~ proCrop + proForageGrass + proShrub + sdMPS, pathAnalysisData)
#(sdMPS, sdEdge)|{proCrop, proForest, proForageGrass, proShrub}
S7 <- lm(sdEdge ~ proCrop + proForest + proForageGrass + proShrub + sdMPS,
pathAnalysisData)
#(sdMPS, proShrub)|{proCrop, proForageGrass, proForest}
S8 <- lm(proShrub ~ proCrop + proForageGrass + proForest + sdMPS, pathAnalysisData)
#(sdMPS, richShrub)|{proCrop, sdEdge, proShrub, proHR}
S9 <- glm(richShrub ~ proCrop + sdEdge + proShrub + proHR + sdMPS, family = "poisson",
pathAnalysisData)
#(proForest, proHR)|{proCrop, proForageGrass, sdMPS,proShrub}
S11.1 <- lm(proHR ~ proCrop + proForageGrass + sdMPS + proShrub + proForest,
pathAnalysisData)
S11.2 <- lm(proForest ~ proCrop + proForageGrass + sdMPS + proShrub + proHR,
pathAnalysisData)
#(proForest, richShrub)|{proCrop, proForageGrass, sdEdge, proShrub, proHR}
S12 <- glm(richShrub ~ proCrop + proForageGrass + sdEdge + proShrub + proHR + proForest,
family = "poisson", pathAnalysisData)
#(sdEdge, proHR)|{proForest, proCrop, proForageGrass, sdMPS, proShrub}
S14.1 <- lm(proHR ~ proForest + proCrop + proForageGrass + sdMPS + proShrub + sdEdge,
pathAnalysisData)
S14.2 <- lm(sdEdge ~ proForest + proCrop + proForageGrass + sdMPS + proShrub + proHR,
pathAnalysisData)
#(proShrub, proHR)|{proCrop, proForageGrass, sdMPS, proForest}
S15.1 <- lm(proHR ~ proCrop + proForageGrass + sdMPS + proForest + proShrub,
pathAnalysisData)
S15.2 <- lm(proShrub ~ proCrop + proForageGrass + sdMPS + proForest + proHR,
pathAnalysisData)

summary(S1.1)
summary(S1.2)
summary(S6)
summary(S7)
```

```
summary(S8)
summary(S9)
summary(S11.1)
summary(S11.2)
summary(S12)
summary(S14.1)
summary(S14.2)
summary(S15.1)
summary(S15.2)

# Next calculate independence claim (C) statistic - the sum of all the log(p values) * -2.
C = 11.07912782

# Calculate the degrees of freedom, df=k2, where k = the number of claims
df=9*2=18

# Use the chi square distribution to see if test statistic and df are significant/non significance.
In R, p-value = 1-pchisq(test statistic, df)
1-pchisq(11.07912782,df=9)

0.2703241

#Parametrized shrub-edge bird model estimates#
s1 <- lm(proForageGrass ~ proCrop, pathAnalysisData)
summary(s1)
s2 <- lm(proHR ~ proCrop + proForageGrass + sdMPS, pathAnalysisData)
summary(s2)
s3 <- lm(sdMPS ~ proCrop, pathAnalysisData)
summary(s3)
s4 <- lm(proForest ~ proForageGrass + proCrop + proShrub, pathAnalysisData)
summary(s4)
s5 <- lm(sdEdge ~ proForest + proCrop + proForageGrass + proShrub, pathAnalysisData)
summary(s5)
s6 <- lm(proShrub ~ proCrop + proForageGrass + proForest, pathAnalysisData)
summary(s6)
s7 <- glm(richShrub ~ proForageGrass + proCrop + sdEdge + proShrub + proHR, family =
"poisson", pathAnalysisData)
summary(s7)

#### Parameterized model ####

#models s1, s2, and s3 are the same as the forest model estimates and significance, need to
model s4-7#
```

```
s1 <- lm(proForest ~ 1, pathAnalysisData)
s2 <- lm(proForest ~ proForageGrass + proCrop + proShrub, pathAnalysisData)
s3 <- lm(proForest ~ proForageGrass + proCrop, pathAnalysisData)
s4 <- lm(proForest ~ proForageGrass, pathAnalysisData)
s5 <- lm(proForest ~ proForageGrass + proShrub, pathAnalysisData)
s6 <- lm(proForest ~ proCrop + proShrub, pathAnalysisData)
s7 <- lm(proForest ~ proCrop, pathAnalysisData)
s8 <- lm(proForest ~ proShrub, pathAnalysisData)
AIC(s1,s2,s3,s4,s5,s6,s7,s8)
summary(s2)

par(mfrow = c(2, 2))
plot(s2)

s9 <- lm(proShrub ~ 1, pathAnalysisData)
s10 <- lm(proShrub ~ proCrop + proForageGrass + proForest, pathAnalysisData)
s11 <- lm(proShrub ~ proCrop, pathAnalysisData)
s12 <- lm(proShrub ~ proCrop + proForageGrass, pathAnalysisData)
s13 <- lm(proShrub ~ proCrop + proForest, pathAnalysisData)
s14 <- lm(proShrub ~ proForageGrass, pathAnalysisData)
s15 <- lm(proShrub ~ proForageGrass + proForest, pathAnalysisData)
s16 <- lm(proShrub ~ proForest, pathAnalysisData)
AIC(s9,s10,s11,s12,s13,s14,s15,s16)
summary(s10)

par(mfrow = c(2, 2))
plot(s10)

s17 <- lm(sdEdge ~ 1, pathAnalysisData)
s18 <- lm(sdEdge ~ proForest + I(proForest^2) + proCrop + proForageGrass + proShrub,
pathAnalysisData)
s19 <- lm(sdEdge ~ proForest + I(proForest^2), pathAnalysisData)
s20 <- lm(sdEdge ~ proForest + I(proForest^2) + proCrop, pathAnalysisData)
s21 <- lm(sdEdge ~ proForest + I(proForest^2) + proForageGrass , pathAnalysisData)
s22 <- lm(sdEdge ~ proForest + I(proForest^2) + proShrub, pathAnalysisData)
s23 <- lm(sdEdge ~ proForest + I(proForest^2) + proCrop + proForageGrass, pathAnalysisData)
s24 <- lm(sdEdge ~ proForest + I(proForest^2) + proCrop + proShrub, pathAnalysisData)
s25 <- lm(sdEdge ~ proForest + I(proForest^2) + proForageGrass + proShrub, pathAnalysisData)
s26 <- lm(sdEdge ~ proCrop, pathAnalysisData)
s27 <- lm(sdEdge ~ proCrop + proForageGrass, pathAnalysisData)
s28 <- lm(sdEdge ~ proCrop + proShrub, pathAnalysisData)
s29 <- lm(sdEdge ~ proForageGrass, pathAnalysisData)
s30 <- lm(sdEdge ~ proForageGrass + proShrub, pathAnalysisData)
s31 <- lm(sdEdge ~ proShrub, pathAnalysisData)
```

```
AIC(s17,s18,s19,s20,s21,s22,s23,s24,s25,s26,s27,s28,s29,s30,s31)
summary(s18)

par(mfrow = c(2, 2))
plot(s18)

s32 <- glm(richShrub ~ 1, family = "poisson", pathAnalysisData)
s33 <- glm(richShrub ~ proForageGrass, family = "poisson", pathAnalysisData)
s34 <- glm(richShrub ~ proForageGrass + proCrop, family = "poisson", pathAnalysisData)
s35 <- glm(richShrub ~ proForageGrass + sdEdge, family = "poisson", pathAnalysisData)
s36 <- glm(richShrub ~ proForageGrass + proShrub, family = "poisson", pathAnalysisData)
s37 <- glm(richShrub ~ proForageGrass + proHR, family = "poisson", pathAnalysisData)
s38 <- glm(richShrub ~ proCrop + sdEdge, family = "poisson", pathAnalysisData)
s39 <- glm(richShrub ~ proCrop + proShrub, family = "poisson", pathAnalysisData)
s40 <- glm(richShrub ~ proCrop + proHR, family = "poisson", pathAnalysisData)
s41 <- glm(richShrub ~ sdEdge + proShrub, family = "poisson", pathAnalysisData)
s42 <- glm(richShrub ~ sdEdge + proHR, family = "poisson", pathAnalysisData)
s43 <- glm(richShrub ~ proShrub + proHR, family = "poisson", pathAnalysisData)
s44 <- glm(richShrub ~ proForageGrass + proCrop + sdEdge, family = "poisson",
pathAnalysisData)
s45 <- glm(richShrub ~ proForageGrass + proCrop + proShrub, family = "poisson",
pathAnalysisData)
s46 <- glm(richShrub ~ proForageGrass + proCrop + proHR, family = "poisson",
pathAnalysisData)
s47 <- glm(richShrub ~ proForageGrass + sdEdge + proShrub, family = "poisson",
pathAnalysisData)
s48 <- glm(richShrub ~ proForageGrass + sdEdge + proHR, family = "poisson", pathAnalysisData)
s49 <- glm(richShrub ~ proForageGrass + proShrub + proHR, family = "poisson",
pathAnalysisData)
s50 <- glm(richShrub ~ proCrop + sdEdge + proShrub, family = "poisson", pathAnalysisData)
s51 <- glm(richShrub ~ proCrop + sdEdge + proHR, family = "poisson", pathAnalysisData)
s52 <- glm(richShrub ~ proCrop + proShrub + proHR, family = "poisson", pathAnalysisData)
s53 <- glm(richShrub ~ sdEdge + proShrub + proHR, family = "poisson", pathAnalysisData)
s54 <- glm(richShrub ~ proForageGrass + proCrop + sdEdge + proShrub, family = "poisson",
pathAnalysisData)
s55 <- glm(richShrub ~ proForageGrass + proCrop + sdEdge + proHR, family = "poisson",
pathAnalysisData)
s56 <- glm(richShrub ~ proForageGrass + proCrop + proShrub + proHR, family = "poisson",
pathAnalysisData)
s57 <- glm(richShrub ~ proForageGrass + sdEdge + proShrub + proHR, family = "poisson",
pathAnalysisData)
s58 <- glm(richShrub ~ proCrop + sdEdge + proShrub + proHR, family = "poisson",
pathAnalysisData)
```

```
s59 <- glm(richShrub ~ proForageGrass + proCrop + sdEdge + proShrub + proHR, family =
"poisson", pathAnalysisData)
s60 <- glm(richShrub ~ sdEdge, family = "poisson", pathAnalysisData)
s61 <- glm(richShrub ~ proCrop, family = "poisson", pathAnalysisData)
s62 <- glm(richShrub ~ proShrub, family = "poisson", pathAnalysisData)
s63 <- glm(richShrub ~ proHR, family = "poisson", pathAnalysisData)
AIC(s32,s33,s34,s35,s36,s37,s38,s39,s40,s41,s42,s43,s44,s45,s46,s47,s48,s49,s50,s51,s52,s53,s5
4,s55,s56,s57,s58,s59,s60,s61,s62,s63)
summary(s44)
summary(s54)
summary(s55)
summary(s59)

par(mfrow = c(2, 2))
plot(s44)
```