

## Appendix A – Supplementary Methods and Results

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### **A1. Methods**

#### *A1.1 Response Variable Derivation*

Given high variability in counts among visits—combined with relatively small sample sizes for some of the counts—we decided to generate seasonal estimates of species richness, evenness, and abundance at a site. Uneven sampling precluded us from merely summing counts across visits for a season. Doing so would bias the data in favor of those sites that were sampled more frequently and result in double-counting of birds observed on repeat surveys. To control for this, we used rarefaction to estimate species richness and evenness (measured as the inverse of Simpson diversity) using package `rareNMtests` in R (Cayuela and Gotelli, 2014; R Core Team, 2015). We used sample-base rarefaction to generate comparable richness estimates across all transect\*season combinations, setting the rarefied number of samples equal to the transect\*season combination with the fewest samples ( $n=2$ ). Sample-based evenness estimates were strongly correlated with richness estimates because of the strong relationship between number of species and number of individuals at poorly-sampled locations. To generate a more independent estimate of evenness, we used individual-based rarefaction, setting the rarefied number of individuals equal to 20. This meant dropping 35 out of 192 transect\*season observations from the analysis, but ensured a reasonable number of individuals, enabling a more robust estimate of evenness.

Abundance was strongly related to the number of repeat samples within a season. Moreover, our chosen sampling method did not enable us to ascertain the identity of individuals counted on different visits, making it impossible to estimate the amount of double-counting over the course of a season. We therefore opted to use the minimum number known alive (MNKA) for each species for a given transect\*season observation (Krebs, 1999). MNKA was estimated as the maximum number of individuals detected on a single visit to a site. MNKA has been used to provide robust estimates of relative abundance when other, more sophisticated metrics cannot be calculated. To avoid a positive bias toward more frequently sampled sites, we restricted our estimate of MNKA to the first two sampling intervals (since all sites were sampled at least twice in a season). We generated an estimate of total bird abundance for a given sample by summing the MNKA across all species detected at a transect\*season observation.

#### *A1.2 Collinearity*

After checking for correlations between continuous covariates, if we suspected a strong association between a continuous and categorical variable, we built a simple linear model including the two variables and dropped one if the model  $R^2$  was greater than 0.25 (analogous to a Pearson correlation of 0.5). For each response variable we used generalized variance inflation

factors (Zuur et al., 2009) to do a final check for collinearity on the predictors selected for the final model.

### *A1.3 Predictors of Rarefied Species Richness, Rarefied Evenness, and Maximum Total Abundance*

We started model building with Boosted Regression Trees (BRTs). In building the BRT model we added a random number dummy variable, with values between 1 and 100, to the set of predictor variables. This allowed us to rapidly assess the predictive ability of the other covariates, with any covariate whose variable importance score fell below the random number being considered unimportant and being dropped from the pool of predictors (Soykan et al., 2014). A second BRT model was then run using the reduced set of predictor variables. This was done to examine the interaction strengths between the remaining predictor variables. BRT models were run using the *dismo* package in R (Hijmans et al., 2013).

The next stage involved building and running Generalized Additive Mixed-Effects Models (GAMMs) in R, for which we used the *gamm4* package (Wood and Scheipl, 2014). Starting with the variables and interactions identified as important in the BRT analysis, we further included a season by water year interaction term in each of the initial GAMM models. After running the initial GAMM model, we dropped any variables or terms with a p-value > 0.10 and re-ran the model (if necessary) with the reduced set of predictor variables.

Next, we used the *lme4* package (Bates et al., 2014) in R for building and running Linear and Generalized Linear Mixed-Effects Models (GLMMs). We approximated non-linear relationships using quadratic and cubic terms in the linear and generalized linear models. As for GAMMs, we dropped any variables or terms with a p-value > 0.10 and re-ran the model (if necessary) with the reduced set of predictor variables.

Finally, we subjected the final LMM/GLMM results to model selection and model averaging.

### *A1.4 Predictors of Maximum Species Abundance*

As a first step, we modeled the individual relationship between each continuous predictor variable and species abundance using GAMMs, with species and site as random effects. We used the estimated degrees of freedom (edf) as a guide in building univariate GLMM models, adding quadratic terms if  $1 < \text{edf} \leq 2$ , adding both quadratic and cubic terms if  $2 < \text{edf} \leq 3$ , and adding quadratic, cubic, and fourth-order terms if  $3 < \text{edf} \leq 4$ . Using the results of the univariate GLMMs as a guide we built a multivariate GLMM with each of the coefficients that had a p-value < 0.10. We then built a second GLMM using those coefficients that had a p-value < 0.10 in the first multivariate GLMM. Since a few of the terms in this second GLMM had p-values > 0.10, we repeated the process again with a further-reduced set of predictors. Finally, we subjected the third multivariate GLMM results to model selection and model averaging.

### *A1.5 Influence of Field Margin Vegetation Structure*

In order to ascertain whether specific characteristics of the field margins explained any variation in species richness beyond what was already explained by the variables included in the aforementioned models, we built a linear mixed-effects model regressing the residuals of the final GLMM model against a measure of vegetation height (along with the square and cube of vegetation height to get at any non-linearities). We separately regressed species richness against the number of vegetation layers (not including both predictors in a single model because they

were strongly correlated). We replicated this analysis for species evenness, maximum total abundance, and maximum species abundance.

### *A1.6 Spatial Autocorrelation of Residuals*

We generated bubble plots, variograms, and directional variograms (Zuur et al. 2009) for all four response variables to evaluate spatial autocorrelation among geographically clustered sites.

## **A2. Results**

### *A2.2 Collinearity*

Vegetation height and number of vertical layers had Pearson's correlation coefficients  $\geq 0.5$  (Tables B7 and B8). This was true for the full dataset and for the reduced dataset (used for species evenness analyses). Moreover, both variables were strongly associated with margin type (F-statistic: 54.55 on 3 and 188 DF, p-value:  $< 2.2e-16$  for Vegetation Height and F-statistic: 86.38 on 3 and 188 DF, p-value:  $< 2.2e-16$  for Number of Vegetation Layers). Since margin type was of greater interest to us due to its management and policy implications, we dropped these two variables from the model. However, recognizing their potential importance as was highlighted in previous work (e.g., Hinsley and Bellamy, 2000), we analyzed the residuals of the final models to see if either vegetation height or number of vegetation layers had any additional explanatory potential beyond that covered by margin type (see *A1.5*, *A2.5*, and Tables B36 and B37).

The generalized variance inflation factors were all below 2, indicating that collinearity was not an issue for the final models.

### *A2.3 Predictors of Rarefied Species Richness, Rarefied Evenness, and Maximum Total Abundance*

BRT analysis singled out six of the 13 covariates as better predicting species richness than a random number (Table B9). The reduced predictor BRT model (Table B10) identified two sets of covariates as interacting strongly-enough to warrant consideration in building GAMM models for species richness (Table B11). When the six variables and the two strongest interaction terms were combined in a GAMM model (Table B12), four of the variables, season, patch area, distance to riparian, and distance to urban were dropped because they were not significant at an alpha level of 0.10 (Table B13). Additionally, the water year by season interaction term—added to all models to control for temporal patterns in the data—was not significant and thus dropped. This left three variables and two interaction terms for the GLMM analysis (Table B14). However, since one of the significant interactions was with a variable that also had quadratic and cubic terms, the final GLMM included 4 interaction terms. Model selection revealed four models that had very strong support (delta values less than two). Each of these included edge type, water year, and the interaction between edge type and water year, differing only in the distance to woodland terms (linear, quadratic, or cubic) and the interaction terms between edge type and distance to woodland (Table B15).

BRT analysis singled out five of the 13 covariates as better predicting species evenness than a random number (Table B16). The reduced predictor BRT model (Table B17) identified three sets of predictors as interacting strongly-enough to warrant consideration in building GAMM models for species evenness (Table B18). When the five variables and three interaction

terms were combined in a GAMM model (Table B19), two of the variables and two of the interaction terms were dropped because they were not significant at an alpha level of 0.10 (Table B20). Since the interaction between water year\*season was significant, it was retained in the model. This left four variables, margin type, season, water year, and distance to woodland (as well as the interaction terms between season and both water year and distance to woodland) for the GLMM analysis (Table B21). Model selection revealed that seven models had the greatest support ( $\Delta < 2$ ). They all included edge type and season, differing in whether they included water year, distance to woodland and the interactions between season and water year and season and distance to woodland (Table B22).

BRT analysis singled out six of the 13 covariates as better predicting maximum total abundance than a random number (Table B23). The reduced predictor BRT model (Table B24) identified two sets of predictors which interacted strongly enough to warrant consideration in building GAMM models for maximum total abundance (Table B25). When the six variables and two strongest interaction terms were combined in a GAMM model (Table B26), four of the variables, water year, adjacent crop, patch area, and landscape variety, were not significant at an alpha level of 0.10; however, the interactions between water year and season and margin type and adjacent crop were statistically significant and therefore adjacent crop and water year were retained for the initial GLMM model. Additionally, the interaction between woodland and landscape variety was not significant and those dropped (Table B27). This left five variables and two interaction terms for the GLMM model (Table B28). Model selection revealed that just a single model had almost all of the support (weight = 1.0); it included all of the coefficients from the reduced-predictor GLMM model (Table B29).

#### *A2.4 Predictors of Species Maximum Abundance*

Univariate GAMMs identified three predictor variables as having potentially non-linear relationships with maximum species abundance (Table B30). Three of the 14 predictor variables were dropped because their univariate GLMM results were not significant at an alpha level of 0.10 (Table B31). The remaining 10 variables were combined in a single multivariate GLMM model, which identified eight predictor variables and one interaction term as having a significant relationship with maximum species richness (Table B32). A second GLMM (Table B33) with this reduced set of predictors identified a quadratic term as not being significant at an alpha level of 0.10, so we generated a final GLMM model (Table B34). Model selection on the final GLMM model revealed the greatest support for the full GLMM model (weight = 0.58), with no other model having a delta value  $< 2$  (Table B35).

#### *A2.5 Influence of Field Margin Structure*

None of the coefficients for models predicting the effects of Vegetation Height or the Number of Vegetation Layers on the residuals from the LMM/GLMM models had a p-value  $< 0.05$ , indicating that these two factors did not explain additional variation in species richness, evenness, maximum total abundance or maximum species abundance beyond what was already explained by the earlier models (Tables B36 & B37). Moreover, none of the models had an  $R^2 > 0.025$  (Tables B36 & B37).

#### *A1.6 Spatial Autocorrelation of Residuals*

None of these plots (not shown) suggested any spatial autocorrelation of the residuals.

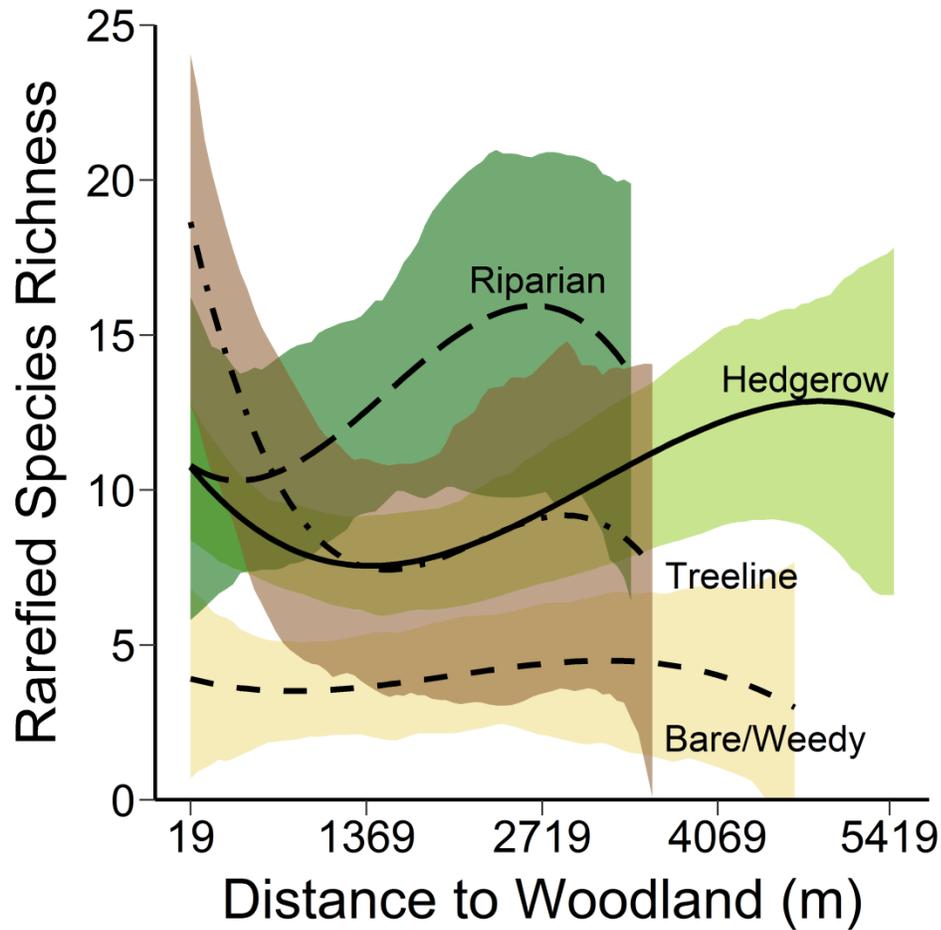
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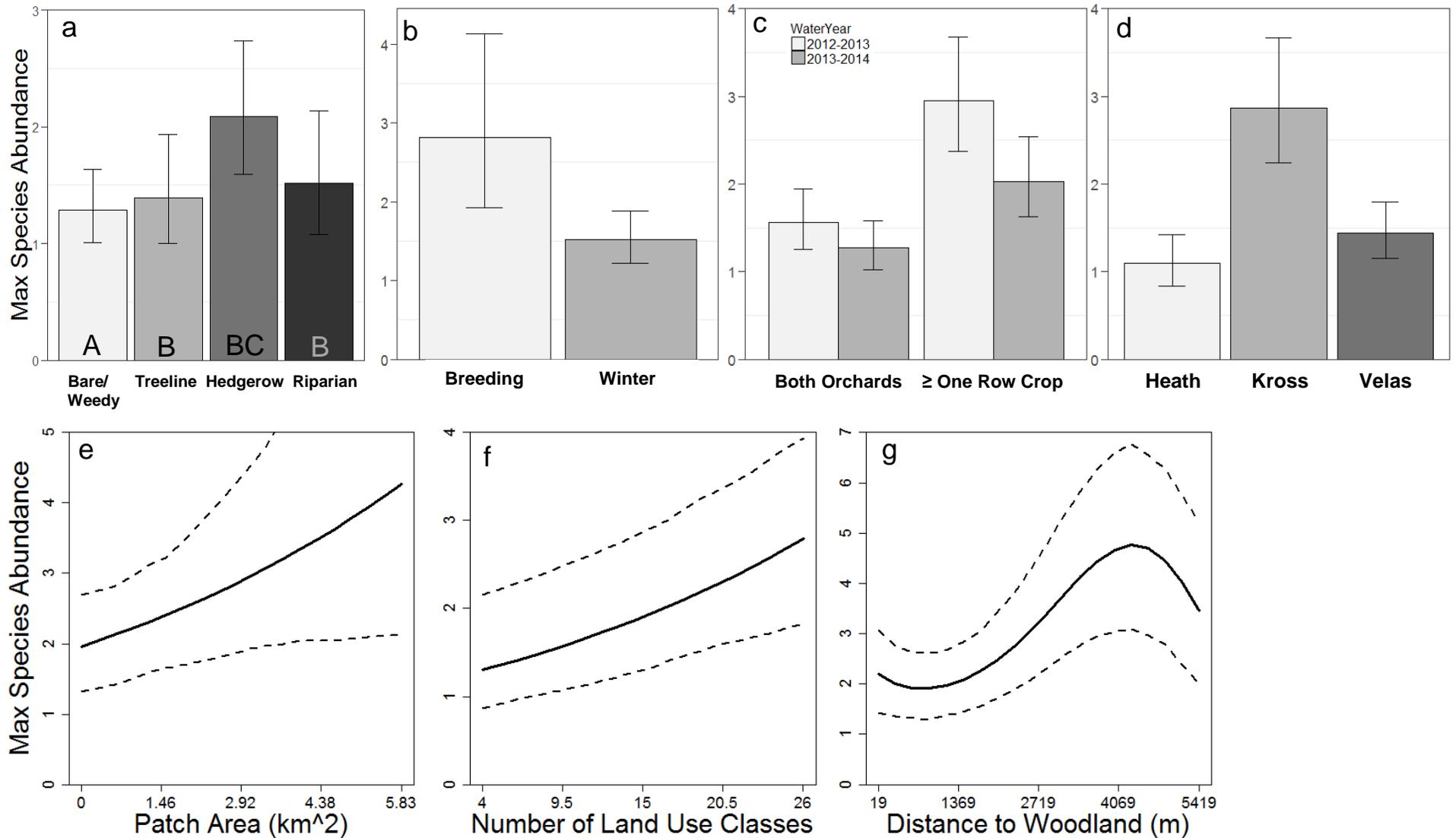
A3. Supplementary Figures



**Figure A1.** Margin type examples from the study area: a) Bare/Weedy, b) Treeline, c) Hedgerow, and d) Riparian. Columns are row crops (left) and orchards (right). Images credit: Treeline left column Sara Kross, all others Sacha Heath.



**Figure A2.** Same as Figure 2b, but with 95% confidence included. Rarefied species richness model-averaged predictions: Richness versus distance to woodland by margin type. 95% confidence intervals for Bare/Weedy (mustard), Treeline (tan), Hedgerow (light green), and Riparian (forest green). Other categorical covariate defaults same as in 2b.



**Figure A3.** Maximum species abundance consensus GLMM model predictions with 95% confidence intervals. Bar heights and solid lines represent the full model-averaged estimates for each variable, controlling the effects of continuous covariates. For all predictions, non-plotted categorical covariates are set to their default values (Margin Type = Hedgerow, Water Year = 2012-2013, Season = Breeding, Adjacent Crop = Both Orchards, Origin = Heath). a) Max species abundance by margin type. b) Max species abundance by water year and season. c) Max species abundance by Adjacent Crop type. d) Max species abundance by project contributing data to this study. e) Max species abundance vs. patch area. f) Max species abundance vs. number of land use classes within 500m of the site. g) Max species abundance vs. distance to woodland.