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Relationships Among Biodiversity Dimensions of Birds in Nebraska

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RELATIONSHIPS AMONG BIODIVERSITY DIMENSIONS OF BIRDS IN NEBRASKA

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Biological diversity, or biodiversity, is a multi-dimensional concept that can be decomposed to measure information about taxonomic, phylogenetic, and functional variation within communities. Although the dimensions of biodiversity are interrelated, the assumption that measuring one dimension of diversity can inform about patterns in another dimension does not necessarily follow from theory or empirical study. The relationships among biodiversity dimensions is not well understood, nor how differences among dimensions could influence conservation decision making. Using the avian community as a study system, we explored the relationships of breadth metrics from the taxonomic, phylogenetic, and functional dimensions among each other and across six gradients of land cover in Nebraska, USA. We found that all three metrics had a high between-sites correlation, yet the within-site correlation was weaker and even slightly negative, which suggests that these metrics could be used as adequate surrogates for one another broadly, yet they would generally be poor predictors locally. We also found substantial differences in spatial scale selection among the diversity metrics, which suggests that these metrics are being influences by different ecological and evolutionary processes. Within each metric's selected spatial scale, land cover relationships were generally similar, yet projected differences in the relationships across land cover resulted

in spatial mismatches, often of substantial magnitude. Differences among diversity metrics may help identify drivers of biodiversity patterns and predict community assembly. Furthermore, the taxonomic metric showed relative insensitivity compared to the phylogenetic and functional metric, suggesting managing for high taxonomic diversity offers a simple and strategic conservation opportunity to preserve phylogenetic and functional diversity as well. Once conservation areas are selected, holistic or intensively managed conservation approaches are recommended.

DEDICATION

To the circus, for always lifting my spirits and teaching that nothing is impossible.

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INTRODUCTION

Biodiversity is a multi-faceted and emergent property of biological communities emerging from ecological and evolutionary processes (Hooper *et al.* 2005; Balvanera *et al.* 2006; Tilman, Isbell & Cowles 2014). Biodiversity is most commonly characterized by measures of taxonomic diversity (e.g., species richness), which are often assumed to approximate other components of biodiversity. However, the rules that govern taxonomic classification are often unable to simultaneously represent the evolutionary and ecological variation found within communities (Swenson 2011; Naeem *et al.* 2016). The phylogenetic and functional dimensions of biodiversity contribute information about different aspects of biodiversity, which provide insight into processes shaping communities and ecosystems not fully encapsulated by taxonomic diversity alone (Cadotte, Carscadden & Mirotchnick 2011; Safi *et al.* 2011; Swenson 2011; Naeem *et al.* 2016). Although the dimensions of biodiversity (i.e., taxonomic, phylogenetic, functional) are interrelated (e.g., Cadotte, Cardinale & Oakley 2008; Flynn *et al.* 2011), the assumption that one dimension is a reliable surrogate for another does not necessarily follow from theory (Faith 1992; Haila & Kouki 1994; Swenson 2011; Naeem *et al.* 2016) or empirical study (Forest *et al.* 2007; Mayfield *et al.* 2010; Chapman *et al.* 2018; Mazel *et al.* 2018; Tucker *et al.* 2018). For example, phylogenetic diversity, which represents variation in evolutionary relatedness and reflects evolutionary and genetic history (Faith 1992; Mace, Gittleman & Purvis 2003; Forest *et al.* 2007), presumably shapes functional diversity, which represents variation in ecological roles represented within communities by linking species to ecosystem productivity, stability, and services (Loreau *et al.* 2001; Hooper *et al.* 2005; Petchey & Gaston 2006; Laureto, Cianciaruso & Samia 2015), because the ecological roles species fill are often influenced by their evolutionary history. However, the degree to which differing evolutionary and ecological forces such as adaptive radiation, convergent evolution, or genetic drift, act within a system ultimately determines relatedness of the taxonomic, phylogenetic and functional dimensions of biodiversity (Swenson 2011).

Failure to account for ecological and evolutionary differences among species can lead to mismatches in observed relationships among biodiversity dimensions (Devictor *et al.* 2010; Meynard *et al.* 2011; Safi *et al.* 2011; Brum *et al.* 2017; Quan *et al.* 2018), and limit our ability to make inferences about unmeasured dimensions or identify the mechanisms driving biodiversity patterns (Swenson & Enquist 2009; Swenson 2011; Naeem *et al.* 2016). To understand the underlying processes and patterns of biodiversity necessitates accounting for the relationships among biodiversity dimensions. One way to gain those insights is by examining the relationships among biodiversity dimensions across a range of environmental conditions and gradients known to affect biodiversity to identify what conditions are associated with mismatches among biodiversity dimensions and the consequences of using one dimension as a surrogate for another.

Here, we explore relationships among taxonomic, phylogenetic, and functional diversity dimensions by quantifying species occupancy across environmental gradients. Specifically, we investigated three dimensions of biodiversity in birds, across natural and anthropogenic gradients of land cover and asked: 1) at what spatial scale do different dimensions of biodiversity relate to land cover, 2) what are the relationships among biodiversity dimensions and various land cover types, 3) are the relationships among biodiversity dimensions consistent across gradients of land cover, and 4) how do the relationships among biodiversity dimensions and land cover contribute to mismatches in predicted biodiversity across space.

METHODS

Study system

Located in the North American Great Plains, the state of Nebraska in the United States harbored substantial variation in natural and anthropogenic land cover (Figure 1. 1; Bishop, Barenberg, Volpe, & Grosse, 2011), making Nebraska an ideal system to examine under what environmental conditions differences among dimensions of biodiversity occur. Although Nebraska was historically home to vast tracts of native grasslands, much of the grassland have been altered to varying degrees to support human needs. Located at the western extent of the 'corn-belt', eastern Nebraska was dominated by intensive row crop agriculture where rain was plentiful and soil was rich, with scattered patches of forest, wetlands, and native grasslands. Across the southern portion of the state, land cover was dominated by matrices of small grain agriculture and pastures in the west and row crop agriculture (e.g., corn, soy beans) in the east. The central and northern-west portion of Nebraska are home to the sand hills where rangeland was dominant due to the sandy soils and lower rainfall, which limited agricultural production. Aside from the sand hills, patches of native habitat were also scattered throughout the state in parks, wildlife management areas, and lands enrolled in the government-sponsored conservation reserve program (CRP), which converted environmentally sensitive land from agriculture to native habitat (Johnson 2000).

Avian point counts

We examined avian biodiversity because birds are abundant, relatively easy to measure, well-studied, evolutionarily (Jetz *et al.* 2012), ecologically diverse (Şekercioğlu, Daily & Ehrlich 2004), and occur across a broad range of anthropogenic and natural gradients. To quantify avian biodiversity, we conducted 500 m fixed radius aural point count surveys during the breeding bird season, from mid-April to late-June of 2016 and 2017, on publicly accessible secondary and tertiary roads (Robbins, Bystrak & Geissler 1986; Mccarthy *et al.* 2012). Survey sites were selected using a modified version of a spatial balanced sampling design, the generalized random tessellation stratified sampling design, that distributed sampling sites randomly within regions of similar dominate land cover to ensure representation of variation in dominant land cover (step 1 in Figure 1. 3; Figure 1. 2; Stevens & Olsen 2004). Using a 30 m resolution land cover product developed by the Rainwater Basin Joint Venture (Figure 1. 1; Bishop 2011), we quantified the proportion of six land cover types (i.e., row crop, grasses, small grain, CRP, wetland, and trees) within a 5 km radius buffer of each pixel across Nebraska. The distributions of the proportions of land cover were split into quartiles, which were equally sampled within each cover type, such that each quartile was represented in the random sampling scheme. Randomly selected sites were relocated to the nearest accessible road and grouped into 'routes' consisting of 7-19 survey sites such that all sites within each route could be visited within one morning following established roadside point count protocols (Jorgensen et al. 2014). Additional routes were created in 2017 to include several Nebraska's Biologically Unique Landscapes, which were primarily managed for declining rare species and unique natural communities (Figure 1. 2; Schneider *et al.* 2011).

Trained observers visited each site within a route up to four times (e.g., the 'robust design' following Williams, Nichols, & Conroy, 2002) during the sampling season (i.e., early May through mid-July within years) in 2016 and 2017. To reduce temporal correlation among visits, we randomized the order of route visitation and starting position. Upon arrival at each point, observers stood at the edge of the road and recorded: date, starting time, UTM coordinates (Garmin eTrex10 GPS, Olathe, Kansas, USA), wind speed, and temperature (Kestrel 1000 wind meter, Houston, Texas, USA). Following a two minute rest period, observers identified and enumerated every bird seen or heard within the following three-minute period (i.e., a visit), which occurred between 15 minutes before sunrise until approximately 10 A.M: the time when avian vocalizations are maximal and most consistent across species (Hutto, Pletschet & Hendricks 1986). We did not perform surveys during inclement weather, including fog, drizzle, prolonged rain, and wind with speeds > 20 km/h (12 mph) as these conditions could have impacted our ability to detect birds.

Species occupancy modeling

Many metrics of biodiversity are sensitive to the number of species and which species occupy a site (Mouchet *et al.* 2010; Pavoine *et al.* 2013), so to obtain robust measures of biodiversity, we must account for known biases and uncertainty inherent in the sampling process. We modeled occupancy of each species detected with hierarchical logistic regression that jointly estimated probability of occupancy and detection probability to account for imperfect detection (step 2 in

Figure 1. 3; Kéry & Schaub, 2011). We then reported model performance.

For each species, counts were collapsed into binary occurrence data for each visit to each site, excluding flyover and unidentified observations. We independently modeled occurrence for each species detected using a Bernoulli-Bernoulli hierarchical logistic regression, in which the probability of site occupancy was modelled as a function of land cover predictors, combined with a detection model accounting for error in estimating true site occupancy as a function of the probability of detection associated with visit-specific covariates (eq. 1 and 2, Figure 1. 4; Kéry & Schaub 2011; Royle & Kéry 2007).

To account for imperfect detection, we modeled our observations ($y_{i,j}$; detections at site i during survey j) as a Bernoulli random variable with probability of success as the product of the true occupancy of the species at the site and detection probability (p), so that detection probability was conditional on occurrence (Kéry & Schaub 2011). We modeled detection probability, p, accounting for multiple observers as a random observer effect (Diefenbach, Brauning & Mattice 2003) and wind speed, time of day, day of the season the survey was conducted, temperature, and cloud cover ($Y_{n\,ij}$ in eq. 1) as fixed effects via a logit link function (eq. 1, Figure 1. 4:Kéry & Schaub, 2011). We included both linear and quadratic effects for time of day, date, and temperature.

We modeled occupancy (z_i=1, if species occupied a site; z_i=0, if not) as another Bernoulli random latent variable controlled by true occupancy probability (Ψ_i) as a fixed effect function of the land cover covariates (grasses, small grain, CRP, trees, wetland; $X_{n\,i}$ in eq. 2) within our sampling radius of 500 m and fixed year effects via a logit link function (eq. 1, Figure 1. 4; Kéry & Schaub 2011). Predictor variables with pairwise Pearson r >0.7 were excluded. We examined linear and quadratic effects for land cover variables with large variation across Nebraska and linear effects only for CRP and wetlands, which had relatively little variation. We performed an orthogonal transformation on land cover variables to remove collinearity between linear and quadratic effects, which can negatively affect model-fit.

Equation 1: Observation process associated with detections

$y_{i,j} \sim Bernoulli\ (z_i * p_{ij})$

$\text{Logit}\ (p_{\ i,j}) = A_{0\ i} + A_1\ Y_{1\ i,j} + A_2\ Y_{1\ i,j}^2 + \ldots\ A_n\ Y_{n\ i,j}$

Priors: $A_n \sim Normal\ (0, 0.1)$

Equation 2: Ecological process associated with true occupancy

$z_i \sim Bernoulli\ (\Psi_i)$

$\text{Logit}\ (\Psi_i) = \beta_{0\ i} + \beta_1\ X_{1\ i} + \beta_2\ X_{1\ i}^2 + \ldots\ \beta_n\ X_{n\ i}$

Priors: $\beta_{\ n} \sim Normal\ (0, 0.1)$

Our models assumed: 1) no false positive detections, 2) occupancy is constant within a year, but could differ between years (i.e., population closure within a sampling season; Kéry & Schaub, 2011), 3) land cover did not significantly change between years, 4) some of the otherwise uncaptured occupancy variation between years can be captured by a year parameter, 5) errors are independent and normally-distributed.

We estimated all models via Bayesian posterior simulation with JAGS (“just another Gibbs sampler;” Plummer 2003) via the rjags (Plummer 2016), and coda packages (Plummer *et al.* 2006) in program R (R Core Team 2018) with one chain of

120,000 of Markov chain Monte Carlo (MCMC) simulations after a 5,000 iteration burn-in period. We assessed parameter convergence visually; all models were determined to be converged after 120,000 iterations. We calculated the mean and 95% credible interval for each parameter based on 120,000 sample iterations.

To examine model performance, we used in-sample validation; we compared the model detection predictions to actual detections were detected individually for each species. We used in-sample validation because we needed as many detections as we could get to inform our occupancy model, which was especially important for rare species. We turned the model's estimated probability of detecting a species at a survey (i.e., 'true occupancy' multiplied by the probability of detecting that species given the survey conditions) into prediction of detection if the estimated probability of detected a species at a survey was greater than prevalence of that species across all surveys (Cramer 2003). This data-based prevalence threshold for modeling checking is considered a simple and effective threshold that minimizes false negative and positive predictions of detection (Liu *et al.* 2005).

As a measure of model fit, we compared the predicted detections and actual detections using the true skill statistic (TSS; TSS = sensitivity + specificity -1) because TSS is largely insensitive to the threshold used to binarize data (Allouche, Tsoar & Kadmon 2006). TSS equally weighted model sensitivity (i.e., the proportion of correctly predicted presences) and specificity (i.e., proportion of correctly predicted absences), and performs well at predicting the distribution of rare species (Allouche *et al.* 2006). TSS values range from -1 to +1, where +1 indicates perfect agreement between predicted and actual detection, values close to zero indicate that prediction was no better than random, and negative values indicate that predicted detection was opposite of actual detection (Allouche *et al.* 2006). Similar to other studies, we considered model fit to be poor if the model's TSS was less than 0.4, adequate if TSS was between 0.4 and 0.75, and excellent if TSS was above 0.75 (Allouche *et al.* 2006).

Taxonomic dimension

We used species richness (SR; the number of species at a site) as our measure for the taxonomic diversity because SR is a commonly used metric to study ecology and evolution and is a measure of taxonomic breadth (Gaston 2000; Gotelli & Colwell 2001; Swenson 2011; Naeem *et al.* 2016).

Phylogenetic dimension

To quantify phylogenetic relationships among bird species, we constructed a phylogenetic hypothesis for the bird species in our final point count dataset based. Because there is uncertainty associated with phylogenetic tree construction, we followed consensus tree building recommendations of Rubolini *et al.* (2015) from a set of equally plausible, but variable, phylogenetic trees of our final set of species. We downloaded 1,000 phylogenetic trees generated from a trimmed subset of the Hackett phylogeny, which was the most complete molecular phylogeny of extant bird species available (Hackett *et al.* 2008; Rubolini *et al.* 2015; compiled from http://www.birdtree.org: Jetz *et al.* 2012). Using the maximum clade credibility criterion (program BEAST; Bouckaert *et al.* 2014), we generated a consensus tree. We assigned the median divergence to branch lengths on the consensus tree to represent time since speciation because median divergence rates avoid misrepresenting potentially skewed posterior distributions of divergence rates (Morrison 2008; Figure S. 1 in supplementary materials).

We then calculated Faith's (1992) phylogenetic diversity (PD), which is the sum of all the branch lengths on the phylogeny connecting the species at a site (R package 'picante' Kembel *et al.* 2010); PD is comparable to SR because PD is also a measure of breadth. Generally, larger values of PD are associated with assemblages containing more distantly related species, and reflect greater unique evolutionary information with a wider scope for future evolutionary adaptation than communities with smaller values of PD (Faith 1992; Mace *et al.* 2003; Faith & Baker 2006). The common ancestral node, or root of the phylogeny, which extends back to include all taxa in the dataset, was included in all calculations of PD so that any combination of clade members at a site would include the evolutionary history since the root (Faith, Reid & Hunter 2004).

Functional dimension

When comparing measures of phylogenetic and functional dimensions, it is important to use a comparable index to avoid misattributing mathematical artefacts for biological pattern (Pavoine *et al.* 2013). To be analogous to PD, we quantified functional diversity (FD; Petchey & Gaston 2002) using the total branch length connecting all co-occurring species at each site based on a functional dendrogram. Similar to a phylogenetic tree, a functional dendrogram also hierarchically clusters species; however, species similarity is quantified based on ecological trait similarities rather than DNA sequence similarity.

We built our functional dendrogram based on 23 functional traits (i.e., four reproductive traits, ten diet traits, one binary activity trait, one body size trait, and seven foraging strategy traits; see Table S. 1 for summary of traits and Table S. 4, Table S. 5, and Table S. 6 for specific values in supplementary materials) similar to traits used to categorize functional diversity of birds in other studies (e.g., Owen L. Petchey, Evans, Fishburn, & Gaston, 2007). Trait information was collected from “The Birds of North America” series from the American Ornithologists’ Society (Rodewald 2015), the “Elton Traits 1.0” species foraging characteristics database for extant birds (Wilman *et al.* 2014), and missing body mass was supplemented with information from the *CRC handbook of avian body masses* (Dunning Jr 2007). To avoid bias in the clustering procedure, variation within each trait was standardized to have a mean of zero and a standard deviation of 1, so that each trait had equal influence on the measure of diversity (Petchey & Gaston 2002, 2006). Final construction entailed arranging species by Gower’s distance, which hierarchically clusters the species parsimoniously by an unweighted pair group method based on the arithmetic mean, (Petchey & Gaston 2002; Podani & Schmera 2006; Mouchet *et al.* 2008). Similar to PD, we quantified FD by summing the branch lengths connecting all co-occurring species at each site on the functional dendrogram from the root (R package ‘picante’ Kembel *et al.* 2010).

Most probable biodiversity measures

Because metrics of biodiversity are often sensitive to the number and which species are included in an assemblage (Faith 1992; Petchey & Gaston 2002; Mouchet *et al.* 2010; Pavoine *et al.* 2013), we estimated the most probable values for each metric to account for the influence rare species could have on diversity metrics in relation to their probability of occupying sites (step 3 in Figure 1. 3). Specifically, we generated 1,000 possible assemblages at each site, with each species’ presence determined by a random binomial draw from its probability of occupancy determined from the species’ occupancy model. We estimated the most probable values of SR, PD, and FD as the mean across the

1,000 bootstrapped assemblages for each site. We centered and scaled the most probable values of SR, PD, and FD (mean: 0; standard deviation: 1) for subsequent analyses.

Biodiversity-land cover relationship modeling

Using the most probable values for each diversity metric, we could address our main research questions regarding the relationships among biodiversity dimensions (step 4 in Figure 1. 3). We modeled each measure in the biodiversity dimension of interest (i.e., PD, FD, SR) using separate models that were linked through examination of their correlations with one another. First, we examined at what spatial scales each diversity metrics responded. Using the selected spatial scales for each land cover type, we estimated the relationships diversity metrics across land cover. We also examined between- and within-site correlations among diversity metrics to estimate how reliably one metric can be used to inform another.

We built a multivariate mixed-effects model with Gaussian error distributions to estimate the relationships between land cover covariates and the diversity metrics (eq. 3). Mixed effects modeling does not assume balanced or complete sampling, and allows for the incorporation of repeated measures (Dingemanse & Dochtermann 2013). Our model had random intercepts for sites, and fixed effects for each year and land-use covariates that we allowed to vary independently for each diversity metric ($Diversity_{w}$; eq. 3). Similar to the occupancy model, we examined linear and quadratic effects for land cover variables with large variation across Nebraska and linear effects only for CRP and wetlands, which had relatively little variation; Land cover variables were orthogonal transformed to remove collinearity between linear and quadratic effects. We ran our model with one MCMC chain for 20,000 iterations after a 5,000 burn-in period with mean-zero, normally distributed uninformative priors with a standard deviation of 0.1 and visually assessed each parameter for convergence.

Equation 3: Ecological process associated with diversity metrics

$$Diversity_{w,\,i} = \Gamma_{0\,w,i} + \Gamma_{1\,w}\, X_{1i}\,[sc_1] + \Gamma_{2\,w}\, X_{1i}^{\,2}\,[sc_1] + \ldots\, \Gamma_{n\,w}\; X_{n\,i}\,[sc_n]$$

Priors: $\Gamma_n \sim \mathit{Normal}\,(0, 0.1)$

$Sc_n \sim cat(w_1, \ldots, w_k)$ for all $w_k = 1$

Because we did not know the spatial scale at which these diversity metrics respond to, we ran the multivariate mixed-effects model to select the most informative spatial scale before estimating effect sizes. We incorporated Bayesian latent indicator scale selection (BLISS; Stuber, Gruber, & Fontaine, 2017) in our multivariate model to determine which spatial scales of land cover variables is most strongly associated with each diversity metric. We evaluated 0.5 km, 1km, 2km, 5km, 10km, 15km, and 20km radius spatial scales (w_k in eq. 3) as candidates for each of the land cover covariates from which BLISS could sample. BLISS uses reversible jump MCMC with each scale as a latent class indicator variable to sample land cover coefficients at each candidate spatial scale in proportion to its probability of being the most informative scale relevant to predicting each diversity metric (Stuber *et al.* 2017). We chose to include row crop along with the other land cover predictors because BLISS performed well with highly correlated variables ($\geq\rho=0.8$; Stuber, Gruber, & Fontaine, 2018; row crop and grasses were correlated at $\rho= -0.8$). We used uniform, discrete priors for each candidate spatial scale, and allowed BLISS to estimate scales independently for each land cover variable and biodiversity metric. We constrained BLISS to sample linear and quadratic effects of land-use variables at the same spatial scale during each sampling iteration. For each variable, we chose the scale with the highest posterior probability for each land cover type as the best spatial scale. We reran the biodiversity model with land cover covariates at their selected scales to better estimate relationships across land cover ($\Gamma_{n\ w}$).

Using the final estimated models for each metric, we created prediction maps by integrating our multivariate biodiversity models with independent land cover variables using raster package (step 5 in Figure 1. 3; Hijmans 2017). Because the biodiversity model was fit on transformed covariates, the resulting model parameters had to be back-transformed from the poly-quadratic transformed data to be applied to the land cover data. Because we modeled the land cover as fixed effects and years as random effects, we chose to project one map for each metric as result of the fixed effects using one year's intercept.

To visualize spatial mismatches among diversity metrics, we rescaled each metrics' prediction map values to range from 0 to 1 and mapped the difference between each pair of diversity metrics in ArcMap (ESRI 2015). The mismatch maps highlight the where differences were predicted to occur and to what degree.

We examined the between and within-site correlation among PD, FD, and SR. To determine whether the correlation between metrics was influenced by land cover variables, we compared correlation estimates from the full model to an intercept-only model. We used zero-mean, normally distributed priors for fixed effects and a weakly informative Wishart distribution (W in eq. 4) for the precision parameter of the multivariate normal distribution (eq. 4). Within-site covariance was estimated as the inverse of the mean precision associated with each combination of diversity metrics (V in eq.4). Within-site correlation was derived from covariance by dividing covariance by the product of the standard deviation of each response variable being compared. Pearson correlation was used to calculate between-site correlations among diversity metrics.

Equation 4: Correlation

$$Diversity_w \sim Normal\ (\mu_w, \tau_w)$$

$$\text{Priors:} \qquad \tau \sim W\ (V, 5)$$

We checked our models for homoscedasticity and normally distributed residuals and assessed the fit of our regression models using R^2 values and root mean square error (RMSE; package ‘caret’: Kuhn *et al.* 2018) in R.

RESULTS

We detected 141 species from 2641 surveys at 781 unique sampling sites; 548 and 549 sites were sampled in 2016 and 2017 respectively, with 415 sites that were visited in both 2016 and 2017 (Table S1 in supplementary materials). Surveys were conducted over 68 days between April 12th through June 30th in 2016 and over 45 days between May 4th to June 22nd in 2017. Each site was visited from 1 – 7 times over the two years, with a mean of 2.4 ± 0.9 replicates per year. Of the species detected, 83 were detected in less than 1% of the surveys, and only 16 species were detected in more than 10% of surveys (Table S. 2 in supplementary materials). Western meadowlark (*Sturnella neglecta*) was detected at the greatest number of sites (693; 89%). Across sites, average SR of detections was 9.69 ± 5.02 and 9.88 ± 3.90 in 2016 and 2017, respectively.

Occupancy modeling of Nebraska birds

Occupancy models for all 141 species attained visual convergence, but model performance varied. TSS was larger than 0.7 for 87% of species' models, which is considered excellent model fit, 12% of models had TSS between 0.4 and 0.7 (i.e., good), however, 0.01% of models (i.e., two species) had TSS lower than 0.4 (i.e., poor model fit; Table S. 2 in supplementary materials).

Across all sites, the most probable SR averaged 50.35 ± 3.79 (min 40, max 60), PD averaged of 1690.88 ± 94.72 (min – max 1424.30 to 1937.20), and FD averaged 2.07 ± 0.10 (1.74 to 2.31 min – max), before they were z-scored to facilitate modeling and interpretation. On average, all diversity metrics were greater in 2016 than 2017.

Multivariate modeling of biodiversity dimensions

Scale selection

BLISS revealed substantial variation in both in the posterior probabilities among land cover types within each biodiversity dimensions and among biodiversity dimensions within land cover types (Figure 1. 5, Figure 1. 6, Figure 1. 7). Selected scales ranging from the smallest candidate scale (0.5 km) to a maximum of 10km. Posterior probability of selected scales ranged from 0.15 (small grain at 10 km for PD) to 0.46 (trees at 4 km for FD) with an average of 0.28. Probability distributions appeared largely unimodal; however, we detected several bimodal patterns (e.g., row crop for FD; Figure 1. 6), and few uniform distributions (e.g., small grains PD, FD, and SR; Figure 1. 5, Figure 1. 6, Figure 1. 7). There were few instances in which the same scale was selected for multiple land cover types within the same diversity metric.

For PD, BLISS tended to select mid-range spatial scales (crop, CRP, grasses, trees), but the smallest scale for wetlands and a relatively large scale for small grain (Figure 1. 5; Table 1. 1). Scale selection was relatively clear for row crop, CRP, grasses, and wetland, but was more ambiguous based on the relatively flat posterior distribution of small grains, and the bimodal distribution of trees. Excluding wetland, BLISS consistently designated larger spatial scales for PD compared with FD. PD also had larger designated spatial scales than SR for half of the land cover variables investigated.

BLISS selected mid-range spatial scales for FD for half of the land cover variables (row crop, small grain, trees), but relatively smaller spatial scales for CRP, grasses, and wetland (Figure 1. 5, Figure 1. 6, Figure 1. 7, Table 1. 1). While the spatial scales selected for FD were almost exclusively smaller than for PD, half of FD land cover variables were selected at the same spatial scale as SR (grasses, small grain, wetland). BLISS selected smaller scales for FD than SR for row crop and CRP, and a larger spatial scale for trees.

Generally, BLISS selected mid-range spatial scales (row crop, CRP, small grain, trees) for SR, but smaller scales for grasses and wetland (Figure 1. 5, Figure 1. 6, Figure 1. 7, Table 1. 1).

Land Cover Relationships

We found that within their selected scales, diversity metrics generally had similar relationships across land cover gradients. We found that PD, FD, and SR had similar negative relationships across CRP and grasses land cover, similar positive relationships with tree cover, and no relationships across the row crop or small grain gradients (Figure 1. 8, Figure 1. 9, Figure 1. 10, Figure 1. 11). FD had a more positive relationship at small percentages of grasses than PD, but the relationships overlapped at higher percentages of grasses (Figure 1. 10). FD and SR demonstrated similar decreasing relationships with increasing percent of wetlands, while PD, although lower on average at small percent of wetland, increased with percent of wetlands (Figure 1. 13).

The most similar land cover relationships (i.e., mean and credible intervals) were often between diversity metrics for which BLISS selected the similar spatial scale: PD and SR across row crop at 4 km and FD at 3 km (Figure 1. 8), PD and SR across CRP at 4 km (Figure 1. 9), FD and SR across small grain at 5 km (Figure 1. 11), and FD and SR across wetlands at 1 km (Figure 1. 13). The most divergent relationships were between PD and the other two metrics across wetlands, yet the difference in spatial scale was the smallest among the possible scales (0.5km; Figure 1. 13).

SR was slightly more centered around zero than PD and FD across grassland (Figure 1. 10).

Biodiversity Correlations

Between-sites, PD, FD, and SR were highly correlated (PD: FD r^2= 0.96, PD:SR r^2= 0.97, FD:SR r^2= 0.98). However, at the within-site level PD and FD were negatively correlated, and SR was slightly negatively correlated with PD and FD (Table 1. 1).Within-site correlations among dimensions did not change after accounting for the fixed effects of land cover variables (Table 1. 1, Table 1. 2).

Model Checking

Visual residual analysis did not indicate model assumption violations. The R^2 values from the multivariate model after scale selection for PD, FD, and SR were 0.012, 0.014, and 0.012, and the RMSE values were 0.992, 0.992, and 0.994, respectively, indicating that our predictor variables have small effects on PD, FD, and SR.

Biodiversity Distribution Maps

We used our multivariate models to predict PD, FD, and SR across the state, which projected the isolated effects of land cover. Diversity metrics showed broad similarities across Nebraska; PD, FD, and SR were predicted to have higher values in the east than the west (Figure 1. 14, Figure 1. 15, Figure 1. 16). Generally, high values of PD, FD, and SR were predicted in similar areas: northwest, along the east border of Nebraska, and in patches in the middle of the state, most of those places had trees. Areas in the east, which have the highest agriculture in the state, were projected to have intermediate to high levels of all three diversity metrics. PD and SR were predicted to have low values in the southwest corner, just north of Colorado, unlike FD. FD was predicted to have low values in the north central Nebraska (Figure 1. 15). SR was generally uniform low to intermediate values throughout north central Nebraska (Figure 1. 16).

When examining the mismatch between PD and FD, we saw that much of the state had relatively similar relative values of PD as FD with 74.4% of Nebraska predicted to be within 5% of each other (Figure 1. 17; yellow). FD was higher than PD for 20.9% of the state (Figure 1. 17; orange), with the highest differences in the southwest. PD was higher than FD in only 4.7% of the state (Figure 1. 17; blue), occurring in small patches in north central and southeastern Nebraska, generally where wetlands occur (Figure 1. 1).

Mismatches between SR and PD and between SR and FD were almost exclusively towards PD and FD respectively (Figure 1. 18, Figure 1. 19). Both PD and FD had higher mismatches in east and south Nebraska than towards the northwest. Areas that were closer to being equal generally followed rivers and were where large contiguous grasslands occurred in the state (e.g., central Nebraska; Figure 1. 18, Figure 1. 19).

DISCUSSION

Understanding the patterns and drivers of biodiversity is one of the core quests for ecologists and evolutionary biologists, yet it is still not known how different dimensions of biodiversity relate to one another and under what conditions biodiversity dimensions differ. Knowledge of the relationships among different diversity metrics can help elucidate whether surrogacy is warranted among dimensions, identify drivers of biodiversity patterns, and predict community assembly.

We explored relationships among breadth metrics in the taxonomic, phylogenetic, and functional dimensions of biodiversity stratified across six land cover gradients to tease apart under what conditions diversity metrics differ. We found that these metrics were adequate surrogates for one another broadly, yet they would serve as poor predictors locally. We detected substantial differences in spatial scale selection among the metrics, with PD generally selecting larger scales than SR and SR selecting larger scales than FD, suggesting that these metrics were associated with different ecological and evolutionary processes. Wetlands showed divergent diversity trends, which could help identify drivers of biodiversity patterns and predict community assembly. Within each metric's selected spatial scale, land cover relationships were generally similar, yet projected differences in the relationships across land cover resulted in spatial mismatches, often of substantial magnitude. Based on our study, we suggest that surrogacy of among these metrics should be viewed with caution and that more studies examine the relationship between biodiversity dimensions and spatial scale.

Correlation and Surrogacy

Often inferences about dimensions have been made from patterns observed in another dimension. Historically, measures of taxonomic diversity (e.g., species richness) have been used to make inferences about phylogenetic and functional diversity, which are often much harder to measure (Safi *et al.* 2011; Swenson 2011). Surrogacy is warranted if metrics consistently co-vary or we understand under what conditions surrogacy is inadequate and correct for them.

The three diversity metrics were highly correlated between sites, suggesting that these metrics could serve as good surrogates for one another broadly. The high between-site correlation could be partly attributed to mathematical constraints as increases in SR necessarily add branch length to PD and FD measures (Faith 1992; Petchey & Gaston 2002; Mouchet *et al.* 2010; Pavoine *et al.* 2013). Yet this mathematical attribute makes biological sense as well; these metrics can be viewed as a measure of breadth so the range of taxonomic, phylogenetic, and functional diversity increases with the addition of species. Breadth is not the only measure of diversity; there are other metrics that examine the distribution and abundance of units that may be more appropriate for the questions being asked (see reviews and guides such as Schleuter *et al.* 2010; Tucker *et al.* 2017). However, if breadth is the primary aspect of diversity being investigated, our results indicated that these metrics could broadly serve as adequate surrogates for one another.

However, evidence for metrics in the taxonomic dimensions being good surrogates for metrics in phylogenetic and functional dimensions is equivocal (Gaston 2000; Webb 2000; Rodrigues & Gaston 2002; Huang, Stephens & Gittleman 2012; Pavoine *et al.* 2013; Winter, Devictor & Schweiger 2013) and typically indicate only partial congruence of SR with PD and FD (Devictor *et al.* 2010; Huang *et al.* 2012; Carvalho *et al.* 2017). Big changes in species membership between sites, which could be associated with the size of available species pools, are probably driving the high between-site correlations. Nebraska had many species that contain the western or eastern most extent of their geographic ranges; Comparing sites that had different species membership based on the available species pools could result in big differences between sites that had different species pools that would drown out smaller fluctuations among diversity metrics between sites that had the same species pool. Examining within-site correlations picked out more minute changes among diversity metrics because the changes in species membership at a site between years was less likely to vary as dramatically compared to differences between sites. We found that within-site correlation was much weaker than between-site correlations among PD, FD, and SR (Table 1. 1). Correlations between SR and the other two metrics were practically zero, meaning that at sites, changes in SR did not correspond with consistent changes in either PD and FD between sampling years. SR's high between-site correlations suggest that SR would be a good surrogate broadly, but the nearly zero within-site correlations suggest that SR would not do a good job predicting specific values of either PD or FD; we recommend that taxonomic surrogacy should be viewed with caution.

Some have also suggested that metrics of phylogenetic diversity could be a surrogate for functional diversity (Faith 1992; Webb *et al.* 2002; Wiens & Graham 2005; Cadotte *et al.* 2008). With advances in phylogenetic analyses and access to genetic data, it has been come easier to examine phylogenetic diversity for many taxonomic clades. Functional diversity lags behind because there is less consensus about what and how to measure functional diversity (Petchey & Gaston 2006; Laureto *et al.* 2015). Our between-site correlations suggest that PD could serve as an adequate surrogate for FD broadly, yet the within-site correlation between PD and FD was negative (Table 1. 1), suggesting that changes in PD at a site between years would result in often inverse changes to FD. Our results are consistent with other studies that have demonstrated that PD is an unreliable surrogate for FD (Pavoine *et al.* 2013; Mazel *et al.* 2018).

One of the questions we asked was whether the relationships among biodiversity dimensions consistent across gradients of land cover. If there are detectable systematic changes among biodiversity dimensions across land cover (e.g., PD consistently decreases at a faster rate compared to SR across a gradient of row crops), then we might be able to detect differences between the correlation structure when we account for land cover. When we compared the within-site correlations in the model that accounted for land cover covariates to the within-site correlations that only had year intercepts, we did not find any differences in the correlations (Table 1. 1, Table 1. 2), suggesting that the correlations between these diversity metrics do not vary substantially in tandem across our land cover gradients. Had we detected systematic differences, surrogacy might have been improved by applying a correction factor under the conditions that produced consistent differences. Here, we did not find our land cover variables to have be substantial effect for which we could apply a correction factor to improve surrogacy.

Scale selection

Our study is also one of the first studies to answer a recent call for investigations of scale-dependency in biodiversity (Pool, Grenouillet & Villéger 2014). Because PD, FD, and SR are aggregate measures of variation in spatial scale selection over all the individual species, we might expect not to find clear selection of spatial scale; BLISS would reflect uniform posterior distributions across scales, like how we found for all three metrics for small grains (Figure 1. 5, Figure 1. 6, Figure 1.7). Uniform posterior distributions indicate insensitivity to differences in spatial scale, such that land cover could be considered equally good or bad at predicting diversity metrics at any scale. However, the often clear selection of spatial scales indicates that many measures are scale sensitive. Additionally, the selection of spatial scales within the middle range of candidate scales (Figure 1. 5, Figure 1. 6, Figure 1.7) indicates that we had a sufficient range of scales from which to consider (Miguet *et al.* 2016). The existence of environmental relationships that are scale-dependent suggests that care should be taken when investigating patterns of biodiversity, as making inferences based on relationships derived from inappropriate scales could lead to incorrect conclusions, and unsuccessful outcomes of biodiversity planning efforts independent of the ability of biodiversity dimensions to predict one another.

Had the metrics been interchangeable, we could expect to see similar selection of spatial scales for all three diversity metrics. However, BLISS revealed substantial differences in spatial scale selection within and among PD, FD, and SR (Figure 1. 5, Figure 1. 6, Figure 1.7). Such clear differences in spatial scale selection are likely not an issue in areas where landscapes are relatively similar across spatial scales, as considering biodiversity at ‘wrong’ spatial scales likely would have little overall impact. However, as differences across scale increase, inappropriately assuming that all diversity metrics respond to the same spatial scales will likely have repercussions. Our BLISS results indicate that inferences made from one metric about other diversity metrics in other dimensions may be unreliable because diversity metrics corresponded with different spatial scales.

The phylogenetic dimension is associated with processes of speciation and extinction (e.g., colonization, dispersal, gene flow, natural selection) that operate across large temporal and spatial scales (Cavender-Bares *et al.* 2009; Jackson & Fahrig 2014; Miguet *et al.* 2016). In our study, BLISS generally selected larger scales for PD than for FD or SR (Table 1. 1). PD is a snapshot of large-scale evolutionary processes, so we could expect PD patterns to manifest on larger spatial scales than with other diversity dimensions. Our result is one of the first empirical examinations between multiple dimensions of biodiversity, especially of the phylogenetic dimension, and spatial scale: an area ripe for hypothesis generating and hypothesis testing investigations.

The functional dimension carries trait-based information that links a community to ecological processes (Mouchet *et al.* 2010). In our study, BLISS generally selected the smallest scales for FD (Figure 1. 6, Table 1. 1). Another study found the distributions of functional traits had stronger associations at smaller spatial scales than larger spatial scales (Kraft & Ackerly 2010). Species clearly benefit from occupying areas where their functional traits offer fitness benefits (Miguet *et al.* 2016). Thus, the set of species at a site is likely to have a range of functional traits that can be used in a relatively small neighborhood; local changes to land cover types and percentages could alter the breadth of functional traits used at a site and impact FD more than PD or SR.

BLISS generally selected mid-ranged scales for SR and these spatial scales were at the same scale as another metric or at intermediate scales between PD and FD (Figure 1. 5, Figure 1. 6, Figure 1.7). Out of the three metrics, SR could be expected to be most associated with intermediate spatial scales; The taxonomic dimension is relatively information-poor, because species names and counts (i.e., SR) contain little to no information about the identity of the species that connect species to ecological or evolutionary processes that produced the observed set of species (Faith 1992; Swenson 2011). As SR could be less associated with ecological and evolutionary processes as PD and FD, the selection of intermediate scales could be a result of averaging ecological and evolutionary patterns.

PD, FD and SR are composite metrics of the multiple species that respond at their specific-spatial scales, which can be expected to reflect the community-wide average of the spatial scales the species use (Jackson & Fahrig 2014; Miguet *et al.* 2016; Stuber *et al.* 2018). Previous research of a subset of the species included here that also used the BLISS method showed that species corresponded to a wide range of spatial scales (Stuber & Fontaine 2018). The corresponding diversity metrics could reflect an average of the species occupying a site. We could not directly investigate this hypothesis in this study because we modeled the mean diversity measures of possible assemblages at each location, thus losing the species-specific resolution in our attempt to minimize the potential overrepresentation of rare species on our species-sensitive diversity metrics.

Land cover relationships

Although BLISS often selected different spatial scales for PD, FD, and SR, most of the relationships with land cover were similar among the three metrics. For some land cover types, the spatial scales that BLISS selected were either close or identical among the diversity metrics (Figure 1. 8, Figure 1. 9, Figure 1. 10, Figure 1. 11, Figure 1. 12, Figure 1. 13). The most similar relationships were indeed between diversity metrics for which BLISS selected the same spatial scales. The similar trends are probably associated with the high between-site correlations among these metrics, with minute differences emerging partly from the differences in land cover variation at different spatial scales.

Most land cover relationships for all three diversity metrics overlapped zero (Figure 1. 8, Figure 1. 9, Figure 1. 10, Figure 1. 11, Figure 1. 12, Figure 1. 13), suggesting weak or non-existent relationships with these environmental characteristics. We could expect small effect sizes for biodiversity metrics for several reasons. First, biodiversity metrics are aggregate measures of the individual species that go into the calculations of those metrics, so effects sizes could be buffered through the exchange of species. Species replacement would not change the SR value, which may also minimally affect PD and FD because these diversity metrics are influenced by the number of species (see Correlation and Surrogacy above). Depending on which species are being exchanged, they could be phylogenetically or functionally similar, which would minimize PD or FD respectively (Loreau *et al.* 2001; Petchey & Gaston 2002). Second, the metrics we used were based on occupancy, meaning that biodiversity metrics would reflect changes in species membership when effect sizes on were strong enough for species to completely appear or disappear from a site. Detecting even small effects could reveal indicate substantial drivers.

We found that PD, FD, and SR had nearly flat relationships with row crops and small grains, but negative relationships with grasses and CRP (Figure 1. 8, Figure 1. 9, Figure 1. 10, Figure 1. 11). Agricultural intensification has been described as a major driver of biodiversity loss worldwide (Tscharntke *et al.* 2005), including the declines in birds (Donald, Green & Heath 2001; Benton, Vickery & Wilson 2003; Flynn *et al.* 2009).

Within our system, row crops were more intensely managed than small grains, and small grains were more intensely used than grassland. Thus, it was surprising that our diversity metrics were not negatively related to agricultural intensification. An apparent discrepancy in the relationship between biodiversity and agricultural intensity could reflect the generality of our land cover labels. In particular, not all grasslands and CRP fields are created equal; having a finer resolution (e.g., having multiple types of grassland to include in the model separately; native grasses, high/low stocked pasture, etc.) could clarify whether our results are consistent across land cover quality.

It was also surprising to see negative relationships between biodiversity metrics and CRP (Figure 1. 9), as the CRP program is often used as a wildlife management tool (Delisle & Savidge 1997) and has been shown to have positive effects on species diversity and population density (Patterson & Best 1996; Best *et al.* 1997; Johnson 2000). Even though we stratified our sampling across a gradient of CRP, our study region did not have many sites with high percentages of CRP (Figure 1. 9); Those weak negative trends could have been influenced by a few sites at the extreme ends that could have been influenced by many factors specific to those few fields. Species composition of birds on CRP fields can change due to factors such as climatic variation, vegetation structure in the CRP field, size of the CRP field, amount of edges, surrounding habitat, type and intensity of management on the CRP field, and fluctuations in the numbers and distribution of bird species (King & Savidge 1995; Johnson 2000), which can influence SR and in turn PD and FD. We suggest closer examination of the effects of quality and quantity of CRP land on avian biodiversity.

Trees was one of the rarer land cover types in our system (Figure 1. 1) so presence of those increase habitat heterogeneity. Trees showed a positive relationship for all three diversity metrics (Figure 1. 12), suggesting that trees add habitat heterogeneity that increase biodiversity. Another study showed that grasslands invaded by woody vegetation typically contained more bird species than those without (Arnold & Higgins 1986). The positive relationship with trees could be due to a few reasons. First, within a primarily grassland or cropland landscape like Nebraska, trees diversify the resources available on a landscape (Benton *et al.* 2003; Stein, Gerstner & Kreft 2014). Second, the detection of trees in our land cover layer would likely be a substantial amount of trees because the resolution of our land cover variables was 30m; likely enough trees to support forest-inhabiting species. Detecting species from both grassland and forest species pools would likely to have a higher SR (and thus PD and FD; see above) than detecting species that only had one species pool.

Our other rare land cover type was wetlands. Like trees, wetlands also diversify the grass- and crop-dominated landscape in Nebraska, so we could expect similar increases to all three biodiversity metrics across a wetland gradient. Another study found a positive relationship between SR of wetland birds and wetland area (Hansson *et al.* 2005). Our study showed a slight negative relationship with SR and FD and a positive relationship with PD across wetlands (Figure 1. 13), the most different trend in our study. Again, the resolution of our land cover layer would necessitate that the detected wetlands are fairly large (cover at least half of a 30m pixel). The number of species that would use wetlands could be fewer than the number of species that would occupy the area had it been terrestrial, so there could be not enough species replacement for SR to be constant as the amount of wetlands increases. Wetlands could attract evolutionarily distant birds (e.g., water fowl, cranes, shore birds; Haukos & Smith 1994), which would increase PD at a faster rate than SR or FD.

Wetlands were the only land cover type that showed divergent trends suggesting wetland land cover is one condition under which biodiversity metrics systematically diverge. Such divergent trends could help identify test ecological theories. In our study, wetlands could serve as an environmental filter that allows species of wide evolutionary histories but only if they have specific functional traits (or are clustered on the functional dendrogram). The species that occur in and around wetlands could display convergent evolution, where functional traits and roles are more similar than would be expected by chance alone. Identifying patterns among metrics in different dimensions can help identify ecological drivers (Swenson & Enquist 2009; Cadotte *et al.* 2011; Safi *et al.* 2011; Spasojevic & Suding 2012; Tucker *et al.* 2017). When relationships between a few metrics could suggest multiple drivers, we suggest using other forms of evidence to discriminate among possible explanations.

Most of the wetland species in this study did not have high detection rates, thus making it difficult to accurately predict where they would occur. Identifying and understanding patterns among diversity metrics offers a way to identify assembly patterns, and potentially rules, that could be more robust than building many uncertain species distribution models. The species that occupy a site may change from year to year, yet understanding the patterns between diversity dimensions can help identify the range of possible species that fit the diversity trends that could occur on a landscape.

SR was slightly more centered around zero than PD and FD across grassland, one of the dominant land cover types in Nebraska (Figure 1. 10). That PD and FD, showed slightly stronger relationships than SR may indicate that SR is less sensitive to land cover variation than other dimensions of biodiversity. SR is a count of species; it does not incorporate any information about evolutionary history or ecological differences. Thus multiple assemblages can have the same SR values, but wildly different levels of PD and FD (Faith 1992; Petchey & Gaston 2006), which are aspects of diversity that are suggested to be more sensitive to drivers of community assembly as they hypothesized to carry information more closely associated with ecological and evolutionary processes (Petchey & Gaston 2006; Safi *et al.* 2011; Swenson 2011). Empirical studies support SR's relative insensitivity across stress gradients compared to PD and FD (Flynn *et al.* 2009; D'agata *et al.* 2014).

Biodiversity distribution maps

Model checking indicated that the relationships we detected across land cover only account for little variation observed in PD, FD, and SR; Our predictive maps reflect the small isolated effects of land cover on the diversity metrics. The diversity distribution maps illustrate relative differences among our diversity metrics when all other potential effects are held constant, so we caution against the use of our models to predict absolute values of diversity.

Highest predicted areas of PD, FD, and SR occurred in sites with high proportions of trees (Figure 1. 14, Figure 1. 15, Figure 1. 16), reflecting the positive relationship with trees in all three diversity dimensions. As these areas were the ones that matched the most across the state, the positive relationship shows how one strong predictor can influence how well diversity dimensions spatially match, an idea that is further supported where there was high congruence between PD and FD (Figure 1. 17). Other areas showed less congruence, where there are fewer trees, so the differences between diversity metrics in those areas were driven by other weaker land cover relationships.

SR varied less across the state compared to PD and FD (Figure 1. 18, Figure 1. 19), potentially reflecting SR's insensitivity to grassland compared to PD and FD. Relative values of SR were predicted to be lower than PD and FD, although the magnitude of difference varied across Nebraska (Figure 1. 18, Figure 1. 19), indicating that SR alone would underestimate the magnitude of change in other dimensions. Increases of SR would correspond with larger increases in PD and FD, but decreases of SR would also correspond with disproportionate declines in PD and FD. Indeed, PD and FD have been detected to have steeper declines than SR along stress gradients (Flynn *et al.* 2009; D'agata *et al.* 2014).

Biodiversity maps generally reflect the high congruence between PD and FD (Figure 1. 17), which was observed in our between-site correlation values and has been detected in other studies (Pool *et al.* 2014). However, substantial mismatches are visible in areas corresponding with differences in land cover relationships. For example, although PD and FD show high congruence, in areas with large proportions of wetlands PD was predicted to be much greater than FD (Figure 1. 17). Even subtle difference in the estimated land cover relationships led to substantial differences in predicted diversity, particularly at the extremes of land cover variation. Spatial mismatches among diversity dimensions have been reported in the literature (Devictor *et al.* 2010; Safi *et al.* 2011;

Thiesen Brum 2015; Brum *et al.* 2017; Quan *et al.* 2018), which pose challenges to the idea of using any one measure as a surrogate for metrics in other dimensions.

Conclusions

Taxonomic, phylogenetic, and functional dimensions of biodiversity offer ways to examine different aspects of biological variation within communities, yet the relationships among the dimensions of biodiversity are not well understood. Our study showed broad similarities among breadth metrics in taxonomic, phylogenetic, and functional dimensions, yet upon closer inspection, correlations were weak within-site, suggesting unreliable surrogacy locally. Furthermore, we identified generally similar relationships across land cover but differences at which spatial scales these diversity metrics respond. Projected differences revealed spatial mismatches, often of substantial magnitude, further cautioning against the use of one metric as a direct surrogate for another.

Quantifying and explaining patterns in biodiversity remains one of the core quests in biology and ecology. We suggest several further directions for the study of biodiversity. As we are one of the first to examine relationships between diversity dimensions and spatial scale, this area is ripe for hypothesis generating. Furthermore, understanding differences among diversity metrics may help identify drivers of biodiversity patterns and predict community assembly. Ultimately, to make robust inferences and predictions about patterns of biodiversity, we must first understand how and why different aspects of biodiversity relate to one another.

FIGURES

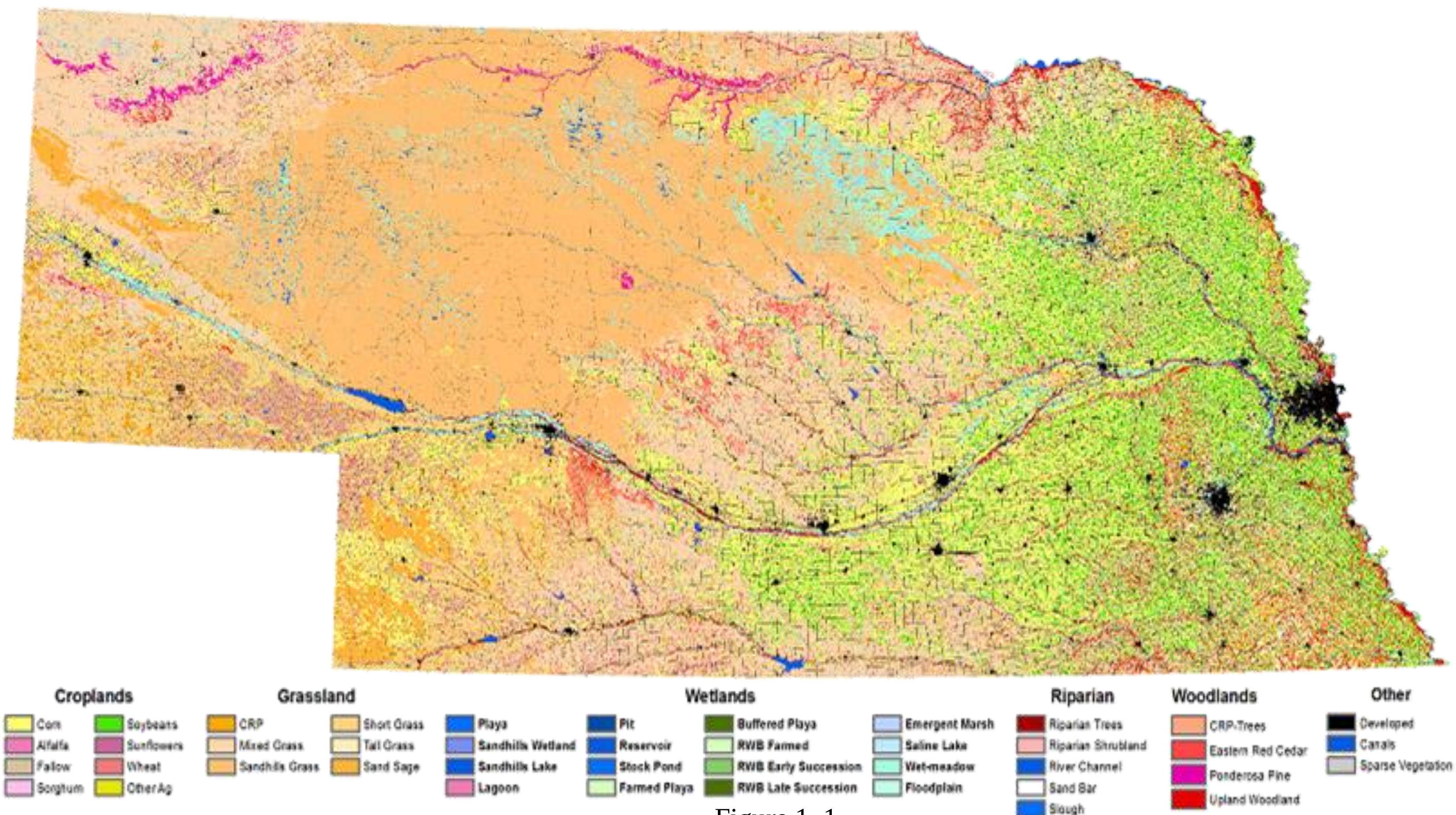

Figure 1. 1

Nebraska land cover reproduced from Rain Water Basin Joint Venture (Bishop *et al.* 2011).

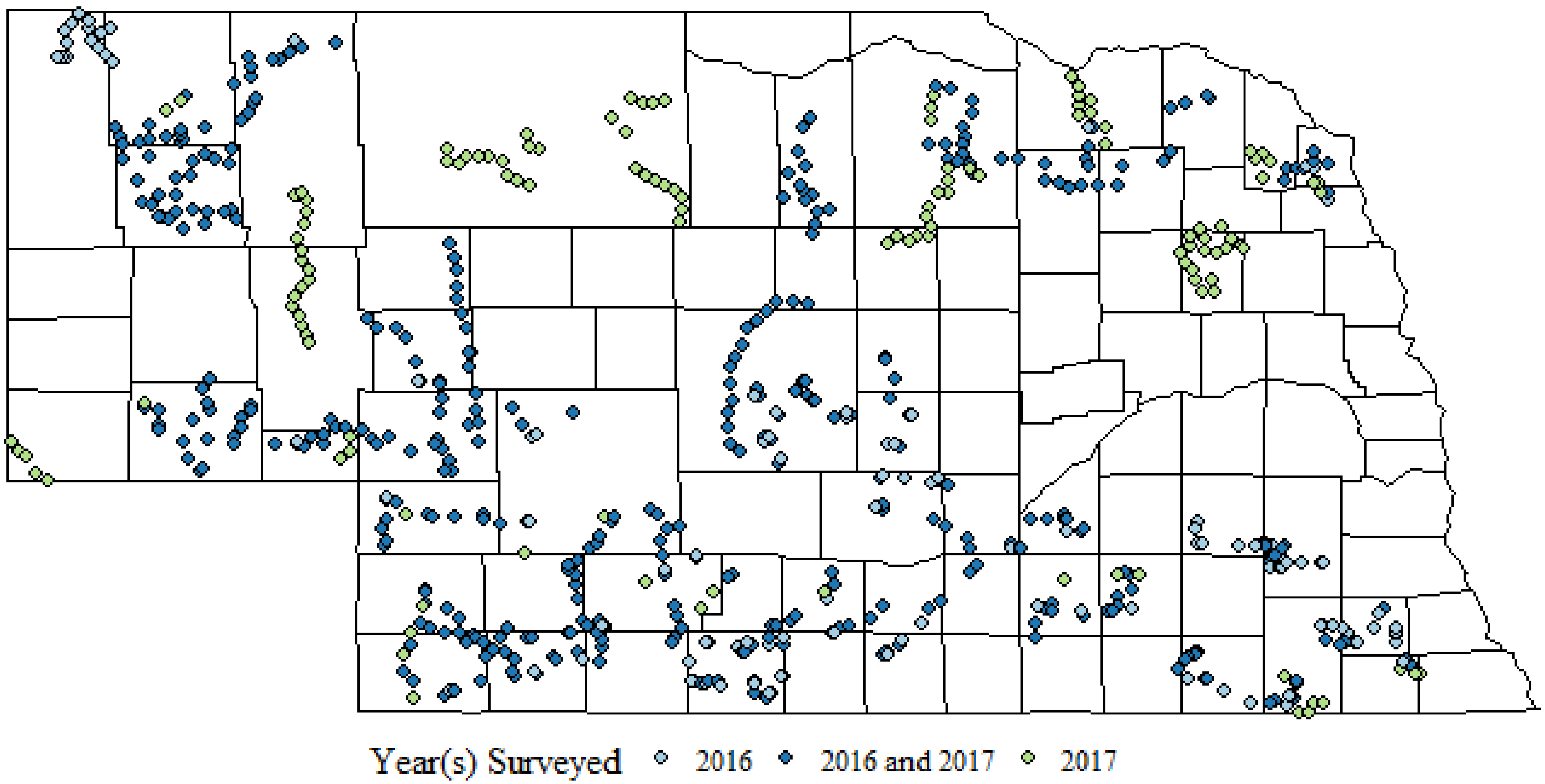

Figure 1. 2

A map of the 2016-2017 survey points throughout the state of Nebraska. Light blue points were visited only in 2016, green points were visited only in 2017, and dark blue points were visited during both years.

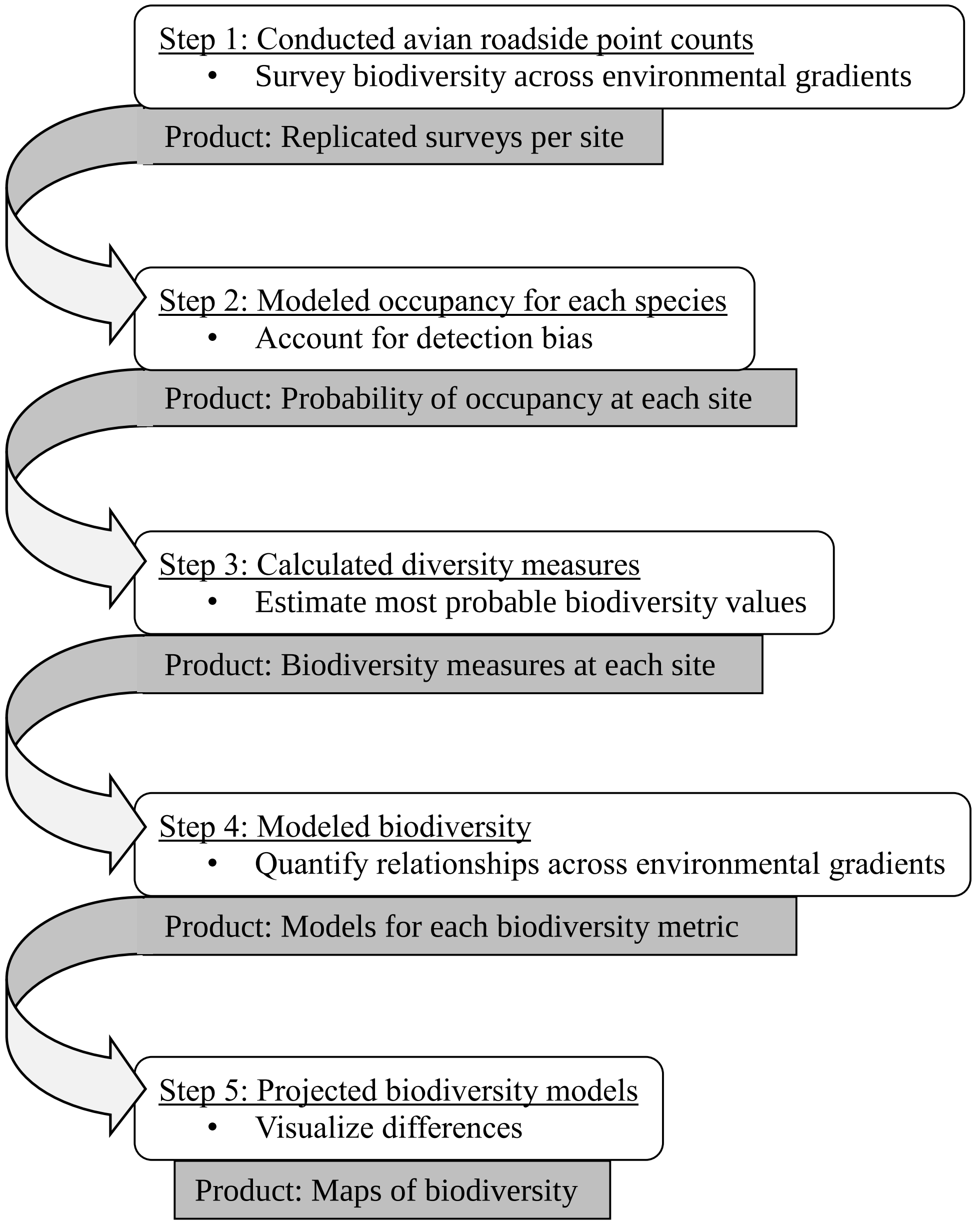

Figure 1. 3

Conceptual framework summarizing methods used to analyze biodiversity patterns of birds in Nebraska, USA. White boxes describe methodological steps with a short justification for that step. Grey text boxes describe the product from each step that was used in the following step.

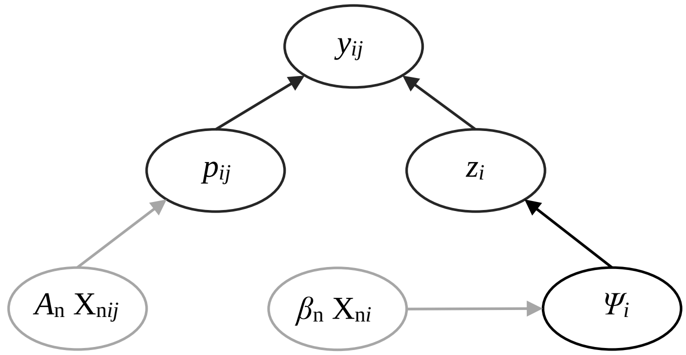

Figure 1. 4

Directed acyclic graph describing the hierarchical Bernoulli-Bernoulli occupancy model used to account for imperfect detection of species based on survey-specific variables. Gray nodes and arrows represent covariate structure while the black nodes and arrows represent non-covariate structure. Notation: y_{ij} is the detection of a species at a survey site i during the jth survey. y_{ij} represents a Bernoulli distribution of the product of the true occupancy (z_i: z_i=1, if species occupied a site; z_i=0, if not) of the species at that site and the probability of detecting the species during that survey (p_{ij}). True occupancy (z_i) is estimated through a Bernoulli logit-linked function that calculated the probability of occupancy (Ψ_i) based on site-specific land-cover covariates (X_{ni}), with intercepts for each year and parameter estimates β_{n}. Detection probability (p_{ij}) at site i during survey j is a logit-linked function with covariates (X_{ni}) and parameter estimates A_{n}.

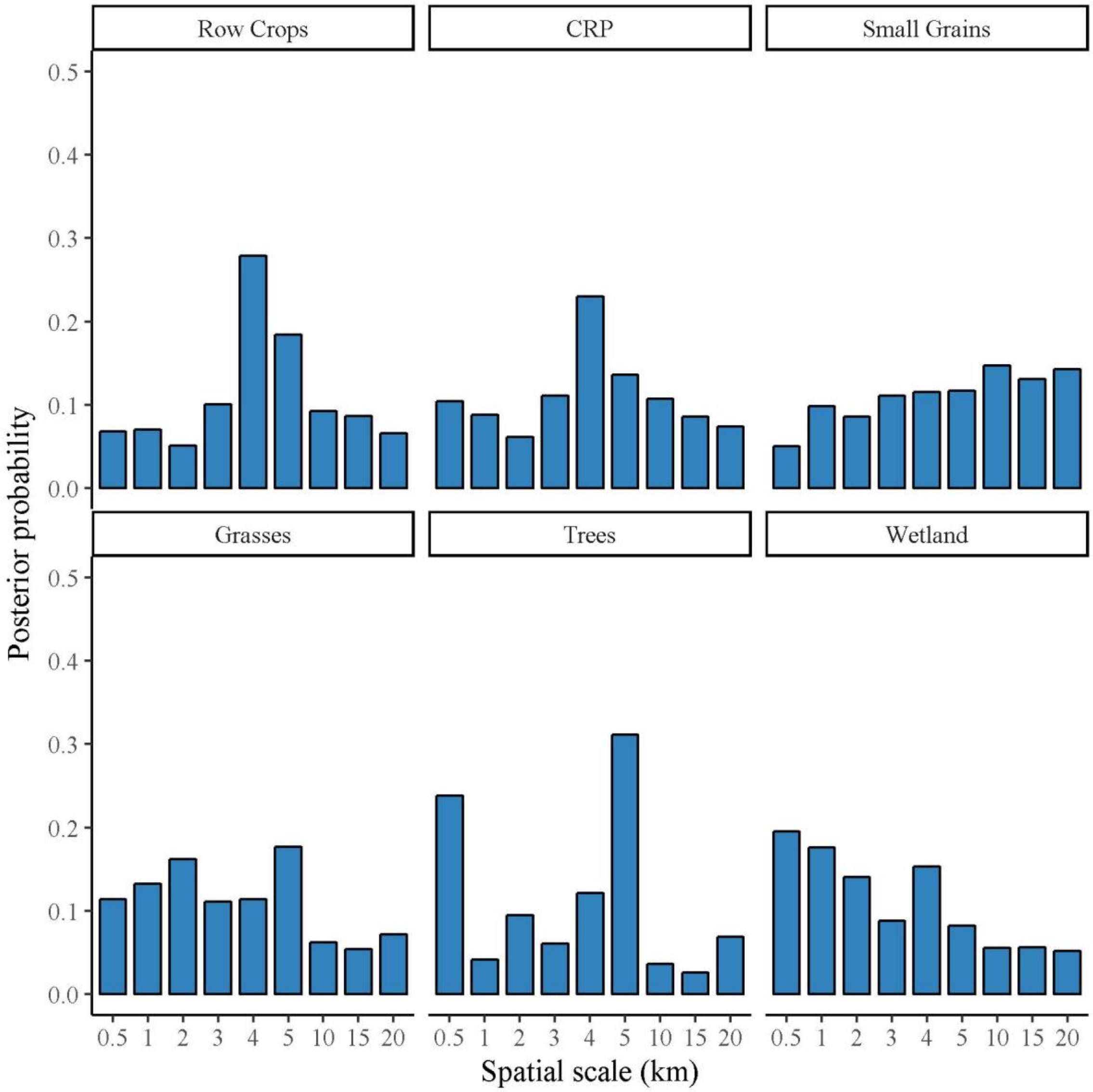

Figure 1. 5

Posterior distributions of the candidate spatial scales (in km) of the land cover predictors row crops, CRP, small grain, grasses, trees, and wetlands for the most probable values of phylogenetic diversity (PD) of breeding birds in Nebraska as estimated by BLISS.

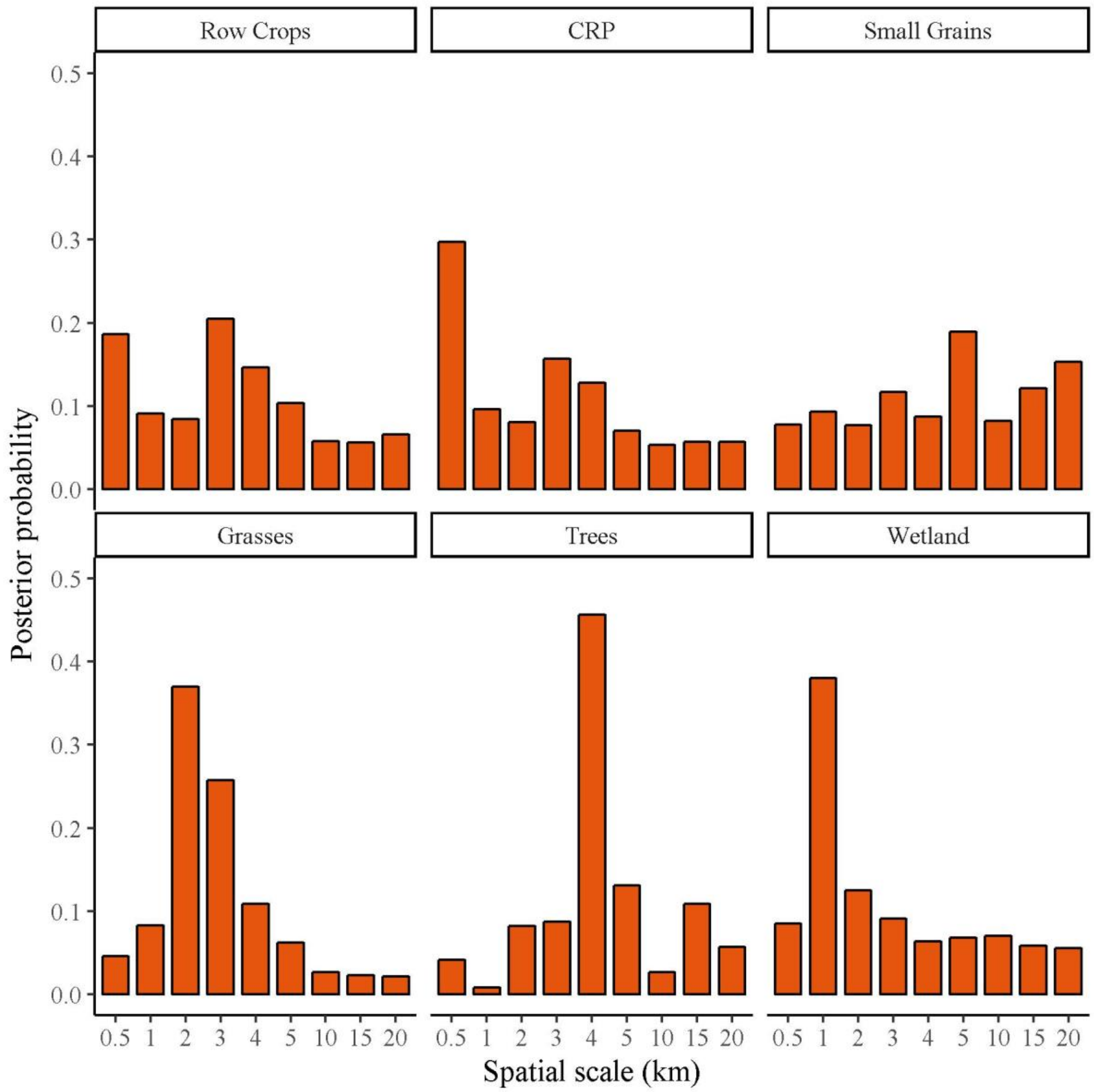

Figure 1. 6

Posterior distributions of the candidate spatial scales (in km) of the land cover predictors row crops, CRP, small grain, grasses, trees, and wetlands for the most probable values of functional diversity (FD) of breeding birds in Nebraska as estimated by BLISS.

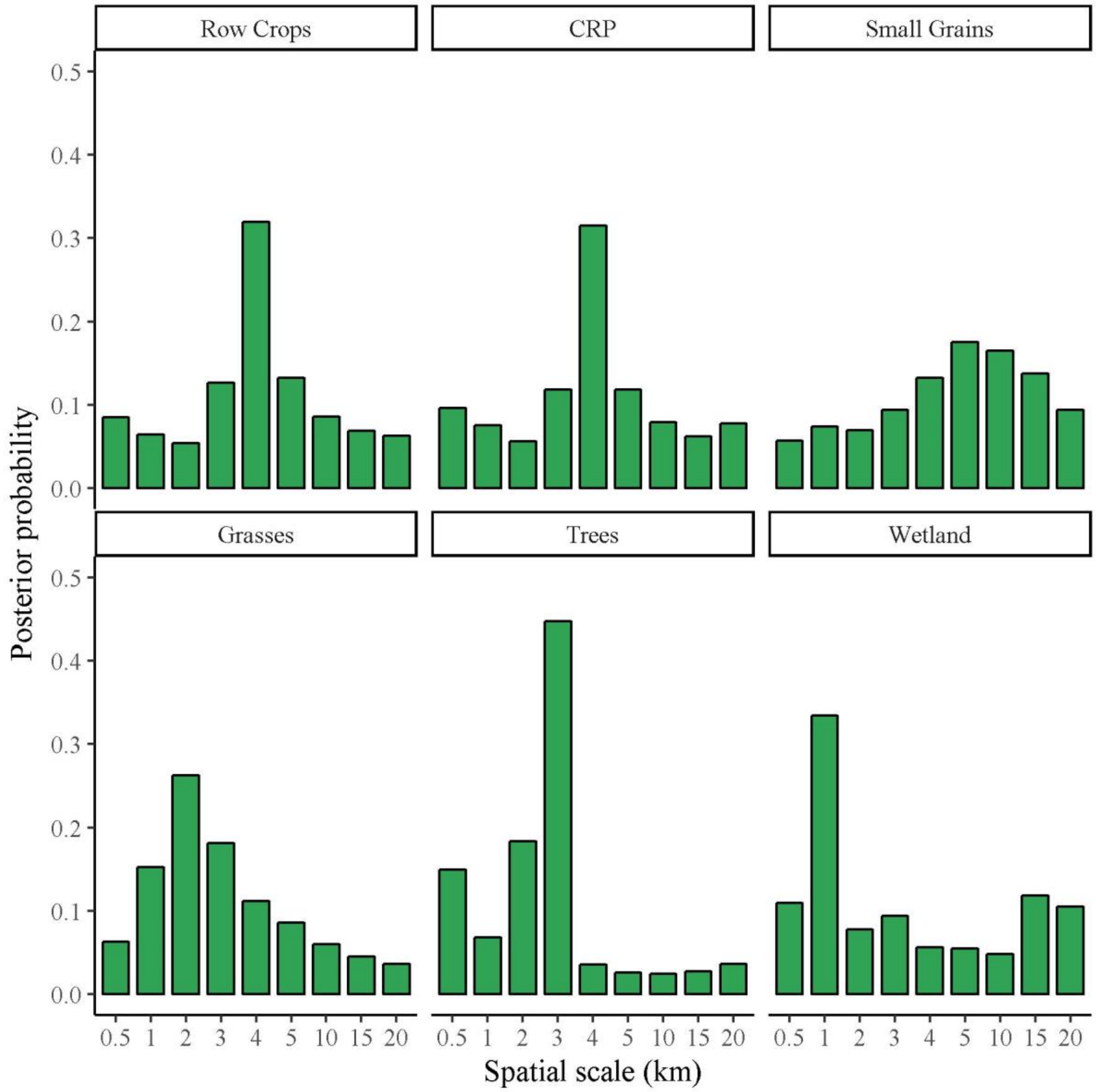

Figure 1. 7

Posterior distributions of the candidate spatial scales (in km) of the land cover predictors row crops, CRP, small grain, grasses, trees, and wetlands for the most probable values of species richness (SR) of breeding birds in Nebraska as estimated by BLISS.

Table 1. 1

Estimated most informative spatial scale, posterior probability of that spatial scale as estimated by BLISS, coefficients (posterior mean) and their associated 95% credible intervals (CI) at the most informative spatial scale for each phylogenetic diversity (PD), functional diversity (FD), species richness (SR), and covariance between each diversity dimension of the birds in Nebraska, USA. Coefficients are associated with orthogonal values of land cover for the biodiversity models and are not back transformed here.

Diversity	**Spatial Scale (km)**	**Scale Posterior Probability**	**Coefficient**	**Posterior mean (95% CI)**
PD	4	0.28	Crops	0.17 (-2.33, 2.59)
			Crops²	-0.37 (-1.81, 1.09)
	4	0.23	CRP	-0.79 (-1.48, -0.10)
	5	0.18	Grasses	-0.96 (-3.18, 1.14)
			Grasses²	0.07 (-0.86, 0.97)
	10	0.15	Small Grains	-0.72 (-2.34, 0.91)
			Small Grains²	0.36 (-0.71, 1.40)
	5	0.31	Trees	1.58 (0.42, 2.76)
			Trees²	-0.30 (-1.16, 0.57)
	0.5	0.2	Wetland	0.20 (-0.60, 0.99)
			Year 1	0.08 (0.00, 0.16)
			Year 2	-0.08 (-0.16, 0.01)
FD	3	0.21	Crops	-0.47 (-2.34, 1.47)
			Crops²	-0.48 (-1.82, 0.87)
	0.5	0.3	CRP	-0.74 (-1.22, -0.26)
	2	0.37	Grasses	-1.83 (-3.36, -0.18)
			Grasses²	0.60 (-0.31, 1.51)
	5	0.19	Small Grains	-0.87 (-2.53, 0.93)

			Small Grains²	0.73 (-0.39, 1.84)
	4	0.46	Trees	2.47 (1.33, 3.65)
			Trees²	-0.48 (-1.34, 0.37)
	1	0.38	Wetland	-0.75 (-1.66, 0.14)
			Year 1	0.02 (-0.06, 0.10)
			Year 2	-0.02 (-0.11, 0.07)
SR	4	0.32	Crops	-0.13 (-1.80, 1.55)
			Crops²	-0.27 (-1.62, 1.09)
	4	0.31	CRP	-0.68 (-1.20, -0.14)
	2	0.26	Grasses	-1.59 (-2.83, -0.27)
			Grasses²	-0.24 (-1.06, 0.58)
	5	0.18	Small Grains	-0.99 (-2.60, 0.74)
			Small Grains²	0.57 (-0.52, 1.64)
	3	0.45	Trees	2.13 (1.02, 3.27)
			Trees²	-0.54 (-1.37, 0.28)
	1	0.33	Wetland	-0.53 (-1.39, 0.32)
			Year 1	0.05 (-0.03, 0.13)
			Year 2	-0.05 (-0.14, 0.04)
PD.FD			Within-site correlation	-0.28 (-0.20, -0.42)
PD.SR			Within-site correlation	-0.07 (-0.06, -0.08)
FD.SR			Within-site correlation	-0.05 (-0.05, -0.06)

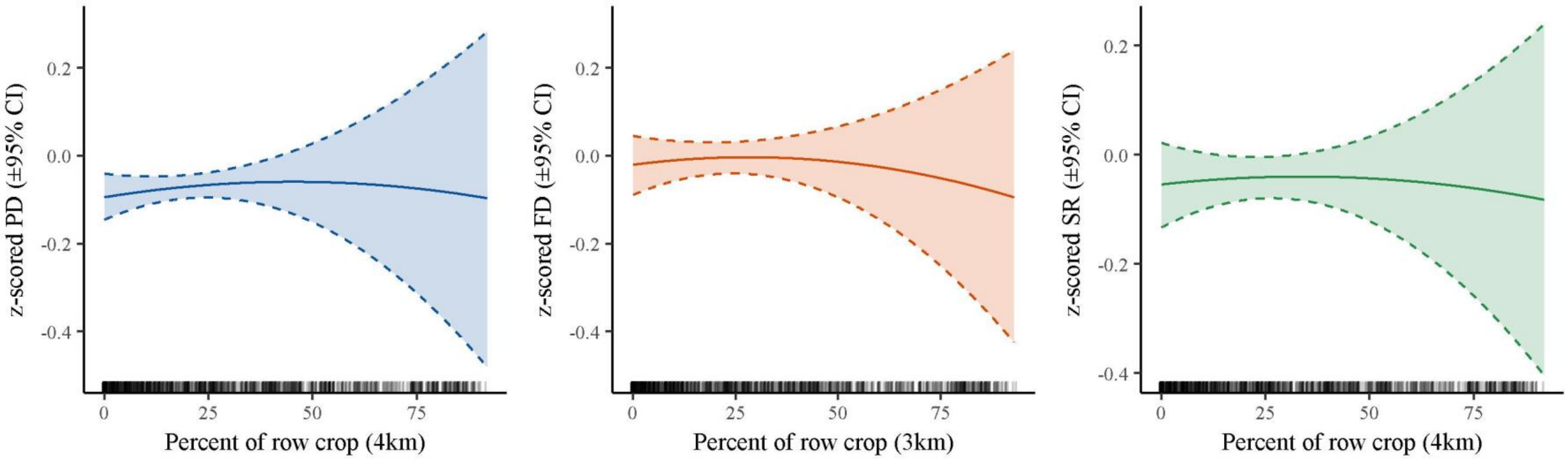

Figure 1. 8

Predicted z-scores of phylogenetic diversity (PD; blue), functional diversity (FD; orange), species richness (SR; green) across percent of a gradient of row crops within a radius of the most informative scale as selected by BLISS (Stuber *et al.* 2017). Solid line represents mean land cover relationships and the lighter ribbon represents 95% credible intervals predicted out to the maximum range of that land cover at selected scales across survey points. The ticks on the x-axis represents the distribution of observed land cover used in model predictions.

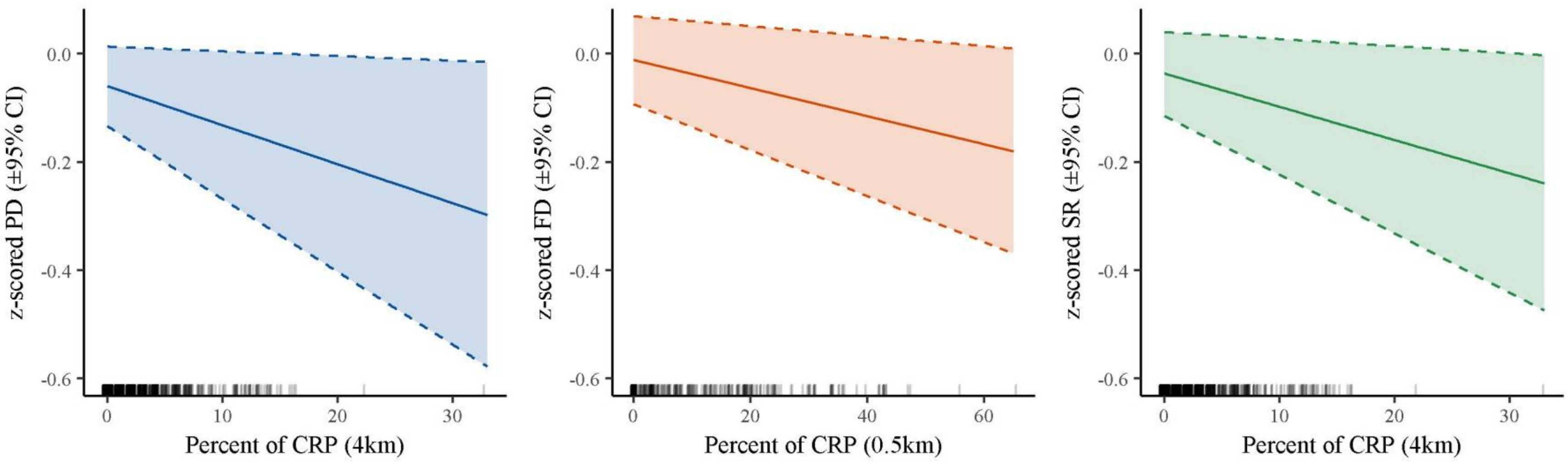

Figure 1. 9

Predicted z-scores of phylogenetic diversity (PD; blue), functional diversity (FD; orange), species richness (SR; green) across percent of a gradient of land enrolled conservation reserve program (CRP) within a radius of the most informative scale as selected by BLISS (Stuber *et al.* 2017). Solid line represents mean land cover relationships and the lighter ribbon represents 95% credible intervals predicted out to the maximum range of that land cover at selected scales across survey points. The ticks on the x-axis represents the distribution of observed land cover used in model predictions.

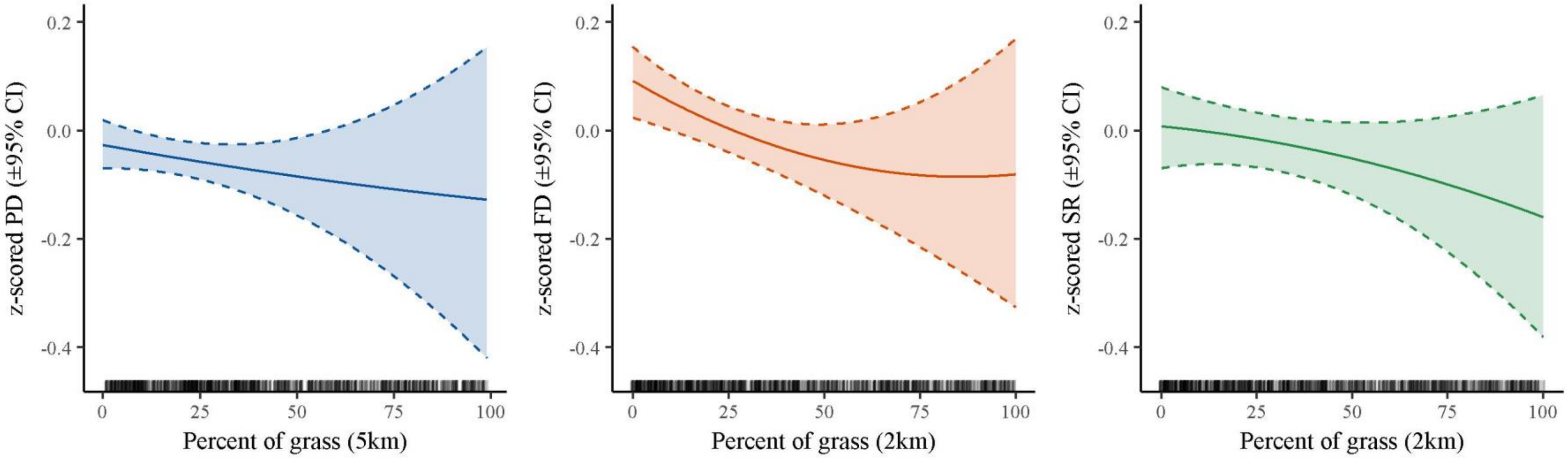

Figure 1. 10

Predicted z-scores of phylogenetic diversity (PD; blue), functional diversity (FD; orange), species richness (SR; green) across percent of a gradient of grasses within a radius of the most informative scale as selected by BLISS (Stuber *et al.* 2017). Solid line represents mean land cover relationships and the lighter ribbon represents 95% credible intervals predicted out to the maximum range of that land cover at selected scales across survey points. The ticks on the x-axis represents the distribution of observed land cover used in model predictions.

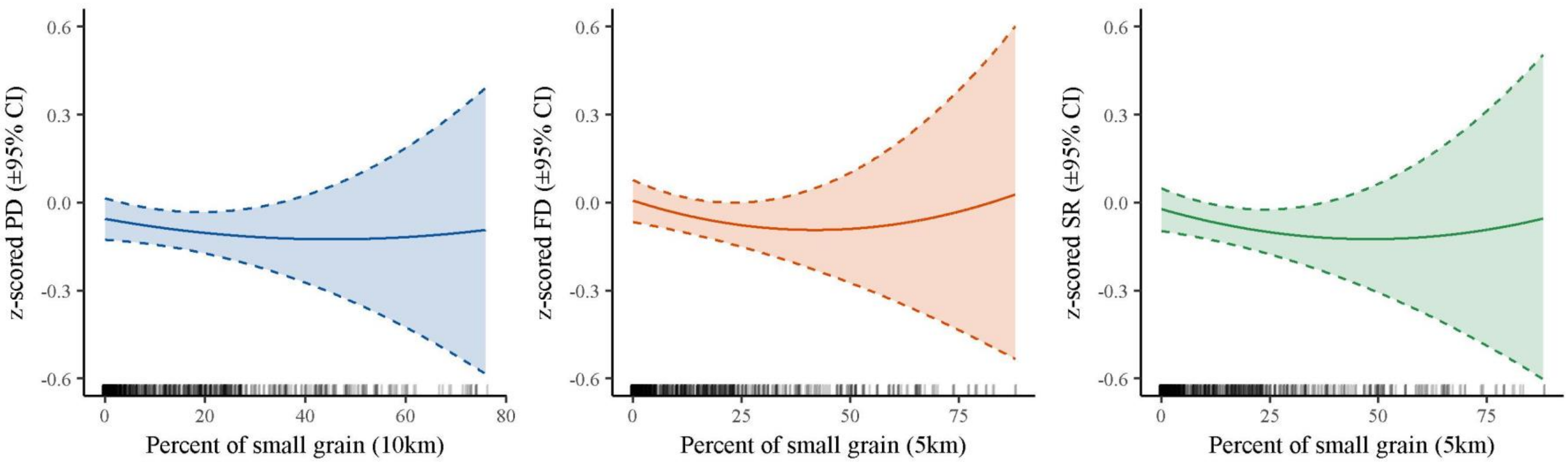

Figure 1. 11

Predicted z-scores of phylogenetic diversity (PD; blue), functional diversity (FD; orange), species richness (SR; green) across percent of a gradient of small grain within a radius of the most informative scale as selected by BLISS (Stuber *et al.* 2017). Solid line represents mean land cover relationships and the lighter ribbon represents 95% credible intervals predicted out to the maximum range of that land cover at selected scales across survey points. The ticks on the x-axis represents the distribution of observed land cover used in model predictions.

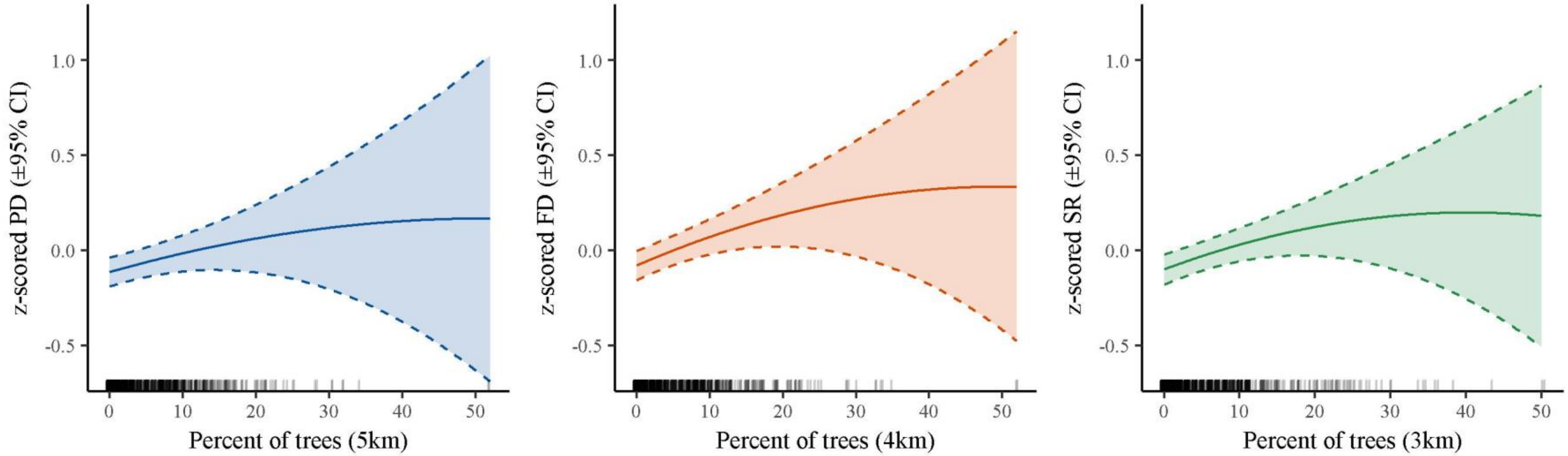

Figure 1. 12

Predicted z-scores of phylogenetic diversity (PD; blue), functional diversity (FD; orange), species richness (SR; green) across percent of a gradient of trees within a radius of the most informative scale as selected by BLISS (Stuber *et al.* 2017). Solid line represents mean land cover relationships and the lighter ribbon represents 95% credible intervals predicted out to the maximum range of that land cover at selected scales across survey points. The ticks on the x-axis represents the distribution of observed land cover used in model predictions.

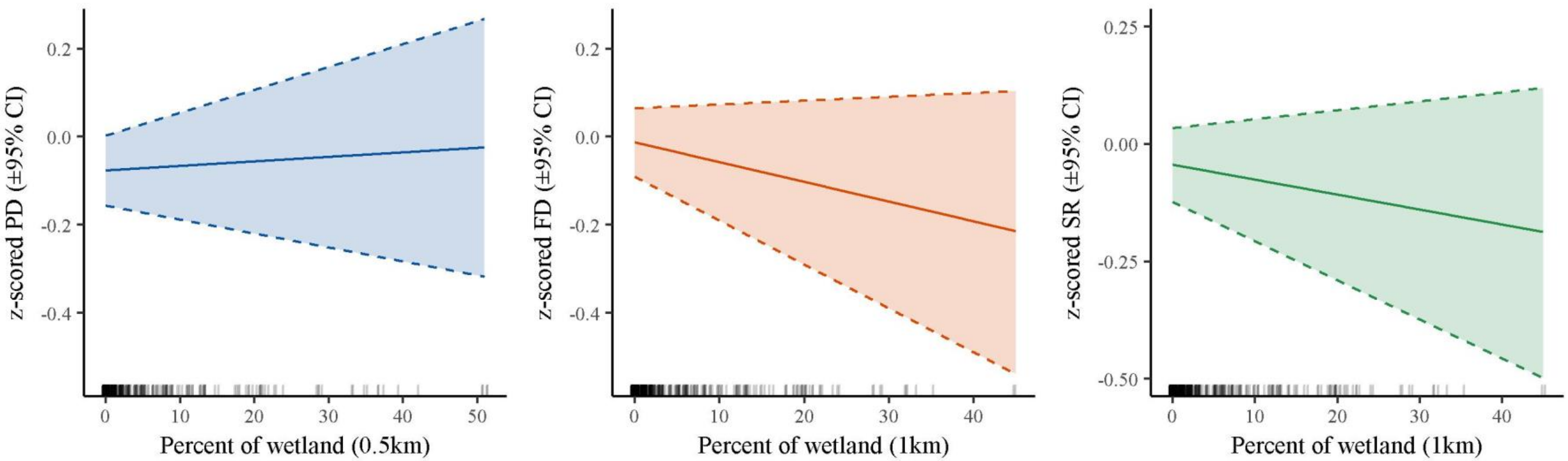

Figure 1. 13

Predicted z-scores of phylogenetic diversity (PD; blue), functional diversity (FD; orange), species richness (SR; green) across percent of a gradient of wetlands within a radius of the most informative scale as selected by BLISS (Stuber *et al.* 2017). Solid line represents mean land cover relationships and the lighter ribbon represents 95% credible intervals predicted out to the maximum range of that land cover at selected scales across survey points. The ticks on the x-axis represents the distribution of observed land cover used in model predictions.

Table 1. 2

Estimated coefficients (posterior mean) and their associated 95% credible intervals (CI) for each year and the covariance between phylogenetic diversity (PD), functional diversity (FD), species richness (SR) of the most probable values for the diversity of birds in Nebraska, USA.

Diversity	**Coefficient**	**Posterior mean (95% CI)**
PD	Year 1	0.08 (0.00, 0.16)
PD	Year 2	-0.08 (-0.16, 0.00)
FD	Year 1	0.03 (-0.05, 0.11)
FD	Year 2	-0.03 (-0.11, 0.05)
SR	Year 1	0.06 (-0.02, 0.14)
SR	Year 2	-0.06 (-0.14, 0.02)
PD.FD	Within-site Correlation	-0.30 (-0.22, -0.47)
PD.SR	Within-site Correlation	-0.07 (-0.06, -0.08)
FD.SR	Within-site Correlation	-0.05 (-0.05, -0.06)

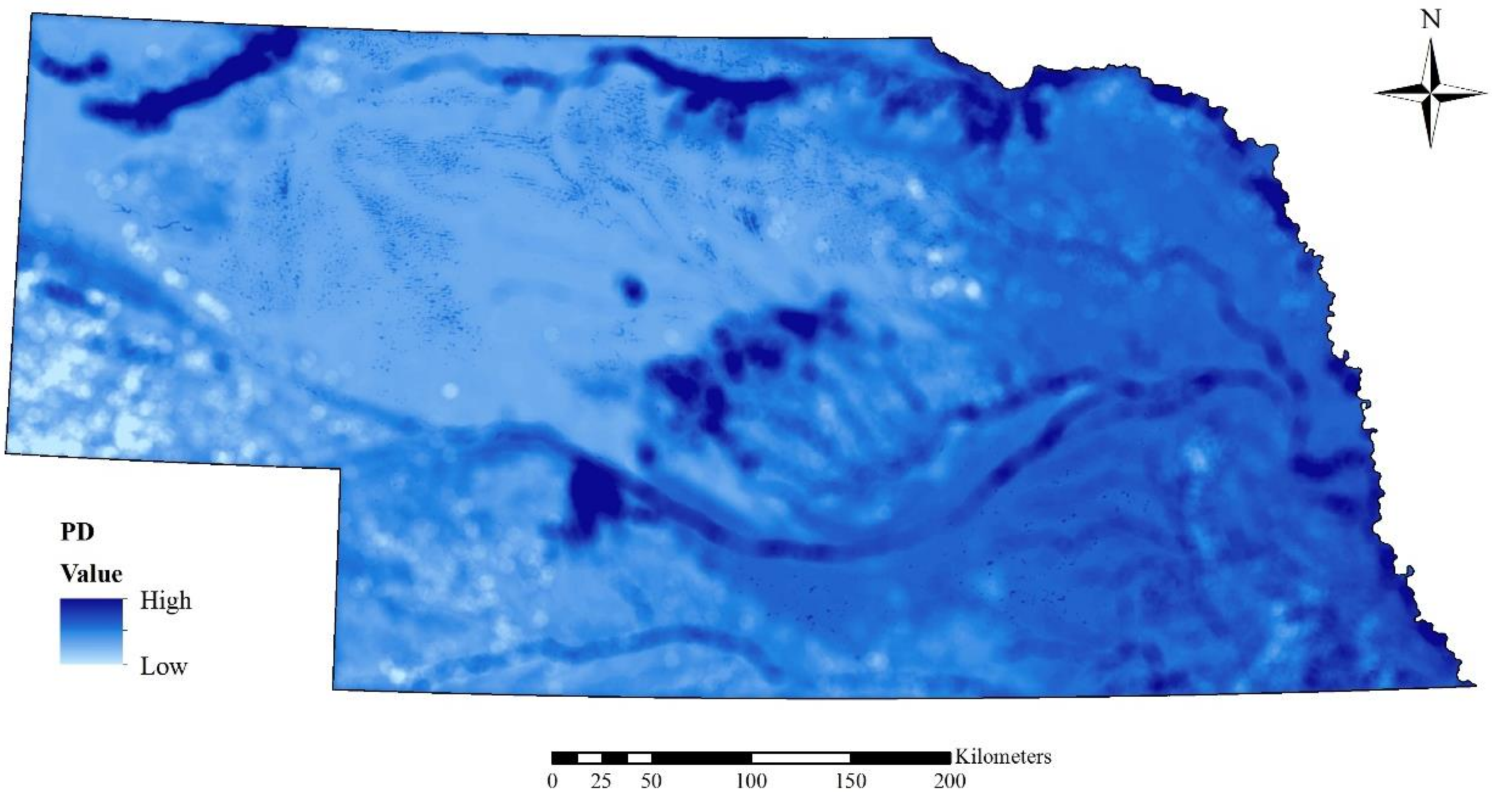

Figure 1. 14

Map of predicted phylogenetic diversity (PD) of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

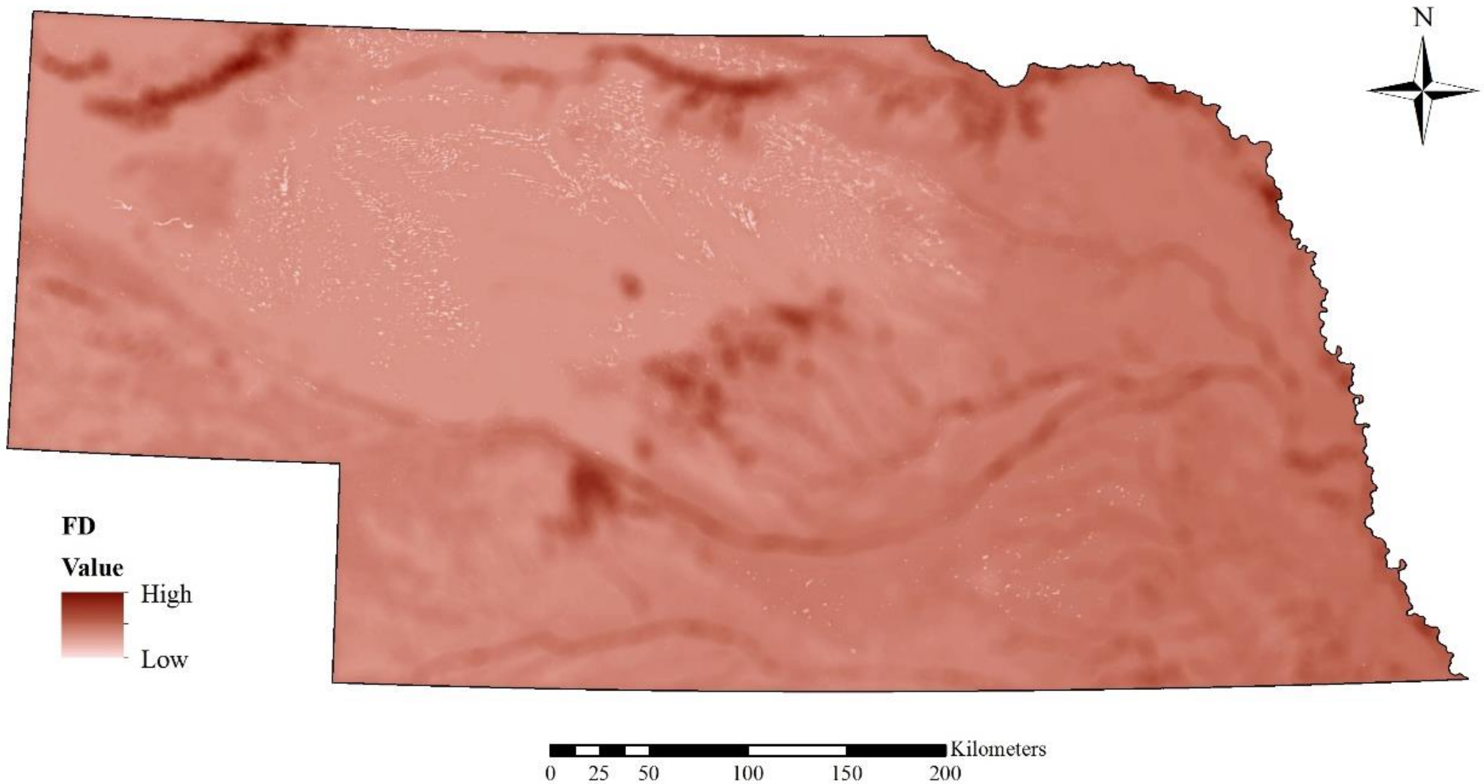

Figure 1. 15

Map of predicted functional diversity (FD) of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

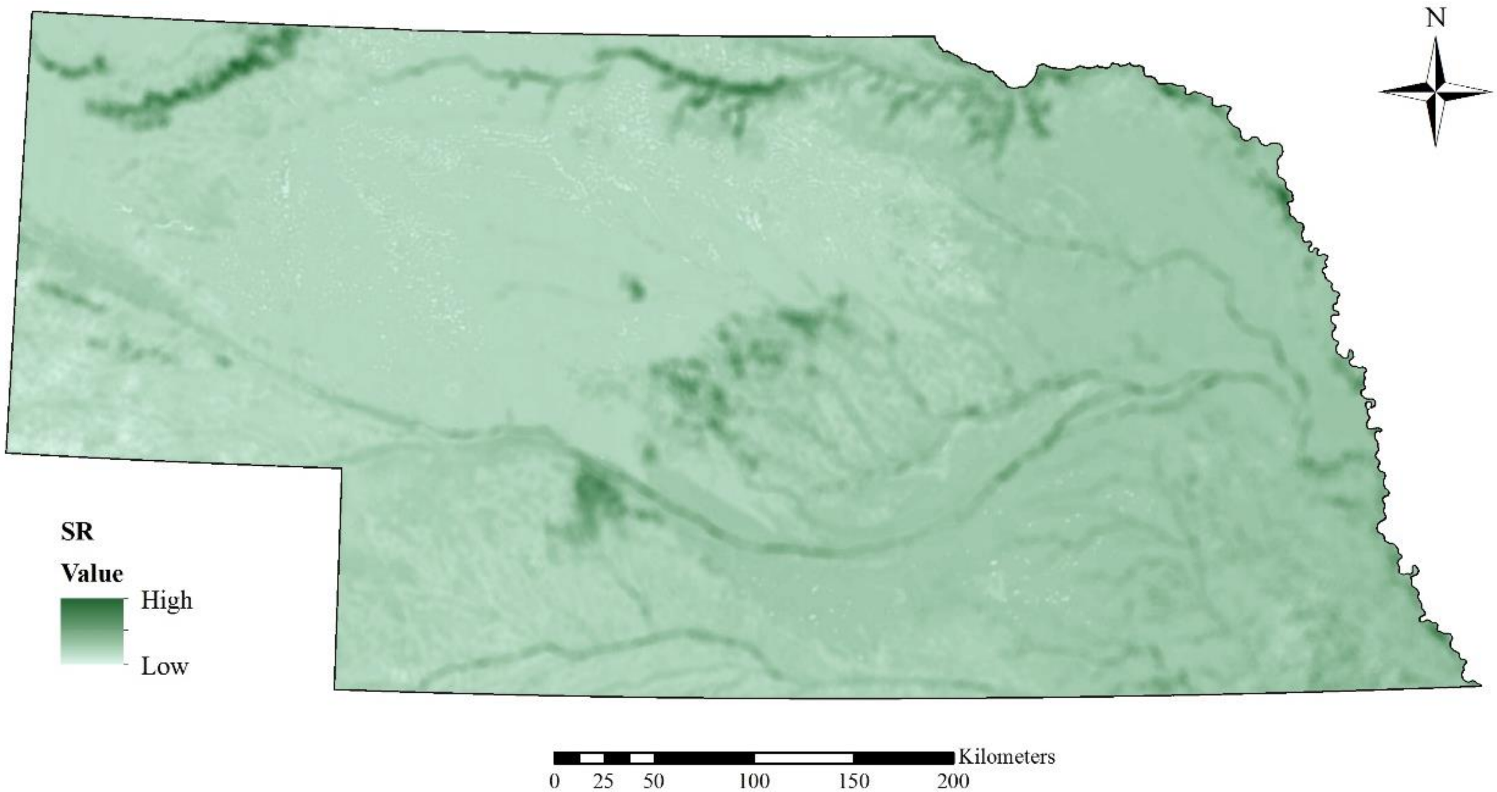

Figure 1. 16

Map of predicted species richness (SR) of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

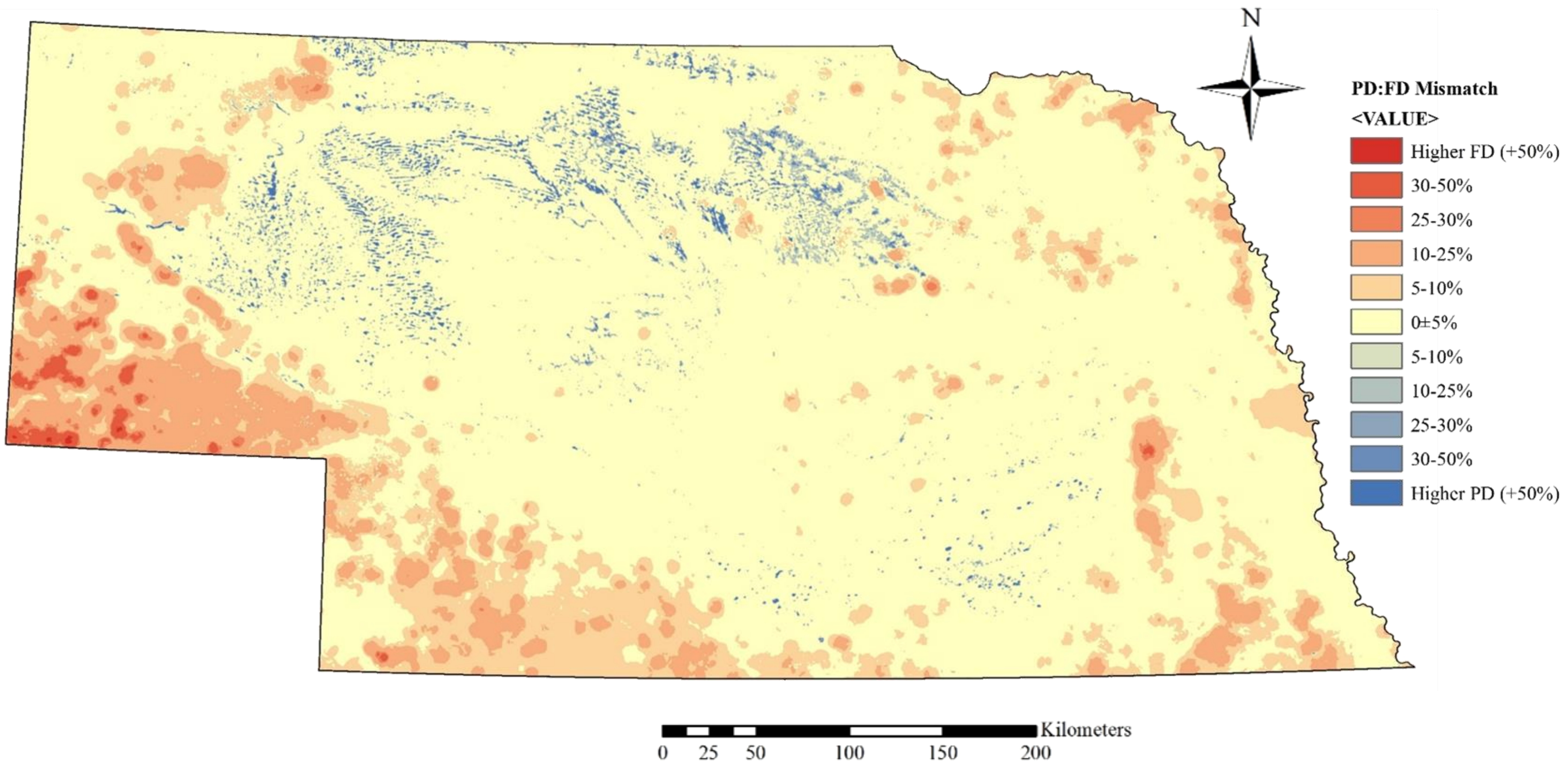

Figure 1. 17

Map of predicted relative phylogenetic diversity (PD) to functional diversity (FD) of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

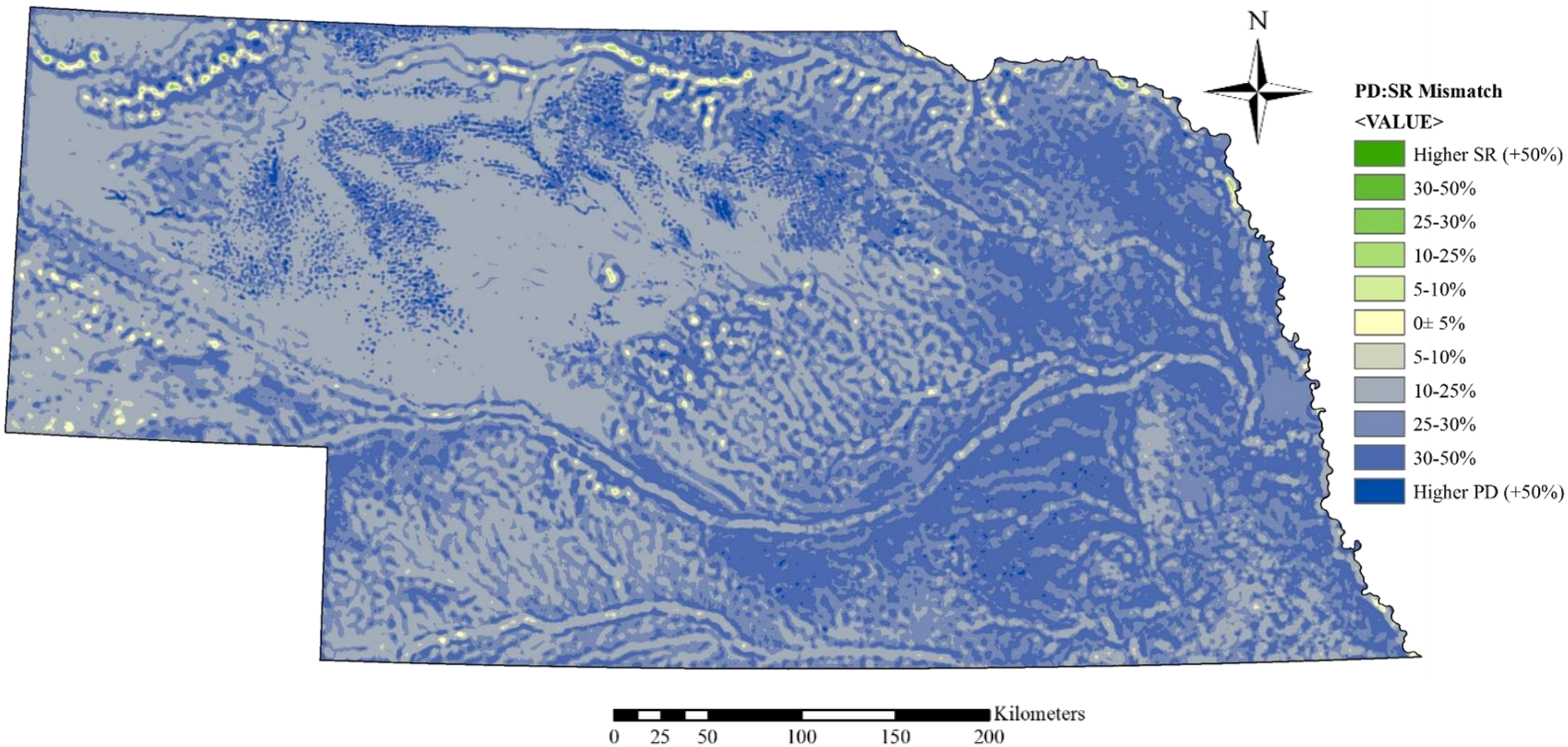

Figure 1. 18

Map of predicted relative phylogenetic diversity (PD) to species richness (SR) of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

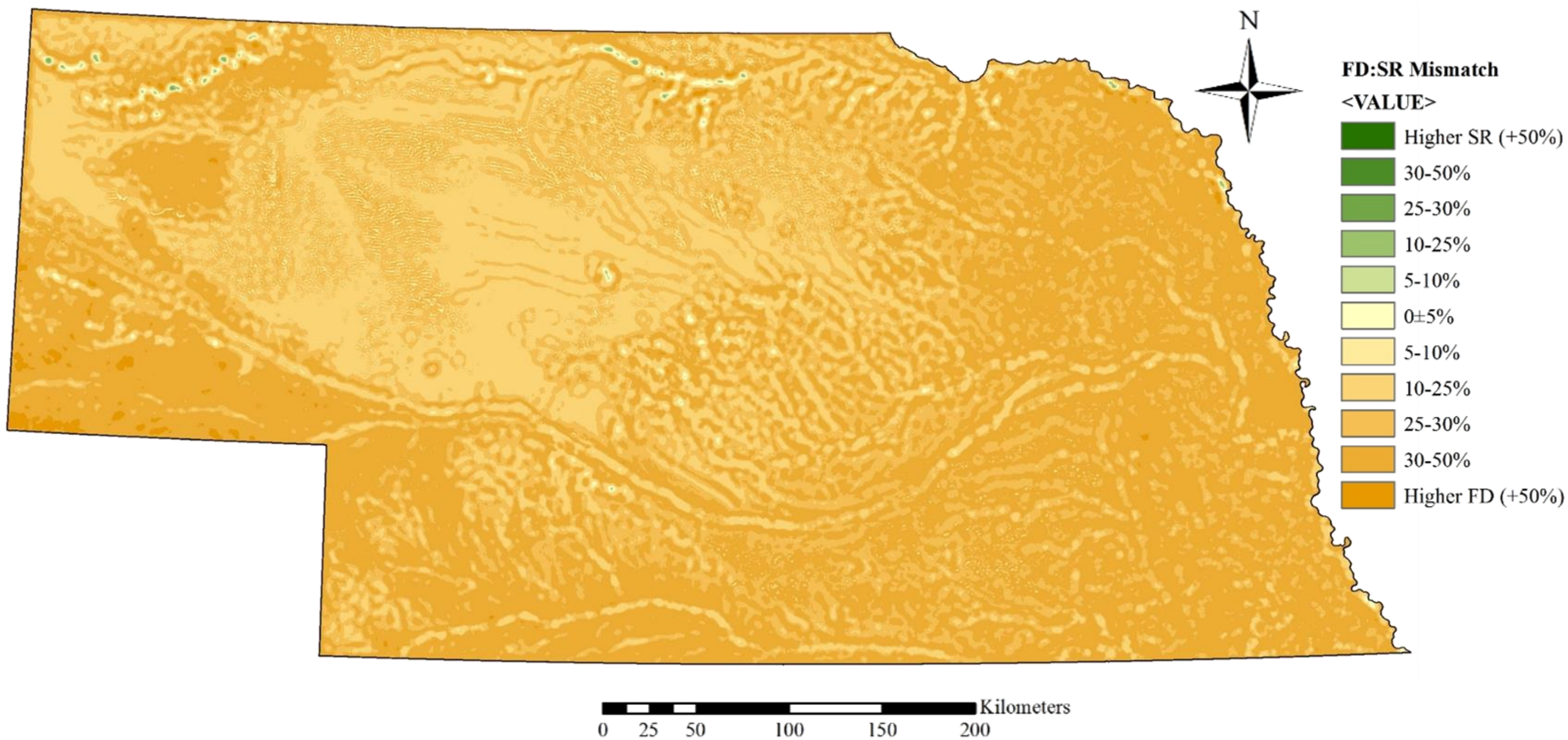

Figure 1. 19

Map of predicted relative functional diversity (FD) to species richness (SR) of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

CHAPTER 2. REFLECTING ON CONSERVATION DECISION MAKING ABOUT DIFFERENT DIMENSIONS OF BIODIVERISTY

INTRODUCTION

Biodiversity is important to human well-being, environmental stability, and ecosystem function, the loss of which is associated with many negative ecosystem changes (Balvanera *et al.* 2006; Díaz *et al.* 2006; Hooper *et al.* 2012; Naeem, Duffey & Zavaleta 2012; Tilman *et al.* 2014; Isbell *et al.* 2015). To promote biodiversity persistence, many organizations have implemented conservation strategies ranging from plans for managing single populations to protecting entire ecosystems (Franklin 1993), but despite ongoing efforts, biodiversity continues to decline (Hoekstra *et al.* 2005; Butchart *et al.* 2010). Thus, there is need to assess how current conservation and management areas encompass biodiversity and determine management approaches that better fulfill conservation goals.

Conservation efforts typically focus on managing taxonomic diversity (e.g., species richness, endemism; (Faith 1992; Reid 1998; Myers *et al.* 2000; Fleishman, Noss & Noon 2006), but recent research suggests that taxonomic diversity is not as closely tied with some conservation goals such as ecosystem stability and long term perseverance (Faith 1992; Forest *et al.* 2007; Mayfield *et al.* 2010; Safi *et al.* 2011; Strecker *et al.* 2011; Pavoine *et al.* 2013; D'agata *et al.* 2014; Mazel *et al.* 2014; Pool *et al.* 2014; Tucker *et al.* 2018). Biodiversity is multi-dimensional, with different dimensions emphasizing different aspects of biological variation that are important for conservation success. For example, the phylogenetic dimension of biodiversity represents evolutionary diversification among species and may act as a proxy for how well a community is able to adapt to future environmental conditions (Faith 1992; Crozier 1997; Mace *et al.* 2003; Forest *et al.* 2007). The functional dimension of biodiversity is associated with variation in species' ecological niches, which is linked to ecosystem productivity, stability, and services (Hooper *et al.* 2005; Petchey & Gaston 2006). Many theoretical and empirical studies show that metrics in taxonomic dimension of biodiversity are often not strongly correlated with metrics in the phylogenetic and functional dimensions (Chapter 1, this volume; Faith 1992; Forest *et al.* 2007; Swenson 2011; Purschke *et al.* 2013). Taxonomic diversity thus may not adequately guide where limited conservation resources could be the most effective in achieving conservation goals.

The first step towards improving the success of conservation plans is to understand their association with different dimensions of biodiversity and where they can be improved. Here, we evaluate how current conservation and management plans capture taxonomic, phylogenetic, and functional dimensions of avian diversity across the landscapes represented in Nebraska, USA. Additionally, we identify where areas of high taxonomic, phylogenetic, and functional diversity are predicted to be, their degree of the overlap, and the distribution of these metrics of diversity in relation to various current conservation and natural resource management plans in Nebraska.

METHODS

Study system

Located in the North American Great Plains, Nebraska, USA, harbors substantial variation in natural and anthropogenic land cover features (Figure 1. 1, Chapter 1, this volume; Bishop, Barenberg, Volpe, & Grosse, 2011), making it an ideal system in which to examine where and in what contexts spatial mismatches among biodiversity dimensions occur and their association with current conservation and natural resource management plans. Located at the western extent of the 'corn-belt', eastern Nebraska is dominated by intensive row crop agriculture where rain is plentiful and soil is rich, with scattered patches of forest, wetlands, and native grasslands. Across the southern portion of the state, land cover is dominated by matrices of small grain agriculture and pastures in the west and row crop agriculture (e.g., corn, soy beans) in the east. The central and northern-west portion of Nebraska are home to the sand hills where rangeland is dominant due to the sandy soils making it difficult to grow crops. Additional patches of more native habitat are scattered throughout the state through parks, wildlife management areas, and lands enrolled in the government-sponsored conservation reserve program (CRP) that funds the conversion of environmentally sensitive land from agriculture to native habitat (Johnson 2000).

Biodiversity data and modeling based on species occupancy

We examined the biodiversity of birds in taxonomic, phylogenetic, and functional dimensions in relation to current conservation and management plans birds are abundant, relatively easy to measure, well-studied, evolutionarily (Jetz *et al.* 2012) and ecologically diverse (Sekercioglu 2006), occur across a broad range of anthropogenic and natural gradients, and are of substantial conservation interest (Schneider *et al.* 2011; Bird Studies Canada & NABCI 2014). We conducted unbounded aural point counts truncated to 500m (Robbins *et al.* 1986) from May to July of 2016 and 2017 on publicly accessible secondary and tertiary roads (Mccarthy *et al.* 2012) across survey sites selected using a modified generalized random tessellation stratified sampling design to ensure representation of variation across the six land cover variables we use in this study (row crop, CRP, grasses, small grains, trees, and wetlands; see Chapter 1, this volume, Stevens & Olsen 2004). Sites were grouped into ‘routes’ consisting of 7-19 survey sites such that all sites within each route could be visited within one morning following established roadside point count protocols (Jorgensen et al. 2014). Within a year, each site was visited up to four times (e.g., the ‘robust design’ following Williams, Nichols, & Conroy, 2002) between 15 minutes before sunrise until approximately 10 A.M, which is when avian vocalizations are the highest and most consistent across species (Hutto *et al.* 1986), over a sampling season (i.e., May through mid-July). Surveys were not conducted during inclement weather, including fog, drizzle, prolonged rain, and wind greater than 20 km/h (12 mph) as these conditions may impact our ability to accurately detect birds.

We modeled probability of occupancy for all species detected throughout the sampling seasons accounting for detection error using Bernoulli-Bernoulli hierarchical, coupled logistic regression via Bayesian posterior simulation with JAGS (see Chapter 1, this volume for full details). We used species richness (SR), the number of species per site, for our metric in the taxonomic dimension. For phylogenetic and functional dimensions, we used Faith’s phylogenetic diversity (PD; Faith 1992), the total branch length needed to connect a rooted phylogeny of the species occupying a site, and functional diversity (FD; Petchey & Gaston 2002), the total branch length needed to connect a rooted functional dendrogram of the species occupying a site. We simulated 1,000 sets of likely assemblages for each site, determined by random binomial draws from the estimated probability of occupancy for each species, and averaged the diversity metrics of the simulated assemblages to estimate diversity without over-representing rare species. We selected the most informative spatial scales for each diversity metric using

Bayesian latent indicator scale selection (BLISS; Stuber, Gruber, & Fontaine, 2017) and then used the most informative scales for each land cover variable to fit a multivariate generalized linear regression describing the relationships between land cover variables and biodiversity dimensions via Bayesian posterior simulation with JAGS. Using the final model, we projected SR, PD, FD and the relative differences among the diversity metrics across Nebraska using ArcGIS and R (ESRI 2015; R Core Team 2018). For details, see Chapter 1, this volume.

Biodiversity hotspots and overlap with conservation plans

Based on projected diversity metric maps, we delineated where the highest 10% of PD, FD, and SR (hereafter high PD, FD, or SR areas respectively, or high diversity areas collectively) occurred. We examined the degree of overlap between areas of high diversity and conservation and management areas by calculating the percentage of delineated conservation areas that overlapped with high diversity areas. Additionally, we relativized PD, FD, and SR to examine how each measure related to the other and to conservation and management plans.

Specifically, we examined Nebraska's Natural Legacy state wildlife action plan (Legacy Plan hereafter), which designated priority areas for conservation action based on preserving endangered and unique wildlife and landscapes (Biologically Unique Landscapes, BULs; Schneider *et al.* 2011). We examined a species-specific management plan in Nebraska: Nebraska Game and Parks Commission's Berggren Plan for ring-necked pheasant (*Phasianus colchicus*), which managed properties to increase pheasant abundance and hunter experience (Nebraska Game and Parks Commission 2016). We also examined a larger scale plan, the North America Bird Conservation Initiative

(NABCI), which developed a hierarchical framework for the conservation of birds within delineated ecoregions from Northern Canada to Northern Mexico (Bird Studies Canada & NABCI 2014). Finally, we examined wildlife management areas, managed by the state wildlife agency, Nebraska Game and Parks Commission (Nebraska Game and Parks Commission 2018).

RESULTS

We used multivariate models to predict PD, FD, and SR across the state (full model output in Chapter 1, this volume), which isolated our detected effects across land cover. Diversity metrics showed broad similarities across Nebraska, predicted to be the highest in the east, and declining westward (Figure 2. 1, Figure 2. 2, Figure 2. 3). Generally, high diversity areas were predicted in similar areas: northwest, along the east border of Nebraska, and in patches in the middle of the state, all places with many trees (Figure 1. 1 in Chapter 1, this volume; Bishop 2011), High diversity areas covered 19,876 km^2 in each diversity dimension. High PD areas and high SR areas were distributed among a similar number of patches (408, 431 patches, respectively) of similar, but largely varying sizes (48.72 ± 230.84 km^2; 47.87 ± 245.74 km^2, respectively). High FD areas were distributed among fewer large patches (262 patches, 76.95 ± 352.25 km^2).

When PD, FD, and SR were relativized, we see that much of the state has similar relative values of PD as FD, with 74.4% of Nebraska predicted to be within 5% of each other (e.g.,

Figure 2. 17; yellow). FD was higher than PD for 20.9% of the state (e.g.,

Figure 2. 17; orange), with the highest differences in the southwest. PD was higher than FD in only 4.7% of the state (e.g.,

Figure 2. 17; blue), occurring in small patches in north central and southeastern Nebraska, generally where wetlands occur. Both PD and FD were predicted to have higher values than SR across most of Nebraska (> 95% for both PD and FD), which included areas reaching more than 30% difference between metrics.

Conservation plans

Legacy Plan's BULs spanned ~43% of Nebraska (85685.9 km^2) and collectively, ~16% of the total area encompassed in BULs overlapped with state's high diversity areas (Table 2. 1). Collectively, BULs encompassed 69%, 68%, and 72% of high PD, FD, and SR areas, respectively. Most of the highest percent overlap occurring in the eastern half of the state in smaller BULs (e.g., Indian Cave Bluffs, Rulo Bluffs, Thurston-Dakota Bluffs; Table 2. 1). Larger BULs were the ones that overlapped high diversity areas most (e.g., Verdigris-Bazile, Pine Ridge, Rainwater Basin; Table 2. 1; Figure 2. 4). Additionally, many BULs closely matched the outlines of large patches of high diversity areas (e.g., Losses Canyons, Pine Ridge, Niobrara River, BULs along the Missouri River; Table 2. 1, Figure 2. 5), and also clusters of small patches of high diversity areas (e.g., Rainwater Basin and for PD; Figure 2. 5).

The areas designated under the Berggren Plan for pheasants spanned ~32% (64454.7 km^2) of Nebraska, but only ~10% of the total area encompassed in the Berggren Plan overlapped with high diversity areas. There was more overlap with high SR areas than high PD and FD areas, but the overlap encompassed ~ 31% of high diversity areas for each metric (6154.1, 6212.7, 6572.0 km^2 for PD, FD, and SR, respectively; Table 2. 2). The Northeast and Central pheasant opportunity area had the highest area of overlap with high diversity areas, but the Central Platte pheasant opportunity area had the highest percent overlap with high diversity areas (Table 2. 2, Figure 2. 8, Figure 2. 9, Figure 2. 10).

NABCI's bird conservation ecoregions covered all of Nebraska. Ecoregions in the east had the highest percentage of area overlapping with high diversity areas of each dimension (e.g., eastern tall grass prairie, prairie pothole; Table 2. 3, Figure 2. 11, Figure 2. 12, Figure 2. 13). The ecoregions with the lowest percentage of overlap with high diversity areas were in the west (i.e., shortgrass prairie, central mixed prairie; Table 2. 3). Central mixed grass prairie overlapped with the highest amount of high diversity areas, yet because the ecoregion was so large, the percentage of that ecoregion with high diversity areas was one of the lowest (e.g., 7820.3 km^2, 6% for PD; Table 2. 3).

Nebraska Game and Parks Commission's wildlife management areas covered less than 1% of Nebraska, the least amount of total area out of the conservation and management plans examined here. However, more than 30% the wildlife management areas overlapped with high diversity areas (249.4 km^2, 33% PD; 245.6 km^2, 32% FD; 289.1 km^2, 38% SR; Table 2. 4), which corresponded to ~ 1% of high diversity areas. Some of the patches that solely overlapped with high PD areas corresponded with wetlands, which had a positive relationship with PD but not FD or SR (Chapter 1, this volume).

Mismatches

There was high congruence among areas of high diversity across the state between diversity dimensions (Figure 2. 4). Mismatches include small patches of high PD in south-central Nebraska without corresponding patches of high FD or SR, and patches of high SR along rivers throughout the state where PD and FD were low (Figure 2. 4).

High FD areas that did not overlap with areas of high PD or SR generally were part of larger patches of high FD in the eastern part of the state (Figure 2. 4).

Areas where PD was predicted to be higher relative to FD generally were in northwestern and south-central Nebraska; These areas often aligned within BULs of the Legacy Plan that were associated with wetlands or rivers (e.g., Cherry County Wetlands, Elkhorn River Headwaters;

Figure 2. 17). Berggren pheasant opportunity areas almost exclusively overlapped areas with higher FD than PD (Figure 2. 18). NACBI central mixed grass prairie and badland and prairies ecoregions almost exclusively contained the areas with higher PD relative to FD (

Figure 2. 19). Other NACBI ecoregions almost exclusively contained areas with higher FD relative to PD except for the southwest portion of the central mixed grass prairie ecoregion which had high FD than PD (

Figure 2. 19). Nebraska Game and Parks Commission's wildlife management areas overlapped areas with higher PD and higher FD relative to other areas. Some small areas of higher PD relative to FD, which were often associated with wetlands.

Areas predicted to have higher FD than PD typically occurred in the southwest and east parts of the state in areas that had more grasslands; Legacy Plan's BULs that encompassed areas of higher FD were generally along the southern border of Nebraska (

Figure 2. 17). Areas of high FD relative to PD generally were well encompassed by the ecoregions on the western and eastern extremes of the state, with few and generally less different areas occurring in the central mixed grass prairie.

DISCUSSION

Here we examined how different metrics in different dimensions of biodiversity, namely taxonomic, phylogenetic, and functional dimensions, varied across a landscape in relation to existing conservation and management plans. We compared plans that were designed with various goals in mind: holistic landscape conservation, single-species prioritization, ecoregion designations, and opportunistic management areas. We find that Nebraska Game and Parks Commission managed lands had the highest percentage of overlap with high diversity areas of all three measures, followed by the Legacy Plan, suggesting that targeted management and holistic approaches could be most effective to provide ancillary benefits to multiple biodiversity dimensions. We demonstrate that SR may be an adequate surrogate for other dimensions of diversity, thus, managing for high SR could result in concurrent conservation of high PD and FD

Management approaches

Nebraska's Natural Legacy Plan

The Legacy Plan BULs had the second largest percent of overlap with high diversity areas of each dimension. Additionally, many BULs closely matched large patches of high diversity areas and clusters of small patches (Figure 2. 5, Figure 2. 6, Figure 2. 7). BULs were designed with the goal to represent a range of components of biological diversity (e.g., species, natural communities; Schneider *et al.* 2011), which may have contributed to its success in matching the outlines of several large patches and clusters of small patches of areas of high biodiversity of birds. The Legacy Plan close matching of the outlines of several large patches and clusters of small patches, especially of PD in southeast Nebraska suggests that a holistic approach may be an effective way to designate areas for conservation of multiple dimensions of biodiversity. Such holistic ecosystem approaches are increasingly being advocated for, as they provide a more feasible approach to protecting the overwhelming variety of biodiversity compared with narrow scope species-specific approaches by focusing on the processes that sustain species, populations, and communities (Franklin 1993).

Furthermore, BUL's were better at encompassing areas of higher PD, than areas of higher FD (

Figure 2. 17), indicating that the Legacy Plan's holistic approach may be better suited to manage for landscapes associated with PD more than FD. Part of the Legacy Plan's mission was to manage for endangered species. Extinction risk is phylogenetically non-random, generally with species that are more phylogenetically unique being at higher risk of extinction than species with many close relatives (Purvis *et al.* 2000). Thus, the Legacy Plan's selection of areas including species at higher risk of extinction could inherently be capturing landscapes with high PD.

Berggren Plan for ring-necked pheasant

The areas designated by the Berggren Plan for pheasants moderately overlapped with areas of high diversity of each dimension (~10%; Table 2. 2) relative to the amount of land outlined in the Berggren Plan. However, the overlap is primarily driven by the four eastern management areas (Figure 2. 8, Figure 2. 9, Figure 2. 10). As the Berggren Plan manages land specifically to increase the abundance of a single species (i.e., ring-necked pheasant) and provide hunting opportunity (Nebraska Game and Parks Commission 2016), it may be surprising that we found any overlap whatsoever. Indeed, often by definition single species management plans focus on maximizing a single habitat type. Based on previous work, increases in CRP was associated with increases pheasant abundance (Jorgensen *et al.* 2014), but we find that areas with relatively high percentages of CRP or grassland have lower PD, FD, and SR than areas with lower percentages (see Chapter 1, this volume). Our results show that SR, PD, and FD were all positively associated with trees, whereas pheasants were predicted to have a negative relationship with trees. Overall, the species-environment relationships that shaped the designation of pheasant focus areas where pheasant abundance is highest (Jorgensen *et al.* 2014; Nebraska Game and Parks Commission 2016) were generally inverse of where we predict the greatest avian diversity, suggesting pheasants many not serve as a good umbrella species (Roberge & Angelstam 2004). The Berggren Plan, however, encompassed more areas that were predicted to have higher FD than PD (Figure 2. 18). The pheasant abundance model (Jorgensen *et al.* 2014) appears to have similar distributions as the areas predicted to have higher FD than PD, indicating managing for pheasants could result in higher increases to FD than PD. Ultimately, prioritizing FD or PD is a policy decision, but our findings suggest that different management plans may serve to balance different policy priorities.

North American Bird Conservation Initiative

Out of the plans we examined, the NABCI was the most closely designed to reflect the diversity targets we assessed (i.e., North American birds vs. Nebraskan birds). The NABCI delineated ecoregion across most of North America considering similar bird communities, habitats, and resource management issues; Within those regions, state and federal government agencies, private organizations and bird initiatives restore and manage land that promote integrated conservation for healthy and abundant bird populations (Bird Studies Canada & NABCI 2014). If outlines for ecoregions were drawn to capture considerable differences among avian assemblages, then we could expect to see substantial differences in biodiversity levels among ecoregions. Generally, the biodiversity levels gradually transitioned across boundaries of ecoregions (Figure 2. 11, Figure 2. 12, Figure 2. 13), which reflects the gradual transitions in land cover across Nebraska (Figure 1. 1; Chapter 1, this volume). Additionally, high biodiversity areas were not contained within select ecoregions, but they were rather scattered within ecoregions and across ecoregion boundaries (Figure 2. 11, Figure 2. 12, Figure 2. 13). Thus, we did not find close alignment between the distribution of biodiversity and the NABCI ecoregion delineations.

However, when we examined the relative differences between PD and FD, we found NABCI ecoregion's outlined where differences between PD and FD manifested well, except in the southwest portion of the central mixed grass prairie of Nebraska, which had more similar values to the shortgrass prairie ecoregion than the central mixed grass prairie ecoregion (

Figure 2. 19). NABCI states that, "Bird Conservation [Eco]Regions should ultimately function as the primary units with which biological foundation issues are resolved, the landscape configuration of sustainable habitats is designed, and priority projects originate (Bird Studies Canada & NABCI 2014). As the primary unit for wildlife management, we must ensure that areas within the unit "encompass similar biological communities… and their boundaries roughly coincide with the area over which key ecological processes most strongly interact" (Olson & Dinerstein 1996). Using one measure of biodiversity might not capture characteristic community changes, but

examining where the relative values between phylogenetic and functional dimensions of biodiversity differ offers a way to identify where substantial changes in community composition of ecological and evolutionary importance occur to improve ecoregion delineation.

Nebraska Game and Parks Commission's Wildlife Management Areas

Nebraska Game and Parks Commission wildlife management areas covered the least amount of land out of the plans examined, but had the highest percentage of its land overlap with high diversity areas. Out of the plans examined, wildlife management areas are likely are the most actively managed for wildlife habitats. These wildlife management areas are often opportunistically acquired by Nebraska Game and Parks Commission through acquisition programs, leases, or donations (Nebraska Game and Parks Commission 2011), yet the management of these scattered areas is often associated with the rare (e.g., trees, wetlands) habitat types, which are positively associated with high biodiversity (Chapter 1, this volume). Wildlife management areas especially overlapped with high PD areas that were not included in high FD and SR areas, many of which contain wetlands, a land cover that was more positively associated with PD than FD and SR (Chapter 1, this volume). As wildlife management areas are typically managed with recreation activity or species specific goals, it was encouraging that wildlife management areas also provided ancillary benefits to avian biodiversity.

Conservation philosophies

Given the increasing pressures to sustain the world's growing human population, it is unlikely that societies will be able to set aside enough land to protect all or most biodiversity (Pimm, Jenkins & Li 2018). Considerations for which dimensions of diversity to prioritize is one of first steps towards actually enacting conservation action. After policy makers, managers, and the public contemplate how much they value the conservation of each dimension of diversity, they still have to decide how to select sites that would fulfill their conservation goals for one or multiple dimensions of biodiversity.

Taxonomic Surrogacy

Measuring taxonomic diversity is the easiest and most common approach of quantifying biodiversity, and thus it is typically the biodiversity dimension considered in planning, monitoring, and evaluating the conservation of biodiversity (Faith 1992; Gotelli & Colwell 2001; Fleishman *et al.* 2006; Swenson 2011). However, evidence suggesting that taxonomic diversity is an adequate surrogate for measures in phylogenetic and functional dimensions is equivocal (Gaston 2000; Webb 2000; Rodrigues & Gaston 2002; Huang *et al.* 2012; Winter *et al.* 2013) and typically indicate only partial congruence of SR with PD and FD (Devictor *et al.* 2010; Huang *et al.* 2012; Carvalho *et al.* 2017). Our study is consistent with previous findings of partial congruence; although we observed areas of high congruence between high diversity areas of PD, FD, and SR (Figure 2. 4), relative values of SR were predicted to be lower than PD and FD, although the magnitude varied erratically across Nebraska (Figure 1. 18, Figure 1. 19, Chapter 1, this volume). Other studies also show that taxonomic measures, such as SR, underestimate changes in the phylogenetic and functional dimensions (Flynn *et al.* 2009; Huang *et al.* 2012; D'agata *et al.* 2014; Mazel *et al.* 2014; Pool *et al.* 2014; Carvalho *et al.* 2017). Empirical evidence is growing to support the semi-independence of diversity dimensions which has substantial implications for how biodiversity conservation is planned and management is conducted.

Differences between the taxonomic dimension and other dimensions may not necessarily be a bad for conservation, as SR general underrepresentation of PD and FD may offer a silver lining for conservation. If SR does not vary as extremely as other dimensions of diversity, as our study and other studies suggest (see above), then a conservation actions that manage land to increase SR, like many current conservation strategies do (Reid 1998; Myers *et al.* 2000), would inherently also manage for high representation of PD and FD. Furthermore, decreases in SR could serve as a 'red flag' for biodiversity decline; decreases in SR would also indicate potentially greater declines in PD and FD as these metrics are broadly correlated (Chapter 1, this volume). Thus, the measuring SR, an easier metric than most metrics in the phylogenetic and functional dimensions, may serve as an adequate surrogate for conservation for other dimensions.

Spatial congruence of high diversity areas could be due to mathematical artefacts of PD, and FD not being measures independent of SR (Chapter 1, this volume) that was probably responsible for inflating the congruence among high diversity areas (Figure 2. 4). Thus, further examination of how reliable SR can be for PD and FD is warranted. Additionally, our study covers a relatively small spatial and taxonomic extent, compared to many similar studies on diversity dimension mismatch. Studies at larger spatial scales tend to show higher divergence among diversity dimensions in a variety of taxa (Devictor *et al.* 2010; Mazel *et al.* 2014; Brum *et al.* 2017; Quan *et al.* 2018) than studies at smaller spatial scales (Strecker *et al.* 2011). Due to other evidence suggesting more independence among dimensions than is suggested here, we recommend taxonomic surrogacy be viewed with caution.

Phylogenetic Gambit

Maximizing PD as a form of conservation decision-making has been increasingly advocated since it was introduced in the 1990s (Vane-Wright, Humphries & Williams 1991; Faith 1992; Crozier 1997; Faith & Baker 2006; Isaac *et al.* 2007; Winter *et al.* 2013). Under the 'phylogenetic gambit' hypothesis, many argue that prioritizing the conservation of PD is the best course of action when all dimensions of diversity cannot be measured or planned for, as the breadth of evolutionary history, measured by PD, also indirectly captures FD. The phylogenetic gambit is a reliable strategy for conservation only if PD captures more FD than random chance. In our study, we observed similarities of PD and FD values within subsections of the plans we examined (Table 2. 1, Table 2. 2, Table 2. 3, Table 2. 4) and high congruence of between PD and FD across Nebraska (~ 75% of Nebraska was within 5%; e.g.,

Figure 2. 17); however, approximately one quarter of Nebraska was predicted to have substantially different PD and FD values due to divergent land cover relationships (> 50%; e.g.,

Figure 2. 17). Similar to other studies (Mazel *et al.* 2018), the phylogenetic gambit can be a decent conservation strategy, but can be unreliable under landscape conditions that favor higher PD relative to FD.

The phylogenetic gambit works when closely related species are more functionally similar that expected by chance. A pattern that arises when trait evolution among closely related species than expected by chance (i.e., phylogenetic niche conservatism; Winter *et al.* 2013; Mazel *et al.* 2018; Quan *et al.* 2018). If evolutionary and ecological processes (e.g., genetic constraints, stabilizing selection favoring ancestral functional traits, neutral drift) drive consistent differences between phylogenetic and functional dimensions of biodiversity (Swenson 2011; Münkemüller *et al.* 2015), then the phylogenetic niche conservatism pattern emerges. However, theoretical and empirical studies of phylogenetic niche conservatism show that the assumption of phylogenetic niche conservatism is rarely and inconsistently met and that the extent of phylogenetic niche conservatism varies across environmental conditions, regions, taxonomic clades, and ecological scales (Wiens & Graham 2005; Pearman *et al.* 2014; Münkemüller *et al.* 2015; Thuiller *et al.* 2015; Mazel *et al.* 2018). Other studies also demonstrate spatial inconsistencies between PD and FD that are likely due to differences in diversity-environment relationships (Devictor *et al.* 2010; Purschke *et al.* 2013; D'agata *et al.* 2014; Chapman *et al.* 2018). Additionally, surrogacy of PD for FD weakens as more species are included in assessing the relationship between PD and FD (Mazel *et al.* 2018), further demonstrating that the phylogenetic gambit is likely an unreliable conservation strategy to capture multiple forms of biodiversity.

Expanding conservation areas

Our results showed high congruence among SR, PD, and FD, which suggests that conservation has flexibility to expand in numerous areas predicted that are predicted to high diversity in all three dimensions (Figure 2. 4). In some cases, under conditions that are expected to have high congruence among diversity dimensions, simple hotspot analyses, like how we outlined areas predicted to have high PD, FD, and SR, could be sufficient to identify areas that maximize multiple dimensions of diversity. For example, we expect diversity dimensions to have the highest congruence when they respond to similar spatial scales and have similar relationships across predictor variables (Chapter 1, this volume).

Numerous frameworks exist for the prioritization of conservation resources (Lamoreux *et al.* 2006), yet most approaches do not incorporate multiple dimensions of biodiversity and thus do not address potential mismatches among diversity dimensions. When diversity dimensions' mismatch, algorithms can help identify areas of potential expansion for conservation biodiversity. One efficient way for maximizing biodiversity is the complementarity-based prioritization, which assesses how much biodiversity is covered in existing protected areas. Then in a stepwise fashion, it is possible to identify further sites which would contribute the greatest amount of biodiversity. Complementarity-based prioritization has been used often in relation to only taxonomic diversity (Reid 1998), but complementarity-based approaches have now also been applied to integrate taxonomic, phylogenetic, and functional dimensions, even in systems that show striking spatial mismatches among dimensions of diversity (Strecker *et al.* 2011; Brum *et al.* 2017). Using prioritization methods, such as complementarity-based prioritization, to maximize multiple dimensions of biodiversity offers an opportunity to expand conservation for multiple dimensions of biodiversity.

Conclusions

Protecting and managing landscapes has long been recognized as one of the key strategies to protect biodiversity; however, the focus and type of management can influence communities and multiple dimensions of biodiversity not typically considered during the planning process. Our study showed high congruence among SR, PD, and FD across a complex landscape, but under certain landscape conditions diversity dimensions differ drastically. The relative insensitivity of SR compared to PD and FD suggest that managing for SR offers a simple and strategic conservation opportunity to preserve PD and FD as well. Depending on the expected relationships among diversity metrics, simple hotspot analyses or more complex prioritization methods, such as complementarity-based approaches, offer ways to identify areas of potential conservation expansion. Once conservation areas are selected, holistic or intensively managed conservation approaches are recommended.

FIGURES

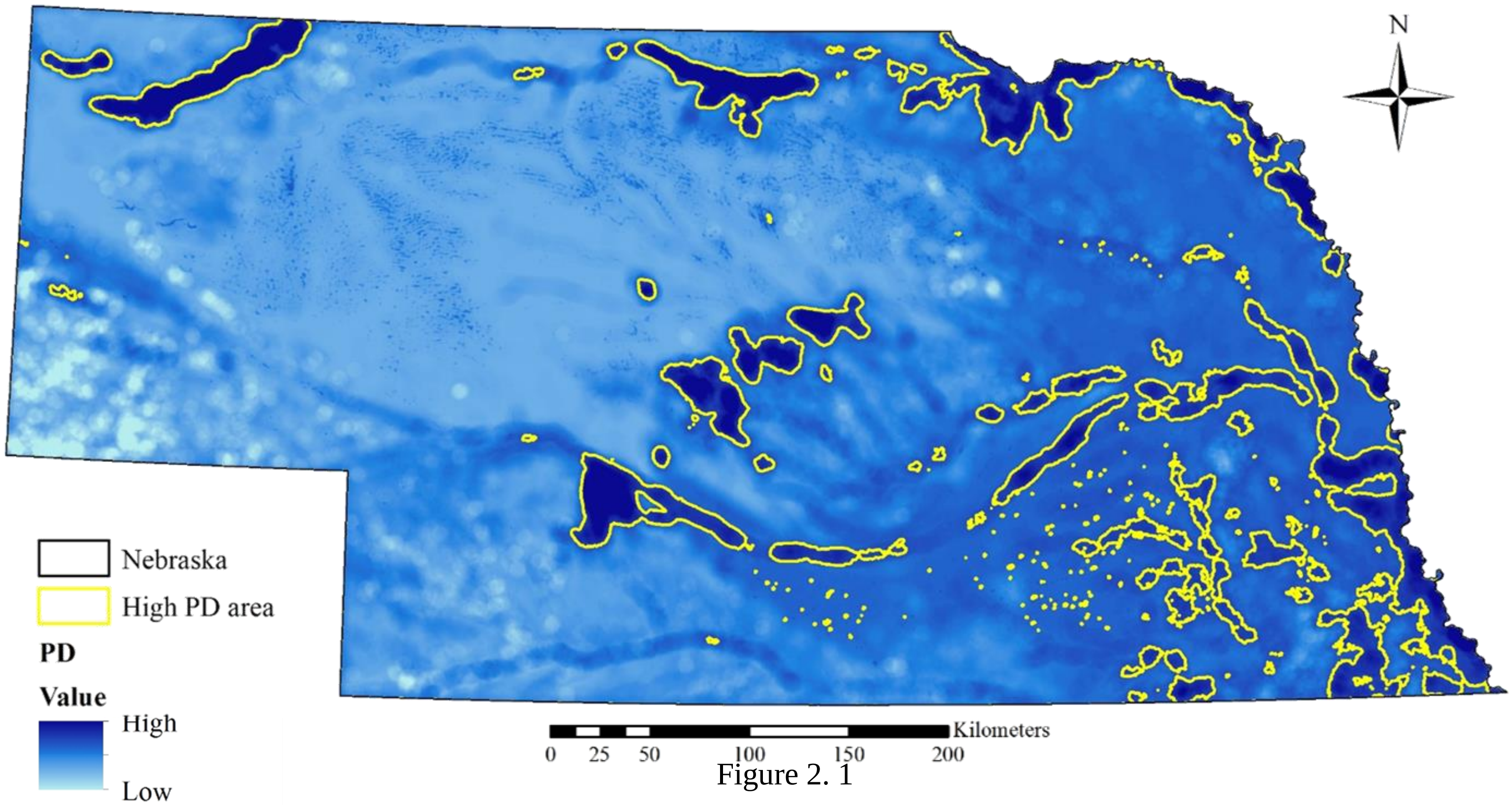

Figure 2. 1

Map of predicted phylogenetic diversity (PD) with the highest 10% of predicted PD values (high PD area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

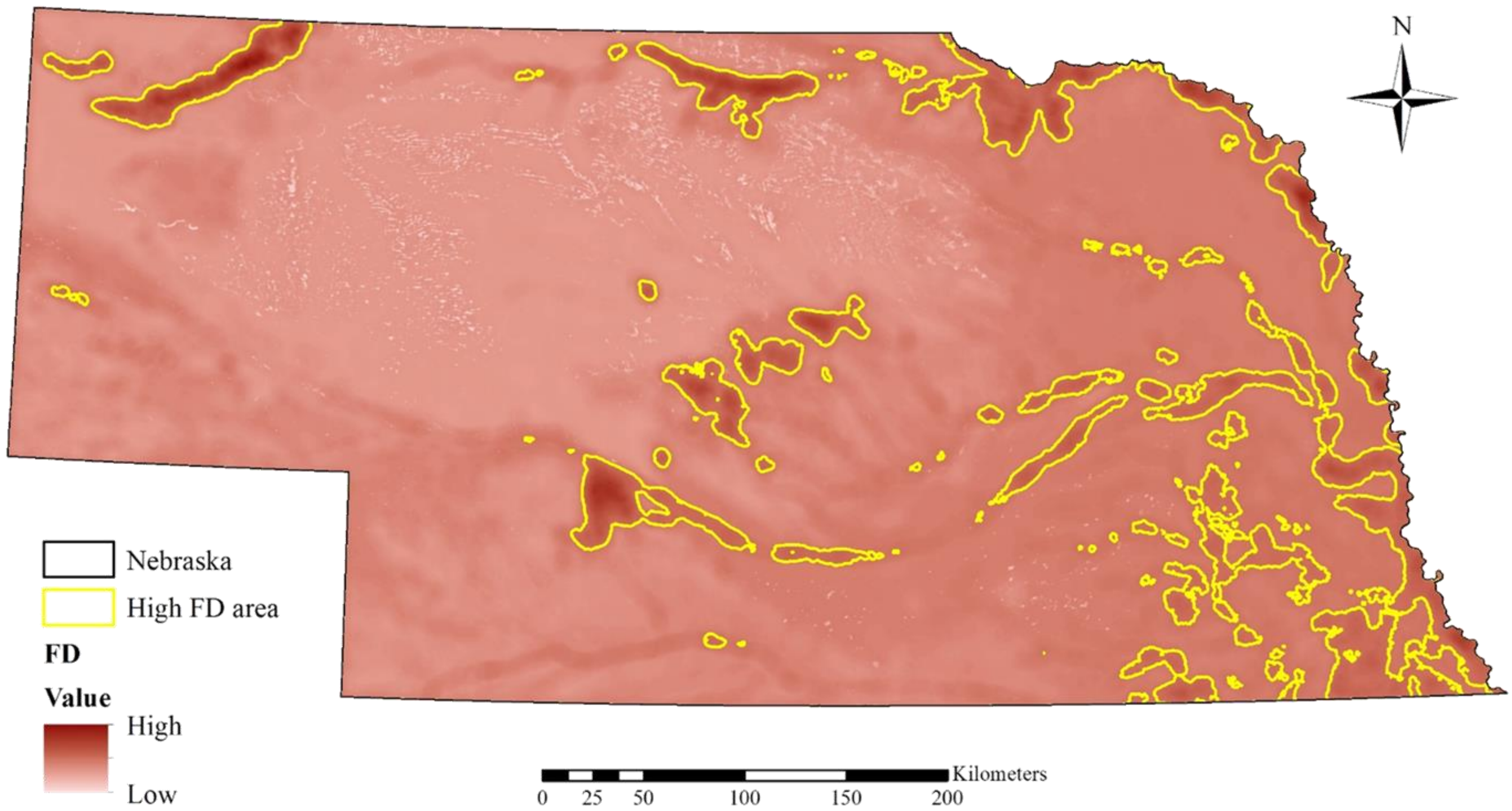

Figure 2. 2

Map of predicted functional diversity (FD) with the highest 10% of predicted FD values (high FD area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

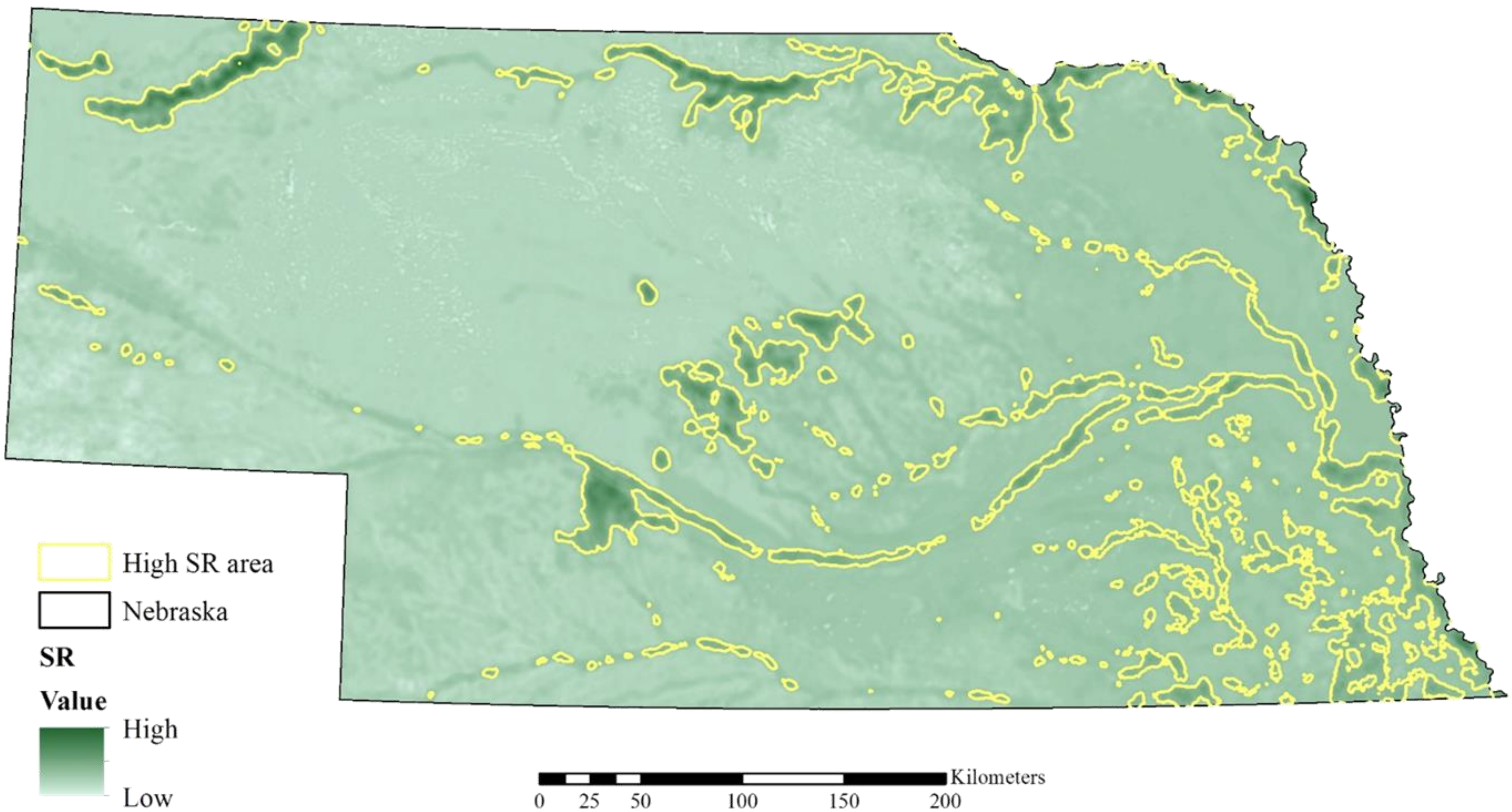

Figure 2. 3

Map of predicted species richness (SR) with the highest 10% of predicted SR values (high SR area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

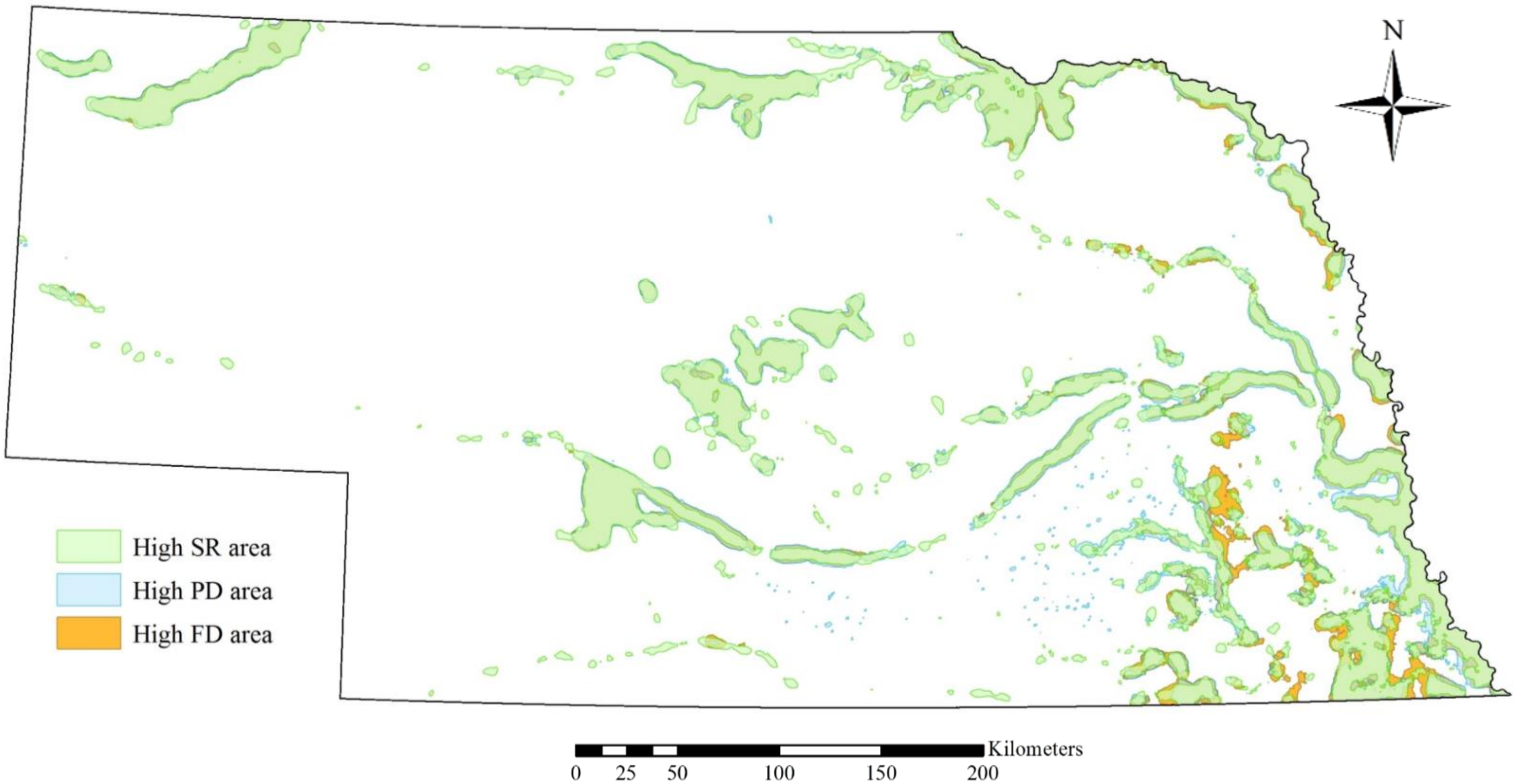

Figure 2. 4

Map of the highest 10% of predicted phylogenetic diversity values (high PD area; blue), the highest 10% of predicted functional diversity values (high FD area; orange), and the highest 10% of species richness values (high SR area; green), of the birds across Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

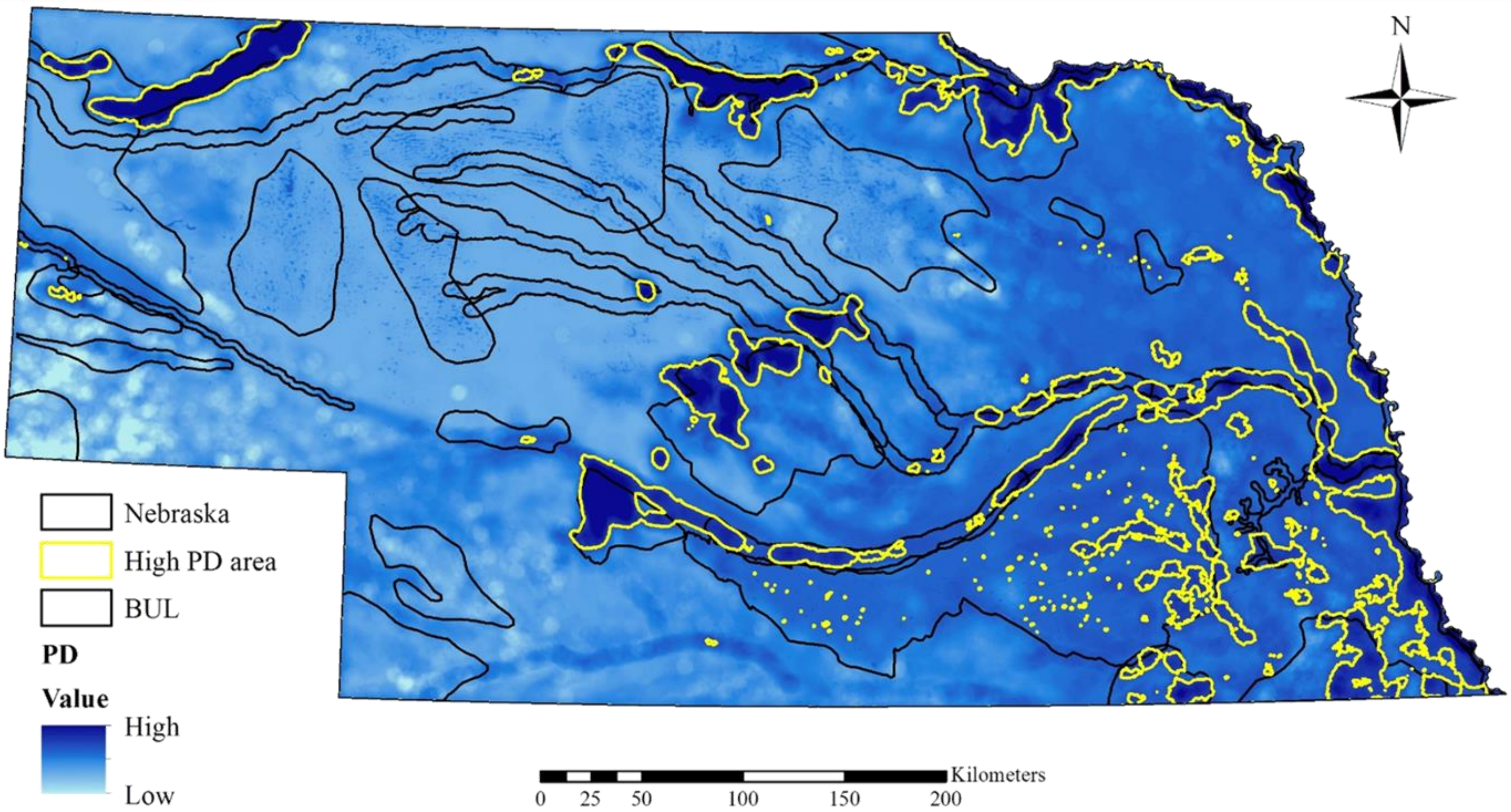

Figure 2. 5

Map of Nebraska’s Natural Legacy Biological Unique Landscapes (BUL) and predicted phylogenetic diversity (PD) with the highest 10% of predicted PD values (high PD area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

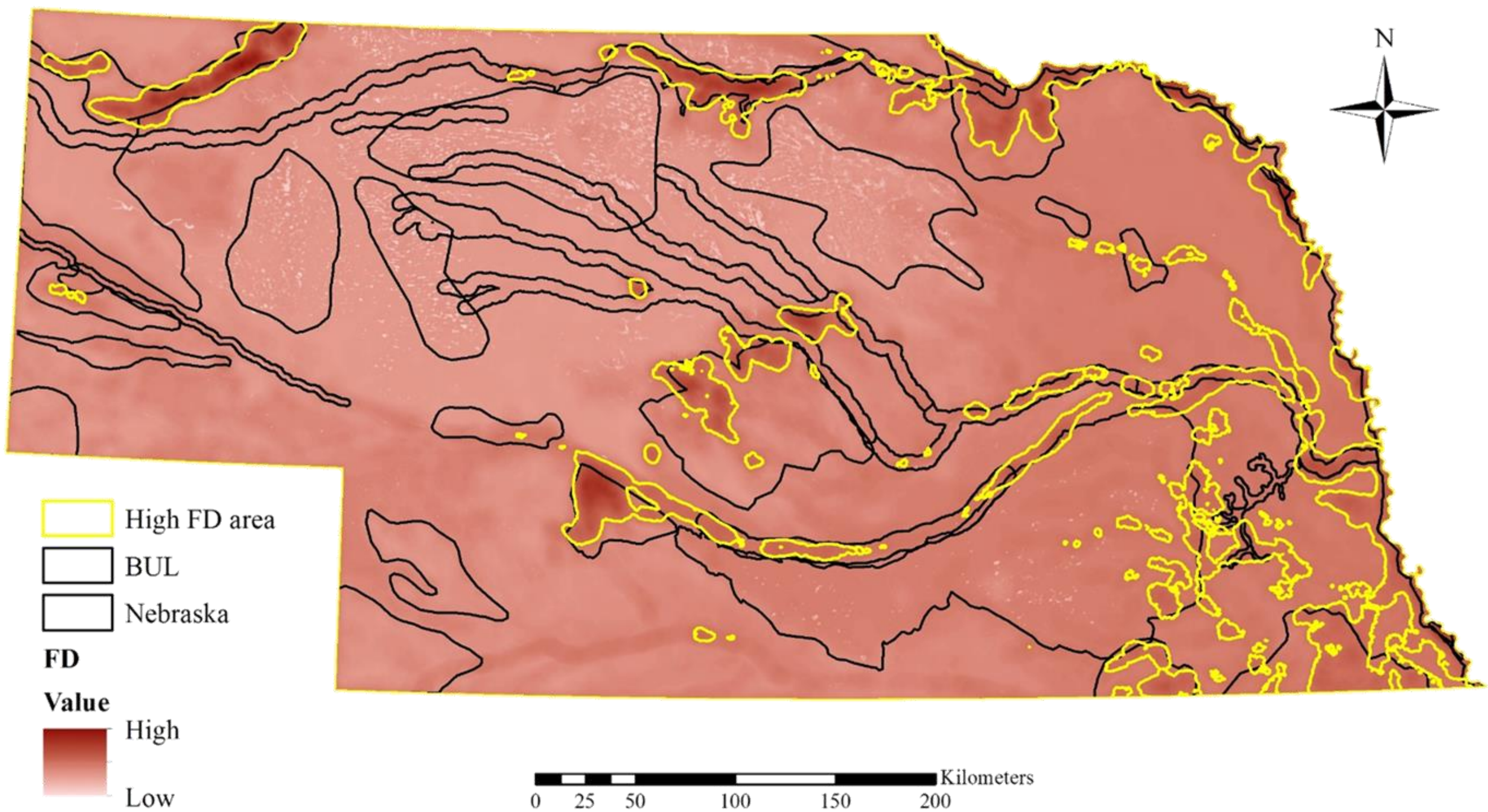

Figure 2. 6

Map of Nebraska's Natural Legacy Biological Unique Landscapes (BUL) and predicted functional diversity (FD) with the highest 10% of predicted FD values (high FD area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

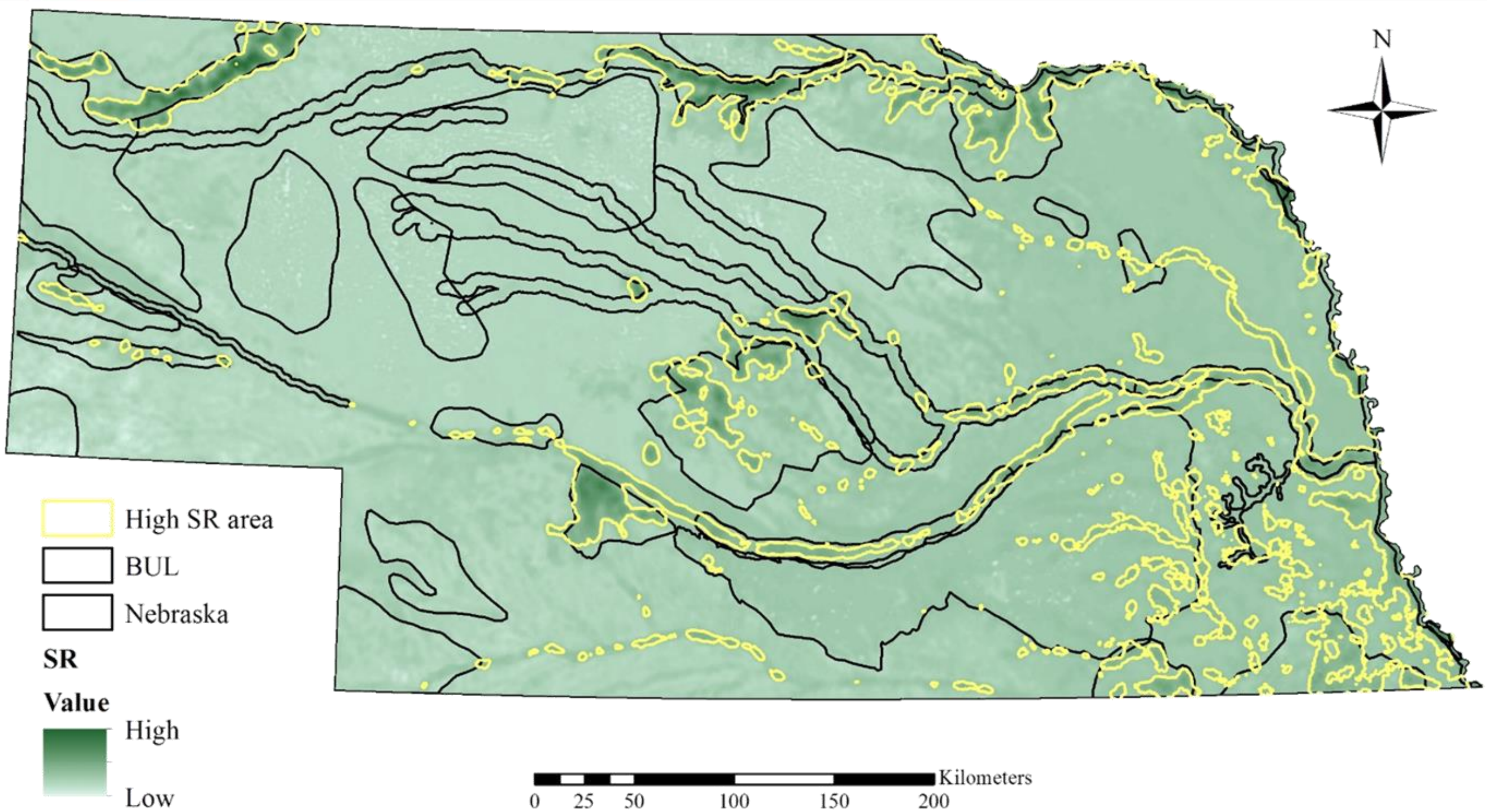

Figure 2. 7

Map of Nebraska's Natural Legacy Biological Unique Landscapes (BUL) and predicted species richness (SR) with the highest 10% of predicted SR values (high SR area) highlighted in yellow of the birds across Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

Table 2. 1

Nebraska's Natural Legacy Biological Unique Landscapes' (BUL) total areas, area of BUL overlapping high diversity area, and proportion of BUL with high diversity measures for phylogenetic diversity (PD), functional diversity (FD), and species richness (SR).

BUL	Area (km^2)	High PD (km^2)	Proportion high PD	High FD (km2)	Proportion high FD	High SR (km^2)	Proportion high SR
Lower Loup Rivers	1167.3	388.5	0.33	355.8	0.30	355.8	0.30
Lower Platte River	1055.1	820.8	0.78	776.4	0.74	753.9	0.71
Snake River	597.3	0.0	0.00	0.0	0.00	0.0	0.00
Missouri River	1790.2	1289.3	0.72	1381.9	0.77	1671.4	0.93
Central Platte River	1703.2	740.6	0.43	612.9	0.36	668.8	0.39
North Platte River	640.7	0.7	0.00	0.0	0.00	8.1	0.01
Middle Loup River	3373.9	80.0	0.02	0.0	0.00	116.5	0.03
North Loup River	2161.1	142.6	0.07	123.5	0.06	169.5	0.08
Calamus River	745.2	0.0	0.00	0.0	0.00	0.0	0.00
Saline Wetlands	430.9	75.0	0.17	91.4	0.21	83.1	0.19

Lower Niobrara River	784.2	400.0	0.51	390.2	0.50	573.8	0.73
Upper Niobrara River	1901.3	1.0	0.00	0.7	0.00	31.8	0.02
Willow Creek Prairies	230.3	0.0	0.00	0.0	0.00	0.0	0.00
Elkhorn Confluence	381.2	0.5	0.00	41.7	0.11	59.4	0.16
Keya Paha	1463.5	33.9	0.02	17.4	0.01	135.1	0.09
Sandstone Prairies	1072.1	405.5	0.38	592.1	0.55	450.9	0.42
Elkhorn River Headwaters	5178.7	0.0	0.00	0.0	0.00	0.0	0.00
Loess Canyons	1367.7	853.9	0.62	845.6	0.62	868.4	0.63
Ponca Bluffs	413.7	374.9	0.91	395.7	0.96	367.8	0.89
Indian Cave Bluffs	67.1	67.1	1.00	67.1	1.00	67.4	1.00
Thurston-Dakota Bluffs	111.7	104.7	0.94	111.7	1.00	111.7	1.00
Rulo Bluffs	12.2	12.2	1.00	12.2	1.00	12.2	1.00
Cherry County Wetlands	7092.0	0.0	0.00	0.0	0.00	2.2	0.00
Dismal River Headwaters	2684.5	0.0	0.00	0.0	0.00	0.0	0.00
Platte Confluence	804.8	11.6	0.01	5.3	0.01	68.2	0.08
Sandhills Alkaline Lakes	3575.5	0.0	0.00	0.0	0.00	0.0	0.00
Sandsage Prairie South	2441.1	0.0	0.00	0.0	0.00	8.9	0.00

Sandsage Prairie North	1724.3	0.0	0.00	0.0	0.00	0.0	0.00
Wildcat Hills North	929.9	42.2	0.05	56.5	0.06	117.8	0.13
Wildcat Hills South	763.8	0.0	0.00	0.0	0.00	69.0	0.09
Central Loess Hills	5676.1	1209.3	0.21	1104.1	0.19	1281.2	0.23
Verdigris-Bazile	2832.1	1642.9	0.58	1689.4	0.60	1567.2	0.55
Southeast Prairies	2343.1	944.2	0.40	1402.8	0.60	1028.1	0.44
Rainwater Basin	15907.4	1408.4	0.09	954.3	0.06	1134.5	0.07
Middle Niobrara	1375.7	889.7	0.65	862.1	0.63	1024.3	0.74
Oglala Grasslands	2895.1	77.1	0.03	79.3	0.03	57.9	0.02
Pine Ridge	2131.5	1515.4	0.71	1501.2	0.70	1489.2	0.70
Panhandle Prairies	4767.5	6.8	0.00	13.6	0.00	15.3	0.00
Kimball Grasslands	1092.8	0.0	0.00	0.0	0.00	0.0	0.00
Total	85685.9	13538.9	0.16	13484.7	0.16	14369.1	0.17

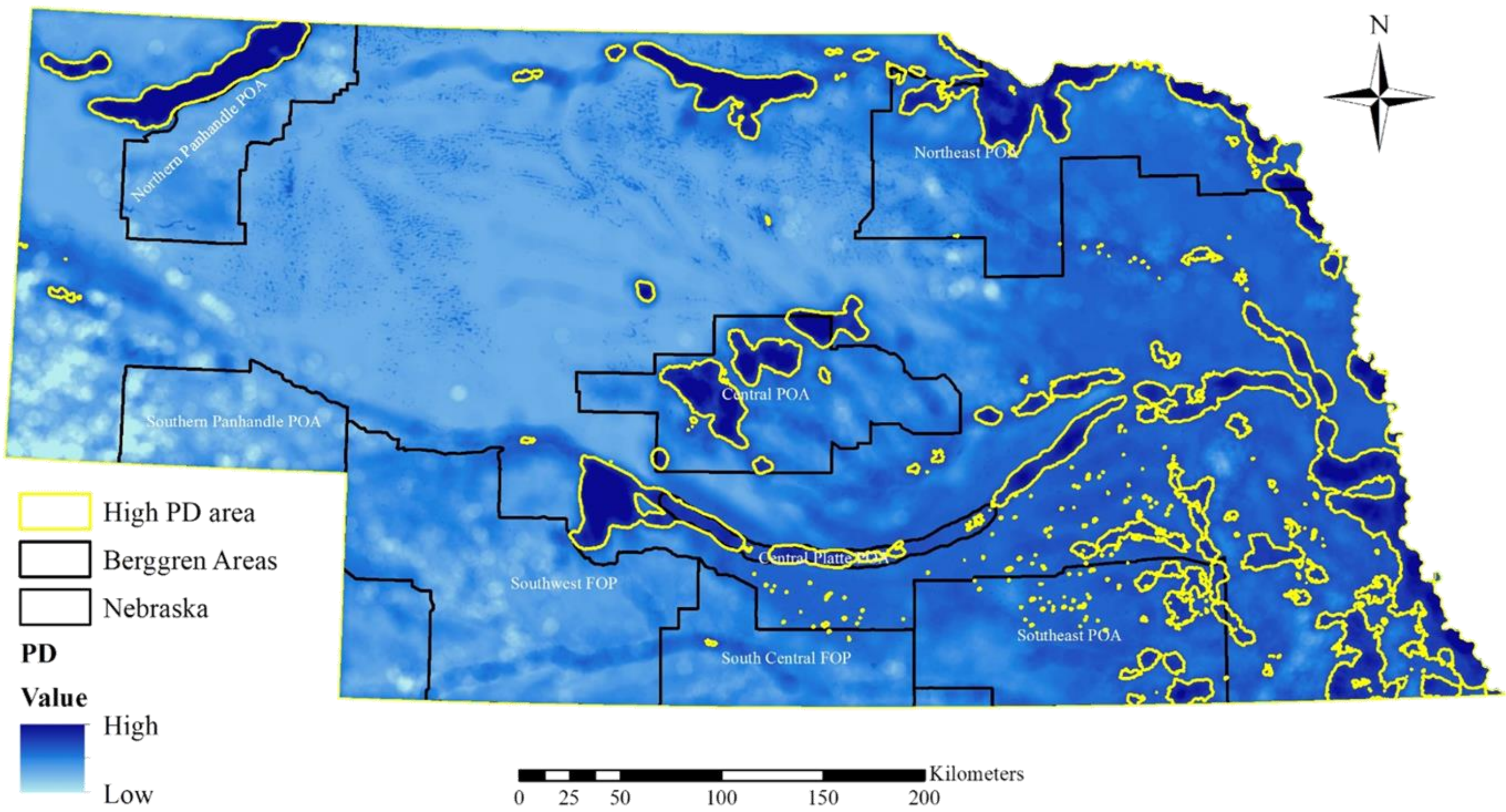

Figure 2. 8

Map of the Berggren Plan for pheasants and predicted phylogenetic diversity (PD) with the highest 10% of predicted PD values (high PD area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

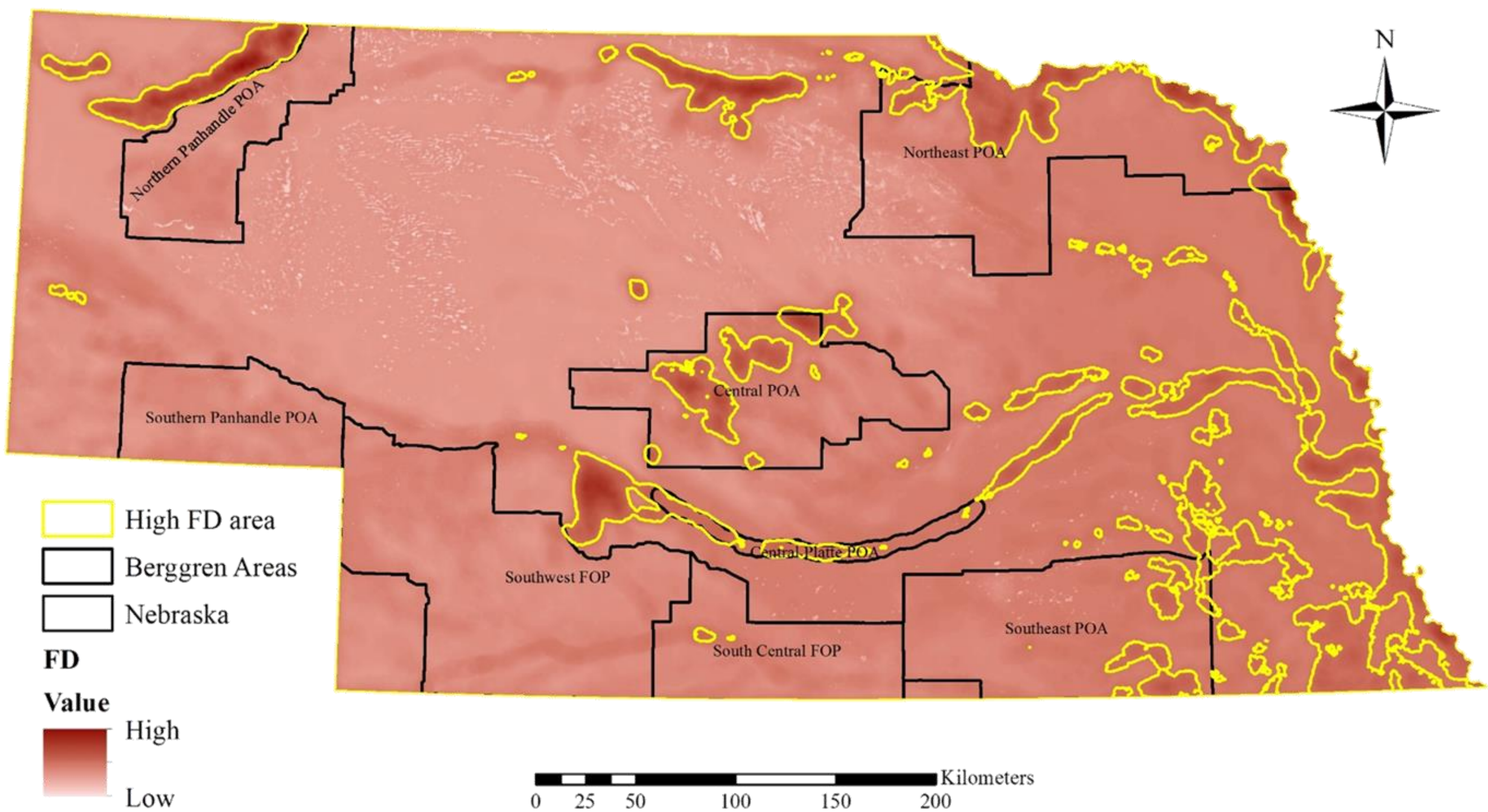

Figure 2. 9

Map of the Berggren Plan for pheasants and predicted functional diversity (FD) with the highest 10% of predicted FD values (high FD area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

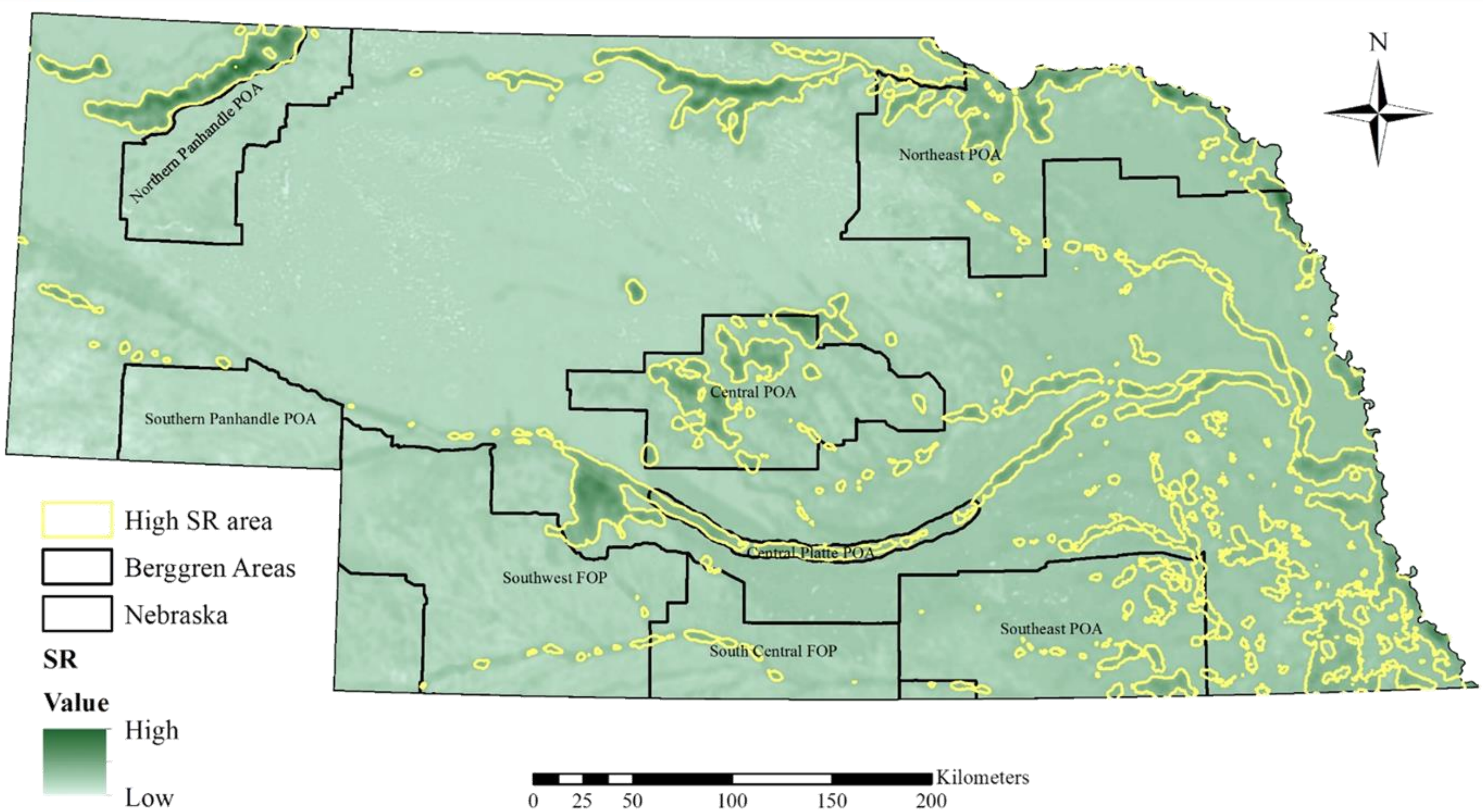

Figure 2. 10

Map of the Berggren Plan for pheasants and predicted species richness (SR) with the highest 10% of predicted SR values (high SR area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

Table 2. 2

The Berggren Plan for pheasants' total areas, area of each pheasant opportunity or focus area overlapping high diversity area, and proportion of pheasant opportunity or focus area with high diversity measures for phylogenetic diversity (PD), functional diversity (FD), and species richness (SR).

Subsection	Area (km^2)	High PD (km^2)	Proportion high PD	High FD (km2)	Proportion high FD	High SR (km^2)	Proportion high SR
Central POA	9128.6	1789.9	0.20	1627.5	0.18	1904.7	0.21
Northern Panhandle POA	5581.3	12.2	0.00	12.4	0.00	16.0	0.00
Southern Panhandle POA	5104.3	0.0	0.00	0.0	0.00	0.0	0.00
Southeast POA	9999.9	974.9	0.10	1095.4	0.11	1051.3	0.11
Northeast POA	13242.4	2633.8	0.20	2767.3	0.21	2592.5	0.20
Central Platte POA	1406.9	734.2	0.52	655.9	0.47	694.2	0.49
Southwest FOP	14298.4	0.9	0.00	2.8	0.00	141.6	0.01
South Central FOP	5693.0	8.3	0.00	51.3	0.01	171.6	0.03
Total	64454.7	6154.1	0.10	6212.7	0.10	6572.0	0.10

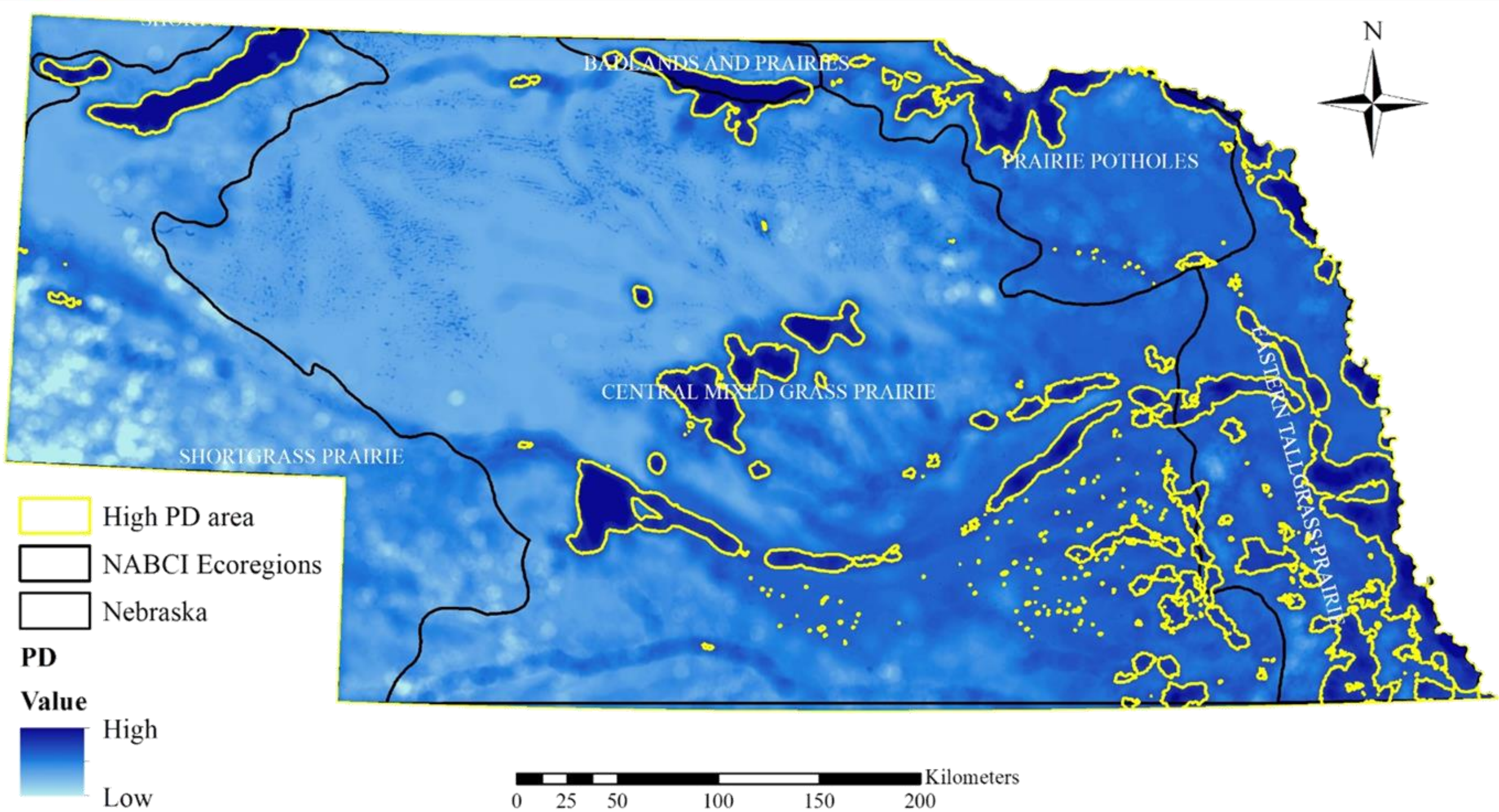

Figure 2. 11

Map of the North American Bird Conservation Initiative's (NABCI) ecoregions and predicted phylogenetic diversity (PD) with the highest 10% of predicted PD values (high PD area) highlighted in yellow of the birds across Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

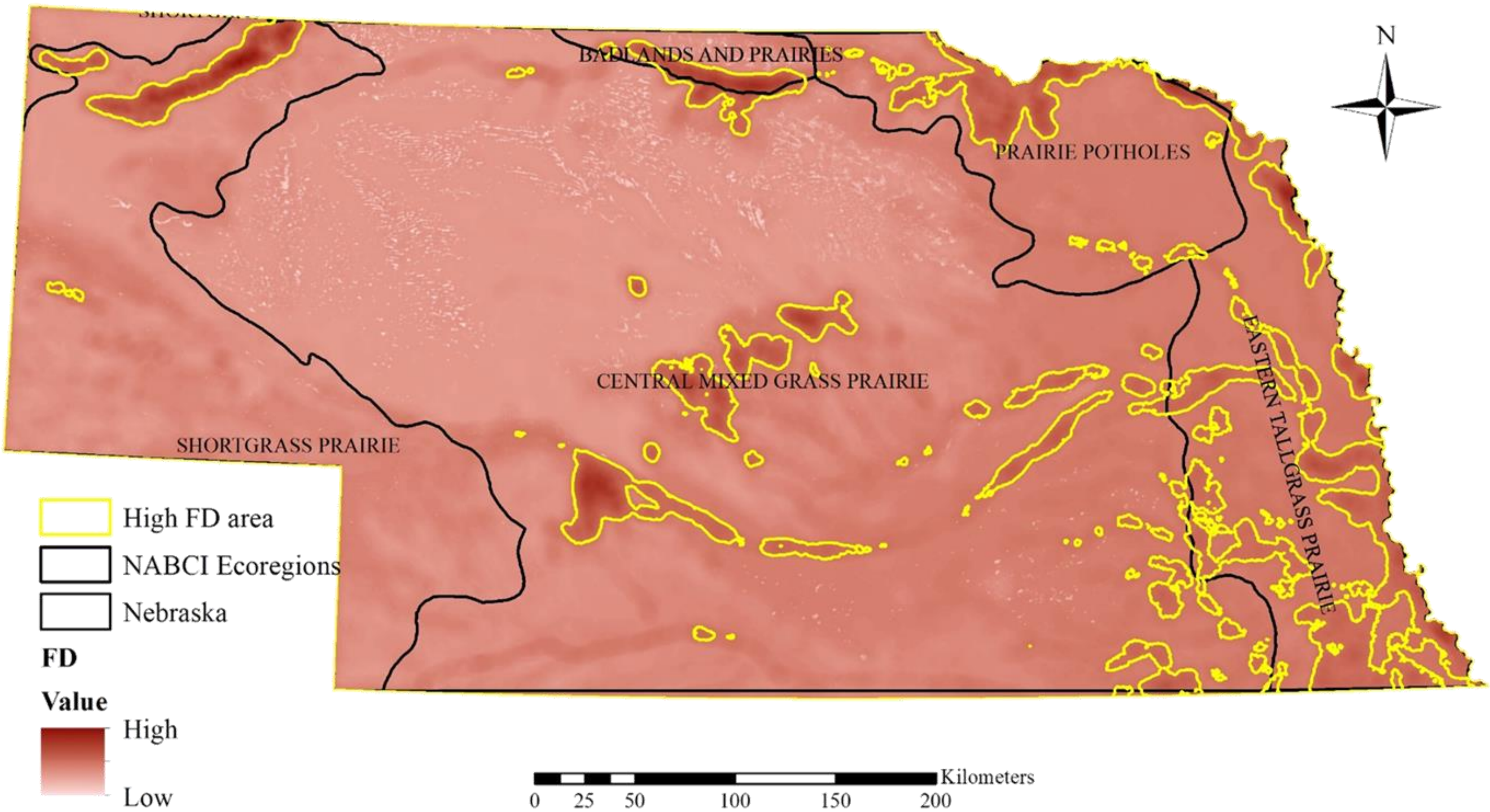

Figure 2. 12

Map of the North American Bird Conservation Initiative's (NABCI) ecoregions and predicted functional diversity (FD) with the highest 10% of predicted FD values (high FD area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

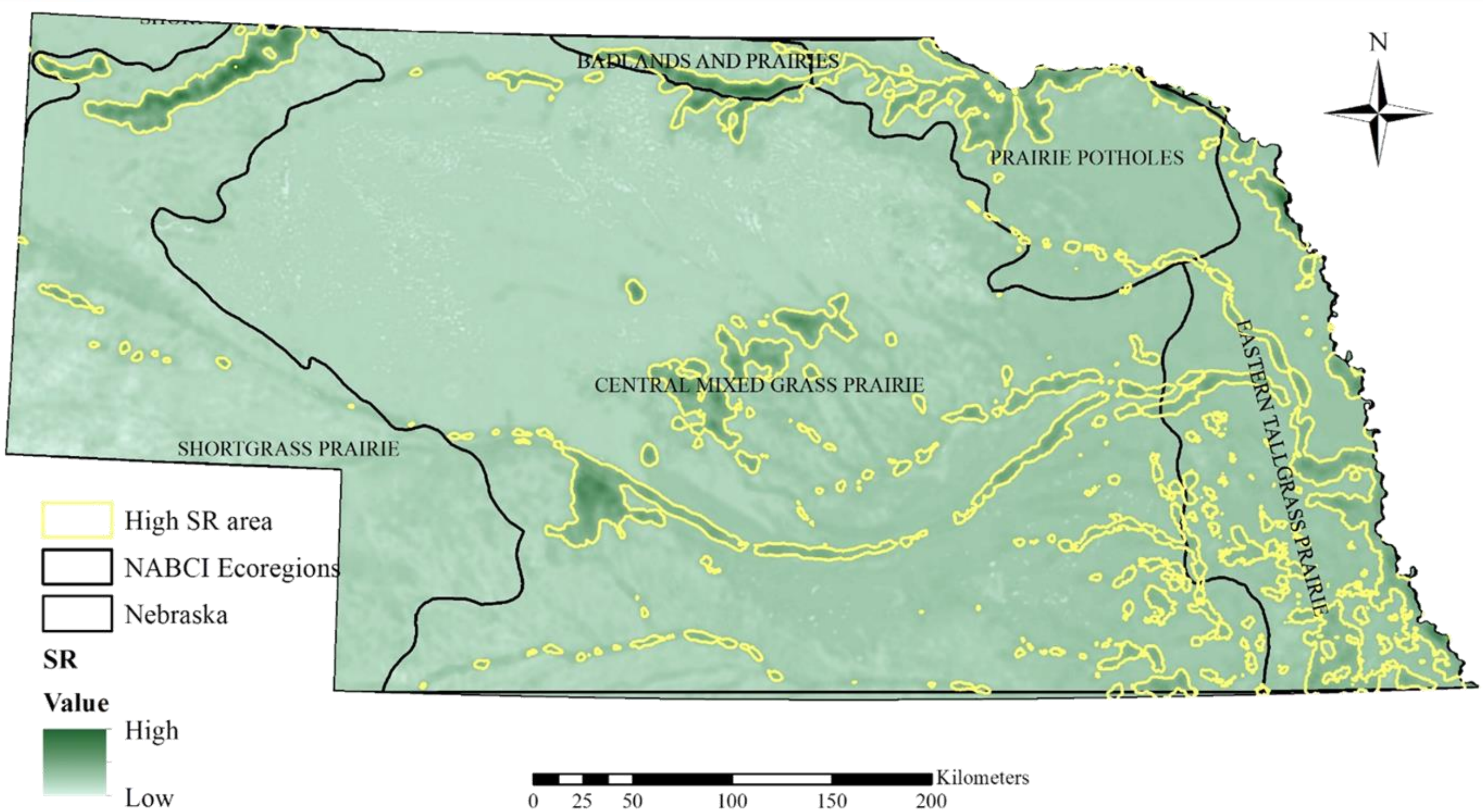

Figure 2. 13

Map of the North American Bird Conservation Initiative's (NABCI) ecoregions and predicted species richness (SR) with the highest 10% of predicted SR values (high SR area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

Table 2. 3

The North American Bird Conservation Initiative ecoregion's total areas, area of each ecoregion overlapping high diversity area, and proportion of ecoregion with high diversity measures for phylogenetic diversity (PD), functional diversity (FD), and species richness (SR).

Ecoregion	**Area (km^2)**	**High PD (km^2)**	**Proportion high PD**	**High FD (km2)**	**Proportion high FD**	**High SR (km^2)**	**Proportion high SR**
Prairie Potholes	15511.5	2421.3	0.16	2625.5	0.17	2855.3	0.18
Badlands and Prairies	4864	775.8	0.16	755.4	0.16	802.5	0.16
Shortgrass Prairie	35297.9	1831.6	0.05	1837.6	0.05	1949.6	0.06
Central Mixed Grass Prairie	120807.3	7820.3	0.06	6958.1	0.06	8430.5	0.07
Eastern Tallgrass Prairie	21969.2	6792.3	0.31	7638.3	0.35	5948.6	0.27

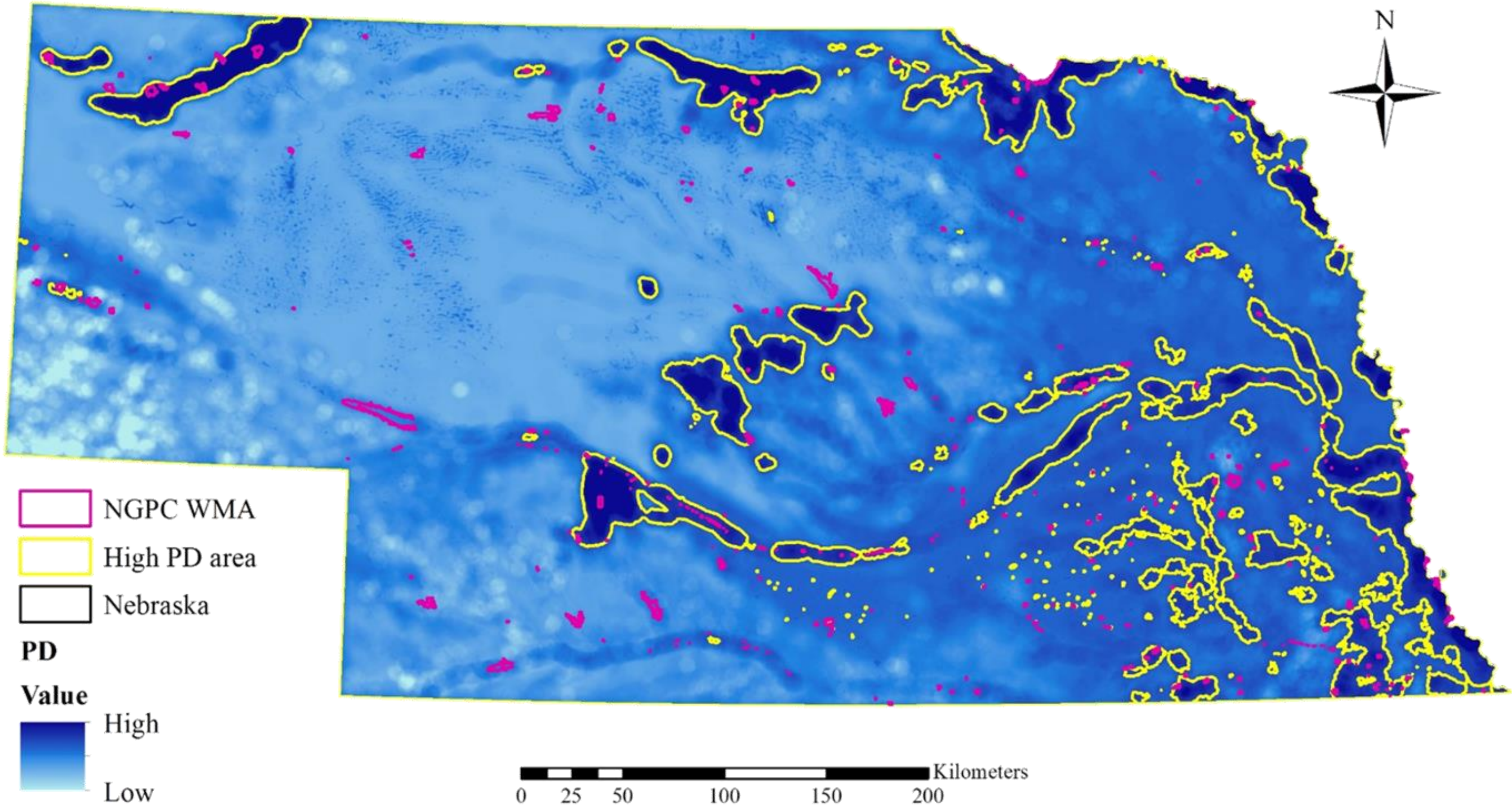

Figure 2. 14

Map of the Nebraska Game and Parks Commission's managed areas (NGPC WMA) ecoregions and predicted phylogenetic diversity (PD) with the highest 10% of predicted PD values (high PD area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

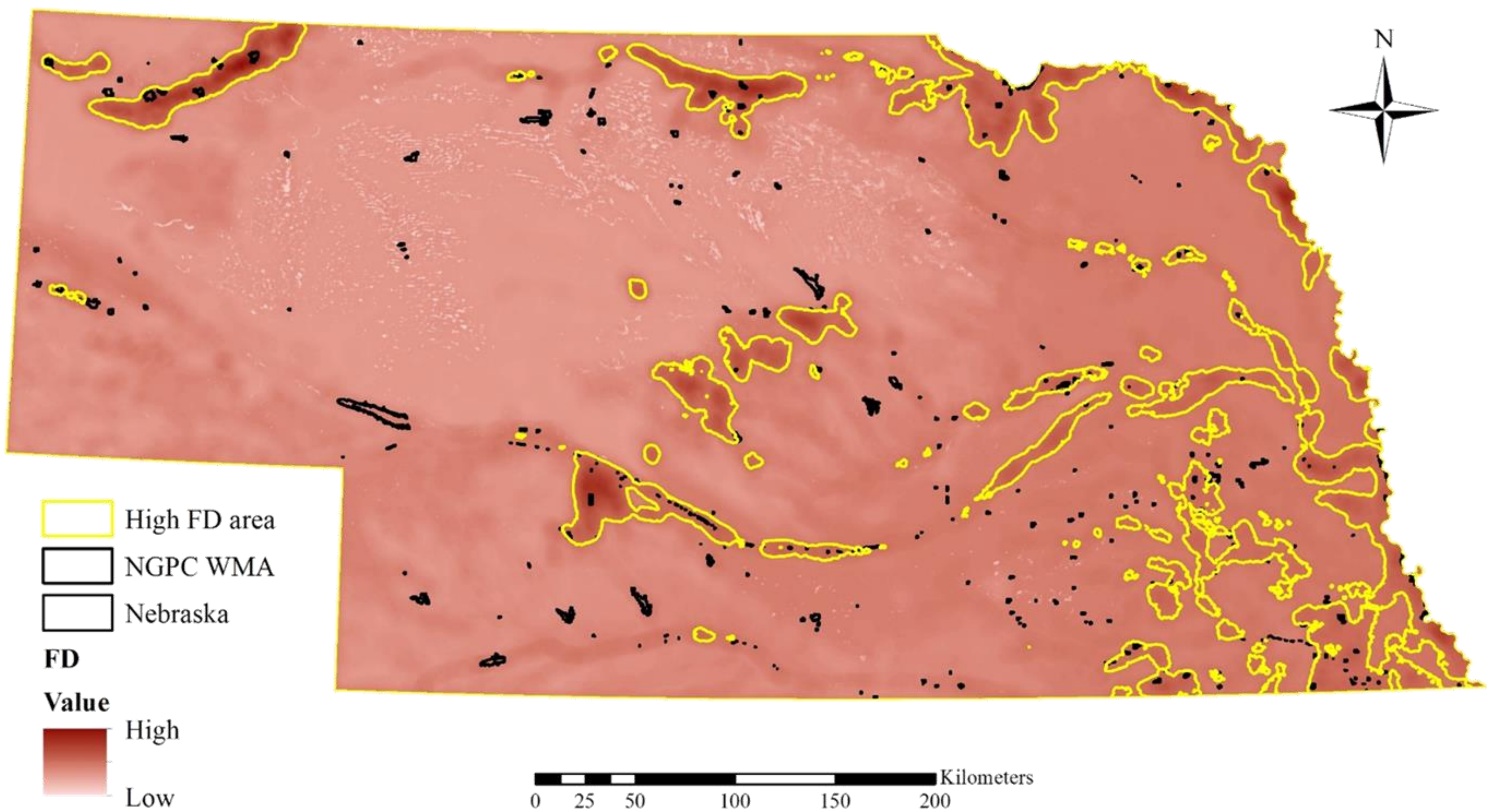

Figure 2. 15

Map of the Nebraska Game and Parks Commission's managed areas (NGPC WMA) ecoregions and predicted functional diversity (FD) with the highest 10% of predicted FD values (high FD area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

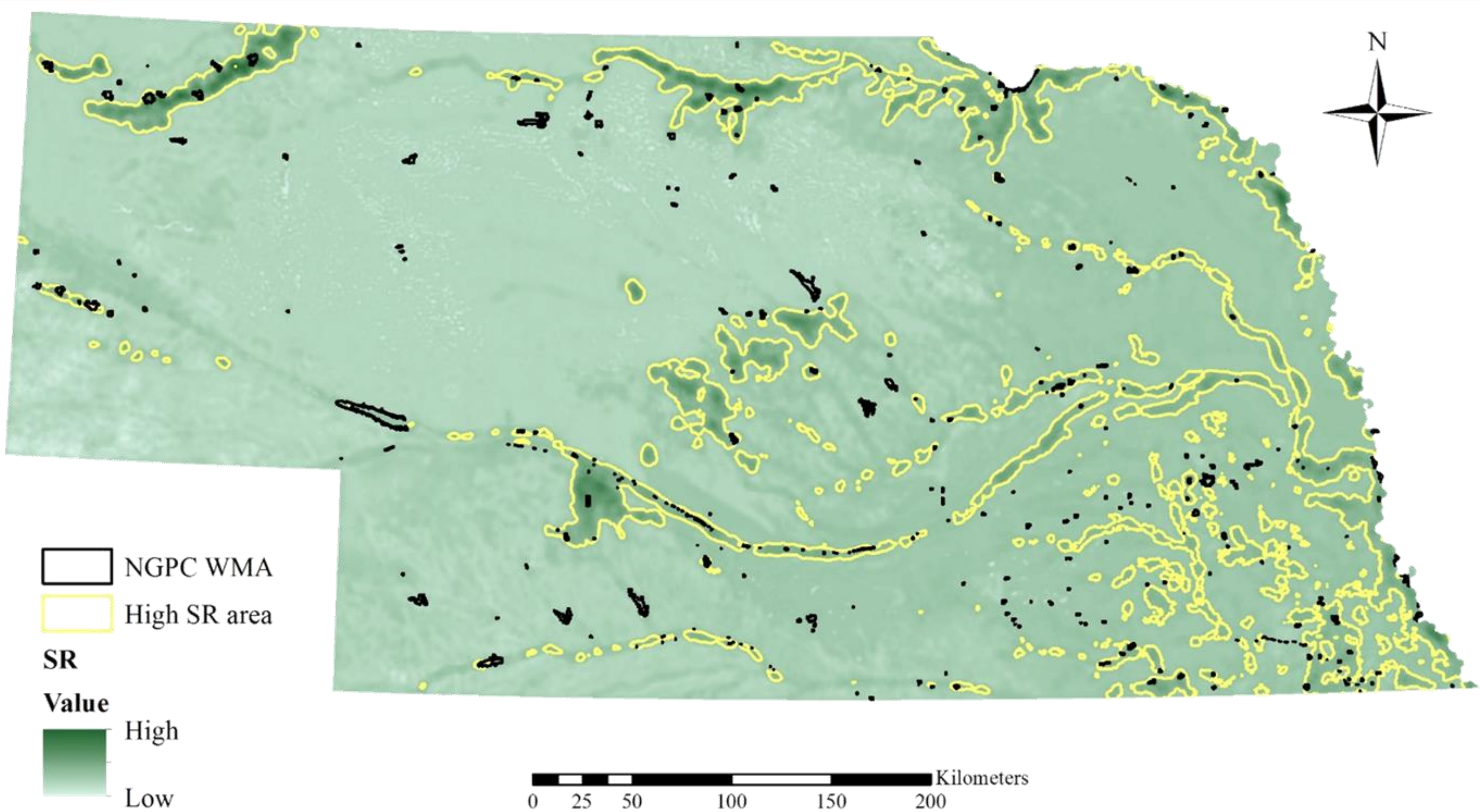

Figure 2. 16

Map of the Nebraska Game and Parks Commission's managed areas (NGPC WMA) ecoregions and predicted species richness (SR) with the highest 10% of predicted SR values (high SR area) highlighted in yellow of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

Table 2. 4

The Nebraska Game and Park Commission's managed areas' total areas, area of overlapping high diversity area, and proportion of managed areas with high diversity measures for phylogenetic diversity (PD), functional diversity (FD), and species richness (SR).

Managed Land	Area (km^2)	High PD (km^2)	Proportion high PD	High FD (km2)	Proportion high FD	High SR (km^2)	Proportion high SR
All 276	766.9	249.4	0.33	245.6	0.32	289.1	0.38

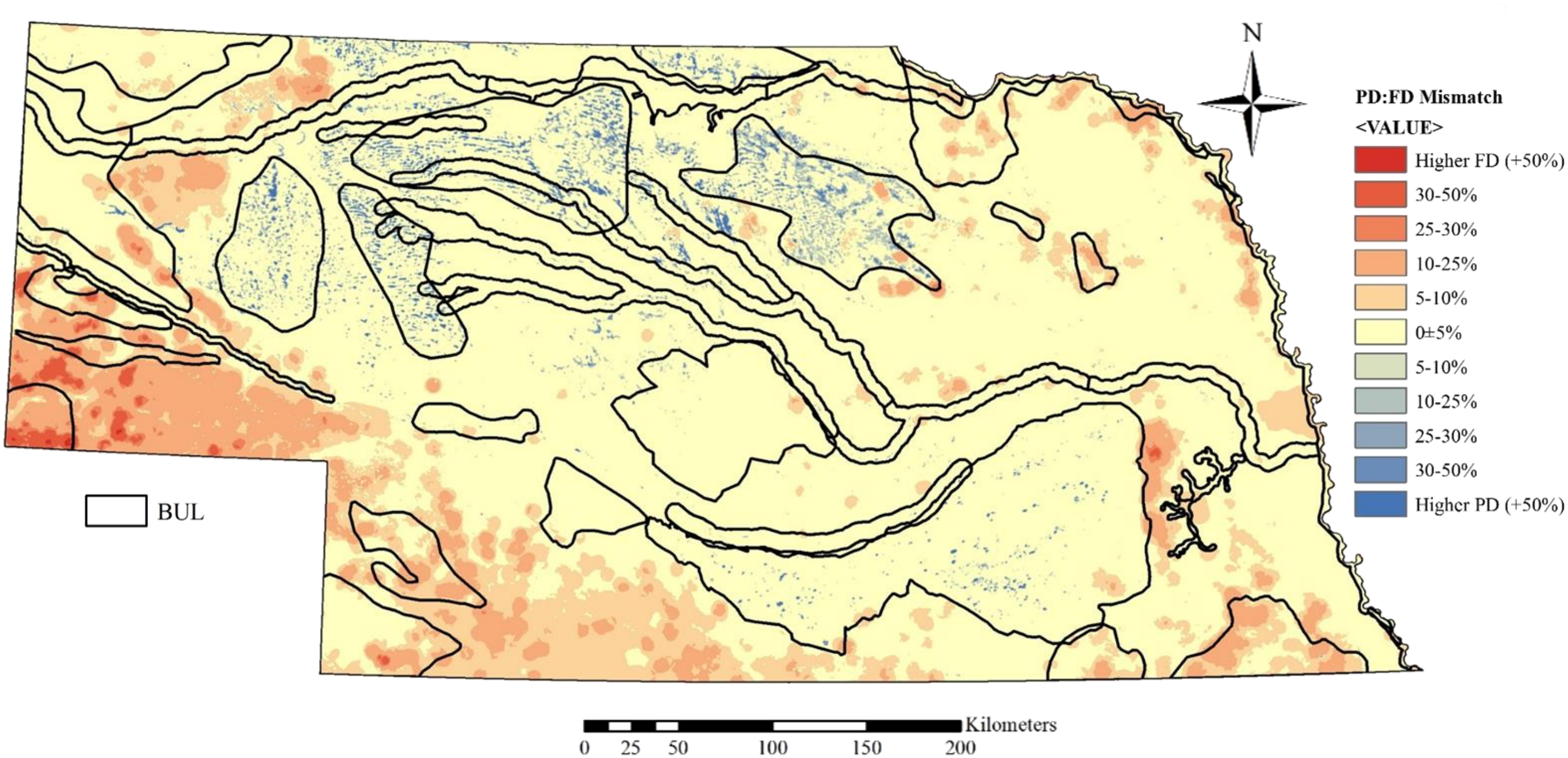

Figure 2. 17

Map of Nebraska's Natural Legacy Biological Unique Landscapes (BUL) and predicted relative phylogenetic diversity (PD) to functional diversity (FD) of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

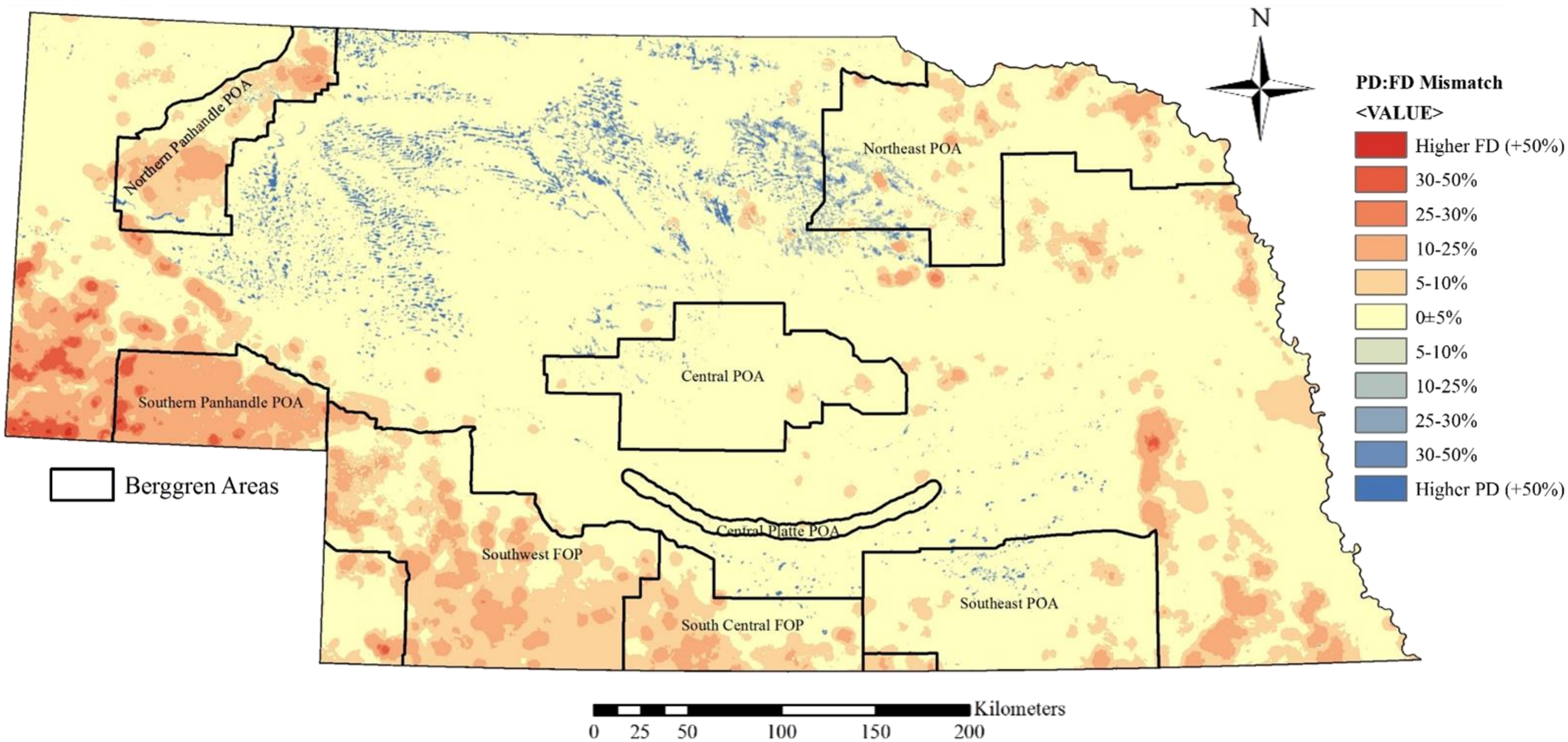

Figure 2. 18

Map of the Berggren Plan for pheasants and predicted relative phylogenetic diversity (PD) to functional diversity (FD) of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

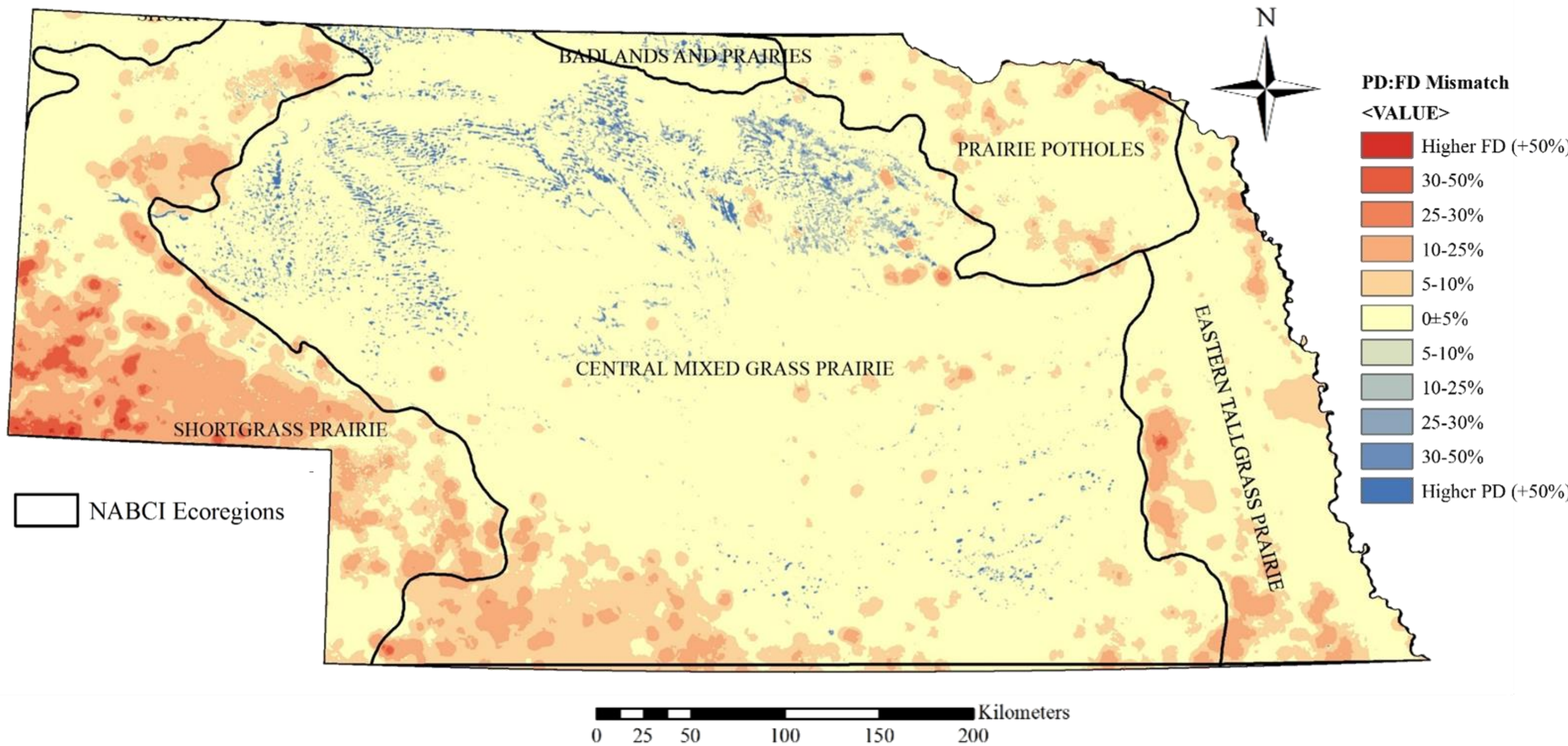

Figure 2. 19

Map of the North America Bird Conservation Initiative's (NABCI) Ecoregions and predicted relative phylogenetic diversity (PD) to functional diversity (FD) of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

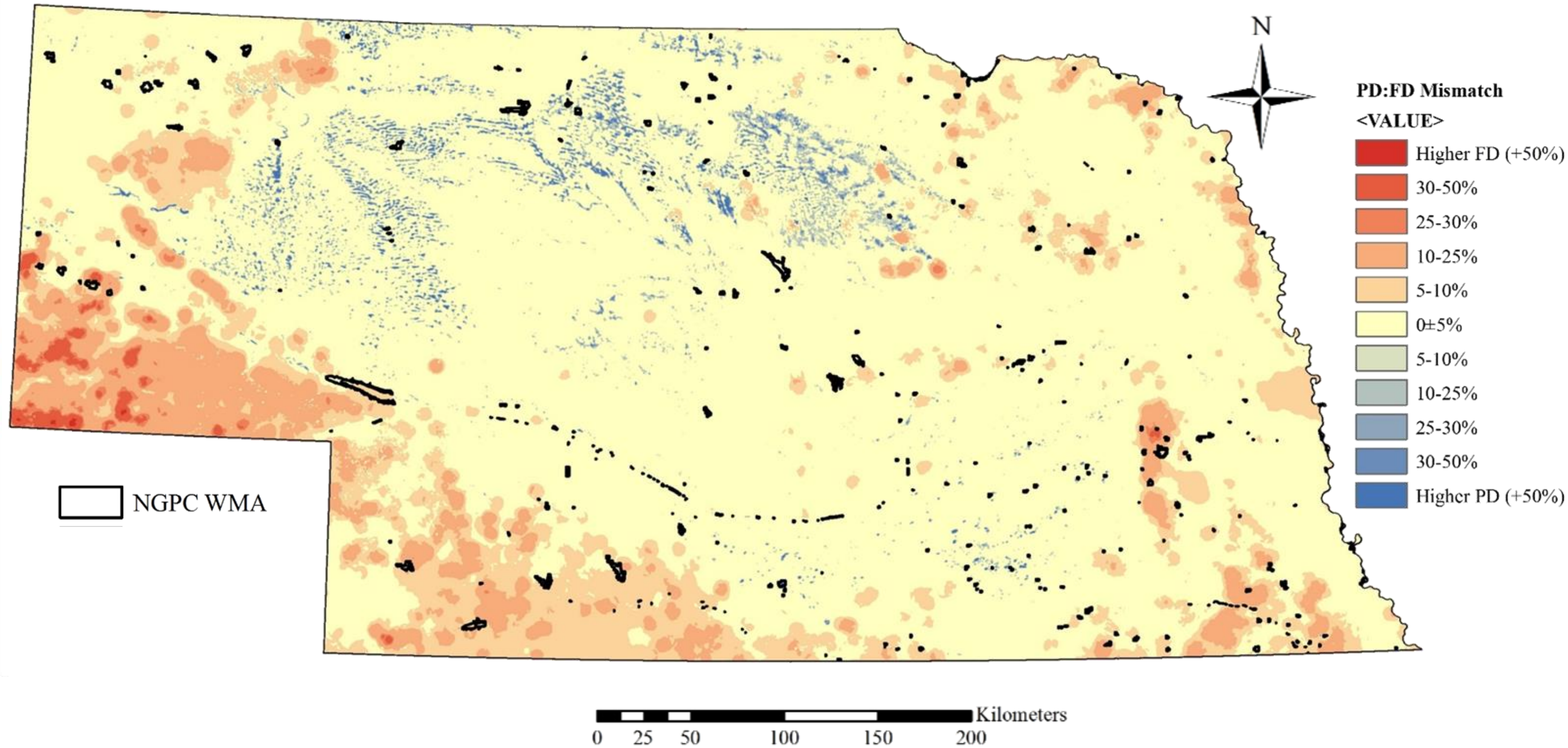

Figure 2. 20

Map of Nebraska Game and Parks Commission's managed lands (NGPC WMA) and predicted relative phylogenetic diversity (PD) to functional diversity (FD) of the birds across the Nebraska, USA across estimated land cover relationship at the spatial scales estimated from Bayesian latent indicator scale selection.

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SUPPLEMENTAL MATERIALS

Table S. 1

Traits included in the creation of the functional dendrogram.

Trait type		Trait	Value type
Resource	1	Body mass	Continuous
quantity	2	Clutch size	Continuous
	3	Mean (no. clutches)	Continuous
	4	Egg length	Continuous
	5	Egg breadth	Continuous
Diet	6	Invertebrates	Percent
	7	Mammals	Percent
	8	Reptiles	Percent
	9	Fish	Percent
	10	Vertebrates (unknown)	Percent
	11	Scavenge	Percent
	12	Fruit	Percent
	13	Nectar or pollen	Percent
	14	Seeds	Percent
	15	Other plant material	Percent
Foraging	16	Below water	Percent
Strategy	17	On water	Percent
	18	On ground	Percent
	19	Below understory	Percent
	20	In middle levels of trees/ bushes	Percent
	21	In canopy	Percent
	22	Aerial	Percent
Foraging period	23	Nocturnal	Binary

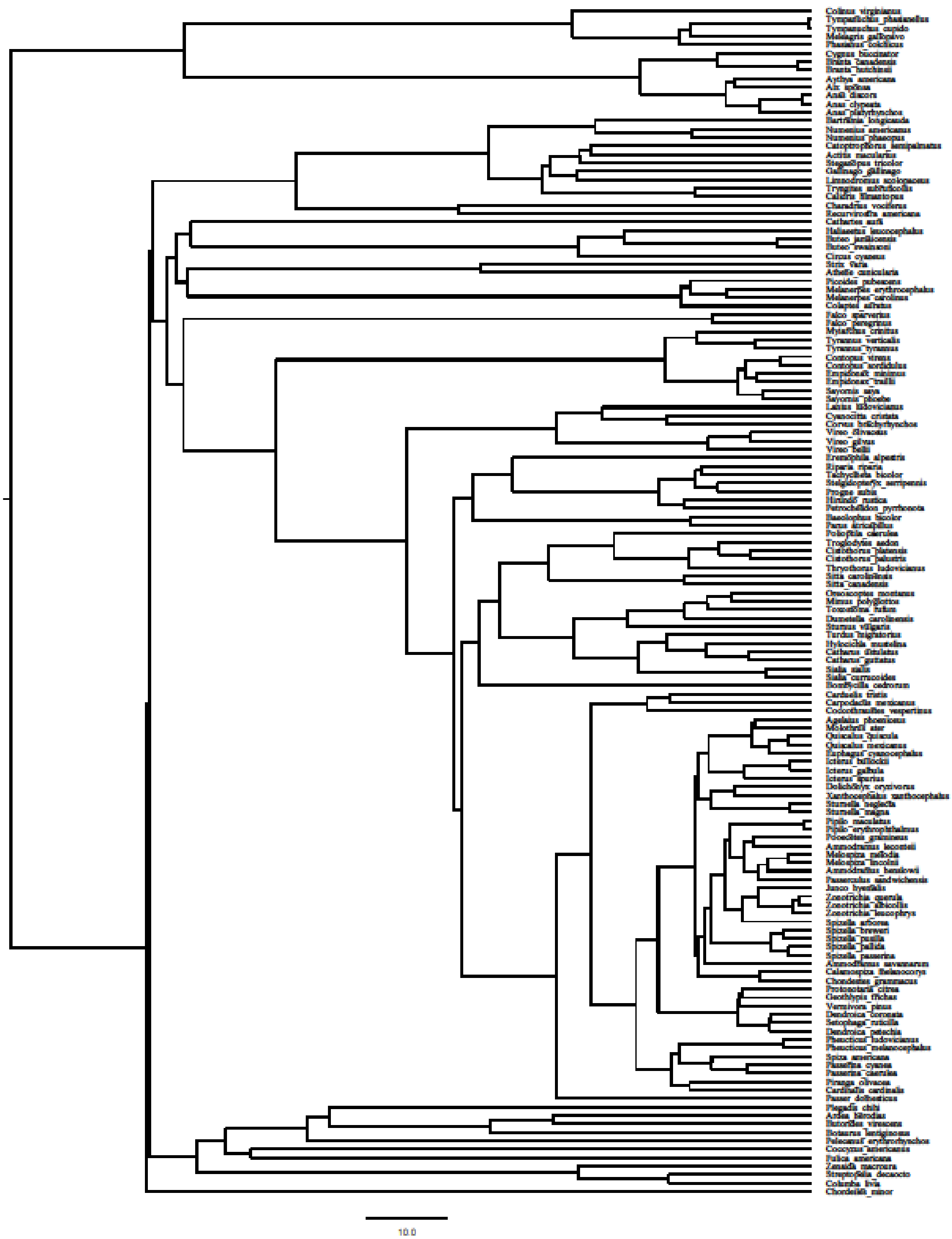

Figure S. 1

Phylogeny of the 141 species detected during point count surveys; phylogeny constructed in program BEAST and Fig Tree (v. 1.4.3). Units are millions of years ago.

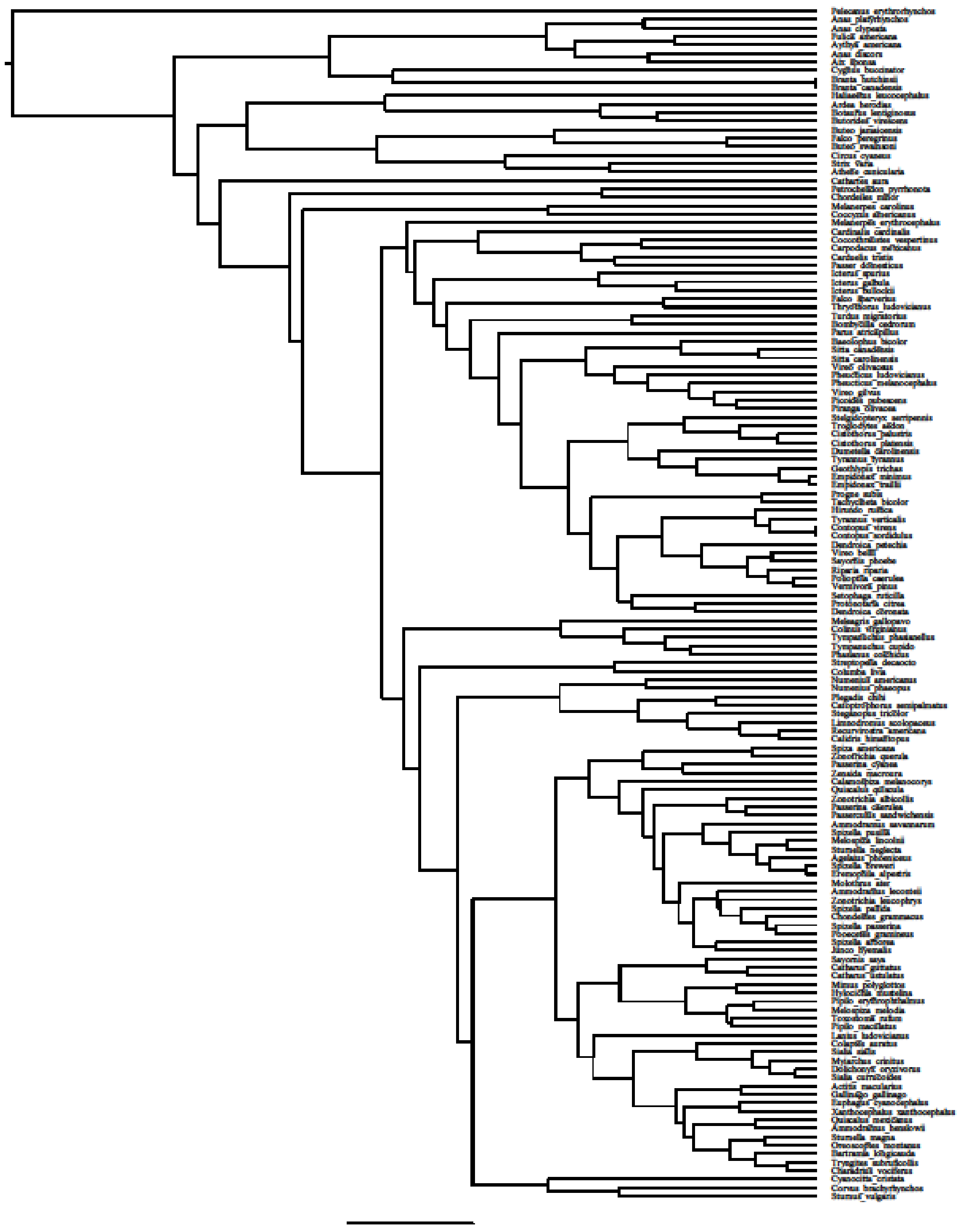

Figure S. 2

Functional dendrogram of the 141 species detected during point count surveys in the 2016 and 2017 field season.

Table S. 2

Species' common name, scientific name, prevalence across surveys, number of times detected, occupancy model checking.

Code	Common Name	Scientific Name	Prevalence	True Skill Statistic	Surveys Detected
AMAV	American Avocet	*Recurvirostra americana*	<0.01	1	4
AMBI	American Bittern	*Botaurus lentiginosus*	<0.01	0.99	10
AMCO	American Coot	*Fulica americana*	<0.01	0.84	14
AMCR	American Crow	*Corvus brachyrhynchos*	0.06	0.93	153
AMGO	American Goldfinch	*Carduelis tristis*	0.05	0.86	135
AMKE	American Kestrel	*Falco sparverius*	<0.01	1	7
AMRE	American Redstart	*Setophaga ruticilla*	<0.01	1	1
AMRO	American Robin	*Turdus migratorius*	0.31	0.76	827
ATSP	American Tree Sparrow	*Spizella arborea*	<0.01	1	1
AWPE	American White Pelican	*Pelecanus erythrorhynchos*	<0.01	1	1
BADO	Barred Owl	*Strix varia*	<0.01	0.86	3
BAEA	Bald Eagle	*Haliaeetus leucocephalus*	<0.01	1	3
BANS	Bank Swallow	*Riparia riparia*	<0.01	1	3

BAOR	Baltimore Oriole	*Icterus galbula*	0.04	0.92	110
BARS	Barn Swallow	*Hirundo rustica*	0.07	0.73	195
BBSA	Buff-breasted Sandpiper	*Tryngites subruficollis*	<0.01	1	1
BCCH	Black-capped Chickadee	*Parus atricapillus*	0.01	0.64	36
BEVI	Bell's Vireo	*Vireo bellii*	0.01	0.99	32
BGGN	Blue-grey Gnatcatcher	*Polioptila caerulea*	<0.01	1	3
BHCO	Brown-headed Cowbird	*Molothrus ater*	0.28	0.41	745
BHGR	Black-headed Grosbeak	*Pheucticus melanocephalus*	<0.01	0.95	2
BLGR	Blue Grosbeak	*Passerina caerulea*	0.02	0.74	51
BLJA	Blue Jay	*Cyanocitta cristata*	0.09	0.89	229
BOBO	Bobolink	*Dolichonyx oryzivorus*	0.03	0.96	84
BRBL	Brewer's Blackbird	*Euphagus cyanocephalus*	<0.01	0.92	8
BRSP	Brewer's Sparrow	*Spizella breweri*	<0.01	1	1
BRTH	Brown Thrasher	*Toxostoma rufum*	0.12	0.83	320
BUOR	Bullock's Oriole	*Icterus bullockii*	<0.01	1	1
BUOW	Burrowing Owl	*Athene cunicularia*	<0.01	1	2

BWTE	Blue-winged Teal	*Anas discors*	0.01	0.98	35
BWWA	Blue-winged Warbler	*Vermivora pinus*	<0.01	1	1
CACG	Cackling Goose	*Branta hutchinsii*	<0.01	1	3
CAGO	Canada Goose	*Branta canadensis*	0.02	0.62	40
CARW	Carolina Wren	*Thryothorus ludovicianus*	<0.01	1	3
CCSP	Clay-coloured Sparrow	*Spizella pallida*	<0.01	0.68	24
CEDW	Cedar Waxwing	*Bombycilla cedrorum*	<0.01	0.84	13
CHSP	Chipping Sparrow	*Spizella passerina*	0.05	0.81	129
CLSW	Cliff Swallow	*Petrochelidon pyrrhonota*	0.02	0.92	57
COGR	Common Grackle	*Quiscalus quiscula*	0.16	0.79	427
CONI	Common Nighthawk	*Chordeiles minor*	0.01	0.99	33
COYE	Common Yellowthroat	*Geothlypis trichas*	0.04	0.62	93
DEJU	Dark-eyed Junco	*Junco hyemalis*	<0.01	1	3
DICK	Dickcissel	*Spiza americana*	0.21	0.64	548
DOWO	Downy Woodpecker	*Picoides pubescens*	<0.01	0.96	6
EABL	Eastern Bluebird	*Sialia sialis*	0.01	0.83	28

EAKI	Eastern Kingbird	*Tyrannus tyrannus*	0.11	0.55	279
EAME	Eastern Meadowlark	*Sturnella magna*	0.07	0.9	195
EAPH	Eastern Phoebe	*Sayornis phoebe*	0.02	0.57	40
EATO	Eastern Towhee	*Pipilo erythrophthalmus*	0.02	0.8	40
EAWP	Eastern Wood-pewee	*Contopus virens*	<0.01	0.79	16
ECDO	Eurasian Collared-dove	*Streptopelia decaocto*	0.03	0.97	71
ETTI	Tufted Titmouse	*Baeolophus bicolor*	<0.01	1	1
EUST	European Starling	*Sturnus vulgaris*	0.03	0.9	77
EVGR	Evening Grosbeak	*Coccothraustes vespertinus*	<0.01	1	1
FISP	Field Sparrow	*Spizella pusilla*	0.11	0.91	283
GBHE	Great Blue Heron	*Ardea herodias*	<0.01	0.76	7
GCFL	Great Crested Flycatcher	*Myiarchus crinitus*	<0.01	0.99	11
GRCA	Grey Catbird	*Dumetella carolinensis*	0.02	0.97	66
GRHE	Green Heron	*Butorides virescens*	<0.01	1	1
GRPC	Greater Prairie-chicken	*Tympanuchus cupido*	0.03	0.96	77

GRSP	Grasshopper Sparrow	*Ammodramus savannarum*	0.32	0.74	840
GTGR	Great-tailed Grackle	*Quiscalus mexicanus*	<0.01	0.87	6
HASP	Harris's Sparrow	*Zonotrichia querula*	<0.01	0.98	7
HESP	Henslow's Sparrow	*Ammodramus henslowii*	<0.01	1	1
HETH	Hermit Thrush	*Catharus guttatus*	<0.01	1	2
HOFI	House Finch	*Carpodacus mexicanus*	<0.01	0.58	7
HOLA	Horned Lark	*Eremophila alpestris*	0.22	0.77	582
HOSP	House Sparrow	*Passer domesticus*	0.01	0.45	39
HOWR	House Wren	*Troglodytes aedon*	0.09	0.93	242
INBU	Indigo Bunting	*Passerina cyanea*	<0.01	1	4
KILL	Killdeer	*Charadrius vociferus*	0.16	0.81	427
LARB	Lark Bunting	*Calamospiza melanocorys*	0.11	0.93	286
LASP	Lark Sparrow	*Chondestes grammacus*	0.05	0.93	123
LBCU	Long-billed Curlew	*Numenius americanus*	<0.01	0.99	15
LBDO	Long-billed Dowitcher	*Limnodromus scolopaceus*	<0.01	1	1

LCSP	Le Conte's Sparrow	*Ammodramus leconteii*	<0.01	1	2
LEFL	Least Flycatcher	*Empidonax minimus*	<0.01	0.93	7
LISP	Lincoln's Sparrow	*Melospiza lincolnii*	<0.01	1	5
LOSH	Loggerhead Shrike	*Lanius ludovicianus*	<0.01	1	12
MALL	Mallard	*Anas platyrhynchos*	0.02	0.98	40
MAWR	Marsh Wren	*Cistothorus palustris*	<0.01	1	7
MOBL	Mountain Bluebird	*Sialia currucoides*	<0.01	1	2
MODO	Mourning Dove	*Zenaida macroura*	0.47	0.37	1236
NOBO	Northern Bobwhite	*Colinus virginianus*	0.17	0.76	451
NOCA	Northern Cardinal	*Cardinalis cardinalis*	0.08	0.89	207
NOFL	Northern Flicker	*Colaptes auratus*	0.04	0.36	102
NOHA	Northern Harrier	*Circus cyaneus*	<0.01	0.91	10
NOMO	Northern Mockingbird	*Mimus polyglottos*	<0.01	0.99	19
NRWS	Northern Rough-winged Swallow	*Stelgidopteryx serripennis*	<0.01	0.86	8
NSHO	Northern Shoveler	*Anas clypeata*	<0.01	0.99	23

OROR	Orchard Oriole	*Icterus spurius*	0.01	0.73	27
PEFA	Peregrine Falcon	*Falco peregrinus*	<0.01	1	1
PROW	Prothonotary Warbler	*Protonotaria citrea*	<0.01	1	3
PUMA	Purple Martin	*Progne subis*	<0.01	1	1
RBGR	Rose-breasted Grosbeak	*Pheucticus ludovicianus*	<0.01	0.69	11
RBNU	Red-breasted Nuthatch	*Sitta canadensis*	<0.01	1	1
RBWO	Red-bellied Woodpecker	*Melanerpes carolinus*	0.04	0.85	109
REDH	Redhead	*Aythya americana*	<0.01	1	1
REVI	Red-eyed Vireo	*Vireo olivaceus*	<0.01	0.95	4
RHWO	Red-headed Woodpecker	*Melanerpes erythrocephalus*	0.05	0.93	137
RNEP	Ring-necked Pheasant	*Phasianus colchicus*	0.37	0.69	990
ROPI	Rock Pigeon	*Columba livia*	<0.01	0.99	17
RTHA	Red-tailed Hawk	*Buteo jamaicensis*	0.01	0.95	39
RWBL	Red-winged Blackbird	*Agelaius phoeniceus*	0.46	0.69	1222
SAPH	Say's Phoebe	*Sayornis saya*	<0.01	0.89	4
SATH	Sage Thrasher	*Oreoscoptes montanus*	<0.01	1	1
SAVS	Savannah Sparrow	*Passerculus sandwichensis*	<0.01	0.93	8

SCTA	Scarlet Tanager	*Piranga olivacea*	<0.01	1	1
SEWR	Sedge Wren	*Cistothorus platensis*	<0.01	0.99	11
SOSP	Song Sparrow	*Melospiza melodia*	0.02	0.97	53
SPSA	Spotted Sandpiper	*Actitis macularius*	<0.01	1	1
SPTO	Spotted Towhee	*Pipilo maculatus*	<0.01	0.99	15
STGR	Sharp-tailed Grouse	*Tympanuchus phasianellus*	<0.01	0.99	13
STSA	Stilt Sandpiper	*Calidris himantopus*	<0.01	1	1
SWHA	Swainson's Hawk	*Buteo swainsoni*	<0.01	1	2
SWTH	Swainson's Thrush	*Catharus ustulatus*	<0.01	1	1
TRES	Tree Swallow	*Tachycineta bicolor*	0.01	0.98	32
TRUS	Trumpeter Swan	*Cygnus buccinator*	<0.01	1	1
TUVU	Turkey Vulture	*Cathartes aura*	0.01	0.52	39
UPSA	Upland Sandpiper	*Bartramia longicauda*	0.1	0.88	262
VESP	Vesper Sparrow	*Pooecetes gramineus*	0.01	0.77	27
WAVI	Warbling Vireo	*Vireo gilvus*	<0.01	0.99	18

WBNU	White-breasted Nuthatch	*Sitta carolinensis*	<0.01	0.87	11
WCSP	White-crowned Sparrow	*Zonotrichia leucophrys*	<0.01	0.98	8
WEKI	Western Kingbird	*Tyrannus verticalis*	0.06	0.91	169
WEME	Western Meadowlark	*Sturnella neglecta*	0.73	0.52	1925
WEWP	Western Wood-pewee	*Contopus sordidulus*	<0.01	1	3
WFIB	White-faced Ibis	*Plegadis chihi*	<0.01	1	1
WHIM	Whimbrel	*Numenius phaeopus*	<0.01	1	1
WIFL	Willow Flycatcher	*Empidonax traillii*	<0.01	1	2
WILL	Willet	*Catoptrophorus semipalmatus*	<0.01	1	3
WIPH	Wilson's Phalarope	*Steganopus tricolor*	<0.01	1	6
WISN	Wilson's Snipe	*Gallinago gallinago*	<0.01	0.93	15
WITU	Wild Turkey	*Meleagris gallopavo*	0.05	0.93	126
WODU	Wood Duck	*Aix sponsa*	<0.01	1	7
WOTH	Wood Thrush	*Hylocichla mustelina*	<0.01	1	1

WTSP	White-throated Sparrow	*Zonotrichia albicollis*	<0.01	1	1
YBCU	Yellow-billed Cuckoo	*Coccyzus americanus*	<0.01	0.83	10
YHBL	Yellow-headed Blackbird	*Xanthocephalus xanthocephalus*	0.02	0.98	48
YRWA	Yellow-rumped Warbler	*Dendroica coronata*	<0.01	0.92	5
YWAR	Yellow Warbler	*Dendroica petechia*	0.04	0.91	118

Table S. 3

Species occupancy modeling outputs for ecological process variables.

Code	Year 1 (2016) (95% CI)	Year 2 (2017) (95% CI)	Grass-linear (95% CI)	Grass-quadratic (95% CI)	Grain-linear (95% CI)	Grain-quadratic (95% CI)	Trees-linear (95% CI)	Trees-quadratic (95% CI)	CRP-linear (95% CI)	Wetland-linear (95% CI)
AMAV	-6.16 (-8.12 , -4.72)	-6.1 (-8.09 , -4.66)	0.77 (-5.32 , 6.81)	-0.05 (-6.09 , 6)	-0.4 (-6.42 , 5.64)	0.2 (-5.86 , 6.22)	-0.37 (-6.43 , 5.63)	0.2 (-5.87 , 6.07)	-0.27 (-6.4 , 5.83)	1.1 (-4.96 , 7.06)
AMBI	-1.99 (-4.57 , 3.53)	-1.5 (-4.23 , 4.59)	1.99 (-4.17 , 8)	0.12 (-5.86 , 6.05)	-0.83 (-6.82 , 5.23)	0.11 (-5.87 , 6.08)	-1.01 (-7.03 , 5.05)	0.79 (-5.25 , 6.8)	-0.87 (-6.9 , 5.18)	2.85 (-3.35 , 8.68)
AMCO	0.52 (-3.09 , 5.91)	1.31 (-2.67 , 6.73)	0.34 (-5.79 , 6.41)	-0.3 (-6.44 , 5.74)	0.09 (-5.92 , 6.14)	0.36 (-5.76 , 6.47)	-0.05 (-6.12 , 6.08)	-0.3 (-6.43 , 5.88)	-0.72 (-6.91 , 5.5)	1.03 (-5.06 , 7.04)
AMCR	-0.93 (-1.43 , -0.33)	-0.57 (-1.12 , 0.14)	-1.5 (-6.03 , 3.06)	0.3 (-4.24 , 4.82)	0.5 (-3.94 , 4.99)	1.01 (-3.39 , 5.55)	1.74 (-2.87 , 6.42)	0.77 (-4.09 , 5.97)	-1.88 (-6.48 , 2.71)	-0.59 (-5.19 , 3.97)
AMGO	-0.03 (-0.91 , 1.78)	0.29 (-0.72 , 2.8)	2.81 (-2.52 , 8)	1.64 (-3.67 , 6.89)	-0.88 (-6.06 , 4.38)	-1.06 (-6.26 , 4.28)	1.39 (-3.8 , 6.65)	-0.19 (-5.18 , 4.96)	-0.19 (-5.52 , 5.25)	-2.3 (-7.78 , 3.52)

AMKE	1.05 (-3.39 , 6.55)	0.66 (-3.72 , 6.19)	-0.25 (-6.34 , 5.92)	-0.38 (-6.5 , 5.77)	0.64 (-5.51 , 6.77)	0.26 (-5.76 , 6.31)	-0.07 (-6.26 , 6.08)	-0.21 (-6.35 , 5.95)	0.18 (-6.01 , 6.3)	-0.33 (-6.47 , 5.84)
AMRE	-2.56 (-7.98 , 4.63)	0.17 (-5.13 , 6.09)	-0.03 (-6.22 , 6.11)	-0.21 (-6.41 , 5.97)	-0.09 (-6.27 , 6.07)	0.07 (-6.13 , 6.24)	-0.05 (-6.24 , 6.07)	-0.02 (-6.22 , 6.16)	-0.07 (-6.2 , 6.11)	-0.08 (-6.3 , 6.06)
AMRO	0.03 (-0.17 , 0.25)	0.38 (0.14 , 0.62)	-2.34 (-5.73 , 1.07)	-1.65 (-5.13 , 1.82)	-3.23 (-6.48 , 0.04)	0.41 (-2.82 , 3.62)	0.02 (-3.59 , 3.65)	-2.8 (-6.51 , 0.78)	1.99 (-1.43 , 5.54)	0.01 (-3.25 , 3.41)
ATSP	-0.07 (-5.11 , 6.04)	-2.55 (-7.76 , 4.01)	0.11 (-6.09 , 6.28)	-0.15 (-6.36 , 6.04)	-0.1 (-6.22 , 6.06)	0.04 (-6.17 , 6.2)	0.69 (-5.5 , 6.89)	0.1 (-6.13 , 6.21)	-0.07 (-6.27 , 6.08)	-0.07 (-6.29 , 6.16)
AWPE	-0.83 (-5.79 , 5.22)	-2.64 (-8.08 , 4.74)	0.03 (-6.11 , 6.17)	-0.31 (-6.45 , 5.86)	0.41 (-5.75 , 6.52)	-0.43 (-6.6 , 5.68)	-0.09 (-6.29 , 6.07)	0.1 (-6.03 , 6.22)	-0.07 (-6.24 , 6.1)	-0.05 (-6.27 , 6.1)
BADO	-3.5 (-8.07 , 1.46)	0.85 (-3.76 , 6.55)	0.09 (-6.06 , 6.25)	0.08 (-6 , 6.19)	-0.19 (-6.36 , 5.97)	0.15 (-5.99 , 6.32)	-0.13 (-6.32 , 6.11)	0.03 (-6.08 , 6.18)	-0.22 (-6.44 , 5.99)	-0.14 (-6.28 , 6.09)
BAEA	-0.94 (-5.27 , 5.03)	0.44 (-4.38 , 6.29)	0.42 (-5.74 , 6.63)	-0.35 (-6.52 , 5.79)	-0.13 (-6.34 , 6.06)	-0.15 (-6.31 , 6.01)	-0.26 (-6.41 , 5.94)	0.18 (-6 , 6.31)	0.15 (-6.05 , 6.26)	1.4 (-4.78 , 7.48)

BANS	-0.67 (-5.39 , 5.67)	0.25 (-4.38 , 6.09)	-0.21 (-6.3 , 5.96)	-0.54 (-6.77 , 5.67)	-0.07 (-6.26 , 6.07)	-0.22 (-6.39 , 5.98)	0.49 (-5.72 , 6.68)	-0.39 (-6.6 , 5.8)	0.37 (-5.74 , 6.54)	-0.18 (-6.35 , 5.95)
BAOR	-0.27 (-1.14 , 1.31)	0.02 (-1.02 , 2.44)	0.39 (-4.82 , 5.66)	-0.2 (-5.49 , 5.1)	-0.97 (-6.11 , 4.33)	-0.49 (-5.89 , 5.07)	0.28 (-5.12 , 5.75)	-0.27 (-5.43 , 4.98)	1.71 (-3.53 , 7.05)	-1.38 (-6.82 , 4.21)
BARS	0.33 (-0.34 , 1.39)	0.72 (-0.09 , 2.37)	-2.95 (-8.25 , 2.42)	-2.85 (-8.12 , 2.58)	0.85 (-4.14 , 5.97)	2.81 (-2.29 , 7.86)	2.14 (-3.1 , 7.51)	0.48 (-4.25 , 5.46)	2.5 (-2.56 , 7.67)	-2.42 (-7.81 , 3.43)
BBSA	-0.41 (-6.17 , 6.11)	-2.64 (-8.15 , 3.86)	-0.07 (-6.19 , 6.15)	-0.23 (-6.43 , 5.92)	0 (-6.13 , 6.19)	-0.17 (-6.26 , 5.97)	-0.09 (-6.27 , 6.1)	0.12 (-6.09 , 6.33)	-0.06 (-6.29 , 6.12)	-0.06 (-6.23 , 6.15)
BCCH	0.7 (-1.89 , 5.61)	1.54 (-1.47 , 6.49)	-1.26 (-7.46 , 5.03)	0.75 (-5.39 , 6.81)	0.41 (-5.53 , 6.31)	0.02 (-5.85 , 5.98)	-0.38 (-6.43 , 5.75)	-0.59 (-6.68 , 5.58)	0.91 (-5.15 , 6.84)	-0.9 (-7.03 , 5.36)
BEVI	-0.7 (-2.45 , 4.08)	-0.92 (-2.61 , 3.39)	0.81 (-4.91 , 6.45)	-0.49 (-6.1 , 5.2)	1.34 (-4.33 , 6.94)	-1.49 (-7.19 , 4.31)	-0.62 (-6.42 , 5.28)	0.66 (-5.23 , 6.55)	-1.68 (-7.51 , 4.29)	-0.15 (-5.89 , 5.59)
BGGN	0.48 (-4.05 , 6.23)	-0.68 (-5.02 , 5.29)	-0.25 (-6.38 , 5.88)	0.65 (-5.55 , 6.82)	-0.28 (-6.47 , 5.86)	0.16 (-6.04 , 6.34)	-0.18 (-6.31 , 6.01)	-0.06 (-6.24 , 6.13)	0.5 (-5.67 , 6.63)	-0.18 (-6.37 , 5.98)

BHCO	1.66 (1.14 , 2.38)	1.46 (0.96 , 2.13)	0.56 (-4.49 , 5.65)	-1.26 (-6.33 , 3.82)	-0.84 (-5.56 , 4.19)	-0.25 (-5.22 , 4.88)	0.12 (-4.82 , 5.4)	-3.33 (-8.36 , 2.41)	-2.21 (-6.94 , 3.02)	2.22 (-2.36 , 7.16)
BHGR	-2.49 (-7.95 , 4.82)	0.62 (-4.07 , 6)	0.32 (-5.82 , 6.5)	-0.02 (-6.19 , 6.14)	-0.14 (-6.34 , 6.05)	0.1 (-6.04 , 6.25)	0.15 (-6.09 , 6.36)	-0.38 (-6.59 , 5.81)	-0.13 (-6.32 , 6.03)	0.07 (-6.13 , 6.24)
BLGR	-0.5 (-1.94 , 1.63)	1.27 (-1.1 , 6.41)	-1.3 (-7.12 , 4.59)	0.23 (-5.61 , 5.95)	2.83 (-3.64 , 8.78)	-1 (-6.38 , 4.51)	-1.25 (-7.11 , 4.68)	0.48 (-5.27 , 6.41)	0.91 (-4.98 , 6.67)	-1.61 (-7.65 , 4.6)
BLJA	-0.42 (-0.83 , 0.06)	-0.55 (-0.96 , -0.09)	-4.35 (-8.7 , -0.02)	0.82 (-3.56 , 5.21)	-0.34 (-4.59 , 3.99)	1.54 (-2.63 , 5.8)	1.73 (-2.74 , 6.31)	-0.56 (-5.24 , 4.53)	-0.76 (-4.99 , 3.52)	-0.73 (-4.94 , 3.54)
BOBO	-1.66 (-2.14 , -1.13)	-1.93 (-2.46 , -1.37)	3.22 (-1.63 , 8.09)	-0.96 (-5.76 , 3.84)	-0.51 (-5.35 , 4.2)	0.55 (-4.21 , 5.3)	-0.79 (-5.9 , 4.19)	-1.76 (-6.92 , 3.24)	-1.43 (-6.46 , 3.43)	7.09 (2.81 , 11.47)
BRBL	-0.04 (-3.94 , 5.74)	1.12 (-3.23 , 6.75)	0.03 (-6.1 , 6.19)	-0.59 (-6.79 , 5.67)	0.35 (-5.72 , 6.37)	-0.89 (-7.05 , 5.27)	-0.13 (-6.31 , 5.98)	-0.27 (-6.4 , 5.9)	0.31 (-5.78 , 6.4)	1.26 (-4.95 , 7.31)
BRSP	-0.77 (-6.57 , 5.63)	-2.92 (-8.45 , 4.57)	0.03 (-6.14 , 6.15)	-0.25 (-6.4 , 5.96)	-0.1 (-6.26 , 6.12)	0.07 (-6.15 , 6.34)	0.76 (-5.45 , 6.96)	0.04 (-6.1 , 6.13)	-0.06 (-6.27 , 6.15)	-0.07 (-6.19 , 6.06)

BRTH	0.11 (-0.33 , 0.64)	0.1 (-0.34 , 0.65)	-1.03 (-5.45 , 3.44)	0.88 (-3.65 , 5.39)	-0.93 (-5.28 , 3.59)	-0.83 (-5.15 , 3.61)	-0.24 (-4.71 , 4.41)	-0.02 (-4.58 , 4.78)	0.33 (-3.97 , 4.86)	-2.63 (-7.21 , 2.11)
BUOR	-2.96 (-8.19 , 3.58)	-0.47 (-5.82 , 6.05)	0.1 (-6.09 , 6.29)	-0.21 (-6.35 , 5.99)	0.03 (-6.13 , 6.14)	-0.29 (-6.43 , 5.85)	-0.09 (-6.26 , 6.08)	0.04 (-6.13 , 6.22)	-0.08 (-6.26 , 6.04)	-0.09 (-6.26 , 6.13)
BUOW	-0.76 (-5.59 , 5.4)	-0.67 (-5.66 , 5.58)	0.51 (-5.73 , 6.69)	0.16 (-5.99 , 6.33)	-0.23 (-6.35 , 5.92)	0.09 (-6.08 , 6.21)	-0.05 (-6.25 , 6.14)	-0.07 (-6.24 , 6.11)	0.02 (-6.15 , 6.22)	0.05 (-6.08 , 6.18)
BWTE	-2.69 (-3.56 , -1.64)	-2.36 (-3.19 , -1.31)	3.63 (-1.65 , 8.92)	1.68 (-3.65 , 6.98)	-0.1 (-5.43 , 5.13)	0.6 (-4.75 , 5.89)	-1.06 (-6.66 , 4.43)	0.02 (-5.53 , 5.45)	-2.81 (-8.49 , 2.71)	4.57 (-0.37 , 9.39)
BWWA	-2.97 (-8.19 , 3.3)	-0.22 (-5.74 , 6.17)	0.03 (-6.14 , 6.24)	-0.22 (-6.42 , 5.92)	-0.11 (-6.3 , 6.03)	0.1 (-6.12 , 6.29)	0.01 (-6.22 , 6.14)	-0.05 (-6.26 , 6.16)	-0.07 (-6.24 , 6.08)	-0.08 (-6.29 , 6.05)
CACG	-1.33 (-5.72 , 4.29)	0.21 (-4.74 , 6.32)	-0.39 (-6.52 , 5.79)	-0.03 (-6.19 , 6.18)	-0.3 (-6.46 , 5.85)	0.19 (-6.02 , 6.36)	0.78 (-5.43 , 6.95)	-0.8 (-6.97 , 5.35)	0.14 (-6.03 , 6.34)	-0.18 (-6.36 , 5.94)
CAGO	1.89 (-1.39 , 6.96)	1.65 (-1.55 , 6.79)	1.04 (-5.14 , 7.14)	0.43 (-5.64 , 6.45)	-1.26 (-7.64 , 5.21)	0.2 (-5.92 , 6.27)	-0.88 (-7.14 , 5.42)	0.18 (-6.01 , 6.29)	-0.7 (-6.87 , 5.53)	0.76 (-5.33 , 6.81)

CARW	-0.27 (-4.51 , 5.83)	-1.15 (-5.41 , 5.16)	0.17 (-5.94 , 6.34)	0.4 (-5.72 , 6.48)	-0.37 (-6.52 , 5.71)	0.24 (-5.95 , 6.41)	0.06 (-6.11 , 6.24)	-0.39 (-6.57 , 5.81)	0.56 (-5.55 , 6.66)	-0.18 (-6.34 , 6.06)
CCSP	2.2 (-1.62 , 7.28)	0.55 (-2.25 , 5)	0.34 (-5.79 , 6.38)	-0.34 (-6.41 , 5.76)	-0.36 (-6.41 , 5.77)	0.23 (-5.84 , 6.38)	1.07 (-5.08 , 7.17)	-1.39 (-7.57 , 4.91)	-0.28 (-6.4 , 5.9)	-0.39 (-6.58 , 5.79)
CEDW	1.23 (-3.18 , 6.79)	0.97 (-3.2 , 6.67)	-0.63 (-6.77 , 5.54)	-0.04 (-6.12 , 6)	-0.45 (-6.62 , 5.81)	-0.21 (-6.27 , 5.82)	0.62 (-5.53 , 6.72)	-0.38 (-6.48 , 5.78)	0.63 (-5.52 , 6.69)	-0.45 (-6.53 , 5.74)
CHSP	-0.23 (-1.09 , 1.08)	0.66 (-0.59 , 3.98)	-0.09 (-5.34 , 5.21)	-0.93 (-6.21 , 4.42)	-0.85 (-6.13 , 4.61)	-2.14 (-7.47 , 3.29)	1.01 (-4.19 , 6.36)	-0.34 (-5.63 , 5.25)	-0.35 (-5.84 , 5.26)	-3.58 (-9.18 , 2.55)
CLSW	-0.11 (-1.28 , 2.87)	-1.36 (-2.33 , -0.05)	-1.48 (-6.94 , 4.09)	0.38 (-5.1 , 5.92)	0.65 (-4.74 , 5.99)	-0.05 (-5.38 , 5.34)	-0.04 (-5.64 , 5.62)	-1.21 (-6.92 , 4.56)	2.67 (-2.85 , 8.13)	-1.44 (-7.16 , 4.43)
COGR	-0.04 (-0.36 , 0.31)	0.24 (-0.12 , 0.65)	-1.3 (-5.39 , 2.83)	-1.02 (-5.29 , 3.24)	0.72 (-3.31 , 4.86)	-2.19 (-6.14 , 1.75)	0.03 (-4.31 , 4.53)	-1.13 (-5.63 , 3.64)	-1.69 (-5.75 , 2.49)	-1.15 (-5.25 , 3.13)
CONI	-0.66 (-2.49 , 3.89)	-0.49 (-2.39 , 4)	2.36 (-3.66 , 8.16)	1.15 (-4.68 , 6.9)	2.34 (-3.44 , 7.99)	0.3 (-5.2 , 5.81)	-1.04 (-6.81 , 4.74)	1.49 (-4.51 , 7.51)	0.46 (-5.24 , 6.2)	0.41 (-5.38 , 6.21)

COYE	1.38 (-0.27 , 5.35)	2.12 (-0.03 , 6.63)	0.51 (-5.43 , 6.43)	0.48 (-5.6 , 6.49)	-0.43 (-6.32 , 5.67)	0.15 (-5.71 , 6.09)	-0.08 (-6 , 5.96)	0.28 (-5.74 , 6.3)	-1.77 (-7.93 , 4.64)	0.74 (-5.03 , 6.54)
DEJU	0.16 (-4.32 , 6.07)	-0.46 (-5.24 , 5.61)	-0.62 (-6.76 , 5.48)	0.2 (-5.91 , 6.36)	-0.32 (-6.46 , 5.8)	0.17 (-5.98 , 6.34)	-0.02 (-6.19 , 6.17)	-0.09 (-6.24 , 6.09)	0.81 (-5.3 , 6.94)	0.03 (-6.13 , 6.25)
DICK	1.58 (0.98 , 2.39)	2.05 (1.18 , 3.66)	-2 (-7.44 , 3.43)	1.48 (-4.01 , 6.91)	0.61 (-4.73 , 6.19)	0.74 (-4.71 , 6.25)	-0.85 (-6.35 , 4.97)	-1.33 (-6.7 , 4.6)	-1.2 (-6.62 , 4.5)	-0.44 (-5.68 , 5.21)
DOWO	0.83 (-3.62 , 6.2)	1.03 (-3.54 , 6.23)	0.12 (-6.05 , 6.22)	0.19 (-5.96 , 6.34)	0.25 (-5.9 , 6.43)	-0.18 (-6.35 , 5.99)	0 (-6.16 , 6.17)	-0.38 (-6.55 , 5.84)	-0.35 (-6.61 , 5.91)	-0.29 (-6.47 , 5.9)
EABL	1.1 (-1.78 , 6.1)	1.58 (-1.56 , 6.55)	-0.52 (-6.59 , 5.65)	-0.49 (-6.54 , 5.61)	-0.04 (-6.05 , 5.99)	0.06 (-5.98 , 6.15)	1.94 (-4.34 , 8.05)	0.75 (-5.28 , 6.67)	0.08 (-5.86 , 6.05)	-0.72 (-6.88 , 5.54)
EAKI	0.62 (-0.1 , 1.9)	0.69 (-0.05 , 2.07)	0.88 (-4.16 , 5.88)	0.58 (-4.47 , 5.55)	0.22 (-4.68 , 5.33)	-0.62 (-5.69 , 4.72)	0.81 (-4.32 , 6.21)	-1.33 (-6.74 , 4.38)	-1.8 (-6.75 , 3.55)	2.28 (-2.62 , 7.46)
EAME	-0.41 (-0.83 , 0.05)	-0.33 (-0.78 , 0.17)	-0.82 (-5.38 , 3.72)	1.95 (-2.68 , 6.6)	1.78 (-2.59 , 6.32)	2.38 (-2.07 , 6.92)	3.5 (-1.21 , 8.3)	-2.28 (-7.19 , 2.79)	-1.96 (-6.5 , 2.64)	1.75 (-2.89 , 6.53)

EAPH	0.44 (-1.71 , 4.85)	2.08 (-1.03 , 6.71)	-0.08 (-6.1 , 5.97)	-0.95 (-7.08 , 5.23)	-0.79 (-6.8 , 5.43)	0.44 (-5.77 , 6.55)	0.74 (-5.29 , 6.73)	-1.19 (-7.34 , 5.05)	0.84 (-5.24 , 6.84)	-0.65 (-6.75 , 5.63)
EATO	1.04 (-1.45 , 6.26)	0.09 (-1.89 , 4.27)	0.67 (-5.3 , 6.57)	-0.69 (-6.54 , 5.25)	-1.38 (-7.32 , 4.84)	0.21 (-5.74 , 6.2)	1.77 (-4.38 , 7.65)	-0.5 (-6.51 , 5.51)	0.29 (-5.62 , 6.18)	-1.09 (-7.17 , 5.17)
EAWP	0.65 (-2.24 , 5.69)	2.32 (-1.43 , 7.05)	0.65 (-5.48 , 6.81)	0.58 (-5.57 , 6.72)	-0.29 (-6.46 , 5.84)	-0.07 (-6.31 , 6.06)	-0.32 (-6.49 , 5.87)	-0.06 (-6.27 , 6.12)	0.22 (-5.97 , 6.37)	-0.44 (-6.63 , 5.76)
ECDO	-1.83 (-2.39 , -1.15)	-1.97 (-2.57 , -1.28)	1.09 (-3.87 , 6.04)	-1.83 (-6.73 , 3.05)	-0.92 (-5.88 , 3.94)	-1.59 (-6.51 , 3.18)	-1.99 (-7.18 , 3.05)	-0.53 (-5.76 , 4.54)	-1.37 (-6.44 , 3.56)	0.73 (-3.98 , 5.3)
ETTI	-3.46 (-8.4 , 3.67)	-1.16 (-5.89 , 5.35)	-0.24 (-6.46 , 5.97)	0.04 (-6.11 , 6.15)	-0.13 (-6.29 , 6.02)	0.05 (-6.21 , 6.24)	1.14 (-5.05 , 7.29)	0.81 (-5.33 , 6.93)	-0.11 (-6.24 , 6.07)	-0.05 (-6.15 , 6.08)
EUST	-0.17 (-1.49 , 2.92)	0.19 (-1.28 , 4.08)	-1.95 (-7.42 , 3.68)	-0.13 (-5.61 , 5.39)	1.56 (-4 , 7.01)	-2.31 (-7.65 , 3.38)	-0.82 (-6.35 , 4.89)	1.13 (-4.69 , 6.99)	-0.51 (-5.91 , 5.08)	-0.47 (-6.02 , 5.23)
EVGR	-0.23 (-5.33 , 5.96)	-2.5 (-7.83 , 4.42)	0.33 (-5.89 , 6.52)	0.3 (-5.85 , 6.48)	-0.14 (-6.33 , 6.05)	0.04 (-6.08 , 6.24)	-0.07 (-6.17 , 6.03)	0.07 (-6.04 , 6.23)	-0.09 (-6.26 , 6.08)	-0.03 (-6.19 , 6.07)

FISP	-0.57 (-0.91 , -0.2)	-0.55 (-0.9 , -0.17)	-1.85 (-5.89 , 2.16)	1.33 (-2.75 , 5.37)	0.49 (-3.4 , 4.49)	-0.68 (-4.62 , 3.36)	1.73 (-2.42 , 5.93)	-2.15 (-6.48 , 2.3)	1.52 (-2.41 , 5.55)	-3.93 (-8.36 , 0.31)
GBHE	-4.37 (-8.4 , -1.09)	1.03 (-2.85 , 6.5)	-0.23 (-6.35 , 5.9)	0.28 (-5.82 , 6.41)	-0.15 (-6.26 , 6.03)	-0.07 (-6.19 , 6.09)	0.43 (-5.66 , 6.51)	-0.04 (-6.2 , 6.06)	0.57 (-5.55 , 6.69)	-0.34 (-6.5 , 5.81)
GCFL	-2.74 (-5.27 , 1.16)	-0.56 (-3.37 , 4.99)	0.57 (-5.52 , 6.57)	-0.54 (-6.56 , 5.57)	-0.87 (-6.89 , 5.14)	0.2 (-5.8 , 6.18)	-0.18 (-6.19 , 5.84)	-0.05 (-6 , 5.88)	1.19 (-4.83 , 7.11)	-0.16 (-6.22 , 5.9)
GRCA	-0.84 (-1.73 , 0.54)	-0.61 (-1.57 , 1.05)	-1.49 (-6.8 , 3.9)	0.38 (-5.03 , 5.75)	0.39 (-4.93 , 5.65)	-0.79 (-6 , 4.46)	0.89 (-4.59 , 6.37)	-0.6 (-5.83 , 4.62)	-0.29 (-5.55 , 5)	-1.56 (-7.17 , 4.16)
GRHE	-0.59 (-6.43 , 5.96)	-2.91 (-8.55 , 4.2)	0.29 (-5.9 , 6.48)	0.11 (-6.02 , 6.29)	-0.12 (-6.29 , 6.06)	0.04 (-6.12 , 6.19)	-0.14 (-6.29 , 5.94)	0.07 (-6.15 , 6.24)	-0.08 (-6.24 , 6.08)	-0.1 (-6.31 , 6.09)
GRPC	-0.63 (-1.55 , 1.13)	-0.84 (-1.69 , 0.65)	1.17 (-4.09 , 6.33)	3.41 (-1.86 , 8.55)	1.39 (-3.78 , 6.58)	0.6 (-4.47 , 5.7)	-1.06 (-6.57 , 4.48)	-1.77 (-7.27 , 3.81)	-1.57 (-6.93 , 3.82)	3.4 (-1.32 , 8.06)
GRSP	0.39 (0.17 , 0.61)	0.27 (0.05 , 0.49)	2.16 (-1.32 , 5.63)	1.43 (-2 , 4.9)	4.89 (1.43 , 8.5)	0.84 (-2.63 , 4.46)	0.07 (-3.49 , 3.77)	2.06 (-1.39 , 5.73)	1.23 (-2.19 , 4.74)	-3.2 (-6.55 , 0.1)

GTGR	-2.11 (-5.61 , 3.35)	0.87 (-3.44 , 6.59)	0.55 (-5.65 , 6.68)	-0.17 (-6.27 , 5.98)	-0.27 (-6.4 , 5.92)	-0.28 (-6.38 , 5.87)	-0.09 (-6.24 , 5.97)	0.02 (-6.11 , 6.15)	-0.41 (-6.57 , 5.8)	0.39 (-5.75 , 6.48)
HASP	0.79 (-3.29 , 6.15)	0.25 (-3.56 , 5.29)	-0.53 (-6.67 , 5.66)	-0.45 (-6.6 , 5.75)	0.36 (-5.79 , 6.45)	-0.11 (-6.23 , 6.03)	0.79 (-5.46 , 6.96)	-0.17 (-6.3 , 5.99)	-0.49 (-6.66 , 5.68)	-0.2 (-6.33 , 5.9)
HESP	-3.68 (-8.73 , 2.56)	-1.59 (-6.59 , 4.79)	0.05 (-6.13 , 6.2)	-0.33 (-6.45 , 5.77)	-0.12 (-6.29 , 6.06)	0.08 (-6.09 , 6.21)	1.27 (-4.91 , 7.42)	1.17 (-4.96 , 7.27)	-0.08 (-6.18 , 6.11)	-0.03 (-6.19 , 6.1)
HETH	-0.16 (-4.94 , 6.16)	-0.05 (-4.97 , 6.2)	0.52 (-5.64 , 6.71)	0.13 (-6.1 , 6.32)	-0.19 (-6.37 , 6.04)	0.13 (-6.07 , 6.3)	-0.13 (-6.27 , 6.1)	0.02 (-6.18 , 6.22)	0.29 (-5.9 , 6.46)	-0.18 (-6.38 , 6.01)
HOFI	1.26 (-2.97 , 6.75)	-4.04 (-8.31 , -0.12)	0.12 (-6.02 , 6.24)	0.12 (-6.05 , 6.29)	-0.29 (-6.5 , 5.86)	-0.12 (-6.24 , 6.06)	-0.32 (-6.45 , 5.83)	0.01 (-6.16 , 6.15)	0.22 (-5.92 , 6.38)	-0.23 (-6.38 , 5.98)
HOLA	0.05 (-0.19 , 0.32)	0.09 (-0.17 , 0.38)	-2.3 (-6.04 , 1.4)	-2.91 (-6.63 , 0.79)	0.49 (-3.06 , 4.13)	0.37 (-3.01 , 3.8)	-0.24 (-4.03 , 3.73)	2.14 (-1.49 , 6.08)	-0.22 (-3.92 , 3.6)	-1.37 (-4.93 , 2.29)
HOSP	2.16 (-0.84 , 6.87)	2.61 (-0.67 , 7.42)	-0.51 (-6.68 , 5.7)	-0.22 (-6.38 , 5.93)	0.33 (-5.7 , 6.37)	0.23 (-5.79 , 6.21)	0.45 (-5.69 , 6.5)	0.32 (-5.89 , 6.56)	0.88 (-5.33 , 7.01)	-0.33 (-6.53 , 5.95)

HOWR	-1.21 (-1.53 , -0.88)	-0.9 (-1.22 , -0.57)	-2.35 (-6.39 , 1.65)	-0.37 (-4.44 , 3.67)	1.34 (-2.52 , 5.2)	1.61 (-2.16 , 5.43)	0.26 (-4.06 , 4.54)	-4.95 (-9.53 , -0.59)	0.46 (-3.43 , 4.32)	-2.07 (-6.29 , 1.93)
INBU	-1.6 (-5.51 , 4.16)	0.49 (-3.96 , 6.2)	0.21 (-5.94 , 6.4)	0.59 (-5.64 , 6.76)	-0.3 (-6.41 , 5.88)	-0.06 (-6.19 , 6.06)	0.48 (-5.66 , 6.52)	0.79 (-5.34 , 6.94)	-0.31 (-6.44 , 5.84)	-0.23 (-6.43 , 5.93)
KILL	0.09 (-0.23 , 0.45)	-0.12 (-0.43 , 0.23)	0.86 (-3.14 , 4.83)	0.89 (-3.08 , 4.86)	0.45 (-3.36 , 4.37)	-0.29 (-4 , 3.47)	-1.13 (-5.26 , 3.1)	0.77 (-3.22 , 4.99)	-0.15 (-4.04 , 3.84)	2.01 (-1.83 , 6.07)
LARB	-1.03 (-1.3 , -0.76)	-1.18 (-1.46 , -0.89)	-0.36 (-4.21 , 3.51)	-0.92 (-4.75 , 2.92)	0.08 (-3.64 , 3.79)	-2.54 (-6.25 , 1.08)	-1.58 (-5.68 , 2.42)	1.53 (-2.32 , 5.29)	-0.49 (-4.4 , 3.36)	-1.15 (-5.15 , 2.72)
LASP	-0.59 (-1.26 , 0.36)	-0.65 (-1.33 , 0.29)	-0.65 (-5.47 , 4.16)	-0.89 (-5.77 , 3.97)	-0.38 (-5.14 , 4.46)	0.25 (-4.57 , 5.08)	2.55 (-2.21 , 7.41)	1.69 (-2.97 , 6.58)	2.43 (-2.27 , 7.16)	-1.27 (-6.27 , 3.77)
LBCU	-2.74 (-4 , -0.42)	-3.96 (-5.61 , -1.72)	3.42 (-2.32 , 9.15)	2.05 (-3.68 , 7.8)	-1.2 (-7.04 , 4.57)	-0.25 (-6.02 , 5.48)	-1.62 (-7.48 , 4.15)	0.88 (-4.88 , 6.52)	-1.47 (-7.38 , 4.35)	0.5 (-5.3 , 6.14)
LBDO	-0.46 (-5.44 , 5.5)	-3.08 (-8.26 , 2.83)	-0.14 (-6.3 , 5.98)	-0.15 (-6.31 , 6.05)	-0.11 (-6.24 , 6.05)	0.06 (-6.13 , 6.22)	-0.13 (-6.33 , 6.03)	0.09 (-6.11 , 6.34)	-0.11 (-6.35 , 6.04)	0.02 (-6.11 , 6.16)

LCSP	-0.53 (-5.16 , 5.54)	-0.47 (-5.12 , 5.57)	0.23 (-5.96 , 6.41)	0.22 (-5.94 , 6.39)	-0.12 (-6.29 , 6.09)	-0.16 (-6.28 , 6.03)	-0.23 (-6.47 , 5.93)	0.16 (-6.04 , 6.35)	0.2 (-6.04 , 6.37)	-0.13 (-6.36 , 6.09)
LEFL	1 (-3.3 , 6.23)	-0.55 (-4.39 , 5.55)	0.64 (-5.65 , 6.82)	-0.05 (-6.21 , 6.14)	-0.45 (-6.62 , 5.64)	0.14 (-5.99 , 6.28)	0.69 (-5.49 , 6.85)	-0.45 (-6.61 , 5.71)	-0.46 (-6.64 , 5.72)	0.28 (-5.88 , 6.37)
LISP	0.47 (-3.96 , 6.21)	-0.27 (-4.31 , 5.14)	-0.3 (-6.5 , 5.86)	-0.16 (-6.33 , 5.97)	-0.35 (-6.64 , 5.86)	-0.06 (-6.2 , 6.07)	0.34 (-5.82 , 6.5)	-0.64 (-6.86 , 5.53)	-0.13 (-6.35 , 6.11)	-0.25 (-6.41 , 5.94)
LOSH	-4.14 (-5.79 , -2.01)	-3.17 (-4.52 , -0.98)	-0.3 (-6.11 , 5.5)	0.57 (-5.22 , 6.38)	2 (-3.71 , 7.63)	0.31 (-5.31 , 5.93)	-1.33 (-7.25 , 4.52)	0.92 (-4.92 , 6.65)	-1.02 (-6.95 , 4.77)	-0.36 (-6.26 , 5.39)
MALL	-0.35 (-2.46 , 4.46)	-0.17 (-2.4 , 5.06)	1.85 (-4.06 , 7.54)	1.22 (-4.61 , 6.92)	0 (-5.65 , 5.67)	0.4 (-5.4 , 6.11)	-1.05 (-6.86 , 4.94)	0.29 (-5.57 , 6.18)	-2.29 (-8.28 , 4.04)	2.35 (-3.71 , 8.06)
MAWR	-3.81 (-6.83 , 0.38)	-1.73 (-4.55 , 4.88)	0.73 (-5.31 , 6.75)	-1.49 (-7.55 , 4.63)	-0.87 (-6.89 , 5.14)	0.57 (-5.46 , 6.57)	-0.51 (-6.58 , 5.56)	0.2 (-5.86 , 6.21)	0.73 (-5.3 , 6.68)	1.52 (-4.47 , 7.4)
MOBL	-1.01 (-5.85 , 5.1)	-0.73 (-5.8 , 5.68)	0.03 (-6.19 , 6.19)	-0.5 (-6.68 , 5.74)	-0.22 (-6.35 , 5.98)	0.13 (-6.02 , 6.25)	-0.15 (-6.34 , 5.99)	0.03 (-6.1 , 6.12)	0.18 (-6.01 , 6.3)	-0.12 (-6.24 , 6.01)

MODO	1.91 (1.52 , 2.4)	2.61 (1.99 , 3.61)	0.28 (-4.77 , 5.31)	-0.08 (-5.29 , 5.01)	3.14 (-1.76 , 8.2)	-0.35 (-5.11 , 4.57)	1.86 (-3.06 , 7.08)	-1.74 (-6.6 , 3.84)	-0.21 (-4.92 , 4.86)	2.87 (-2 , 8.06)
NOBO	0.08 (-0.31 , 0.51)	0.56 (0.1 , 1.14)	-0.22 (-4.52 , 4.14)	1.05 (-3.32 , 5.43)	2.46 (-1.78 , 6.93)	-1.17 (-5.4 , 3.17)	3 (-1.4 , 7.6)	-3.91 (-8.61 , 0.89)	0.76 (-3.57 , 5.33)	-2.03 (-6.24 , 2.37)
NOCA	-0.23 (-0.72 , 0.38)	-0.13 (-0.65 , 0.52)	-0.76 (-5.42 , 3.92)	-2.35 (-7.09 , 2.38)	-1.24 (-5.84 , 3.45)	0.79 (-3.91 , 5.6)	3.29 (-1.42 , 8.19)	-1.97 (-6.64 , 2.89)	-1.07 (-5.71 , 3.69)	-4.44 (-9.45 , 0.66)
NOFL	1.61 (-0.25 , 5.62)	3.08 (0.25 , 7.47)	-0.73 (-6.88 , 5.53)	0.23 (-5.83 , 6.26)	-0.23 (-6.3 , 5.82)	0.36 (-5.84 , 6.42)	0.82 (-5.2 , 6.85)	-0.8 (-6.61 , 5.23)	-0.41 (-6.48 , 5.75)	-0.52 (-6.6 , 5.64)
NOHA	1.02 (-2.9 , 6.47)	0.15 (-3.33 , 5.56)	0.39 (-5.67 , 6.45)	0.72 (-5.44 , 6.79)	-0.62 (-6.77 , 5.57)	0.2 (-5.96 , 6.31)	-0.31 (-6.49 , 5.89)	-0.07 (-6.2 , 6.01)	1.13 (-5.05 , 7.26)	-0.38 (-6.52 , 5.81)
NOMO	-2.1 (-3.46 , -0.46)	-1.31 (-2.7 , 0.65)	-2.18 (-7.95 , 3.56)	1.32 (-4.5 , 7.16)	2.74 (-2.87 , 8.41)	1.25 (-4.33 , 6.86)	-0.07 (-6.05 , 5.91)	-1.32 (-7.25 , 4.64)	0.68 (-5.03 , 6.4)	-1.06 (-7.16 , 4.97)
NRWS	1.12 (-2.85 , 6.09)	0.35 (-3.4 , 5.62)	-0.28 (-6.49 , 5.88)	-0.23 (-6.31 , 5.9)	0.16 (-5.94 , 6.22)	0.04 (-6.12 , 6.21)	0.52 (-5.62 , 6.68)	-0.49 (-6.63 , 5.65)	0.23 (-5.88 , 6.42)	-0.28 (-6.47 , 5.9)

NSHO	-3.17 (-4.09 , -2.08)	-3.24 (-4.18 , -2.12)	2.15 (-3.38 , 7.64)	1.75 (-3.8 , 7.29)	-0.56 (-6.17 , 4.84)	0.27 (-5.26 , 5.75)	-2.05 (-7.8 , 3.61)	1.13 (-4.51 , 6.65)	-2.09 (-7.87 , 3.54)	2.99 (-2.35 , 8.1)
OROR	0.68 (-2.22 , 5.15)	1.99 (-1.72 , 6.97)	0.1 (-5.86 , 6.09)	0.36 (-5.69 , 6.35)	0.33 (-5.58 , 6.38)	0.33 (-5.59 , 6.27)	0.2 (-5.94 , 6.23)	-0.52 (-6.62 , 5.56)	-0.76 (-6.9 , 5.55)	-0.4 (-6.6 , 5.85)
PEFA	-0.45 (-5.75 , 5.94)	-2.73 (-8.19 , 4.67)	-0.32 (-6.49 , 5.85)	0.26 (-5.95 , 6.43)	-0.13 (-6.27 , 6.04)	0.07 (-6.13 , 6.24)	-0.08 (-6.29 , 6.1)	-0.03 (-6.19 , 6.12)	-0.04 (-6.18 , 6.17)	-0.06 (-6.21 , 6.02)
PROW	-0.53 (-5.42 , 5.86)	0.6 (-4.4 , 6.39)	-0.09 (-6.29 , 6.1)	-0.3 (-6.51 , 5.87)	0.19 (-5.97 , 6.33)	-0.04 (-6.19 , 6.1)	-0.02 (-6.16 , 6.08)	-0.14 (-6.27 , 6.06)	-0.25 (-6.41 , 5.87)	0.04 (-6.14 , 6.2)
PUMA	-0.34 (-5.41 , 5.73)	-2.99 (-8.02 , 3.15)	-0.22 (-6.37 , 5.95)	0.12 (-6.07 , 6.3)	-0.13 (-6.34 , 6.12)	0.07 (-6.11 , 6.16)	-0.1 (-6.27 , 6.07)	0.08 (-6.16 , 6.24)	-0.09 (-6.3 , 6.08)	-0.06 (-6.26 , 6.11)
RBGR	1.31 (-2.33 , 6.67)	1.75 (-1.92 , 6.74)	-0.37 (-6.54 , 5.77)	-0.26 (-6.4 , 5.92)	-0.57 (-6.82 , 5.67)	0.28 (-5.98 , 6.47)	0.99 (-5.24 , 7.2)	-0.24 (-6.34 , 5.81)	0.79 (-5.4 , 6.95)	-0.11 (-6.27 , 6.09)
RBNU	-2.61 (-7.99 , 4.35)	-0.32 (-5.39 , 5.62)	0.04 (-6.19 , 6.26)	-0.27 (-6.49 , 5.9)	-0.14 (-6.32 , 6.02)	0.07 (-6.11 , 6.34)	-0.01 (-6.16 , 6.17)	-0.1 (-6.33 , 6.05)	-0.07 (-6.26 , 6.17)	0.01 (-6.19 , 6.18)

RBWO	-0.15 (-0.91 , 1.03)	0.33 (-0.64 , 2.21)	-1.4 (-6.69 , 3.96)	1.9 (-3.66 , 7.37)	2.3 (-2.84 , 7.48)	1.57 (-3.65 , 6.81)	0.62 (-4.79 , 6.12)	-1.56 (-7.08 , 4.12)	-1.01 (-6.22 , 4.43)	-0.44 (-6.04 , 5.35)
REDH	-0.2 (-5.75 , 5.73)	-2.57 (-8 , 4.04)	-0.07 (-6.3 , 6.13)	-0.25 (-6.41 , 5.88)	-0.04 (-6.17 , 6.14)	0.02 (-6.12 , 6.19)	0.08 (-6.12 , 6.27)	-0.28 (-6.43 , 5.94)	-0.09 (-6.3 , 6.11)	-0.05 (-6.23 , 6.12)
REVI	-1.42 (-5.11 , 4.66)	0.67 (-3.45 , 6.43)	0.18 (-5.99 , 6.35)	-0.16 (-6.26 , 5.96)	-0.39 (-6.58 , 5.78)	0.25 (-5.91 , 6.43)	-0.36 (-6.54 , 5.82)	0.32 (-5.82 , 6.51)	0 (-6.1 , 6.14)	-0.06 (-6.21 , 6.08)
RHWO	-1.08 (-1.57 , -0.5)	-0.72 (-1.24 , -0.09)	-1.39 (-5.95 , 3.2)	1.25 (-3.38 , 5.89)	0.33 (-4.05 , 4.79)	2 (-2.48 , 6.49)	3.41 (-1.29 , 8.17)	0.45 (-4.58 , 5.84)	-1.97 (-6.62 , 2.6)	-0.84 (-5.47 , 3.64)
RNEP	0.77 (0.53 , 1.02)	0.85 (0.6 , 1.12)	0.97 (-2.83 , 4.71)	2.01 (-1.72 , 5.74)	0.27 (-3.2 , 3.81)	-2.01 (-5.36 , 1.33)	0.33 (-3.41 , 4.25)	-0.27 (-3.85 , 3.52)	1.69 (-1.86 , 5.42)	-0.37 (-3.83 , 3.27)
ROPI	-3.97 (-5.57 , -1.78)	-2.42 (-3.66 , 0.5)	0.87 (-4.82 , 6.58)	1.49 (-4.25 , 7.19)	-1.34 (-7.07 , 4.32)	0.18 (-5.54 , 5.9)	0.63 (-5.18 , 6.34)	0.96 (-4.86 , 6.64)	-0.87 (-6.67 , 4.84)	-0.51 (-6.4 , 5.27)
RTHA	0.44 (-1.76 , 5.62)	-0.69 (-2.42 , 3.12)	0.88 (-4.87 , 6.52)	2.25 (-3.82 , 8.04)	-0.34 (-6.05 , 5.42)	1.56 (-4.15 , 7.17)	-0.85 (-6.62 , 5.12)	1.44 (-4.8 , 7.59)	-0.15 (-5.95 , 5.73)	-0.99 (-6.99 , 5.1)

RWBL	0.8 (0.6 , 1.02)	0.6 (0.4 , 0.81)	1.3 (-2.07 , 4.68)	-0.59 (-4.02 , 2.82)	-0.44 (-3.64 , 2.79)	0.48 (-2.64 , 3.66)	-3.35 (-6.74 , 0.04)	-0.5 (-3.89 , 2.91)	-1 (-4.25 , 2.35)	3.49 (-0.19 , 7.5)
SAPH	-3.73 (-8.27 , 2.31)	0.71 (-3.66 , 6.04)	0.73 (-5.51 , 6.9)	0.41 (-5.74 , 6.59)	-0.21 (-6.32 , 5.99)	-0.01 (-6.14 , 6.1)	-0.27 (-6.45 , 5.87)	0.24 (-5.93 , 6.41)	-0.26 (-6.48 , 5.9)	-0.05 (-6.23 , 6.13)
SATH	-1.92 (-7.71 , 4.98)	0.12 (-5.03 , 5.92)	-0.25 (-6.43 , 5.95)	0.24 (-5.97 , 6.4)	-0.13 (-6.3 , 6.1)	0.03 (-6.15 , 6.25)	-0.06 (-6.26 , 6.11)	0.08 (-6.09 , 6.26)	-0.09 (-6.27 , 6.03)	-0.03 (-6.21 , 6.14)
SAVS	0.47 (-3.02 , 5.9)	-1.05 (-4.33 , 4.76)	1.07 (-5.18 , 7.19)	0.84 (-5.25 , 6.94)	0.13 (-5.95 , 6.18)	-0.52 (-6.6 , 5.59)	-0.5 (-6.66 , 5.65)	0.2 (-5.95 , 6.41)	-0.68 (-6.8 , 5.48)	-0.36 (-6.47 , 5.8)
SCTA	-3 (-8.15 , 3.36)	-0.44 (-5.47 , 5.77)	0.19 (-5.98 , 6.36)	-0.08 (-6.27 , 6.11)	-0.1 (-6.19 , 6.05)	0.05 (-6.1 , 6.19)	-0.07 (-6.25 , 6.09)	0.1 (-6.08 , 6.22)	0.37 (-5.82 , 6.51)	-0.07 (-6.22 , 6.09)
SEWR	-1.92 (-4.66 , 2.61)	-0.29 (-3.49 , 5.41)	0.15 (-5.86 , 6.15)	-0.22 (-6.22 , 5.8)	-0.02 (-6.04 , 5.92)	0.28 (-5.83 , 6.27)	-0.53 (-6.57 , 5.54)	-0.06 (-6.12 , 5.97)	0.39 (-5.6 , 6.3)	1.31 (-4.76 , 7.36)
SOSP	-0.69 (-1.98 , 2.61)	-0.78 (-2.03 , 2.14)	-2.63 (-8.12 , 3.03)	0.34 (-5.16 , 5.76)	1.71 (-3.72 , 7.08)	-0.29 (-5.54 , 5.02)	0.24 (-5.36 , 5.85)	-1.08 (-6.7 , 4.66)	0.87 (-4.58 , 6.28)	0.98 (-4.47 , 6.35)

SPSA	-0.57 (-5.67 , 5.51)	-2.42 (-7.97 , 4.66)	0.04 (-6.1 , 6.22)	-0.26 (-6.46 , 5.92)	-0.08 (-6.25 , 6.06)	0.04 (-6.14 , 6.19)	-0.04 (-6.23 , 6.08)	-0.1 (-6.26 , 6.02)	-0.05 (-6.2 , 6.13)	1.26 (-4.94 , 7.47)
SPTO	-0.76 (-3.43 , 4.89)	-1.15 (-3.72 , 4.22)	1.43 (-4.6 , 7.37)	0.02 (-5.9 , 5.98)	-0.43 (-6.44 , 5.57)	-0.75 (-6.67 , 5.22)	0.43 (-5.58 , 6.44)	-1.61 (-7.6 , 4.54)	-0.89 (-6.96 , 5.12)	-0.61 (-6.63 , 5.39)
STGR	-1.62 (-4.53 , 4.33)	-1.04 (-4.03 , 5.33)	1.74 (-4.42 , 7.78)	1.23 (-4.77 , 7.15)	-0.16 (-6.08 , 5.69)	0.43 (-5.47 , 6.3)	-0.82 (-6.81 , 5.21)	0.25 (-5.73 , 6.16)	-0.19 (-6.17 , 5.75)	0.92 (-5.13 , 6.86)
STSA	-2.5 (-8.09 , 4.47)	-0.15 (-5.53 , 6.14)	-0.28 (-6.55 , 6)	0.27 (-5.87 , 6.42)	0.01 (-6.17 , 6.16)	-0.21 (-6.42 , 5.98)	-0.04 (-6.19 , 6.11)	0.01 (-6.17 , 6.23)	-0.07 (-6.21 , 6.14)	0.62 (-5.57 , 6.86)
SWHA	-0.4 (-4.78 , 5.78)	-3.28 (-8.26 , 3.75)	0.58 (-5.54 , 6.71)	0.38 (-5.8 , 6.57)	-0.22 (-6.37 , 5.91)	0.08 (-6.11 , 6.24)	0.01 (-6.13 , 6.14)	-0.21 (-6.37 , 5.93)	-0.19 (-6.39 , 6.02)	-0.15 (-6.29 , 5.99)
SWTH	-2.24 (-7.81 , 4.63)	0.4 (-5.3 , 6.15)	0.2 (-5.98 , 6.4)	-0.06 (-6.3 , 6.11)	-0.13 (-6.31 , 6.12)	0.05 (-6.1 , 6.12)	0.11 (-6.09 , 6.23)	-0.23 (-6.43 , 5.95)	-0.07 (-6.24 , 6.04)	0.14 (-6.04 , 6.32)
TRES	-1.3 (-2.62 , 1.75)	-1.56 (-2.9 , 1.15)	0.49 (-5.1 , 6)	0.97 (-4.66 , 6.52)	-0.15 (-5.69 , 5.39)	-2.1 (-7.67 , 3.53)	-2.13 (-7.94 , 3.72)	0.56 (-5.16 , 6.31)	1.26 (-4.21 , 6.67)	-0.61 (-6.35 , 5.14)

TRUS	-1.1 (-5.99 , 4.83)	-2.71 (-8.31 , 4.54)	0.39 (-5.78 , 6.58)	0.41 (-5.72 , 6.6)	-0.17 (-6.38 , 5.97)	0.04 (-6.13 , 6.25)	-0.13 (-6.29 , 6.07)	0.11 (-6.09 , 6.25)	-0.1 (-6.32 , 6.05)	-0.07 (-6.22 , 6.09)
TUVU	1.31 (-1.3 , 6.21)	1.77 (-1.18 , 6.96)	0.13 (-5.93 , 6.15)	-0.91 (-6.97 , 5.33)	0.21 (-5.77 , 6.21)	0.14 (-5.84 , 6.11)	0.82 (-5.27 , 6.79)	0.02 (-6.02 , 6.16)	0.31 (-5.77 , 6.36)	-0.29 (-6.4 , 5.95)
UPSA	-0.59 (-0.94 , -0.2)	-0.4 (-0.77 , 0.01)	2.09 (-2.03 , 6.25)	1.09 (-3.06 , 5.24)	-2.58 (-6.7 , 1.57)	0.42 (-3.64 , 4.5)	-0.48 (-4.73 , 3.83)	2.26 (-1.51 , 6.1)	-0.62 (-4.8 , 3.55)	2.64 (-1.55 , 7.16)
VESP	1.48 (-1.7 , 6.38)	2.09 (-1.42 , 7.15)	-0.94 (-7.13 , 5.33)	0.85 (-5.42 , 6.98)	-0.24 (-6.35 , 5.87)	-0.06 (-6.21 , 6.04)	-0.28 (-6.41 , 5.89)	0.35 (-5.81 , 6.52)	0 (-6.05 , 6.1)	-0.08 (-6.01 , 5.88)
WAVI	-0.14 (-2.79 , 5.07)	0.13 (-2.63 , 5.39)	-0.12 (-6.1 , 5.88)	0.12 (-5.79 , 6.07)	-1.34 (-7.5 , 4.88)	0.51 (-5.46 , 6.5)	-0.45 (-6.48 , 5.59)	-0.4 (-6.46 , 5.64)	0.81 (-5.24 , 6.77)	-0.71 (-6.82 , 5.39)
WBNU	0.14 (-3.24 , 5.39)	1.71 (-2.42 , 6.89)	0.59 (-5.54 , 6.74)	0.2 (-5.92 , 6.3)	-0.09 (-6.19 , 6.11)	-0.13 (-6.24 , 6.03)	-0.19 (-6.32 , 5.93)	-0.37 (-6.48 , 5.83)	0.02 (-6.04 , 6.12)	-0.4 (-6.51 , 5.77)
WCSP	1.1 (-3.44 , 6.74)	0.36 (-3.92 , 6.3)	-0.3 (-6.46 , 5.81)	-0.41 (-6.56 , 5.72)	0.48 (-5.64 , 6.5)	0.7 (-5.37 , 6.73)	0.99 (-5.17 , 7.07)	0.08 (-6.04 , 6.24)	-0.47 (-6.66 , 5.75)	-0.1 (-6.24 , 6.08)

WEKI	-0.28 (-0.86 , 0.48)	-0.34 (-0.91 , 0.41)	-0.9 (-5.61 , 3.85)	3.93 (-0.83 , 8.72)	2.14 (-2.36 , 6.81)	1.68 (-2.79 , 6.3)	0.34 (-4.45 , 5.29)	-0.96 (-5.89 , 4.21)	-2.67 (-7.5 , 2.24)	0.46 (-4.18 , 5.26)
WEME	2.23 (1.91 , 2.58)	2.21 (1.89 , 2.57)	4.92 (0.47 , 9.37)	-1.58 (-6.02 , 2.85)	4.1 (-0.18 , 8.6)	-1.39 (-5.64 , 3.01)	-2.52 (-6.87 , 2.15)	2.18 (-2.1 , 7.02)	-1.47 (-5.51 , 2.76)	1.83 (-2.49 , 6.45)
WEWP	-1.19 (-5.61 , 4.98)	0.03 (-4.62 , 5.91)	-0.4 (-6.54 , 5.74)	-0.1 (-6.3 , 6.13)	0.86 (-5.19 , 6.94)	1.49 (-4.73 , 7.61)	0.59 (-5.53 , 6.72)	0.35 (-5.79 , 6.45)	0.01 (-6.17 , 6.22)	0.13 (-6 , 6.26)
WFIB	-2.96 (-8.26 , 4.19)	-0.58 (-5.82 , 5.59)	0.26 (-5.91 , 6.43)	0.07 (-6.09 , 6.25)	-0.12 (-6.32 , 6.01)	0.04 (-6.13 , 6.21)	-0.12 (-6.25 , 6.04)	0.07 (-6.1 , 6.24)	-0.1 (-6.24 , 6.02)	0.37 (-5.77 , 6.56)
WHIM	-0.2 (-5.8 , 5.97)	-2.47 (-8.18 , 4.74)	-0.15 (-6.32 , 6.04)	0.04 (-6.12 , 6.24)	-0.08 (-6.22 , 6.06)	0.05 (-6.16 , 6.23)	0.03 (-6.16 , 6.27)	-0.18 (-6.35 , 5.95)	0.33 (-5.82 , 6.52)	-0.05 (-6.22 , 6.09)
WIFL	-0.16 (-5.55 , 5.82)	-0.36 (-5.48 , 5.63)	0.62 (-5.49 , 6.77)	0.55 (-5.67 , 6.68)	-0.23 (-6.37 , 5.96)	0.11 (-6.09 , 6.31)	-0.17 (-6.36 , 6.01)	0.17 (-6.01 , 6.44)	-0.13 (-6.31 , 6.09)	-0.09 (-6.26 , 6.11)
WILL	-0.16 (-4.83 , 5.74)	-0.88 (-5.63 , 5.44)	0.67 (-5.58 , 6.89)	0.18 (-6.06 , 6.33)	-0.34 (-6.52 , 5.87)	0.2 (-5.97 , 6.39)	-0.27 (-6.41 , 5.87)	0.23 (-5.98 , 6.38)	-0.18 (-6.34 , 5.97)	0.31 (-5.83 , 6.42)

WIPH	-3.87 (-5.94 , 0.95)	-4.25 (-6.48 , -0.23)	1.12 (-4.82 , 7.07)	0.19 (-5.81 , 6.14)	0.79 (-5.13 , 6.64)	0.46 (-5.45 , 6.38)	-0.7 (-6.72 , 5.27)	0.38 (-5.63 , 6.25)	-0.6 (-6.63 , 5.4)	0.85 (-5.15 , 6.73)
WISN	-0.51 (-3.15 , 4.5)	0.72 (-2.53 , 6.38)	1.3 (-4.85 , 7.38)	-0.68 (-6.71 , 5.4)	-0.81 (-6.98 , 5.32)	0.18 (-5.89 , 6.27)	-0.6 (-6.73 , 5.47)	-0.07 (-6.19 , 6)	-0.17 (-6.22 , 5.89)	3.52 (-3.06 , 9.72)
WITU	-0.79 (-1.42 , 0.07)	-0.56 (-1.25 , 0.38)	1.76 (-3.02 , 6.54)	-0.39 (-5.2 , 4.4)	1.46 (-3.19 , 6.24)	-0.86 (-5.48 , 3.83)	-0.58 (-5.54 , 4.47)	-0.09 (-5.19 , 5.16)	-1.32 (-6.17 , 3.55)	-0.02 (-4.85 , 4.91)
WODU	0.29 (-3.72 , 5.79)	-0.07 (-3.98 , 5.74)	0.65 (-5.48 , 6.76)	0.13 (-6.03 , 6.25)	-0.61 (-6.8 , 5.59)	0.34 (-5.76 , 6.45)	0.9 (-5.29 , 7.07)	0.38 (-5.68 , 6.47)	0.2 (-5.89 , 6.34)	0.06 (-6.12 , 6.19)
WOTH	-0.41 (-5.4 , 5.58)	-3.01 (-7.88 , 3.81)	0.09 (-6.04 , 6.22)	-0.29 (-6.46 , 5.88)	-0.13 (-6.29 , 6.02)	0.08 (-6.09 , 6.19)	0.84 (-5.36 , 7.05)	0.22 (-5.91 , 6.39)	-0.06 (-6.26 , 6.13)	-0.07 (-6.24 , 6.1)
WTSP	-2.82 (-8 , 4.03)	-0.52 (-5.35 , 6.02)	0.03 (-6.14 , 6.24)	-0.29 (-6.45 , 5.89)	-0.12 (-6.28 , 6.04)	0.1 (-6.01 , 6.34)	-0.1 (-6.26 , 6.12)	0.12 (-6.04 , 6.29)	0.91 (-5.24 , 7.06)	-0.05 (-6.2 , 6.07)
YBCU	-1.55 (-4.01 , 1.87)	1.8 (-2.02 , 6.65)	-0.17 (-6.32 , 5.9)	-0.59 (-6.67 , 5.5)	0.41 (-5.7 , 6.5)	-1.13 (-7.24 , 5.01)	0.3 (-5.75 , 6.33)	0.24 (-5.91 , 6.3)	0.28 (-5.78 , 6.4)	-0.37 (-6.55 , 5.81)

YHBL	-2.51 (-3.12 , -1.82)	-2.67 (-3.33 , -1.95)	2.34 (-2.72 , 7.44)	1.48 (-3.65 , 6.63)	-1.1 (-6.26 , 3.92)	1.3 (-3.81 , 6.37)	-1.73 (-7.14 , 3.55)	-0.74 (-6.14 , 4.51)	-3.03 (-8.5 , 2.29)	2.46 (-2.48 , 7.17)
YRWA	1.07 (-3.2 , 6.75)	-1.15 (-5.03 , 4.84)	0 (-6.19 , 6.13)	0.12 (-6.03 , 6.25)	-0.26 (-6.44 , 5.92)	-0.01 (-6.11 , 6.15)	-0.27 (-6.44 , 5.92)	0.1 (-6.07 , 6.27)	-0.34 (-6.53 , 5.88)	-0.14 (-6.29 , 6)
YWAR	-0.57 (-1.21 , 0.25)	0 (-0.74 , 1.06)	0.9 (-4.22 , 5.95)	-1.96 (-7.13 , 3.26)	-0.32 (-5.32 , 4.72)	1.11 (-3.68 , 5.94)	3.42 (-1.79 , 8.69)	-2.81 (-8.18 , 2.66)	-2.76 (-7.96 , 2.44)	-1.27 (-6.31 , 3.96)

Table S. 4

Species' resource quantity functional traits for species detected in Nebraska, USA. Body mass (g) is the geometric mean of average values provided for both sexes from Dunning Jr 2007 through Elton Traits 1.0 database; Wilman *et al.* 2014. Mean clutch size, mean number of clutches during a breeding period (excluding re-nesting attempts due to failure), mean egg length (mm) and mean egg breath (mm) were extracted from the Birds of North America online database (Rodewald 2015). When different reproductive traits estimates were reported, then we prioritized reporting a value by the most complete information, the largest sample size, closest geographic site of the study to Nebraska when multiple studies had similar sample sizes, and recent studies. If mean values were not reported, we took the median value of the range of values provided for that trait. If raw data were reported, then the mean was calculated in R.

Alpha code	Body mass (g)	Mean clutch size	Mean number of clutches	Mean egg length (mm)	Mean egg breadth (mm)
AMAV	304	3.8	1.0	49.5	34.2
AMBI	706	3.8	1.0	48.6	36.6
AMCO	637	9.0	1.0	48.7	33.5
AMCR	449	4.8	1.0	29.1	41.4
AMGO	13	5.2	1.0	16.5	12.4
AMKE	115	4.8	1.1	35.1	28.4
AMRE	8	3.8	1.0	16.1	12.6
AMRO	79	3.5	1.5	28.4	20.7
ATSP	18	5.0	1.0	19.2	14.5
AWPE	5608	2.0	1.0	87.1	57.1
BADO	711	2.4	1.0	50.6	43.3
BAEA	4701	1.9	1.0	7.1	5.5

BANS	13	4.9	1.0	17.2	12.4
BAOR	33	4.4	1.0	23.0	15.5
BARS	18	4.7	1.0	19.3	13.8
BBSA	62	4.0	1.0	38.1	27.0
BCCH	11	7.0	1.0	1.5	1.2
BEVI	9	3.8	1.0	17.5	12.8
BGGN	6	4.5	1.8	14.6	11.5
BHCO	40	4.3	3.8	21.5	16.4
BHGR	47	3.4	1.0	24.5	17.8
BLGR	27	3.6	1.0	21.9	16.2
BLJA	88	4.0	2.0	28.0	20.4
BOBO	31	5.1	1.0	21.7	16.2
BRBL	62	5.0	1.0	25.7	18.9
BRSP	11	3.0	2.0	17.0	16.6
BRTH	69	4.1	1.1	26.9	19.7
BUOR	38	5.0	1.0	23.8	15.9
BUOW	151	8.0	1.0	32.1	26.2
BWTE	359	10.1	1.0	46.4	33.3
BWWA	9	4.6	1.0	15.7	12.3
CACG	2812	4.8	1.0	84.9	57.6
CAGO	2812	4.8	1.0	84.9	57.6
CARW	19	4.8	1.4	19.0	14.8
CCSP	11	4.0	1.0	17.1	12.7
CEDW	32	4.2	1.9	22.1	15.6
CHSP	12	3.7	1.0	17.6	12.9
CLSW	22	3.5	1.0	20.4	14.0
COGR	105	4.8	1.0	28.8	21.4
CONI	79	2.0	1.0	21.7	31.0
COYE	10	4.0	1.0	17.4	13.4
DEJU	20	3.9	1.0	20.0	15.3
DICK	26	4.0	1.0	20.8	15.7

DOWO	26	4.8	1.0	19.4	15.1
EABL	28	4.5	2.1	20.9	16.5
EAKI	40	3.4	1.0	24.1	17.9
EAME	92	4.8	1.0	27.8	20.4
EAPH	20	5.0	2.0	19.2	14.7
EATO	40	3.9	2.0	23.1	17.0
EAWP	14	3.0	1.0	18.2	13.7
ECDO	149	1.9	4.5	31.3	24.1
ETTI	22	5.7	1.0	18.4	14.1
EUST	77	4.3	2.0	29.8	21.4
EVGR	57	3.5	1.0	23.4	16.6
FISP	13	3.7	2.9	17.8	13.4
GBHE	2523	3.2	1.0	63.6	39.8
GCFL	32	5.0	1.0	22.6	17.2
GRCA	35	3.4	2.0	23.9	17.7
GRHE	202	2.8	1.0	37.5	29.2
GRPC	870	12.1	1.0	42.4	31.7
GRSP	18	4.3	2.0	18.6	14.4
GTGR	160	3.7	1.0	31.8	21.9
HASP	36	3.5	1.0	22.2	16.5
HESP	13	3.8	1.0	18.3	14.1
HETH	30	3.4	1.0	22.7	17.0
HOFI	21	4.6	1.9	19.0	14.0
HOLA	33	3.2	2.0	21.5	15.7
HOSP	27	5.1	2.0	21.6	15.6
HOWR	11	6.4	2.0	16.6	12.7
INBU	15	3.4	1.0	18.8	14.2
KILL	96	4.0	1.0	37.9	27.1
LARB	38	3.6	1.0	21.8	16.9
LASP	29	4.1	1.0	20.2	16.0
LBCU	584	4.0	1.0	65.3	46.1

LBDO	104	3.9	1.0	43.0	31.0
LCSP	13	4.5	1.0	17.9	13.5
LEFL	10	4.0	1.0	16.6	12.9
LISP	17	4.2	1.0	19.6	14.6
LOSH	52	6.4	1.0	25.0	18.7
MALL	843	8.7	1.0	56.5	41.1
MAWR	11	5.0	2.0	16.3	12.6
MOBL	30	5.7	1.5	21.9	16.6
MODO	119	2.0	1.0	28.0	22.0
NOBO	172	13.0	1.0	30.0	25.0
NOCA	43	3.0	1.7	24.9	18.6
NOFL	131	6.5	1.0	2.8	2.2
NOHA	393	4.4	1.0	46.0	35.6
NOMO	49	3.8	2.0	18.5	24.5
NRWS	16	6.3	1.0	18.3	13.2
NSHO	613	10.1	1.0	52.3	36.8
OROR	19	5.0	1.3	20.7	14.5
PEFA	760	3.7	1.0	53.4	41.7
PROW	14	4.8	1.5	18.5	14.7
PUMA	54	5.0	1.0	24.3	17.4
RBGR	42	4.0	1.0	24.3	17.6
RBNU	10	2.8	1.0	15.7	12.1
RBWO	70	4.3	1.0	25.3	18.8
REDH	1076	10.5	1.0	60.2	43.4
REVI	16	3.1	1.0	20.4	14.8
RHWO	72	4.8	1.0	25.1	19.2
RNEP	1120	10.6	1.0	45.0	36.0
ROPI	354	2.0	6.5	38.4	28.6
RTHA	1101	2.9	1.0	59.6	47.5
RWBL	51	3.3	1.7	24.7	17.8
SAPH	21	4.5	2.0	20.0	15.4

SATH	44	3.5	1.0	24.5	18.0
SAVS	20	4.1	1.0	19.4	14.6
SCTA	28	3.4	1.0	23.3	16.5
SEWR	9	6.9	1.4	16.7	12.1
SOSP	22	4.1	2.0	20.4	15.7
SPSA	40	4.0	1.0	32.0	24.0
SPTO	39	3.4	1.5	24.1	18.0
STGR	882	10.9	1.0	43.1	32.3
STSA	57	3.9	1.0	36.5	25.5
SWHA	947	2.3	1.0	57.1	44.4
SWTH	30	3.5	1.0	23.2	16.7
TRES	21	5.6	1.0	18.8	13.4
TRUS	11071	5.0	1.0	114.5	73.1
TUVU	1518	1.9	1.0	71.3	48.6
UPSA	159	4.0	1.0	45.0	32.5
VESP	26	4.0	1.0	20.9	15.5
WAVI	14	3.8	2.0	18.6	13.6
WBNU	21	7.3	1.0	19.0	14.0
WCSP	28	4.6	1.0	21.3	15.9
WEKI	40	4.1	1.0	23.7	17.4
WEME	100	4.8	1.0	28.1	20.6
WEWP	13	3.0	1.0	18.1	13.7
WFIB	617	3.4	1.0	52.0	36.7
WHIM	365	3.7	1.0	58.1	40.0
WIFL	13	3.6	1.0	18.0	13.7
WILL	246	3.9	1.0	53.5	38.0
WIPH	59	4.0	1.0	33.2	23.6
WISN	113	3.9	1.0	39.3	28.4
WITU	5791	10.5	1.0	61.5	46.5
WODU	658	11.4	2.0	49.9	38.5
WOTH	50	3.7	2.0	25.5	19.1

WTSP	24	4.0	1.0	21.0	15.4
YBCU	64	3.0	1.0	30.6	23.1
YHBL	63	0.8	1.0	26.3	18.1
YRWA	12	3.6	1.0	17.7	13.3
YWAR	10	4.5	1.0	16.6	12.7

Table S. 5

Species' diet functional traits for species detected in Nebraska, USA. Diet preferences (i.e., estimates of percent use, with all categories summing to 100%) were accessed from the Elton Traits 1.0 database (Wilman *et al.* 2014).

Alpha code	**Invertebrates**	**Mammals and birds**	**Reptiles and amphibians**	**Fish**	**Vertebrates (general or unknown)**	**Scavenge**	**Fruit**	**Nectar**	**Seeds**	**Plant material**
AMAV	80	0	0	0	0	0	0	0	20	0
AMBI	20	0	20	60	0	0	0	0	0	0
AMCO	20	0	0	0	0	0	0	0	40	40
AMCR	20	10	10	10	0	20	20	0	10	0
AMGO	10	0	0	0	0	0	0	10	60	20
AMKE	60	20	20	0	0	0	0	0	0	0
AMRE	80	0	0	0	0	0	10	0	10	0
AMRO	50	0	0	0	0	0	50	0	0	0
ATSP	50	0	0	0	0	0	0	0	50	0
AWPE	0	0	0	100	0	0	0	0	0	0
BADO	10	70	10	10	0	0	0	0	0	0
BAEA	0	30	20	30	0	20	0	0	0	0
BANS	100	0	0	0	0	0	0	0	0	0
BAOR	60	0	0	0	0	0	20	20	0	0
BARS	80	0	0	0	0	0	10	0	10	0

BBSA	80	0	0	0	0	0	0	0	20	0
BCCH	60	0	0	0	0	0	20	0	20	0
BEVI	90	0	0	0	0	0	10	0	0	0
BGGN	100	0	0	0	0	0	0	0	0	0
BHCO	40	0	0	0	0	0	0	0	60	0
BHGR	70	0	0	0	0	0	20	0	10	0
BLGR	40	0	0	0	0	0	20	0	30	10
BLJA	20	10	10	0	0	0	20	0	40	0
BOBO	60	0	0	0	0	0	30	0	10	0
BRBL	100	0	0	0	0	0	0	0	0	0
BRSP	50	0	0	0	0	0	0	0	50	0
BRTH	50	0	0	0	0	0	30	0	20	0
BUOR	60	10	0	0	0	0	0	30	0	0
BUOW	20	70	10	0	0	0	0	0	0	0
BWTE	10	0	0	0	0	0	0	0	30	60
BWWA	100	0	0	0	0	0	0	0	0	0
CACG	0	0	0	0	0	0	10	0	0	90
CAGO	0	0	0	0	0	0	10	0	0	90
CARW	60	0	20	0	0	0	10	0	10	0
CCSP	20	0	0	0	0	0	0	0	60	20
CEDW	20	0	0	0	0	0	70	0	0	10
CHSP	40	0	0	0	0	0	0	0	60	0

CLSW	100	0	0	0	0	0	0	0	0	0
COGR	40	10	0	10	0	0	0	0	40	0
CONI	100	0	0	0	0	0	0	0	0	0
COYE	100	0	0	0	0	0	0	0	0	0
DEJU	30	0	0	0	0	0	0	0	70	0
DICK	0	0	0	0	0	0	0	0	100	0
DOWO	80	0	0	0	0	0	10	0	10	0
EABL	70	0	0	0	0	0	30	0	0	0
EAKI	70	0	10	0	0	0	10	0	10	0
EAME	70	0	0	0	0	0	10	0	20	0
EAPH	90	0	0	0	0	0	10	0	0	0
EATO	30	0	0	0	0	0	30	0	40	0
EAWP	90	0	0	0	0	0	10	0	0	0
ECDO	10	0	0	0	0	0	30	0	40	20
ETTI	60	0	0	0	0	0	0	0	40	0
EUST	20	0	10	0	0	10	30	10	20	0
EVGR	10	0	0	0	0	0	20	0	40	30
FISP	40	0	0	0	0	0	0	0	60	0
GBHE	30	10	10	50	0	0	0	0	0	0
GCFL	60	0	0	0	0	0	40	0	0	0
GRCA	60	0	0	0	0	0	40	0	0	0
GRHE	30	0	30	40	0	0	0	0	0	0

GRPC	20	0	0	0	0	0	10	0	50	20
GRSP	60	0	0	0	0	0	0	0	40	0
GTGR	80	0	0	0	0	0	0	0	20	0
HASP	10	0	0	0	0	0	0	0	90	0
HESP	70	0	0	0	0	0	0	0	30	0
HETH	80	0	0	0	0	0	20	0	0	0
HOFI	10	0	0	0	0	0	30	0	30	30
HOLA	50	0	0	0	0	0	0	0	50	0
HOSP	10	0	0	0	0	0	0	0	60	30
HOWR	80	0	0	0	0	0	0	0	0	20
INBU	0	0	0	0	0	0	0	0	100	0
KILL	90	0	0	0	0	0	0	0	10	0
LARB	30	0	0	0	0	0	10	0	60	0
LASP	30	0	0	0	0	0	0	0	70	0
LBCU	90	0	0	0	0	0	10	0	0	0
LBDO	60	0	0	0	0	0	0	0	20	20
LCSP	20	0	0	0	0	0	0	0	80	0
LEFL	90	0	0	0	0	0	10	0	0	0
LISP	50	0	0	0	0	0	0	0	50	0
LOSH	70	10	10	0	0	10	0	0	0	0
MALL	40	0	10	10	0	0	0	0	20	20
MAWR	100	0	0	0	0	0	0	0	0	0

MOBL	60	0	0	0	0	0	30	0	10	0
MODO	0	0	0	0	0	0	0	0	90	10
NOBO	0	0	0	0	0	0	0	0	70	30
NOCA	20	0	0	0	0	0	10	0	0	70
NOFL	70	0	0	0	0	0	20	0	10	0
NOHA	10	70	10	0	0	10	0	0	0	0
NOMO	50	0	0	0	0	0	50	0	0	0
NRWS	100	0	0	0	0	0	0	0	0	0
NSHO	60	0	0	0	0	0	0	0	20	20
OROR	40	0	0	0	0	0	20	30	0	10
PEFA	10	80	10	0	0	0	0	0	0	0
PROW	70	0	0	0	0	0	10	10	10	0
PUMA	100	0	0	0	0	0	0	0	0	0
RBGR	50	0	0	0	0	0	20	0	20	10
RBNU	50	0	0	0	0	0	0	0	50	0
RBWO	30	10	10	0	0	0	20	10	20	0
REDH	10	0	0	0	0	0	0	0	20	70
REVI	60	0	0	0	0	0	20	0	20	0
RHWO	60	0	0	0	10	0	0	0	20	10
RNEP	10	0	0	0	0	0	30	0	30	30
ROPI	10	0	0	0	0	0	0	0	60	30
RTHA	10	60	30	0	0	0	0	0	0	0

RWBL	50	0	0	0	0	0	0	0	50	0
SAPH	90	0	0	0	0	0	10	0	0	0
SATH	80	0	0	0	0	0	10	0	10	0
SAVS	40	0	0	0	0	0	20	0	30	10
SCTA	80	0	0	0	0	0	10	0	0	10
SEWR	100	0	0	0	0	0	0	0	0	0
SOSP	40	0	0	0	0	0	30	0	30	0
SPSA	80	0	0	20	0	0	0	0	0	0
SPTO	50	0	0	0	0	0	20	0	30	0
STGR	10	0	0	0	0	0	10	0	10	70
STSA	80	0	0	0	0	0	0	0	20	0
SWHA	30	60	10	0	0	0	0	0	0	0
SWTH	60	0	0	0	0	0	40	0	0	0
TRES	90	0	0	0	0	0	10	0	0	0
TRUS	10	0	0	0	0	0	0	0	20	70
TUVU	0	0	0	0	0	100	0	0	0	0
UPSA	70	0	0	0	0	0	0	0	30	0
VESP	50	0	0	0	0	0	0	0	50	0
WAVI	80	0	0	0	0	0	10	0	0	10
WBNU	50	0	0	0	0	0	0	0	50	0
WCSP	10	0	0	0	0	0	10	0	70	10
WEKI	90	0	0	0	0	0	10	0	0	0

WEME	50	0	0	0	0	0	0	0	50	0
WEWP	90	0	0	0	0	0	10	0	0	0
WFIB	80	0	10	10	0	0	0	0	0	0
WHIM	60	0	0	0	0	0	20	0	10	10
WIFL	90	0	0	0	0	0	10	0	0	0
WILL	80	0	0	20	0	0	0	0	0	0
WIPH	80	0	0	0	0	0	0	0	20	0
WISN	80	0	0	0	0	0	0	0	10	10
WITU	20	0	0	0	0	0	20	0	20	40
WODU	0	0	0	0	0	0	0	0	50	50
WOTH	60	0	0	0	0	0	40	0	0	0
WTSP	20	0	0	0	0	0	20	0	50	10
YBCU	60	10	20	0	0	0	10	0	0	0
YHBL	100	0	0	0	0	0	0	0	0	0
YRWA	70	0	0	0	0	0	10	10	10	0
YWAR	100	0	0	0	0	0	0	0	0	0

Table S. 6

Species' diet functional traits for species detected in Nebraska, USA. Foraging strategies (i.e., estimates of percent use, with all categories summing to 100%) and time of activity (i.e., whether the species mainly foraged nocturnally) were accessed from the Elton Traits 1.0 database (Wilman *et al.* 2014).

Alpha code	**Below water**	**Around water surface**	**On ground**	**In tree understory**	**In middle of trees**	**In tree canopy**	**Aerial**	**Nocturnal**
AMAV	0	50	50	0	0	0	0	0
AMBI	0	70	30	0	0	0	0	0
AMCO	50	50	0	0	0	0	0	0
AMCR	0	0	80	20	0	0	0	0
AMGO	0	0	33	33	33	0	0	0
AMKE	0	0	50	40	10	0	0	0
AMRE	0	0	0	0	80	20	0	0
AMRO	0	0	20	40	40	0	0	0
ATSP	0	0	60	20	20	0	0	0
AWPE	100	0	0	0	0	0	0	0
BADO	0	10	60	20	10	0	0	1
BAEA	0	40	30	0	10	10	10	0
BANS	0	0	0	40	60	0	0	0

BAOR	0	0	30	10	20	40	0	0
BARS	0	0	30	30	40	0	0	0
BBSA	0	0	100	0	0	0	0	0
BCCH	0	0	0	20	80	0	0	0
BEVI	0	0	0	50	50	0	0	0
BGGN	0	0	0	50	50	0	0	0
BHCO	0	0	80	10	10	0	0	0
BHGR	0	0	10	0	40	50	0	0
BLGR	0	0	100	0	0	0	0	0
BLJA	0	0	40	20	20	20	0	0
BOBO	0	0	100	0	0	0	0	0
BRBL	0	0	100	0	0	0	0	0
BRSP	0	0	100	0	0	0	0	0
BRTH	0	0	80	20	0	0	0	0
BUOR	0	0	30	20	20	30	0	0
BUOW	0	0	80	10	10	0	0	1
BWTE	0	100	0	0	0	0	0	0
BWWA	0	0	0	50	50	0	0	0
CACG	0	40	60	0	0	0	0	0
CAGO	0	40	60	0	0	0	0	0
CARW	0	0	40	40	20	0	0	0
CCSP	0	0	80	10	10	0	0	0

CEDW	0	0	0	40	40	0	20	0
CHSP	0	0	80	10	10	0	0	0
CLSW	0	0	0	0	0	0	100	0
COGR	0	0	70	20	10	0	0	0
CONI	0	0	0	10	0	0	90	1
COYE	0	0	0	80	20	0	0	0
DEJU	0	0	60	10	30	0	0	0
DICK	0	0	100	0	0	0	0	0
DOWO	0	0	0	20	40	40	0	0
EABL	0	0	100	0	0	0	0	0
EAKI	0	0	0	80	20	0	0	0
EAME	0	0	100	0	0	0	0	0
EAPH	0	0	0	50	50	0	0	0
EATO	0	0	80	20	0	0	0	0
EAWP	0	0	33	33	33	0	0	0
ECDO	0	0	80	10	10	0	0	0
ETTI	0	0	20	20	40	20	0	0
EUST	0	0	80	20	0	0	0	0
EVGR	0	0	0	50	50	0	0	0
FISP	0	0	100	0	0	0	0	0
GBHE	0	60	40	0	0	0	0	0
GCFL	0	0	100	0	0	0	0	0

GRCA	0	0	0	80	20	0	0	0
GRHE	0	80	20	0	0	0	0	0
GRPC	0	0	100	0	0	0	0	0
GRSP	0	0	80	20	0	0	0	0
GTGR	0	0	80	10	10	0	0	0
HASP	0	0	90	10	0	0	0	0
HESP	0	0	80	10	10	0	0	0
HETH	0	0	50	50	0	0	0	0
HOFI	0	0	33	33	33	0	0	0
HOLA	0	0	100	0	0	0	0	0
HOSP	0	0	50	50	0	0	0	0
HOWR	0	0	0	100	0	0	0	0
INBU	0	0	40	40	20	0	0	0
KILL	0	0	100	0	0	0	0	0
LARB	0	0	50	10	10	20	10	0
LASP	0	0	80	10	10	0	0	0
LBCU	0	20	80	0	0	0	0	0
LBDO	0	50	50	0	0	0	0	0
LCSP	0	0	80	20	0	0	0	0
LEFL	0	0	0	80	20	0	0	0
LISP	0	0	100	0	0	0	0	0
LOSH	0	0	80	10	10	0	0	0

MALL	20	60	20	0	0	0	0	0
MAWR	0	0	0	100	0	0	0	0
MOBL	0	0	100	0	0	0	0	0
MODO	0	0	60	40	0	0	0	0
NOBO	0	0	100	0	0	0	0	0
NOCA	0	0	40	20	20	20	0	0
NOFL	0	0	100	0	0	0	0	0
NOHA	0	0	100	0	0	0	0	0
NOMO	0	0	70	30	0	0	0	0
NRWS	0	0	30	70	0	0	0	0
NSHO	20	80	0	0	0	0	0	0
OROR	0	0	30	50	20	0	0	0
PEFA	0	0	20	20	20	20	20	0
PROW	0	0	0	20	80	0	0	0
PUMA	0	0	20	20	20	20	20	0
RBGR	0	0	20	20	30	30	0	0
RBNU	0	0	0	33	33	33	0	0
RBWO	0	0	0	0	20	60	20	0
REDH	50	50	0	0	0	0	0	0
REVI	0	0	0	0	20	80	0	0
RHWO	0	0	20	20	60	0	0	0
RNEP	0	0	100	0	0	0	0	0

ROPI	0	0	80	20	0	0	0	0
RTHA	0	0	0	0	33	33	33	0
RWBL	0	0	90	10	0	0	0	0
SAPH	0	0	50	50	0	0	0	0
SATH	0	0	100	0	0	0	0	0
SAVS	0	0	80	10	10	0	0	0
SCTA	0	0	10	10	40	40	0	0
SEWR	0	0	0	100	0	0	0	0
SOSP	0	0	70	30	0	0	0	0
SPSA	0	20	80	0	0	0	0	0
SPTO	0	0	70	30	0	0	0	0
STGR	0	0	100	0	0	0	0	0
STSA	0	50	50	0	0	0	0	0
SWHA	0	0	20	20	20	20	20	0
SWTH	0	0	50	50	0	0	0	0
TRES	0	0	20	20	20	20	20	0
TRUS	0	100	0	0	0	0	0	0
TUVU	0	0	100	0	0	0	0	0
UPSA	0	0	100	0	0	0	0	0
VESP	0	0	80	10	10	0	0	0
WAVI	0	0	0	20	30	50	0	0
WBNU	0	0	0	33	33	33	0	0

WCSP	0	0	80	10	10	0	0	0
WEKI	0	0	30	30	40	0	0	0
WEME	0	0	100	0	0	0	0	0
WEWP	0	0	33	33	33	0	0	0
WFIB	0	80	20	0	0	0	0	0
WHIM	0	20	60	20	0	0	0	0
WIFL	0	0	0	80	20	0	0	0
WILL	0	70	30	0	0	0	0	0
WIPH	0	80	20	0	0	0	0	0
WISN	0	20	80	0	0	0	0	0
WITU	0	0	90	10	0	0	0	0
WODU	0	80	20	0	0	0	0	0
WOTH	0	0	80	20	0	0	0	0
WTSP	0	0	90	10	0	0	0	0
YBCU	0	0	0	0	40	60	0	0
YHBL	0	0	90	10	0	0	0	0
YRWA	0	0	0	50	50	0	0	0
YWAR	0	0	0	20	80	0	0	0