IMPACTS OF DISTANT DRIVERS ON LANDSCAPES AND BIODIVERSITY

By

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ABSTRACT

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Global biodiversity is increasingly impacted by distant drivers. With societies more connected than ever before, natural resource consumption has expanded beyond administrative and political boundaries. International food trade in particular has profound impacts on land-use and socioeconomic and environmental outcomes. At the same time, global biodiversity is threatened at an unprecedented scale, with many of the causes obfuscated by complexities of distant, interacting socioecological systems. Understanding the ultimate drivers of biodiversity change and translating them to local biodiversity outcomes is integral to addressing conservation challenges in the age of globalization. This dissertation analyzes the impacts of international trade on biodiversity in an agroecosystem undergoing land-use change driven by global markets. Chapter 1 provides background on the study region, Heilongjiang Province, and describes disruption of soybean production in the area due to changes in global trade. Chapter 2 is a systematic review of studies on distant drivers of biodiversity change. Across all taxa, harmful impacts on biodiversity were the most frequent outcome reported, with distant impacts of trade and tourism most frequently studied. In Chapter 3, satellite imagery was classified into landcover classes to create high-fidelity maps of the agriculture-dominated study landscape. By utilizing phenological, synthetic aperture radar, and vegetation/soil index data, accuracies of 91%- 80% were achieved. In Chapter 4 these landcover maps were used to calculate landscape metrics. These metrics were then used to analyze relationships between landscape structure (i.e., composition and configuration) and bird communities. Functional biodiversity indices derived from life history and morphological traits were examined in addition to taxonomic measures. Though no discernable differences between taxonomic and functional community metrics were observed, several significant relationships between landscape structure and biodiversity metrics were found. Crop diversity, natural landcover, and edge metrics, were positively correlated with bird richness. Aggregation of patches, corn area, and soybean area were negatively correlated. We also compared landscape structure and biodiversity between two regions impacted by global soybean trade. Despite the more impacted region having lower crop diversity and natural area, there was no difference in biodiversity between the two regions. The more impacted region also had more rice area, demonstrating that negative biodiversity impacts may be mitigated by rice cultivation. Chapter 5 built on the previous chapter by modeling bird occupancy to assess species-specific relationships with landscape structure. Results indicated that increased crop diversity significantly increased occupancy of birds at both the taxonomic and functional level, particularly for birds belonging to less common functional groups. Percentage of natural area was not as important as expected, while metrics related to landscape configuration had very few significant impacts on occupancy. Increases in rice area were not as detrimental to bird occupancy as increases in corn and soybean. In fact, soybean area exhibited more significant negative relationships with bird occurrence than corn, suggesting that decreases in soybean area due to global trade may have benefitted bird biodiversity in the case of a monocultural landscape. However, due to the prevalence of small-scale farming practices, the more likely outcome would be a decrease in crop diversity due to soybean fields being converted to more profitable crops (e.g., corn, rice). By linking global trade, changes in landcover/use, landscape structure, and local bird communities in the same context, the results of this dissertation highlight the need for integrated biodiversity studies that place ecosystems in the broader context of globalization.

This dissertation is dedicated to the common and unexciting species of birds that have adapted to
living in human-modified landscapes and contribute to the health of the ecosystems we all rely
on. I'll still refer to you as ‘trash birds’, but it is from a place of love and respect (and a force of
habit). I hope you continue to fill everyday life with color and song
for generations to come.

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I also need to thank my lab mates for their comradery and support over the past six years. I especially want to thank Kelly Kapsar, for her willingness to listen and commiserate as we worked towards finishing our degrees during a global pandemic. Last, but certainly not least, I need to thank Dr. Anna Herzberger for her friendship since my first day as a grad student, when I hopped on a plane to China with zero understanding of what I was getting myself into. I don't think I would have finished this degree without her words of encouragement and unwavering belief in my abilities.

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I owe an unending gratitude to my parents. To my mother, Candee Morris, thank you for always being there, for instilling the value of education in me, and for your example of always living with an open mind. To my father, Joseph Hovis, thank you for the informal ecological education you gave me throughout my childhood, for picking up the phone when I needed someone to talk birds with, and for enabling my book addiction as both a child and an adult. To you both, I would never be where I am today without the sacrifices you made and your desire to provide Savanna and I with a better life. I hope you are proud of the person I have become.

Finally, I need to thank my partner in life, Kelsen Case. Listing all the ways in which I received support from you would be longer than this entire dissertation, so I will restrain myself. Thank you for the past eight years and for persevering with me during the long-distance of the first five. Your endless patience, love, and sense of humor have been a constant source of joy, especially during the more difficult times. A bonus thank you to my furry companions that I’ve had throughout this process. In particular, to the late and great Catticus, who I adopted in my second month of grad school to ease the loneliness and uncertainty during that time in my life. Thanks buddy, wish you were here to see me graduate and to immediately lay on my diploma the second I turn around.

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CHAPTER 1: INTRODUCTION

1.1 Overview

As the world continues to develop, boundaries between natural and human systems become less clear and more complicated (J. Liu et al., 2013). Today's global trade market blurs these boundaries even further by connecting distant, coupled human and natural systems (CHANS) all around the globe. This presents new challenges for sustainability, as many countries now consume resources far beyond their borders, with consequences felt not by the consumers but the unseen ecosystems and individuals that provide these resources (Chaudhary & Kastner, 2016; Prell et al., 2017; Weinzettel et al., 2013; Xu et al., 2020).

Concurrently, the human population is growing exponentially, thereby exacerbating resource demand. As of 2019, the world population was approximately 7.56 billion (U.S. Census Bureau, 2019). As many countries find their domestic resources inadequate to meet basic human needs, such as food, they turn to global trade (Odorico et al., 2014). Additionally, types of commodities demanded by countries is shifting to more animal-based products as development results in more affluent populations (Robinson & Pozzi, 2011). The combination of these factors has led to sky-rocketing demands in the food trade which subsequently impacts the CHANS that produce these highly traded commodities (Tilman et al., 2011).

Importing countries often obtain environmental benefits (e.g., increased land allocation for biodiversity conservation and restoration rather than food production) (De Fraiture et al., 2004; Lenzen et al., 2012; Nimubona, 2012; Walz & Wellisch, 1997), whereas exporting countries experience environmental degradation (e.g., from converting land for food production) (Lambin & Meyfroidt, 2011; Lenzen et al., 2012). However, little empirical evidence on the environmental impacts of global trade in importing countries is available (but see Sun et al. 2018) as most research has been conducted on exporting countries (J. Sun et al., 2018). The assumption that importing countries always receive environmental benefits from global trade must be further tested (J. Liu, 2020), for it is crucial to identify environmental costs and benefits borne by both importing and exporting countries to secure global environmental sustainability and food security (Tanentzap et al., 2015).

1.2 Global Soybean Trade

One of the most globally traded crops is soybean (*Glycine max*). The soybean trade network is among the largest in the world (Leff et al., 2004). The three largest nodes within this network are the United States (US), Brazil, and China (Reenberg & Fenger, 2011; Schaffer-Smith et al., 2018). Soybeans are mainly used for human consumption, livestock feed, and industrial purposes. Soybeans are also valued for their ability to fix atmospheric nitrogen and are commonly grown in rotation with other crops to maintain soil fertility (Hymowitz, T., Newell, 1981). Soybeans are one of the only commodity crops to significantly increase in acreage, increasing 45% from 1980-2009 (Reenberg & Fenger, 2011). For comparison, corn acreage increased by 21% during the same time period. Acceleration of the soybean trade is unprecedented in terms of scale and consequences of this rapid growth are still unclear.

Despite domesticating the soybean over 3000 years ago (Hymowitz, 1970), China is now the world's largest importer of soybeans; importing more than 84 million tons of soybeans in 2015 or 64% of total global soybean imports (Figure 1) (FAOSTAT Database, 2017). The rise in soybean imports to China can be attributed to two major factors: reduction of the soybean tariff in 2001, when China joined the World Trade Organization (L. Li et al., 2017); and for livestock feed to meet the rising demand for animal products as China's population becomes more affluent (Gale, 2015). The majority of China's soybean imports are from Brazil and the US where climate, vast field sizes, and genetically modified varieties lower cost of production significantly

(Yao et al., 2018). The majority of domestically grown soybeans, however, are grown in northeast China where growing seasons are short and farms are small, with non-contiguous fields of various crops (L. Li et al., 2017). Additionally, cultivation of genetically modified soybeans (and other crops) is explicitly outlawed by the Chinese government (Reenberg & Fenger, 2011).

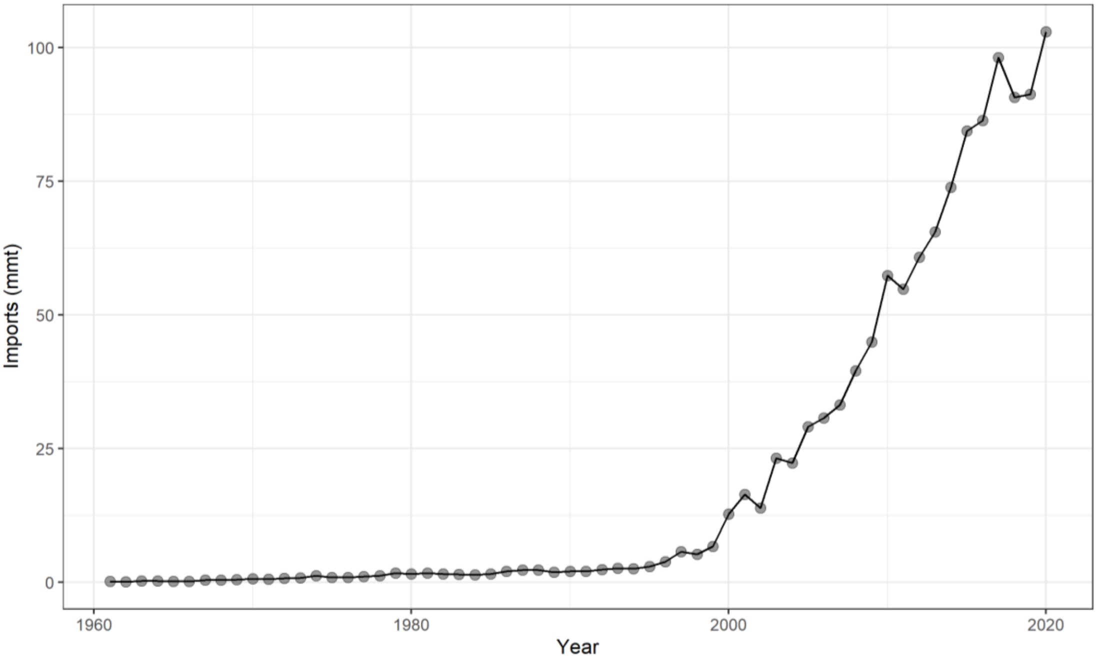


Figure 1: Chinese soybean imports from 1960-2020 (FAOSTAT)

In addition to socioeconomic effects, soybean production for global trade has numerous environmental impacts. Research identified threats in Brazil to both the Cerrado (savannah) and Amazonian forests as well as spillover feedbacks driving cattle expansion (Fearnside, 2002; le Polain de Waroux et al., 2017; Vanwey et al., 2013). However, less research has been conducted on environmental effects in soybean importing countries. The assumption of increased environmental benefits may not hold true in China due to the disruption of its domestic soybean production and the subsequent impact on the agroecosystem.

1.3 Agroecosystems

Agricultural landscapes are oftentimes overlooked with regards to biodiversity conservation. This is largely due to the patch-matrix paradigm that has dominated the field of landscape ecology for the greater part of the field's history (Lausch et al., 2015). Briefly, the patch-matrix model is that habitat is fragmented by disturbance, usually human driven, which breaks up the habitable areas into patches, which are then separated by unsuitable areas (i.e. the matrix, often human-dominated lands) (Rutledge, 2003). The patch-matrix model was conceptualized with the inhospitable (to terrestrial animals) ocean as the matrix separating hospitable islands (MacArthur & Wilson, 1967). However, terrestrial landscapes oftentimes offer a more subtle gradient between hospitable and inhospitable habitats. There is a growing body of work demonstrating that matrix habitats can play important roles in how species utilize and move about landscapes, and this literature calls for more comprehensive approaches to landscape characterization (Fahrig, 2001; Prugh et al., 2008). Recently, landscape ecologists have espoused treating the "matrix", or non-habitat areas of the landscape, as part of the functioning ecosystem landscape mosaic, rather than disregarding it as barren a wasteland (Fahrig et al., 2011; Vasseur et al., 2013).

Agricultural land is a prime example of a heavily human-modified landscape. Many natural elements persist, but humans manage a majority of the inputs and outputs as well as configuration and composition. Using the PMM framework, farmland would be treated as matrix for wildlife, while considering uncultivated forest or grassland areas as habitat patches. However, agricultural lands can house a multitude of species assemblages. The question remains, what kind of agricultural landscapes offer the greatest habitat potential? There is consensus that landscape heterogeneity positively contributes to biodiversity, however, widespread intensification of farming operations has reduced heterogeneity of farmlands (i.e. larger fields, more agrichemicals, bigger machinery, mono-cropping etc.) (Benton et al., 2003).

The fields of agroecology and landscape ecology are simultaneously moving towards functional views of ecosystem and biodiversity characteristics. Functional views consider the role an organism or habitat plays within the broader ecosystem. By utilizing mainstay landscape pattern and composition metrics, relationships between landscape, species diversity, and ecosystem services can be quantified to aid in comprehending mechanistic patterns and processes of human-modified landscapes (Fahrig et al., 2011). These concepts have been applied to both theoretical and empirical situations (Gil-Tena et al., 2015; Vasseur et al., 2013). Vasseur et al.'s (2013) approach demonstrated how the oftentimes hidden landscape mosaic (i.e., temporal changes or chemical inputs) affects arthropod habitat suitability in farmland. Gil-Tena et al. (2015) evaluated bird occurrence and landscape heterogeneity within and among landscape patches, and focused on functional biodiversity rather than taxonomic biodiversity (e.g. insectivorous, seed eating, raptors etc.) (Gil-Tena et al., 2015). Both studies found that higher heterogeneity across the landscape resulted in higher biodiversity opportunity (Gil-Tena et al., 2015; Vasseur et al., 2013).

1.4 Conceptual Framework

In this dissertation, I utilized the telecoupling framework to guide my research questions, as the concept is well suited to understanding and quantifying complex interactions between coupled human and natural systems (J. Liu et al., 2013). The framework distinguishes sending, receiving, and spillover systems with defined boundaries as well as relevant environmental and socioeconomic causes, effects and agents (Figure 2). Systems are connected by flows which can be tangible (e.g., people, materials, organisms) or intangible (e.g., knowledge, technology, capital). The role a system plays (i.e., sending, receiving, or spillover) depends on the flow of interest (e.g., soybeans) and direction(s) of said flow. Sending systems have outward direction of flow (e.g., origin, source, exporter) while receiving systems flow inward (e.g., destination, recipient, importer). Spillover systems affect or are being affected by flows between sending and receiving systems (e.g., stopover, third party). Agents are defined as decision-makers in a system and can have either direct or indirect impacts on flows. Causes and effects of a system are often linked via feedbacks, and they are defined as components that influence emergence/dynamics of telecouplings and as consequences of telecouplings, respectively.

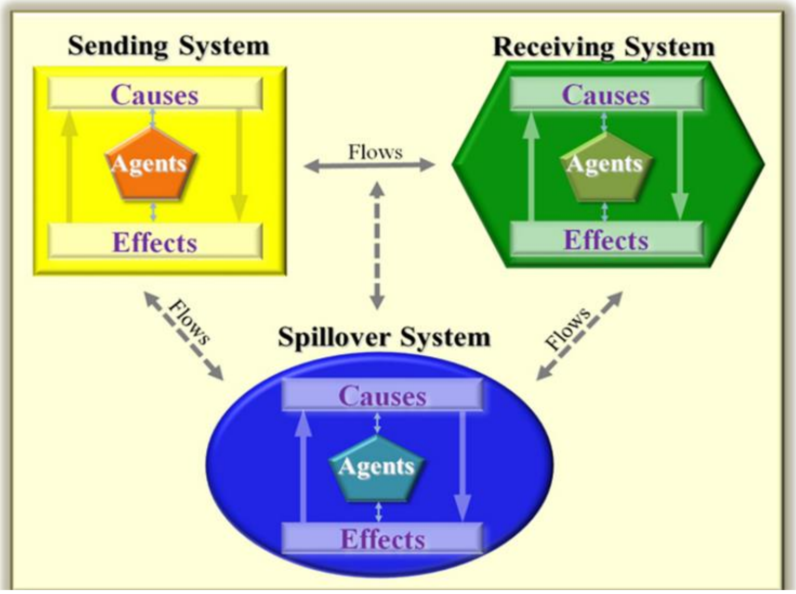


Figure 2: Conceptual Framework Diagram of Telecoupling (Taken from Liu et al. 2013)

In the context of this dissertation, we focus on flow of soybeans from Brazil to China. On that basis, Brazil as the sending system and China is the receiving system. and the United States is the spillover system. For our purposes, the US is defined as a spillover system as it is a major competitor to Brazil in the soybean market and exports a large share of its soybeans to China, however it is not the focus of this specific study. Cause and effect linked to soybean price in China (i.e., low priced Brazil soybeans outcompete domestically grown soybeans in China) and land use change (i.e., farmers in China shift crop types because they cannot compete with soybeans), respectively. A multitude of other cause and effects exist for this system, but this dissertation centers on soybean price and land use change. In this system, farmers are a primary agent as they make decisions on growing soybeans based on market prices. Land use change causes a secondary effect on biodiversity. The magnitude and significance of relationships between crop price, farmers, land use, and biodiversity are the focus of this dissertation.

1.5 Study System

The study site is Heilongjiang province in northeast China (Figure 3). Heilongjiang's biome is temperate broadleaf/mixed forests with a climate characterized by long, harsh winters and short, mild summers which allow for a single-crop growing season (Olson et al., 2001; *Weather and Climate*, 2016). Heilongjiang is the top agrarian producer in China. Until recently, the main crop was soybean, accounting for up to one third of total national production (Survey Office of the National Bureau of Statistics in Heilongjiang, 2013). Soybeans (*Glycine max*) are a nitrogen-fixing legume belonging to Fabaceae that typically grow to be ~50cm on average. The other two main crops are corn and paddy rice. Corn (*Zea mays*; Poaceae) is a tall cereal grass (2-3m) that produces 1-3 ears of corn per plant. Rice (*Oryza sativa*; Poaceae) is also a cereal grass traditionally grown in paddies that are flooded with 10cm or more of water throughout their growing cycle to limit competition from weeds.

In recent years, this region has undergone significant changes in land use/cover change (LULCC) as influence of global trade grows in the Chinese agriculture market. Due to cheap soybean imports from abroad, Heilongjiang's small-scale farmers struggle to sell their soybean harvests for profit. From 2009-2013, soybean cultivation in Heilongjiang dropped from 4 million ha to 2.4 million ha as farmers switched to growing more profitable crops such as corn and paddy rice (J. Sun et al., 2015; Survey Office of the National Bureau of Statistics in Heilongjiang, 2013).

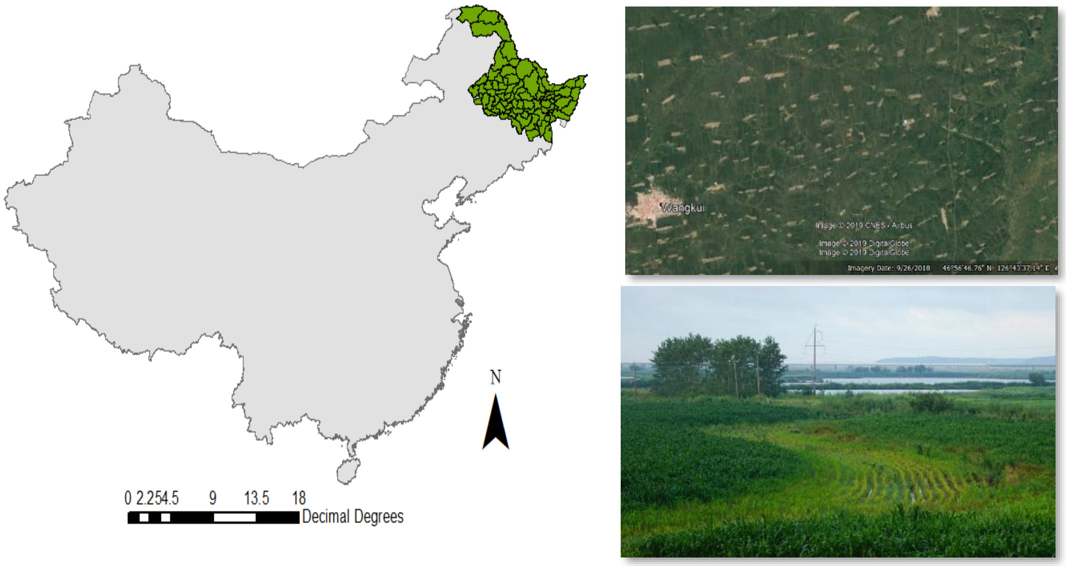


Figure 3: Map of Heilongjiang Province (left), Google Earth Image showing village and cropland juxtaposition (top right), and example of typical farmland (bottom right)

As previously stated, Heilongjiang's primary industry is agriculture therefore the majority of land is dedicated to cultivation. The only remnants of primary forest, once home to Siberian tigers, exist in the northwest of the province where the main industry is forestry (Muldavin, 1997). Despite being dominated by farmland, Heilongjiang is a unique agroecosystem, dominated by small-scale farmers. These farmers tend to manage 3-10 ha and are quick to respond to changing crop markets. The landscape is typified by villages scattered across the landscape, with fields of varying crop type and size in the surrounding vicinity (Figure 3). This type of agricultural landscape creates a diverse crop mosaic landscape, which can host a number of species that support overall biodiversity of the region (Y. Liu et al., 2013). Under current trends of crop conversion, it is not clear what impacts on biodiversity will be.

1.6 Dissertation Objectives

Chapter 2 synthesizes empirical evidence from scientific publications over the past decade that measured impacts of different telecoupling flows on biodiversity.

Chapter 3 describes the process of producing high fidelity landcover maps of the study region using satellite imagery and machine learning.

Chapter 4 evaluates relationships between structure (i.e., composition and configuration) of an agricultural landscape and taxonomic and functional biodiversity for birds at the community-level.

Chapter 5 evaluates species-specific relationships between agricultural landscape structure and bird occupancy at taxonomic and functional levels.

CHAPTER 2: COMPLEX IMPACTS OF TELECOUPLING ON GLOBAL BIODIVERSITY

In collaboration with
Veronica Frans, Kelly Kapsar, Aurora Torres, Yuqian Zhang, Min-Gon Chung, Yingjie Li,
Ruishan Chen, Emily Dean, Anna Herzberger, Ming Lei, Xutong Wu, Ying Xing, Jianguo Liu

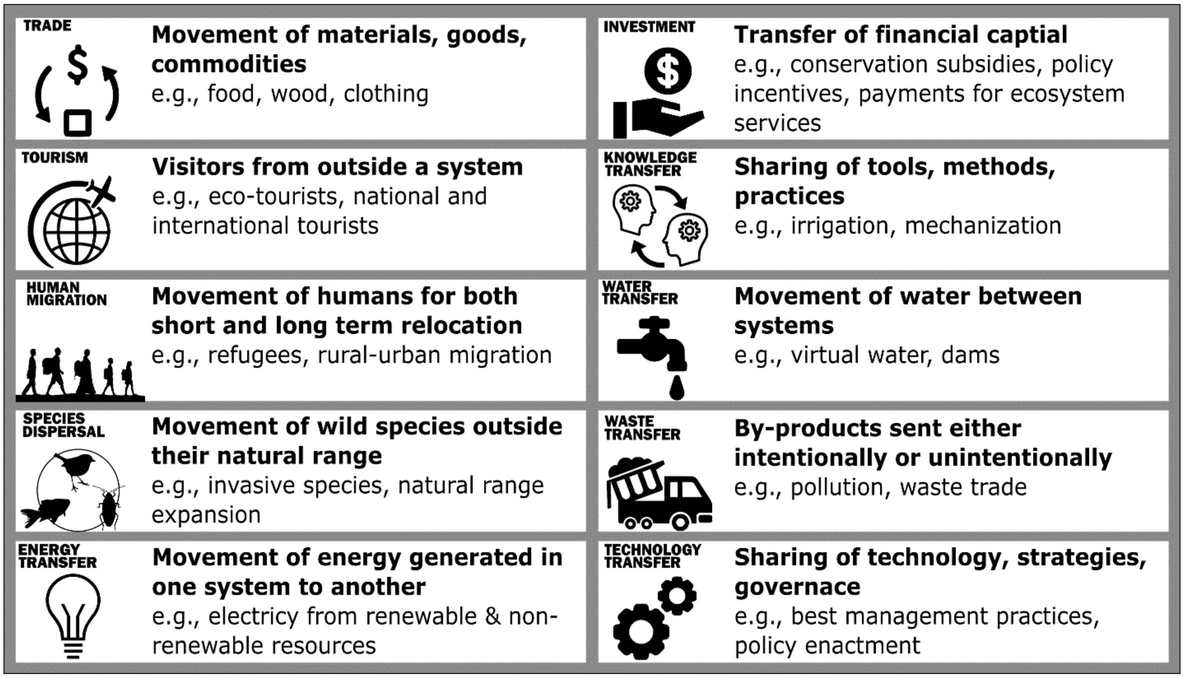
Abstract

As the world becomes more interconnected, underlying causes of the global biodiversity crisis often extend beyond local systems. Human-nature interactions over distances (i.e., telecouplings, which expand and integrate disciplinary concepts such as trade and tourism) are increasing in magnitude and complexity, yet knowledge about their impacts on biodiversity is scattered and fragmented. Here, we synthesized empirical evidence from scientific publications in the past decade that specifically measured impacts of telecouplings on biodiversity. Impacts reported as significant were categorized as “beneficial”, “harmful”, or “changed” based on direction of the biodiversity-telecoupling relationship (e.g., increased tourist disturbance linked to decreased species richness). Results indicated that harmful impacts were the most frequent outcome across all taxa (51%), though there were also beneficial impacts (11%). Among the 10 types of telecouplings, the most common telecouplings connected to observed impacts were tourism (46%) and trade (26%). We also found few studies occurring in Africa and Oceania, despite being the locations of many important biodiversity hotspots. Our study provides the first integrated assessment of evidence for impacts of telecouplings on biodiversity, and sheds light on how telecoupling-mediated mechanisms have complex cascading consequences for biodiversity. Further efforts to study telecoupling impacts on biodiversity will be critical for addressing the biodiversity crisis post-2020.

2.1 Introduction

Global biodiversity is threatened at an unprecedented scale and addressing the causes of these threats is essential to slow or reverse biodiversity declines. Modern species extinctions are occurring 1,000 times more frequently than historical background extinction rates (Díaz et al., 2019; S. L. Pimm et al., 2014) with species declines extending across taxa (Alroy, 2015; Arthington et al., 2016; Bek et al., 2017; Böhm et al., 2013; Ceballos et al., 2015; Darwall & Freyhof, 2015; S. Pimm et al., 2006; Sodhi et al., 2008; van Klink et al., 2020; Wake & Vredenburg, 2008). Approximately one million species of plants and animals are currently facing extinction due to human activity (Díaz et al., 2019). Understanding the underlying mechanisms that cause biodiversity loss is a key priority for assuring and enhancing the wellbeing of both humans and nature (Hooper et al., 2012; Mace et al., 2012; Oliver et al., 2015). Ultimate causes of biodiversity loss may originate locally and/or emerge from distant regions. Traditionally, research has focused on local causes of biodiversity loss, such as deforestation and habitat fragmentation. However, globalization has drastically altered the use of natural resources as well as patterns of resource consumption (Chaudhary & Kastner, 2016; Dorninger et al., 2021). As the world becomes more interconnected, resources and goods are increasingly consumed outside production systems. For example, local farming in many places is predominantly driven by international demand for commodity crops rather than local food requirements (Headey, 2011). Identifying only the local causes of biodiversity loss will oftentimes not provide enough information to discern or address the mechanisms ultimately driving reductions in biodiversity (Carrasco et al., 2017). Understanding the impacts of globalization on biodiversity requires an integrated approach that includes both local and distant interactions between humans and nature.

The telecoupling framework is such an integrated tool (J. Liu et al., 2013). The term ‘telecoupling’ refers to human-nature interactions over distances (J. Liu et al., 2013). It expands and integrates disciplinary concepts such as trade, tourism, migration, and investment (Figure 4). It encompasses local and distant systems as well as underlying mechanisms driving biodiversity impacts. In the context of this paper, we consider the location experiencing biodiversity impacts as the ‘local’ system. Telecoupling types are categorized by the content of the flows transferred between systems (Figure 4). Many different types of telecouplings have been associated with threats to biodiversity. In rural areas, for example, waste transfer in the form of agricultural run-off results in distance effects on distant and biodiverse regions, such as the “dead zone” in the Gulf of Mexico (Del Giudice et al., 2020; Osterman et al., 2009). Similarly, wild species in southeast Asia are increasingly threatened by the palm oil trade as their habitats are destroyed and converted to plantations to meet global demand (Fitzherbert et al., 2008). The role of telecouplings in global biodiversity changes is increasingly recognized (Chan et al., 2020) and has been highlighted in important international venues and publications (e.g., 2021 Nobel Prize Summit and 2019 Global Assessment Report on Biodiversity and Ecosystem Services sponsored by the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services). However, knowledge about the impacts of telecoupling on biodiversity is fragmented and scattered, and research synthesizing impacts is lacking.



TRADE **Movement of materials, goods, commodities** e.g., food, wood, clothing	INVESTMENT **Transfer of financial captial** e.g., conservation subsidies, policy incentives, payments for ecosystem services
TOURISM **Visitors from outside a system** e.g., eco-tourists, national and international tourists	KNOWLEDGE TRANSFER **Sharing of tools, methods, practices** e.g., irrigation, mechanization
HUMAN MIGRATION **Movement of humans for both short and long term relocation** e.g., refugees, rural-urban migration	WATER TRANSFER **Movement of water between systems** e.g., virtual water, dams
SPECIES DISPERSAL **Movement of wild species outside their natural range** e.g., invasive species, natural range expansion	WASTE TRANSFER **By-products sent either intentionally or unintentionally** e.g., pollution, waste trade
ENERGY TRANSFER **Movement of energy generated in one system to another** e.g., electricy from renewable & non-renewable resources	TECHNOLOGY TRANSFER **Sharing of technology, strategies, governace** e.g., best management practices, policy enactment

Figure 4: Overview of telecoupling types (bold) with examples.

A global overview assessing the relationships between telecoupling and biodiversity is urgently needed. Previous studies have examined the influence of single telecouplings (e.g., trade (Green et al., 2019); tourism (Brandt & Buckley, 2018) on biodiversity or on specific taxa (e.g., birds (Marques et al., 2019)), yet no studies have synthesized the influence of telecouplings across taxa, telecoupling types, and geographic regions. Given the potentially unique responses of specific taxa to different telecouplings, understanding these relationships is crucial to more effectively conserve biodiversity (J. Liu, 2021; J. Liu et al., 2016). This issue is particularly salient and timely as scientists and stakeholders around the world are developing the Post-2020 Biodiversity Framework (*Convention on Biological Diversity*, 2020), which will serve as a global biodiversity conservation blueprint for the next decade. Establishing the degree to which telecouplings impact biodiversity across taxa, telecoupling types, and geographic regions is essential to inform the next era of conservation in a globalized world.

To address this need, we conducted a global synthesis of telecoupling impacts on biodiversity. Our review assessed empirical studies from 2010 to 2019 that quantified the impacts of telecouplings on biodiversity, defined here as the variety of organisms across levels of biological organization. Of the 7,306 unique articles resulting from our initial search, 131 articles (1.8%) reported biodiversity indicators and their relationship with telecouplings. From this synthesis, we assessed the impacts of telecouplings on biodiversity and highlighted knowledge gaps to inform future research and conservation efforts.

2.2 Methods

We synthesized studies that quantified biodiversity change in the context of telecoupling published between 2010 and 2019. We curated studies for our synthesis by first conducting a literature search, then implementing multiple rounds of abstract and full text screenings to check that each study met our inclusion criteria. Once the initial screenings were complete, each article underwent a full-text assessment to extract data on the type of biodiversity and telecoupling studied, the study location, the metrics researchers reported, direction of the biodiversity impact, and significance of the impact. Overall impact was then determined for each article by taking the mode of all reported impact directions (e.g., beneficial, harmful) reported for each taxon. Each step of our research process – literature search, inclusion criteria, data extraction and analysis – is detailed below.

2.2.1 Literature Search

We implemented a systematic review by adapting the workflow of PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) (Moher et al., 2010; Sato et al., 2013). To synthesize impacts of telecouplings on biodiversity using information from peer-reviewed literature, we focused on research articles published within the past decade (2010-2019) and written in English. The literature search was conducted with Web of Science on December 20, 2019, using terms pertaining to four primary categories: biodiversity, impact, scale, and telecoupling. We used several keywords for each primary category. For example, terms such as “impact”, “effect”, “consequence”, and “influence” were included for the impact category, and “trade”, “migration”, “technology transfer” were for the telecoupling category (Hull & Liu, 2018). We finalized the search string based on different combinations of keywords, while excluding potentially ambiguous ones (see Box 1 in appendix for search string).

2.2.2 Inclusion Criteria

To only include articles relevant to the research objectives, we conducted two rounds of screening (title/abstract screening and full-text assessment) based on specific inclusion criteria we developed (Box 2 in appendix). We only included articles that met all five of the following criteria: (1) measured impacts on biodiversity of animal and plant species (excluding other taxa such as fungi, bacteria); (2) investigated the study species in relation to a particular telecoupling process; (3) reported direct outcomes in the form of a quantitative relationship, (4) were observational or experimental studies; and (5) were written in English. Subsequently, synthesis efforts, such as meta-analyses and literature reviews, fell outside the scope of this review. For example, a review by Scheele et al. provides strong evidence of the negative impacts of disease spread (chytridiomycosis) facilitated by humans but was not included in our synthesis due to the difficulty of identifying specific telecoupling processes related to species decline and the fact that many of the articles used to inform their meta-analysis were published prior to 2010 (Scheele et al., 2019).

For the first round of screening, we checked only the title and abstract for these criteria using the *metagear* package in R (Lajeunesse, 2016). Articles that were immediately identified as missing one or more of our criteria were removed prior to the full-text assessment. If it was unclear whether an article met the five criteria from the abstract, a full-text assessment was conducted to provide more context prior to deciding on inclusion or exclusion.

2.2.3 Data extraction and analysis

Once all articles were assessed for inclusion/exclusion criteria, each eligible paper was coded to extract information on study characteristics (e.g., telecoupling types, region; see Table 2 in appendix for codebook) and each biodiversity value reported (e.g., metric type, impact, significance; see Table 2 in appendix for codebook). To enhance inter-coder reliability (i.e., the concordance rate of individuals coding the same articles), all coders were initially trained by reading common abstracts and then having group discussions to determine an article's eligibility based on inclusion and exclusion criteria. Group decisions were made on articles with unclear eligibility; three additional coders independently assessed them, and a majority rule was used for the article's eligibility decision.

After all eligible articles were coded, we documented number of biodiversity values reported for a given taxa (e.g., occurrence values for multiple species, composition changes for multiple community structures) and their relationship with the telecoupling studied (i.e., impact). Impacts reported as significant were categorized as "beneficial", "harmful", or "changed" based on direction of the biodiversity-telecoupling relationship. Statistically insignificant relationships, neutral relationships, or cases of model disagreement were categorized as "unclear" impacts. The category with the greatest number of relationships determined overall impact for a given article. Articles with equal numbers in one or more categories were considered 'mixed'. All data were synthesized and visualized using R, version 4.1.0716 .

2.3 Results

Overall, telecouplings were more frequently associated with statistically significant harmful (51%) rather than beneficial (11%) impacts on biodiversity, and several impacts showed statistically significant changes in species communities (6%). There were, however, articles where telecoupling impacts on biodiversity were not straightforward, with 25% of articles resulting in ‘unclear’ (non-significant, neutral, disagreement) and 7% ‘mixed’ impacts (articles with equal numbers in one or more categories of impacts). The scale of the studies in our review ranged from local landscapes (Amira et al., 2018) to global assessments (Nishijima et al., 2016). We found biodiversity impacts driven by a wide array of complex mechanisms that ultimately affected many indicators of biodiversity (see Table 2 in appendix for list of indicator types). Some examples of impacted biodiversity indicators included changes in distribution (e.g., avoidance of recreation infrastructure in habitat (Coppes et al., 2017), density (e.g., trampling disturbance due to tourists (Sarmento & Santos, 2012), abundance (e.g., declining populations due to trapping for pet trade (Harris et al., 2017), and productivity (e.g., altered species interactions via alien species introduction (Nobre et al., 2019). Across the 131 articles, we recorded 788 cases of biodiversity indicators impacted by telecoupling (Figure 7, Table 3 in appendix).

2.3.1 Impacts across taxa

Harmful impacts on biodiversity were more frequent than beneficial impacts across all taxa (Table 4 in appendix). Mammals had the largest proportion of harmful impacts reported (80%), followed by invertebrates (48%), birds and plants (both 46%), and fish (40%). We found 4 studies recorded for reptiles and amphibians with harmful impacts (3 and 1 respectively). Similarly, most (75%) studies using indicators combining multiple taxa found harmful impacts. Birds were the most studied taxon (28%), followed by invertebrates (24%), vascular plants (21%), mammals (11%), and fish (11%; Table 3 in appendix). A much smaller set of articles studied reptiles and amphibians (4% and 1% of articles, respectively). Only four articles (3%) analyzed telecoupling impacts on more than one taxon simultaneously. Our assessment also revealed that there were relatively more beneficial impacts on birds and plants, potentially because conservation initiatives usually contribute to creation or bolstering of habitats at smaller scales, rather than those with large or restrictive habitat requirements (Balduino et al., 2017; Dale et al., 2017; Sanderson et al., 2016).

Birds experienced more harmful (46%) and unclear (22%) impacts than beneficial (16%) (Figure 5, Table 4 in appendix). Harmful impacts to birds were associated with trade (9 articles; e.g., impact of trade agreements and farming intensification (Reif & Vermouzek, 2019)) in addition to knowledge transfer and human migration. Tourism was also associated with harmful impacts to birds (7 articles; e.g., effects of road or trail use (Wolf et al., 2013)). Beneficial impacts for birds were mainly associated with knowledge transfer (50% of beneficial bird impacts [3 articles]; e.g., biodiversity-friendly farming practices (Martín et al., 2012)), tourism (e.g., disturbed park areas had higher abundances for some species (Huhta & Sulkava, 2014)), and species dispersal (e.g., non-native shrub offered more food resources for woodland bird species (Arizaga et al., 2013)). Instances of trade interacting with other telecouplings also resulted in beneficial impacts: knowledge transfer (conservation policy informed by prices of crops for trade (Hyun et al., 2013)) and energy transfer (forest fragmentation for transferring natural gas increased abundances of some bird species (Farwell et al., 2016)).

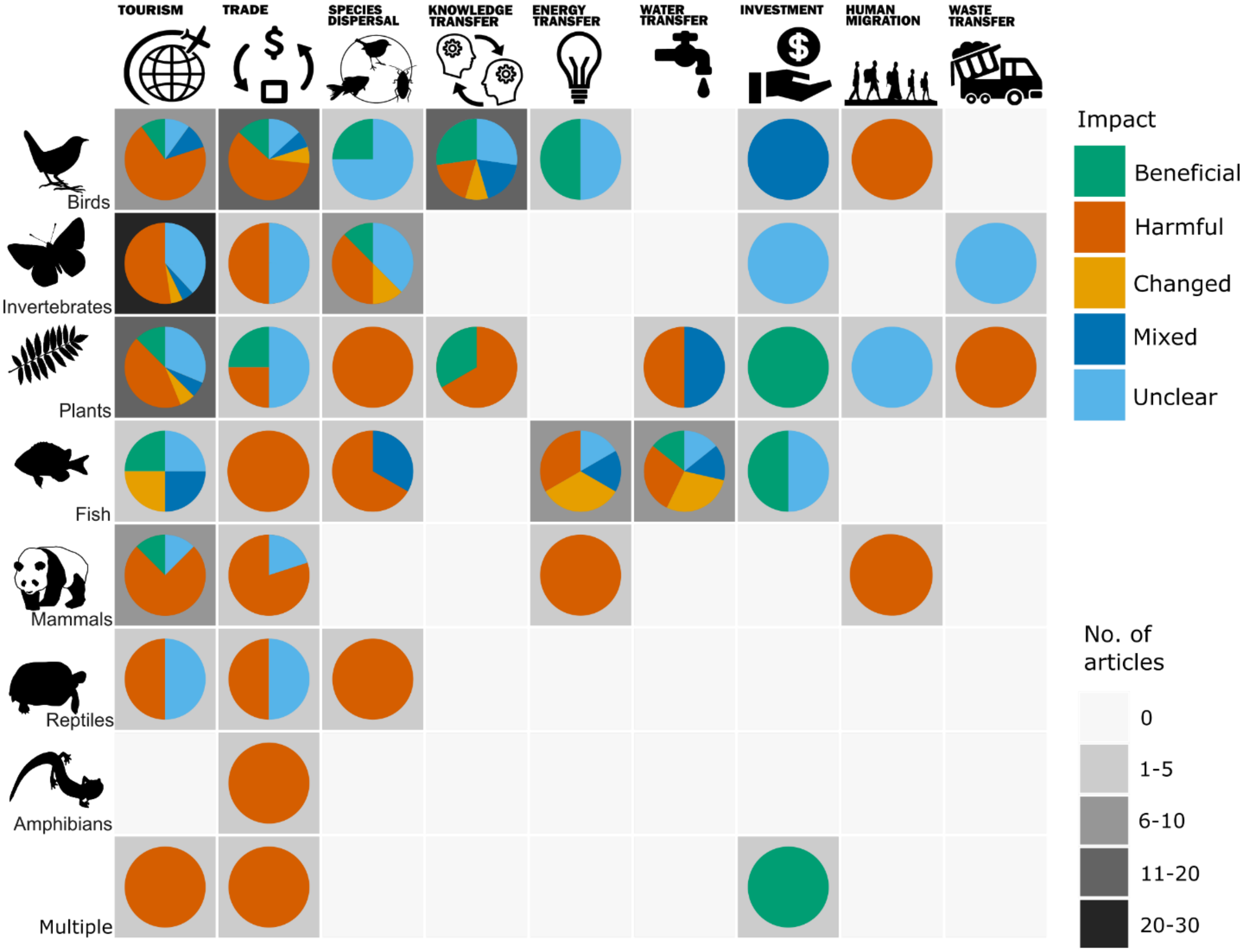


Figure 5: Reported impacts of telecouplings on biodiversity for each taxon in the examined articles. Each pie chart shows the relative proportion of impacts found across articles for each taxon and telecoupling type (Figure 2.1). Beneficial, harmful, and changed impacts indicate a significant relationship between biodiversity and telecoupling was found. Unclear impacts indicate non-significant, neutral, or disagreeing results within a study and mixed impacts mean an article had equal numbers of indicators in one or more categories (e.g., increased abundance of one species, decreased for another). The background of the pie chart indicates the number of articles in a given category (white to black). Articles that considered multiple telecoupling types were counted for each type reported.

Invertebrates were found to be most associated with harmful (48%) and unclear (39%) impacts, with only one study demonstrating beneficial impacts of telecouplings (Figure 5, Table 4 in appendix). Studies reporting harmful impacts were most often related to tourism (11 articles; e.g., impact of trampling on reef communities (Santos et al., 2015)), as well as species dispersal (e.g., release of popular aquarium corals that outcompete native species (Mantelatto et al., 2018)) and trade (e.g., decreased soil fauna diversity in tropical forest converted to rubber plantations for trade (Singh et al., 2019)). The single instance of beneficial impacts was related to species dispersal (e.g., benthic community benefitting from the introduction of a non-native fish that altered the functioning of the lakes' trophic and increased productivity (Nobre et al., 2019)).

Plant biodiversity was associated more with harmful (46%) and unclear (29%) impacts than beneficial (14%) (Figure 5, Table 4 in appendix). Tourism was frequently associated with harmful impacts to plant biodiversity (7 plant articles, e.g., plant community disturbance due to tourist activity (Šilc et al., 2016)). In addition to tourism, plants were negatively impacted by telecouplings related to species dispersal (2 plant articles, non-native plants inhibiting native species diversity (Fukami et al., 2013)) as well as knowledge transfer (dissemination of information regarding mismatch between habitat needed and habitat protected (Assédé et al., 2018)), trade (e.g., community market access and local plant richness (Oldekop et al., 2018)), water transfer and waste transfer (run-off contaminants inhibit growth of saltmarsh plant species and allow for the encroachment of exotic and mangrove species (Geedicke et al., 2018)). For plants, most beneficial associations occurred with tourism (e.g., intermediate disturbance caused by tourists (Czortek et al., 2018)), investment, and knowledge transfer (policy and incentives to start game farms decreased vegetation loss (Mokotjomela & Nombewu, 2020)) with one instance related to trade (e.g., wood pellet trade resulted in improved overall forest condition (Dale et al., 2017)).

For mammals, the majority of telecoupling impacts were harmful (80%), with remaining impacts being 7% beneficial and 13% unclear (Figure 5, Table 4 in appendix). Harmful impacts on mammal biodiversity were associated with tourism (e.g., tourist presence deterring species with low tolerance for human activity (Zhou et al., 2013)), trade (e.g., impact of commercial livestock on local species (Moraga et al., 2015)), human migration (e.g., increased hunting resulting from migrant populations increasing demand for bushmeat (Remis & Jost Robinson, 2012)), and energy transfer (e.g., effect of oil-spills on marine mammals (Balmer et al., 2018)). The only instance of beneficial impacts was related to tourism (more visitors increased wildlife protections resulting in higher elephant numbers (Selier et al., 2016)).

Fish experienced mostly harmful impacts (40%) with some instances of significant community changes (20%) and even fewer beneficial outcomes (13%) (Figure 5, Table 4 in appendix). Harmful impacts on fish biodiversity were the most frequent (40%) and associated with trade (3 articles; e.g., unmanaged harvest for the aquarium trade(Santos et al. 2015)) as well as species dispersal (e.g., introduced aquaculture species led to a reduction of native species (Cuvin-Aralar, 2016)), energy transfer, and water transfer (e.g., cascaded dams and reservoirs impeded movement of eggs, larvae and young fish more than a single dam (Yang et al., 2017)). Most studies reporting significant changes to fish communities were associated with hydroelectric dams (i.e., water and energy transfer) and physical barriers to movement they created (Lima et al., 2018; Sá-Oliveira et al., 2015). Additionally, one study demonstrated significant changes to fish behavior due to tourist activity (Lima et al., 2014). Beneficial impacts on fish biodiversity were recorded for tourism (e.g., tourist feeding fish resulted in high fish abundance (Balduino et al., 2017)), water transfer, and investment (e.g., investment in restoration efforts for dam removal increased number of lamprey nests (Lasne et al., 2015)).

Although reptiles and amphibians were studied in relatively fewer articles, some significant impacts of telecoupling were found (Figure 5, Table 4 in appendix). Impacts on reptile biodiversity were either harmful (60%; 3 articles) or unclear (40%; 2 articles). The three cases of harmful impacts were associated with species dispersal (e.g., spread of parasite from invasive turtle species to native species (Meyer et al., 2015)), tourism (e.g., tourism development resulted in reptile populations (Krawczyk et al., 2019)), and trade (e.g., population declines due to the pet trade (Flecks et al., 2012)). For amphibians, while we had a small sample size that prevented us from assessing impacts adequately, one study related trade to harmful impacts on amphibian communities (e.g., community market access and frog richness (Oldekop et al., 2018)).

2.3.2 Impacts across telecoupling types

Most articles investigated changes in biodiversity associated with impacts of tourism (46%) and trade (26%). Species dispersal and knowledge transfer were the next most common telecouplings studied, representing 13% and 10% of articles, respectively. The remaining telecouplings (energy transfer, investment, human migration, water transfer, and waste transfer) were each studied in <10 articles (Table 5 in appendix). No studies looked at the impact of technology transfers. Some articles studied impacts of multiple, interacting telecouplings on biodiversity (18%). In these cases, we attributed the impacts to all telecoupling types mentioned in the article.

In general, biodiversity was negatively impacted by telecouplings. Over half of the articles for trade and tourism showed harmful impacts. Trade was reported as harmful in 64% of the articles (e.g., biodiversity loss due to human consumption of traded goods (Wilting et al., 2017)). For tourism, 53% were categorized as harmful (e.g., human trampling at tourist destinations (Farris et al., 2013)). Species dispersal, the third most frequent telecoupling studied, was associated with harmful impacts in 44% of the articles (e.g., impacts of invasive species on local species communities (Van Bocxlaer & Albrecht, 2015)).

Some types of telecouplings had relatively more beneficial impacts on biodiversity. Compared to other telecoupling types, investment and knowledge transfer had higher proportions of beneficial impacts on biodiversity (43% and 21% respectively; Table 5 in appendix). Beneficial impacts on biodiversity were mostly linked with policy initiatives committed to halting biodiversity loss by driving conservation investments (Waldron et al., 2017), knowledge transfer to promote ecological restoration efforts (Sieges et al., 2014), transitions from intensive production to ecological production methods (e.g., agro-environmental schemes (Gamero et al., 2017)), and the creation of protected areas (Kleijn et al., 2014).

In some articles, we also observed mixed impacts (i.e., equal contributions of beneficial, harmful, changed, or unclear impacts). For example, tourism was sometimes beneficial (e.g., income from tourism funding conservation efforts (Selier et al., 2016)) or harmful (e.g., tourism disturbance (Coppes et al., 2017)). Differential impacts may also reflect different tolerance levels among species (Shochat et al., 2010), with sensitive species being lost (e.g., Bronze-tailed Peacock-pheasant [*Polyplectron chalcurum*] or capercaillie [*Tetrao urogallus*] avoiding roads and other infrastructure (Coppes et al., 2017; Harris et al., 2017)), less sensitive species resisting, and some non-native, introduced species thriving (e.g., the highly invasive snail, *Melanoides tuberculata,* in Lake Malawi (Van Bocxlaer & Albrecht, 2015)). Thus, depending on the relative proportion of declining, resisting, and thriving species within a focal system, telecouplings may change local species assemblages (Reyes-Martínez et al., 2015), leading to biotic homogenization or a loss of community uniqueness (Thomas et al., 2014). Likewise, conservation policies involving knowledge transfer and investment can also result in mixed impacts. For example, a review of the European Union’s agriculture policy showed that despite the intended beneficial biodiversity impacts of farmland conservation incentives, harmful impacts also occurred due to agricultural intensification encouraged by policymakers (Gamero et al., 2017).

2.3.3 Impacts across regions

There was a bias in distribution of locations for studies regarding telecoupling impacts on biodiversity. Studies most commonly occurred in Brazil (15%), the United States (10%), and China (8%). However, when aggregated to the continental scale, Europe (23%) was the most frequent study continent. The remaining articles were distributed across South America (20%), Asia (19%), North America (17%), Africa (8%), Oceania (8%), and Antarctica (2%), with global studies representing 4% of all the articles. The relative scarcity of studies in Africa and Oceania is concerning, as they are home to many of the world's most valuable (and threatened) biodiversity hotspots (Habel et al., 2019). The distribution of studies across habitats was also biased. Most articles investigated impacts on biodiversity in terrestrial habitats (57%), whereas 19% and 17% of articles examined impacts on biodiversity in marine and freshwater habitats, respectively (Table 6 in appendix).

The direction of telecoupling impacts on biodiversity also varied geographically. Harmful impacts were most frequent across all continents, apart from North America, where 50% of the impacts were unclear. Europe had the largest number of beneficial impacts compared to other

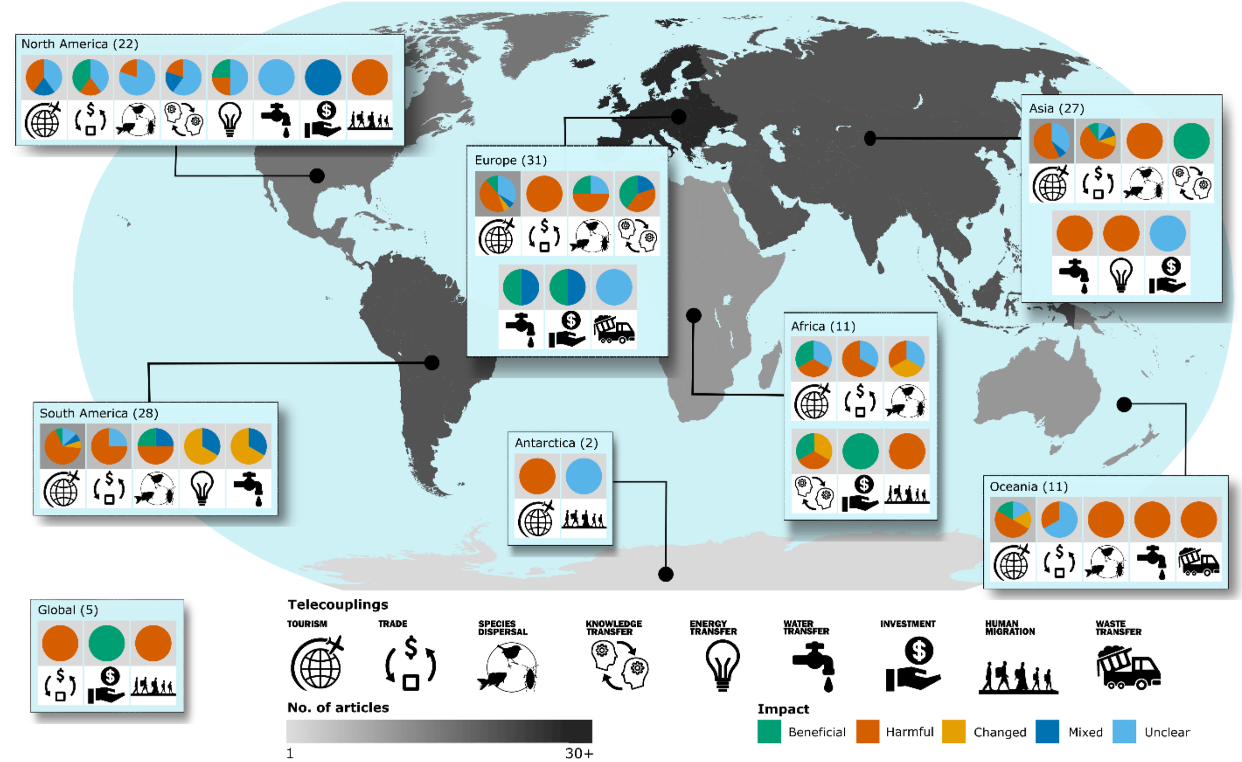


Figure 6: Reported impacts of telecouplings on biodiversity by continent. Each pie chart shows the relative proportion of impacts (i.e., beneficial, harmful, changed, mixed, unclear) found across articles for each continent and telecoupling type (Figure 4). The background of the pie chart and the color of each continent indicates the number of articles in each category (white to black). Articles that consider multiple telecoupling types are replicated for each type's pie chart.

continents. Of the five global studies, four reported harmful impacts of telecoupling while the remaining one demonstrated beneficial impacts (Figure 6**,** Table 7 in appendix).

The types of telecouplings studied in the context of biodiversity impacts differed by continent as well. Tourism studies occurred mostly in Europe, Asia, and South America and trade studies were mainly concentrated in Asia and South America. Trade and tourism were also common telecouplings in North America, in addition to species dispersal, knowledge transfer, and energy transfers. For Africa, tourism, trade, species dispersal, and knowledge transfer were equally studied, whereas studies in Oceania focused on tourism and trade. The two studies that looked at telecoupling impacts on biodiversity in Antarctica were related to tourism and human migration. Finally, studies conducted on a global scale mostly focused on trade with one study each related to investment and human migration. Across all continents, investment, human migration, and waste transfer were the least studied (Figure 6**,** Table 7 in appendix**).**

2.4 Research Challenges & Recommendations

Telecouplings are increasing in magnitude and scope as the world becomes more interconnected and populations grow (Borrelli et al., 2020; Powers & Jetz, 2019; Stehfest et al., 2019). They will likely continue to have significant impacts on global biodiversity. In our analysis, we found abundant evidence of telecouplings driving biodiversity change. However, the percentage of studies that explicitly acknowledged, identified, and quantified relevant telecouplings and their impacts on biodiversity was small in the literature (1.8%). Thus, more extensive and empirical studies on telecoupling impacts and mechanisms are urgently needed. Additionally, there is a need for studies that link environmental changes driven by telecoupling to specific indicators of biodiversity. Finally, of the studies that considered telecouplings as a driver of biodiversity changes, the majority were biased towards certain taxa, locations, and metrics.

2.4.1 Mechanisms behind impacts of telecoupling on biodiversity

This study provides evidence demonstrating the profound impacts of telecoupling on biodiversity. However, the specific mechanisms that led to these impacts were less studied and thus are less clear. Here, we define mechanisms as the processes driving biodiversity impacts involved in a particular *flow* of materials, energy, people, products, capital, information, and organisms. Other important components of the telecoupling framework are factors influencing emergence and dynamics of flows (*causes*), socioeconomic and environmental consequences of the telecoupling (*effects*, which includes cascading impacts on biodiversity), and the relevant *systems* (*local* and *distant*) (Table 1).

Table 1: Examples of biodiversity impacts present in our sample and their potential telecoupled mechanisms

Telecoupling type	Trade	Tourism	Species Dispersal	Knowledge Transfer	Energy Transfer
Distant System	Food importing countries	Country with eco-tourists	Native range of introduced species	International regulators	Energy company
Local System	Food exporting country	Country with eco-tourism attractions	Region species introduced to	Nation under regulation	Location of energy extraction
Causes	High global food demand	Eco-tourism industry established	Economic need in local community	Alternative production encouraged by regulators	Increased energy demand
Effects	Deforestation for more cropland and habitat loss	Tourist spending reinforcing wildlife protections	Non-native species introduced for production, altered species community	Widespread use of practice improves habitat quality	Contamination event leading to habitat degradation
Biodiversity Impact	Increased extinction risk	Increased wildlife abundance	Decreased native species dominance	Increased wildlife populations	Displacement of wildlife populations
	(Green et al., 2019)	(Selier et al., 2016)	(Cuvin-Aralar, 2016)	(Martín et al., 2012)	(Balmer et al., 2018)

More studies should connect observed changes in biodiversity to both local and distant drivers so that the mechanisms can be better understood. To illustrate the full application of the telecoupling framework, we outlined potential mechanisms of telecoupling impacts on biodiversity in five articles with examples for each component (Table 1). In general, mechanisms vary greatly across telecoupling types. For example, agricultural trade caused by international demand can result in harmful biodiversity impacts by increasing the need for land conversion and thus habitat loss in the local system. In the case of tourism, biodiversity often benefits from the economic incentives to preserve wildlife. It should be noted that, due to the inherent complexity of telecouplings, accurately identifying and quantifying each component of the telecoupling framework can be challenging. Thus, after an initial mechanism is established, further investigations should take place to validate the proposed model and uncover new research avenues. This holistic approach is necessary to fully understand biodiversity dynamics.

2.4.2 Explicitly identify and define potential telecouplings

Many of the studies we found did not directly examine telecoupling impacts, with most telecouplings being briefly mentioned or inferred by us. For example, we classified studies involving production of globally traded commodities in the local system as influenced by trade, even if authors did not directly identify the regions that ultimately received the commodities. Explicit links between observed biodiversity changes due to telecouplings are essential to understand the mechanisms and achieve more effective management and sustainability interventions with less trade-offs. For instance, policies to mitigate deforestation in the Amazon for soybean production and trade have resulted in increased deforestation and threats to biodiversity in another biodiversity hotspot, the Brazilian Cerrado region (Dou et al., 2018). Findings from research like this can help avoid similar spillover effects on biodiversity in other systems. Whenever possible and appropriate, researchers should identify all relevant human-nature interactions in their local system and those relevant distant systems (Table 1). Doing so ensures that all important drivers of change are accounted for and may also lead to unexpected avenues for further investigation.

2.4.3 Connect environmental change to biodiversity indicators

There is a pressing need to bridge the gap between studies connecting telecouplings to environmental change and those quantifying biodiversity's relationship to environmental variables. Many studies on telecouplings quantified direct and local environmental impacts, but rarely included biodiversity indicators in their assessment. Research that simultaneously measures telecouplings' impact on the environment and biodiversity should be a priority for future research. To overcome logistical challenges of such an undertaking, researchers can also use existing studies, datasets, and/or models to link telecouplings with biodiversity. For example, researchers have successfully combined socioeconomic models for material flow and economic trade with biodiversity models to quantify extinction risk for species of concern in the Brazilian Cerrado (Green et al., 2019). Such innovative approaches to telecoupling and biodiversity research can play a large role in future biodiversity conservation.

2.4.4 Apply the telecoupling framework to understudied taxa and geographic regions

More studies need to be conducted on those taxa and geographic regions underrepresented in the current literature. The scientific literature assessing telecoupling impacts on biodiversity focused on certain locations, taxa, and biodiversity metrics. Most articles focused on birds, plants, and invertebrates in terrestrial habitats. Amphibians, reptiles, fishes, and mammals were comparatively under-studied, which may have implications for understanding threatened species and conservation prioritization. Moreover, only four studies used biodiversity indicators including more than one taxon (Marquardt et al., 2019; Seshadri & Ganesh, 2011; Waldron et al., 2017; Wilting et al., 2017). Bridging this research gap with multi-taxa studies may facilitate more comprehensive conservation policies to limit biodiversity loss. Additionally, many studies were concentrated in Brazil, the United States, and China. In contrast, studies rarely occurred in Africa, the Middle East, and South and Southeast Asia. The disproportionately low number of scientific studies on these regions is concerning, as they are forecasted to experience increased rates of development in the coming decades (Bren d'Amour et al., 2017). This limited number of studies could lead policy makers to underappreciate the importance of telecouplings in those regions. Finally, our study revealed differential use of various biodiversity metrics. Most articles reported compositional and structural components of biodiversity, using metrics such as species presence or absence, richness, and abundance. In contrast, impacts on movement, population dynamics, or functional metrics were rarely assessed. Assessments of biodiversity should be conducted using a wide variety of indicators to better understand telecoupling impacts on ecological processes that in turn shape biodiversity. Studies addressing one or more of these gaps will be essential for informing biodiversity conservation.

2.5 Conclusions

This paper synthesizes impacts of 10 different types of telecoupling on 7 major taxa across all continents. It is also timely as the world is developing the Post-2020 Global Biodiversity Framework. Impacts of telecoupling are often beyond the control of local people, highlighting greater challenges in biodiversity conservation and the increasing need for global collective actions.

Slowing the trajectory of biodiversity loss requires an integrative approach to conservation. Amid the current biodiversity crisis, it is imperative that policy and intervention strategies be tailored to the ultimate causes of species loss. The causes of biodiversity decline are often intertwined with both local drivers and telecouplings. Our synthesis demonstrates the need for more research that empirically assesses biodiversity change in the context of distant system interactions. Of the studies that identified telecouplings linked to biodiversity change, impacts varied widely across taxa, regions, and telecoupling types. Despite some instances where telecouplings benefitted biodiversity, it was clear that most impacts of telecouplings were overwhelmingly harmful. This further highlights the importance of understanding the dynamics and interactions of the human and natural components of telecoupled systems if leverage points for intervention are to be found. Policy aiming to reduce biodiversity declines needs to consider telecouplings in addition to local drivers. Collaboration among governments, industries, and communities in local and distant systems will be essential. Halting biodiversity loss is a global challenge that will require system-based solutions. Utilizing integrated and interdisciplinary approaches, such as the telecoupling framework, will bring us closer to these solutions and a more sustainable future in a telecoupled world.

APPENDIX

2A.1 Supplemental Methods

Box 1: Search string

(TS = ((Biodiversity OR "Biological diversity") AND (abundan* OR densit* OR "population size" OR "population-level" OR "species distribution" OR *diversity OR "species richness" OR "species composition" OR "species evenness" OR "number of species" OR biomass) AND (impact* OR effect$ OR affect* OR influenc*) AND (transboundary OR intercontinental OR distal OR teleconnection$ OR telecoupl* OR "far away" OR external OR trade OR touris* OR migrat* OR "information dissemination" OR "technology transfer" OR "knowledge transfer" OR "foreign investment" OR "international aid" OR "international cash transfer" OR "international remittance" OR "payment for ecosystem services" OR "virtual land" OR "virtual water" OR "virtual energy" OR "human migration" OR refugee$ OR immigra* OR “disease spread” OR “foreign direct investment” OR “labor migration”)) NOT TS=(trade-off$ OR simulation))(TS = ((Biodiversity OR "Biological diversity") AND (abundan* OR densit* OR "population size" OR "population-level" OR "species distribution" OR *diversity OR "species richness" OR "species composition" OR "species evenness" OR "number of species" OR biomass) AND (impact* OR effect$ OR affect* OR influenc*) AND (transboundary OR intercontinental OR distal OR teleconnection$ OR telecoupl* OR "far away" OR external OR trade OR touris* OR migrat* OR "information dissemination" OR "technology transfer" OR "knowledge transfer" OR "foreign investment" OR "international aid" OR "international cash transfer" OR "international remittance" OR "payment for ecosystem services" OR "virtual land" OR "virtual water" OR "virtual energy" OR "human migration" OR refugee$ OR immigra* OR “disease spread” OR “foreign direct investment” OR “labor migration”)) NOT TS=(trade-off$ OR simulation))

Box 2: Inclusion and Exclusion Criteria

1. BIODIVERSITY: Does it measure impacts on biodiversity? Here, our definition of biodiversity refers to the variety of organisms across levels of biological organization. This includes any animal and plant species, at any life stage, at terrestrial, freshwater, or marine realms. EXCLUDE (irrelevant) if there is no measurement of impacts on biodiversity or impacts are assessed for other taxa (e.g., fungi, bacteria). If unclear from the information provided in the title/abstract, answer YES (full paper to be screened). INCLUDE papers that look at proxy measures (e.g., land-use change or habitat) if it is in the context of a specific species or group of species.

2. INTERVENTION: Does the study investigate the impacts of telecouplings on the study species? (i.e., Effect/Impact of ______ on biodiversity). This includes "trade, tourism, species dispersal, human migration, the spread of diseases, knowledge transfer, information dissemination, technology transfer, international investments, international cash transfer, international remittance, payments for ecosystem services, virtual land or water or energy"… or direct mention of telecoupling INCLUDE papers that have inferred telecoupings (e.g. a paper discussed local biodiversity variation due to tourism without specifying tourist source; a paper mentioned local landscape change impact on biodiversity because of agricultural food trade in general). EXCLUDE (teleconnections) papers analyzing the impacts of teleconnections (e.g., natural long-distance seed dispersal) as this revision focuses only on human-nature interactions (couplings). EXCLUDE papers focused on "ecosystem services" generally (if no biodiversity metric is mentioned).

3. OUTCOME: Does this study report direct outcomes in the form of a quantitative effect of the intervention? Studies should quantify the relationship between couplings and biodiversity responses at metacommunity, community, population or species levels. This can include population abundance, species presence/absence, species richness/abundance among other response variables. We will include all outcomes (beneficial, harmful, direct and indirect) associated with any aspect of couplings. EXCLUDE studies that report qualitative outcomes or do not report outcomes at all.

4. STUDY CLASS: Is this an observational study? This can include manipulated experiments (i.e., researcher has control over the variable of interest and the response to/ manipulating it is measured), or non-manipulative studies (sometimes called observational or natural experiments) occur when the researcher takes advantage of changes that have happened (by using existing data) or are about to happen (by taking measurements, i.e. making observations) to understand its effect. If the study is a simulation study (i.e., individual-based models or population viability analysis) = EXCLUDE (modeling study); unless the study contains potentially useful field-collected data that was used to validate the model. Also, any recent reviews that you deem to have potentially relevant references (i.e., the review is relevant but simply not primary literature = EXCLUDE (relevant review) but write down the title, to screen later at full-text; time permitting, we will go through those references to ensure we're capturing all relevant papers. Similarly, if the item is an entire conference proceeding including multiple abstracts of potential relevance = EXCLUDE. All other situations = EXCLUDE (i.e., policy discussions, conceptual frameworks, strictly modeling, or irrelevant reviews, or the coder determined the study is not relevant at all).

5. LANGUAGE: Is the full text written in English?

Table 2: Codebook

Category	Variable Name	Variable Type	Type of Question	Response Options	Description
Screening Confirmation	Biodiversity Impact	Text	Short answer, text	-	What is the specific "biodiversity" being studied in this article? (e.g., Polar bear population dynamics)
	Telecoupling	Text	Short answer, text	-	In your own words, what is the external process that is impacting biodiversity in the focal system(s)?
	Quantitative	Text	Short answer, text	-	What are the specific quantitative variables that were collected/analyzed in relation to the impact of the telecoupling on the studied biodiversity metric?
	Study Type	Text	Multiple choice (single response)	True False	This study is based on observations and/or experiments. It is not a simulation study (e.g., climate forecasting) or review paper.
Identifiers	Paper ID Code	Text	Short answer, numerical	-	NA
	Coder Name	Text	Short answer, text	-	NA
	Year Published	Continuous (Integer)	Short answer, numerical	2010-2020	NA
	First Author's Last Name	Text	Short answer, text	-	NA
Biodiversity	Taxonomic Focus	Text	Checkboxes	Bird Mammal Reptile Amphibian Fish Invertebrate Plant Other	Check the boxes for the taxonomic groups for which data were collected, analyzed, and/or synthesized during the study.
	Biodiversity Indicator (single species)	Text	Multiple choice (single response)	Abundance/Density Occurrence Within-Species diversity Population dynamics NA	Abundance/Density – number of individuals, individuals/unit area, biomass Occurrence – presence, range, persistence, NOT detections (if separate from occurrence) Within species diversity – genetic diversity, age structure, etc. Population dynamics – survival, fitness, reproduction, mortality, etc. If indicator is at multiple or habitat level, select NA
	Biodiversity Indicator (multiple species)	Text	Multiple choice (single response)	Diversity index Richness Evenness Composition Abundance/Density Occurrence NA	Diversity index – Shannon-wiener, Simpson's, Inverse Simpson's, etc. Richness – number of species Evenness – relative abundance Composition – what species make up the community? Abundance/Density - number of individuals, individuals/unit area, biomass Occurrence - presence, range, persistence, NOT detection (if separate from occurrence) If indicator is at single or habitat level, select NA
	Biodiversity Indicator (habitat)	Text	Multiple choice (single response)	Amount Quality	Amount – e.g. land use change from non-habitat to habitat (must be in the context of specific species) Quality – pollution, connectance, disturbance, etc. If indicator is at single or multiple level, select NA

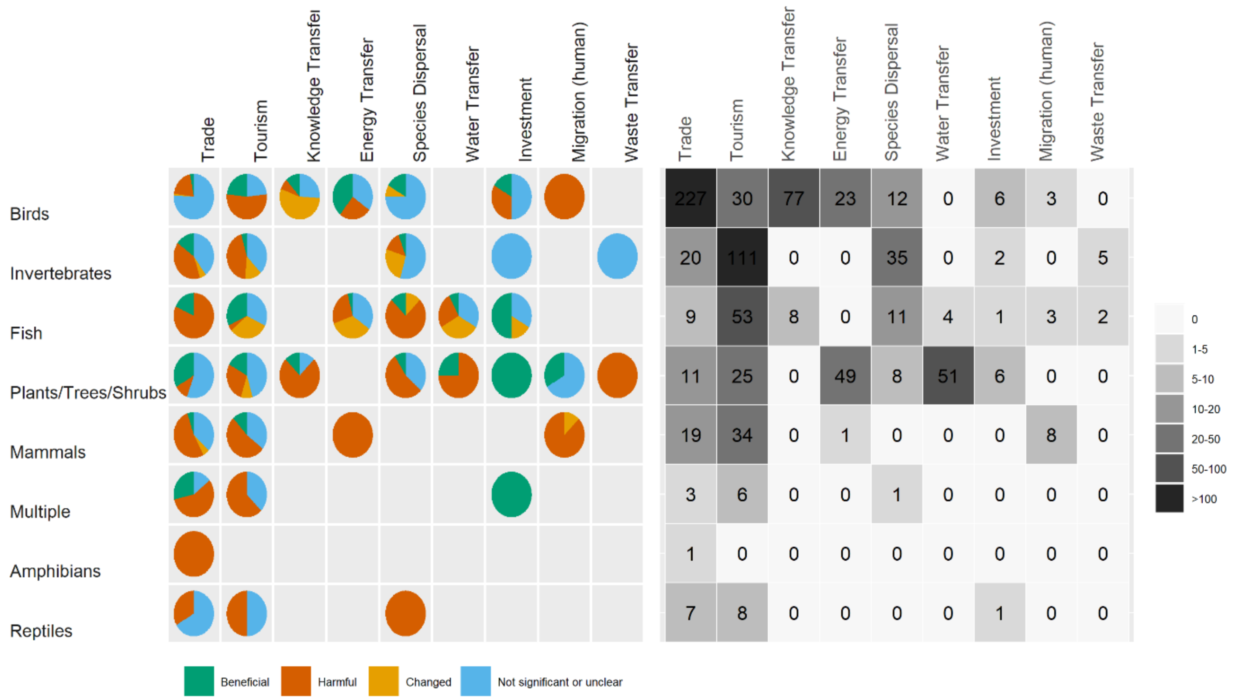
Table 2 (cont’d)

Telecoupling Variables	Specific Telecoupled Flow Type(s)	Text	Short answer, text	-	State the specific external flow(s) that were analyzed in relation to their impact on focal system biodiversity. For example, if international trade data were analyzed, which commodities were used to evaluate trade?
	Telecoupled Flow Category	Text	Checkboxes	Trade Migration (human) Migration (non-human) Species Dispersal Tourism Knowledge Transfer Technology Transfer Investment Water Transfer Waste Transfer Other	Check the boxes for the variables that were analyzed as they flowed **between** countries, multi-country regions, or continents.
	Impact of Telecoupling	Text	Multiple choice (single response)	Beneficial Neutral Harmful Changed Unclear	Beneficial = Biodiversity improved as a result of the telecoupling process Neutral = Biodiversity did not change a result of the telecoupling process Harmful = Biodiversity declined as a result of the telecoupling process Changed = Biodiversity changed but no determination of direction could be made (e.g., change in community composition)
	Impact of Telecoupling (Unclear)	Text	Short answer, text	-	If you selected "Unclear" above, please briefly state the situation. Otherwise, leave blank.
	Significance of telecoupling	Text	Multiple choice (single response)	True False Not evaluated	The impact of the telecoupling process on biodiversity was statistically significant (p<= 0/5).
Study Characteristics	Habitat	Text	Checkboxes	Terrestrial Freshwater Marine Not specified/Global study	For descriptions, see https://askabiologist.asu.edu/explore/biomes
	Number of Countries Analyzed	Continuous (Integer)	Short answer, numerical	1-200	State the total number of countries included in the analysis (regardless of the number of focal countries listed in the "Scale of Analysis" section).
	Countries Analyzed	Text	Short answer, text	-	If <10 countries were analyzed, please write the country names here. Otherwise, leave blank.
	Continent(s) represented	Text	Checkboxes	North America South America Asia Europe Africa Antarctica Australia Unclear/unknown	Check boxes for all continents from which data were collected/analyzed.

2A.2 Supplemental Results

2A.2.1 Total vs Overall Impacts

We documented a total of 788 telecoupling impacts on biodiversity within the 131 eligible articles from our review (Figure 7). Telecouplings were more frequently associated with statistically significant harmful (30%) rather than beneficial (10%) impacts with biodiversity, and a considerable number of impacts showed statistically significant changes in species communities (13%). However, most articles (70%) reported multiple cases of biodiversity impacts (e.g., occurrence values for multiple species, composition changes for multiple community structures). Furthermore, the total number of impacts per article was highly variable (range of 1-162). Therefore, we also evaluated the overall impact (see methods for details). When aggregated to the article level, the relative frequency of harmful impacts increased from 30% to 51%, while the proportion of beneficial impacts remained almost the same (from 10% to 11%). The percentage of unclear impacts decreased from 47% to 25%, indicating that there were some articles reporting many relationships associated with unclear biodiversity impacts. When these results were aggregated into an overall impact value for each study, the relative contribution of unclear relationships decreased (Table 3).



	Trade	Tourism	Knowledge Transfer	Energy Transfer	Species Dispersal	Water Transfer	Investment	Migration (human)	Waste Transfer
Birds	227	30	77	23	12	0	6	3	0
Invertebrates	20	111	0	0	35	0	2	0	5
Fish	9	53	8	0	11	4	1	3	2
Plants/Trees/Shrubs	11	25	0	49	8	51	6	0	0
Mammals	19	34	0	1	0	0	0	8	0
Multiple	3	6	0	0	1	0	0	0	0
Amphibians	1	0	0	0	0	0	0	0	0
Reptiles	7	8	0	0	0	0	1	0	0

Figure 7: The impact of different telecoupling types on biodiversity across taxa (n=788). For articles that considered multiple telecoupling types, their relationships appear in >1 column.

Table 3: Taxa proportion at individual indicator level and article level (n = number of studies)

Taxa	**Indicators (n = 788)**		**Articles (n = 131*)**	
	n	%	n	%
Birds	361	47.07%	37	28.24%
Invertebrates	165	21.51%	31	23.66%
Fish	92	11.99%	15	11.45%
Plants	88	11.47	28	21.37%
Mammals	55	07.17%	15	11.45%
Reptiles	10	1.30%	5	3.82%
Amphibians	1	0.13%	1	0.76%
Multiple	16	2.09%	4	3.05%

*some articles reported on more than one taxon

Table 4: Percentage of telecoupling impacts across taxa (n = number of studies)

Taxa (n)	Beneficial	Harmful	Changed	Mixed	Unclear
Birds (37)	16% (6)	46% (17)	5% (2)	11% (4)	22% (8)
Plants (28)	14% (4)	46% (13)	4% (1)	7% (2)	29% (8)
Invertebrates (31)	3% (1)	48% (15)	6% (2)	3% (1)	39% (12)
Fish (15)	13% (2)	40% (6)	20% (3)	13% (2)	13% (2)
Mammals (15)	7% (1)	80% (12)	-	-	13% (2)
Reptiles (5)	-	60% (3)	-	-	40% (2)
Amphibians (1)	-	-	100% (1)	-	-
Multiple (4)	25% (1)	75% (3)	-	-	-

Table 5: Percentage of telecoupling impacts across telecoupling types (n = number of studies)

Telecoupling (n)	Beneficial	Harmful	Changed	Mixed	Unclear
Tourism (62)	8% (5)	53% (33)	5% (3)	6% (4)	27% (17)
Trade (36)	8% (3)	64% (23)	3% (1)	3% (1)	22% (8)
Spp. Dispersal (18)	11% (2)	44% (8)	6% (1)	6% (1)	33% (6)
Investment (7)	43% (3)	-	-	29% (2)	29% (2)
Knowledge Transfer (14)	29% (4)	29% (4)	7% (1)	14% (2)	21% (3)
Water Transfer (9)	11% (1)	33% (3)	22% (2)	22% (2)	11% (1)
Energy Transfer (9)	11% (1)	33% (3)	22% (2)	11% (1)	22% (2)

Table 6: Percentage of telecoupling impacts across habitats (n = number of studies)

Habitat (n)	Beneficial	Harmful	Changed	Mixed	Unclear
Terrestrial (75)	13% (10)	55% (41)	3% (2)	7% (5)	23% (17)
Marine (25)	4% (1)	56% (14)	8% (2)	4% (1)	28% (7)
Freshwater (22)	14% (3)	36% (8)	14% (3)	9% (2)	27% (6)
Terrestrial/Freshwater (4)	-	-	25% (1)	-	75% (3)
Terrestrial/Marine (2)	-	100% (2)	-	-	-
Freshwater/Marine (1)	100% (1)	-	-	-	-
Not specified /Global study (2)	100% (1)	100% (1)	-	-	-

Table 7: Percentage of telecoupling impacts across regions (n = number of studies)

Region (n)	Beneficial	Harmful	Changed	Mixed	Unclear
Europe (31)	19% (6)	42% (13)	3% (1)	10% (3)	26% (8)
Asia (27)	4% (1)	67% (18)	4% (1)	7% (2)	19% (5)
S. America (28)	7% (2)	61% (17)	11% (3)	7% (2)	14% (4)
N. America (22)	9% (2)	32% (7)	-	9% (2)	50% (11)
Oceania (11)	9% (1)	55% (6)	9% (1)	-	27% (3)
Africa (11)	18% (2)	46% (5)	18% (2)	-	18% (2)
Antarctica (2)	-	50% (1)	-	-	50% (1)
Global (5)	20% (1)	80% (4)	-	-	-

CHAPTER 3: LANDCOVER CLASSIFICATION OF A HETEROGENEOUS AGROECOSYSTEM

Abstract

The global food trade drives changes, both environmental and economical, all over the world. China is the world’s largest importer of soybeans, importing over half of the world’s traded supply annually. However, their domestic soybean farmers have struggled to compete in the global market. This has resulted in a rapid conversion of land to other crops, and the complex landscape created by small-scale farming has made characterizing and understanding this change challenging. The ability to accurately map this region is the first step to understanding the environmental and social consequences of this globally driven change. By using high-resolution imagery across different periods of the growing season and utilizing a random forest classifier with an object-based approach, we were able to generate highly accurate landcover maps (91% training, 80% testing). Furthermore, merging similar landcover classes (e.g., rain-fed crop, natural area) increased the accuracy substantially. We found that most important parameters in our analysis consisted mainly of both synthetic aperture radar (SAR) and short-wave infrared (SWIR) indices from earlier in the growing season. The resulting map from this customizable and transferable workflow will be vital for understanding the impact of landscape change on biodiversity.

3.1 Introduction

3.1.1 Background

Agricultural landscapes can oftentimes be overlooked in terms of biodiversity conservation efforts (Norris, 2008). This is largely due to the patch-matrix paradigm dominating the field of landscape ecology for the greater part of its history (Forman & Godron, 1981; Wiens, 1976). More recently, the “matrix”, or non-habitat areas of the landscape, is increasingly being treated as part of the functioning ecosystem, rather than disregarded as a barren wasteland. This has inspired numerous theories and frameworks in the fields of agro- and landscape ecology that aim to examine the biodiversity potential of agricultural landscapes that were traditionally labeled as part of the ‘matrix’(Benton et al., 2003; Fahrig et al., 2011; Perfecto & Vandermeer, 2010).

In order to quantify the effects of landscape structure (i.e., composition and configuration) on ecological processes, a variety of landscape metrics have been developed, however they require reliable landcover/use maps to produce meaningful measures. Advances in remote-sensing technology and processing software have enabled researchers to produce more detailed analyses of heterogeneous landscapes. However, those advances are now at a point where the scale of images is so fine that traditional remote sensing methods are ineffective. Now, many scientists are looking to object-based remote sensing, which is a classification method based on objects rather than pixels.

With the advent of widely available satellite imagery at fine spatial resolutions, researchers have the ability to characterize heterogeneous landscapes at resolutions that could not be achieved previously (Lausch et al., 2015). For instance, a commonly used resolution is NASA’s 30m/pixel Landsat mission (USGS US Dept of the Interior, 2017). Up until recently, this was considered a fine spatial resolution. However, today there are many satellites, such as Sentinel-2, offering finer resolutions (10m/pixel) (European Space Agency, 2017). This is particularly relevant for regions with high landscape heterogeneity, like small-scale agriculture (Figure 8). In this example, farmers may grow multiple crops within a 30x30m area and wildlife species often utilize even smaller areas. However, increased resolution does present a challenge during classification due to increased pixel variation (Fahrig et al., 2011).

Figure 8: Typical farmland structure in the United States (left) versus Heilongjiang (right). For comparison, the red point in the center of the image is surrounded by a buffer of 1000m.

The area of GEOgraphic-Object-Based Image Analysis (GEOBIA) emerged as an alternative to pixel-based image analysis methods. Pixel-based methods of image classification treat each pixel as separate from its neighbors and leaves out the context of the pixel entirely. Pixel-based methods are still widely used and are extremely applicable when the target of an image is less than or equal to pixel size. However, there are many applications where this is not the case, and the recent onset of accessible and extremely high-resolution imagery has made GEOBIA more popular among geographers. When using an object-based approach, the image first goes through a process where similar pixels are grouped into objects based on their attributes. The same classification methods used for pixel-based methods can then be applied to these objects. The main benefit of segmenting the image first is that it retains its context and there is less misclassification within objects due to pixel-pixel variation (i.e., salt and pepper effect).

Machine-learning algorithms are commonly applied to GEOBIA. Duro et al. compared three different algorithms, decision tree (DT), random forest (RF), and support vector machine (SVM), using both pixel and object-based classification. They found that pixel-based showed no significant difference across the three algorithms, though object based showed a significantly different result with DT. Also, classifications using either RF or SVM gave the most valuable depiction of cropland, regardless of pixel or object based, though, the pixel-based method took less computational time. However, they concluded that there was no obvious advantage over the other when it comes to pixel or object based (Duro et al., 2012).

Random forest is a machine learning method of classification that has shown to be one of the more reliable methods of classification due to it using both decision trees and sub-setting (similar to bootstrapping) to improve prediction while controlling for over-fitting (Belgiu & Drăguţ, 2014; Gislason et al., 2006). The algorithm is trained on a subset of validated data (i.e., ground truth) and produces multiple decision trees for each observation, which then assign a class based on the majority outcome. Many studies and reviews have tested RF against other classification methods, and it reliably performs the best. Its superior performance is attributed to the fact that it can deal with both high data dimensionality as well as multicollinearity, things that are extremely common in large data sets. However, RF can be sensitive to sample design and tends to favor classes with a large number of training samples. It is also preferred because there are only two parameters that are user defined (number of trees and the number of features used to split a node), whereas other methods have much more ambiguity for the user to define.

Researchers have also explored and examined current methods strictly within the object-based sphere. After examining a case study in China, Li et al determined that among seven GEOBIA methods, they found that RF was the most accurate classifier when varying the different segmentation variables (M. Li et al., 2016). In fact, RF is one of the most commonly used methods in GEOBIA classification, and it is a promising avenue as more high quality and high-volume data are created. For example, satellite programs like Sentinel offer unprecedented ability to further discriminate landcover types as spectral differences can be parsed more easily. This is expected to be extremely useful for mapping agriculture (Lebourgeois et al., 2017).

An example of a study that merged these two methods, did so by mapping irrigation in Africa (Vogels et al., 2019). By using a higher spatial resolution than would be allowed for pixel-based methods, they showed that there was more irrigation in the region than one would infer from maps made using coarser resolutions. This result brings into question our understanding of the world through the lens of these potentially inaccurate data products, and we should expect many of them to be challenged or corrected in the future.

3.1.2 Objectives

Recent research, including empirical remote sensing studies in our study region of Heilongjiang, China, have indicated cropland conversions in importing countries in response to international trade (J. Sun et al., 2015; van Vliet et al., 2015). Farmer land-use decisions are affected by multiple factors such as climate, resources, and crop prices, among others (Lutz, 1998; S. A. Wood et al., 2014). As global trade increases, small farmers struggle to compete when their markets are flooded with cheap imports (Tilt, 2008). Crop price plays a large part in determining what small-scale farmers choose to grow from one year to another and whether they plant a single crop type or diversify (Di Falco & Perrings, 2005; Michler & Josephson, 2017; D.

Wood & Lenné, 1999). Additionally, as small farmers in developing countries become integrated in a global commodity market, they have to consider risk and market uncertainty more than ever before (Hao, 2010). With more farmers reacting to global markets by altering their cultivation strategies, the structure of agroecosystems changes as well.

While some global landcover maps exist, they are not at the resolution needed to accurately capture the heterogeneity of the study region nor do they differentiate between crop types (Figure 8). The inherent inaccuracies and limitations of these products are also difficult to ascertain. Furthermore, accurately classifying crop types can be challenging as they often have very similar spectral characteristics, and many crop classification methods focus on using single-source optical data. However, recent advances in sensor capabilities and data processing techniques have enabled the use of both optical and radar data, which enhances the performance of crop classification, particularly in the context of crop identification (C. Liu et al., 2019; Orynbaikyzy et al., 2019). Additionally, many crop classification methods leave out non-crop classes which limits their applicability to landscape-level analyses (Kang et al., 2018; You et al., 2021; Zhang et al., 2020; Zhong et al., 2016). Therefore, the main objective of this analysis is to create high fidelity landcover maps of our study region that distinguish between the region’s major crops (soybean, corn, and rice) as well as other non-crop classes (wetland, forest, grassland, built-up) at a fine spatial resolution to facilitate calculation of landscape metrics relevant to agricultural structure and biodiversity.

3.2 Methods

Excluding field data collection, the entire process of creating landcover maps occurred in Google Earth Engine (GEE). To see each step of the workflow, see the diagram in Figure 9. The accessibility of imagery in GEE as well as their ever-growing library of processing and analysis tools makes it an ideal platform to create custom landcover maps for many applications.

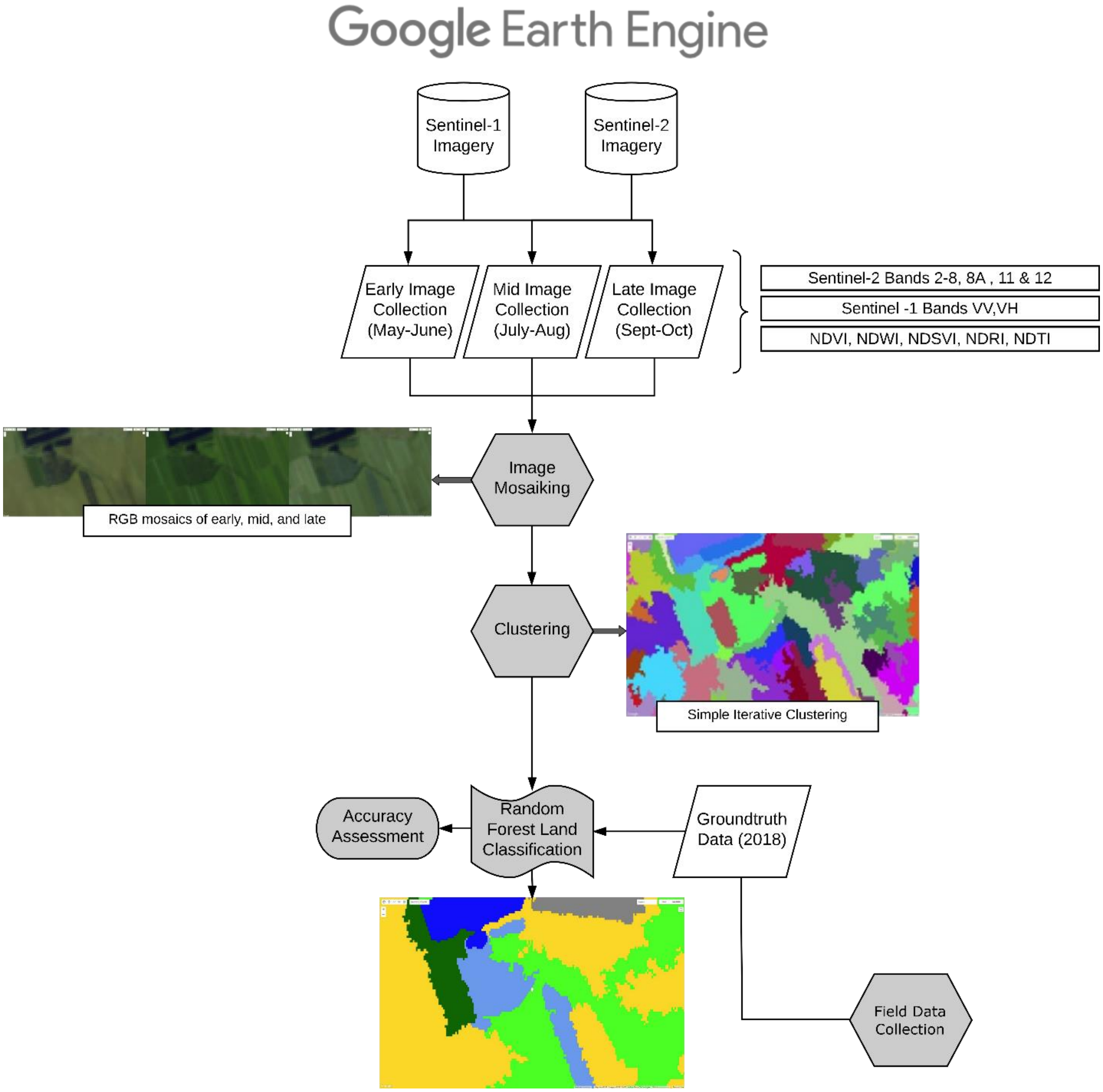


Figure 9: Workflow diagram for the landcover classification in Google Earth Engine.

3.2.1 Study System

Heilongjiang province in northeast China produces much of the country's grain (Figure 10). With a climate characterized by long, harsh winters and short, mild summers, only a single crop growing season is possible (Figure 11) (Olson et al., 2001; *Weather and Climate*, 2016). The three main crops grown in the region are soybean, corn, and paddy rice. However, with the growing influence of global trade and cheap imports of soybeans, farmers have switched to growing more corn and rice in recent years. From 2009-2013, soybean cultivation decreased by nearly 40% (4 million to 2.4 million ha) (J. Sun et al., 2015; Survey Office of the National Bureau of Statistics in Heilongjiang, 2013).

As previously stated, Heilongjiang's main industry is agriculture therefore the majority of land is dedicated to agriculture. Heilongjiang is primarily cultivated by smallholder farmers (farm sizes around 3-10 ha). The landscape is typified by villages scattered across the landscape, with fields of varying crop type, size, and shape in the surrounding vicinity (Figure 8).

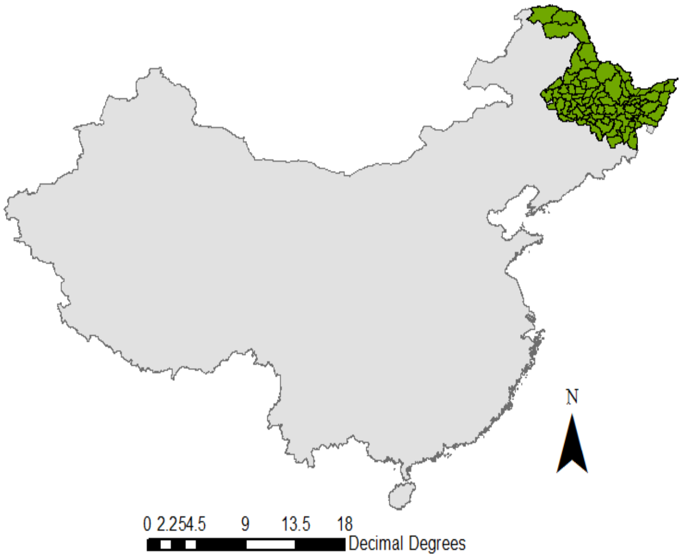


Figure 10: Map of Heilongjiang Province, China.

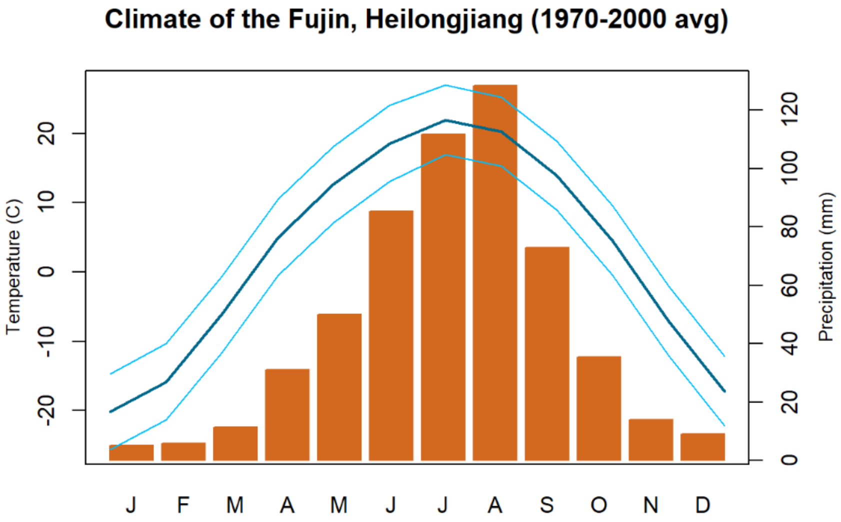


Figure 11: Climate of Heilongjiang Province from 1970-2000 (mean temperature in dark blue, min/max in light blue, and average precipitation in orange.

3.2.2 Ground Truth Data Collection

In the summer of 2018, we collected ground truth data across Heilongjiang (Figure 12). Points were selected in areas with at least 100m^2 of a single landcover class for nine classes: built up, corn, forest, grassland, 'other crop', rice, soybean, water, & wetland (Table 8). Due to accessibility and logistical constraints, most points were collected along roadsides to increase the overall sample size for each class. In addition to ground truth points collected in the field, additional points were collected using satellite imagery to supplement the non-crop classes that were under-represented in the field data. Of the points collected, 30% were withheld as testing data for classification accuracy assessment. The number of samples per land class can be found in the table below (Table 8).

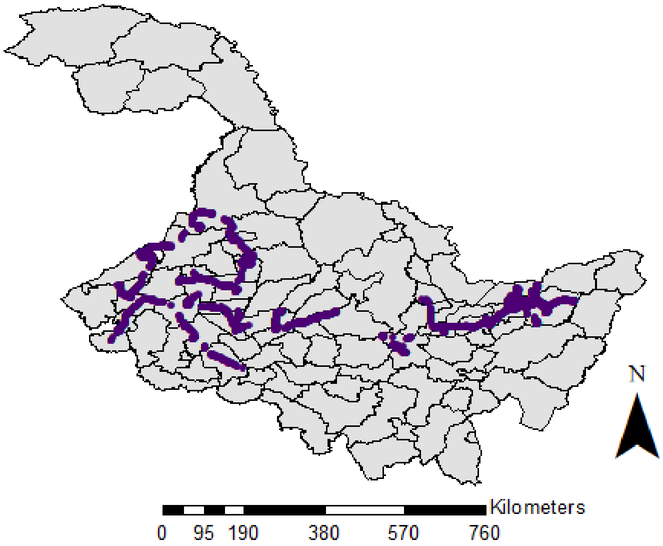


Figure 12: Map of Heilongjiang and location of field ground truth points

Table 8: Class definitions and ground truth totals

Class	Training	Testing	Total	Description
Corn	1365	535	1900	Rain-fed cropland planted with corn (*Zea mays*)
Soybean	855	390	1245	Rain-fed cropland planted with soybeans (*Glycine max*)
Rice	1095	492	1587	Flooded paddy rice (*Oryza sativa*)
'Other crop'	117	71	188	Cropland planted with an alternative crop (e.g., potato, tobacco, rapeseed, cucumber, watermelon, etc.)
Forest	351	149	500	Forestland, typically early successional. Either mixed species stands for single planted stands
Grassland	362	143	505	Both scrub and grassland (vegetation no taller than 3 m) in dry soil.
Wetland	183	86	269	Saturated land with some vegetation cover
Water	188	63	251	Body of water >1m deep
Built-up	332	167	499	Villages, roads, greenhouses, etc.
Total	4848	2096	6944	

3.2.3 Imagery Acquisition & Processing

Shapefiles of each bird point location (collected in 2017 & 2018, see Chapter 4) as well as ground truth points (collected in 2018) with 2000m buffers were used to filter Sentinel-2 Level-1C (i.e., top of atmosphere, orthorectified) imagery in Google Earth Engine. Unfortunately, Level-2A (i.e., surface reflectance) images were not available in our study area for either year. Three time periods throughout the growing season were used to create the filtered collections: early (5/1-6/30), mid (7/1-8/31), and late (9/1-10/31). The ground truth collection (the collection with the largest extent) contained around 35 Sentinel-2 tiles. Only images with <20% cloudy pixel percentages were included[1]. The resulting size of the image collections for 2017 and 2018 are presented in the table below (Table 9). Since Sentinel-2B was not launched until March 2017, there were significantly fewer images available in 2017 as the satellite was still in the ramp-up phase during most of the growing season (Sudmanns et al., 2020). The Sentinel-1 collections were filtered using the same workflow as the optical imagery (Table 9).

Table 9: Total number of images in for each collection (2017 samples, 2018 samples, and ground truth samples) that were used for the image mosaicking process.

	Sentinel - 2			Sentinel - 1		
	2017	2018	Ground truth (2018)	2017	2018	Ground truth (2018)
Early	36	176	284	101	90	97
Mid	42	103	171	67	63	69
Late	76	187	293	70	48	53

Five vegetation indices were calculated for all images in each collection before calculating the median value for all pixels (see Table 10 for specific band designations and index definitions). In addition to the commonly used vegetation (NDVI)(Rouse & Haas, 1974) and water indices (NDWI)(Gao, 1996), we also derived three additional indices known to aid in crop type separation, particularly between corn and soybean (Kang et al., 2018; Zhang et al., 2020; Zhong et al., 2016). The first two combined the visible and SWIR bands to provide information on vegetation senescence (NDSVI)(Qi et al., 2002) and residue (NDRI)(Gelder et al., 2009). The final index was calculated using bands just in the SWIR region to provide information on the tillage state of a pixel/object (NDTI)(Van Deventer et al., 1997).

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[1] One site was filtered at 60% cloudy pixels to ensure image availability in the early season for 2017. Before adding them to the entire collection, we checked that no cloudy pixels occurred within the 2km sample area.

Table 10: Data layers used for classification

Sensor (res.)	Abbrev.	Name	Approx. Band Center/Calculation
Sentinel-2 (10 m)	B2	Blue	490 nm
	B3	Green	560 nm
	B4	Red	660 nm
	B8	Near infrared (NIR)	830 nm
	NDVI	Normalized difference vegetation index	(B8-B4)/B8+B4
	NDWI	Normalized difference water index	(B3-B8)/B3+B8
Sentinel-2 (20 m)	B5	Red edge 1	700 nm
	B6	Red edge 2	740 nm
	B7	Red edge 3	780 nm
	B8A	Near infrared narrowband	860 nm
	B11	Short wave infrared 1 (SWIR)	1610 nm
	B12	Short wave infrared 2 (SWIR)	2200 nm
	NDTI	Normalized differential tillage index	(B11-B12)/(B11+B12)
Sentinel-2 (10m & 20m)*	NDSVI	Normalized difference senescent vegetation index	(B11-B4)/(B11+B4)
	NDRI	Normalized difference residue index	(B4-B12)/(B4+B12)
Sentinel-1 C-band SAR (10 m)	VV	Single co-polarization, vertical transmit/vertical receive	5.4 GHz (~5.5 cm wavelength C-band)
	VH	Dual-band cross-polarization, vertical transmit/horizontal receive	5.4 GHz (~5.5 cm wavelength C-band)

*Final resolution of indices is 20m

Since Sentinel data are collected at a relatively fine spatial resolution (10 and 20m), we segmented the images into objects prior to classification rather than just classifying individual pixels. Doing so reduces error due to spectral variability within a landcover class and preserves features such as field borders/margins. Before initializing segmentation, we stacked the early, mid, and late mosaics for each sample (2017, 2018, GT). To initiate the clustering algorithm, we set a seed grid over the mosaics with 20 pixels between each seed and used B2, B3, B4, B8, NDVI, NDWI, NDSVI, NDRI, and NDTI as clustering variables. Finally, the target bands for classification were extracted. The 60m resolution bands (B1, B9, B10) and the SAR layers (HH, HV) were excluded. We then ran the mosaics through an image segmentation algorithm based on simple non-iterative clustering (Figure 13). The parameters used can be found in the table below (Table 11). After the segmentation, the band and index means were calculated for each segment. In GEE, composite (i.e., mosaicked) images do not have a specific resolution until it is specified by the user. For this application, we exported the final rasters at 10m for all data layers.

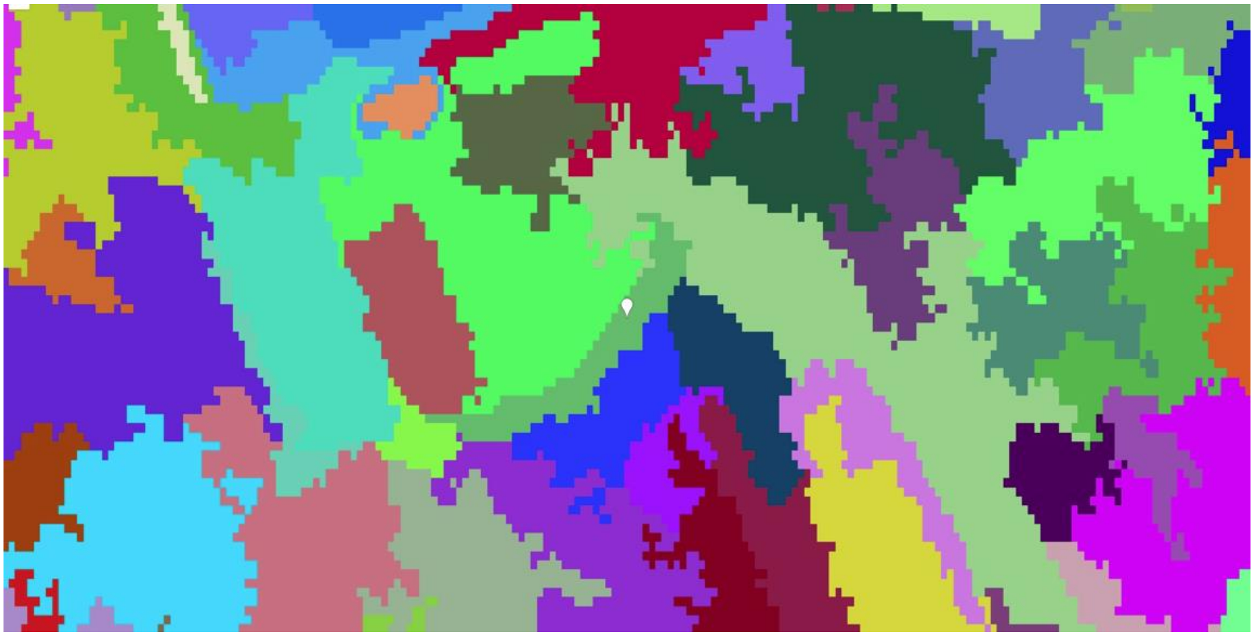


Figure 13: Example result from the simple non-iterative clustering algorithm

Table 11: Parameters for simple non-iterative clustering algorithm in GEE

Argument	Value	Details
`image`	*image*	*The input image for clustering.*
`size`	*5*	*The superpixel seed location spacing, in pixels. If 'seeds' image is provided, no grid is produced. Default = 5*
`compactness`	*1*	*Compactness factor. Larger values cause clusters to be more compact (square). Setting this to 0 disables spatial distance weighting. Default = 1*
`connectivity`	*8*	*Connectivity. Either 4 or 8. Default = 8*
`neighborhoodSize`	*64*	*Tile neighborhood size (to avoid tile boundary artifacts). Defaults to 2 * size. Default = null*
`seeds`	*defined by seed grid*	*If provided, any non-zero valued pixels are used as seed locations. Pixels that touch (as specified by 'connectivity') are considered to belong to the same cluster. Default = null*

3.2.4 Landcover Classification

For the classification of image segments, we used a RF classifier trained on ground truth (GT) points collected during the 2018 field season. The data layers used for the image segment classification were the mean value for bands 2-8, 8A, 11, 12, NDVI, NDWI, NDSVI, NDRI, NDTI, VV, & VH (17 for each time period, total of 51) in each cluster (Table 10). Seventy percent of the points were randomly chosen to train the RF classifier with the remaining 30% set aside for training. The number of trees was set to 450, with all other parameters set to default (Table 12). The trained classifier was then run on the 2018 and 2017 samples. To assess the performance of the classifier, we calculated overall, user, and producer accuracies for both the training and testing ground truth points as well as F- score metrics for each class. We also derived variable importance for the RF algorithm in GEE to compare across the bands used in the classifier.

Table 12: Parameters for Random Forest Classifier in Google Earth Engine

Argument	Type	Details
`numberOfTrees`	*Integer, default: 1*	*The number of Rifle decision trees to create per class.*
`variablesPerSplit`	*Integer, default: 0*	*The number of variables per split. If set to 0 (default), defaults to the square root of the number of variables.*
`minLeafPopulation`	*Integer, default: 1*	*The minimum size of a terminal node.*
`bagFraction`	*Float, default: 0.5*	*The fraction of input to bag per tree.*
`outOfBagMode`	*Boolean, default: false*	*Whether the classifier should run in out-of-bag mode.*
`seed`	*Integer, default: 0*	*Random seed.*

3.3 Results & Discussion

3.3.1 Accuracy Assessment

The re-substitution and validation accuracies (i.e., training and testing accuracies) were assessed for the final classified image. Overall training accuracy was 91% whereas the testing accuracy was 80%. The kappa value for the training data was 0.89 for the training data, reflecting a high level of agreement, and the testing data's kappa value of 0.76, while slightly lower, still indicates a substantial level of agreement (Table 13).

The accuracy of each class varied somewhat. For the training data, both the producer and user accuracies of built-up, forest, grassland, rice, water, and wetland were above 90%. Corn had a producer's relatively high producer accuracy at 92%, but a lower user accuracy (83%) due to a higher number of commission errors (false positives). The soybean and 'other crop' class had low producer accuracies (76.7% and 76.9%) with slightly better user accuracies (86.8% and 90.6%) due to a higher number of omission errors (false negatives).

For the testing data, wetland was the only class with both user and producer accuracies above 90%. Rice was relatively accurate with a producer and user accuracy of 92.9% and 89.9%, respectively. Similarly, water had a producer and user accuracy of 85.7% and 92.1%. The forest, grassland, and built-up classes had moderate levels of accuracy with user accuracies all around 78% and producer accuracies ranging from 83-88%. In contrast, the three rain-fed -crop classes all performed relatively poorly. Corn, soybean, and ‘other crop’ had a producer’s accuracy of 78.3%, 62.1%, and 52.1% and a user accuracy of 68.6%, 77.9%, and 81.7%. Similar to the testing data, the difference in producer and user accuracies can be attributed to higher numbers of commission errors in corn and omission errors in soybean and ‘other crop’.

Looking at the confusion matrices (Table 14,Table 15) for the training and testing data, we can see the majority of commission errors for corn occurred in the soybean class, with most omission errors in soybean being incorrectly classified as corn. The ‘other crop’ class was most often confused with both corn and soybean. The ‘other crop’ class’s low performance can also be attributed to the fact that it had a low number of ground truth points compared to the rest of the classes. Ground truth supplementation was conducted by visually inspecting satellite imagery so identifying pixels containing crops other than rice, corn, and soybean was not feasible. That being said the performance of this classification method to correctly identify the crops in Heilongjiang performs similarly to (if not better than) recent mapping efforts (You et al., 2021).

Table 13: Accuracy assessment for training data: producer accuracy (PA), user accuracy (UA)

	Training		**Testing**	
	PA	UA	PA	UA
built-up	95.783	93.373	82.635	78.443
corn	92.015	83.223	78.318	68.598
forest	97.443	98.580	87.919	85.906
grassland	93.094	96.685	86.014	78.322
othercrop	76.923	90.560	52.113	81.690
rice	96.986	97.260	92.886	89.837
soybean	76.725	86.784	62.051	77.949
water	96.277	100	85.714	92.063
wetland	100	99.454	93.023	94.186
OVERALL	**91.277**	-	**80.2**	-
KAPPA	**0.893**	-	**0.759**	-

Table 14: Training confusion matrix

		Predicted									
		built-up	corn	forest	grassland	othercrop	rice	soy	water	wetland	TOTAL
Reference	built-up	318	3	1	1	0	5	4	0	0	332
	corn	6	1256	1	3	1	4	94	0	0	1365
	forest	1	7	343	0	1	0	0	0	0	352
	grassland	5	14	0	337	0	4	1	0	1	362
	othercrop	1	13	1	0	90	4	8	0	0	117
	rice	6	15	0	5	2	1062	5	0	0	1095
	soybean	2	175	2	3	7	10	656	0	0	855
	water	1	2	0	0	0	3	1	181	0	188
	wetland	0	0	0	0	0	0	0	0	183	183
ALL											4849

Table 15: Testing confusion matrix

		Predicted									
		built-up	corn	forest	grassland	othercrop	rice	soy	water	wetland	TOTAL
Reference	built-up	138	7	3	5	1	9	2	1	1	167
	corn	12	419	9	6	4	21	64	0	0	535
	forest	7	3	131	1	0	4	3	0	0	149
	grassland	2	10	2	123	0	2	1	0	3	143
	othercrop	3	18	1	0	37	0	12	0	0	71
	rice	6	9	3	8	4	457	4	1	0	492
	soybean	5	118	3	8	4	10	242	0	0	390
	water	0	2	0	2	0	4	0	54	1	63
	wetland	1	1	0	1	0	0	0	3	80	86
ALL											2096

To improve the overall accuracy and quality of data derived from the classification map, the rain-fed crop classes (i.e., corn, soybean, and ‘other crop’) were merged into one class (Table 16). The original landcover maps that contained 9 landcover classes were also re-classified to just three classes (built-up, cropland, and natural landcover) to facilitate calculation of various landscape metrics (e.g., percent of natural landcover).

Table 16: Merged classification schemes

Original Classes	*Rain-fed crop*	*Reclassified*
n = 9	n = 7	n = 3
built-up	built-up	built-up
rice	rice	cropland
corn	rain-fed crop	cropland
soybean	rain-fed crop	cropland
‘other crop’	rain-fed crop	cropland
forest	forest	natural
grassland	grassland	natural
water	water	natural
wetland	wetland	natural

For the rain-fed crop classification, overall training and testing accuracies increased substantially to 97.38% (+6.08%) and 90.70% (+10.5%) respectively (Table 17). The reclassification of just 3 classes (built-up, cropland, and natural) resulted in even more accurate classifications with a training accuracy of 98.23% (+6.93%) and a testing accuracy of 93.61% (+13.41%) (Table 18).

For both reclassified maps, the producer and user’s accuracy for the training data was above 90% across all landcover classes. For the testing data, the merged rain-fed crop map had the highest accuracies in the wetland, rain-fed crop, and rice classes (accuracies ≥90%). The remaining classes all had accuracies at 78% or higher (Table 17). The accuracy assessment of the testing data for the simple reclassification found cropland class to be the most accurate, followed by natural and built-up classes (Table 18). The confusion matrices for each reclassification can be found in Table 19-Table 22.

Table 17: Accuracy assessment for training and testing data of rain-fed crop reclassification

	Training		Testing	
	PA	UA	PA	UA
built-up	97.853	92.638	82.635	78.443
forest	97.443	98.580	87.919	85.906
grassland	93.094	96.685	86.014	78.322
rain-fed crop	98.373	97.945	92.169	95.281
rice	96.986	97.260	92.886	89.837
water	95.767	100.000	85.714	92.063
wetland	100.000	99.454	93.023	94.186
OVERALL	**97.381**	-	**90.697**	-

Table 18: Accuracy assessment for training and testing data of reclass reclassification

	Training		Testing	
	PA	UA	PA	UA
built-up	95.796	92.793	82.635	78.443
natural	96.225	98.435	90.930	88.889
cropland	99.096	98.688	95.632	96.707
OVERALL	**98.227**	-	**93.607**	-

Table 19: Rain-fed crop training confusion matrix

		Predicted							
		built-up	forest	grassland	rain-fed crop	rice	water	wetland	TOTAL
Reference	built-up	319	1	1	7	5	0	0	333
	forest	1	343	0	8	0	0	0	352
	grassland	5	0	337	15	4	0	1	362
	rain-fed crop	10	4	6	2298	18	0	0	2336
	rice	6	0	5	22	1062	0	0	1095
	water	2	0	0	3	3	181	0	189
	wetland	0	0	0	0	0	0	183	183
	ALL								4850

Table 20: Rain-fed crop testing confusion matrix

		Predicted							
		built-up	forest	grassland	rain-fed crop	rice	water	wetland	TOTAL
Reference	built-up	138	3	5	10	9	1	1	167
	forest	7	131	1	6	4	0	0	149
	grassland	2	2	123	11	2	0	3	143
	rain-fed crop	20	13	14	918	31	0	0	996
	rice	6	3	8	17	457	1	0	492
	water	0	0	2	2	4	54	1	63
	wetland	1	0	1	1	0	3	80	86
	ALL								2096

Table 21: Reclass training confusion matrix

		Predicted			
		built-up	natural	cropland	TOTAL
Reference	built-up	319	2	12	333
	natural	8	1045	33	1086
	cropland	16	15	3400	3431
	ALL				4850

Table 22: Reclass testing confusion matrix

		Predicted			
		built-up	natural	cropland	TOTAL
Reference	built-up	138	10	19	167
	natural	10	401	30	441
	cropland	26	39	1423	1488
	ALL				2096

We also calculated the F-score for each of the original and merged classes. F-score is a metric that combines both precision and recall performance of a classifier and ranges from ‘worst’ to ‘best’ using values between 0 and 1 (Table 23). The majority of classes exhibited high F-score values, for both the training and testing data (>0.8). The classes with the lowest F-scores were corn, soybean, and ‘other crop’ classes in the original classified map. However, the F-scores of the merged rain-fed crop class for both training and testing data were above 0.9.

Table 23: F-scores for each class

All classes	**built-up**	**corn**	**soy**	**other**	**rice**	**forest**	**grass-**	**wetland**	**water**
Train	0.944	0.881	0.807	0.826	0.971	0.980	0.948	0.997	0.978
Test	0.809	0.747	0.674	0.612	0.915	0.870	0.828	0.936	0.885
Rain-fed crop	**built-up**	**rain-fed crop**	**rice**	**forest**	**grassland**	**wetland**	**water**		
Train	0.944	0.980	0.971	0.980	0.948	0.997	0.978		
Test	0.809	0.936	0.915	0.870	0.828	0.936	0.885		
Reclassified	**built-up**	**cropland**	**natural**						
Train	0.944	0.989	0.973						
Test	0.809	0.961	0.900						

3.3.2 Variable Importance

Two variables were distinctly important compared to the rest of the variables used in the RF classifier (Figure 14**,** Table 24). The top-ranking variable was the Sentinel-1 C-band cross polarized VH data for the early time period. The next most important variable was NDTI (normalized difference tillage index) from the early time period. The next two variables in the ranking were also indices from the early period: NDWI (normalized difference water index and NDSVI (normalized difference senescent vegetation index). The NDTI for both the late and mid time periods were the next highest ranked, resulting in all three phenological periods for the same metric ranking in the top ten ranked variables. It is also notable that the seven of the top ten variables were derived from the early time period, highlighting the importance of indices from early in the growing season.

Comparing two of the top data layers, VH and NDTI, across all three time periods one can see there is significant variability (Figure 15). For the VH data, the peak occurs early in the season, decreases significantly during the height of the growing season and the increases slightly around harvest time (Figure 15**,** a-c). NDTI showed a similar pattern, though not as pronounced (Figure 15**,** d-f). You can also observe the relatively constant values for the water (dark blue) and built-up (gray) regions in each image band image when comparing to the classified image (Figure 15**,** g).

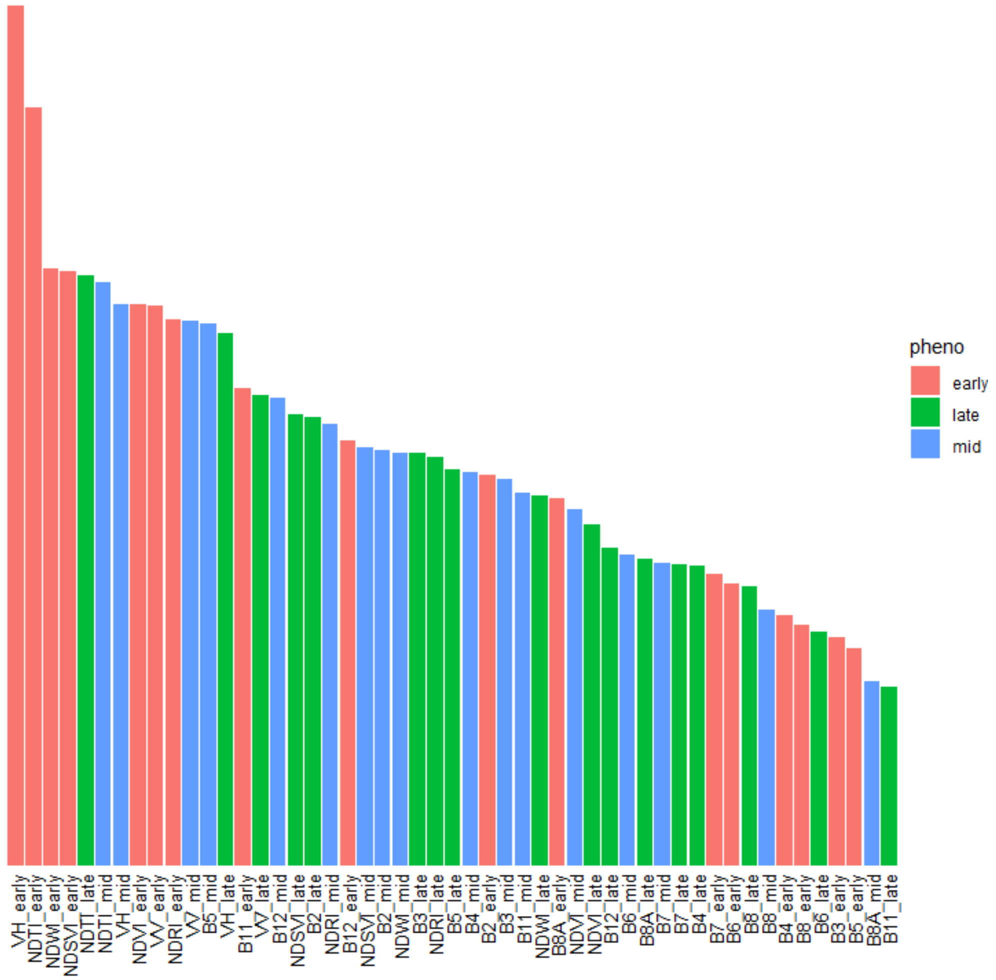


Figure 14: Bar graph of data layer importance for random forest classification

Table 24: Data layer ranked by variable importance

rank	band	importance		rank	band	importance
1	VH_early	724.016		**27**	B4_mid	575.268
2	NDTI_early	691.432		**28**	B2_early	574.638
3	NDWI_early	640.533		**29**	B3_mid	573.473
4	NDSVI_early	639.248		**30**	B11_mid	568.819
5	NDTI_late	638.017		**31**	NDWI_late	568.045
6	NDTI_mid	636.149		**32**	B8A_early	567.087
7	VH_mid	628.957		**33**	NDVI_mid	563.617
8	NDVI_early	628.829		**34**	NDVI_late	558.595
9	VV_early	628.559		**35**	B12_late	551.397
10	NDRI_early	623.969		**36**	B6_mid	549.361
11	VV_mid	623.755		**37**	B8A_late	547.822
12	B5_mid	622.738		**38**	B7_mid	546.712
13	VH_late	619.534		**39**	B7_late	546.118
14	B11_early	602.069		**40**	B4_late	545.718
15	VV_late	600.015		**41**	B7_early	542.923
16	B12_mid	598.964		**42**	B6_early	540.137
17	NDSVI_late	593.742		**43**	B8_late	539.084
18	B2_late	592.968		**44**	B8_mid	531.535
19	NDRI_mid	590.811		**45**	B4_early	530.072
20	B12_early	585.410		**46**	B8_early	526.940
21	NDSVI_mid	583.504		**47**	B6_late	524.495
22	B2_mid	582.286		**48**	B3_early	522.843
23	NDWI_mid	581.532		**49**	B5_early	519.542
24	B3_late	581.379		**50**	B8A_mid	508.663
25	NDRI_late	580.274		**51**	B11_late	507.015
26	B5_late	576.418				

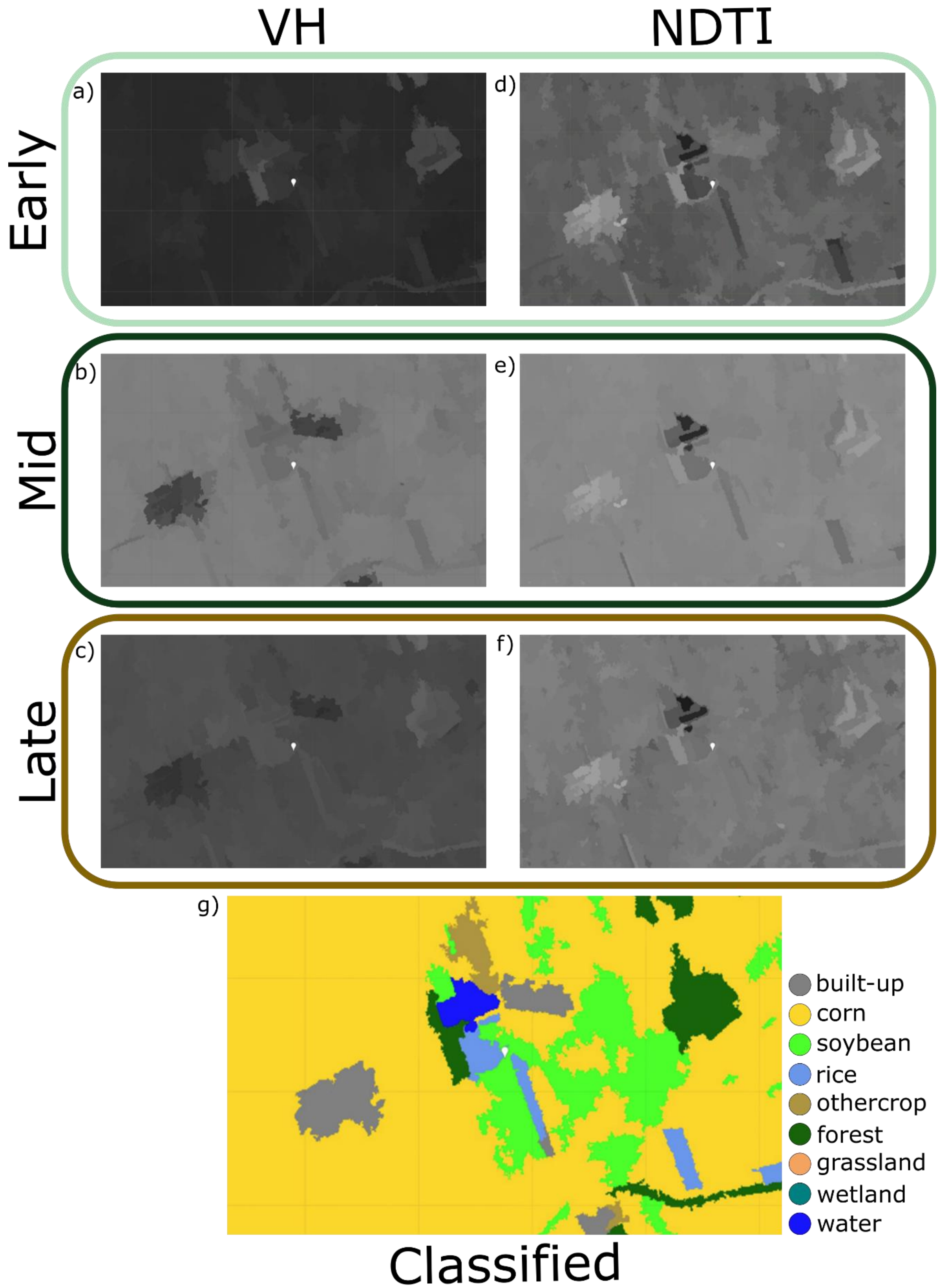


Figure 15: Phenological difference between two of the most important data layers, VH (a-c) and NDTI (d-f) for all three time periods compared to the final classification (g).

3.4 Conclusions

This chapter demonstrates a workflow that produces high fidelity landcover classification for a heterogeneous agricultural landscape. By utilizing fine spatial resolution data from both optical and SAR sensors at multiple points during the growing season and using an object-based approach, we were able to achieve an accuracy of >80% on the validation data. Merging the rain-fed crop classes further increased the accuracy to >90%. Evaluating the performance of each data layer in our RF classifier solidified the importance of phenological data, as many of the top bands were from earlier in the growing season. We also found that indices involving the SWIR region were among the top-ranking variables. This entire process was performed in Google Earth Engine and could easily be transferred to other regions and time periods, so long as the user supplies the appropriate amount of ground truth data for each target class. The final classified maps can be used for several applications, including landcover dynamics and inventories as well as the calculation of landscape metrics for landscape-level analyses.

CHAPTER 4: LANDSCAPE STRUCTURE AND BIRD DIVERSITY IN AGROECOSYSTEMS OF NORTHEAST CHINA

Abstract

International food trade drives land use/cover change, having consequences for wildlife that utilize agroecosystems. To explore this, we assessed bird communities and landscape structure in the agricultural region of Heilongjiang Province in northeastern China. We examined the relationship between functional and taxonomic measures of bird diversity and landscape metrics (both compositional and configurational). We found that several landscape metrics significantly related to bird metrics, though there was little difference in the relationships of between bird diversity and landscape structure when comparing taxonomic versus functional diversity. Crop diversity as well as natural landcover and edge metrics positively correlated with bird richness, while patch aggregation and rain-fed crop (e.g., corn, soybean) percentage were negatively related. We also found that paddy rice in our study region supported functionally different bird species compared to soybean and corn. Finally, we compared regions in Heilongjiang impacted by global trade and found that those with a larger decrease in soybean cultivation had lower levels of crop diversity as well as higher amounts of rice area. There were no significant regional differences in bird diversity, however, which indicates that negative impacts to bird diversity due to soybean conversion (and a decrease in crop diversity) may be mitigated by increases in rice cultivation rather than corn.

4.1 Introduction

4.1.1 Background

Agroecosystems are a multi-functional landscapes that not only can be utilized for food production, but also serve as habitat for a multitude of species that provide ecosystem services and support robust ecosystems (Godfray & Garnett, 2014). To understand species' contributions to ecosystem function in agroecosystems, research is undergoing a shift that focuses on functional, rather than purely taxonomic diversity. This provides a more holistic perspective as functional diversity often serves as an indicator of the wide range of ecosystem services on which humans and food production rely (S. A. Wood et al., 2015).

Scientists often study ecosystems using taxonomic definitions to group or separate species. However, taxonomic metrics alone may not provide insight about the functioning of an ecosystem (Cadotte et al., 2011). Many common functional biodiversity metrics are trait-based, though they can also be based on environmental gradients, biotic interactions, and energetic/reproductive performance (Mcgill et al., 2006). Furthermore, studies that examine both functional and taxonomic biodiversity often find contrasting results (Edie Stewart M. et al., 2018; Jacoboski & Hartz, 2020; W. Li et al., 2021).

To understand landscape characteristics that promote biodiversity, we often use metrics to quantify various aspects of landscape heterogeneity. Here, we focus on structural landscape heterogeneity, which distinguishes landcover types by their geographic characteristics. Alternatively, some researchers classify landcover based on species-specific resource needs (Fahrig et al., 2011). There are two components of structural landscape heterogeneity that are typically considered: composition and configuration. Composition refers to the identity of landcover types found in a landscape while configuration is defined by the spatial layout of various landcover types (Fahrig & Nuttle, 2005). There are numerous metrics that can be used to characterize a landscape, but care must be taken to avoid using correlated and redundant metrics simultaneously (Frazier & Kedron, 2017). Additionally, in the context of biodiversity, it remains unclear which spatial resolution is the most appropriate to apply, and what extent to calculate landscape metrics for the most informative results (Fahrig et al., 2011).

There is a need to understand and quantify characteristics of agricultural landscapes that bolster biodiversity. There have been some attempts to create and assess habitat descriptors, mainly in Europe (Herzog et al., 2017). They recommend seven descriptors (richness, diversity, patch size, linearity, crop richness, shrub habitat amount, and tree habitat amount) as well as a semi-natural habitat descriptor which is interpreted differently across farm type. However, these descriptors only assess potential habitat quality and do not address realized biodiversity in terms of number of species (or functional groups) of a landscape. Other studies have found that general heterogeneity mediates farmland bird diversity rather than crop diversity (Redlich et al., 2018). However this does not seem to be true in regions that also farm paddy rice (M. B. Lee & Goodale, 2018).

4.1.2 Research Questions

Using geo-located samples of bird diversity and landcover maps, we aim to determine the relationship between agricultural landscape characteristics and bird diversity in taxonomic and functional contexts in our study region of Heilongjiang Province in northeastern China. Our research questions are listed below.

Q1: What is the impact of global trade on landscape structure?

Q2: What is the relationship between landscape structure and bird diversity?

Q3: What is the relationship between crop diversity and functional/taxonomic bird biodiversity?

Q4: What is the relationship between landscape structure and functional bird community traits?

4.2 Methods

4.2.1 Bird Data Collection

In the summer of 2017 and 2018, we collected bird data at 37 sites across Heilongjiang. At each site, we conducted a series of point counts (2-9 per site depending on conditions) for a total of 207 bird samples (Figure 16). These geolocated data were collected using a point count method (Bibby, 2000; Hutto, 1986). All birds seen or heard were recorded (both species and abundance) within 50m (2017) or 100m (2018) for three, three-minute intervals. Only those birds seen within a 50m range were used for this analysis. Additionally, birds flying over the sample point were not counted unless they were actively using the air space (e.g., swallows feeding over a field, kestrel hovering while hunting). Birds recorded as present in previous time intervals were re-recorded since each interval was treated as a separate sample.

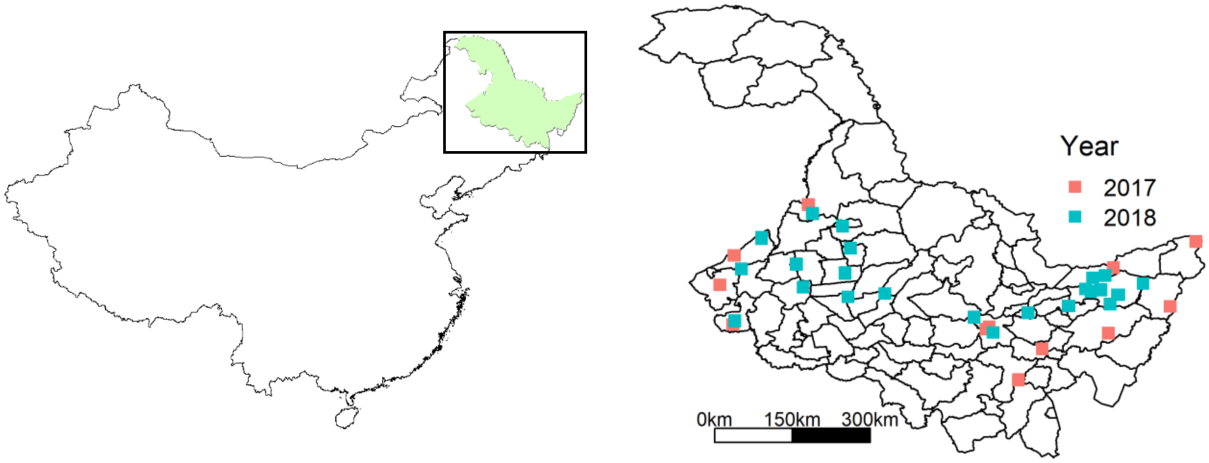


Figure 16: Map of Heilongjiang and location of sites where bird biodiversity was sampled. Counties in the Qiqihar (west) and Jiamusi (east) prefectures are outlined in black.

4.2.2 Biodiversity Indices

We calculated taxonomic richness (TR) at the family-level as many species were difficult to distinguish in the field (e.g., swallow species often occurred in mixed flocks). The taxonomic diversity metrics we examined were richness (i.e., number of families) and the Shannon index.

As seen in (1.1), the Shannon index (H) is based on the summation across species abundances, where p^i is the proportional abundance of species i and b is the log base (natural log), which balances the importance of both abundant and rare species (Morris et al., 2014). The *vegan* package in R was used for this calculation (Oksanen et al., 2020; R Core Team, 2021).

$$H = -\sum_{i} p_i log_b p_i \qquad \textbf{(1.1)}$$

Before calculating functional diversity indices, we created a trait matrix for all families present in our sample (Table 34). In addition to average body mass, we also collected information on different suites of binary traits: habitat preference (wetland, water, grassland, open woodland, forest, and forest edge), diet (insects, fish, small mammals, small birds, other invertebrates, grains, nestlings/eggs, herps, plant matter, fruits, and carrion), foraging behavior (stalking, bark gleaning, hovering, hawking, scanning, foliage gleaning, continuous aerial feeding, ground foraging, sallying diving, dabbling, and probing [see Table 33 for definitions]), nesting behavior (ground nester), and migratory status (summer, winter, resident, migration route, and scarce). The majority of the information was gathered from the Birds of the World database as well as field guides (Billerman et al., 2020; Brazil, 2009). The final trait frequency for each family is listed in Table 25.

Next, we created functional groups based on the trait matrix by inspecting the dendrogram created by clustering the families using the Ward method (Petchey & Gaston, 2006; Ward, 1963). Each suite of traits was weighted as follows: mass (1), habitat preference (1.25), diet (1.5), foraging behavior (1.5), ground nester (1), and migratory status (1). The diet and foraging traits were weighted the most to prioritize traits that may contribute to ecosystem services/disservices related to agriculture (e.g., pest-control, crop destruction, seed predation).

In addition to functional group richness, we calculated functional dispersal as well as the community weighted means (CWM) of each trait for each sample. Functional dispersion (FDis) is the mean distance in a functional space from the centroid, weighted towards the most abundant species (Laliberté & Legendre, 2010), and the CWM of each trait allowed us to assess community functional composition (Lavorel et al., 2008). All binary trait variables were treated as continuous, so higher values of CWM indicate higher frequencies of a given trait. The functional diversity metrics were calculated using the *FD* package in R (Laliberté et al., 2014; Laliberté & Legendre, 2010; R Core Team, 2021).

Table 25: Summary of trait frequency for families (n=30)

		freq	*perc (%)*
Habitat Preference	Wetland	20	66.7
	Open woodland	18	60.0
	Grassland	17	56.7
	Forest Edge	13	43.3
	Forest	11	36.7
	Water	8	26.7
Diet	Insects	27	90.0
	Other invertebrates	27	90.0
	Grains & seeds	14	46.7
	Plant matter	12	40.0
	Small herps	11	36.7
	Fruits & berries	10	33.3
	Nestlings & eggs	8	26.7
	Fish	7	23.3
	Small mammals	5	16.7
	Small birds	5	16.7
	Carrion	2	6.7
Foraging Behavior	Ground foraging	17	56.7
	Foliage gleaning	15	50.0
	Sallying	6	20.0
	Hovering	5	16.7
	Diving	5	16.7
	Probing	5	16.7
	Hawking	4	13.3
	Scanning	3	10.0
	Continuous aerial	3	10.0
	Dabbling	2	6.7
	Stalking	1	3.3
	Bark gleaning	1	3.3
Nesting & Migration	Ground nester	12	40.0
	Summer	23	76.7
	Migratory	23	76.7
	Resident	10	33.3
	Migration route	4	13.3
	Scarce	1	3.3
	Winter	0	0.0

4.2.3 Landscape Metrics

The classified landcover rasters (see chapter 3) for 2017 and 2018 were exported at a GEE scale of 10 and used to calculate landscape metrics using the *landscapemetrics* R package (Hesselbarth et al., 2019; R Core Team, 2021). Nineteen samples were removed from this analysis due to uncertainty in the land cover classification, resulting in a final sample size of 188. All metrics were calculated at three different extents: 250m, 500m, & 1000m (Figure 17). Different extents were used to identify the single extent, by landscape metric, that incorporated the greatest amount of variability.

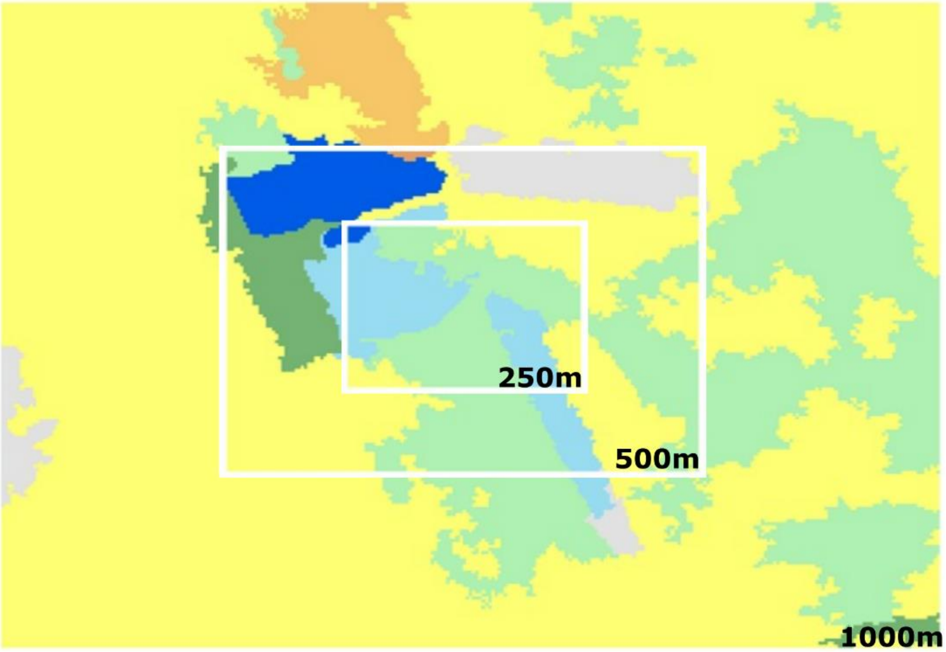


Figure 17: Comparison of the three extents chosen for landscape metric calculation at the same site

Six different metrics were calculated at each extent. Depending on the metric type, calculations were conducted at the landscape or class level (Table 26). For the crop diversity metric (MSIDI_crop), the input landscape contained only the four crop classes (corn, soybean, rice, and 'other crop') with the other classes masked (Figure 18).

Table 26: Landscape metric definitions, input, equations, and descriptions (Hesselbarth et al., 2019; Laliberté & Legendre, 2010). The 'reclassified' landcover input merged similar landcover classes so that there were only 3 classes contained in the raster (built-up, natural, and cropland).

Metric Name	*Landcover input (level)*	*Formula*	*Description*
Modified Simpson's diversity index (MSIDI)	Crop classes (landscape)	$-ln\sum_{i=1}^{m} P_i^2$ P_i = landscape area proportion of class i m = number of classes	Value of 0 indicates only one patch in landscape. Metrics increases (no limit) as the number of patches (with equal proportions) increases.
Mean patch area (AREA_MN)	All classes (landscape)	$mean(AREA[patch_{ij}])$	A landscape with all small patches has a value of 0 and increases (no limit) as patch areas increase. Unit in hectares.
Aggregation index (AI)	All classes (landscape)	$\left[\sum_{i=1}^{m}\left(\frac{g_{ii}}{\max g_{ii}}\right)P_i\right] * 100$ g_{ii} = the number of like adjacencies $\max g_{ii}$ = the max number of like adjacencies of class i	Ranges from 0-100. Values of 0 indicate completely disaggregated classes. Values of 100 for completely aggregated classes in a landscape. Unit in percent.
Total edge length (TE)	All classes (landscape)	$\sum_{k=1}^{m} e_{ik}$ e_{ik}= total edge length i = target class k = all other classes	Value of 0 if all cells in a landscape raster are edge cells or if the landscape only contains one class. Increases (no limit) as landscape fragmentation increases. Unit in meters.
Edge density (ED)	All classes (landscape)	$\frac{E}{A} * 10000$ E = total edge length A = the total area	Value of 0 indicates only one patch is present (landscape boundary not included). Value increases (no limit) as the number of patches increase. Unit in meters.
Percent of landscape (PLAND)	Reclassified All classes (class)	$\frac{\sum_{j=1}^{n} a_{ij}}{A} * 100$ a_{ij} = the area of patch j n = number of patches A = the total landscape area	Value of 100 indicates only one patch of target class is present in landscape. Approaches 0 as class area decreases. Unit is percent.

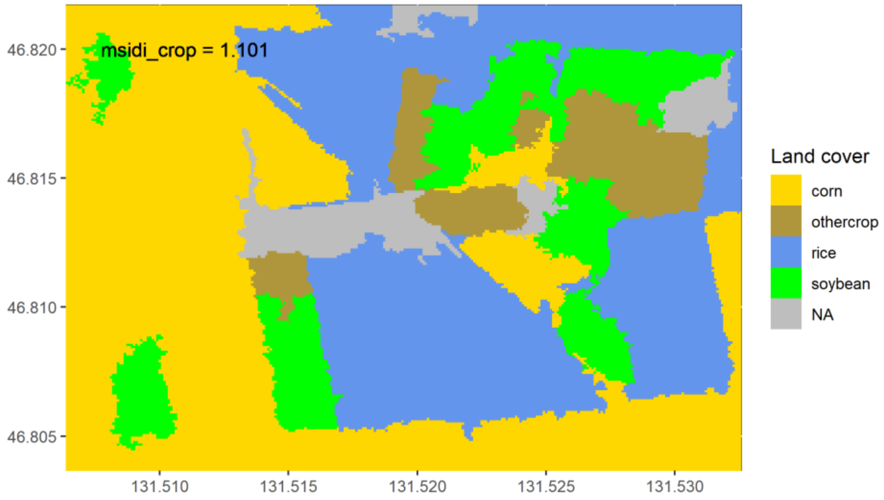


Figure 18: Example landscape input for crop diversity. All non-crop classes (i.e., built-up, forest, grassland, wetland, and water were masked (NA).

4.2.4 Prefecture Case Study

To evaluate impacts of global trade on landscape and bird biodiversity in Heilongjiang, we compared two prefectures (Jiamusi and Qiqihar) with differing degrees of landcover change as portrayed by soybean planting area. Due to limited availability of Sentinel imagery during our study period, we used annual soybean maps derived from Landsat imagery created by another group of researchers to inform our selection of the regions (X. Li et al., 2021). The entire province experienced growth in soybean area beginning in 2002. However, around 2010, there was a sharp decrease in soybean area across all prefectures, though the degree of decline was not equal.

Qiqihar is located in the western half of the province and covers over 42,000 km^2. Prior to 2000, Qiqihar had the most soybean planted area in the province (X. Li et al., 2021). After the increase in the early 2000s, the planted area dropped slightly in Qiqihar resulting in another prefecture surpassing the planted soybean area of Qiqihar (X. Li et al., 2021). The Jiamusi prefecture is located on the eastern side of Heilongjiang and is slightly smaller than Qiqihar (~31,000 km^2). Compared to Qiqihar, Jiamusi grew fewer soybeans between 2000-2018, though it did go from being the 5th largest grower in 2000 to the 3rd in 2009 (X. Li et al., 2021). However, Jiamusi experienced a more severe drop in soybean area compared to Qiqihar, with soybean planting area dropping below the pre-increase level in 2018 (Figure 19). Using soybean area decline as a proxy for the impact of soybean imports on landscape and bird diversity, we selected Jiamusi as an example of greater impact and Qiqihar as an example of the impact. Each prefecture has a similar number of samples, with 53 and 55 in Jiamusi and Qiqihar, respectively (Figure 20).

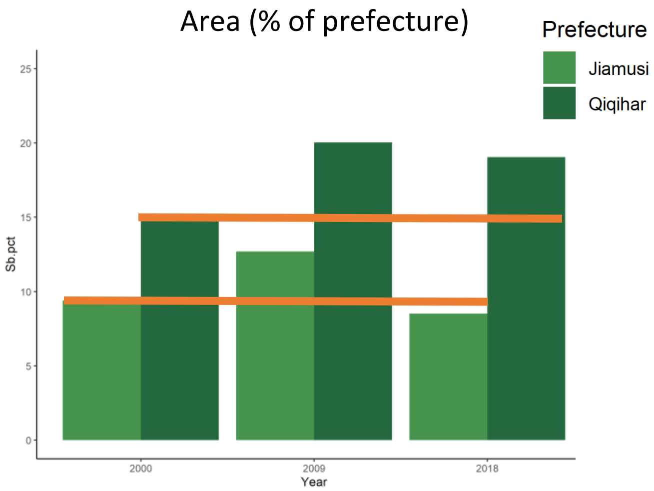


Figure 19: Soybean area decline for Jiamusi and Qiqihar prefectures. The orange lines highlight the difference in soybean area between 2000 and 2018.

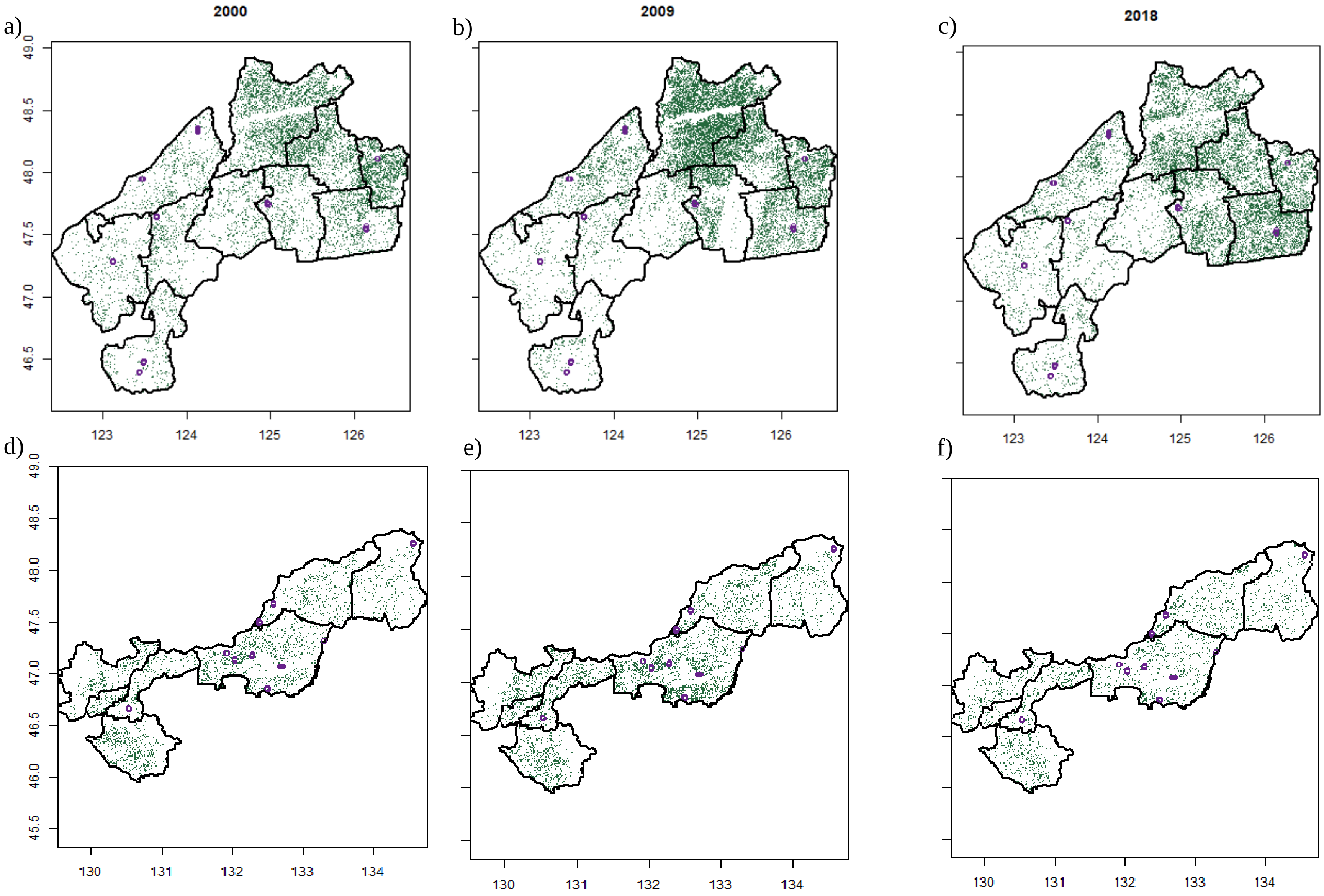


Figure 20: Soybean area in 2000 (a,d), 2009 (b,e), and 2018 (c,f) for Qiqihar (a-c) and Jiamusi (d-f). Data from X. Li et al. 2021. Bird/landscape samples are depicted by purple points.

4.3 Results

4.3.1 Biodiversity results

After inspecting the dendrogram created by clustering the families based on the trait matrix, we chose to assess functional group diversity using 15 groups (Figure 21). This value was determined based on inspection of a range of group number values. Though other grouping schemes could be argued, the 15 groups we created made ecological sense without masking functionally unique families and were therefore well-suited to our research objectives. The group membership for each family can be found in Table 27.

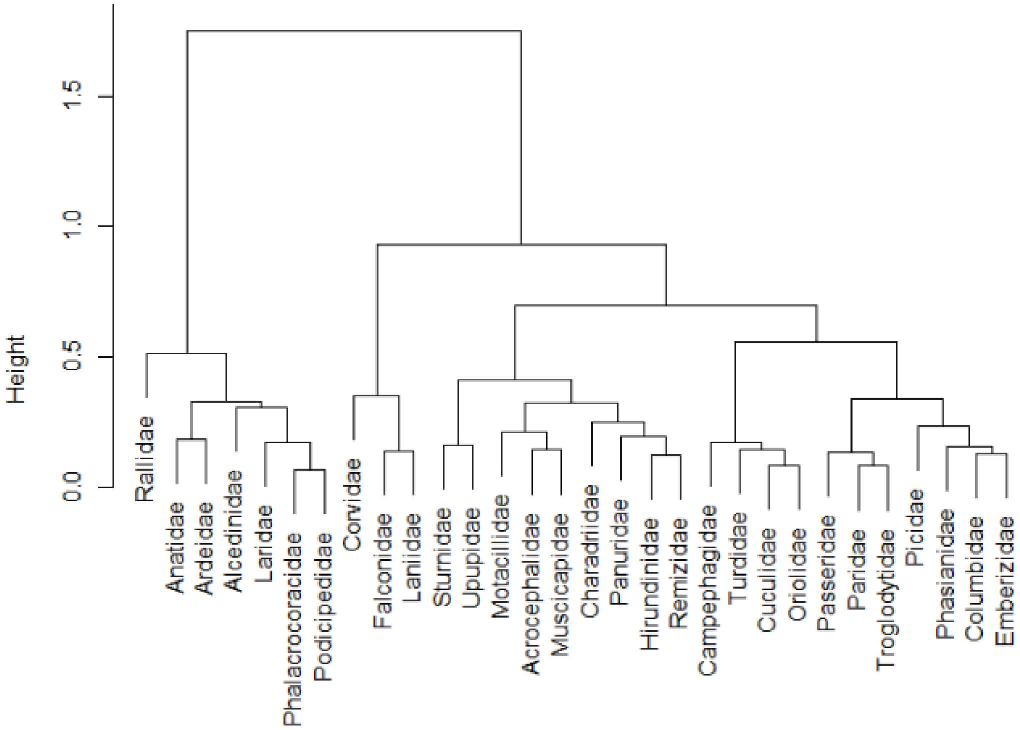


Figure 21: Cluster dendrogram of families based on functional traits

Table 27: Family membership to functional groups and occurrence for all sampled prefectures in Heilongjiang, Jiamusi, and Qiqihar (OW=old world).

			All (n=188)		**Jiamusi (n=53)**		**Qiqihar (n=55)**	
Group	**Family**	**Description**	Fam Occ	Grp Occ	Fam Occ	Grp Occ	Fam Occ	Grp Occ
1	Acrocephalidae	Reed warbs	63	65	26	26	14	14
1	Muscicapidae	OW Flycatchers	3		0		0	
2	Alcedinidae	Kingfisher	1	1	0	0	0	0
3	Anatidae	Ducks	2	4	1	2	1	1
3	Ardeidae	Herons	3		1		1	
4	Campephagidae	Cuckooshrike	1	14	1	3	0	7
4	Cuculidae	Cuckoos	7		1		5	
4	Oriolidae	Orioles	3		1		2	
4	Turdidae	Thrushes	3		0		0	
5	Charadriidae	Shorebirds	5	5	3	3	0	0
6	Columbidae	Doves	17	45	7	13	3	5
6	Emberizidae	OW Buntings	29		7		1	
6	Phasianidae	Pheasants	1		0		1	
7	Corvidae	Crows & Jays	34	34	12	12	13	13
8	Falconidae	Falcons	10	20	4	8	2	2
8	Laniidae	Shrikes	10		4		0	
9	Hirundinidae	Swallows	65	70	10	10	26	30
9	Panuridae	Reed Tits	1		0		1	
9	Remizidae	Penduline Tits	7		0		6	
10	Laridae	Gulls	1	4	0	2	1	2
10	Phalacrocoracidae	Cormorants	2		2		0	
10	Podicipedidae	Grebes	2		0		2	
11	Motacillidae	Wagtails & Pipits	3	3	0	0	0	0
12	Paridae	Tits	2	33	0	4	0	13
12	Passeridae	OW Sparrows	30		3		13	
12	Troglodytidae	Wrens	1		1		0	
13	Picidae	Woodpeckers	1	1	0	0	1	1
14	Rallidae	Rails	3	3	0	0	2	2
15	Sturnidae	Starlings	1	3	1	1	0	0
15	Upupidae	Hoopoe	2		0		0	

Across all samples, the most frequently occurring families were Hirundinidae (swallows), Acrocephalidae (reed warblers), and Corvidae (corvids) (Table 27). These three families were the most common in Jiamusi and Qiqihar as well, with reedwarblers occurring more in Jiamusi and swallows occurring more in Qiqihar. The most common functional groups differed between the two prefecture. Across the entire sample area and in Qiqihar, swallows/reedtits (group 9) occurred more frequently while reedwarb/flycatchers (group 1) were more common in Jiamusi.

We also investigated relative frequencies of bird communities based on functional groups. In general, many of the communities we found were unique, with only a couple of occurrences across all 188 points. The most common community only contained species from group 1 (reedwarb/flycatcher) followed by communities compromised solely of families from group 9 (swallow/reedtit) (Table 28). These two groups were also found in several other of the most common communities, including one where they co-occur. Unlike with the taxonomic frequency, Jiamusi had the same most common functional group as the rest of the region (reedwarb/flycatcher) while Qiqihar’s most common group was the swallow/reedtit group.

Table 28: Most frequent communities.

ALL (n=188)			**Jiamusi (n=53)**			**Qiqihar (n=55)**		
comm.	Freq	*description*	*comm.*	*Freq*	*description*	*comm.*	*Freq*	*description*
group1	21	reedwarb/flycatcher	group1	10	reedwarb/flycatcher	group9	6	swallow/reedtit
group9	13	swallow/reedtit	group6	3	dove/bunting/pheasant	group12	5	sparrow/tit
group12	12	sparrow/tit	group7	3	crow/magpie	group1 group9	4	reedwarb/flycatcher swallow/reedtit
group6	10	dove/bunting/pheasant	group1 group5 group6	2	reedwarb/flycatcher shorebird/lapwing dove/bunting/pheasant	group9 group12	3	swallow/reedtit sparrow/tit
group1 group9	8	reedwarb/flycatcher swallow/reedtit	group1 group8	2	reedwarb/flycatcher falcon/shrike	group4 group7 group9	2	thrush/cuckoo/oriole crow/magpie swallow/reedtit
group6 group9	8	dove/bunting/pheasant swallow/reedtit	group1 group9	2	reedwarb/flycatcher swallow/reedtit	group7	2	crow/magpie
group9 group12	8	swallow/reedtit sparrow/tit	group9 group12	2	swallow/reedtit sparrow/tit	group7 group9 group12	2	crow/magpie swallow/reedtit sparrow/tit
group7	6	crow/magpie						
group1 group6	5	reedwarb/flycatcher dove/bunting/pheasant						
group8	4	falcon/shrike						

The richness metrics were calculated by aggregating observations for all 3 intervals recorded for each point. TR ranged from 0-9 with a mean of 1.66 (Table 29). The number of functional groups (FGR) had a similar mean to TR (1.62) and ranged from 0-8 (Table 29). Finally, we mapped the richness metrics across the study region (Figure 23) and found no significant differences between Jiamusi and Qiqihar.

Table 29: Summary table of the richness metrics calculated at the point level for all Heilongjiang prefectures (n=188), Jiamusi (n=53), and Qiqihar (n=55)

	All Prefectures		Jiamusi (more impacted)		Qiqihar (less impacted)	
	mean	sd	mean	sd	mean	sd
n.sp	1.66	1.37	1.60	1.55	1.73	1.58
FGR[*]	1.62	1.28	1.58	1.52	1.64	1.32
[*] Number of groups (15) determined based on visual inspection of dendrograms produced using the ward method of clustering.						

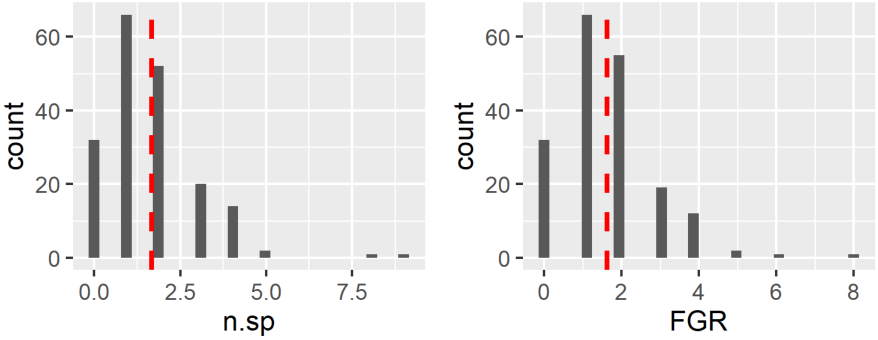


Figure 22: Histograms of the three richness metrics with the mean depicted by the red vertical line: number of families (n.sp) and functional group richness (FGR)

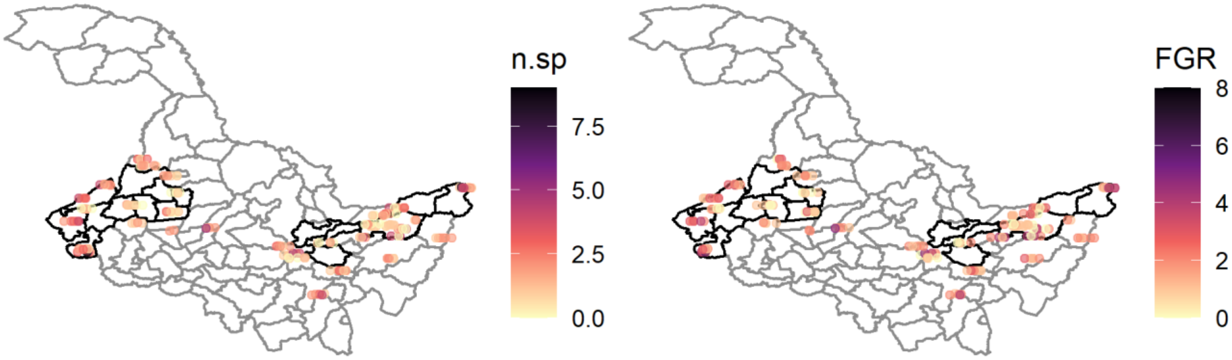


Figure 23: Map of richness metrics: number of families (n.sp) and unctional group richness (FGR). Counties in the Qiqihar (west) and Jiamusi (east) prefectures are outlined in black.

The abundance-weighted metrics were calculated at the interval level first, and then averaged at the point level. Comparing these two levels of analysis, the mean values of these metrics did not differ greatly (Table 30). Therefore, we will focus on the point-level results. Shannon (H) diversity ranged from 0-1.53 with a mean of 0.217 (Table 30) with a distribution clearly skewed to the right (Figure 24). For the 156 points where functional dispersal (FDis) could be calculated, many had a FDis value of zero, indicating the presence of a single species (Figure 24). The largest value of FDis in our sample was 0.221, with a mean of 0.043 (Table 31). Finally, we mapped the abundance-weighted metrics across the study region (Figure 25) and found no difference between the Qiqihar and Jiamusi (p-value > 0.05) (Table 31).

Table 30: Summary table of the abundance-weighted biodiversity metrics averaged across all intervals (n=564) and at the point-level for all samples (n=188).

	Intervals		Points	
	mean	sd	mean	sd
H	0.198	0.354	0.217	0.309
FDis*	0.047	0.066	0.043	0.052
* Could not be calculated for communities with 0 species present (32 points)				

Table 31: Summary table of the abundance-weighted biodiversity metrics at the point-level for Jiamusi (n=53) and Qiqihar (n=55).

	Jiamusi (more impacted)		Qiqihar (less impacted)	
	mean	sd	mean	sd
H	0.22	0.34	0.22	0.31
FDis*	0.04	0.06	0.04	0.05
* Could not be calculated for communities with 0 species present (13 and 12 points for Jiamusi and Qiqihar respectively)				

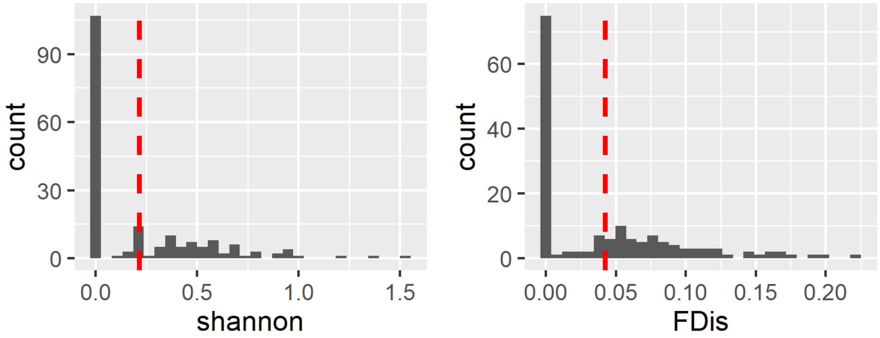


Figure 25: Histograms of the abundance-weighted biodiversity metrics at the point-level with the mean depicted by the red vertical line: Shannon-Weiner index (shannon) and functional dispersion (FDis).

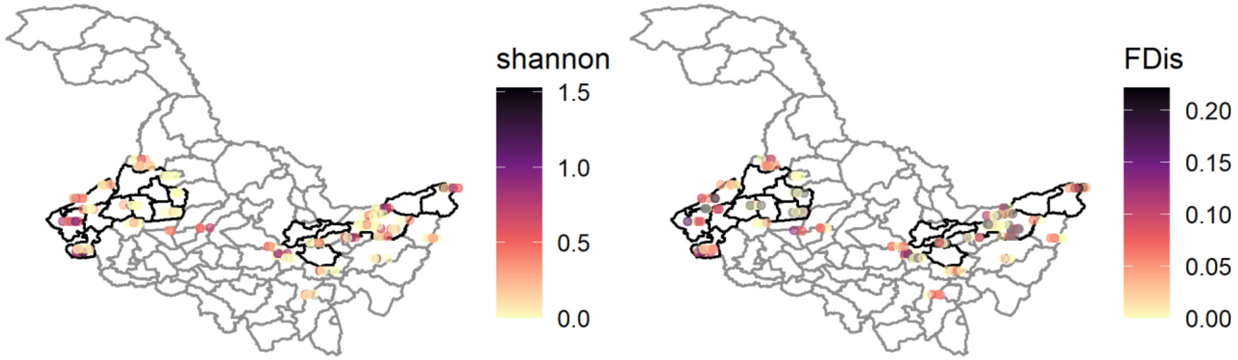


Figure 24: Map of abundance-weighted biodiversity indices at the point-level: Shannon-Weiner index (shannon) and functional dispersion (FDis). Note that the gray points represent missing values (where 0 species are present for FDis. Counties in the Qiqihar (west) and Jiamusi (east) prefectures are outlined in black.

4.3.2 Landscape metric results

A summary of the landscape metrics calculated for each extent can be found in Table 32. Crop diversity at the largest extent was significantly higher in Qiqihar. Percent natural area was also significantly higher at the 500m and 1000m extents in Qiqihar, while rice at the highest extent was significantly higher in Jiamusi. Though soybean area mean was not significantly different between the Jiamusi and Qiqihar samples, Qiqihar had more samples with higher soybean percentage (Figure 26).

Table 32: Summary table of all landscape metrics at the small (250m), medium (500m), and large (1000m) extents. Bold values indicate significant differences between Jiamusi and Qiqihar (p-value < 0.1).

	All HLJ		**Jiamusi (more impacted)**		**Qiqihar (less impacted)**	
	mean	*sd*	*mean*	*sd*	*mean*	*sd*
msidi_crop_250m	0.30	0.33	0.35	0.37	0.35	0.32
msidi_crop_500m	0.36	0.34	0.36	0.37	0.41	0.34
msidi_crop_1000m	0.42	0.33	**0.38**	**0.34**	**0.49**	**0.31**
mn_patch_250m	6.03	5.38	4.79	3.83	5.59	5.37
mn_patch_500m	10.32	9.68	8.71	4.81	9.02	7.29
mn_patch_1000m	14.11	6.45	13.61	6.90	12.98	5.41
ai_250m	96.70	2.02	96.26	1.75	96.36	1.98
ai_500m	96.82	1.51	96.50	1.45	96.55	1.39
ai_1000m	96.82	1.21	96.70	1.24	96.58	1.19
te_250m	2.51x10^{3}	1.51x10^{3}	2.86x10^{3}	1.37x10^{3}	2.72x10^{3}	1.51x10^{3}
te_500m	9.30x10^{3}	4.23x10^{3}	1.01x10^{4}	4.19x10^{3}	1.01x10^{4}	3.92x10^{3}
te_1000m	3.56x10^{4}	1.28x10^{4}	3.67x10^{4}	1.36x10^{4}	3.83x10^{4}	1.23x10^{4}
ed_250m	99.54	60.11	113.52	54.43	107.81	60.22
ed_500m	92.34	42.05	100.39	41.67	100.06	39.02
ed_1000m	88.41	31.75	90.96	33.76	94.74	30.83
p_nat_250m	15.35	22.22	10.78	12.72	14.29	20.00
p_nat_500m	15.63	19.64	**9.96**	**8.94**	**14.44**	**15.49**
p_nat_1000m	16.68	18.65	**9.14**	**6.88**	**15.62**	**13.53**
p_soy_250m	15.86	26.25	11.31	14.24	11.83	24.19
p_soy_500m	14.40	22.30	9.62	10.41	12.27	22.12
p_soy_1000m	13.41	18.81	8.57	8.39	11.53	18.45
p_corn_250m	29.35	32.02	32.55	34.91	37.19	32.51
p_corn_500m	29.93	29.50	35.57	34.68	35.43	28.35
p_corn_1000m	29.65	27.00	36.25	33.02	33.02	24.10
p_rice_250m	33.35	36.71	37.23	35.53	31.43	34.69
p_rice_500m	31.81	34.05	36.32	34.81	29.29	30.85
p_rice_1000m	29.62	30.15	**37.29**	**33.64**	**26.70**	**25.54**

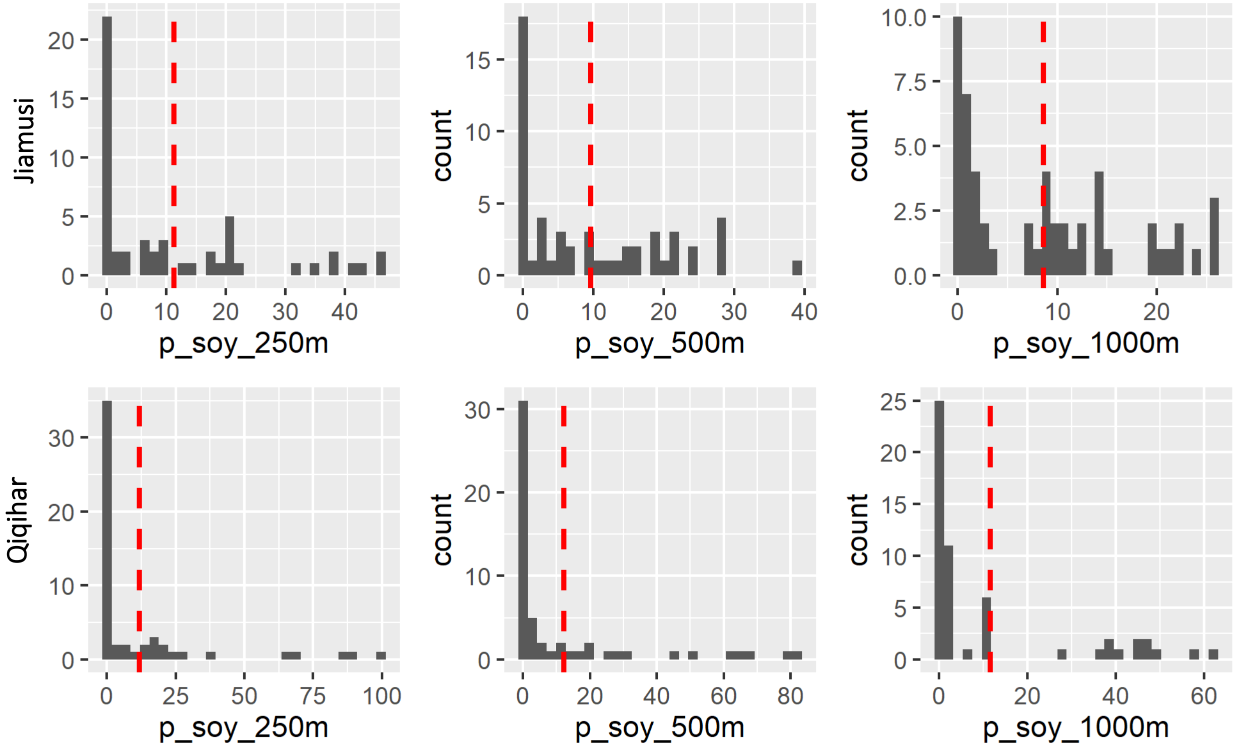
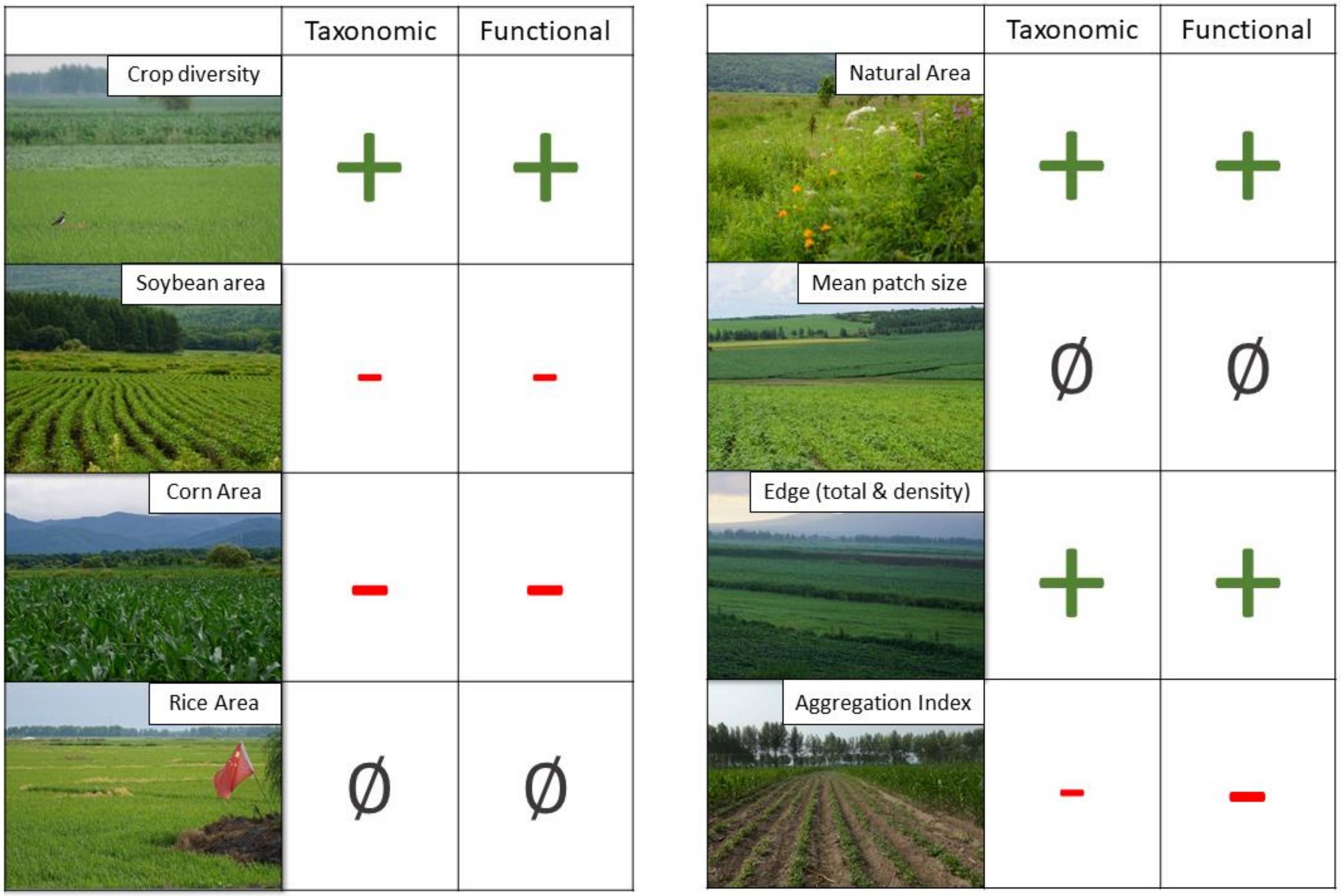


Figure 26: Histograms of percent soybean (p_soy) for Jiamusi (top) and Qiqihar (bottom).

4.3.3 Bird Diversity & Landscape Relationship

While examining relationships between landscape structure and bird diversity across all samples, we found little differences between taxonomic or functional measures of bird diversity. However, we observed some significant relationships (p-value < 0.1) between bird diversity and landscape structure. Taxonomic (n.sp) and functional group richness (FGR) exhibited similar relationships across all landscape metrics (Figure 27). Both were significantly and positively correlated with crop diversity and percent natural landcover for all extents, with the degree of correlation increasing slightly as extent decreased (Figure 28). Total edge and edge density were also positively correlated with these richness metrics (Figure 27). For TR, the edge metric relationships were stronger at the largest extent while the FGR relationships were strongest at the smallest extent (Figure 29).

On the other hand, aggregation was significantly and negatively correlated with taxonomic and functional group richness (Figure 27). Percent soybean and corn were also negatively correlated with TR and FGR (Figure 27). Soybean area was only moderately significant (p-values < 0.1) for the 500m and 1000m extents, while corn was significantly correlated for all extents (Figure 30). Neither mean patch size nor percent rice were significantly correlated with these biodiversity metrics (Figure 27).



	Taxonomic	Functional
Crop diversity	+	+
Soybean area	-	-
Corn Area	-	-
Rice Area	Ø	Ø

	Taxonomic	Functional
Natural Area	+	+
Mean patch size	Ø	Ø
Edge (total & density)	+	+
Aggregation Index	-	-

Figure 27: Correlations between taxonomic richness (n.sp) and functional richness (function group richness). The size of each sign corresponds to the number of extents (250m, 500m 1000m) that were significantly positive (+) or negative (-). Metrics with no significant relationships are denoted by the null sign (Ø).

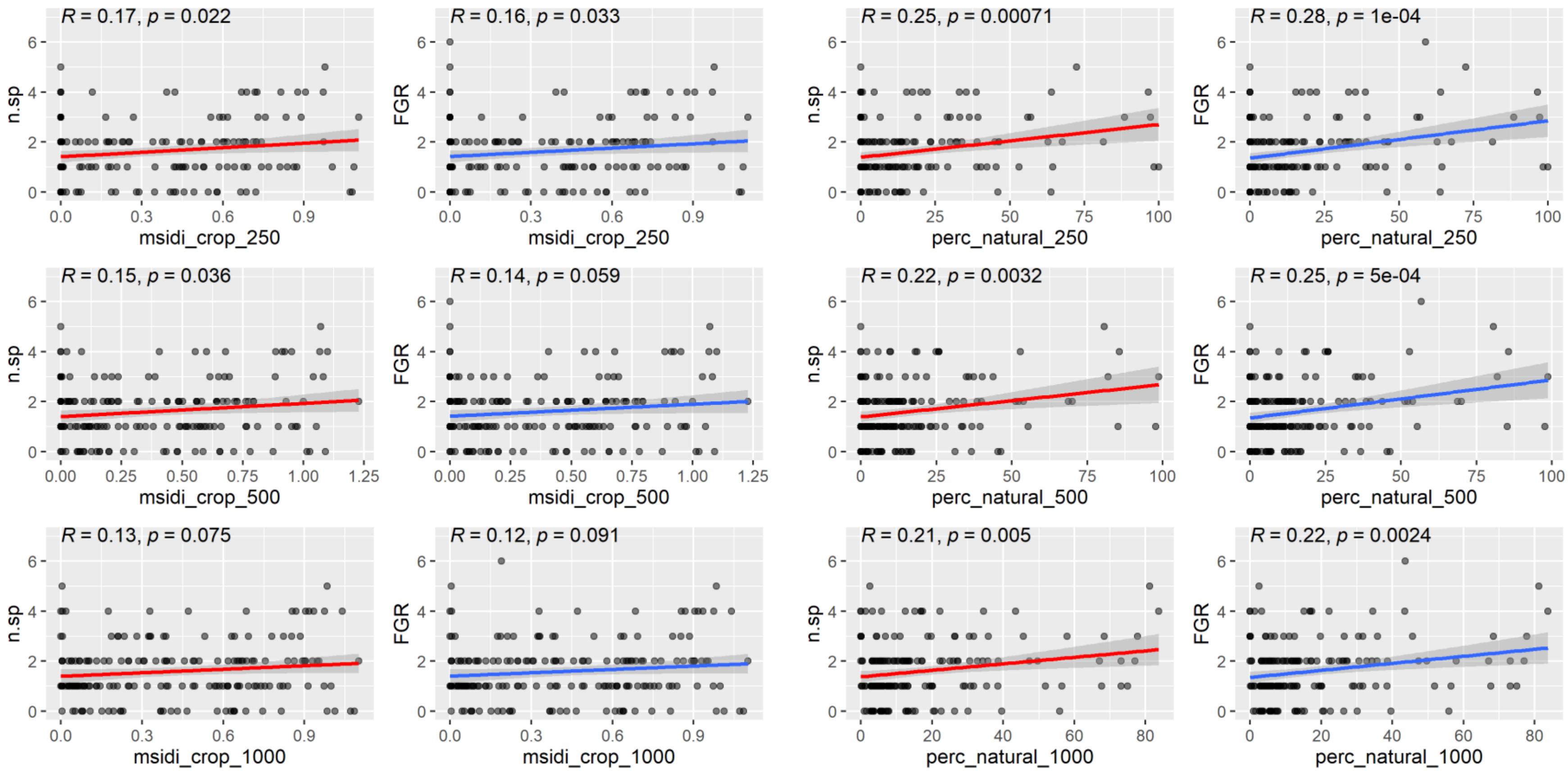


Figure 28: Taxonomic richness (n.sp, red) and functional group richness (FGR, blue) relationships with crop diversity (left) and percent natural landcover (right). Pearson's correlation (R) and p-value (p) for each relationship is also included in the top left corner of each

Figure 29: Taxonomic richness (n.sp, red) and functional group richness (FGR, blue) relationships with total edge (top left), edge density (top right) and aggregation index (bottom). Pearson's correlation (R) and p-value (p) for each relationship is also included in the top left corner of each plot.

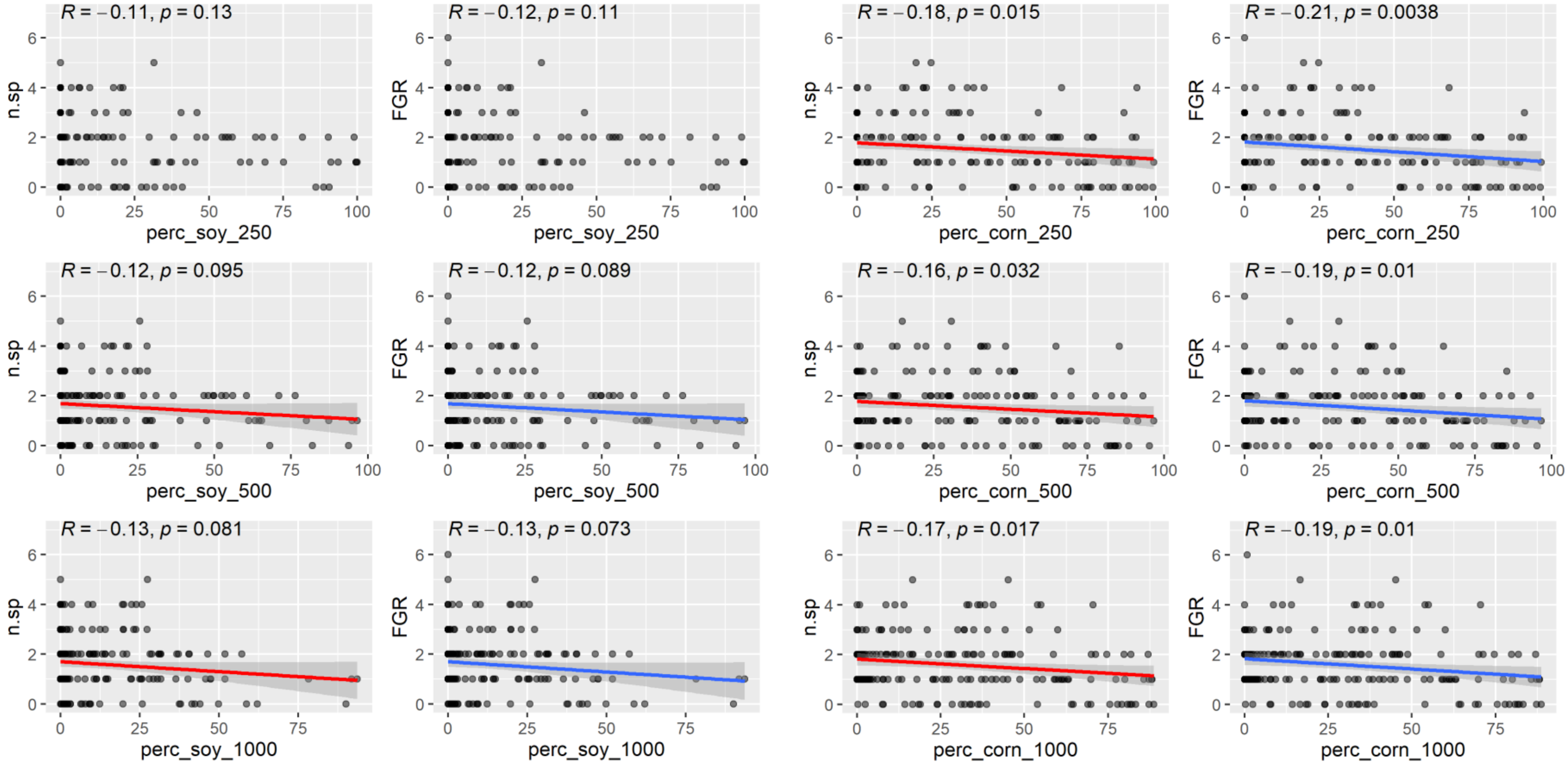


Figure 30: Taxonomic richness (n.sp, red) and functional group richness (FGR, blue) relationships with percent soybean (left) and percent corn (right). Pearson's correlation (R) and p-value (p) for each relationship is also included in the top left corner of each plot.

We found some significant correlations between the abundance-weighted bird diversity metrics, Shannon (H) and functional dispersion (FDis), and landscape structure (Figure 31). Unlike with richness, crop diversity was substantially less related to H and FDis, with just the 500m extent being positively related to FDis (Figure 32). On the other hand, percent natural landcover, total edge, and edge density were all positively correlated across all extents (Figure 31-Figure 33). Aggregation was negatively related across all extents for both H and FDis (Figure 31, Figure 33). H and FDis were negatively correlated across all extents of soybean percentage while corn area was only negatively correlated with H at the 1000m extent (Figure 31, Figure 34). Neither mean patch size nor percent rice were related to the H and FDis biodiversity metrics (Figure 31, Figure 40).

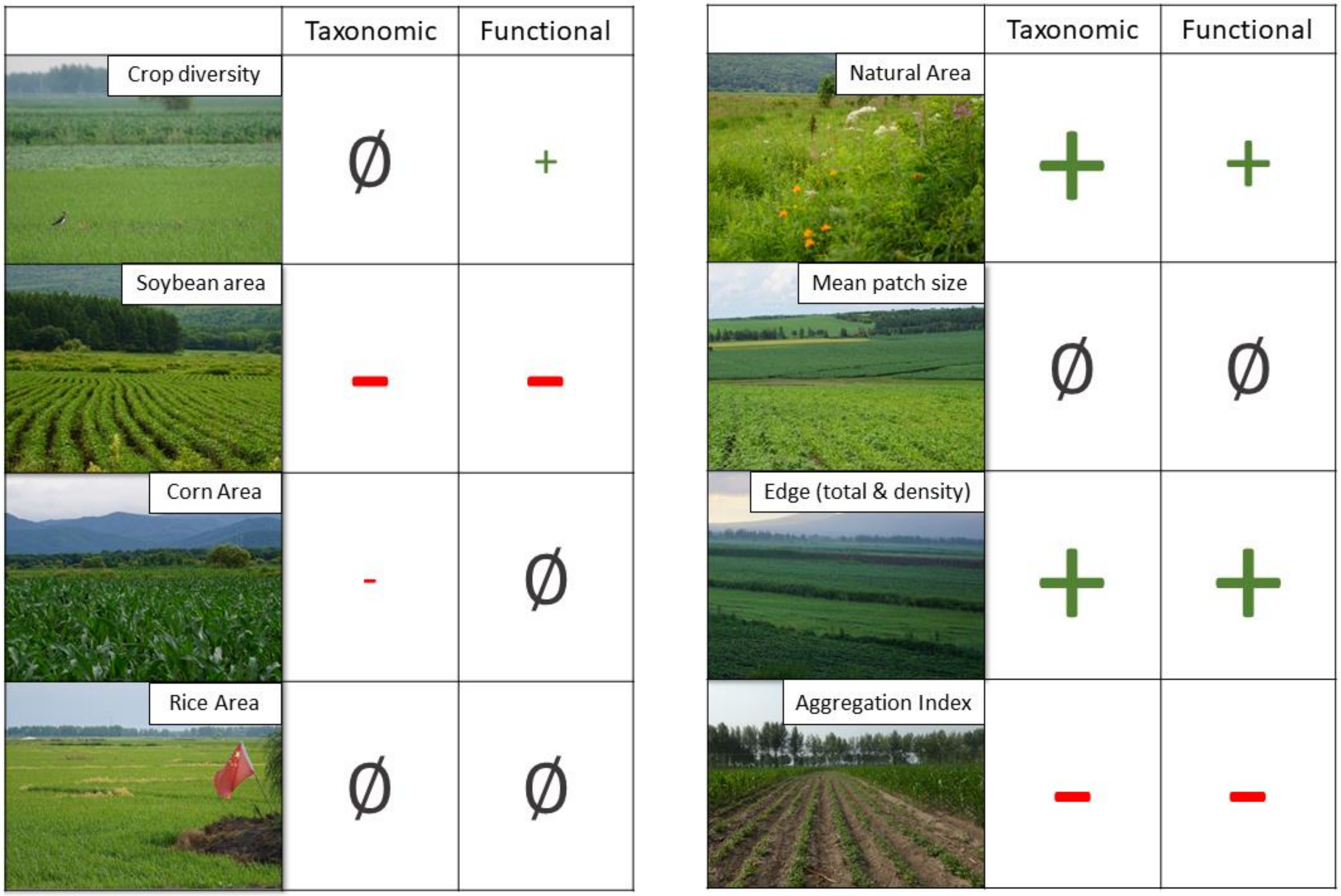


Figure 31: Correlations between Shannon's diversity index (taxonomic) and functional dispersal (functional). The size of each sign corresponds to the number of extents (250m, 500m 1000m) that were significantly positive (+) or negative (-). Metrics with no significant relationships are denoted by the null sign (Ø).

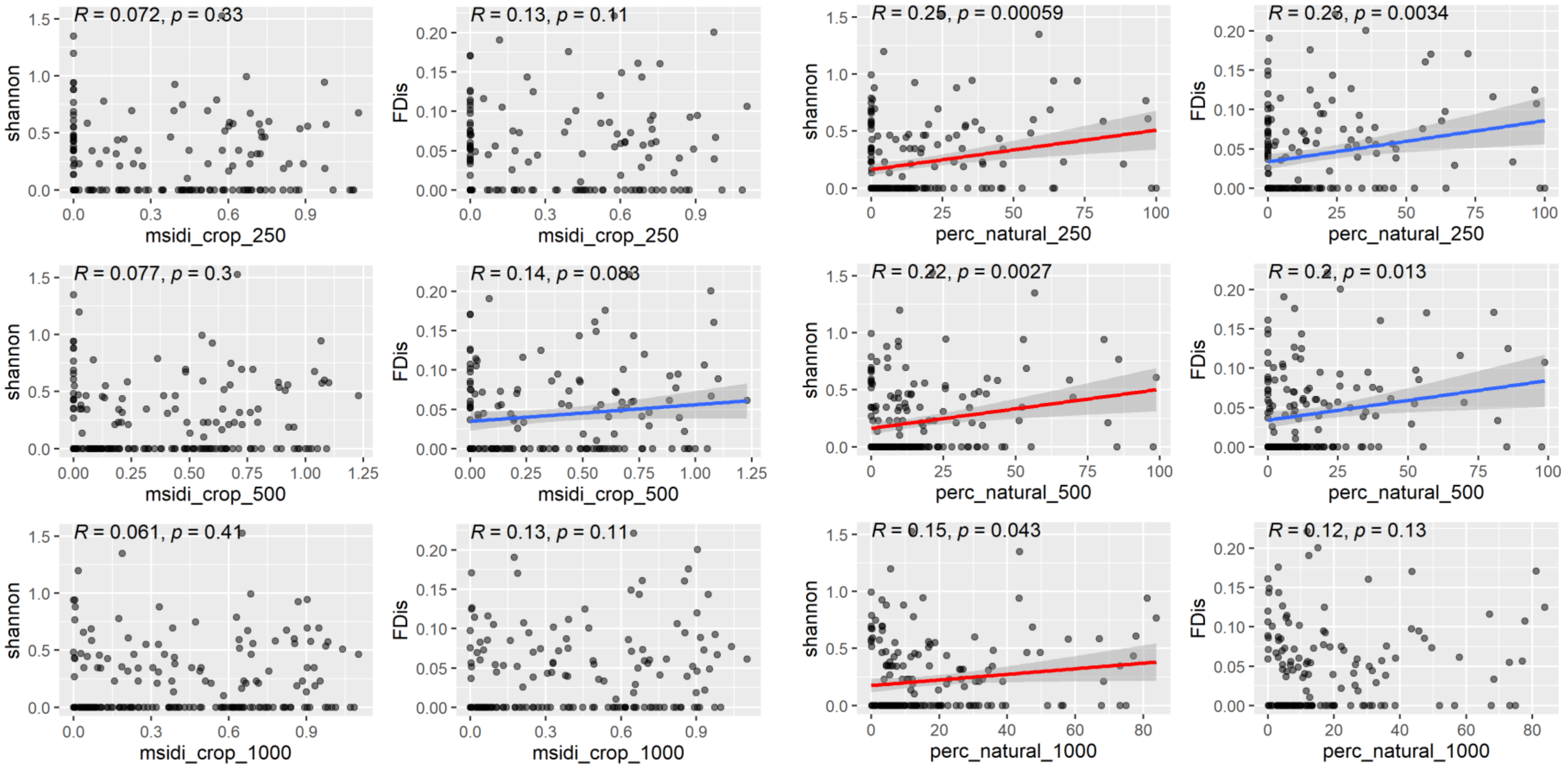


Figure 32: Shannon-Weiner (shannon, red) and functional dispersal (FDis, blue) relationships with crop diversity (left) and percent natural landcover (right). Pearson's correlation (R) and p-value (p) for each relationship is also included in the top left corner of each plot.

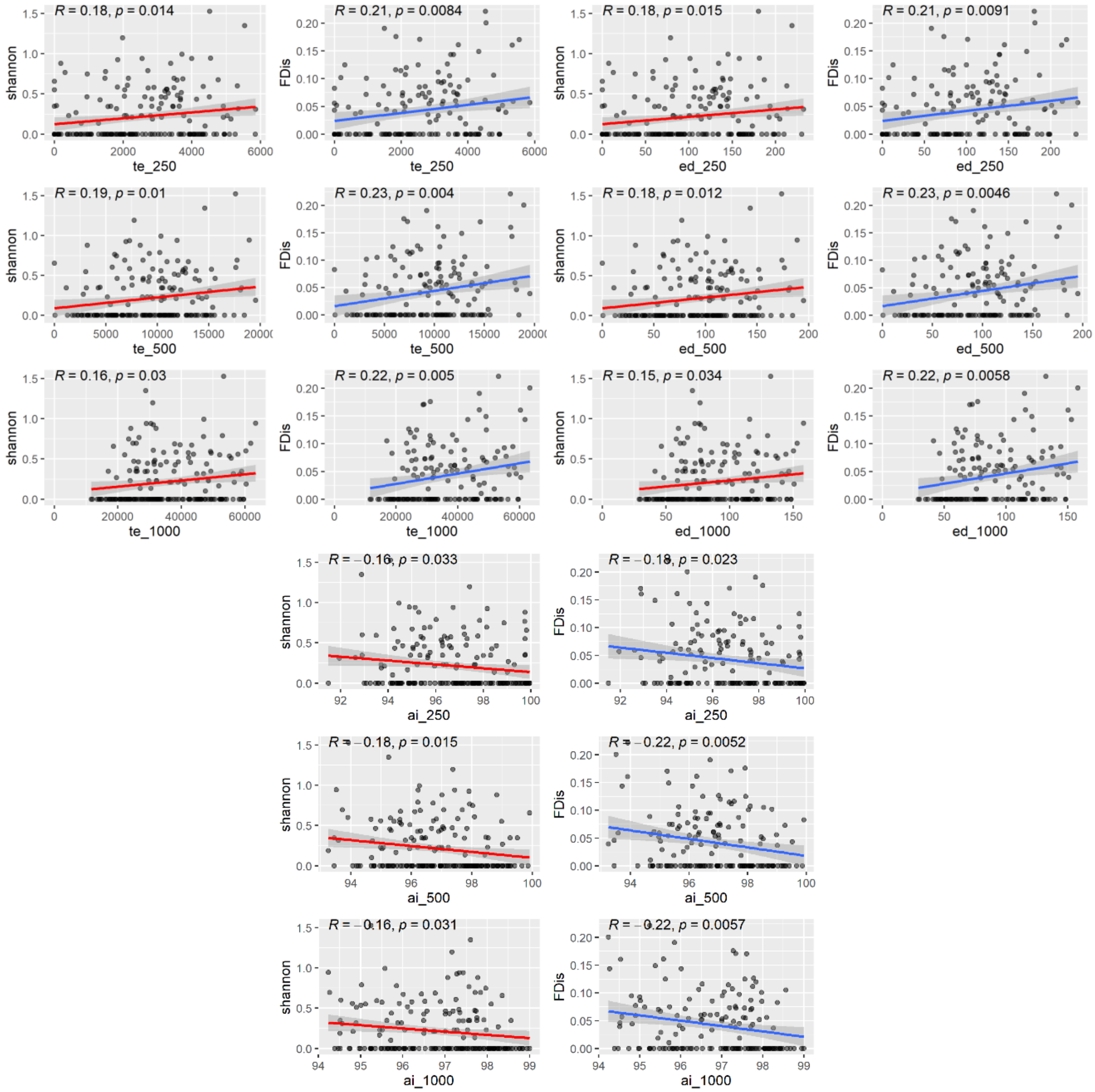


Figure 33: Shannon-Weiner (shannon, red) and functional dispersal (FDis, blue) relationships with total edge (top left), edge density (top right) and aggregation index (bottom). Pearson's correlation (R) and p-value (p) for each relationship is also included in the top left corner of each plot.

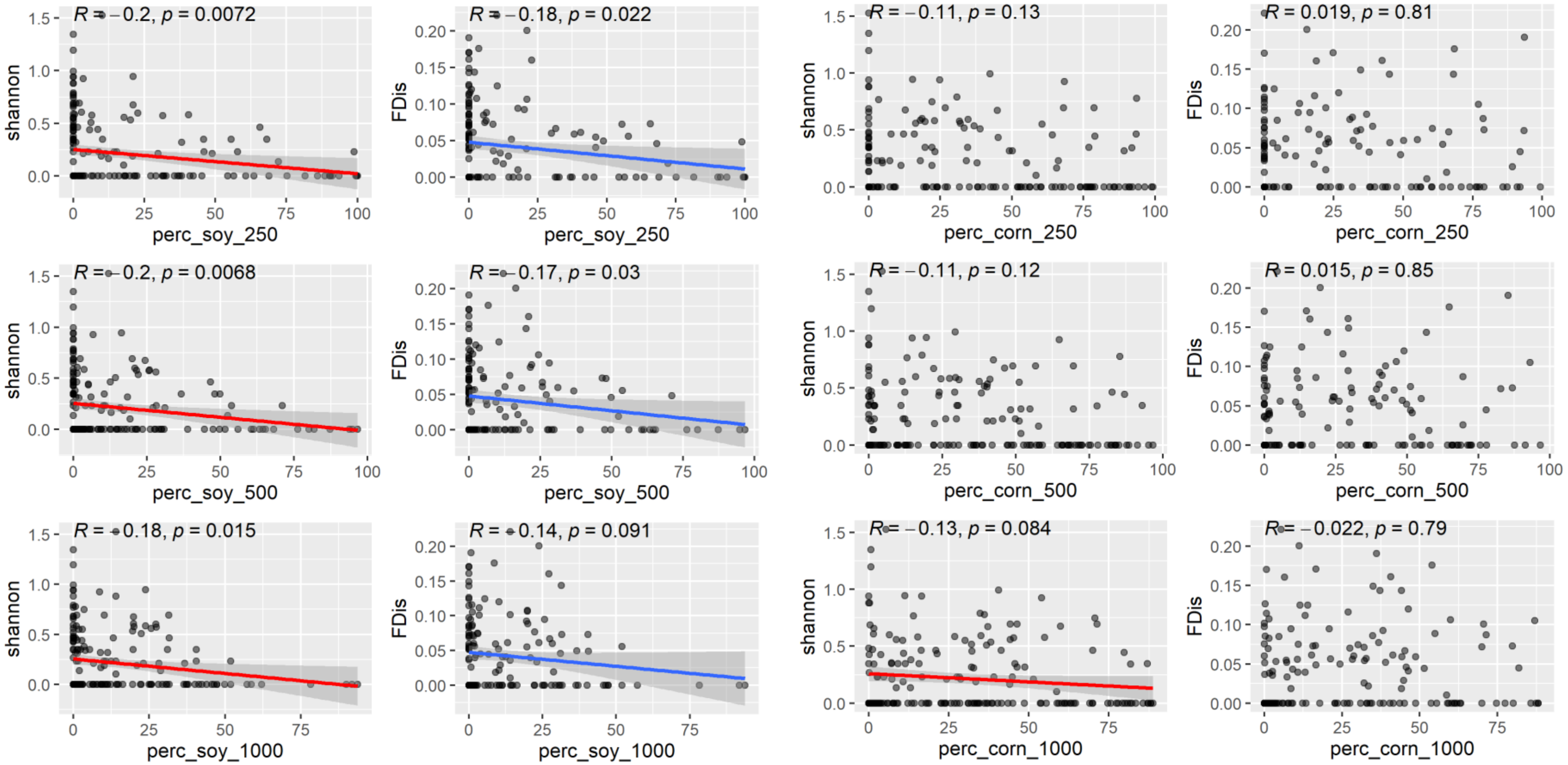


Figure 34: Shannon-Weiner (shannon, red) and functional dispersal (FDis, blue) relationships with percent soybean (left) and percent corn (right). Pearson's correlation (R) and p-value (p) for each relationship is also included in the top left corner of each plot.

4.3.4 Community Weighted Means and Landscape

We detected 29 significant correlations between crop diversity and various CWM values. Note that all these significant relationships were found to be positive except one. Average mass was positively correlated with crop diversity calculated at 250m and 500m (Table 35). Within the habitat preference traits, the forest trait was positively correlated with crop diversity at all extents (Table 35). The majority of the diet traits (6 out of 11) were positively related to crop diversity as well (Table 36). The impact of crop diversity was not as strong when considering the suite of foraging traits. Only bark gleaning, hawking, and scanning exhibited significant relationships in our sample (Table 37). The ground nesting trait was also correlated with crop diversity at the largest extent (Table 38). Finally, the presence of resident species was positively related with crop diversity at all extents, while those that passed through the region on migration were positively correlated at the medium and largest extents of crop diversity (Table 38). The relative relationships between the CWM for habitat, diet, foraging behavior, and migration and crop diversity at 1000m can be found in Figure 35.

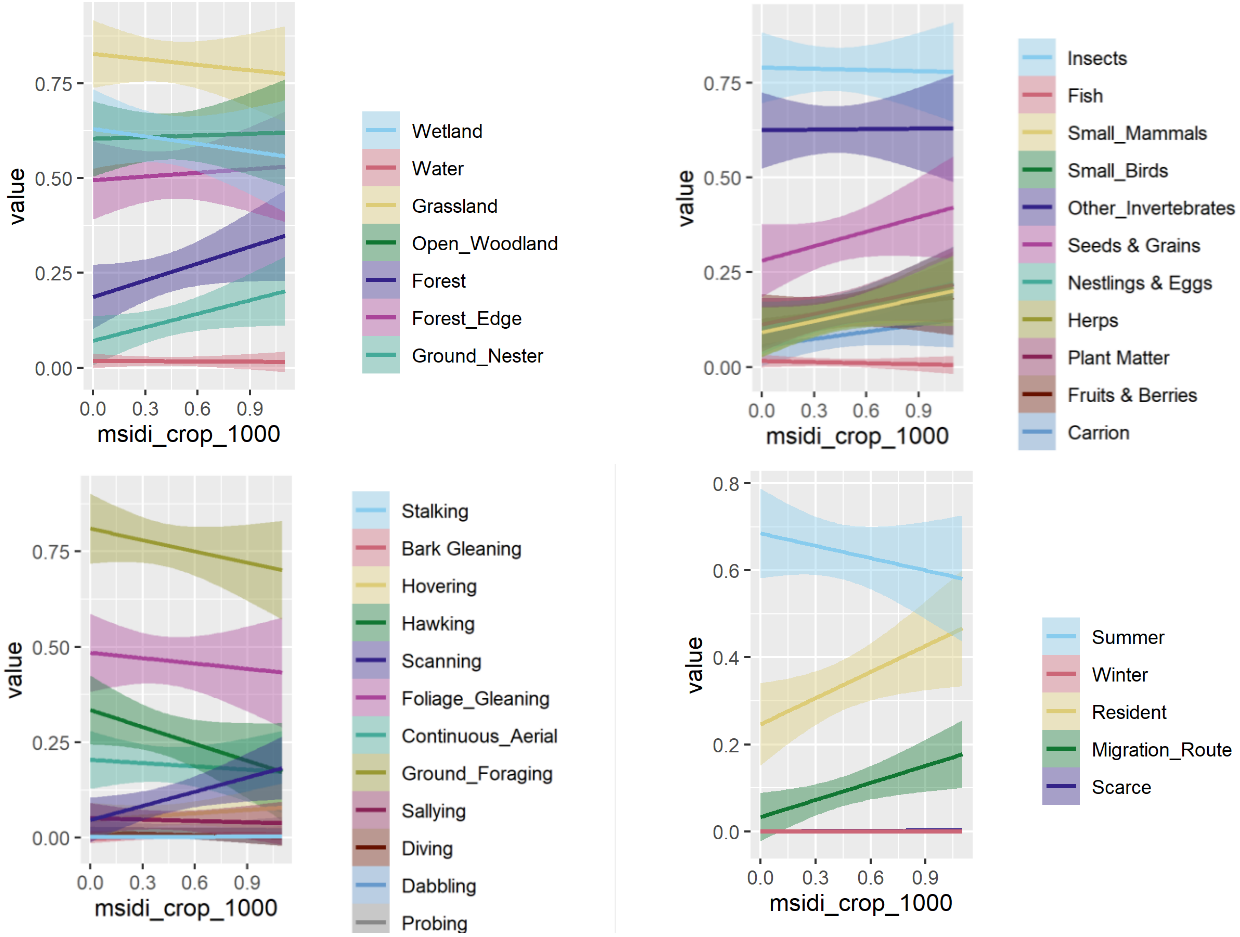


Figure 35: Linear relationships of crop diversity at the 1000m extent and the habitat, diet, foraging behavior, and migration community weighted means.

Percentage of soybean, corn, and paddy rice was found to be significantly related to many of the CWM traits (26, 54, and 55 for soybean, corn, and rice area respectively). We found that there were many instances where percentage of rain-fed crops (soybean and corn) and rice paddy had opposite relationships with various CWMs. Both corn and rice percent were correlated with average body mass, positively and negatively respectively (Table 35). Every habitat preference trait, except for forest was negatively correlated with corn and positively correlated with rice. Additionally, forest preference was negatively correlated with paddy rice area and positively related to soybean (Table 35).

As with habitat preference, the direction of the significant relationships of the rain-fed crops and rice paddy within the diet trait CWMs were often reversed. Percent corn crop was correlated with 6 of the diet traits we recorded, 7 significant relationships were found with rice percentage, and 2 diet traits were correlated with soybean area (Table 36). Fruit and carrion diets CWMs were positively correlated with corn and negatively correlated with rice. Additionally, diets that include nestlings/eggs were negatively correlated with rice. Insect, fish, and invertebrate diet CWMs were positively related to rice and negatively with corn. Seed diets were positively correlated with soybean area and negatively with rice area. Diets with plant matter were positively correlated with soybean area and negatively with corn. Herptiles (reptiles and amphibians), small birds, and mammal diet CWMs were not significantly related to either crop percentage (Table 36).

The significant foraging behavior CWMs that were positively correlated with rice (and negatively correlated with both corn and soybean) were hawking and ground foraging (Table 37). Foliage gleaning was also positively correlated with rice but only negatively correlated with corn. Scanning behavior was negatively correlated with rice and positively corelated with corn. Finally, sallying was negatively correlated with corn while dabbling was positively related with rice area. Birds that typically nest on the ground were positively associated with soybean area but negatively correlated with corn (Table 38). Finally, the migration statuses of bird communities were significantly correlated with crop area (Table 38). Corn was negatively correlated with both summer migrants and those that pass through the regions during their migration. Soybean was negatively related to summer migrants and positively correlated with migration route and resident species. Rice area negatively correlated with resident species and positively correlated to summer migrants. The relative relationships between the CWM for habitat, diet, foraging behavior, and migration and the different crop areas at 1000m can be found in (Figure 36-Figure 38).

The edge metrics, total edge and edge density were also significantly related to many CWM traits. The majority of the relationships were positive with a few negative relationships (Table 35-Table 38). Aggregation also had several significant relationships with a number of functional traits, with most of them being negative. Mean patch size and natural landcover area had relatively fewer significant correlations with CWM values, with mostly negative relationships for mean patch size (9 out of 10) and mostly positive for natural area (15 out of 16) (Table 35-Table 38).

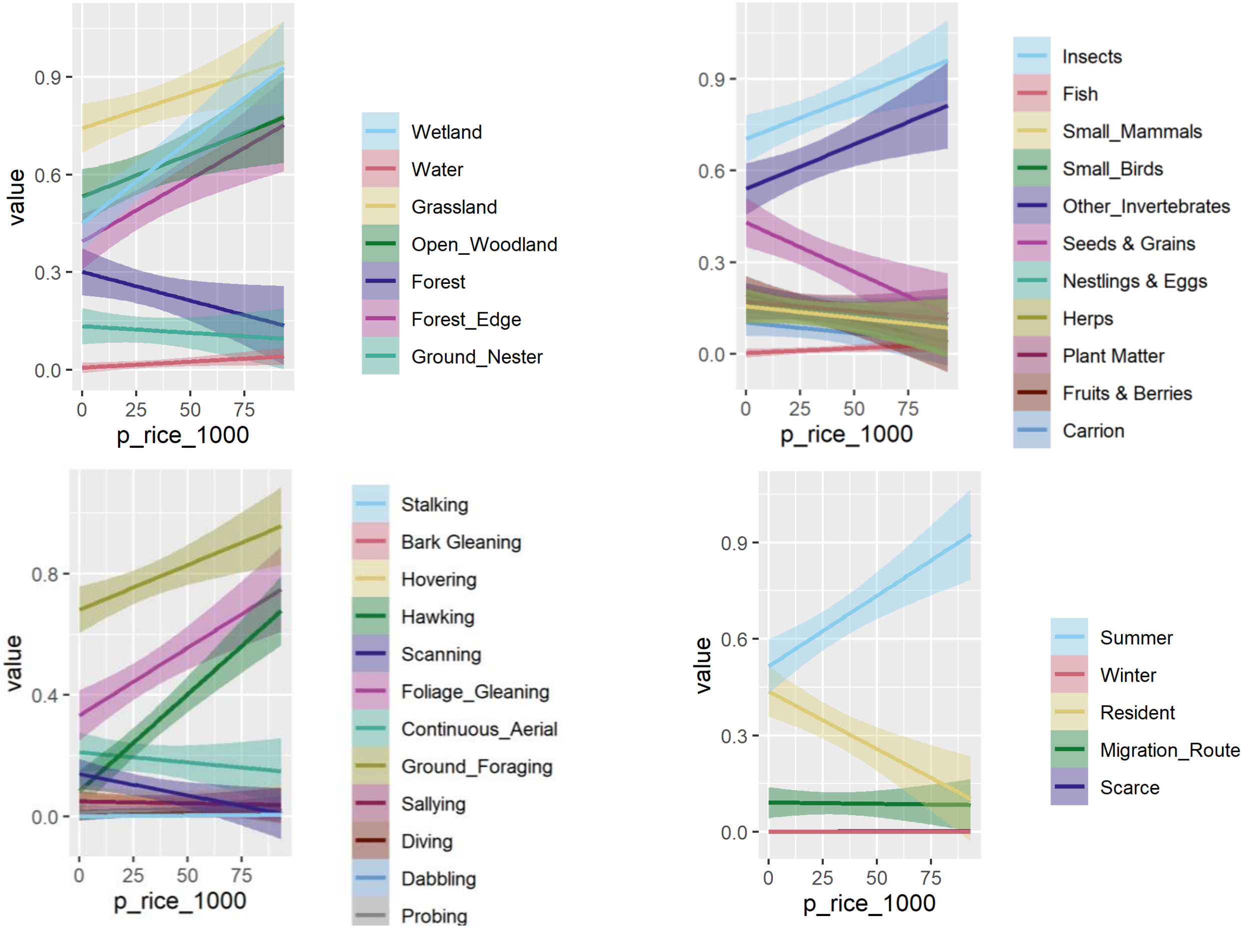


Figure 36: Linear relationships of rice paddy percentage at the 1000m extent and the habitat, diet, foraging behavior, and migration community weighted means.

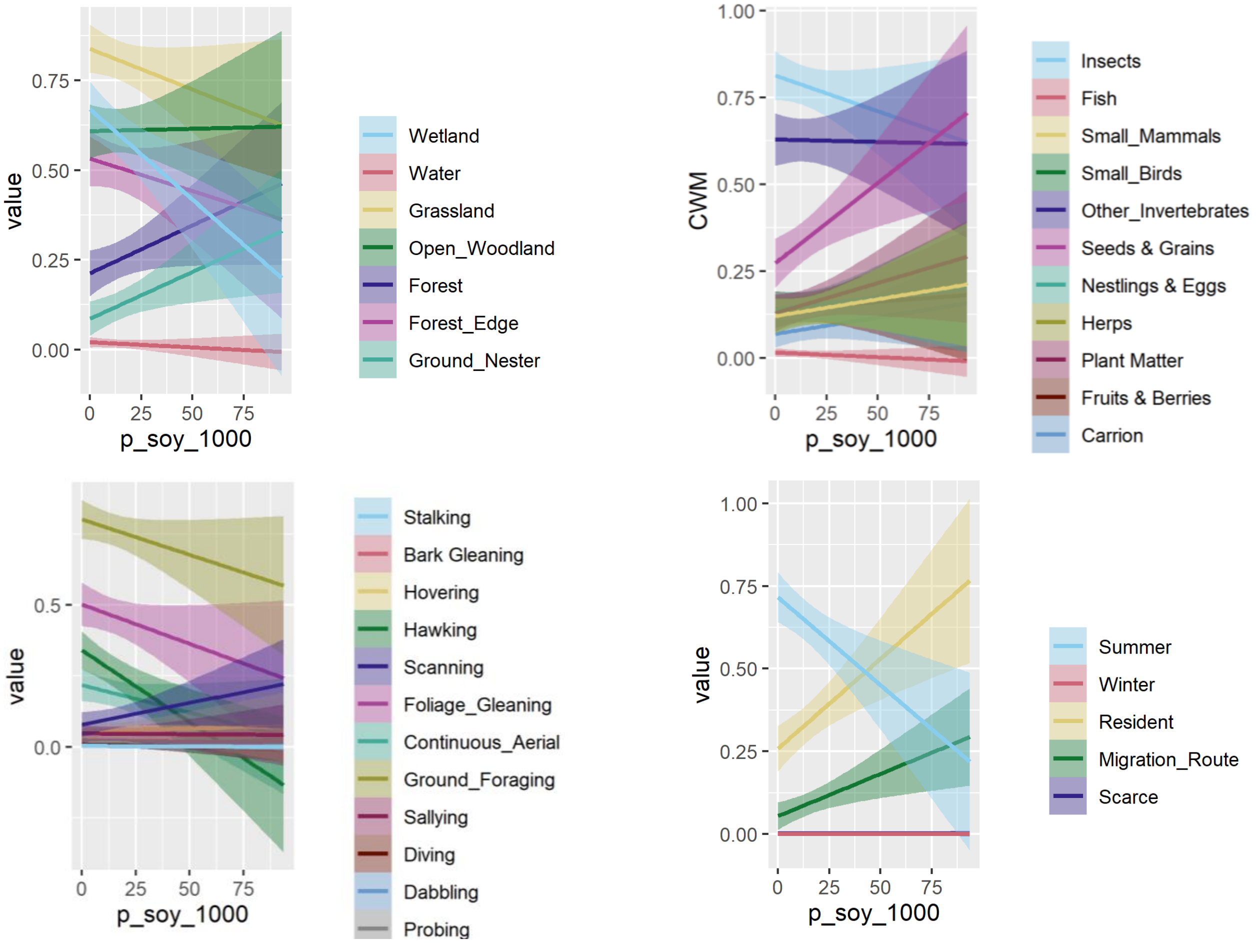


Figure 37: Linear relationships of soybean percentage at the 1000m extent and the habitat, diet, foraging behavior, and migration community weighted means.

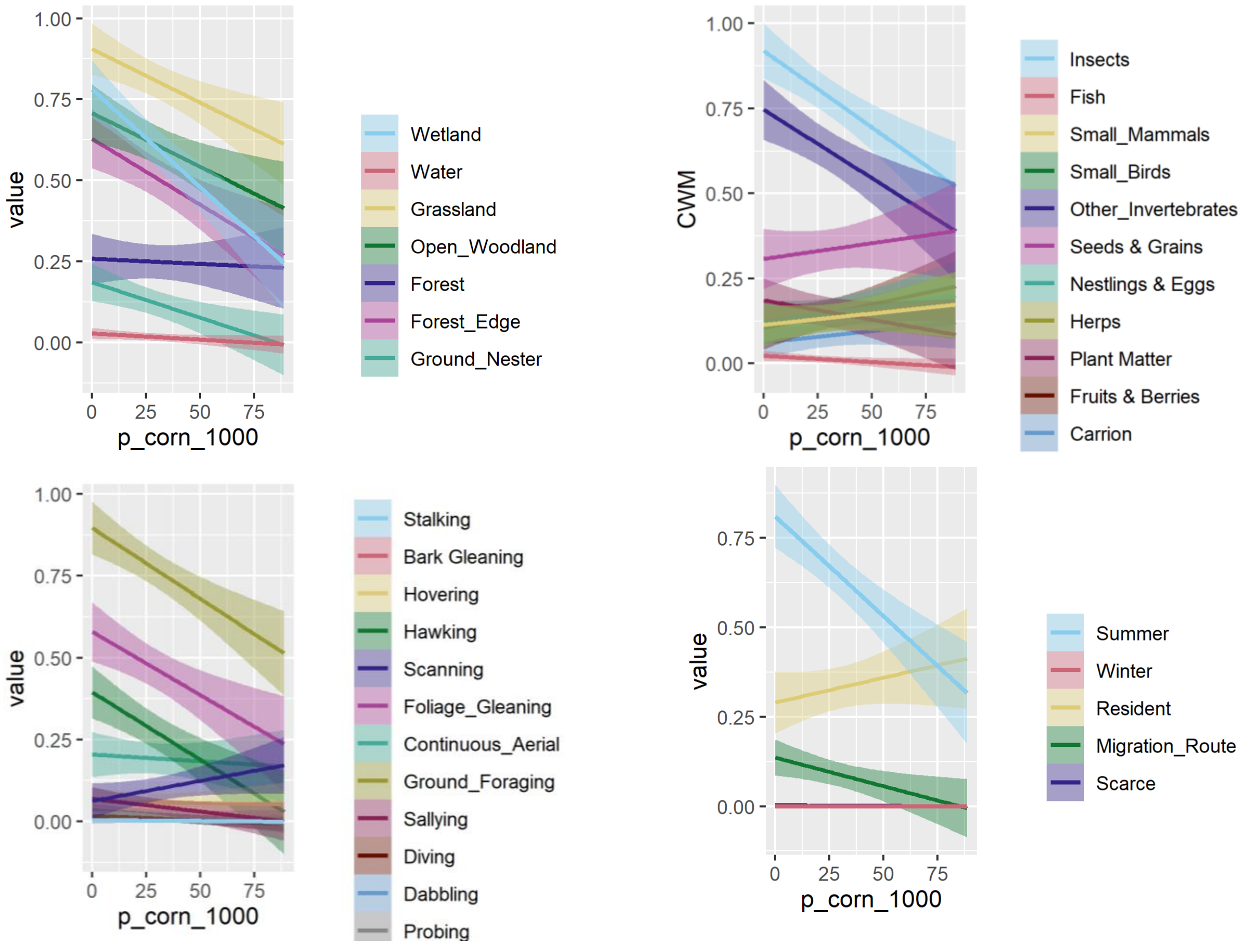


Figure 38: Linear relationships of corn percentage at the 1000m extent and the habitat, diet, foraging behavior, and migration community weighted means.

4.4 Discussion

This chapter examined the relationship between landscape structure (compositional and configurational) and bird diversity using both taxonomic and functional measures of biodiversity across multiple scales. For percent crop area, both soybean and corn had significant negative correlations with taxonomic and functional diversity while paddy rice had no significant relationships. This implies that landscapes with more rain-fed crop area (i.e., fields that are not flooded like with paddy rice) support fewer bird species/functional groups. This is further supported by studies reporting high levels of species diversity associated with paddy rice farming practices (Amira et al., 2018) and highlights the importance of considering crops separately as the resources they provide can differ by species/taxa (Gil-Tena et al., 2015).

Soybean area positively correlated with some functional traits of birds. Soybean area was significantly positively correlated with ground nesting, while corn was negatively correlated (rice was not significant). Of the 30 families observed in our study, 40% have the ground nesting trait meaning soybean cultivation may be conducive to the breeding ecology for many species in this agroecosystem. Furthermore, there may be population-level consequences for these species if soybean area loss limits the amount of nesting habitat past a certain point. Additionally, both migratory (i.e., species that pass through during migration) and non-migratory traits positively correlated with soybean area, while summer migrants were positively correlated with rice area. In the context of these two important life history strategies, both soybean and rice area positively impact different bird groups, while corn decreases the frequency of these traits in the bird community.

We also found that crop diversity and natural landcover were positively correlated with bird biodiversity. The fact that natural area has a positive relationship with biodiversity is expected, however the significant correlation of crop diversity with both taxonomic and functional biodiversity is notable, as not all studies agree with this finding (Martin et al., 2020; Redlich et al., 2018). However there are a number of studies that produced similar results (M. B. Lee & Goodale, 2018; D. Li et al., 2020; Lindsay et al., 2013). A possible explanation for this discrepancy is the presence of paddy rice in our study region as it is able to support species that fields of rain-fed crops cannot (e.g., herons, ducks).

Crop diversity also had several positive correlations with various functional traits which could have implications for various ecosystem services (Figure 35, Table 35-Table 38). For example, CWM for small mammal diet preference increased with crop diversity, which could help control local rodent populations (Fischer et al., 2018; Pejchar et al., 2018; O. M. Smith et al., 2021). Furthermore, five of the six significant traits were those associated with a carnivorous diet (e.g., small birds, carrion). Similar to soybean percentage, crop diversity was also significantly correlated with the ground nesting, migratory-route, and resident functional traits.

Higher values of edge metrics (total edge and edge density) were correlated with biodiversity (both taxonomic and functional) while higher levels of aggregation were associated with lower biodiversity. This indicates that landscapes dominated by a small number of landcover classes do not support high levels of bird diversity, similar to our finding on crop diversity. It is interesting that both edge metrics were found to be important for biodiversity but not mean patch size despite the two being closely related (i.e., smaller patch size increases edge metrics) as well as other studies finding field size significantly related to species richness (Martin et al., 2020). However, the study by Martin et al. (2020) did not include natural landcover in their analysis. The semi-natural strips that occur in field margins are known to be beneficial to both bird and general biodiversity in a landscape (Blaix & Moonen, 2020; Kujawa et al., 2020; Meichtry-Stier et al., 2018). This disagreement may be evidence that semi-natural field edges could mediate the effect of patch size on farmland biodiversity. However, it should be noted that we limited the potential effect of patch size by using a maximum extent of 1000m.

In order to understand the impacts of global trade on Heilongjiang's agroecosystem, this chapter links landcover change (i.e., soybean area loss) to landscape structure and bird biodiversity. From 2000-2018, cheap soybean imports drove many Chinese soybean farmers to switch to more profitable crops in our study region (Gale et al., 2019; X. Li et al., 2021; J. Sun et al., 2018). Using soybean area decrease as a proxy for global trade impact, we compared landscape and biodiversity metrics in two regions of Heilongjiang that experienced a decline in soybean area, with one exhibiting a greater degree of loss than the other.

The samples in the more impacted region (Jiamusi) had significantly lower levels of crop diversity (i.e., number of crops and evenness of crop area). Additionally, the Jiamusi samples had less natural landcover percentage and higher rice percentage. However, the two regions had the same levels of both functional and taxonomic biodiversity.

While the difference in crop diversity can be linked to the differing amounts of soybean area loss, the relationship between the amount of natural landcover and global trade is not as clear. From 2000-2018, cropland in Heilongjiang expanded substantially with most of the land being converted from wetland, grassland, and forests. However, the intensity of the expansion was not the same between our two case study prefectures. The more highly impacted region in our study, Jiamusi, is located in the Sanjiang plain, which experienced higher rates of cropland expansion (increase of 6.8%). In the Songnen plain where Qiqihar (the less impacted area) is located, cropland increased by 3.56% (Chen et al., 2022). The factors driving this expansion are linked to a number of factors including food security, economic pursuit, and national policies (Chen et al., 2022). The degree to which global soybean imports effects these factors is not yet clear. For example, the demand for the high-quality rice grown in Heilongjiang has recently boomed within China while the profitability of soybeans has decreased due to global trade, pushing farmers towards rice cultivation rather than soybean. However, uncovering the causal link between these socioeconomic factors and landcover change is challenging and warrants further research.

In the context of global trade, we observed that highly impacted regions (i.e., more soybean loss) had lower levels of crop diversity as well as lower levels of natural landcover. While we cannot say whether the difference of natural landcover amount is related to global trade, we would expect a region with less natural landcover and lower levels of crop diversity to have lower biodiversity based on the relationships we found. However, we did not find a significant difference for either taxonomic or functional biodiversity between the degrees of global trade impact. Therefore, it is possible that the higher amount of rice in the highly impacted region mitigated the expected decline in biodiversity due to global trade. In the typical heterogeneous landscape of Heilongjiang farmland, the conversion of soybean fields to another crop due to low prices, decreased the crop diversity of the landscape (i.e., reduced crop richness and/or evenness). However, if they were converted to rice instead of corn, the impact to bird communities was less detrimental.

In general, we saw little to no discernable differences in the significance, direction, or strength of the relationships when using taxonomic versus functional indicators (e.g., species richness versus functional group richness). This finding does not agree with similar studies that do report differing relationships of taxonomic/functional diversity and landscape structure (Birkhofer et al., 2018; Flynn et al., 2009; M.-B. Lee & Martin, 2017; Morelli et al., 2018). This disparity could be related to the relatively small functional space due to environmental filtering inherent in our study region (Barragán et al., 2011; Duflot et al., 2014). Extending the amount of time spent sampling (particularly for the abundance-weighted indices) may help reduce this issue.

A quick note on the impact of scale. We found that some relationships became significant at different scales in some cases. However, we also had many instances where scale did not matter (i.e., all scales were either significant or insignificant). Therefore, if researchers wish to use landscape metrics to model biodiversity, we suggest exploring a number of extents to select the appropriate extent to use (while also accounting for collinearity among landscape variables).

There were some additional limitations to this study. First, there is a need for data from across the seasons. For example, this region serves as an important migratory route for many species, including some cranes (Austin et al., 2018). Exploring these landscape-biodiversity relationships during the harvest/fall season may uncover important temporal dynamics associated this agroecosystem (M.-B. Lee & Martin, 2017; Vasseur et al., 2013). Additionally, collecting more data across a wider range of landscape metric values (e.g., natural landcover) may help to confirm these relationships as well as performing additional analyses that include multiple variables and account for imperfect species detections.

4.5 Conclusions

This chapter helps contribute to our current understanding of how landscape structure mediates farmland biodiversity, which is necessary to promote the multi-functionality of agricultural systems. We found that many aspects of landscape structure can influence both taxonomic and functional biodiversity. Additionally, the fact that our findings are not in complete agreement with some existing studies suggest that these relationships are dependent on the characteristics of a given agroecosystem, and that broad generalizations are not possible using these methods alone. Finally, we show that global trade impacted regions growing soybeans by decreasing crop diversity. This could translate to negative consequences for biodiversity but may be mitigated by rice cultivation.

APPENDIX

Table 33: Table of foraging behavior definitions (M.-B. Lee & Martin, 2017; Remsen & Robinson, 1990; Ruxton & Hansell, 2011)

Behavior	**Definition**
stalking	walking slowly or standing, waiting for prey/food to be within reach
bark gleaning	plucking or picking food from bark surface and underneath
hovering	aerial maneuver where bird maintains location while searching for prey, dives onto prey from aerial position
hawking	catching and feeding on prey in the air
scanning	watching an area before attacking prey
foliage gleaning	plucking or picking food from surface of leaves and other foliage
continuous aerial feeding	similar to hawking, but flies for much longer periods of time
ground foraging	plucking or picking food from the ground surface
sallying	catching prey in the air, then returning to perch to feed
diving	specific to aquatic locations, bird dives below surface for food (may dive from water surface or from the air)
dabbling	specific to aquatic locations, bird submerges head/neck below the surface to feed
probing	inserting bill into soft substrate to capture food underneath

Table 34: Trait matrix for families observed in study area (n=30).

	Mass			**Habitat Preference**						**Diet**											**Forage Behavior**												**Nesting & Migration**						
	Mass Low (g)	Mass High (g)	Avg. Mass (g)	Wetland	Water	Grass	Open Woodland	Forest	Forest Edge	Insects	Fish	Small mammals	Small birds	Other invertebrates	Grain & seeds	Nestlings & eggs	Small herps	Plant matter	Fruits and berries	Carrion	Stalking	Bark gleaning	Hovering	Hawking	Scanning	Foliage Gleaning	Continuous Aerial	Ground	Sallying	Diving	Dabbling	Probing	Ground Nester	Summer	Winter	Resident	Migration route	Scarce	Migratory
Acrocephalidae	18.25	29.5	23.88	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0	0	1	0	0	0	0	1
Alcedinidae	19	40	29.5	1	1	0	0	0	0	1	1	0	0	1	0	0	0	1	1	0	0	0	1	0	1	0	0	0	1	1	0	0	1	1	0	1	0	0	1
Anatidae	750	1500	1125	1	1	0	0	0	0	1	1	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	1
Ardeidae	649.4	1421.6	1035.5	1	1	0	0	0	0	1	1	1	1	1	0	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1
Campephagidae	20	28	24	0	0	0	1	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	0	1	0	1
Charadriidae	80.5	665	372.75	1	1	1	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	1	0	0	1	0	1
Columbidae	144.75	267	205.88	0	0	1	1	1	1	0	0	0	0	1	1	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	1	0	0	1
Corvidae	245.33	354	299.67	0	0	1	1	1	1	1	0	1	1	1	1	1	1	0	1	1	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	1	0	0	0
Cuculidae	106	133	119.5	1	0	1	1	1	1	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	1
Emberizidae	14	25.4	19.7	1	0	1	1	1	1	1	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	1	1	0	1	1	0	1
Falconidae	118.75	263.25	191	1	0	1	1	0	1	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	1	0	1	0	0	1
Hirundinidae	17	27.33	22.167	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0	0	1
Laniidae	44.67	79	61.833	1	0	1	1	1	1	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	0	0	0	1	1	0	0	0	0	1	0	0	0	0	1
Laridae	69.5	112.5	91	1	1	0	0	0	0	1	1	0	0	1	0	0	1	0	0	0	0	0	1	1	0	0	1	0	0	1	0	0	1	1	0	0	1	0	1
Motacillidae	17.2	27.13	22.167	1	0	1	1	0	1	1	0	0	0	1	1	0	0	0	1	0	0	0	1	0	0	0	0	1	1	0	0	1	1	1	0	0	0	0	1
Muscicapidae	13	17	15	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0	1
Oriolidae	65	100	82.5	0	0	0	1	1	1	1	0	0	0	1	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	1
Panuridae	12	18	15	1	0	0	0	0	0	1	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	1	0	0	0	0	1
Paridae	2	15	8.5	0	0	0	1	1	0	1	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	1	0	0	0
Passeridae	17	30	23.5	0	0	1	1	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
Phalacrocoracidae	1810	2810	2310	1	1	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1
Phasianidae	545	1990	1267.5	1	0	1	1	0	1	1	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	1	0	0	0
Picidae	17	69	43	1	0	0	1	1	1	1	0	0	0	1	1	1	0	1	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0
Podicipedidae	130	236	183	1	1	0	0	0	0	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1
Rallidae	273	516	394.5	1	1	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	0	1	0	1	1	1	1	1	0	0	0	0	1
Remizidae	7.5	12	9.75	1	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	1
Sturnidae	55	100	77.5	0	0	1	1	0	0	1	0	0	0	1	1	0	1	1	1	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0
Troglodytidae	6	12	9	0	0	0	1	1	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	1	0	0	0
Turdidae	60	72	66	0	0	0	0	1	1	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0	0	1
Upupidae	46	89	67.5	0	0	1	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0	1

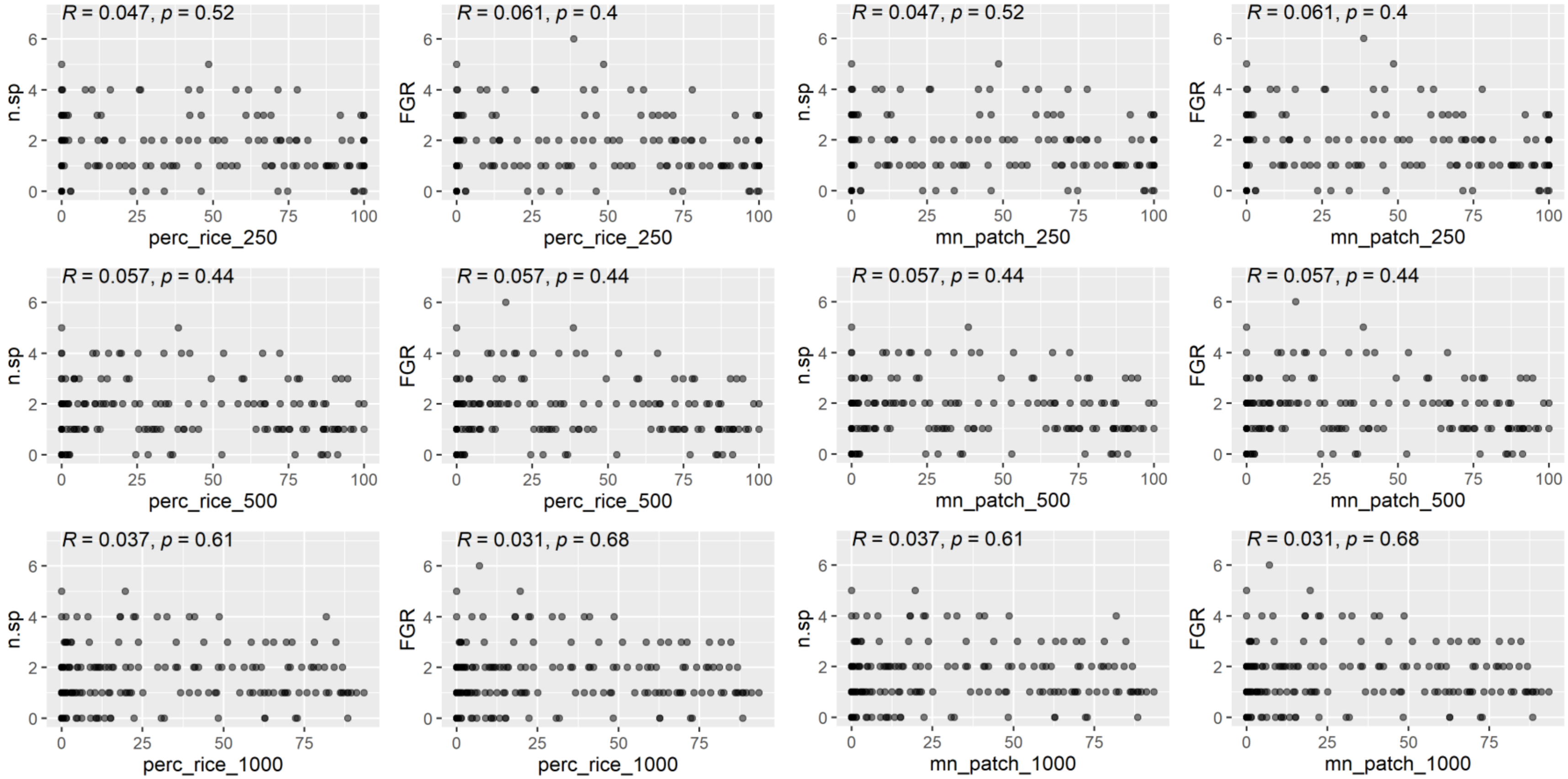


Figure 39: Taxonomic richness (n.sp, red) and functional group richness (FGR, blue) relationships with mean patch size (left) and percent rice (right). Pearson's correlation (R) and p-value (p) for each relationship is also included in the top left corner of each plot.

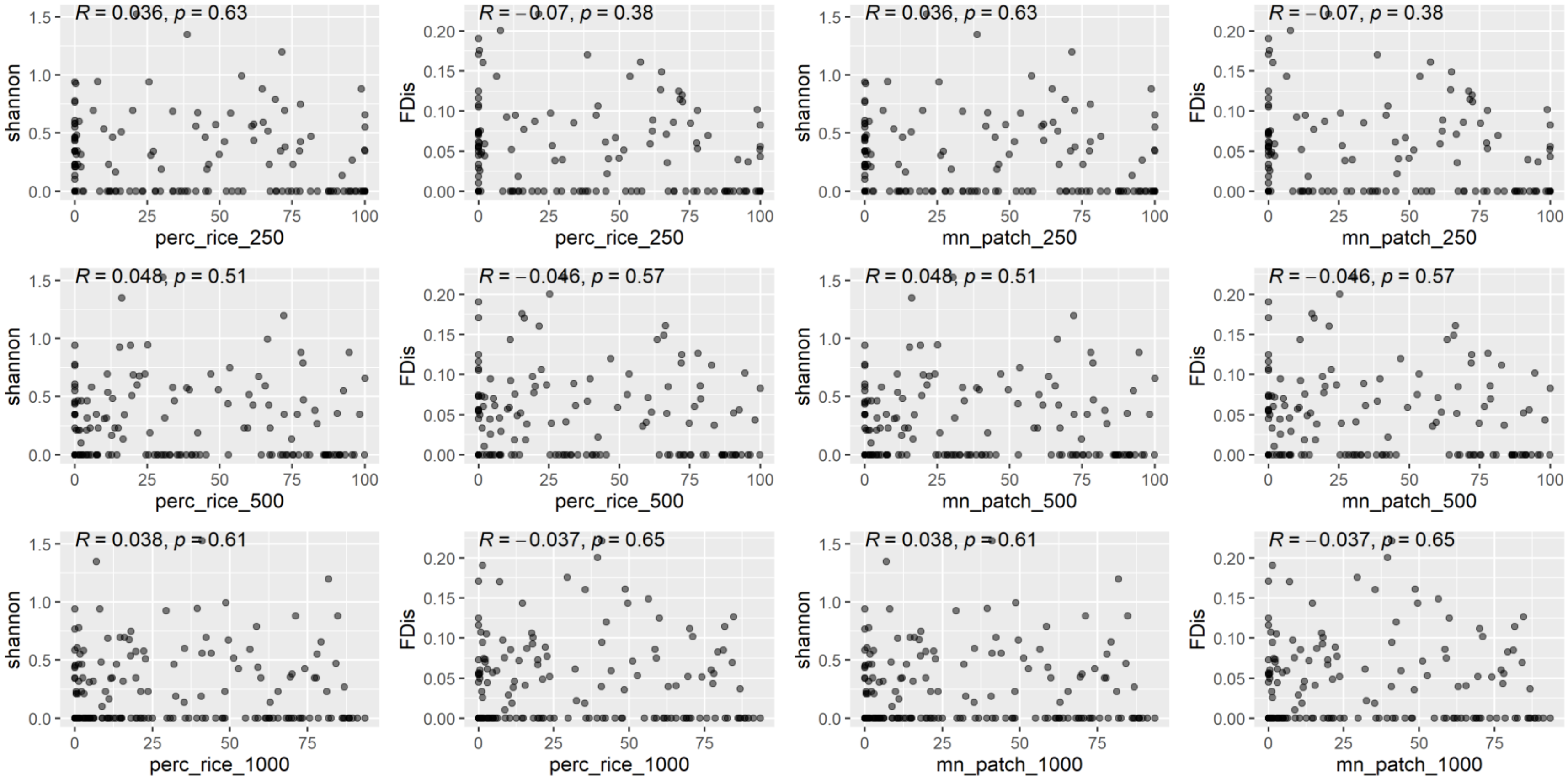


Figure 40: Shannon-Weiner (shannon, red) and functional dispersal (FDis, blue) relationships with mean patch size (left) and percent rice (right). Pearson's correlation (R) and p-value (p) for each relationship is also included in the top left corner of each plot.

Table 35: Pearson’s correlation values between CWM for mass and habitat preference and landscape structure metrics. Positive and negative correlation values >|0.1| are highlighted in green and red, respectively. P-values ⩽0.1 are highlighted in blue.

	R.AvgMassGrams	p.AvgMassGrams	R.Wetland	p.Wetland	R.Water	p.Water	R.Grassland	p.Grassland	R.Open_Woodland	p.Open_Woodland	R.Forest	p.Forest	R.Forest_Edge	p.Forest_Edge
msidi_crop_250m	0.21	0.01	-0.08	0.29	0.11	0.15	-0.01	0.95	0.01	0.86	0.14	0.05	0.05	0.49
msidi_crop_500m	0.15	0.06	-0.07	0.36	0.07	0.33	-0.02	0.82	0.04	0.58	0.15	0.03	0.06	0.45
msidi_crop_1000m	0.10	0.20	-0.05	0.51	-0.01	0.90	-0.04	0.57	0.01	0.88	0.13	0.07	0.02	0.74
mn_patch_250m	-0.08	0.30	0.04	0.58	-0.11	0.13	0.04	0.61	0.05	0.48	-0.01	0.87	0.05	0.50
mn_patch_500m	-0.08	0.32	0.05	0.51	-0.08	0.25	0.03	0.70	0.00	0.98	0.00	0.95	0.04	0.58
mn_patch_1000m	-0.04	0.65	0.05	0.54	0.00	0.97	-0.01	0.88	0.05	0.50	-0.05	0.52	0.06	0.41
ai_250m	-0.14	0.09	0.07	0.35	-0.10	0.17	-0.01	0.88	-0.03	0.63	-0.01	0.91	0.00	0.99
ai_500m	-0.17	0.04	0.11	0.14	-0.12	0.09	0.01	0.91	-0.04	0.63	0.01	0.87	0.02	0.75
ai_1000m	-0.12	0.13	0.05	0.48	-0.01	0.88	-0.02	0.73	0.00	0.95	0.02	0.81	0.03	0.71
te_250m	0.16	0.05	-0.05	0.46	0.13	0.07	0.02	0.83	0.04	0.55	0.03	0.65	0.02	0.81
te_500m	0.17	0.03	-0.10	0.18	0.15	0.04	0.00	0.99	0.04	0.57	0.01	0.91	-0.02	0.80
te_1000m	0.14	0.09	-0.05	0.48	0.02	0.75	0.03	0.72	0.00	0.97	0.00	0.98	-0.03	0.72
ed_250m	0.16	0.05	-0.05	0.46	0.13	0.08	0.01	0.85	0.04	0.55	0.04	0.63	0.02	0.80
ed_500m	0.17	0.03	-0.10	0.19	0.15	0.05	0.00	0.99	0.04	0.60	0.01	0.91	-0.02	0.79
ed_1000m	0.13	0.10	-0.05	0.48	0.02	0.76	0.02	0.74	0.00	0.95	0.00	0.98	-0.03	0.71
p_nat_250m	0.05	0.55	0.07	0.37	0.03	0.70	0.06	0.39	0.05	0.53	0.19	0.01	0.08	0.28
p_nat_500m	0.02	0.79	0.05	0.49	0.02	0.79	0.02	0.74	0.00	0.99	0.17	0.02	0.03	0.65
p_nat_1000m	-0.07	0.39	0.09	0.20	-0.03	0.70	0.05	0.53	-0.05	0.45	0.14	0.06	-0.02	0.83
p_soy_250m	-0.03	0.67	-0.11	0.14	-0.05	0.51	-0.04	0.63	0.02	0.83	0.19	0.01	-0.04	0.57
p_soy_500m	0.00	0.98	-0.16	0.03	-0.05	0.52	-0.07	0.34	0.01	0.93	0.14	0.06	-0.07	0.34
p_soy_1000m	0.04	0.65	-0.21	0.00	-0.07	0.36	-0.11	0.12	0.01	0.93	0.14	0.06	-0.08	0.29
p_corn_250m	0.22	0.01	-0.35	0.00	-0.16	0.03	-0.25	0.00	-0.25	0.00	-0.09	0.20	-0.29	0.00
p_corn_500m	0.24	0.00	-0.35	0.00	-0.13	0.07	-0.23	0.00	-0.23	0.00	-0.02	0.82	-0.25	0.00
p_corn_1000m	0.21	0.01	-0.37	0.00	-0.13	0.08	-0.24	0.00	-0.21	0.00	-0.02	0.75	-0.25	0.00
p_rice_250m	-0.20	0.01	0.32	0.00	0.11	0.13	0.17	0.02	0.16	0.03	-0.18	0.02	0.23	0.00
p_rice_500m	-0.19	0.02	0.34	0.00	0.10	0.18	0.18	0.01	0.19	0.01	-0.16	0.03	0.26	0.00
p_rice_1000m	-0.16	0.05	0.35	0.00	0.14	0.06	0.17	0.02	0.19	0.01	-0.15	0.04	0.26	0.00

Table 36: Pearson's correlation values between CWM for diet preference and landscape structure metrics. Positive and negative correlation values >|0.1| are highlighted in green and red, respectively. P-values ≤0.1 are highlighted in blue.

	R.Insects	p.Insects	R.Fish	p.Fish	R.Small_Mammals	p.Small_Mammals	R.Small_Birds	p.Small_Birds	R.Invertebrates	p.Invertebrates	R.Seeds & Grains	p.Seeds & Grains	R.Nestlings/Eggs	p.Nestlings/Eggs	R.Herps	p.Herps	R.Plant Matter	p.Plant Matter	R.Fruits & Berries	p.Fruits & Berries	R.Carrion	p.Carrion
msidi_crop_250m	-0.03	0.73	0.04	0.57	0.20	0.01	0.20	0.01	0.03	0.67	0.07	0.37	0.22	0.00	0.21	0.00	0.05	0.46	0.19	0.01	0.20	0.01
msidi_crop_500m	-0.01	0.86	0.02	0.79	0.18	0.02	0.18	0.02	0.05	0.48	0.11	0.12	0.19	0.01	0.18	0.01	0.10	0.15	0.13	0.09	0.15	0.03
msidi_crop_1000m	-0.01	0.91	-0.04	0.55	0.12	0.11	0.12	0.11	0.00	0.96	0.10	0.16	0.12	0.10	0.12	0.09	0.10	0.16	0.06	0.41	0.09	0.20
mn_patch_250m	-0.02	0.80	-0.10	0.19	-0.19	0.01	-0.19	0.01	0.02	0.80	0.03	0.67	-0.21	0.00	-0.20	0.01	0.11	0.15	-0.06	0.42	-0.13	0.07
mn_patch_500m	0.01	0.94	-0.07	0.36	-0.09	0.21	-0.09	0.21	-0.02	0.83	-0.02	0.75	-0.10	0.18	-0.10	0.16	0.02	0.84	-0.03	0.71	-0.02	0.84
mn_patch_1000m	0.03	0.72	0.04	0.59	-0.09	0.20	-0.09	0.20	0.04	0.56	0.00	0.99	-0.08	0.27	-0.10	0.16	0.01	0.93	-0.04	0.61	-0.01	0.92
ai_250m	-0.04	0.55	-0.08	0.26	-0.19	0.01	-0.19	0.01	-0.07	0.37	0.00	0.98	-0.23	0.00	-0.20	0.00	0.12	0.09	-0.12	0.09	-0.14	0.05
ai_500m	-0.02	0.78	-0.09	0.24	-0.23	0.00	-0.23	0.00	-0.07	0.36	-0.01	0.87	-0.23	0.00	-0.24	0.00	0.12	0.09	-0.10	0.19	-0.13	0.07
ai_1000m	-0.03	0.70	0.02	0.80	-0.19	0.01	-0.19	0.01	0.00	0.99	0.03	0.67	-0.18	0.02	-0.20	0.01	0.13	0.07	-0.07	0.37	-0.10	0.18
te_250m	0.05	0.46	0.10	0.16	0.21	0.00	0.21	0.00	0.08	0.26	0.01	0.86	0.25	0.00	0.22	0.00	-0.09	0.20	0.13	0.07	0.15	0.04
te_500m	0.04	0.63	0.11	0.15	0.23	0.00	0.23	0.00	0.08	0.28	0.03	0.67	0.24	0.00	0.25	0.00	-0.10	0.18	0.10	0.16	0.14	0.05
te_1000m	0.03	0.65	-0.01	0.92	0.20	0.01	0.20	0.01	0.00	0.97	-0.01	0.87	0.18	0.01	0.21	0.00	-0.11	0.13	0.08	0.30	0.11	0.14
ed_250m	0.05	0.47	0.10	0.16	0.21	0.00	0.21	0.00	0.08	0.26	0.01	0.86	0.25	0.00	0.23	0.00	-0.09	0.21	0.13	0.07	0.15	0.04
ed_500m	0.03	0.64	0.10	0.15	0.23	0.00	0.23	0.00	0.08	0.30	0.03	0.70	0.24	0.00	0.25	0.00	-0.10	0.18	0.10	0.17	0.14	0.06
ed_1000m	0.03	0.67	-0.01	0.91	0.20	0.01	0.20	0.01	0.00	0.99	-0.01	0.85	0.18	0.01	0.21	0.00	-0.11	0.13	0.07	0.31	0.10	0.15
p_nat_250m	0.08	0.25	0.04	0.55	0.10	0.18	0.10	0.18	0.08	0.27	0.03	0.67	0.11	0.12	0.11	0.12	0.12	0.11	0.10	0.16	0.00	0.95
p_nat_500m	0.04	0.55	0.03	0.69	0.03	0.65	0.03	0.65	0.03	0.65	0.03	0.69	0.04	0.55	0.05	0.53	0.14	0.05	0.09	0.22	-0.05	0.50
p_nat_1000m	0.06	0.40	-0.01	0.93	-0.03	0.65	-0.03	0.65	-0.03	0.66	0.03	0.68	-0.02	0.82	-0.03	0.71	0.15	0.04	0.03	0.64	-0.09	0.21
p_soy_250m	-0.02	0.77	-0.06	0.42	-0.01	0.88	-0.01	0.88	0.01	0.93	0.25	0.00	-0.02	0.77	-0.02	0.84	0.20	0.01	0.01	0.89	0.06	0.39
p_soy_500m	-0.05	0.50	-0.06	0.43	0.02	0.78	0.02	0.78	0.00	0.97	0.23	0.00	0.01	0.93	0.02	0.81	0.14	0.06	0.00	0.97	0.07	0.31
p_soy_1000m	-0.10	0.18	-0.07	0.34	0.06	0.38	0.06	0.38	-0.01	0.93	0.21	0.00	0.04	0.56	0.06	0.39	0.11	0.14	0.03	0.71	0.08	0.27
p_corn_250m	-0.27	0.00	-0.13	0.08	0.06	0.38	0.06	0.38	-0.30	0.00	0.04	0.58	0.08	0.26	0.05	0.47	-0.18	0.01	0.12	0.11	0.11	0.15
p_corn_500m	-0.28	0.00	-0.12	0.09	0.10	0.17	0.10	0.17	-0.28	0.00	0.06	0.40	0.12	0.10	0.09	0.22	-0.12	0.09	0.15	0.04	0.12	0.09
p_corn_1000m	-0.31	0.00	-0.14	0.06	0.06	0.38	0.06	0.38	-0.25	0.00	0.06	0.41	0.08	0.29	0.05	0.48	-0.10	0.16	0.13	0.09	0.08	0.27
p_rice_250m	0.17	0.02	0.10	0.18	-0.10	0.18	-0.10	0.18	0.19	0.01	-0.26	0.00	-0.12	0.10	-0.10	0.17	-0.08	0.27	-0.19	0.01	-0.14	0.06
p_rice_500m	0.19	0.01	0.09	0.21	-0.11	0.15	-0.11	0.15	0.21	0.00	-0.24	0.00	-0.12	0.10	-0.11	0.14	-0.07	0.37	-0.18	0.01	-0.13	0.08
p_rice_1000m	0.21	0.00	0.13	0.08	-0.08	0.28	-0.08	0.28	0.21	0.00	-0.24	0.00	-0.09	0.22	-0.08	0.27	-0.06	0.40	-0.17	0.02	-0.10	0.19

Table 37: Pearson's correlation values between CWM for foraging behavior and landscape structure metrics. Positive and negative correlation values >|0.1| are highlighted in green and red, respectively. P-values ≤0.1 are highlighted in blue.

	R.Stalking	p.Stalking	R.Bark Gleaning	p.Bark Gleaning	R.Hovering	p.Hovering	R.Hawking	p.Hawking	R.Scanning	p.Scanning	R.Foliage_Gleaning	p.Foliage_Gleaning	R.Continuous_Aerial	p.Continuous_Aerial	R.Ground_Foraging	p.Ground_Foraging	R.Sallying	p.Sallying	R.Diving	p.Diving	R.Dabbling	p.Dabbling	R.Probing	p.Probing
msidi_crop_250m	-0.02	0.76	0.09	0.20	0.04	0.58	-0.09	0.24	0.24	0.00	0.01	0.95	-0.02	0.79	-0.07	0.35	-0.04	0.57	0.04	0.61	0.05	0.50	0.04	0.56
msidi_crop_500m	-0.02	0.81	0.14	0.06	0.06	0.39	-0.10	0.18	0.21	0.00	0.00	0.95	-0.06	0.40	-0.07	0.33	-0.04	0.60	0.01	0.86	0.03	0.70	0.05	0.52
msidi_crop_1000m	0.02	0.78	0.11	0.14	0.05	0.49	-0.12	0.09	0.16	0.03	-0.04	0.63	-0.03	0.69	-0.08	0.26	-0.02	0.76	-0.06	0.40	-0.05	0.51	-0.01	0.93
mn_patch_250m	-0.04	0.59	-0.03	0.73	-0.14	0.06	0.04	0.58	-0.16	0.03	0.11	0.14	-0.03	0.63	0.07	0.32	-0.10	0.18	-0.08	0.27	-0.07	0.34	-0.09	0.22
mn_patch_500m	-0.04	0.61	-0.02	0.79	-0.13	0.07	0.04	0.61	-0.05	0.46	0.10	0.16	0.02	0.77	0.05	0.47	-0.10	0.18	-0.05	0.48	-0.04	0.55	-0.08	0.27
mn_patch_1000m	0.05	0.51	0.09	0.20	-0.16	0.03	0.09	0.23	-0.09	0.23	0.16	0.03	-0.10	0.17	0.01	0.87	-0.07	0.35	0.04	0.59	0.04	0.56	-0.06	0.41
ai_250m	-0.11	0.15	-0.06	0.42	-0.11	0.14	-0.02	0.76	-0.17	0.02	0.04	0.57	0.01	0.87	0.03	0.67	-0.07	0.33	-0.04	0.57	-0.02	0.76	-0.02	0.74
ai_500m	-0.08	0.29	0.01	0.92	-0.17	0.02	-0.01	0.91	-0.20	0.01	0.12	0.10	0.05	0.53	0.05	0.46	-0.08	0.25	-0.05	0.52	-0.05	0.52	-0.07	0.35
ai_1000m	-0.01	0.88	0.04	0.63	-0.18	0.01	-0.01	0.92	-0.20	0.01	0.13	0.07	-0.06	0.41	0.01	0.84	-0.03	0.70	0.04	0.60	0.03	0.64	-0.04	0.61
te_250m	0.11	0.15	0.08	0.30	0.12	0.09	0.02	0.78	0.19	0.01	-0.03	0.68	-0.02	0.81	-0.03	0.65	0.07	0.31	0.06	0.41	0.04	0.60	0.04	0.60
te_500m	0.08	0.26	0.02	0.84	0.18	0.01	0.00	0.96	0.21	0.00	-0.11	0.12	-0.04	0.57	-0.05	0.52	0.09	0.23	0.07	0.37	0.06	0.40	0.09	0.24
te_1000m	0.02	0.81	-0.02	0.77	0.18	0.01	-0.01	0.91	0.21	0.00	-0.13	0.09	0.06	0.41	-0.01	0.86	0.02	0.77	-0.03	0.69	-0.03	0.71	0.04	0.54
ed_250m	0.11	0.14	0.08	0.29	0.13	0.08	0.02	0.79	0.19	0.01	-0.03	0.67	-0.02	0.79	-0.04	0.63	0.08	0.30	0.06	0.42	0.04	0.60	0.04	0.60
ed_500m	0.08	0.27	0.01	0.84	0.18	0.01	0.00	0.95	0.20	0.00	-0.12	0.12	-0.04	0.59	-0.05	0.51	0.09	0.23	0.06	0.38	0.06	0.41	0.08	0.25
ed_1000m	0.02	0.80	-0.02	0.78	0.18	0.01	-0.01	0.91	0.21	0.00	-0.13	0.08	0.06	0.41	-0.02	0.83	0.02	0.75	-0.03	0.68	-0.03	0.70	0.04	0.55
p_nat_250m	0.06	0.42	-0.01	0.93	0.15	0.05	0.00	0.98	0.04	0.63	0.04	0.59	0.08	0.28	0.09	0.23	0.16	0.03	0.01	0.87	-0.02	0.84	-0.04	0.60
p_nat_500m	0.02	0.74	-0.01	0.94	0.13	0.08	-0.07	0.34	-0.03	0.70	-0.02	0.80	0.10	0.16	0.06	0.41	0.23	0.00	0.01	0.91	-0.02	0.79	0.00	0.98
p_nat_1000m	-0.03	0.68	-0.01	0.86	0.09	0.20	-0.16	0.03	-0.06	0.43	-0.08	0.26	0.19	0.01	0.04	0.58	0.21	0.00	-0.01	0.92	-0.03	0.69	0.00	0.95
p_soy_250m	-0.05	0.50	0.00	0.99	-0.07	0.35	-0.29	0.00	0.04	0.56	-0.06	0.38	-0.05	0.47	-0.04	0.55	0.02	0.81	-0.05	0.51	-0.04	0.61	0.01	0.85
p_soy_500m	-0.05	0.53	0.00	0.97	-0.04	0.56	-0.27	0.00	0.09	0.24	-0.10	0.17	-0.08	0.26	-0.09	0.21	-0.02	0.83	-0.05	0.52	-0.04	0.56	0.00	0.98
p_soy_1000m	-0.03	0.63	-0.01	0.87	0.01	0.84	-0.25	0.00	0.12	0.12	-0.12	0.10	-0.11	0.12	-0.12	0.10	-0.01	0.94	-0.07	0.36	-0.06	0.43	-0.02	0.81
p_corn_250m	-0.10	0.16	0.06	0.40	-0.01	0.86	-0.31	0.00	0.16	0.03	-0.29	0.00	0.02	0.82	-0.32	0.00	-0.10	0.16	-0.10	0.16	-0.09	0.23	-0.07	0.34
p_corn_500m	-0.11	0.15	0.01	0.85	0.00	0.95	-0.31	0.00	0.17	0.02	-0.25	0.00	0.00	0.96	-0.30	0.00	-0.10	0.16	-0.10	0.19	-0.08	0.29	-0.08	0.29
p_corn_1000m	-0.09	0.23	0.01	0.90	-0.02	0.83	-0.29	0.00	0.13	0.07	-0.24	0.00	-0.03	0.64	-0.30	0.00	-0.12	0.09	-0.12	0.12	-0.10	0.19	-0.10	0.18
p_rice_250m	0.05	0.54	-0.04	0.60	-0.02	0.78	0.49	0.00	-0.18	0.01	0.26	0.00	-0.04	0.55	0.21	0.00	-0.02	0.83	0.10	0.18	0.10	0.19	0.01	0.84
p_rice_500m	0.08	0.30	0.00	0.98	-0.05	0.53	0.50	0.00	-0.18	0.02	0.30	0.00	-0.06	0.45	0.23	0.00	-0.04	0.63	0.08	0.25	0.09	0.22	0.02	0.83
p_rice_1000m	0.08	0.25	0.03	0.70	-0.05	0.53	0.50	0.00	-0.17	0.02	0.31	0.00	-0.06	0.39	0.23	0.00	-0.02	0.76	0.12	0.10	0.13	0.07	0.05	0.47

Table 38: Pearson's correlation values between CWM for the ground nesting trait/migration status and landscape structure metrics. Positive and negative correlation values >|0.1| are highlighted in green and red, respectively. P-values ≤0.1 are highlighted in blue.

	R.Ground_Nester	p.Ground_Nester	R.Summer	p.Summer	R.Winter	p.Winter	R.Resident	p.Resident	R.Migration_Route	p.Migration_Route	R.Scarce	p.Scarce
msidi_crop_250m	0.01	0.93	-0.05	0.50	NA	NA	0.13	0.09	0.03	0.70	0.06	0.41
msidi_crop_500m	0.09	0.20	-0.07	0.34	NA	NA	0.18	0.01	0.13	0.07	0.07	0.32
msidi_crop_1000m	0.14	0.05	-0.07	0.34	NA	NA	0.16	0.03	0.18	0.01	0.05	0.48
mn_patch_250m	0.06	0.44	0.06	0.41	NA	NA	0.01	0.88	0.09	0.22	-0.05	0.49
mn_patch_500m	0.00	0.96	0.05	0.48	NA	NA	-0.04	0.55	0.03	0.66	-0.05	0.53
mn_patch_1000m	0.02	0.82	0.00	0.96	NA	NA	-0.06	0.45	0.00	0.95	-0.07	0.31
ai_250m	0.16	0.03	0.06	0.44	NA	NA	-0.02	0.79	0.19	0.01	-0.09	0.20
ai_500m	0.12	0.10	0.11	0.15	NA	NA	-0.07	0.37	0.15	0.05	-0.14	0.05
ai_1000m	0.13	0.09	0.05	0.53	NA	NA	-0.05	0.53	0.11	0.12	-0.10	0.19
te_250m	-0.13	0.07	-0.04	0.57	NA	NA	0.04	0.62	-0.16	0.03	0.10	0.18
te_500m	-0.10	0.19	-0.10	0.19	NA	NA	0.08	0.26	-0.12	0.10	0.14	0.05
te_1000m	-0.11	0.13	-0.05	0.51	NA	NA	0.06	0.39	-0.10	0.18	0.10	0.17
ed_250m	-0.13	0.07	-0.04	0.57	NA	NA	0.04	0.61	-0.16	0.03	0.10	0.18
ed_500m	-0.10	0.19	-0.09	0.20	NA	NA	0.08	0.27	-0.12	0.11	0.14	0.05
ed_1000m	-0.11	0.14	-0.05	0.51	NA	NA	0.06	0.40	-0.10	0.19	0.10	0.17
p_nat_250m	0.05	0.50	0.15	0.04	NA	NA	0.05	0.51	-0.02	0.82	0.03	0.68
p_nat_500m	0.12	0.11	0.13	0.07	NA	NA	0.03	0.73	0.00	0.98	0.02	0.77
p_nat_1000m	0.19	0.01	0.16	0.03	NA	NA	0.03	0.67	0.07	0.31	-0.02	0.80
p_soy_250m	0.32	0.00	-0.13	0.07	NA	NA	0.25	0.00	0.33	0.00	-0.02	0.83
p_soy_500m	0.25	0.00	-0.19	0.01	NA	NA	0.25	0.00	0.27	0.00	-0.01	0.92
p_soy_1000m	0.18	0.01	-0.23	0.00	NA	NA	0.25	0.00	0.20	0.01	0.00	0.97
p_corn_250m	-0.21	0.00	-0.38	0.00	NA	NA	0.06	0.42	-0.23	0.00	-0.07	0.36
p_corn_500m	-0.20	0.01	-0.34	0.00	NA	NA	0.08	0.25	-0.19	0.01	-0.06	0.39
p_corn_1000m	-0.21	0.00	-0.34	0.00	NA	NA	0.09	0.21	-0.18	0.01	-0.07	0.37
p_rice_250m	-0.09	0.20	0.31	0.00	NA	NA	-0.27	0.00	-0.05	0.52	-0.02	0.74
p_rice_500m	-0.07	0.35	0.31	0.00	NA	NA	-0.26	0.00	-0.02	0.76	0.00	0.97
p_rice_1000m	-0.04	0.54	0.30	0.00	NA	NA	-0.27	0.00	-0.01	0.89	0.03	0.71

CHAPTER 5: MODELING BIRD OCCUPANCY IN A CHANGING AGROECOSYSTEM

Abstract

International food trade drives global land use change, with consequences for wildlife that utilize agroecosystems. Most studies on trade-driven land use change focus on conversion of natural habitats to cropland in countries that produce and export agricultural goods. Importing countries, however, undergo more indirect land use shifts. Imports have substantial effects on domestic crop prices, sometimes resulting in crop switching and abandonment by farmers in the importing country and altering the agricultural landscape. To explore these drivers shaping the landscape of agroecosystems, we analyzed relationships between bird species-level occupancy and agricultural landscape metrics in a region heavily impact by global trade. Our results indicated that increased crop diversity significantly increased occupancy of many birds at taxonomic and functional levels. Crop diversity was particularly important for less commonly surveyed functional groups. Percentage of natural landcover was not as important as expected, while metrics related to landscape configuration had few significant impacts on occupancy. Increases in rice area had fewer negative impacts to bird occupancy compared to increases in corn and soybean. Furthermore, we found more bird groups were negatively impacted by soybean area than corn, though this was more apparent at the taxonomic level. By combining remotely sensed landscape characteristics with bird diversity observations, this study provides a better understanding of how global trade and land use change may ultimately impact agroecosystems.

5.1 Introduction

5.1.1 Background

Environmental sustainability and food security are two of the greatest global challenges in modern times (Berry et al., 2014; Foley et al., 2005; Godfray & Garnett, 2014; Willett et al., 2019). Up until the mid-20th century, food demands were met by local producers but are now increasingly satisfied through international trade (Porkka et al., 2013; Sandström et al., 2014; V. H. Smith & Glauber, 2020; Tarrant, 1985). Recent research indicates cropland conversions are occurring in importing countries in response to international trade (J. Sun et al., 2015; van Vliet et al., 2015). Farmer land-use decision making is affected by multiple factors such as climate, resources, and crop prices, among others (Lutz, 1998; S. A. Wood et al., 2014). As global trade increases, farmers with smaller operations struggle to compete when markets are flooded with cheap imports (Tilt, 2008). Crop price plays a large role in determining what small-scale farmers choose to grow and whether they plant a single crop type or diversify (Di Falco & Perrings, 2005; Michler & Josephson, 2017; D. Wood & Lenné, 1999). Additionally, as small-scale farmers in developing countries become integrated in a global commodity market, they must consider risk and market uncertainty more than ever before (Hao, 2010). Responses of farmers to global markets contribute to socioeconomic drivers that ultimately shape landscapes of agroecosystems.

Research that links global trade, changes in landcover/use, and local biodiversity in the same context is lacking. Due to challenges associated with linking social and ecological data, many studies default to measuring landcover change alone or using a species area relationship to evaluate biodiversity impacts (Chaudhary & Brooks, 2019; Estrada et al., 2019; Newbold et al., 2015; Sala et al., 2000). While informative at broad scales, this approach often over-simplifies the complex relationships species have with their habitat at the local scale (Souza et al., 2015). Moreover, many studies on landcover change focus on destruction of “natural” habitat to assess impacts on biodiversity. Subsequently, the biodiversity potential of farmland is often overlooked (Norris, 2008).

The level of biodiversity that can be sustained in a predominantly agrarian region depends on farming practices that shape the landscape. For example, soil management (tilling), marginal land care (mowing), and chemical inputs (fertilizer and pesticide application) can all impact suitability of farmland for both animal and plant species (Billeter et al., 2008; Geiger et al., 2010; Humbert et al., 2012; Sapkota et al., 2012). It is also understood that landscape heterogeneity, in general, supports high levels of biodiversity (Fahrig et al., 2011; MacArthur & MacArthur, 1961; Tews et al., 2004) -- though too much heterogeneity can have negative impacts due to fragmentation or inadequate patch sizes of habitat (Allouche et al., 2012). Studies in agriculture have found heterogeneity across all landcover classes, including semi-natural, natural, built-up, and other features can positively effect biodiversity (Benton et al., 2003; Firbank et al., 2008; M.-B. Lee & Martin, 2017). However, those measures of heterogeneity are often outside the scope of conservation strategies that could be employed to increased farmland biodiversity. In terms of landscape structure, farmers have control on the types of crops they grow, where they grow them on their land, and their management of marginal land/field edges (Aguilar et al., 2015; Hayden et al., 2021; Jupiter, 2020, 2020; Preissel et al., 2017). Unless they decide to take land out of production (which may not be ideal for either the farmer’s bottom line or food security (Garibaldi et al., 2017; Kremen & Merenlender, 2018; Tscharntke et al., 2012)), their control over other aspects of the landscape is restricted. However, if relationships between biodiversity and actionable landscape metrics (e.g., percentage of natural area to inform land sparing amounts, crop diversity to inform how many crops to grow in a given area) were understood, they could be more easily translated to conservation strategies focused on farmers.

5.1.2 Research Goal

The goal of this study is to assess relationships between landscape structure (i.e., composition and configuration) and bird diversity in a region highly impacted by global trade. Specifically, this study looked at relationships between bird occupancy and landscape metrics using a multi-species occupancy modeling approach and assessed occupancy of taxonomic and functional bird groups. By gathering empirical wildlife data and linking it with landscape metrics, this chapter bridges the gap between landcover and a metric of local biodiversity that often exists in CHANS research and places it into context of the global interconnected CHANS encompassing the soybean trade.

5.2 Methods

5.2.1 Bird Data

In the summer of 2017 and 2018, we collected bird biodiversity data at 207 different points across Heilongjiang. These geolocated data were collected using a point count method (Bibby, 2000; Hutto, 1986). All birds seen or heard were recorded within a 50m (2017) or 100m (2018) radius for three, three-minute intervals. The use of temporal intervals allows for the calculation of detection probabilities (Zipkin et al. 2010). If individuals were not identifiable to the species, they were put into a non-specific category (e.g., crow spp, swallow spp). We also evaluated bird occurrence from a functional perspective by grouping each family into 15 different groups based on morphological and life history traits (see chapter 3). The composition of the functional groups was a mixture of single-family groups as well those that combined several similar families. Each group was also given an alias to aid in the interpretation of the results.

5.2.2 Landscape Metrics

To portray landcover around each bird survey point, landscape metrics were derived from classified landcover rasters (see chapters 3-4). Nineteen samples were removed from this analysis due to uncertainty in the land cover classification, resulting in a final sample size of 188. All metrics were calculated using the R package *landscapemetrics* at three different extents: 250m, 500m, and 1000m (Hesselbarth et al., 2019). We calculated seven landscape metrics to use as predictors of bird occupancy in our model (Table 39). The landscape-level metrics we selected for our model included the modified Simpson's diversity index of crop cover classes (msidi_crop), mean patch size (mn_patch), and aggregation index (ai). At the class level, we chose to include percent natural area, percent soybean, percent corn, and percent rice. These metrics were chosen based on previous work as well as our research goal of evaluating both landscape composition and configuration (Gil-Tena et al., 2015; M. B. Lee & Goodale, 2018; D. Li et al., 2020; Liao et al., 2020; C. Wood et al., 2017). To capture the largest range of variation for each metric, the extent which demonstrated the most variability (i.e., largest distance between end points of a boxplot) was identified for each metric. The correlations between each metric were also calculated to ensure the predictors in the model were not severely colinear (i.e., correlation > 0.7).

Table 39: Landscape metrics selected for model. The ‘Reclass’ input refers the landcover raster that merged crop classes (soybean, corn, rice, and other) into one ‘cropland’ class and the natural classes (forest, grassland, wetland, and water) into one ‘natural’ class.

Metric	*Unit*	*Level*	*Type*	*Input*
MSIDI	none	landscape	diversity	Crop classes only
AREA_MN	hectares	landscape	area & edge	All classes
AI	percentage	landscape	aggregation	All classes
PLAND_Natural	percentage	class	area & edge	Reclass
PLAND_Corn	percentage	class	area & edge	All classes
PLAND_Soy	percentage	class	area & edge	All classes
PLAND_Rice	percentage	class	area & edge	All classes

5.2.3 Occurrence Model

To assess relationship between landscape structure and bird diversity, we utilized a multispecies hierarchical occupancy model (M.-B. Lee & Martin, 2017; Zipkin et al., 2010) (Zipkin et al. 2010). The model estimates occupancy using a Bayesian approach while accounting for imperfect detection. All variables were standardized prior to running the model. Since the radius for point counts was increased from 50m to 100m in 2018, the detection and occurrence means were also calculated separately to account for unequal effort between the years (MacKenzie, 2018).

Our model is structured as a typical hierarchical occupancy model with two connected regression models estimating the ecological and detection processes separately (Kéry & Schaub, 2012). The occupancy state for species i at point j is a binary variable where a species occurs at point j when Occ_{ij} = 1 and Occ_{ij} = 0, otherwise. The occurrence state (1.1) was modeled as the outcome of a Bernoulli random variable where $pOcc_{ij}$ is the probability species i occurs at point j. The analysis of the model used data augmentation to allow for estimations of the number of families (or groups) that were unobserved during sampling. As described in Royle et al. 2007 and Zipkin et al. 2010, this is achieved by modifying the occurrence process with w_i (Royle, Dorazio, and Link 2007; Zipkin et al. 2010). For the taxonomic and functional level models, the dataset was augmented with 30 and 15 zeroes, respectively.

$$Occ_{ij} \sim Bern(pOcc_{ij} * w_i) \tag{1.1}$$

We modeled the detection state similarly (1.2), with detection being determined by detection probability for species i at point j during interval k and occupancy state (i.e., whether or not species i is actually at point j).

$$Det(i,j,k) \sim Bern\left(pDet_{ijk} * Occ_{ij}\right) \tag{1.2}$$

Since we expected occurrence and detection probabilities to vary by species, landscape structure, and survey characteristics, a logit link function was used to incorporate these effects. We modeled occurrence probability (1.3) using a linear combination of crop diversity, aggregation index, mean patch size, percent natural landcover, percent rain-fed crop cover, and percent rice cover as well as longitude to account for underlying species distributions that differed from east to west. The $Occ17_i$ term is the occurrence probability for species i, when all other covariates are equal to their mean. The $Occ18_i$ term exists to modify occurrence probability for samples collected in 2018 (Ind_j = 1).

$$\begin{gathered} logit(pOcc_{ij}) = Occ17_i + Occ18_i Ind_j + MSIDIcrop_j \beta_{1i} + MNpatch_j \beta_{2i} + \\ AI_j \beta_{3i} + PLANDnat_j \beta_{4i} + PLANDsoy_j \beta_{5i} + PLANDcorn_j \beta_{6i} + \\ PLANDrice_j \beta_{7i} + LONG_j \beta_{8i} \end{gathered} \tag{1.3}$$

For detection probability (1.4), we included the time of the sample (calculated as the number of minutes after sunrise) as a predictor in addition to the $Det17_i$ and $Det18_i$ terms.

$$logit(pDet_{ijk}) = Det17_i + Det18_i Ind_j + sunrise_{jk}\, \alpha_i \tag{1.4}$$

An important characteristic of this modeling approach links the species-level processes to a community-level component, where all species parameters are drawn from a shared distribution. This allows for the species-specific parameters to be treated as random effects that are governed by community hyperparameters. These hyperparameters were assumed to be normally distributed with a parameter-specific mean of μ and standard deviation of σ. Similarly, μ and σ were also specified for all species-level parameters.

We conducted a Bayesian analysis of the model using the programs R and WinBUGS (Lunn et al., 2000; R Core Team, 2021). We defined independent, diffuse prior distributions for the community hyperparameters (see appendix for model code) and ran the model with 3 chains of 75,000 iterations after a 75,000 burn-in and thinned by 10. Model convergence was evaluated using the Gelman diagnostic (Brooks & Gelman, 1998).

5.3 Results

5.3.1 Model data

A total of 2444 bird observations were made across all 188 point-count locations and intervals, spanning 13 orders and 30 families (Table 40). The majority of species were passerines from the Hirundinidae (swallow), Acrocephalidae (reed warbler), Corvidae (crow/magpie), Passeridae (old world sparrow), and Emberizidae (bunting) families (Table 40). At the species level, 46 unique species were identified. The most frequent group in our sample (group 9) consisted of swallows and reed tits (swallow/reedtit) followed by group 1 (reedwarb/flycather) and group 7 (crow/magpie) (Table 42).

Table 40: Frequency of bird order and family in sample

Order	**#**	**Family**	**#**
Passeriformes	2080	Hirundinidae	727
Columbiformes	104	Acrocephalidae	468
Charadriiformes	60	Corvidae	321
Falconiformes	59	Passeridae	284
Pelicaniformes	43	Emberizidae	118
Anseriformes	28	Columbidae	104
Cuculiformes	28	Falconidae	59
Gruiformes	11	Remizidae	53
Galliformes	9	Laniidae	42
Phoenicopteriformes	4	Ardeidae	41
Piciformes	4	Charadriidae	32
Bucerotiformes	3	Anatidae	28
Coraciiformes	1	Cuculidae	28
		Laridae	28
		Oriolidae	13
		Rallidae	11
		Muscicapidae	10
		Panuridae	10
		Motacillidae	9
		Paridae	9
		Phasianidae	9
		Turdidae	8
		Picidae	4
		Podicipedidae	4
		Sturnidae	3
		Troglodytidae	3
		Upupidae	3
		Campephagidae	2
		Phalacrocoracidae	2
		Alcedinidae	1

Table 41: Functional group composition and species frequency

Group	*Spp*	*Family*	*Order*	*Freq*
1	reed_warbler	Acrocephalidae	Passeriformes	351
1	black_browed_reed_warbler	Acrocephalidae	Passeriformes	106
1	thick-billed_warbler	Acrocephalidae	Passeriformes	6
1	oriental_reed_warbler	Acrocephalidae	Passeriformes	5
1	stonechat	Muscicapidae	Passeriformes	10
2	common_kingfisher	Alcedinidae	Coraciiformes	1
3	duck_spp	Anatidae	Anseriformes	28
3	bittern_spp	Ardeidae	Pelicaniformes	18
3	great_egret	Ardeidae	Pelicaniformes	10
3	gray_heron	Ardeidae	Pelicaniformes	7
3	purple_heron	Ardeidae	Pelicaniformes	5
3	striated_heron	Ardeidae	Pelicaniformes	1
4	ashy_minivet	Campephagidae	Passeriformes	2
4	common_cuckoo	Cuculidae	Cuculiformes	28
4	black_naped_oriole	Oriolidae	Passeriformes	13
4	thrush_spp	Turdidae	Passeriformes	7
4	siberian_thrush	Turdidae	Passeriformes	1
5	shorebird_spp	Charadriidae	Charadriiformes	23
5	northern_lapwing	Charadriidae	Charadriiformes	9
6	dove_spp	Columbidae	Columbiformes	46
6	pigeon	Columbidae	Columbiformes	45
6	spotted_dove	Columbidae	Columbiformes	10
6	oriental_turtle_dove	Columbidae	Columbiformes	3
6	bunting_spp	Emberizidae	Passeriformes	76
6	chestnut-earred_bunting	Emberizidae	Passeriformes	24
6	black_faced_bunting	Emberizidae	Passeriformes	10
6	meadow_bunting	Emberizidae	Passeriformes	7
6	reed_bunting	Emberizidae	Passeriformes	1
6	ring-neck_pheasant	Phasianidae	Galliformes	9
7	eurasian_magpie	Corvidae	Passeriformes	308
7	crow_spp	Corvidae	Passeriformes	12
7	eurasian_jay	Corvidae	Passeriformes	1
8	eurasian_kestrel	Falconidae	Falconiformes	36
8	amur_falcon	Falconidae	Falconiformes	11
8	eurasian_hobby	Falconidae	Falconiformes	7
8	falcon_spp	Falconidae	Falconiformes	5
8	brown_shrike	Laniidae	Passeriformes	33
8	gray_shrike	Laniidae	Passeriformes	5
8	shrike_spp	Laniidae	Passeriformes	4
9	swallow_spp	Hirundinidae	Passeriformes	685
9	red-rumped_swallow	Hirundinidae	Passeriformes	26
9	barn_swallow	Hirundinidae	Passeriformes	16
9	bearded_reedling	Panuridae	Passeriformes	10
9	chinese_penduline_tit	Remizidae	Passeriformes	53
10	white_wing_tern	Laridae	Charadriiformes	25
10	tern_spp	Laridae	Charadriiformes	3
10	great_cormorant	Phalacrocoracidae	Pelicaniformes	2
10	little_grebe	Podicipedidae	Phoenicopteriformes	4
11	white_wagtail	Motacillidae	Passeriformes	4
11	pipit_spp	Motacillidae	Passeriformes	3
11	olive-backed_pipit	Motacillidae	Passeriformes	2
12	tit_spp	Paridae	Passeriformes	9
12	eurasian_tree_sparrow	Passeridae	Passeriformes	284
12	eurasian_wren	Troglodytidae	Passeriformes	3
13	woodpecker_spp	Picidae	Piciformes	4
14	common_moorhen	Rallidae	Gruiformes	8
14	common_coot	Rallidae	Gruiformes	2
14	crake_spp	Rallidae	Gruiformes	1
15	common_starling	Sturnidae	Passeriformes	3
15	common_hoopoe	Upupidae	Bucerotiformes	3

Table 42: Functional group frequency and group aliases.

Group Aliases	*Group*	*Freq*
swallow/reedtit	group_9	790
reedwarb/flycatcher	group_1	478
crow/magpie	group_7	321
sparrow/tit	group_12	296
dove/bunting/pheasant	group_6	231
falcon/shrike	group_8	101
heron/duck	group_3	69
thrush/cuckoo/oriole	group_4	51
tern/grebe	group_10	34
shorebird/lapwing	group_5	32
rail	group_14	11
pipit/wagtail	group_11	9
hoopoe/starling	group_15	6
woodpecker	group_13	4
kingfisher	group_2	1

As expected, variation of each landscape metric varied among extents (Table 43). Two metrics had the greatest spread at the largest extent (mean patch and rice percentage). Crop diversity, aggregation, percent corn maximized variation at 500m and the percentage of natural landcover and soybean variation peaked at the smallest extent (250m). For the most part, none of the metrics were highly correlated, however, aggregation and mean patch size were moderately correlated (R = 0..57) as well as corn and rice area (R = -0.59) (Figure 41).

Table 43: Data variation for each metric across all extents (250m, 500m, and 1000m).

	spread				250m		500m		1000m	
metric (standardized)	max	250m	500m	1000m	max	min	max	min	max	min
msidi_crop	500	3.35	3.58	3.37	2.43	-0.92	2.53	-1.06	2.07	-1.29
mn_patch	1000	1.36	1.44	3.47	0.48	-0.89	0.69	-0.75	2.24	-1.23
ai	500	4.20	4.42	3.94	1.61	-2.58	2.05	-2.37	1.81	-2.13
pland_natural	250	3.05	2.32	2.53	2.12	-0.93	1.43	-0.89	1.62	-0.91
pland_soybean	250	3.36	2.69	3.17	2.33	-1.03	1.82	-0.88	2.34	-0.83
pland_corn	500	3.38	3.39	3.31	1.84	-1.54	2.09	-1.31	2.15	-1.16
pland_rice	1000	2.95	3.04	3.11	1.43	-1.52	1.73	-1.31	2.02	-1.09

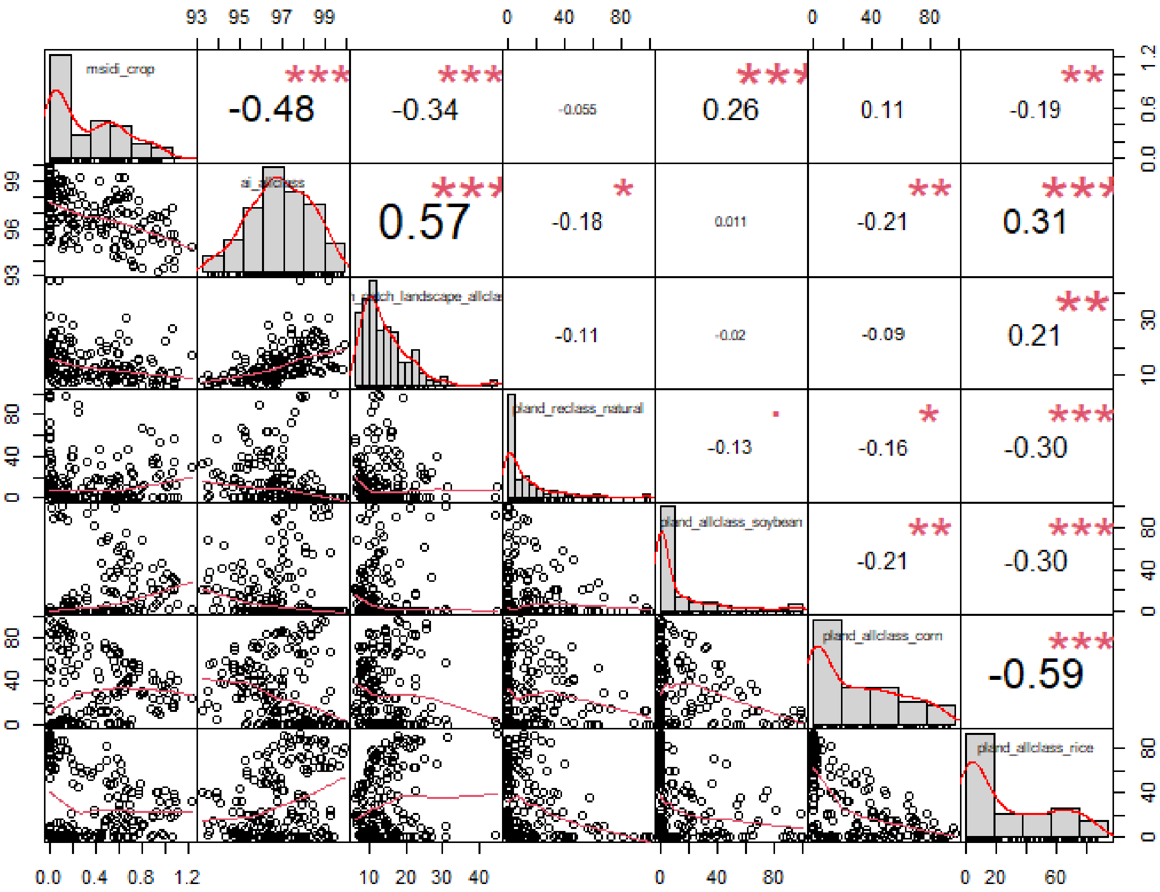


Figure 41: Correlogram for metrics selected as model predictors.

5.3.2 Taxonomic model results

At the community-level, all landscape parameters had 90% Bayesian credible intervals (BCIs) that contained zero (Table 44). Crop diversity (msidi_crop) was the only variable indicating marginal significance, suggesting that greater crop diversity corresponded to higher bird occurrence probabilities (Table 44).

Table 44: Estimates of hyperparameters for the taxonomic occurrence model

parameter	mean	sd	lower	upper
occurrence 17	-5.04	2.49	-7.53	-2.56
occurrence 18	0.42	0.93	-0.50	1.35
detection 17	0.15	0.65	-0.50	0.80
detection 18	0.15	0.35	-0.20	0.50
msidi_crop	0.25	0.32	-0.06	0.57
mn_patch	-0.07	0.34	-0.41	0.26
ai	-0.08	0.39	-0.47	0.31
pland_nat	0.19	0.36	-0.17	0.54
pland_soy	-0.34	0.46	-0.80	0.12
pland_corn	-0.28	0.47	-0.75	0.18
pland_rice	-0.16	0.53	-0.68	0.37
long	-0.10	0.65	-0.74	0.55
sunrise	-0.04	0.43	-0.47	0.38

The number of bird families with significant and nearly significant coefficient estimates (i.e., BCI crossed zero by <0.1) varied across the different landscape metrics. At the family level, higher crop diversity significantly associated with higher occupancy probabilities for 5 of the 30 families (Figure 43). Additionally, all but one family (Laridae) had positive mean estimates and several additional families had 90% credible intervals that crossed 0 by <0.1 (e.g., Remizidae, Charadriidae, Figure 43).

Only one family, Hirundinidae, showed significant effects of mean patch size (positive) and no families were significant for aggregation (Figure 44). The means for patch size were mostly negative. For the aggregation parameter, family means were distributed more equally between positive and negative effects (Figure 44). Panuridae and Anatidae were nearly significant, with a positive mean estimate.

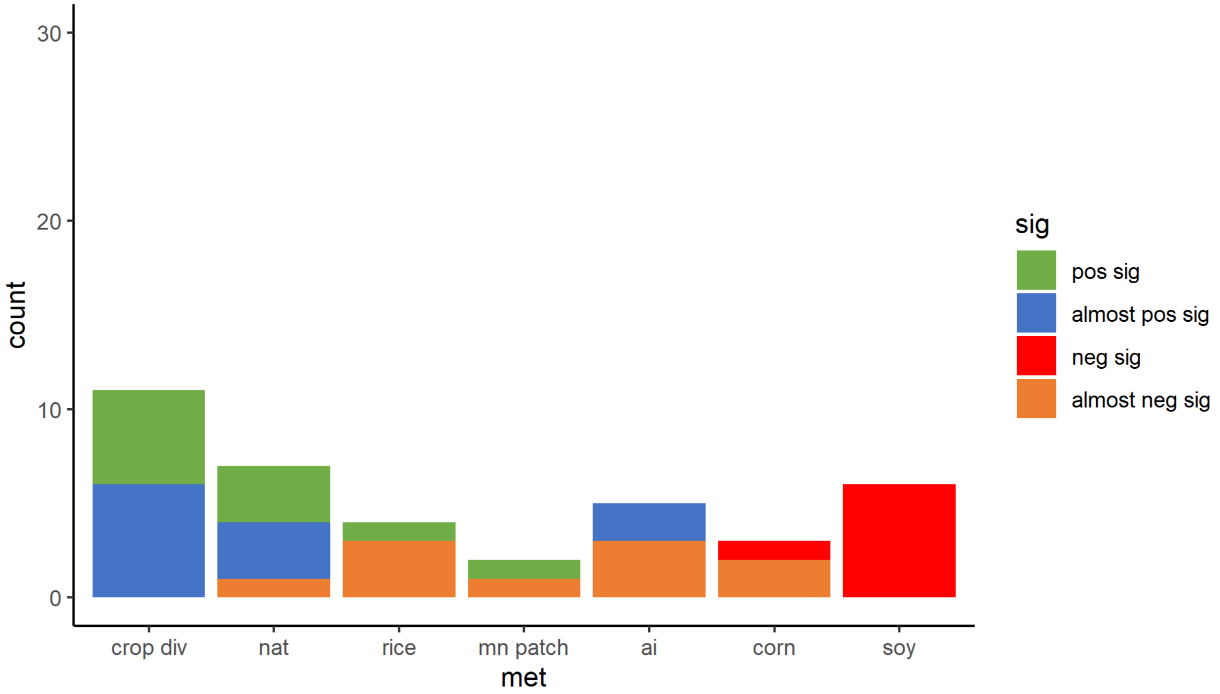


Figure 42: Number of bird families with significant and nearly significant coefficient estimate means (green, blue = positive, red, orange = negative) for each landscape metric: crop diversity (crop div), natural area (nat), rice area (rice), mean patch size (mn patch), aggregation of patches (ai), corn area (corn), and soybean area (soy).

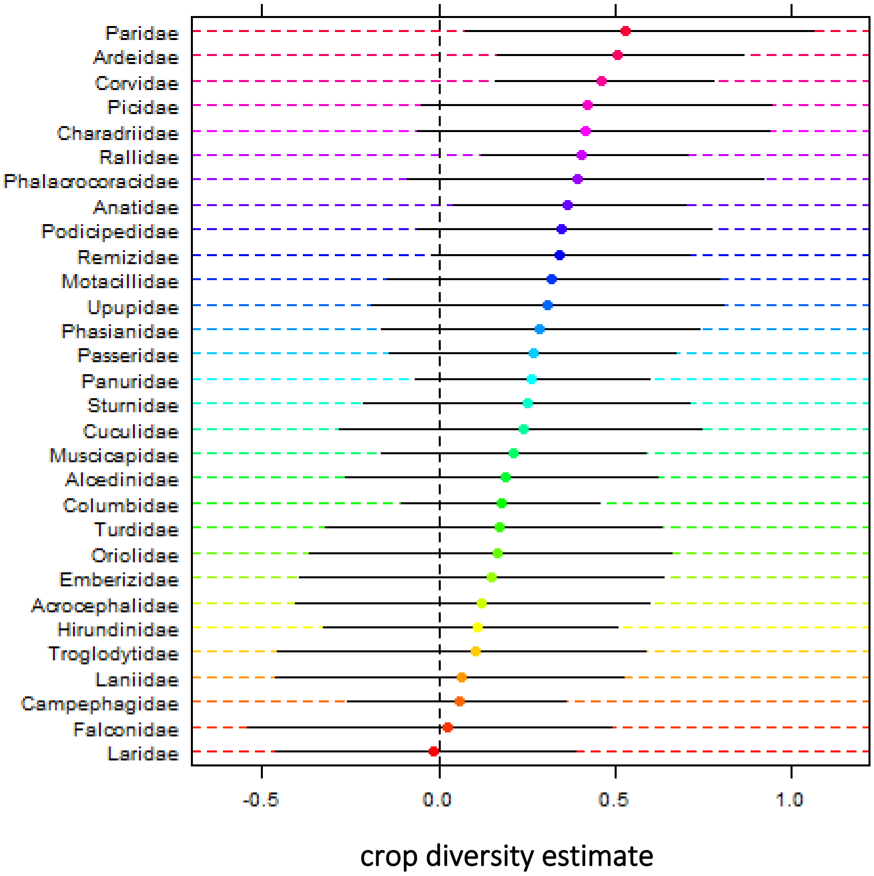
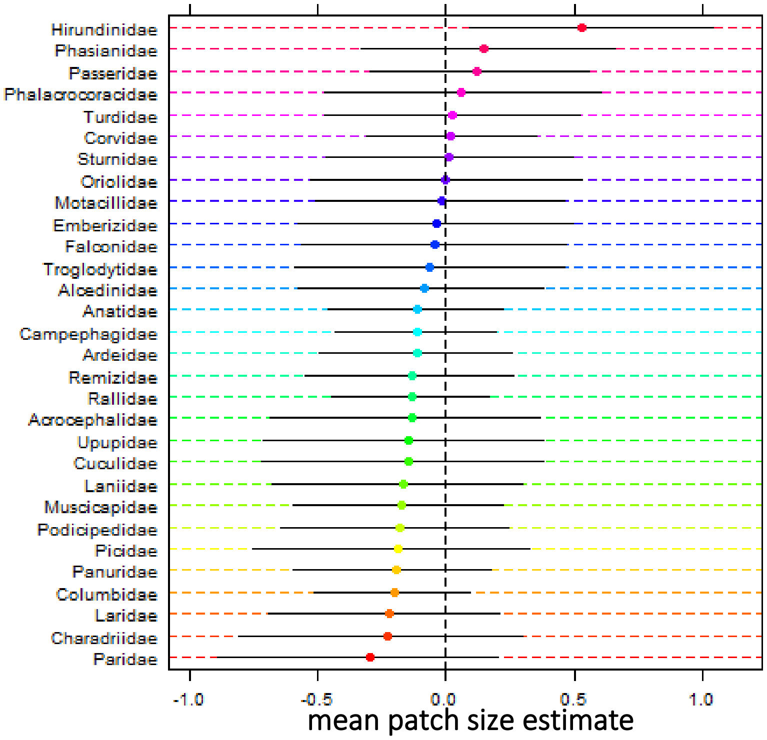


Figure 43: Dot plot showing the family-specific mean estimates with 90% Bayesian credible intervals for crop diversity. Five families had positive estimates with BCIs that did not cross 0 (Corvidae, Ardeidae, Anatidae, Rallidae, Paridae)



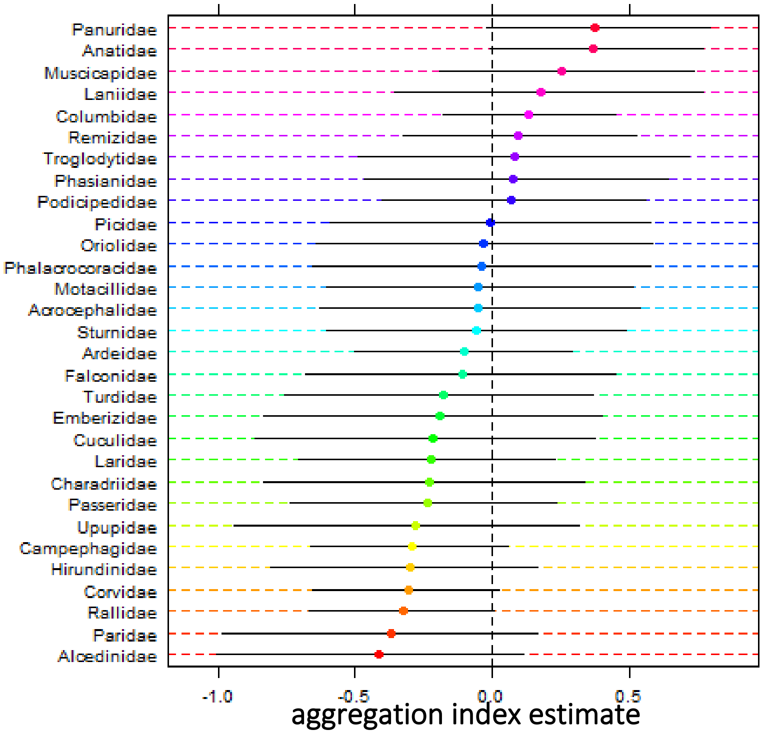


Figure 44: Dot plots showing the family-specific mean estimates with 90% credible intervals for mean patch area and aggregation index.

For the percent natural landcover area metric, Panuridae, Troglodytidae, and Phasianidae were the only families significantly more likely to occur as natural landcover increased, though most of the non-significant groups also had positive mean estimates (Figure 45). Some families had negative means (e.g., Corvidae and Campephagidae) but were not significant. For the crop percent area metrics, the majority of families exhibited negative associations (Figure 45). Soybean area was significantly and negatively associated with Hirundinidae, Corvidae, Passeridae, Remizidae, Ardeidae, and Laridae families. The Corvidae family was significantly, negatively related to corn planted area with Anatidae and Falconidae being nearly significant and negative. Rice paddy area was positively associated with Corvidae occurrence (Figure 45).

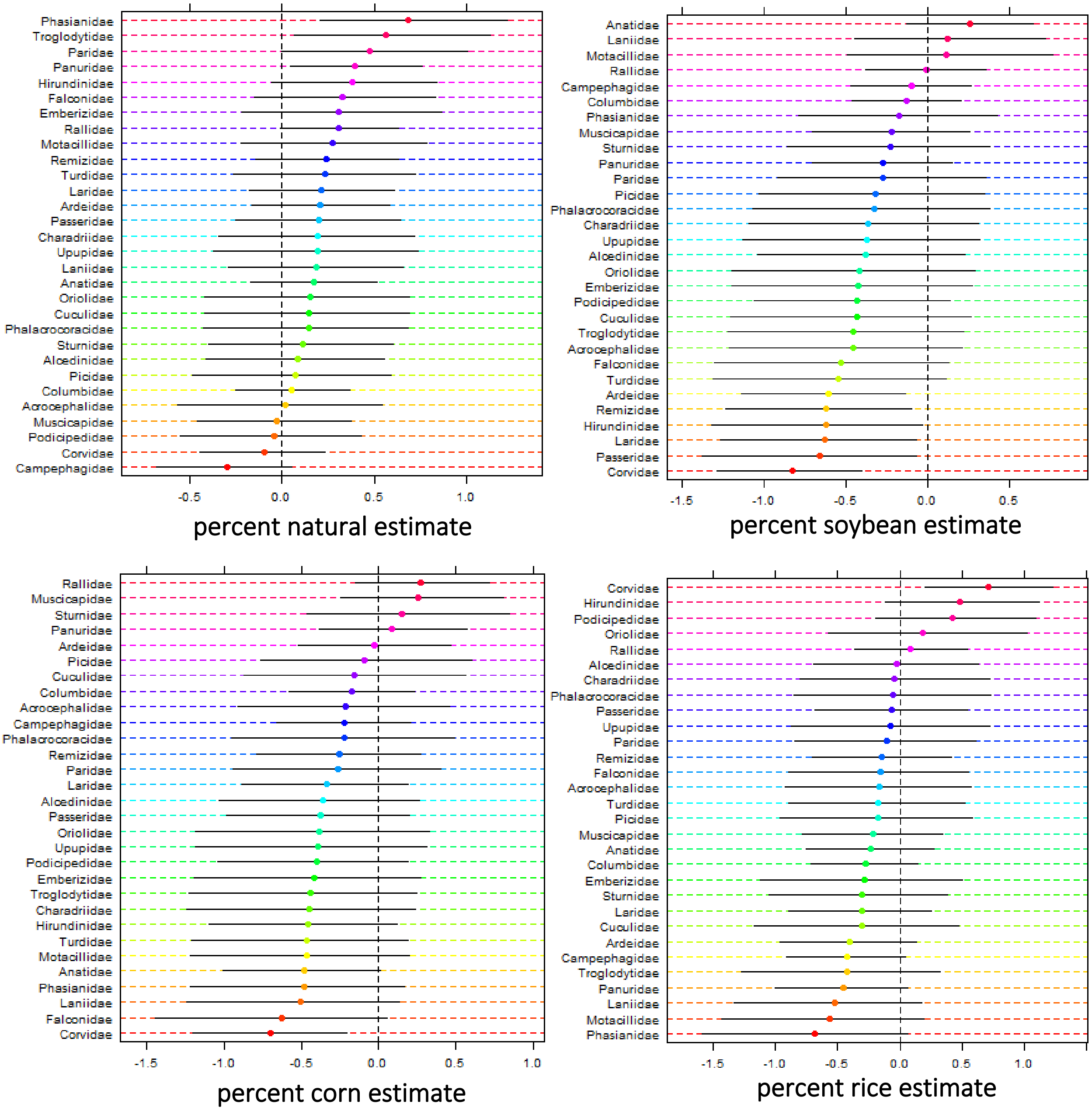


Figure 45: Dot plots showing the family-specific mean estimates with 90% Bayesian credible intervals for percent area natural landcover (forest, wetland, grassland), soybean, corn, and rice paddy.

Longitude was included in the occurrence model as a covariate to address potential underlying regional differences of species distribution between eastern and western halves of the province. Families more likely to occur in the western half of the province include Musciapidae, Falconidae, Sturnidae, Columbidae, Campephagidae, Lariidae, and Rallidae. Those occurring more in the eastern side include Anatidae and Corvidae. The minutes after sunrise covariate for detection was only significant for species in the Columbidae family (Figure 46).

No estimates for detection in 2018 have BCI's that exclude zero, implying that the increase in radius between the two years did not impact detection significantly (Figure 47). Some of the families that occurred more often in 2018 due to the increased sample radius include Ardeidae, Hirundidae, Campephagidae, and Rallidae.

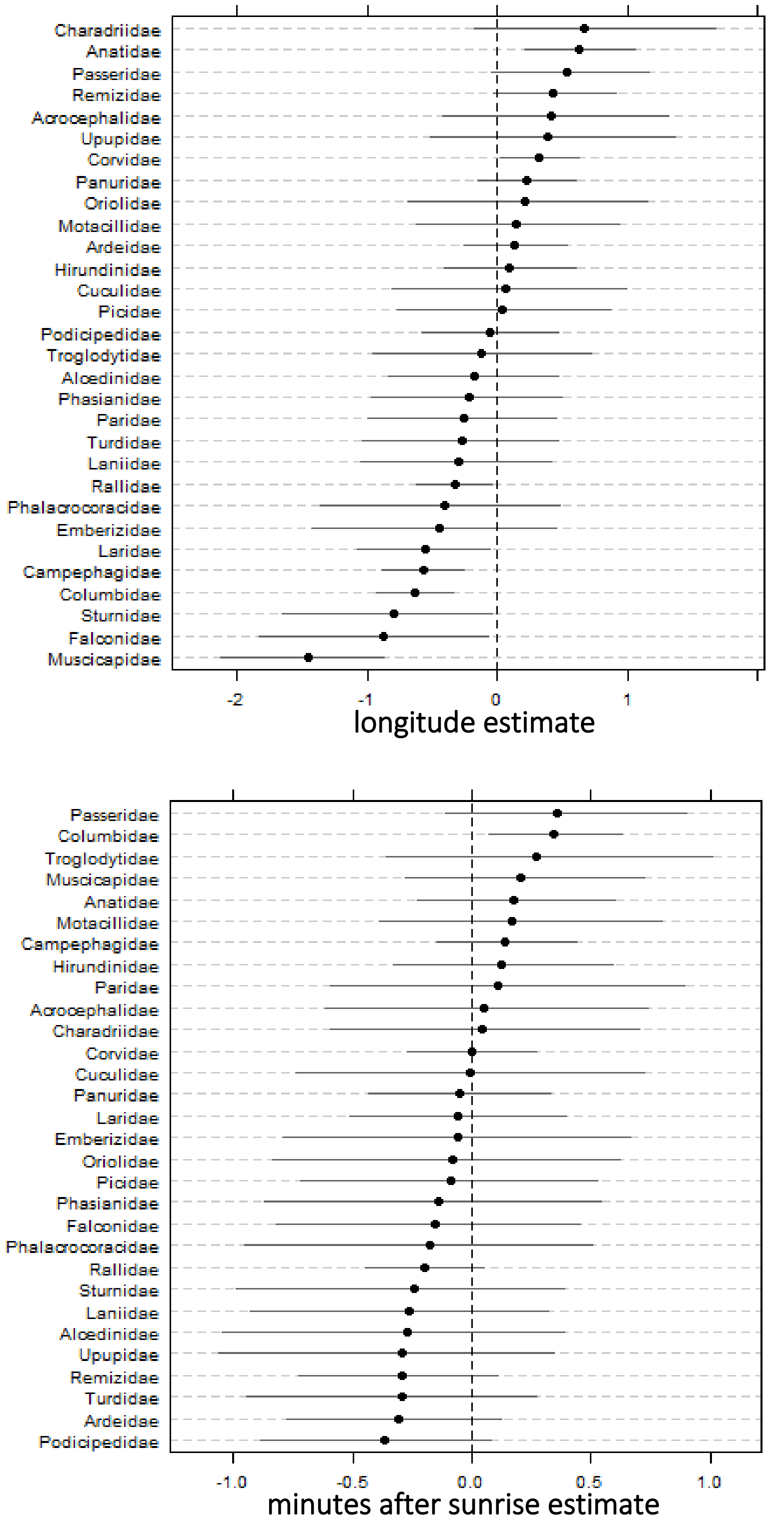


Figure 46: Dot plots showing the family-specific mean estimates with 90% credible intervals for longitude and minutes after sunrise, which were used as covariates in the occurrence and detection models respectively.

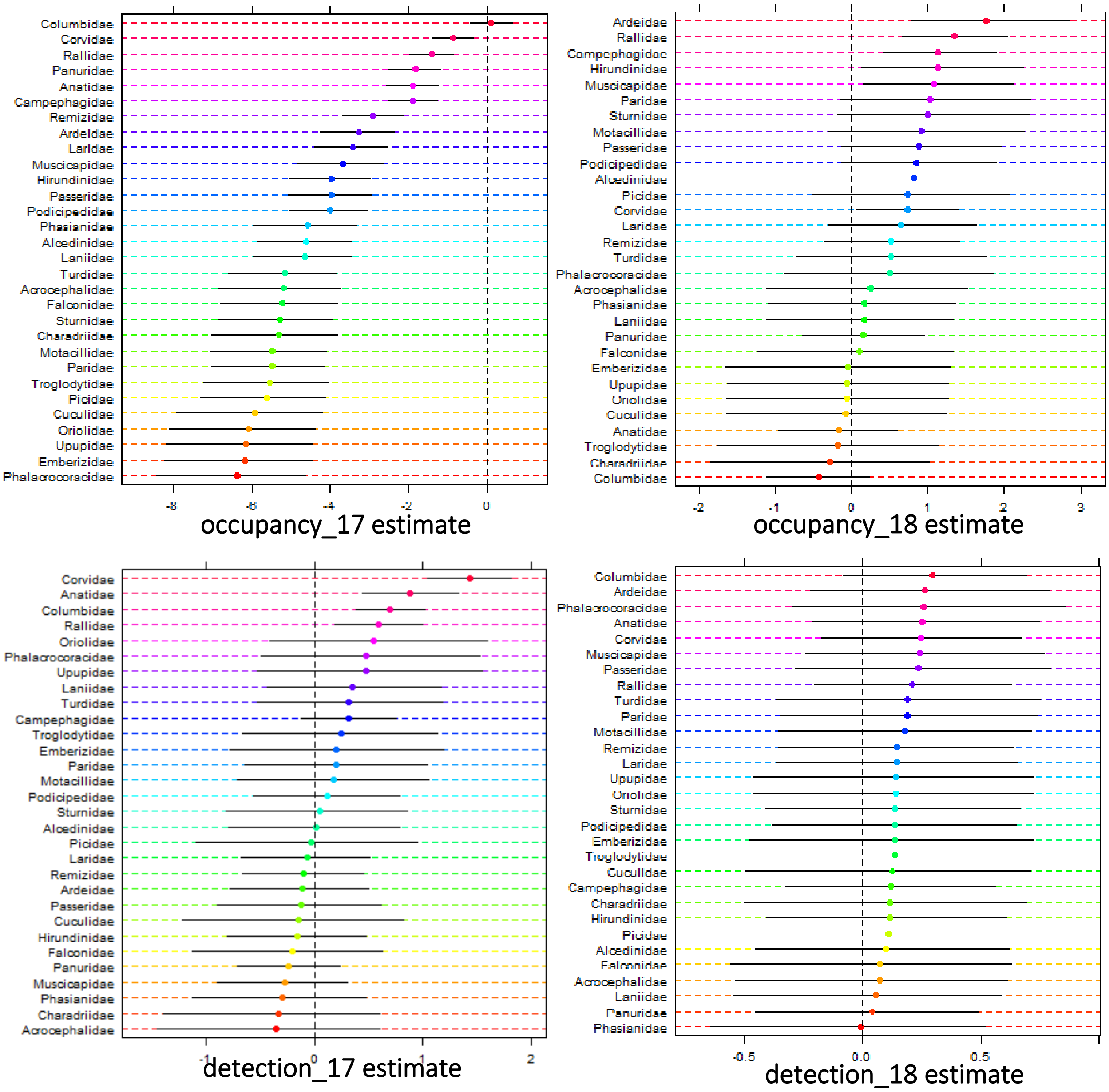


Figure 47: Dot plots showing the family-specific mean estimates with 90% credible intervals for occurrence and detection.

Most of the most abundant bird families (>30 observations) had occupancy probabilities higher than the mean across all crop diversity levels. Corvidae, Columbidae, and Ardeidae demonstrated the largest increases in occupancy probability as crop diversity increased (Figure 48). The remaining five families (11 total) were less impacted by crop diversity and had relationships similar to the community mean. Hirundinidae demonstrated a substantial positive relationship with mean patch size. Most families had a neutral or slightly positive relationship with percent natural area, except Corvidae which decreased in occupancy probability as natural area increased.

For the percent crop area metrics, most families had a negative relationship as the landscape becomes more dominated by a given class, especially in the case of corn and soybean area (all negative). The negative relationship between soybean area and occurrence was significant for 5 of the most common families while corn was only significant for one. Rice area had negative, non-significant relationships with Columbidae and Ardeidae occupancy and a significant, positive relationship in the case of Corvidae (Figure 48).

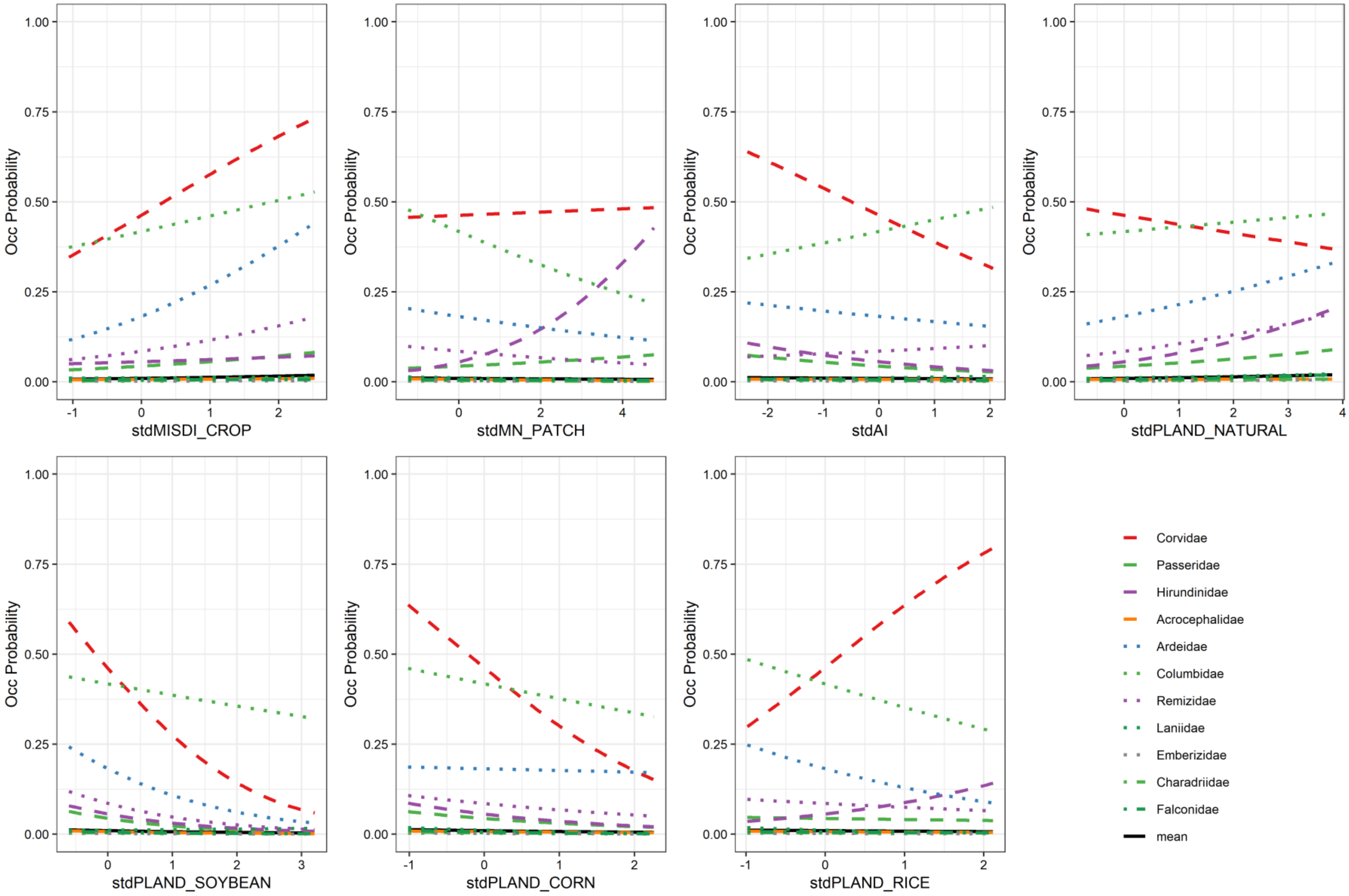


Figure 48: All landscape metric relationships with occurrence probability for the most abundant families (>30 observations)

5.3.3 Functional model results

For the functional model, positive values of crop diversity (MSIDI_crop) corresponded to higher occurrence probabilities at the community-level, compared to the taxonomic model, which had a credible interval that crossed zero (Table 45). All other landscape covariates had 90% credible intervals that contained zero.

Table 45: Estimates of hyperparameters for the functional occurrence model

parameter	mean	sd	lower	upper
occurrence 17	-3.33	2.54	-5.88	-0.79
occurrence 18	0.43	0.84	-0.41	1.26
detection 17	0.27	0.60	-0.33	0.86
detection 18	0.24	0.36	-0.12	0.59
msidi_crop	0.35	0.34	0.01	0.69
mn_patch	-0.09	0.37	-0.46	0.27
ai	-0.08	0.48	-0.56	0.40
pland_nat	0.16	0.35	-0.19	0.51
pland_soybean	-0.34	0.51	-0.85	0.16
pland_corn	-0.26	0.49	-0.76	0.23
pland_rice	-0.02	0.55	-0.57	0.53
long	-0.08	0.45	-0.53	0.37
sunrise	-0.13	0.44	-0.57	0.31

The number of bird groups with significant and nearly significant coefficient estimates (i.e., BCI crossed zero by <0.1) varied across the different landscape metrics (Figure 49). At the group level, higher crop diversity was significantly associated with higher occupancy probabilities for 8 of the 15 groups (Figure 50). Additionally, all groups had positive mean estimates and several additional families had BCIs that barely crossed zero (e.g., reedwarb/flycatcher, woodpecker). Only the dove/bunting/pheasant group was significantly impacted by patch size. The majority of the groups had mean estimates that were negative, with the woodpecker and shorebird/lapwing groups being nearly significant (Figure 51). The shorebird/lapwing group was significantly, positively impacted by aggregation index with the crow/magpie and hoopoe/starling groups being nearly significant with negative estimates (Figure 51).

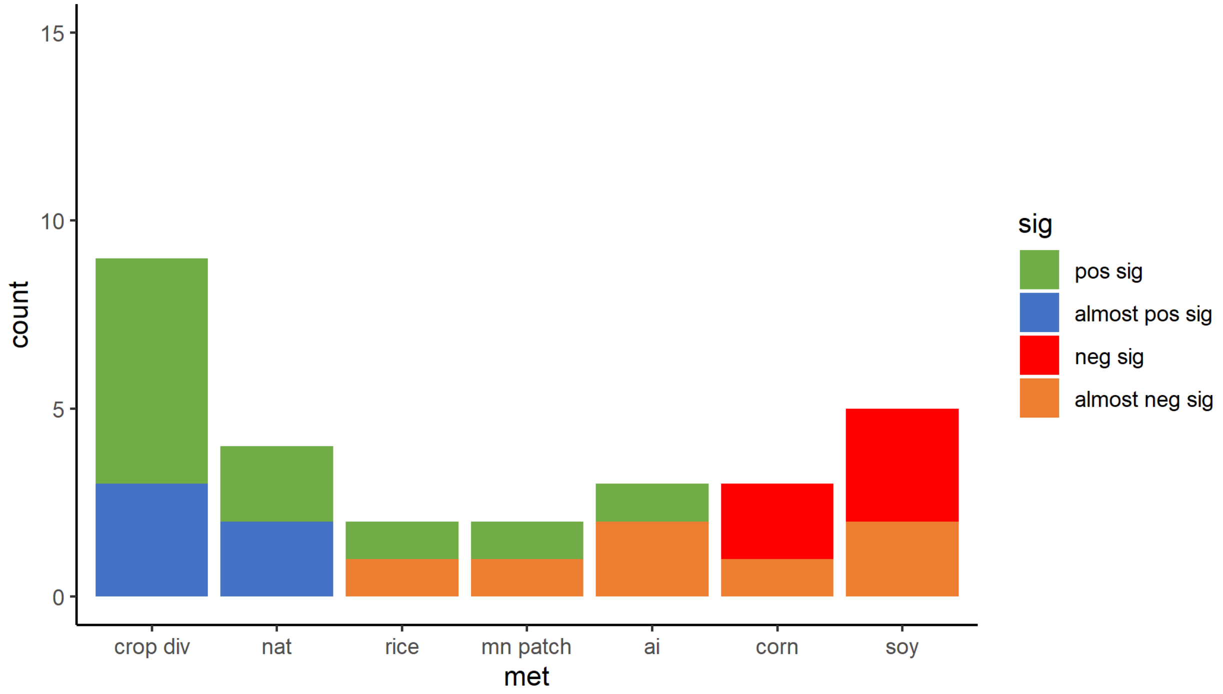


Figure 49: Number of bird groups with significant and nearly significant coefficient estimate means (green, blue = positive, red, orange = negative) for each landscape metric: crop diversity (crop div), natural area (nat), rice area (rice), mean patch size (mn patch), aggregation of patches (ai), corn area (corn), and soybean area (soy).

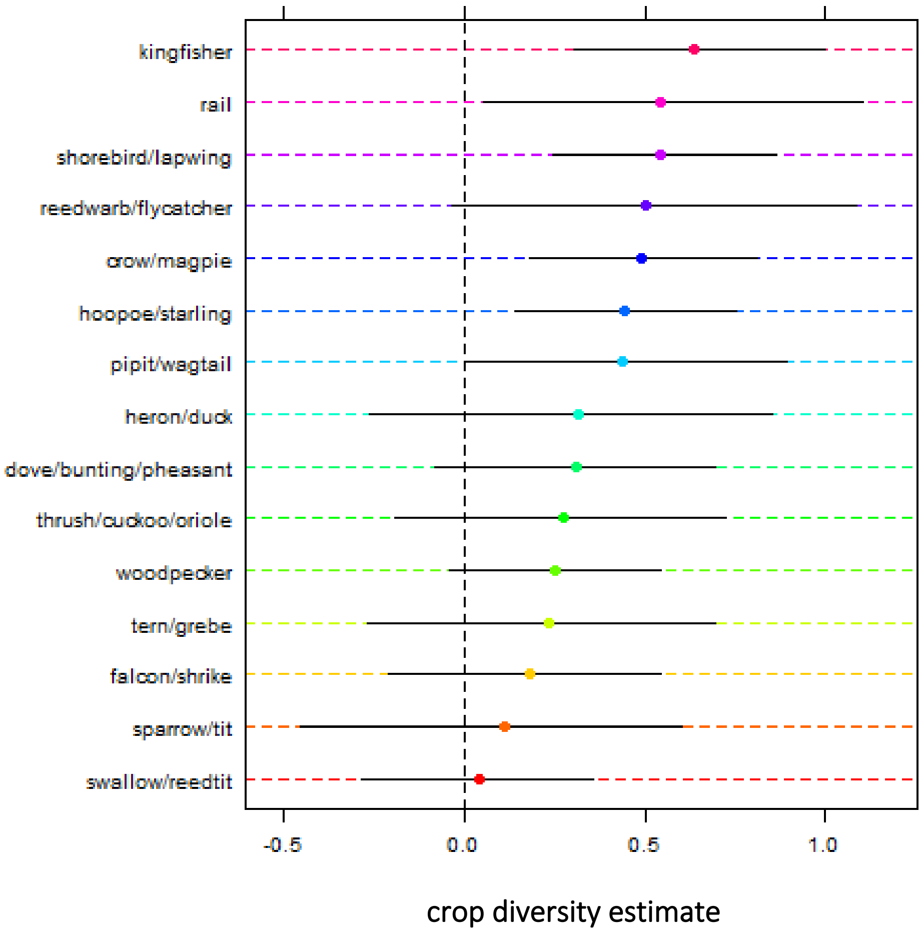


Figure 50: Dot plot showing the group-specific mean estimates with 90% Bayesian credible intervals for crop diversity. Six groups had positive estimates with BCIs that did not cross 0 (crow/magpie, shorebird/lapwing, rail, pipit/wagtail, hoopoe/starling, kingfisher)

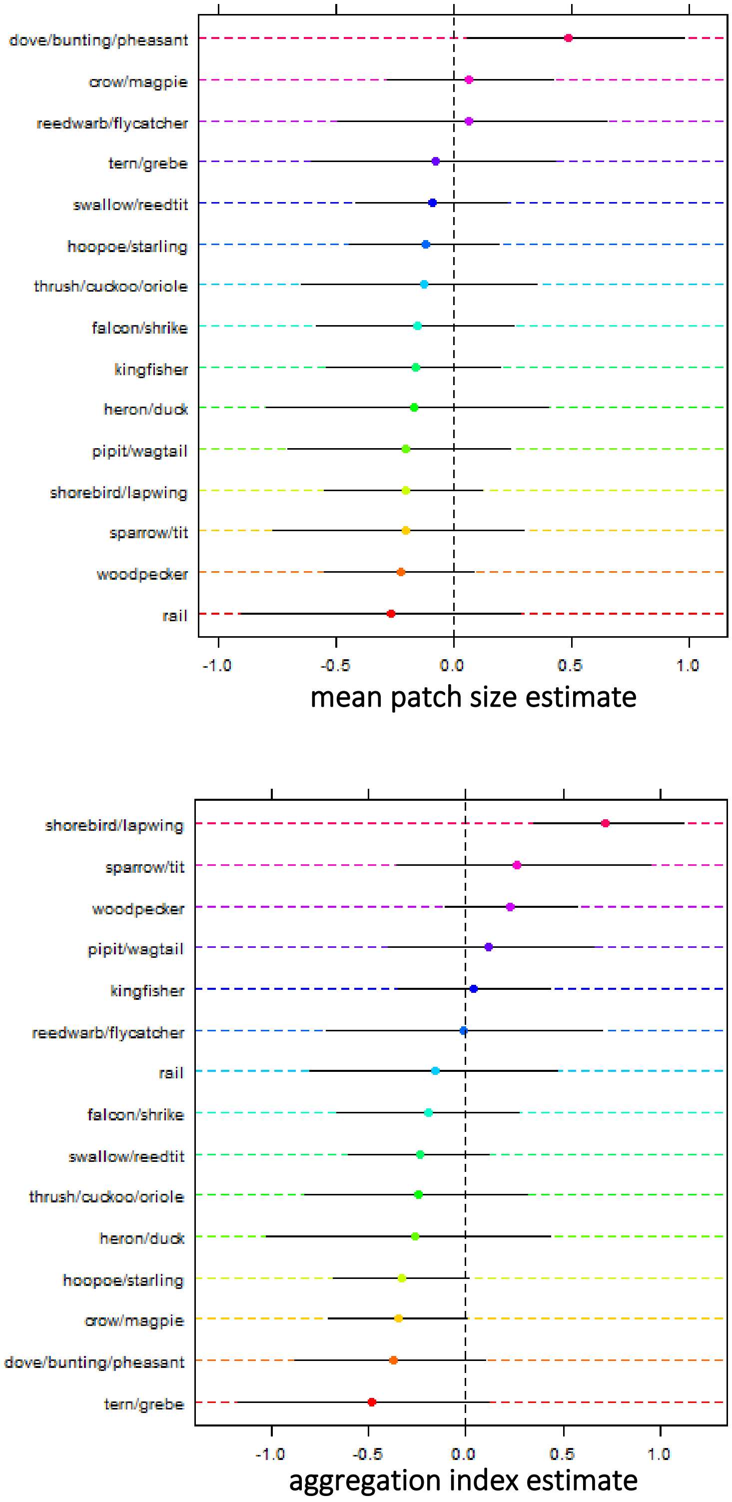


Figure 51: Dot plots showing the group-specific mean estimates with 90% credible intervals for mean patch area and aggregation index.

For the percent natural landcover area metric, the falcon/shrike and shorebird/lapwing groups were significantly more likely to occur as natural landcover increased (Figure 52). For soybean and corn area, the majority of groups exhibited negative associations. Soybean area was significantly and negatively associated with the crow/magpie, dove/bunting/pheasant, and kingfisher groups with the thrush/cuckoo/oriole and falcon/shrike groups being nearly significant (Figure 52). Corn area was negatively related to the thrush/cuckoo/oriole and crow/magpie groups with the falcon/shrike also being nearly significant (Figure 52). Rice paddy area was only positively related to the crow/magpie group (Figure 52).

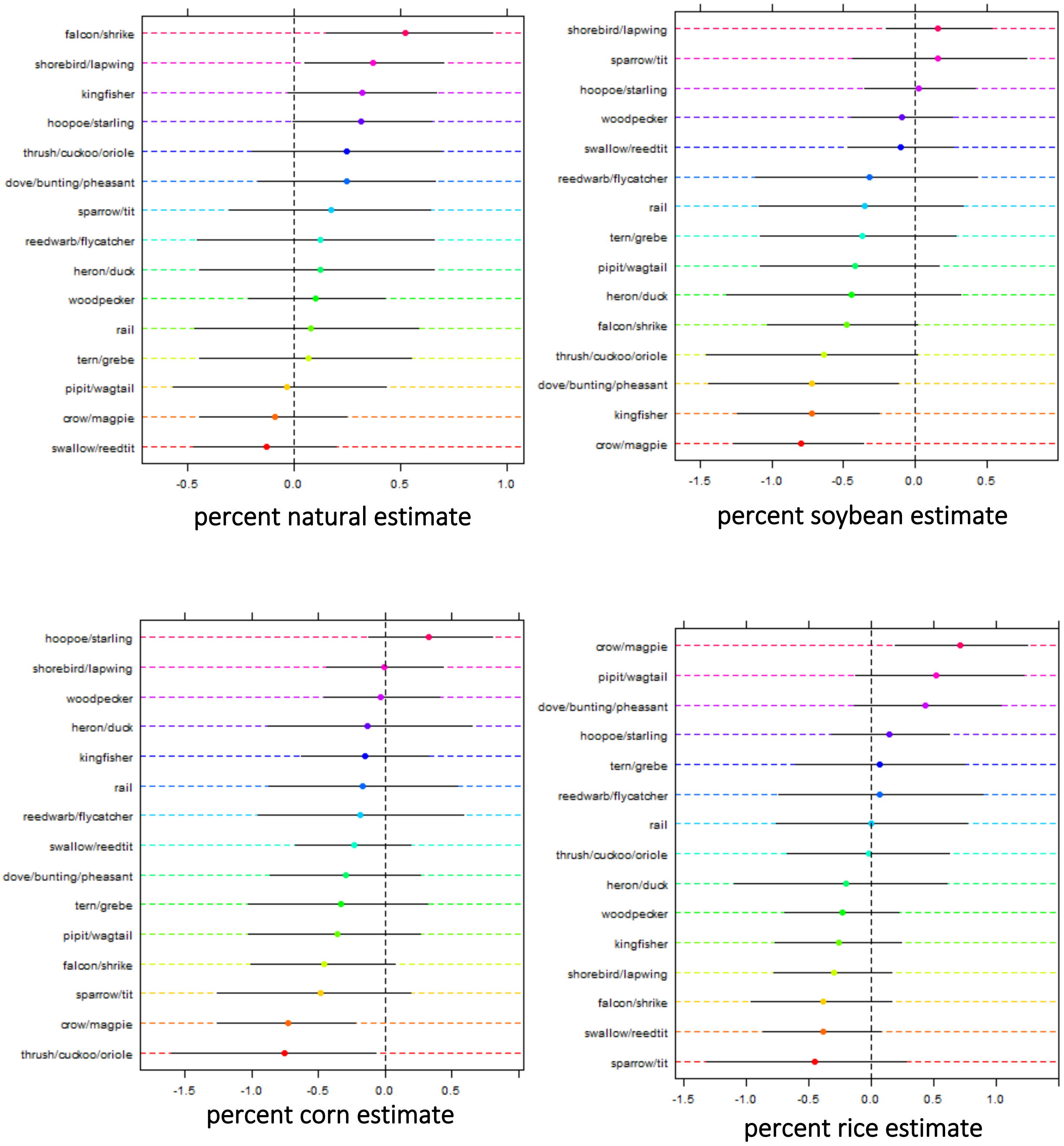


Figure 52: Dot plots showing the group-specific mean estimates with 90% Bayesian credible intervals for percent area natural landcover (forest, wetland, grassland), soybean, corn, and rice paddy.

Groups that were more likely to occur in the western half of the province included the woodpecker, swallow/reedtit, falcon/shrike, and hoopoe/starling groups (Figure 53). Those occurring more in the eastern side include the shorebird/lapwing, crow/magpie, dove/bunting/pheasant, and kingfisher groups. The minutes after sunrise covariate for detection was only significant for the kingfisher (negative) and woodpecker groups (positive) (Figure 53).

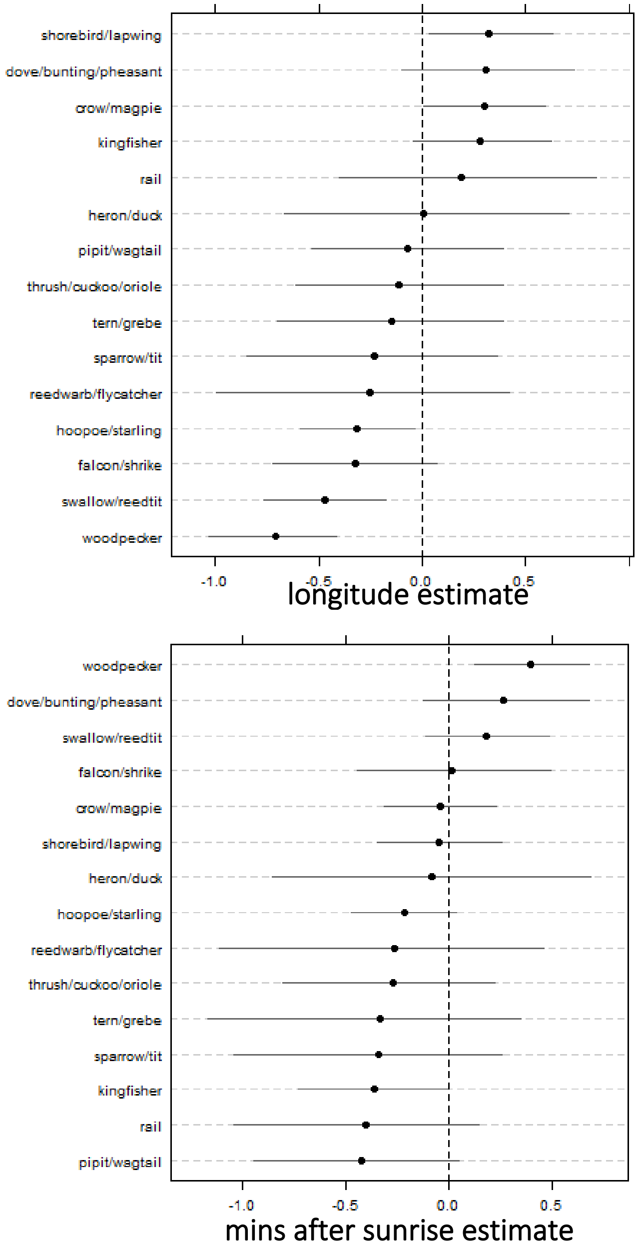


Figure 53: Dot plots showing the group-specific mean estimates with 90% credible intervals for longitude and minutes after sunrise, which were used as covariates in the occurrence and detection models respectively.

As with the taxonomic model, the mean estimates for the occurrence and detection parameters demonstrate that the difference between the two years was most significant for occurrence (Figure 54). Some of the groups that occurred more often in 2018 due to the increased sample radius include the hoopoe/starling , kingfisher, dove/bunting/pheasant, , swallow/reedtit , and crow/magpie groups (Figure 54).

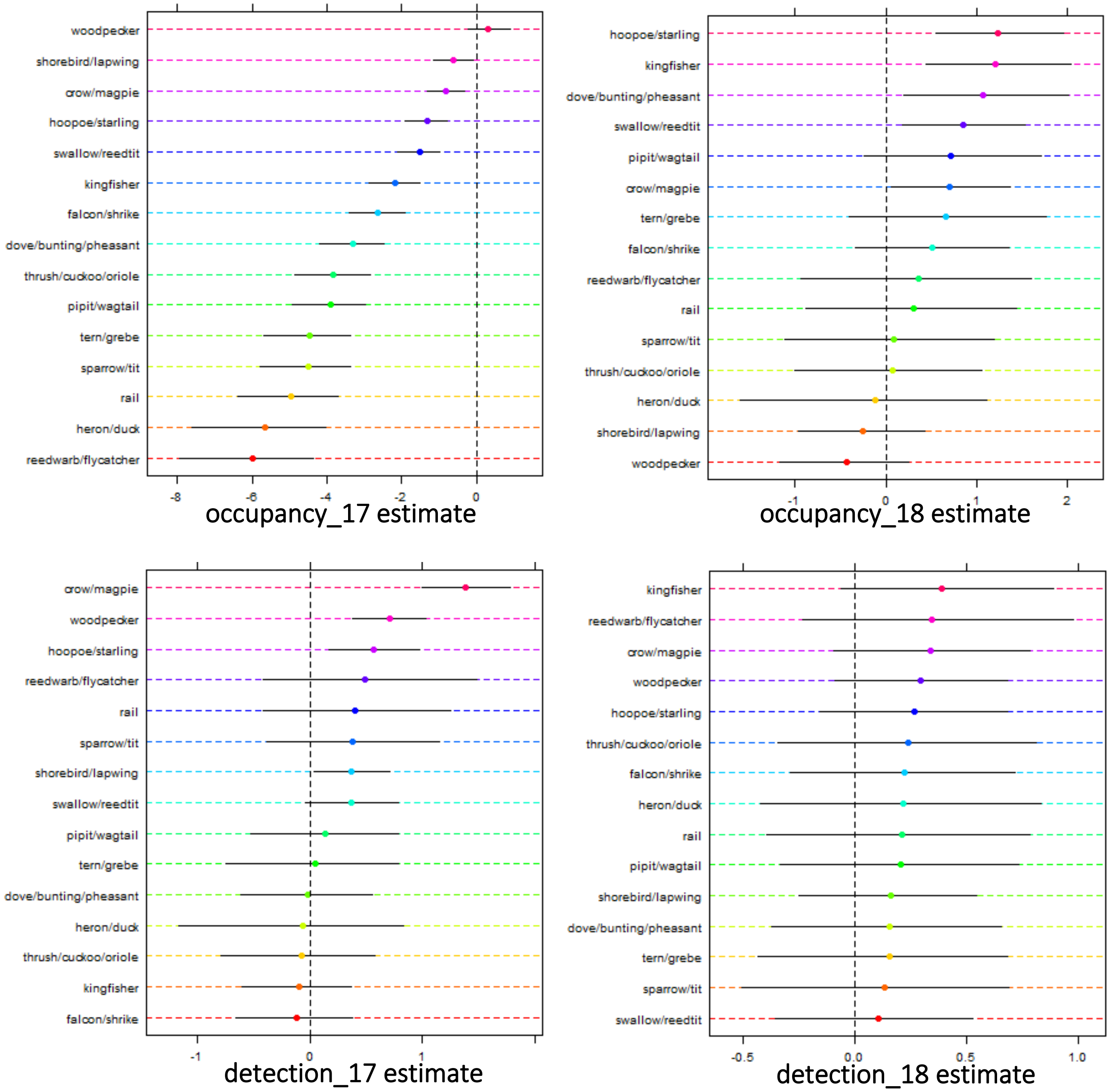


Figure 54: Dot plots showing the group-specific mean estimates with 90% credible intervals for occurrence and detection.

Finally, we examined the relationship between occurrence probability for each functional group and the landscape metrics and found differing effects (Figure 55). Looking at the most abundant bird groups (>30), half of the groups had occupancy probabilities higher than the mean across all crop diversity levels. Crow/magpie and shorebird/lapwing in particular had the largest increases in occupancy probability as crop diversity increased. The dove/bunting/pheasant group occupancy increased with mean patch size and the other groups were negatively impacted. The aggregation index significantly increased occupancy for shorebird/lapwings, while the other groups had negative relationships. Percent natural landcover positively impacted the occupancy of the shorebird/lapwing, falcon/shrike, and dove/bunting/pheasant groups while negatively impacting the crow/magpie and swallow/reedtit groups. The relationships with soybean area and corn were similar, with the shorebird/lapwing group increasing in occupancy more with soybean percentage. Increasing rice area decreased occupancy probability for the swallow/reedtit, shorebird/lapwing, and falcon/shrike and increased for the dove/bunting/pheasant and crow/magpie groups (though the rice parameter was only significant for the crow/magpie group).

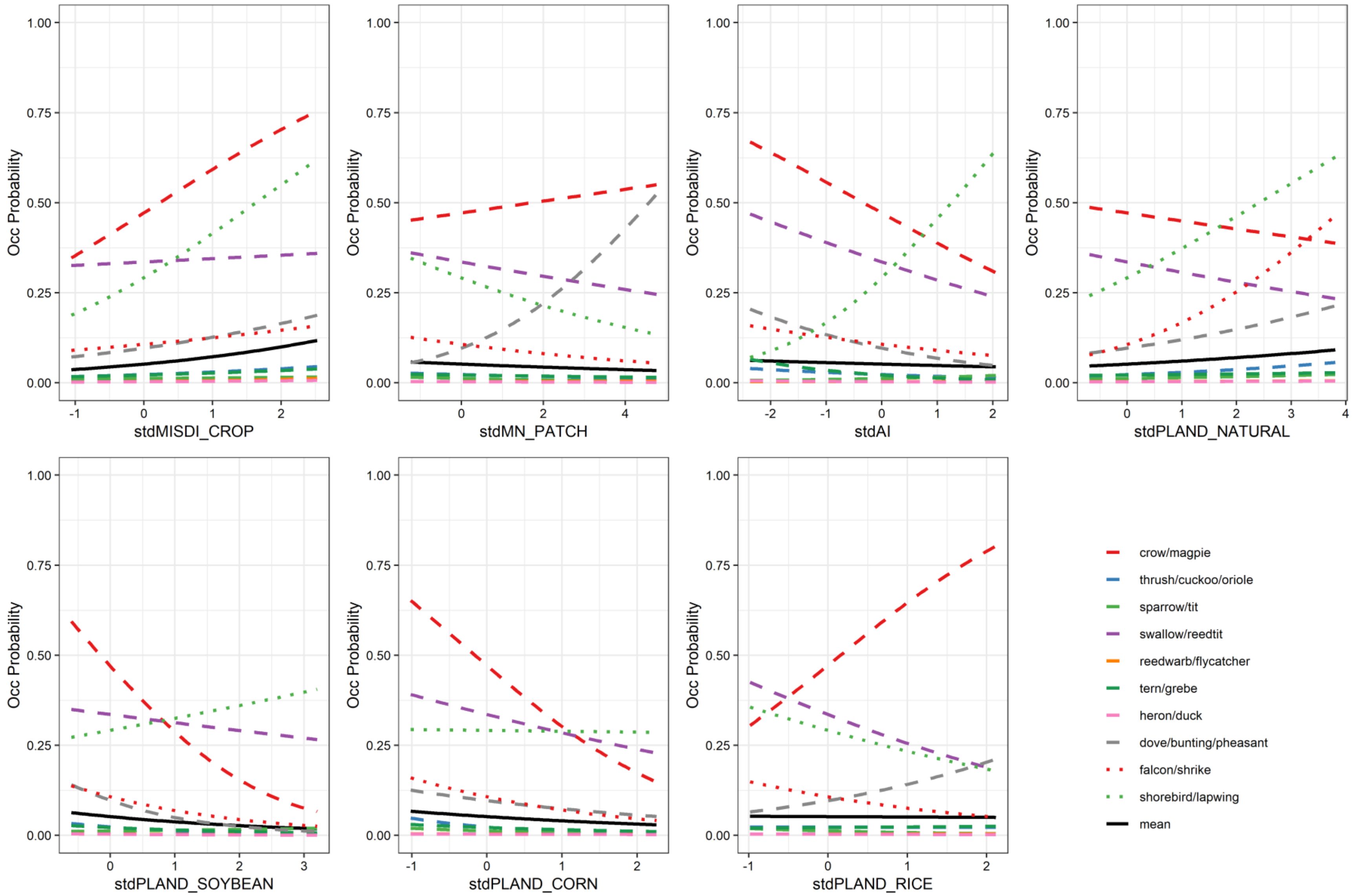


Figure 55: All landscape metric relationships with occurrence probability for the most abundant groups (>30 observations)

5.4 Discussion & Conclusion

We found that different bird families and functional groups have different relationships to landscape structure. Our results show that crop diversity (MSIDI of corn, rice, soybean, and ‘other crop’) had the most substantial impact on bird diversity. Higher crop diversity increased mean occupancy for nearly all bird families and functional groups and was significant for many of the rarer families and functional groups, particularly for the latter. Of the five groups that had fewer than 30 observations, four had significant, positive parameter estimates for crop diversity (rail, pipit/wagtail, hoopoe/starling, kingfisher).

We saw differences between our taxonomic and functional groupings when modeling occupancy. For crop diversity, a majority of the functional groups were significantly more likely to occur as crop diversity increased compared to the taxonomic model. This disparity between taxonomic and functional highlights that fact that landscape-biodiversity relationships are both complex and context-dependent as well as heavily influenced by the method used to define functional diversity (Hevia et al., 2016; M.-B. Lee & Martin, 2017). Several studies corroborate our finding that a positive relationship between crop diversity and biodiversity exists (M. B. Lee & Goodale, 2018; D. Li et al., 2020; Lindsay et al., 2013) yet others found no effect in agricultural systems (Fahrig et al., 2015; Martin et al., 2020; Redlich et al., 2018).

We also found the percent of natural area (i.e., forest, grassland, and wetland) was not nearly as important as we expected. The amount of natural landcover was significant in some cases, but the effect size was often similar to or smaller than the other percent area metrics. A few groups even had negative estimates for natural area (e.g., Corvids). Only a handful of bird groups had significantly positive parameter estimates/credible intervals. This may be due to an under sampling of natural habitat, though range of percent natural area (250m) was 0.027-100%.

The metrics in our model that were more configurational in nature (mean patch area & aggregation) were not as significant for the bird groups in our dataset. This is in contrast with several studies that report mean patch size as a significant predictor of biodiversity in agricultural landscapes (Fahrig et al., 2015; Martin et al., 2020). However, it should be noted that we limited the potential effect of patch size by using a maximum extent of 1000m. It is possible there would be a significant effect if mean patch size were calculated at a larger extent.

All significant parameter estimates for percent corn and soybean were negative, while rice area only had a positive, significant estimate for Corvidae and the crow/magpie group. At the taxonomic level, soybean area had more significantly negative estimates (six families) compared to corn (one family). Furthermore, the six families that had significant, negative coefficient estimates for soybean area were some of the most commonly observed in our sample (i.e., >28 observations). The disparity between soybean and corn’s impact lessened when looking at functional group occupancy. Soybean was negatively associated with two groups and corn with one, as well as one shared between the two (crow/magpie). A possible explanation for this difference is that the lack of perching opportunities for birds in soybean fields. For example, shrikes (Laridae family) were often observed perching on corn stalks or trees while scanning for prey. That is not possible in a landscape dominated by soybean fields.

Given that rice area had no negative parameter estimates, this implies landscapes completely dominated by rain-fed crops are substantially less habitable than those dominated by paddy rice, potentially due to some of the more biodiversity-friendly practices related to rice cultivation (e.g., flooding for weed control, rice-fish cultures)(Amira et al., 2018; Y. Sun et al., 2015; C. Wood et al., 2017). Further validation of this model would enhance its predictive ability as well as provide insight for agroecosystems with similar landscape characteristics (i.e., paddy rice, high heterogeneity).

Overall, we found that different crop types support different bird families and groups and that, in general, landscapes that have high crop diversity (in terms of both number of crops and relative abundance) maximized occupancy for the most bird species. This suggests that monocultures, even at the relatively fine scale of 500m, decrease a landscape’s ability to support bird biodiversity.

Therefore, in the context of global trade impacts, if a region that was only growing soybeans converted some land to different crops, then there may have been a benefit to bird biodiversity. However, we observed that the more highly impacted region had less crop diversity after experiencing soybean area loss. Given the prevalence of small-scale farming in Heilongjiang, it is more likely that soybean patches within a crop mosaic (with many crops and heterogenous crop field sizes) were converted to more profitable crops, thus decreasing overall crop diversity. In addition to decreasing occupancy for all bird families/groups, this likely had an outsized, negative impact on rarer bird functional groups (which may have consequences for the ecosystem as whole). That being said, if soybean area was converted to rice, the detrimental impacts to biodiversity may have been less severe compared to corn as rice had no significantly negative parameter estimates for occupancy.

As these results show, cultivated land is more than capable of supporting a wide array of bird species. Furthermore, while many of the species in this agroecosystem are considered common, many are experiencing decreasing populations. For example, the Northern Lapwing (*Vanellus vanellus*) is a common sight in Heilongjiang landscapes growing rice, corn, and soybeans and is considered 'near threatened' by the IUCN red list. Bird conservation in this region does not necessarily need to focus on increasing natural habitat, but rather, maintaining the heterogeneity of the landscape, including the diversity of crops grown, at a relatively fine scale. Challenges to the idea that farmland cannot be wildlife habitat are essential for the future sustainability of global food systems and biodiversity, in China and across the globe (Kremen & Merenlender, 2018; L. Li et al., 2020). As farmers become more involved in global markets, their practices often scale-up to reduce costs and maximize yields, resulting in more monocultural landscapes. Preserving the crop diversity of farmland, especially in the case of a landscape that combines rain-fed crops and paddy rice, will be vital for many of the bird species that rely on crop mosaics.

APPENDIX

Model Code for WinBUGS:

```
model{

# Define prior distributions for community-level model parameters
omega ~ dunif(0,1)

# grand means
mean ~ dunif(0,1)
mu.u0 <- log(mean) - log(1-mean)

mean2 ~ dunif(0,1)
mu.u1 <- log(mean2) - log(1-mean2)

mean3 ~ dunif(0,1)
mu.v0 <- log(mean3) - log(1-mean3)

mean4 ~ dunif(0,1)
mu.v1 <- log(mean3) - log(1-mean3)

mu.a1 ~ dnorm(0, 0.001) # MSIDI_CROP
mu.a2 ~ dnorm(0, 0.001) # MN_PATCH_ALLCLASS
mu.a3 ~ dnorm(0, 0.001) # AI_ALLCLASS
mu.a4 ~ dnorm(0, 0.001) # PLAND_NATURAL
mu.a5 ~ dnorm(0, 0.001) # PLAND_SOYBEAN
mu.a6 ~ dnorm(0, 0.001) # PLAND_CORN
mu.a7 ~ dnorm(0, 0.001) # PLAND_RICE
mu.a8 ~ dnorm(0, 0.001) # LONGITUDE
mu.b1 ~ dnorm(0, 0.001) # SUNRISE

tau.u0 ~ dgamma(0.1,0.1)
tau.u1 ~ dgamma(0.1,0.1)

tau.v0 ~ dgamma(0.1,0.1)
tau.v1 ~ dgamma(0.1,0.1)

tau.a1 ~ dgamma(0.1,0.1)
tau.a2 ~ dgamma(0.1,0.1)
tau.a3 ~ dgamma(0.1,0.1)
tau.a4 ~ dgamma(0.1,0.1)
tau.a5 ~ dgamma(0.1,0.1)
tau.a6 ~ dgamma(0.1,0.1)
tau.a7 ~ dgamma(0.1,0.1)
tau.a8 ~ dgamma(0.1,0.1)
tau.b1 ~ dgamma(0.1,0.1)

# Species loop (i)
for (i in 1:(n+nzeroes)) {

# Create priors for species i from the community level prior distributions
    w[i] ~ dbern(omega)
    u0[i] ~ dnorm(mu.u0, tau.u0)
    u1[i] ~ dnorm(mu.u1, tau.u1)

    v0[i] ~ dnorm(mu.v0, tau.v0)
    v1[i] ~ dnorm(mu.v1, tau.v1)
```

```
    a1[i] ~ dnorm(mu.a1, tau.a1)
    a2[i] ~ dnorm(mu.a2, tau.a2)
    a3[i] ~ dnorm(mu.a3, tau.a3)
    a4[i] ~ dnorm(mu.a4, tau.a4)
    a5[i] ~ dnorm(mu.a5, tau.a5)
    a6[i] ~ dnorm(mu.a6, tau.a6)
    a7[i] ~ dnorm(mu.a7, tau.a7)
    a8[i] ~ dnorm(mu.a8, tau.a8)

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

## Likelihood ##

# Create a loop to estimate the Z matrix (true occurrence for species i at
point j)

# Point loop (j)
    for (j in 1:J) {
                    logit(psi[j,i]) <- u0[i] + u1[i] * Year[j] +
                    a1[i]*std.MSIDI_CROP[j] + a2[i]*std.MNPATCH_ALLCLASS[j] +
                    a3[i]*std.AI_ALLCLASS[j] + a4[i]*std.PLAND_NATURAL[j] +
                    a5[i]*std.PLAND_SOYBEAN[j] + a6[i]*std.PLAND_CORN[j] +
                    a7[i]*std.PLAND_RICE[j] + a8[i]*std.long[j]

                    mu.psi[j,i] <- psi[j,i]*w[i]
                    Z[j,i] ~ dbern(mu.psi[j,i])

#Create a loop to estimate detection for species i at point k during sampling
period k
        for (k in 1:K[j]) {
                            logit(p[j,k,i]) <-  v0[i] + v1[i] * Year[j] +
                            b1[i]*std.sunrise[j,k]

                            mu.p[j,k,i] <- p[j,k,i]*Z[j,i]
                            X[j,k,i] ~ dbern(mu.p[j,k,i])

                } #k
       } #j

} #i

# Sum all species observed (n) and unobserved species (n0) to find the
# total estimated richness
n0 <- sum(w[(n+1):(n+nzeroes)])
N <- n + n0

# Create a loop to determine point level richness estimates for the
# whole community and for subsets or assemblages of interest.
for(j in 1:J){
Nsite[j]<- inprod(Z[j,1:(n+nzeroes)],w[1:(n+nzeroes)])
} #j
```

CHAPTER 6: SYNTHESIS

This dissertation is part of a larger project aimed at investigating the socioeconomic and environmental impacts of global soybean trade across distances using the telecoupling framework. Broadly, the work in this dissertation explores biodiversity impacts of telecoupling. Furthermore, this study goes beyond quantifying environmental impacts solely as land use change with assumed biodiversity implications by translating landscape change due to global trade to explicit consequences for bird diversity. In chapter two, a systematic review of the distant drivers of global biodiversity change was conducted. After conducting full-text analyses of 131 studies and synthesizing impacts of ten types of distant drivers and seven taxonomic groups, negative impacts on biodiversity were found to be the most frequent outcome reported. Some instances of beneficial and species composition change were observed as well. The most common type of drivers studied were trade and tourism. Despite containing some of the world's most important biodiversity hotspots, substantially fewer studies were conducted in Africa and Oceania, compared to other developed continents. This synthesis highlights the need for more biodiversity research that empirically assesses biodiversity change in the context of globalization.

Chapter three reports on the process of creating the landcover maps used to inform the landscape variables used in later chapters. Studies that use landscape characteristics to explain biodiversity patterns are only as good as the landcover maps input. Of the landcover maps available to researchers, many have significant limitations (coarse spatial resolution, limited temporal and geographic availability, class schemes that are too generalized) in addition to the inherent inaccuracies common to all remotely sensed products. The resulting landcover map had a fine enough spatial resolution to capture the heterogeneity of the farming landscape in

Heilongjiang and achieved a high level of accuracy by utilizing the large library of remotely sensed data and computing power of Google Earth Engine.

The fourth chapter contributes to the scientific community's understanding of how landscape structure mediates the biodiversity of agroecosystems and places these relationships in the context of global trade impacts. In order to assess biodiversity and landscape relationships at the functional level, life history and morphological traits were collected for each bird family observed in this study, allowing for the calculation of community functional metrics as well as the creation of functional groups. After analyzing the relationships of several landscape metrics with taxonomic and functional bird community diversity metrics, significant correlations between landscape structure and biodiversity were found. Crop diversity, natural landcover, and edge metrics were positively correlated with richness while aggregation and rain-fed crop (i.e., corn and soybean) area were both negatively related. No relationship with mean patch size was found, contrary to other studies' findings. This disagreement is likely due to inherent differences between agroecosystems that primarily cultivate rain-fed crops (i.e., corn, soybean) and those that farm paddy rice. In the context of global trade impact, crop diversity appears to be negatively impacted as farmers convert soybean fields to other crops, such as corn and rice. However, growing paddy rice versus a crop such as corn may be beneficial for functional diversity as different bird groups and community traits are associated with flooded rice paddies. As growing food security challenges necessitate the use of land for food production, understanding how to design these landscapes to bolster biodiversity will be necessary for the health of ecosystems across the world.

The fifth and final chapter models the relationship between landscape structure and group-specific occupancy at both taxonomic and functional levels. Using a hierarchical modeling structure and Bayesian analysis, estimates of landscape metric effects were obtained for each group and at the community-level. Overall, crop diversity significantly increased occupancy of birds for taxonomic and functional groups. However, the percentage of natural landcover was not as important as expected, and metrics related to landscape configuration (i.e., mean patch size, aggregation index) had fewer significant impacts on occupancy. The effects of rice, corn, and soybean area differed as well. Increases in rice area were not detrimental to bird occupancy whereas increases in corn and soybean area had significant negative effects for a number of bird families and functional groups. Soybean area in particular exhibited more significant negative associations with bird families, which suggests that conversion away from soybean due to global trade in a soybean monoculture may have been beneficial for some bird species, especially when those fields were converted to paddy rice. However, in the typical heterogeneous landscape of Heilongjiang farmland, it is more likely that the conversion of soybean fields to another crop decreased the crop diversity of the landscape, which was a much more important contributor to bird occupancy. By combining remotely sensed landscape characteristics with biodiversity observations, this chapter provides a better understanding of how global trade and land use change may ultimately impact agroecosystems and can help inform farmland biodiversity conservation strategies.

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