**CHAPTER 4**

**Comparison of avian guild richness, species abundance, and nest success in   
harvested and non-harvested forested landscapes**

**INTRODUCTION**

**Long-term changes in bird populations**

In the forests of the eastern United States, landscapes have been altered significantly in the last century, with tradeoffs associated with different forest bird guilds. Bird species that breed in early-successional forest habitat, such as chestnut-sided warblers (*Setophaga pensylvanica*), eastern towhees (*Pipilo erythrophthalmus*), and yellow-breasted chats (*Icteria virens*), are strongly associated with herbaceous or shrubby areas in the stand initiation/establishment or regeneration phase, with low canopy basal area (Sheehan et al. 2014). In contrast, bird species that breed in mature forest habitat, such as blue-headed vireos (*Vireo* *solitarius*), ovenbirds (*Seiurus aurocapilla*), and wood thrushes (*Hylocichla mustelina*), are associated with late-successional stands in the canopy transition or old-growth/gap dynamics stages, with high canopy basal area (Sheehan et al. 2014). Thus, there are differential benefits to early-successional vs. mature forest birds when there are changes in composition (i.e., amount of different habitat patch types without regard to spatial attributes) and configuration (i.e., spatial characteristics of individual habitat patches, requiring spatial information and usually aggregated across patches at the class or landscape level) of forested landscapes. Historically, such changes in the eastern United States over hundreds of years have comprised a loss of old-growth forests followed more recently by a decrease in age-class diversity and structural complexity within second-growth forests (e.g., Schulte et al. 2007) and loss of early-successional habitats dominated by grass, shrubs, or young trees (Askins 2001, Trani et al. 2001). Concomitantly, there have been severe and widespread population declines in shrubland-dependent species (Litvaitis 1993, Hunter et al. 2001, DeGraaf and Yamasaki 2003), with the removal of early-successional habitat from the landscape thought to be the primary reason driving those trends (Kelley et al. 2008). Thus, optimizing diversity across the forest-associated bird guilds likely calls for mosaic landscapes that contain a variety of forest age classes or successional stages (Loehle et al. 2005, Mitchell et al. 2008).

**Bird responses to harvest intensity**

Increasing variation in composition and configuration within forested landscapes can be accomplished by timber management or silvicultural practices. For instance, harvesting forests can lead to patches that are distinct, more fragmented, less connected, and smaller (Boucher et al. 2015). These forests also contain more edge area and are subjected to more frequent and more severe uniformly-sized disturbance from periodic, repeated harvest regimes. Within stands, even-aged silvicultural systems (e.g., clearcuts) can create homogenous vertical and horizontal structure (Kuuluvainen et al. 1996), but at a landscape scale, timber rotation length can change the age-class distribution of forests, increasing the proportions of early-successional or young forest (Hejl et al. 1995). In contrast, non-harvested forested landscapes (i.e., no timber harvest within >80 years) are usually characterized by occasional large-scale disturbances and frequent small-scale disturbances, which allow for a finer-grained mosaic of different successional phases (Bengtsson et al. 2000). Thus, landscape-scale structural heterogeneity is generally higher in harvested forests managed in an even-aged system whereas within-stand structural heterogeneity might be higher in non-harvested landscapes (Dettki and Esseen 1998), particularly those subject to historic natural disturbance regimes (e.g., fire). Ultimately, harvests increase the availability of early-successional forest habitat, which leads to increased abundance of early-successional and some generalist bird species (Duguay et al. 2001, McDermott and Wood 2009). Especially in forest-dominated landscapes, timber harvest can be a useful management tool to support a diversity of bird species.

Whether within a harvested or non-harvested landscape, birds are sensitive to landscape change in terms of composition. Several studies suggest that songbird abundance in forested landscapes is influenced more by the quantity of different habitats in the landscape rather than the spatial arrangement of those habitats (e.g., Lichstein et al. 2002). Higher proportions of early-successional habitats in harvested landscapes can also result in significantly higher abundances of early-successional and generalist bird species (Drapeau et al. 2000). A study from a harvested forest found that certain forest interior-edge (e.g., black-capped chickadees [*Poecile atricapillus*], dark-eyed juncos [*Junco hyemalis*], eastern towhees) and forest interior (e.g., ovenbirds, black-throated blue warblers [*Setophaga caerulescens*], scarlet tanagers [*Piranga* *olivacea*]) species are sensitive to both landscape composition and landscape configuration metrics, such as contrast-weighted edge density, number of patches, and percent core area (Weakland 2000). Other studies also linked mature forest bird species with landscape composition (Becker et al. 2012), as well as amount of core area, area-weighted mean shape index (i.e., metric of the shape complexity of patches of all cover types derived by measuring the perimeter-to-area ratio weighted by the size of its patches), and interspersion-juxtaposition index (i.e., a measure of the intermixing of cover types relative to the maximum intermixing possible) (Becker 2010).

In addition to the amount of habitat present in the landscape, landscape configuration features, such as habitat patch area, are important predictors of bird abundance (Crozier and Niemi 2003). Other aspects of landscape configuration include core area and edge density. Howell et al. (2000) found that the abundances of Acadian flycatchers (*Empidonax virescens*), red-eyed vireos, scarlet tanagers, and yellow-throated vireos (*Vireo flavifrons*) were all positively associated with mean mature forest patch size; the abundances of Carolina wrens (*Thryothorus ludovicianus*) and northern parulas (*Setophaga americana*) were positively related to mature forest core area; and the abundance of blue-gray gnatcatchers (*Polioptila* *caerulea*) responded negatively to edge density, while abundances of blue jays (*Cyanocitta cristata*), brown-headed cowbirds (*Molothrus ater*), and eastern wood-pewees (*Contopus virens*) responded positively to edge density. Early-successional and shrubland bird abundance is also related positively to patch size of their corresponding habitat (DeGraaf and Yamasaki 2003, Chandler et al. 2009, Lehnen and Rodewald 2009, Shake et al. 2012). For instance, Askins et al. (2007) found that eastern towhees and shrubland generalists are found in higher abundances in larger forest openings. On the other hand, the size of early-successional habitat patches can negatively affect mature forest birds. For instance, forest-interior and interior-edge guild abundances decreased after specific thresholds in timber harvest within a heavily forested central Appalachian landscape (Becker et al. 2011). Another study found that 0.4-ha clearcut openings resulted in the movement of several forest-interior species away from openings and subsequently decreased abundance in and adjacent to openings (Germaine et al. 1997).

Landscape composition and particularly configuration can affect nest success. At a fundamental level, nesting songbird distributions can be dictated by habitat cover within the landscape (Drolet and Desrochers 1999). Composition within forested landscapes further influences avian nesting success by altering interactions between nest predators and nesting birds (Rodewald and Yahner 2001). Configuration can also affect nest survival, as nest predators concentrate near edges (Gates and Gysel 1978), so increased edge density or the abrupt creation of edge due to timber harvest in a managed forest could lower nest success. Nest success of wood thrush in the Monongahela National Forest in West Virginia was found to be positively related to mean shape indices and mean patch fractal dimension of mature forest (both indicative of higher complexity of mature forest patch shapes) and negatively related to an interspersion-juxtaposition index (i.e., measure of the relative interspersion of mature forest patches) and proportion of open habitat (Williams 2002).

Avian population and community processes operate across a broader scale than local patches (Bennett et al. 2004). Patterns of bird species composition and diversity are related to landscape composition, such as proportions of forest types and ages (Drapeau et al. 2000, Carrara et al. 2015), and landscape configuration, such as patch sizes and edge density. Greater landscape age heterogeneity is associated with greater overall species richness (Loehle et al. 2005, Mitchell et al. 2008). In addition, in a study of the effects of group-selection opening size on breeding bird habitat use in a bottomland forest, species richness in 0.06-, 0.13-, 0.26-, and 0.5-ha openings increased as opening size increased, due to the increased use of larger openings by early-successional and edge-associated species (Moorman and Guynn, Jr. 2015). Furthermore, mature forest edge is positively associated with generalist richness but negatively with specialist species richness (Jones et al. 2000). Beyond species richness, landscape changes can ultimately result in shifts in community composition and diversity (i.e., turnover) (Parody et al. 2001), as conversion of guild-specific preferred habitat to less suitable habitat can lead to reductions in guild richness (Aratrakorn et al. 2006, Zurita et al. 2006). In summary, landscape structure may affect forest bird assemblages through effects on both total number of species and on temporal rates of community composition change.

**Knowledge gap**

Forest managers often aim to balance or combine the economic benefits of timber harvest with the maintenance of wildlife habitat, biodiversity, and ecosystem function. Forest songbirds exhibit varying responses to timber harvest (Thompson et al. 1992, Annand and Thompson III 1997, Robinson and Robinson 1999), which can alter forest composition, configuration, and connectivity on a landscape scale (e.g., Spies et al. 1994). Thus, timber management can be potentially used as a landscape-level tool to promote both early-successional and mature forest songbird populations and diversity (Petit et al. 1995). However, we have an incomplete understanding of how birds respond over time to landscape-level factors. Except for a few recent studies, such as Kellner et al. (2019), previous studies have traditionally focused on forest patches in agricultural landscapes (e.g., Freemark and Merriam 1986, van Dorp and Opdam 1987, McIntyre 1995, Villard et al. 1999, Lee et al. 2002) or in landscapes that are either exclusively harvested or non-harvested (not both simultaneously), or they examined avian responses at control and harvested sites on limited (i.e., stand- and patch-level) scales (e.g., (Crawford et al. 1981, DeGraaf et al. 1998, McDermott et al. 2011), neglecting landscape-level trends. Furthermore, these studies tend to be short-term, lasting 1–3 years, and may not reflect the full temporal response to the management practices under study (Sallabanks et al. 2000, Loehle et al. 2005). Thus, long-term research is needed to investigate the response of bird communities to landscape-level factors in both harvested and non-harvested forests through time. Specifically, I aim to answer the following questions: (1) How do early-successional and forest-interior breeding birds respond to landscape composition and configuration over time, and (2) are those relationships and trends modified by the intensity (i.e., type) of timber harvest in the surrounding landscape?

**Purpose, objectives, and hypotheses**

The purpose of this study was to quantify long-term avian responses to landscape-scale forest management and compare changes over time in avian diversity, abundance, and population dynamics from two Central Appalachian forested landscapes that varied in timber harvest intensity. My specific objectives were to examine the influence and effect of interactions between time and landscape-level timber harvest intensity on breeding season songbird guild richness, focal species abundance, and focal species nest success. I focused on 2 landscapes with diverging forest management prescriptions: (1) an actively harvested landscape with >70% of its area experiencing diameter-limit harvest, two-age harvest, or clear-cutting during the study period (1993–2009), and (2) a minimally harvested landscape with <1% of its area experiencing two-age harvest or clear-cutting approximately 10–15 years prior to the study period.

In this study, I tested the hypothesis that long-term temporal trends in forest songbird communities and populations during the breeding season are mediated by landscape-level forest management. I predicted that trends over time in diversity, abundance, and nest success would vary by guild designation and landscape (i.e., level of timber harvest intensity). For example, in the actively harvested landscape, I expected that early-successional and edge-associated species would respond positively over time, whereas forest-interior and forest-gap species would respond negatively over time. In contrast, in the minimally harvested landscape, I expected that early-successional and edge-associated species would respond negatively over time, while forest-interior and forest-gap species would show little to no response. Taking a holistic approach, I assessed the statistical significance and effect sizes of interactions between time and landscape-level timber harvest intensity for overall species richness, the number of species belonging to 4 habitat guild designations, the abundance of 14 focal songbird species, and the nest success of 6 focal songbird species (Table 1).

**METHODS**

**Study area**

Sampling points and nest search plots for this study were spread throughout 2 study areas within the Central Appalachians region (Figures 1–3). I used data from a total of 1,186 sampling points and 50 nest search plots (Figures 2–3), consisting of 166 sampling points and 20 nest search plots in the actively harvested MeadWestvaco Wildlife and Ecosystem Research Forest (WERF), which is located in Randolph County, West Virginia, and 1020 sampling points and 30 nest search plots in the minimally harvested Monongahela National Forest (MNF), which encompasses portions of nine counties (Preston, Tucker, Grant, Randolph, Pendleton, Pocahontas, Webster, Nicholas, and Greenbrier) in eastern West Virginia. All sampling points used in this study were located in forest stands that experienced varying levels and types of recent or ongoing timber harvest (ranging from no harvest to clear-cutting), and distances between sampling points were at least 200 m.

Research in the actively harvested WERF was conducted from 1996–1998 (Weakland 2000), 2001–2003 (Dellinger 2005), and 2007–2009 (Becker 2010). The WERF encompasses 3,080 ha and was established in 1994 by the Westvaco Corporation to study the effects of industrial forest management practices on ecosystem processes and wildlife within a primarily 70–90 year-old even-aged mature forest. Located within the Central Appalachians (Allegheny Mountains) physiographic province, regional topography within the WERF consists of narrow valleys with small, high-gradient streams and broad ridges oriented south-southwest to north-northeast (Becker et al. 2011). Annual average precipitation is >160 cm per year (Strausbaugh and Core 1977), and elevation ranges from 734–1,180 m. Vegetation communities in the WERF are variable across that elevational gradient. At high elevations (>1,000 m), red spruce (*Picea rubens*) and eastern hemlock (*Tsuga canadensis*) dominate. At mid-elevations (850–1,000 m), northern hardwoods such as red maple (*Acer rubrum*), American beech (*Fagus grandifolia*), and black cherry (*Prunus serotina*) are most prevalent. Meanwhile, low-elevation sites (<850 m) consist of cove hardwood and mixed mesophytic plant communities (northern red oak [*Quercus rubra*], black birch [*Betula lenta*], and tulip-poplar [*Liriodendron tulipifera*]) and xeric oak-hickory communities (black oak [*Quercus velutina*], scarlet oak [*Q. coccinea*], and hickory [*Carya* spp.]). Non-forest cover in the study area is limited to grassy cover along road edges, gas well openings, and log landings.

Research in the minimally harvested MNF was conducted from 1993–1994 (Nichols), 1995–1996 (Duguay), 1996–1997 (Demeo), 1998–2000 (Williams), and 2001–2009. The MNF was placed under federal protection in 1920 and encompasses nearly 688,000 ha, of which 54% (371,906 ha) is owned and overseen by the U.S. Forest Service. The MNF stretches across a latitudinal range of nearly 200 km and lies within two physiographic provinces, the Central Appalachians (Allegheny Mountains) and the Ridge and Valley. The eastern section of the Monongahela National Forest, which overlaps the Ridge and Valley physiographic province, lies in the rain shadow of the Allegheny Mountains, so it receives significantly less precipitation (~75 cm/year) compared to the rest of the forest, which experiences 115–150 cm/year (Clarkson 1966). Elevation within the MNF ranges from 275–1,480 m. In terms of forest composition, the MNF is comprised primarily of 70–100 year-old stands with high regional tree diversity and 4 major forest zones (mixed mesophytic, northern hardwoods, red spruce, and dry oaks) (McCay et al. 1997, DeMeo 1999). Mixed mesophytic forests are present at low elevations (<900 m), with northern red oak, sugar maple (*Acer saccharum*), hickory, and tulip-poplar as the dominant species (Madarish et al. 2002). At increasing elevations, there is a transition in stand dominance to northern hardwoods, including American beech, sugar maple, and black cherry (*Prunus serotina*) (Stephenson 1993). At the highest elevations (>1,150 m), remnant boreal forest ecosystems consist of red spruce. In the eastern MNF, dry oaks are common in the Ridge and Valley area, consisting of white (*Q. alba*), chestnut (*Q. prinus*), scarlet, and black oaks, as well as pines (*Pinus* spp).

**Harvest history**

During its establishment in 1994, the WERF was comprised of secondary forests that were established by natural regeneration following large-scale logging from 1916–1928 (Keyser and Ford 2005). Timber had been sporadically thinned and harvested since the 1930’s, resulting in numerous logging roads and skidder trails transecting the forest. Since its initial establishment, much of the WERF had been actively managed using even-aged timber harvesting through clear-cuts, shelterwood cuts, and uneven-age or partial harvesting via single-tree selection and high-grade harvests of mature sawtimber (Dellinger et al. 2007*b*). Prior to 1997, several timber harvests had been conducted, including diameter-limit harvests, two-age harvests, and regeneration (seed-tree) harvests, but the majority of the WERF remained mature deciduous or mixed forest (Figure 4). From 1997–1998, additional forest stands were harvested using a variety of methods (e.g., diameter-limit harvests, two-age harvests, regeneration harvests, clear-cuts). More stands were harvested throughout the years, and nearly 50% of the WERF had experienced some type of harvest by 2003 (Figure 4). In 2007, management shifted to primarily uneven-aged techniques, and by 2009, at least 70% of the WERF had been harvested to some degree (Figure 4). Thus, the WERF served as an actively harvested landscape for this study.

The MNF is comprised of mature, second-growth Appalachian hardwood forests. A 100–120 year timber harvest rotation applies to most areas of the MNF not designated as Wilderness Areas, and the vast majority of the MNF had not been harvested nor majorly disturbed within 50 years prior to the study period. Therefore, most of the sampling points within the MNF were located in relatively intact areas with high (>60%) core area (DeMeo 1999). A small subset of the sampling points was in forest stands in the Cheat and Greenbrier Ranger Districts of the MNF that had experienced two-age harvest or clear-cutting between 1979 and 1986 for a study on the effects of two-age harvests (Miller et al. 2006). However, the area of the harvested stands accounted for <1% of the total area of public lands in the MNF. Thus, the MNF served as a minimally harvested landscape for this study.

**Guild designations**

To compare temporal trends for overall species richness and guild richness in the actively harvested landscape and the minimally harvested landscape, I considered a subset of the 114 total avian species that were detected across all surveys in all years from the 2 study areas. Specifically, I limited the richness analyses to 62 passerine and near-passerine species (see Appendix A for full list) with breeding ranges that encompassed the 2 study areas and that had ≥10 detections. I also excluded wetland-associated songbirds (e.g., red-winged blackbirds [*Agelaius phoeniceus*]) because they were incidental to the focal habitat types, as well as corvids and waterthrushes because they are not well-sampled with breeding songbird point count surveys.

Habitat-related guild designations for the 62 songbird species were assigned based on breeding habitat and comprised 4 categories (Appendix A): (1) early-successional and edge-associated (i.e., primarily breed or found in grasslands, shrub/scrub, or young forest; or along forest edges, such as the interface of early-successional and mature forest); (2) forest-interior (i.e., generally breed or found in the core area of mature forest); (3) forest-gap (i.e., generally breed or found in or near small forest gaps within the core area of mature forest); and (4) forest generalist (i.e., associated with forest but no preference for early-successional vs. mature forest).

**Focal species**

To compare temporal trends in focal species abundance in the actively harvested landscape and the minimally harvested landscape, I selected a total of 14 songbird species across the 4 guild designations (Table 1): 3 early-successional and edge-associated species, 4 forest-interior species, 4 forest-gap species, and 3 forest generalist species. Species selection was based on relative frequency; for each guild designation, I included the 3 species with the highest relative frequency. For the forest-interior guild and forest-gap guild, I additionally included a species of regional conservation concern with the highest relative frequency.

To assess temporal trends in focal species nest success in the actively harvested landscape and the minimally harvested landscape, I selected 6 species from the 14 songbird species listed above as focal species for abundance analyses (Table 1): 2 early-successional and edge-associated species, 3 forest-interior species, and 1 forest-gap species. Species selection was based on sample size; these were the 6 species that had sample sizes of at least 70 total nests across the 2 study areas and a minimum of 15 nests from each study area.

**Bird count data**

Avian point count survey data were collected at the 2 study areas from 1996–1998, 2001–2003, and 2007–2009 at 166 WERF sampling points and from 1996–2009 at 1020 MNF sampling points. In the WERF, point count surveys were conducted within a 50-m fixed radius at locations selected systematically from available points on a 241 x 241 m forest inventory grid (Figure 2) established in 1995 by Westvaco Forest Resources (prior to extensive timber harvesting). An average of 110 points were surveyed each year, and locations were mostly consistent across time periods. In the MNF, point count surveys were conducted along 109 generally extensive linear transects (up to 2,500 m in length) with 10–12 sampling points (Figure 3). Of the 109 total transects, at least 44 transects were oriented at right angles to contours to capture maximum variation in elevation and landforms.

Avian point count surveys were not collected every year at all sampling points. The number of years of data associated with each sampling points ranged 2–9 years (mean = 5.9 ± 2.5 years) in the WERF and 1–12 years (mean = 4.0 ± 2.8 years) in the MNF. Within a year that avian point count survey data were collected, the number of repeated visits (i.e., replicate surveys) ranged from 1–3 visits (mean = 2.0 ± 0.2 visits) in the WERF and 1–4 visits (mean = 1.3 ± 0.5 visits) in MNF. I included all replicate surveys per sampling point per year in my data analyses, for a total of 14,504 replicate surveys across 4,999 stacked site × year combinations.

At both study areas, avian point count surveys were conducted from mid-May to early July (i.e., during the bird breeding season) and consisted of 10-minute stationary counts, during which a single observer recorded all individuals heard or seen. Surveys began within 30 minutes of sunrise and continued until approximately 4 hours after sunrise. No surveys were conducted on days with rain, heavy fog, or high wind speed, following the guidelines of Ralph et al. (1993). Up to 4 detection covariates were recorded for each survey: date, start time, wind code, and sky code. While date was recorded for all surveys, a subset of surveys was missing start times (68% of MNF data), wind codes (73% of MNF data), or sky codes (73% of MNF data).

The 10-minute point count survey was divided into 2 time intervals (i.e., within-survey replicates): 0–5 minutes and >5–10 minutes. Individual birds were only recorded the first time they were observed, following removal sampling methods. For each record, observers indicated the corresponding time interval and distance band (≤50 m or >50 m). To limit detection variability due to distance, I restricted all data analyses to birds detected within 50 m.

**Nest success data**

Avian nest monitoring survey data were collected at the 2 study areas from 1996–1998, 2001–2003, and 2007–2009 from 20 WERF nest search plots and from 1993–1999 at 30 MNF nest search plots (Figures 2–3). Throughout the breeding season, field technicians looked for active nests within the nest search plots. Nests that were located through both systematic searching efforts and opportunistic observations were then monitored from mid-May until mid-July. During the monitoring period, field technicians checked each nest a minimum of every 3–4 days until the nesting attempt was complete and identified as either successful or failed. From the nest monitoring records, I used the following data for each nest location: bird species, success or failure during the incubation period, and success or failure during the brooding period.

Nest search plots varied in size and location among sampling years and between study areas (Figures 2–3). In the WERF, there were 8 45-ha nest search plots during 1996–1998 and 12 20-ha nest search plots during 2001–2003 and 2007–2009. The nest search plots were distributed randomly throughout 3 elevational blocks and encompassed either non-harvested areas with intact, predominantly mature hardwood forest, lightly harvested areas that retained closed canopy conditions, or heavily harvested areas with early-successional vegetation. In the MNF, 31 stands were intensively searched for nests during 1993–1998 (Duguay et al. 2001), with search effort distributed relatively evenly between stands. From 1996 to 1999, nest searches occurred within 40-ha (200-m wide × 2,000-m long, oriented perpendicular to prevailing slopes) plots that were established along 2 transects in each of 5 2,500-ha study areas that were randomly located within the mixed mesophytic vegetation zone of the MNF; the study areas ranged from 42–81% in core forest area (DeMeo 1999). Nest searching protocols followed the methodology of the national BBird program of nest search plot monitoring (BBird 1996). In 1998 and 1999, additional nests (outside the established nest search plots) in the northwestern region of the MNF (within Tucker and Randolph counties) were located through behavioral cues and systematic searches of likely nesting habitat (Williams 2002).

My objective was to compare temporal trends in nest success between the actively harvested landscape and the minimally harvested landscape, but the time periods of nest monitoring at the 2 study areas did not fully overlap (WERF: 1996–1998, 2001–2003, and 2007–2009 vs. MNF: 1993–1999). Therefore, I made the following assumptions: (1) trends from MNF data collected from 1993 to 1999 were representative of long-term trends; and (2) there was no outside, unconsidered systemic confounding factor (e.g., stochastic weather extremes, climate change, invasive species introduction) influencing trends from WERF data collected after 1999.

**Environmental data**

The full set of site covariates for the guild richness analyses and focal species abundance analyses included year of data collection, landscape-scale harvest intensity, an interaction between year and landscape-scale harvest intensity, and 9 environmental variables that were included to control for their known effects (Table 2). Landscape-scale harvest intensity was a dummy variable where 1 = actively harvested landscape (i.e., WERF) and 0 = minimally harvested landscape (i.e., MNF). The first 3 controlling environmental variables were topographical factors: elevation, aspect, and topographical position index (TPI). Mean elevation, mode aspect, and mode TPI within 50 m of each sampling point were calculated or derived using Shuttle Radar Topography Mission digital elevation data. The next controlling environmental variable was stand age. To calculate mode stand age within 50 m of each sampling point, I used GIS datasets from the WERF and from the MNF that mapped forest stands in each study area and provided stand-scale attribute information. The 5 remaining controlling environmental variables were proportions of landcover classifications, including 3 forest types (all forest [i.e., any type of mature forest], mixed forest, and conifer forest) within 50 m of each sampling point, shrub cover within 50 m of each sampling point, and all forest (i.e., any type of mature forest) within 1 km of the sampling point. To determine land cover proportions, I downloaded the 2001, 2004, 2006, and 2008 National Land Cover Databases (NLCD), which all have a resolution of 30 m (Jin et al. 2019). All calculations were made using land cover data from the closest year available (i.e., I used the 2001 NLCD data for surveys conducted in 2002 or earlier, 2004 NLCD data for surveys conducted in 2003 or 2004, 2006 NLCD data for surveys conducted in 2005–2007, and 2008 NLCD data for surveys conducted in 2008 or 2009).

**Data analysis**

*Determining overall species and guild richness from a hierarchical community model*

To calculate overall species richness and guild richness at each sampling point in each year of the study, I estimated the individual species occupancy of the 62 passerine and near-passerine species (Appendix A) simultaneously in a hierarchical community model (see Appendix B for JAGS code) and then derived the corresponding sums for all species and each guild designation (Zipkin et al. 2010). The hierarchical community model facilitated a multi-species approach to estimating individual species occurrence probabilities (Dorazio and Royle 2005, Dorazio et al. 2006). Following the modeling framework of Zipkin et al. (2010), species-specific occurrence and detection processes within the hierarchical community model were related to one another through a community-level hierarchical component, which assumed that each of the species parameters were random effects, governed by “hyper-parameters” (i.e., drawn from a community-level distribution). Linking individual species occurrence probabilities through this community-level hierarchical component leads to improved precision of species-specific estimates (Kéry and Royle 2008, Zipkin et al. 2009).

Occurrence *Zs,y,sp* was defined as a binary variable in which *Zs,y,sp* = 1 if species *sp* occurs within 50 m of sampling point *s* in year *y*. The occurrence state was assumed to be the outcome of a Bernoulli random variable, denoted by:

*Zs,y,sp* ~ *Bernoulli*(*Ψs,y,sp*)

where *Ψs,y,sp*is the probability that species *sp* occurs at sampling point *s* in year *y*. I further used a logit link to model linear relationships between occurrence probability (*Ψs,y,sp*) and 9 site covariates, which consisted of elevation, aspect, TPI, stand age, proportion of all forest / mixed forest / conifer forest / shrub within 50 m, and proportion of all forest within 1 km (Table 2). All continuous site covariates were centered and scaled prior to analysis. In addition, because my data included repeated observations at each sampling point over the course of multiple years, the hierarchical community model also incorporated a random site effect.

Given the observed data *Ys,y,r,sp*, where *r* is a within-survey replicate (i.e., 5-minute time interval during the 10-minute point count survey period) across all survey replicates (i.e., repeated visits to the sampling point during the sampling year), I defined the detection model for species *sp* at sampling point *s* in year *y* during replicate *r* as:

*Ys,y,r,sp* ~ *Bernoulli*(*ps,y,r,sp* × *Zs,y,sp*)

where *ps,y,r,sp* is the detection probability of species *sp* for the *r*th replicate at sampling point *s* in year *y*, given that species *sp* is present at sampling point *s* in year *y*. I further used a logit link to model linear relationships between detection probability (*ps,y,r,sp*) and 4 detection covariates, which consisted of ordinal day (centered and scaled prior to analysis), time since sunrise (measured as decimal hours and centered and scaled prior to analysis), a dummy variable for wind (0 = wind codes of 0, 1, or 2; 1 = wind codes >2), and a dummy variable for sky (0 = sky codes of 0, 1, or 2; 1 = sky codes >2). I also incorporated a species-specific random observer effect in the hierarchical community model.

Because a subset of avian point count surveys conducted in the MNF lacked data pertaining to time, wind code, or sky code, I imputed those detection covariate values. I assumed that time since sunrise was a Gaussian random variable, and that the wind and sky dummy variables were Bernoulli random variables. Imputation was informed by the observed data and accounted for uncertainty, with values drawn from a posterior distribution of each detection variable (Gelman et al. 1995).

Ultimately, the hierarchical community model yielded species-specific estimates of latent occupancy (*Zs,y,sp*) for species *sp* at each sampling point *s* in each year *y* based on observed data from replicate surveys. I then derived the overall species richness for each sampling point in each year by summing the occupancy of the 62 passerine and near-passerine species, as in the following equation:

Similarly, I derived guild-specific richness by summing the occupancy of the subset of songbird species that belonged to each habitat guild designation (Appendix A).

I constructed the hierarchical community model in a Bayesian framework, implemented with Markov chain Monte Carlo methods. For all community-level and species-specific parameters, I used prior distributions which were meant to provide little information; all gamma prior distributions, often used for variance parameters, had a shape parameter of 0.1 and rate parameter of 0.1, and all Gaussian prior distributions, such as for the community-level slope coefficients for each site covariate, had a mean of 0 and precision of 0.01 (Appendix B). I fit the models in JAGS (Plummer 2003) using the “jagsUI” package (Kellner and Meredith 2021) in Program R (R Core Team 2022). I used the “jags” function to run 3 chains of 5,000 iterations for the hierarchical community model, with a burn-in of 3,000 iterations and thinning rate of 2 iterations, which resulted in 3,000 posterior draws and reasonable convergence (R̂ ≤ 1.1) (Gelman et al. 2014).

*Determining relationships with harvest intensity over time for overall species and guild richness*

After I derived detection-corrected overall species and guild richness from the hierarchical community model, I then incorporated those estimates into corresponding generalized linear mixed effects models, with overall species or guild richness as the response variable and incorporating an interaction between time and landscape-level harvest intensity as a predictor variable. To propagate uncertainty from the original hierarchical community model results, I ran 3,000 iterations of the generalized linear mixed effects models for overall species richness and for each guild designation, cycling through the values from each of the 3,000 posterior draws. In result, the models yielded a posterior distribution of 3,000 for each slope coefficient, from which I derived the mean and 95% credible intervals. Thus, the estimated effects on overall species and guild richness were calculated as derived quantities (Kery and Royle 2016).

For each generalized linear mixed effects model, I assumed the number of species at each site in each year (i.e., overall species richness or guild richness) to be a Poisson random variable and used a log link to model relationships with controlling topographical and habitat factors and an interaction between year and landscape-level harvest intensity. All continuous predictor variables were centered and scaled prior to analysis. The total number of slope coefficients was 14 (resulting in a ratio of ~85 sites to 1 slope coefficient; Bolker et al. 2008), corresponding to year, landscape-level harvest intensity, year × landscape-level harvest intensity, elevation, aspect, aspect squared, TPI, stand age, stand age squared, proportion of all forest within 50 m, proportion of mixed forest within 50 m, proportion of conifer forest within 50 m, proportion of shrub within 50 m, and proportion of all forest within 1 km. Because my data included repeated observations at each sampling point over the course of multiple years, all of the generalized linear mixed effects models also incorporated a random site effect for log expected richness.

I fit all generalized linear mixed effects models using the “lme4” package (Bates et al. 2015) in Program R (R Core Team 2022). Specifically, I used the “glmer” function with family = “poisson”, optimizer = “bobyqa” (i.e., a specific optimizing function used by the model), and nAGQ = 0. The nAGQ is the number of points per axis for evaluating the adaptive Gauss-Hermite approximation to the log-likelihood. A value of zero uses a form of parameter estimation for generalized linear mixed effects models by optimizing the random effects and the fixed-effects coefficients in the penalized iteratively reweighted least squares step.

*Determining relationships with landscape-level harvest intensity over time for abundance of individual focal species*

To quantify and compare temporal trends in the abundance of specific focal species during the breeding season, I estimated the abundance of 14 songbird species (Table 1) independently in stacked N-mixture models (Royle 2004) (see Appendix C for JAGS code). For the abundance model within the hierarchical stacked N-mixture model, I assumed that species count was a Poisson random variable and used a log link to model relationships with controlling topographical and habitat factors and an interaction between year and landscape-level harvest intensity. All continuous predictor variables were centered and scaled prior to analysis. The total number of slope coefficients was 14, corresponding to same site covariates as for the generalized linear mixed effects models. Because my data included repeated observations at each sampling point over the course of multiple years, the stacked N-mixture models also incorporated a random site effect for log expected count.

For the detection model within the hierarchical stacked N-mixture model, I assumed that the observed count was a binomial random variable and modeled the probability of detection for the each within-survey replicate, using the same methods as for the hierarchical community model. I further used a logit link to model linear relationships between detection probability and 4 detection covariates, which consisted of ordinal day (centered and scaled prior to analysis), time since sunrise (measured as decimal hours and centered and scaled prior to analysis), a dummy variable for wind (0 = wind codes of 0, 1, or 2; 1 = wind codes >2), and a dummy variable for sky (0 = sky codes of 0, 1, or 2; 1 = sky codes >2). I used the same methods as for the hierarchical community model to impute study region-specific detection covariates for avian point count surveys from the MNF that were lacking data on time, wind code, or sky code.

The stacked N-mixture models were constructed in a Bayesian framework, implemented with Markov chain Monte Carlo methods. For all model parameters, I used prior distributions which were meant to provide little information; gamma prior distributions had shape and rate parameters of 0.01 or 0.1, and Gaussian prior distributions had a mean of 0 and precision of 0.01 (Appendix C). I fit the models in JAGS (Plummer 2003) using the “jagsUI” package (Kellner and Meredith 2021) in Program R (R Core Team 2022). I used the “autojags” function to run 3 chains for each model with a burn-in of 2,000–21,000 iterations (Appendix D), thinning rate of 3 iterations, and iteration increment of 3,000; models iteratively ran until reasonable convergence (R̂ ≤ 1.1) was achieved (Gelman et al. 2014), resulting in 3,000 posterior draws.

*Determining relationships with harvest intensity over time for nest success of individual focal species*

To quantify and compare temporal trends in nest success of specific focal species during the breeding season, I estimated the overall probability of nest success of 6 songbird species (Table 1) independently in conditional binomial models (see Appendix E for JAGS code). I assumed that observed nest success was a Bernoulli random variable and modeled both the probability of nest success during the incubation period and the probability of nest success during the brooding period, which was conditional upon nest success during the incubation period. Thus, given the observed nest success data *Ys,sp,1:2*, where *Ys,sp,1* = 1 if the nest of species *sp* at nest location *s* survived the incubation period and *Ys,sp,2* = 1 if the nest of species *sp* at nest location *s* survived the brooding period and successfully fledged at least 1 offspring, I defined the nest success model as:

*Ys,sp,1* ~ *Bernoulli*(*p.incubations,sp*)  
*Ys,sp,2* ~ *Bernoulli*(*p.broodings,sp*) × *Ys,sp,1*

where *p.incubations,sp* is the probability of nest success during the incubation period and *p.incubations,sp* is the probability of nest success during the brooding period, dependent upon the nest fate during the incubation period. The probability of overall nest success (*p.overalls,sp*) for species *sp* at nest location *s* was then calculated as the product of the probabilities of nest success during the incubation and brooding periods, as in the following equation:

*p.overalls,sp = p.incubations,sp* × *p.broodings,sp*

For both the probabilities of nest success during the incubation and brooding periods, I further used a logit link to model their relationships with 5 site covariates, which consisted of year, landscape-level timber harvest intensity, an interaction between year and landscape-level timber harvest intensity, a dummy variable for harvest history within the nest search plot (0 = no recent harvest; 1 = recent harvest), and a dummy variable for whether the nest search plot was dominated by mature forest (0 = no; 1 = yes). I also incorporated a species-specific and period-specific random nest search plot effect in the conditional binomial model.

The conditional binomial models were constructed in a Bayesian framework, implemented with Markov chain Monte Carlo methods. For all model parameters, I used prior distributions which were meant to provide little information; gamma prior distributions had shape and rate parameters of 0.01, and Gaussian prior distributions had a mean of 0 and precision of 0.01 (Appendix E). I fit the models in JAGS (Plummer 2003) using the “jagsUI” package (Kellner and Meredith 2021) in Program R (R Core Team 2022). I used the “autojags” function to run 3 chains for each model with a burn-in of 2,000–21,000 iterations (Appendix D), thinning rate of 3 iterations, and iteration increment of 3,000; models iteratively ran until reasonable convergence (R̂ ≤ 1.1) was achieved (Gelman et al. 2014), resulting in 3,000 posterior draws.

*Determining significance of interactions*

For all of the guild richness models, focal species abundance models, and focal species nest success models, relationships with individual variables were considered significant when the 95% credible intervals of their slope coefficient values did not overlap zero (Table 3, Figures 5–7). Similarly, interactions between year and landscape-scale harvest intensity were considered significant when the 95% credible intervals of their effective slope coefficient values did not overlap zero (Table 4). I defined an effective slope coefficient as the effect of a 1-unit change in time given specific levels of landscape-scale harvest intensity (i.e., actively harvested landscape vs. minimally harvested landscape).

**RESULTS**

**Effects of harvest intensity over time on overall species and guild richness**

Figure 8

**Effects of harvest intensity over time on focal species abundance**

Figure 9

**Effects of harvest intensity over time on focal species nest success**

Figure 10

**DISCUSSION**

[summary of key results]

[breakdown of key result concerning guild richness; reference to previous literature]

[breakdown of key result concerning focal species abundance; reference to previous literature]

[breakdown of key result concerning focal species nest success; reference to previous literature]

[holistic summation combining consistent results across guild richness, abundance, and nest success]

**Conclusions**

[repeat key result and put in context of why important; state conservation / management implications]

**Acknowledgments**

This research was supported by the National Science Foundation Graduate Research Fellowship under Grant No. DGE-1102689. I thank the previous West Virginia University graduate students who were responsible for field data collection at the two study sites.

**Literature Cited**

**Tables**

Table 1. List of the common name, scientific name, 4-letter species code, and habitat-related guild designation of the 14 songbird species used in the focal species analyses. The habitat-related guild designation indicates the primary breeding habitat of the species, such that: species in the early-successional and edge-associated (ESEA) guild breed in open habitat, shrub/scrub, or young forest, or along forest edges, such as the interface of early-successional and mature forest; species in the forest-interior (INT) guild breed in the core area of mature forest; species in the forest-gap (GAP) guild breed in or near small forest gaps within the core area of mature forest; and species in the forest generalist (GEN) guild are associated with forest but have no preference for early-successional vs. mature forest. All 14 species were focal species for assessing temporal trends in abundance, and 6 species (with bolded common names and 4-letter species codes) were focal species for assessing temporal trends in nest success. An asterisk following the common name indicates a species of regional conservation concern (i.e., listed as an Appalachian Mountains Joint Venture Priority Species or North American Bird Conservation Initiative’s Watch List species).

|  |  |  |  |
| --- | --- | --- | --- |
| **Common Name** | **Scientific Name** | **Code** | **Guild** |
| Chestnut-sided warbler | *Setophaga pensylvanica* | CSWA | ESEA |
| **Eastern towhee\*** | *Pipilo erythrophthalmus* | **EATO** | ESEA |
| **Indigo bunting\*** | *Passerina cyanea* | **INBU** | ESEA |
| Black-throated green warbler | *Setophaga virens* | BTNW | INT |
| **Dark-eyed junco** | *Junco hyemalis* | **DEJU** | INT |
| **Red-eyed vireo** | *Vireo olivaceus* | **REVI** | INT |
| **Wood thrush**\* | *Hylocichla mustelina* | **WOTH** | INT |
| American redstart | *Setophaga ruticilla* | AMRE | GAP |
| Cerulean warbler\* | *Setophaga cerulea* | CERW | GAP |
| Hooded warbler\* | *Setophaga citrina* | HOWA | GAP |
| **Veery** | *Catharus fuscescens* | **VEER** | GAP |
| American robin | *Turdus migratorius* | AMRO | GEN |
| Black-capped chickadee\* | *Poecile atricapillus* | BCCH | GEN |
| White-breasted nuthatch | *Sitta carolinensis* | WBNU | GEN |

Table 2. List, detailed description, and data source of the 11 site covariates used in the guild richness and focal species abundance analyses, comprising 2 focal variables, 3 topographical variables, and 6 habitat variables.

|  |  |  |
| --- | --- | --- |
| **Variable** | **Description (Unit)** | **Data Source (resolution)** |
| Year | Year of data collection; variable type: discrete; range: 1996–2009 | Bird survey data |
| Landscape-scale Harvest Intensity | Harvest intensity at the landscape level, corresponding to study area; variable type: dummy; 1 = actively harvested (i.e., WERF), 0 = minimally harvested (i.e., MNF) |
| Elevation | Mean elevation (m) within 50 m of each sampling point; variable type: continuous; range: 353–1,395 m | Shuttle Radar Topography Mission digital elevation data (~20–25 m), Consultative Group on International Agricultural Research – Consortium for Spatial Information |
| Aspect | Mode aspect (degrees) within 50 m of each sampling point; variable type: continuous; bounded between 0 and 360 degrees |
| Topographical Position Index (TPI) | Mode TPI within 50 m of each sampling point; higher positive values indicate ridges, lower positive values indicate upper to mid slopes, values near 0 indicate flat areas, higher negative values indicate lower slopes, and lower negative values indicate valleys; variable type: continuous; range: -3.500–2.375 |
| Stand Age | Mode stand age within 1 km of the edge of the wildlife opening; variable type: discrete; range: 0–180 years | GIS datasets of WERF and MNF forest stands |
| Proportion All Forest | Proportion of any type of mature forest cover (including deciduous, mixed, and coniferous) / mixed forest cover / coniferous forest cover / shrub cover within 50 m of the sampling point; variable type: continuous; bounded between 0 and 1 | 2001 / 2004 / 2006 / 2008 National Land Cover Database (30 m), U.S. Geological Survey |
| Proportion Mixed Forest |
| Proportion Conifer Forest |
| Proportion Shrub |
| Proportion All Forest within 1 km | Proportion of any type of mature forest cover (including deciduous, mixed, and coniferous) within 1 km of the sampling point; variable type: continuous; bounded between 0 and 1 |

Table 3. Statistical significance (indicated by bold type) of slope coefficients for the predictor variables (YR = year, LSHI = landscape-scale harvest intensity, EL = elevation, ASP = aspect, TPI = topographic position index, AGE = stand age, PAF = proportion of all forest within 50 m, PMF = proportion of mixed forest within 50 m, PCF = proportion of conifer forest within 50 m, PS = proportion of shrub cover within 50 m, and PAFkm = proportion of all forest within 1 km) corresponding to overall species richness (ALL), guild (ESEA, INT, GAP, and GEN) richness, focal songbird species abundance (see Table 1 for species codes), and focal songbird species nest success, arranged by guild designation.

Table 4. Statistical significance (indicated by bold type) of the effective slope coefficients for year on overall species richness (ALL), guild (ESEA, INT, GAP, and GEN) richness, focal songbird species abundance (see Table 1 for species codes), and focal songbird species nest success in an actively harvested landscape and minimally harvested landscape.

**FIGURES**

Figure 1. Location and extent of the 2 study areas in West Virginia.

Figure 2. Locations of the sampling points and nest search plots in the WERF.

Figure 3. Locations of the sampling points and nest search plots in the MNF

Figure 4. Harvest history of WERF.

Figure 5. Whisker plots for overall species richness and guild richness (see Appendix A for guild designations and associated forest songbird species), displaying the slope coefficients of the predictor variables (i.e., site covariates), which consisted of year, XXXX, and proportion of any type of forest cover within 1 km (Proportion Forest). Points are located at the mean values for the posterior distributions and the corresponding whiskers encompass the 95% credible intervals. Black points with closed circles and black whiskers indicate statistical significance (i.e., credible intervals do not overlap zero).

Figure 6. Whisker plots for each focal species for abundance analyses (Table 1), displaying the slope coefficients of the predictor variables (i.e., site covariates), which consisted of year, XXXX, and proportion of any type of forest cover within 1 km (Proportion Forest). Points are located at the mean values for the posterior distributions and the corresponding whiskers encompass the 95% credible intervals. Black points with closed circles and black whiskers indicate statistical significance (i.e., credible intervals do not overlap zero). Color of the 4-letter species code indicates its guild designation (dark blue = north guild, red = south guild, light blue = trailing guild, and orange = general guild), and the bird silhouette indicates its taxonomic family (warbler, thrush, or flycatcher).

Figure 7. Whisker plots for each focal species for nest success analyses (Table 1), displaying the slope coefficients of the predictor variables (i.e., site covariates), which consisted of year, XXXX, and proportion of any type of forest cover within 1 km (Proportion Forest). Points are located at the mean values for the posterior distributions and the corresponding whiskers encompass the 95% credible intervals. Black points with closed circles and black whiskers indicate statistical significance (i.e., credible intervals do not overlap zero). Color of the 4-letter species code indicates its guild designation (dark blue = north guild, red = south guild, light blue = trailing guild, and orange = general guild), and the bird silhouette indicates its taxonomic family (warbler, thrush, or flycatcher).

Figure 8. Plots of year x study area interaction for guild richness

Figure 9. Plots of year x study area interaction for focal species abundance

Figure 10. Plots of year x study area interaction for focal species nest success

**APPENDICES**

**Appendix A**

Table of the 62 passerine and near-passerine species considered in the guild richness analyses.

Table A1. List of the common name, scientific name, 4-letter species code, relative frequency, taxonomic family, habitat-related guild designation, and focal species status of all 62 passerine and near-passerine species considered for the guild richness analyses. Relative frequency is the number of detections across all breeding bird point count surveys from all sampling points in the study. The habitat-related guild designation indicates the primary breeding habitat of the species, such that: species in the early-successional and edge-associated (ESEA) guild breed in open habitat, shrub/scrub, or young forest, or along forest edges, such as the interface of early-successional and mature forest; species in the forest-interior (INT) guild breed in the core area of mature forest; species in the forest-gap (GAP) guild breed in or near small forest gaps within the core area of mature forest; and species in the forest generalist (GEN) guild are associated with forest but have no preference for early-successional vs. mature forest.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Common Name**  **(*Scientific Name*)** | **Species Code** | **Relative Frequency** | **Taxonomic Family** | **Guild** | **Focal Species** |
| Chestnut-sided Warbler  (*Setophaga pensylvanica*) | CSWA | 600 | Parulidae | ESEA | 1 |
| Eastern Towhee  (*Pipilo erythrophthalmus*) | EATO | 718 | Passerellidae | ESEA | 1 |
| Indigo Bunting  (*Passerina cyanea*) | INBU | 589 | Cardinalidae | ESEA | 1 |
| American Goldfinch  (*Spinus tristis*) | AMGO | 89 | Fringillidae | ESEA | 0 |
| Brown-headed Cowbird  (*Molothrus ater*) | BHCO | 163 | Icteridae | ESEA | 0 |
| Blue-winged Warbler  (*Vermivora cyanoptera*) | BWWA | 110 | Parulidae | ESEA | 0 |
| Carolina Wren  (*Thryothorus ludovicianus*) | CARW | 14 | Troglodytidae | ESEA | 0 |
| Cedar Waxwing  (*Bombycilla cedrorum*) | CEDW | 216 | Bombycillidae | ESEA | 0 |
| Chipping Sparrow  (*Spizella passerina*) | CHSP | 40 | Passerellidae | ESEA | 0 |
| Common Yellowthroat  (*Geothlypis trichas*) | COYE | 60 | Parulidae | ESEA | 0 |
| Eastern Phoebe  (*Sayornis phoebe*) | EAPH | 16 | Tyrannidae | ESEA | 0 |

Table A1. Continued.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Common Name**  **(*Scientific Name*)** | **Species Code** | **Relative Frequency** | **Taxonomic Family** | **Guild** | **Focal Species** |
| Field Sparrow  (*Spizella pusilla*) | FISP | 34 | Passerellidae | ESEA | 0 |
| Gray Catbird  (*Dumetella carolinensis*) | GRCA | 132 | Mimidae | ESEA | 0 |
| Mourning Dove  (*Zenaida macroura*) | MODO | 17 | Columbidae | ESEA | 0 |
| Mourning Warbler  (*Geothlypis philadelphia*) | MOWA | 42 | Parulidae | ESEA | 0 |
| Northern Cardinal  (*Cardinalis cardinalis*) | NOCA | 24 | Cardinalidae | ESEA | 0 |
| Song Sparrow  (*Melospiza melodia*) | SOSP | 75 | Passerellidae | ESEA | 0 |
| Yellow-billed Cuckoo  (*Coccyzus americanus*) | YBCU | 64 | Cuculidae | ESEA | 0 |
| Black-throated Green Warbler  (*Setophaga virens*) | BTNW | 2458 | Parulidae | INT | 1 |
| Dark-eyed Junco  (*Junco hyemalis*) | DEJU | 1719 | Passerellidae | INT | 1 |
| Red-eyed Vireo  (*Vireo olivaceus*) | REVI | 3135 | Vireonidae | INT | 1 |
| Wood Thrush  (*Hylocichla mustelina*) | WOTH | 610 | Turdidae | INT | 1 |
| Acadian Flycatcher  (*Empidonax virescens*) | ACFL | 708 | Tyrannidae | INT | 0 |
| Black-and-white Warbler  (*Mniotilta varia*) | BAWW | 641 | Parulidae | INT | 0 |
| Blackburnian Warbler  (*Setophaga fusca*) | BLBW | 608 | Parulidae | INT | 0 |
| Black-throated Blue Warbler  (*Setophaga caerulescens*) | BTBW | 1162 | Parulidae | INT | 0 |
| Blue-headed Vireo  (*Vireo solitarius*) | BHVI | 1636 | Vireonidae | INT | 0 |
| Brown Creeper  (*Certhia americana*) | BRCR | 150 | Certhiidae | INT | 0 |
| Canada Warbler  (*Cardellina canadensis*) | CAWA | 558 | Parulidae | INT | 0 |
| Golden-crowned Kinglet  (*Regulus satrapa*) | GCKI | 437 | Regulidae | INT | 0 |
| Hairy Woodpecker  (*Leuconotopicus villosus*) | HAWO | 318 | Picidae | INT | 0 |
| Hermit Thrush  (*Catharus guttatus*) | HETH | 384 | Turdidae | INT | 0 |

Table A1. Continued.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Common Name**  **(*Scientific Name*)** | **Species Code** | **Relative Frequency** | **Taxonomic Family** | **Guild** | **Focal Species** |
| Least Flycatcher  (*Empidonax minimus*) | LEFL | 71 | Tyrannidae | INT | 0 |
| Magnolia Warbler  (*Setophaga magnolia*) | MAWA | 1153 | Parulidae | INT | 0 |
| Ovenbird  (*Seiurus aurocapilla*) | OVEN | 788 | Parulidae | INT | 0 |
| Pileated Woodpecker  (*Dryocopus pileatus*) | PIWO | 168 | Picidae | INT | 0 |
| Pine Warbler  (*Setophaga pinus*) | PIWA | 79 | Parulidae | INT | 0 |
| Purple Finch  (*Haemorhous purpureus*) | PUFI | 35 | Fringillidae | INT | 0 |
| Red-breasted Nuthatch  (*Sitta canadensis*) | RBNU | 198 | Sittidae | INT | 0 |
| Rose-breasted Grosbeak  (*Pheucticus ludovicianus*) | RBGR | 443 | Cardinalidae | INT | 0 |
| Scarlet Tanager  (*Piranga olivacea*) | SCTA | 1084 | Cardinalidae | INT | 0 |
| Swainson's Thrush  (*Catharus ustulatus*) | SWTH | 126 | Turdidae | INT | 0 |
| Winter Wren  (*Troglodytes hiemalis*) | WIWR | 541 | Troglodytidae | INT | 0 |
| Worm-eating Warbler  (*Helmitheros vermivorum*) | WEWA | 237 | Parulidae | INT | 0 |
| Yellow-rumped Warbler  (*Setophaga coronata*) | YRWA | 83 | Parulidae | INT | 0 |
| American Redstart  (*Setophaga ruticilla*) | AMRE | 568 | Parulidae | GAP | 1 |
| Cerulean Warbler  (*Setophaga cerulea*) | CERW | 125 | Parulidae | GAP | 1 |
| Hooded Warbler  (*Setophaga citrina*) | HOWA | 580 | Parulidae | GAP | 1 |
| Veery  (*Catharus fuscescens*) | VEER | 1070 | Turdidae | GAP | 1 |
| Eastern Wood-Pewee  (*Contopus virens*) | EAWP | 314 | Tyrannidae | GAP | 0 |
| Great-crested Flycatcher  (*Myiarchus crinitus*) | GCFL | 90 | Tyrannidae | GAP | 0 |
| Northern Parula  (*Setophaga americana*) | NOPA | 113 | Parulidae | GAP | 0 |
| Yellow-throated Vireo  (*Vireo flavifrons*) | YTVI | 44 | Vireonidae | GAP | 0 |

Table A1. Continued.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Common Name**  **(*Scientific Name*)** | **Species Code** | **Relative Frequency** | **Taxonomic Family** | **Guild** | **Focal Species** |
| American Robin  (*Turdus migratorius*) | AMRO | 533 | Turdidae | GEN | 1 |
| Black-capped Chickadee  (*Poecile atricapillus*) | BCCH | 702 | Paridae | GEN | 1 |
| White-breasted Nuthatch  (*Sitta carolinensis*) | WBNU | 449 | Sittidae | GEN | 1 |
| Blue-gray Gnatcatcher  (*Polioptila caerulea*) | BGGN | 147 | Polioptilidae | GEN | 0 |
| Downy Woodpecker  (*Picoides pubescens*) | DOWO | 206 | Picidae | GEN | 0 |
| Northern Flicker  (*Colaptes auratus*) | NOFL | 134 | Picidae | GEN | 0 |
| Red-bellied Woodpecker  (*Melanerpes carolinus*) | RBWO | 51 | Picidae | GEN | 0 |
| Tufted Titmouse  (*Baeolophus bicolor*) | TUTI | 195 | Paridae | GEN | 0 |
| Yellow-bellied Sapsucker  (*Sphyrapicus varius*) | YBSA | 24 | Picidae | GEN | 0 |

**Appendix B**

JAGS model code for the guild richness analyses.

model {

### PRIORS

# COMMUNITY-LEVEL MODEL PARAMETERS (OCCUPANCY)

community.occupancy.a ~ dlogis(0,1) #this assumes a logistic prior

community.occupancy.tau ~ dgamma(0.1, 0.1)

# COMMUNITY-LEVEL MODEL PARAMETERS (DETECTION)

community.detection.b ~ dlogis(0,1) #this assumes a logistic prior

community.detection.tau ~ dgamma(0.1, 0.1)

# COMMUNITY-LEVEL PARAMETERS FOR SITE COVARIATE SLOPE COEFFICIENTS

for (sitecov in 1:n.sitecovs) {

mu.alpha[sitecov] ~ dnorm(0, 0.01)

tau.alpha[sitecov] ~ dgamma(0.1, 0.1)

}

# COMMUNITY-LEVEL PARAMETERS FOR DETECTION COVARIATE SLOPE COEFFICIENTS

for (detcov in 1:n.detcovs) {

mu.beta[detcov] ~ dnorm(0, 0.01)

tau.beta[detcov] ~ dgamma(0.1, 0.1)

}

# SPECIES-SPECIFIC PRIORS FROM THE COMMUNITY-LEVEL PRIOR DISTRIBUTIONS

for (species in 1:n.species) {

# INTERCEPTS

alpha0[species] ~ dnorm(community.occupancy.a, community.occupancy.tau)

beta0[species] ~ dnorm(community.detection.b, community.detection.tau)

# SLOPE COEFFICIENTS FOR SITE COVARIATES

for (sitecov in 1:n.sitecovs) {

alpha[species, sitecov] ~ dnorm(mu.alpha[sitecov],

tau.alpha[sitecov])

}

# RANDOM SITE EFFECT

tau.rse[species] ~ dgamma(0.1, 0.1)

for (site in 1:n.sites) {

random.site.effect[species, site] ~ dnorm(alpha0[species],

tau.rse[species])

}

# SLOPE COEFFICIENTS FOR DETECTION COVARIATES

for (detcov in 1:n.detcovs) {

beta[species, detcov] ~ dnorm(mu.beta[detcov], tau.beta[detcov])

}

# RANDOM OBSERVER EFFECT

tau.roe[species] ~ dgamma(0.1, 0.1)

for (observer in 1:n.observers) {

random.observer.effect[species, observer] ~ dnorm(beta0[species],

tau.roe[species])

}

}

# NOTES: Loop over all species.

# PARAMETERS FOR IMPUTATION OF DETECTION COVARIATES

# WIND CODE

wind.prob ~ dbeta(1, 1)

# SKY CODE

sky.prob ~ dbeta(1, 1)

### LIKELIHOOD

# IMPUTATION OF DETECTION COVARIATES

for (site in 1:n.sites){

for (year in 1:n.years[site]) {

for (replicate in 1:n.replicates[site, year]) {

time.array[site, year, replicate] ~ dnorm(0, 1)

wind.array[site, year, replicate] ~ dbern(wind.prob)

sky.array[site, year, replicate] ~ dbern(sky.prob)

}

}

}

# NOTES: Loop over sites, years, and replicates.

for (species in 1:n.species) {

# Loop to estimate Z (true occurrence) for each species at each site

for (site in 1:n.sites){

for (year in 1:n.years[site]) {

# OCCUPANCY MODEL

logit(psi[site, year, species]) <- inprod(alpha[species,

1:n.sitecovs],

sitecov.array[site, year, 1:n.sitecovs]) +

random.site.effect[species, site]

# ESTIMATING OCCUPANCY

Z[site, year, species] ~ dbern(psi[site, year, species])

# Estimate detection of each species at each site during each

# sampling replicate

# Loop over each replicate for each site (variable number of

# replicates depending on site and year; n.visits x 2 replicates)

for (replicate in 1:n.replicates[site, year]) {

# DETECTION MODEL

logit(p[site, year, replicate, species]) <- beta[species, 1] \*

day.array[site, year, replicate] +

beta[species, 2] \*

time.array[site, year, replicate] +

beta[species, 3] \*

time.array[site, year, replicate] \* time.array[site, year, replicate] +

beta[species, 4] \*

wind.array[site, year, replicate] +

beta[species, 5] \*

sky.array[site, year, replicate] +

random.observer.effect[species,

observer.id.array[site, year, replicate]]

# ESTIMATING PROBABILITY OF DETECTION

mu.p[site, year, replicate, species] <- p[site, year,

replicate, species] \*

Z[site, year, species]

Y[site, year, replicate, species] ~ dbern(mu.p[site, year,

replicate, species])

} # end replicate loop

} #end year loop

} #end site loop

} #end species loop

### DERIVED QUANTITIES

# Loop to determine site-level richness estimates for the whole community

# and for subsets or assemblages of interest

for (site in 1:n.sites) {

for (year in 1:n.years[site]) {

site.species.richness[site, year] <- sum(Z[site, year, 1:n.species])

es.ea.guild.richness[site, year] <- inprod(Z[site, year,

1:n.species],

es.ea.guild[1:n.species])

forest.interior.guild.richness[site, year] <- inprod(Z[site, year,

1:n.species],

forest.interior.guild[1:n.species])

forest.gap.guild.richness[site, year] <- inprod(Z[site, year,

1:n.species],

forest.gap.guild[1:n.species])

generalist.guild.richness[site, year] <- inprod(Z[site, year,

1:n.species],

generalist.guild[1:n.species])

}

} #end site loop

}

**Appendix C**

JAGS model code for the focal species abundance analyses.

model {

### PRIORS

for (species in 1:n.species) {

# INTERCEPTS

alpha0[species] ~ dnorm(0, 0.01) #intercept for abundance model

beta0[species] ~ dnorm(0, 0.01) #intercept for detection model

# SLOPE COEFFICIENTS FOR SITE COVARIATES

for (alpha.index in 1:n.alphas) {

alpha[species, alpha.index] ~ dnorm(0, 0.01)

}

# RANDOM SITE EFFECT

tau.rse[species] ~ dgamma(0.01, 0.01) #for random site effects

for (site in 1:n.sites){

random.site.effect[species, site] ~ dnorm(alpha0[species],

tau.rse[species])

}

# NOTES: Loop over the number of unique sites

# SLOPE COEFFICIENTS FOR DETECTION COVARIATES

for (detcov in 1:n.detcovs) {

beta[species, detcov] ~ dnorm(0, 0.01)

}

# RANDOM OBSERVER EFFECT

tau.roe[species] ~ dgamma(0.01, 0.01)

for (observer in 1:n.observers) {

random.observer.effect[species, observer] ~ dnorm(beta0[species],

tau.roe[species])

}

}

# NOTES: Loop over each focal species.

# PARAMETERS FOR IMPUTATION OF DETECTION COVARIATES

# TIME

time.mu ~ dnorm(0, 0.01)

time.tau ~ dgamma(0.1, 0.1)

# NOTE: Normal distribution.

# WIND CODE

wind.prob ~ dbeta(1, 1)

# SKY CODE

sky.prob ~ dbeta(1, 1)

### LIKELIHOOD

# IMPUTATION OF DETECTION COVARIATES

for (site in 1:n.sites){

for (year in 1:n.years[site]) {

for (visit in 1:n.visits[site, year]) {

time.array[site, year, visit] ~ dnorm(time.mu, time.tau)

wind.array[site, year, visit] ~ dbern(wind.prob)

sky.array[site, year, visit] ~ dbern(sky.prob)

}

}

}

# NOTES: Loop over sites, years, and visits.

# ESTIMATE ABUNDANCE AND DETECTION PROBABILITY

for (species in 1:n.species) {

# Loop to estimate N (true abundance) for each species at each site

for (site in 1:n.sites) {

for (year in 1:n.years[site]) {

# ABUNDANCE MODEL

log(lambda[site, year, species]) <- alpha[species, 1] \*

sitecov.array[site, year, 1] +

alpha[species, 2] \*

sitecov.array[site, year, 2] +

alpha[species, 3] \*

sitecov.array[site, year, 3] +

alpha[species, 4] \*

sitecov.array[site, year, 4] +

alpha[species, 5] \*

sitecov.array[site, year, 4] \*

sitecov.array[site, year, 4] +

alpha[species, 6] \*

sitecov.array[site, year, 5] +

alpha[species, 7] \*

sitecov.array[site, year, 6] +

alpha[species, 8] \*

sitecov.array[site, year, 6] \*

sitecov.array[site, year, 6] +

alpha[species, 9] \*

sitecov.array[site, year, 7] +

alpha[species, 10] \*

sitecov.array[site, year, 8] +

alpha[species, 11] \*

sitecov.array[site, year, 9] +

alpha[species, 12] \*

sitecov.array[site, year, 10] +

alpha[species, 13] \*

sitecov.array[site, year, 11] +

alpha[species, 14] \*

sitecov.array[site, year, 1] \*

sitecov.array[site, year, 2] +

random.site.effect[species, site]

# sitecov.array: 1 = study area, 2 = year, 3 = elevation,

# 4 = aspect, 5 = TPI, 6 = stand age, 7 = proportion all forest,

# 8 = proportion mixed forest, 9 = proportion conifer forest,

# 10 = proportion shrub, 11 = proportion all forest within 1 km

# ESTIMATING ABUNDANCE

N[site, year, species] ~ dpois(lambda[site, year, species])

for (visit in 1:n.visits[site, year]) {

# OBSERVATION PROBABILITY

Y[site, year, visit, 1, species] ~ dbin(p[site, year, visit,

1, species],

N[site, year, species])

z[site, year, visit, 1, species] <- N[site, year, species] –

Y[site, year, visit, 1,

species]

for (i in 2:n.replicates) {

Y[site, year, visit, i, species] ~ dbin(p[site, year,

visit, i,

species],

z[site, year, visit, i-1,

species])

z[site, year, visit, i, species] <- N[site, year, species]

- sum(Y[site, year,

visit, 1:i,

species])

}

# Loop to estimate detection each species at each site

for (replicate in 1:n.replicates) {

# DETECTION MODEL

logit(p[site, year, visit, replicate, species]) <-

beta[species, 1] \* day.array[site, year, visit] +

beta[species, 2] \* time.array[site, year, visit] +

beta[species, 3] \* time.array[site, year, visit] \*

time.array[site, year, visit] +

beta[species, 4] \* wind.array[site, year, visit] +

beta[species, 5] \* sky.array[site, year, visit] +

random.observer.effect[species,

observer.id.array[site, year,

visit]]

}

# NOTES: Loop over each replicate for each site.

} # end visit loop

} # end year loop

} # end site loop

} # end species loop

}

**Appendix D**

Table of model information for overall species richness, the 4 habitat-related guild designations considered in the guild richness analyses, the 14 focal songbird species considered in the species abundance analyses, and the 6 focal songbird species considered in the species nest success analyses.

Table D1. List of the 4 habitat-related guild designations and 14 focal songbird species (see Table 1 for species codes), with corresponding information for the abundance and nest success models that includes the number of chains (Chains), total iterations (Total), burn-in (Burn), thinning rate (Thin), and resulting posterior iterations (Posterior). The habitat-related guild designation indicates the primary breeding habitat of the species (see Appendix A for precise definitions), and includes 4 categories: early-successional and edge-associated (ESEA), forest-interior (INT), forest-gap (GAP), and forest generalist (GEN).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Guild** | **Species** | **Model** | **Chains** | **Total** | **Burn-In** | **Thin** | **Posterior** |
| ALL |  |  | 3 |  |  |  |  |
| ESEA | |  | 3 |  |  |  |  |
|  | CSWA | Abundance | 3 |  |  |  |  |
|  | EATO | Abundance | 3 |  |  |  |  |
|  |  | Nest Success | 3 |  |  |  |  |
|  | INBU | Abundance | 3 |  |  |  |  |
|  |  | Nest Success | 3 |  |  |  |  |
| INT | |  | 3 |  |  |  |  |
|  | BTNW | Abundance | 3 |  |  |  |  |
|  | DEJU | Abundance | 3 |  |  |  |  |
|  |  | Nest Success | 3 |  |  |  |  |
|  | REVI | Abundance | 3 |  |  |  |  |
|  |  | Nest Success | 3 |  |  |  |  |
|  | WOTH | Abundance | 3 |  |  |  |  |
|  |  | Nest Success | 3 |  |  |  |  |
| GAP | |  | 3 |  |  |  |  |
|  | AMRE | Abundance | 3 |  |  |  |  |
|  | CERW | Abundance | 3 |  |  |  |  |
|  | HOWA | Abundance | 3 |  |  |  |  |
|  | VEER | Abundance | 3 |  |  |  |  |
|  |  | Nest Success | 3 |  |  |  |  |
| GEN | |  | 3 |  |  |  |  |
|  | AMRO | Abundance | 3 |  |  |  |  |
|  | BCCH | Abundance | 3 |  |  |  |  |
|  | WBNU | Abundance | 3 |  |  |  |  |

**Appendix E**

JAGS model code for the focal species nest success analyses.

model {

### PRIORS

# INTERCEPTS

ISM.alpha0 ~ dnorm(0, 0.01) #intercept for incubation success model (ISM)

BSM.alpha0 ~ dnorm(0, 0.01) #intercept for brooding success model (BSM)

# SLOPE COEFFICIENTS FOR SITE COVARIATES

for (alpha.index in 1:n.alphas) {

ISM.alpha[alpha.index] ~ dnorm(0, 0.01) #for incubation success model

BSM.alpha[alpha.index] ~ dnorm(0, 0.01) #for brooding success model

}

# RANDOM PLOT EFFECT

ISM.tau.rpe ~ dgamma(0.01, 0.01) #for incubation success model

BSM.tau.rpe ~ dgamma(0.01, 0.01) #for brooding success model

for (nest.plot in 1:n.nest.plots){

ISM.random.plot.effect[nest.plot] ~ dnorm(ISM.alpha0, ISM.tau.rpe)

BSM.random.plot.effect[nest.plot] ~ dnorm(BSM.alpha0, BSM.tau.rpe)

}

# NOTES: Loop over the number of nest search plots

### LIKELIHOOD

for (nest in 1:n.nests){

Y[nest, 1] ~ dbern(p.incubation[nest])

Y[nest, 2] ~ dbern(p.brooding[nest] \* Y[nest, 1])

# NOTE: probability of nest success during brooding period is

# conditional on nest success during incubation period

logit(p.incubation[nest]) <- ISM.alpha[1] \* sitecov.matrix[nest, 1] +

ISM.alpha[2] \* sitecov.matrix[nest, 2] +

ISM.alpha[3] \* sitecov.matrix[nest, 3] +

ISM.alpha[4] \* sitecov.matrix[nest, 4] +

ISM.alpha[5] \* sitecov.matrix[nest, 1] \*

sitecov.matrix[nest, 2] +

ISM.random.plot.effect[nest.plot.index[nest]]

# sitecov.matrix: 1 = study area, 2 = year, 3 = nest search plot with

# harvest history, 4 = nest search plot in mature forest

logit(p.brooding[nest]) <- BSM.alpha[1] \* sitecov.matrix[nest, 1] +

BSM.alpha[2] \* sitecov.matrix[nest, 2] +

BSM.alpha[3] \* sitecov.matrix[nest, 3] +

BSM.alpha[4] \* sitecov.matrix[nest, 4] +

BSM.alpha[5] \* sitecov.matrix[nest, 1] \*

sitecov.matrix[nest, 2] +

BSM.random.plot.effect[nest.plot.index[nest]]

# sitecov.matrix: 1 = study area, 2 = year, 3 = nest search plot with

# harvest history, 4 = nest search plot in mature forest

p.overall[nest] <- p.incubation[nest] \* p.brooding[nest]

} # end nest loop

}