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Joshua Perry Harris

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# ESTIMATING WILDLIFE BIODIVERSITY OF PINE PLANTATION EDGES OF CONTRASTING ROTATIONAL STAGES: A CASE STUDY

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ESTIMATING WILDLIFE BIODIVERSITY OF PINE PLANTATION EDGES OF  
CONTRASTING ROTATIONAL STAGES: A CASE STUDY

By

Joshua Perry Harris, B.S. Forest Wildlife Management

Presented to the Faculty of the Graduate School of

Stephen F. Austin State University

In Partial Fulfillment

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For the Degree of  
Master of Science

STEPHEN F. AUSTIN STATE UNIVERSITY  
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CONTRASTING ROTATIONAL STAGES: A CASE STUDY

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## ABSTRACT

Plantation edges are a tangible landscape feature that can be manipulated by altering harvest strategies, stand delineation, and regulation methods on a landscape scale. Determining whether a difference in biodiversity values exist between structurally varied edge types created by pine plantations in East Texas could identify forest management improvements for wildlife biodiversity. Biodiversity has been estimated within varied endemic and exotic plantation systems but few studies have evaluated plantation edges of contrasting rotational stages.

An individual large Timberland Investment Management Organization (TIMO) manages a fragmented strip of pine plantations between the Davy Crockett and Angelina National Forests of East Texas. These plantations are of specific interest because of their abundance, similar management objectives, and uniform silvicultural practices. Lack of a clear understanding of how, or if, wildlife biodiversity varies in the edges between plantations prompted this evaluation of biodiversity. Structural differences between plantation edges are presumed to be the main mechanism that would create observed differences in the diversity and abundance of wildlife.

Diversity and abundance of vertebrate species and family richness of invertebrates was estimated amongst three loblolly pine (*Pinus taeda* L.) plantation edge types of contrasting rotational phases. Three edge types were defined based on combinations of structurally different stands created via forest thinning on sampled lands (A=pre-thin/post thin, B= pre-thin/pre-clearcut, and C=post thin/pre-clearcut).

For two summer seasons (May-August, 2015-2016) richness and abundance data was collected on birds, medium sized-mammals, and small mammals, using double observer point counts, motion camera traps, and Sherman traps, respectively. Invertebrate families were sampled for richness using pitfall traps. Utilizing richness and abundance data collected, two indices of diversity (Shannon's, Simpson's reciprocal), two measures of species evenness (Shannon's, Simpson's reciprocal), and two measures of community dominance (Beta diversity, Berger-Parker index) were calculated. The two samples for each animal group observed were also extrapolated out to six samples using sample based rarefaction curves (SBRC) generated with the software EstimateS.

Data analysis was designed to determine which edge type had the most species detected (richness, alpha diversity), the dissimilarity between edge type species (beta diversity), and the dissimilarity between the number of individuals within each edge type (Berger-Parker Index). Information about how the rarity or commonness of species observed within each edge type affected each's diversity (Shannon Index, Simpson's Reciprocal Index) was also calculated. The

richness of each animal group within each edge type based on extrapolated samples (SBRC) was estimated to account for the small sample size.

Richness and abundance of vertebrates was similar amongst edges during 2015 and increased with stand ages during 2016. However, diversity indices, community dominance, and evenness of vertebrates failed to detect a difference amongst edge types for each season. Additionally, confidence intervals for sample based rarefaction curves for the three edge types overlapped, preventing the identification of a difference with only six extrapolated samples. However, twenty-one of the fifty-five invertebrate families were found exclusively in edge type B.

Regardless, no one-edge type emerged as having elevated value for wildlife. Rather, each edge type provided a piece of the open pine habitat conditions to which many of these species are accustomed. The similar ratio and evenly distributed spatial orientation of stand types amongst sampled lands on the landscape provide a variety of stand structures for wildlife. The landscape heterogeneity of structurally varied stands, throughout the sampled matrix, can be attributed to forest certification standards adopted by the land managers. According to these findings, timberlands between the Davy Crockett and Angelina National Forests are already being managed with landscape scale considerations; however, this study is only a snapshot of biodiversity estimates for a two-year span encompassing six similar but varied sites. Increasing the

number of replicates through subsequent sampling would allow for the statistical analysis of any detectable differences between edge types.



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## RICHNESS AND DIVERSITY OF PLANTATION EDGES

## INTRODUCTION

It is estimated that half of the terrestrial flora and fauna on Earth are found in forested ecosystems (Hassan et al. 2005); however, global deforestation trends and conversion of natural forests to agriculture or plantation monocultures are major threats to global wildlife biodiversity (Stephens and Wagner 2007). As of 2007, the global area of natural or semi-natural forests was decreasing at a rate of 13 million hectares each year, only 2-3 million hectares of which are being converted to plantation forestry (Thompson et al. 2011, FAO 2007, FAO 2006). According to Hansen et al. (2010), North America experienced the greatest gross forest cover loss (GFCL) (forest “cover” loss indicates the clearcutting of stands not land conversion to other uses) during 2000-2005 with the United States ranking 4th globally in GFCL among countries with over one million square kilometers of forest cover lost. With 87% of forested lands in the southern United States in private ownership, biodiversity conservation cannot be accomplished on public lands alone (Miller et al. 2009, Zobrist et al. 2005).

Before European settlement, an estimated 81 million hectares of pine, oak, and other mixed forests dominated the American South, in which longleaf pine (*Pinus palustris* Mill.) savannah (~24 million hectares) is estimated to have

thrived (Zobrist et al. 2005). These stands were mostly comprised of a single species overstory, a sparse mid-story, and a species rich understory (Zobrist et al. 2005). The primary disturbance regime in these forests was frequent natural and anthropogenic fire that perpetuated the fire resistant longleaf pines and allowed for large, long lived (600 years plus) trees (Zobrist et al. 2005). These lands were replaced with other southern yellow pine species (primarily *Pinus taeda* L.) that could better suit the needs of the timber industry. Today dozens of threatened or endangered wildlife species utilize the remaining 1.2 million hectares of longleaf pine forest, of which less than 5,000 hectares are regarded as old growth (Zobrist et al. 2005).

Despite the compositional and structural differences between historic open pine and current intensively managed forest conditions, plantations can provide habitat for many forest species (Greene et al. 2016, Zobrist et al. 2005). Greene et al. (2016) argue that managed pine forests that receive mid-rotational silvicultural activities such as prescribed fire, chemical treatment, or forest thinning can provide habitat for wildlife species adapted to and favoring open pine conditions. Additionally, young planted forests provide early successional habitats dense with graminoid bunches, diverse forbs, and singing perches needed for pine-grassland avian species such as the Bachman's sparrow (*Aimophila aestivallis*), eastern kingbird (*Tyrannus tyrannus*), yellow-billed

cuckoo, northern bobwhite, prairie warbler (*Dendroica discolor*), greater roadrunner (*Geococcyx californianus*), American woodcock (*Scolopax minor*), and the eastern towhee (*Pipilo erythrocephalus*).

Having early successional habitat scattered throughout this matrix of planted pine is beneficial to other species groups as well. Small mammals and invertebrates benefit from the increased sunlight in early successional habitat that promotes dense herbaceous and forb layers that provide food and cover from aerial predators (Kellner and Swihart 2014). The retention of logging debris on cutover lands benefits avian, small mammal and insect groups by providing substrate and microsite movement pathways (Kellner and Swihart 2014).

As these early successional habitats mature, they enter the stem exclusion stage as the canopy closes. This limits and in some cases totally restricts use of those stands by certain species. As the structure of these forests shift, so do their vegetative composition and density. Closed canopy avian species such as the tufted titmouse and Carolina chickadee eventually will replace the early successional specialists such as eastern kingbirds (*Tyrannus tyrannus*) and prairie warblers (*Setophaga discolor*) in growing stands. However, the dynamic nature of the plantation matrix allows for a mix of stand types in varied stages of development, in close proximity to each other, which provides a plethora of stand and edge types, and facilitates species dispersal.

Structural (density, debris abundance, canopy cover), compositional (floral and faunal diversity), and functional (stand stage, productivity, management practices) bio-indicators of forest diversity have been identified for stand level plantation management (Smith et al. 2008). Amongst these bio-indicators, stand stage, a multivariate classification of stand structure, is the most effected by forest thinning activities (Smith et al. 2008). Because thinning is a necessary management practice in planted and natural forests grown for timber, it is the easiest functional bio-indicator of biodiversity to change (Smith et al. 2008). Stand structure is strongly correlated with species richness, and so the use of a small number of stages (pre-thin, post-thin, pre-clearcut) can be used to summarize biodiversity changes over each forest cycle (Smith et al. 2008). When these stages of stand development created by stand age and forest thinning are adjacent to each other, they create unique edges of unknown value to wildlife diversity.

Owens et al. (2014) argue that intensively managed pine species plantations can support more birds than the historically disturbed landscapes. Intensively managed *Pinus spp.* plantations are managed and maintained more so today than historically. Models developed to determine the relationship between avian richness, abundance, and breeding score (a measure of breeding activity) were all positively correlated with non-woody vegetation height, density,

and heterogeneity within planted forests (Owens et al. 2014). Successional changes in these young forests steadily facilitated a 15-power increase in breeding activity in only 5 years and avian richness doubled over this time (Owens et al. 2014).

Numerous evaluations of wildlife diversity within planted forests have been conducted on stands of varied structure (Calladine 2009, Lindenmayer et al. 2009, McWethy 2009, Smith et al. 2008, and Constantine et al. 2005). What we propose is the evaluation of wildlife diversity amongst combinations of stand structures, or edges, between timber stands of three stand stages. The spatial and temporal shifting of plantation stands within a forest-dominated landscape is what is so intriguing about utilizing their edges more efficiently. The value of edges for wildlife depends on their spatial configuration (MacDonald 2003), productivity (McWethy et al. 2009), and structure (Smith et al. 2008), which are controlled through management decisions. If managers of large land bases undertake stand level management for biodiversity, then their practices are likely to support increased biodiversity across the landscape (Zobrist et al. 2005). The scale for such management could extend throughout the American Southeast where pine species are endemic and grown commercially on 19% of privately owned forestlands (Greene et al 2016, Owens et al. 2014).

It is widely accepted that planted forest monocultures are less biologically diverse than naturally regenerated primary or secondary forests (Thompson et al. 2011, Jactel and Brockerhoff 2007, Zobrist et al. 2005, and Hartley 2002).

Planted forests are often treated with herbicides during planting site preparation to reduce herbaceous and woody competition to the crop species. Prescribed fire, which reduces litter layers, coarse woody debris, and mid-story density, are also common in planted forest monocultures to reduce fuel loads that could endanger investments, limit accessibility to humans, and compete with crop species for space, light, and nutrients. Additionally, these planted forests are often harvested prior to trees reaching sizes and ages necessary for habitation by several cavity nesting woodland bird, and mammal species. Despite these limitations, planted forests are still more beneficial to wildlife than urban or agricultural land uses (Hartmann et al. 2010, Brockerhoff et al. 2008, and Stephens and Wagner 2007).

Biodiversity within plantation forests is important because more biodiverse stands have been shown to be more productive (Hartley 2002, Jactel and Brockerhoff 2007) and resilient to perturbation (Hansen et al. 2001). The presence and abundance of several insectivorous species can offset, reduce, or stop damaging insect outbreaks and limit dangerous forest disease vectors that can have detrimental effects in monocultures (Jactel and Brockerhoff 2007).

Additionally, the presence and abundance of game species such as white tailed deer and feral hogs allow landowners to utilize their timberlands as hunting leases that offer annual returns on their long-term forestry investments (Zobrist et al. 2005). Tracking forest productivity and diversity together allow for direct comparisons of the benefits diverse wildlife communities provide plantation forests and facilitate the marriage between conservation and industry.

Managing plantation forests as efficiently as possible can also help curb the loss of biodiversity from the conversion of naturally regenerated forests to other uses (Hartmann et al. 2010). Increasing forested patch sizes and providing corridors for wildlife moving through plantation forests from one natural forest patch to another are examples of those management strategies (Lindenmayer et al. 2009, Miller et al. 2009, MacDonald 2003, Hartley 2002, Lindenmayer 1999, Norton 1998). For instance, area of forested patches of wildlife habitat could be increased by establishing forest plantations of regionally endemic species adjacent to naturally regenerated forests (Miller et al. 2009, Norton 1998). Thus, intensively managed commercial plantations, which comprise 19% of privately owned forests in the southern United States (Greene et al. 2016), may be more beneficial for wildlife and ecosystem functions than currently known once spatial, temporal, and site specific characteristics are better understood (Stephens and Wagner 2007, Hartley 2002).



The use of plantation forests to provide ecosystem services (such as erosion prevention, pest control, pollination, clean water, food, mitigation of climate change, control of disease vectors, ecosystem stability, and goods in the form of timber) is becoming more and more necessary given current forestry trends (Thompson et al. 2011). Increased biodiversity in forest stands enhances the delivery of certain ecosystem services, while a reduction in diversity results in the degradation of certain ecosystem services (Thompson et al. 2011). These trends illustrate the need and opportunity for plantation managers in North America to consider implementing creative management practices to promote wildlife biodiversity. Managing for both timber production and species conservation is possible, but will require insight regarding specific management practices and their effects on wildlife (Lindenmayer 1999, Hansen et al. 1991).

Biodiversity conservation efforts in the forestry industry currently include certification programs such as the Sustainable Forestry Initiative (SFI), which has become a leading force in sustainable forest management in the United States (SFI 2015-2019). Globally, 323 million hectares (ca. 8%) of commercial forests have become certified through one of the many certification agencies. These lands produce 25% of the world's timber (Moore et al. 2012). Timber plantations and natural forests certified under such programs utilize management practices that are beneficial to biodiversity conservation (Hagan et al. 2005). For instance,

SFI certified forest lands have increased emphasis on the writing of management plans, controlling invasive species, adhering to best management practices (BMP's) for water quality and soil retention, and planning for biodiversity and habitat conservation (Hagan et al. 2005).

The notion of altering forest management practices to promote wildlife biodiversity, while minimizing economic loss, is not a new concept (Franklin and Foreman 1987). In fact, this subject has been studied in multiple ecosystems and with varied species compositions, rotation lengths, and harvest strategies (Pryke and Samways 2012, Stephens and Wagner 2007, Carnus et al. 2006, MacDonald 2003, Hartley 2002, Norton 1998, Hansen et al. 1991, and Franklin and Foreman 1987). For example, a comparison of harvest strategies on Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco) plantations in the U.S. Pacific Northwest called for the retention of biological corridors and forest patches among cutover lands to enhance inter-patch movement of species, reduce wind effects, and provide edge and cover for wildlife (Franklin and Foreman 1987). Similarly, Norton (1998) argued that forest management strategies in New Zealand could be altered to improve biological corridors without reducing timber production by adopting a landscape management approach and ensuring that there are always mature plantation stands adjacent to younger plantation stands.

Progress towards improving conditions for wildlife within these various planted forest ecosystems began with recognizing the positive relationship between biodiversity and forest productivity (Thompson et al. 2011, Klenner et al. 2009, Brockerhoff et al. 2008, Jactel and Brockerhoff 2007, Stephens and Wagner 2007, MacDonald 2003, Hartley 2002). Several studies have been conducted looking at the effects of forest features and silvicultural actions on diversity. For instance, some of their findings indicate that the abundance of snags and coarse woody debris (CWD) (Hansen et al. 1991), canopy openness (Greene et al. 2016), rotation length (Andreu et al. 2008, Carnus et al. 2006), and understory composition and structure (Hartley 2002) are all linked to forest biodiversity.

Improving forest productivity by improving forest biodiversity can be a delicate balancing act because too much or too little of certain management actions can have adverse effects for both biodiversity and productivity. Limiting the stem exclusion stage through more severe pre-commercial and commercial thinning earlier in a rotation has been recommended to promote biodiversity through understory development (Andreu et al. 2008, Carnus et al. 2006); however, once the canopy is open, the mid-story hardwoods and vines will have to be controlled lest the understory be shaded out and diversity diminished (Andreu et al. 2008, Zobrist et al. 2005). Extending rotation lengths has also

been recommended for and attributed to increases in biodiversity (Carnus et al. 2006), but doing so may not coincide with the goals of stakeholders and the fluctuations of timber markets (Zobrist et al. 2005, Hartley 2002). Managing for biodiversity within commercial timberlands does not have to be a significant economic burden on landowners. By identifying any detectable differences in wildlife diversity amongst forest edges and carefully evaluating management decisions such as stand delineation and regulation, we hypothesize that plantation stands and edges can be arranged in a way that is least detrimental to biodiversity and connectivity on the landscape, while maintaining viable production and revenue levels.

This case study focused on the planning for wildlife biodiversity and connectivity in a landscape dominated by plantation forests, specifically on the management of edges between plantations. We defined these edges as the ecotone between structurally different stands of timber being grown with the same management strategy but on different timelines. These edges are currently created over space and time depending on timber markets, site productivity, real estate trends, and decisions made by land managers in regulating a large forested land base.

By determining if biodiversity differences and/or similarities exist among edges in loblolly pine (*Pinus taeda* L.) tracts in East Texas, we will be able to

ascertain if changes to plantation edge ratios and locations would benefit wildlife on a landscape scale (Thompson et al. 2011, Jactel and Brockerhoff 2007), or if current management strategies already account for these factors. Wildlife biodiversity estimates will reflect local stand level conditions, but the scope of this project will include landscape scale considerations for southern yellow pine plantation management in the southern United States.

## METHODS

### Study Area

The Davy Crockett and Angelina National Forests, located approximately 32 kilometers apart in the eastern region of the Pineywoods of Texas ([tpwd.texas.gov](http://tpwd.texas.gov)), are the oldest and largest contiguous patches of forested lands in the region. These forests have different forest management objectives than the plantation matrix between them, allowing for natural regeneration and increased vertical structural complexity. These National Forests are 70-80 year old even aged forests approaching old growth conditions, where the original cohort is allowed to die naturally and structural conditions including large diameter live and dead trees, multiple cohorts, a diverse composition, and canopy gaps created by natural and anthropogenic disturbances develop over time.

These forests are not used for timber; however, the frequent use of prescribed fire by forest managers has created an almost homogeneous structure throughout much of their total area. Prescribed fire is used to reduce fuel loads that could lead to dangerous wildfires, but this favors fire resistant floral species and contributes to the forest homogeneity. These older and larger forested patches benefit certain faunal species that require forest interior habitats

and older trees but have limited use for other early successional habitat specialists. Due to the heterogeneity and fragmentation of forest age ranges within timberlands, one may argue that these planted timberlands offer a more diverse range of niches for wildlife than the National Forests. This study was designed to estimate species' richness, abundance and biodiversity in edges created within the timberlands of that matrix.

Stand-replacing disturbance did occur on this landscape prior to the widespread establishment of plantation forests, but not on the same scale or level of fragmentation as today (Van Lear et al. 2004, and Noss1988). Stand rotational phases on sampled lands, based on forest thinning's, are very similar and evenly distributed spatially, which is intuitive considering the constant need for harvestable timber stands (Figures 3-6). The similar ratio of stand rotational phases and distribution on the sampled landscape helps to reduce any error that may have occurred had there been an unequal proportion or clumping effect of one or more edge types.

#### Edge Types and Sampling Site Selection

Data were collected during the summer months (June-August) of 2015 and 2016, on six 4-hectare sites, using sampling techniques targeting invertebrates, birds, small and medium-sized mammals. We avoided sampling

areas close to major roads, residential areas, and streamside management zones to minimize the effects of those features on observations of biodiversity. We also excluded sites where logging roads were inaccessible due to rutting from forest harvests. These limitations greatly reduced available edges to sample.

Edge treatments were defined based on a chronosequence approach (Smith et al. 2008) that uses the thinning regime on sampled lands as a separator for three stand stages of development that correspond closely to stand age in these intensely managed forests. Current management strategies on sampled lands result in thinning between 11 and 18 years after planting and less productive sites can be clear-cut as early as 18 years post planting. This strategy creates three stand structural phases that occur within each rotation; pre-thin, post-thin, and pre-harvest, which were used to define the three edge types (pre-thin / post-thin, pre-thin / pre-clearcut, and post-thin / pre-clearcut). Sites were selected based on the combination of available stand types that encompassed each edge type using ArcGIS software (Version 10.2.2, ESRI 2011) and maps provided by the land managers (Figures 1-6). The collective sites available for sampling yielded one dataset of the three edge types in 2015 and one replicate for each in 2016 (Figure 2).



Once edges were identified, we defined a 100m x 200m section on each side of each edge where sampling was conducted (Figure 7). The study area for each site was four hectares with two hectares on each side of sampled edges. Ten sampling lanes were established 20m apart in these sections to facilitate movement of field technicians while deploying traps (Figure 8). These sampling lanes also aided the detection of medium mammals with motion sensing trail cameras, because without them visibility would have been only a few feet in certain instances and the likelihood of detecting present individuals would have been greatly reduced. Additionally, without these sampling lanes, sampling small mammals systematically would not have been possible, but rather traps would only have been placed biasedly in areas accessible to humans.

### Sampling Techniques

Edges were sampled for invertebrates using pitfall traps for five consecutive days each sampling season. Each trap array was confined to a one meter square comprised of five 0.47-liter plastic cups arranged with one trap in the center and one at each corner. One cup was placed in the ground at ground level; a second cup, of equal size, was placed inside the first and a few cubic centimeters of rubbing alcohol and water was added to kill any invertebrates that fell into each cup. Four trap arrays were placed along sampling lanes perpendicular to each edge with two arrays on either side of the edge, one at 10

meters and one at 20 meters, for five nights for twenty trap nights per survey per site. Two out of the ten sampling lanes were randomly sampled each survey. Samples were collected on the fifth day. Insects trapped were stored in glass containers filled with ethanol for identification in the lab. Once in the lab, collected specimens were sorted and identified to family using entomology guides for North America (Marshall 2006, Arnett and Thomas 2001).

Avian biodiversity and abundance were estimated using the independent double observer method as described by Nichols et al. (2000). Point counts were located 50m from the plantation edge within each stand and 130m from each other to maintain sample independence (Figure 8) (Calladine et al. 2009). Each point was a 50m diameter circle, so every bird seen or heard within 25m of the point center was recorded. All sites were comprised of four point counts per season and each point was sampled by both observers simultaneously for ten minutes. The distance to detected birds and time of detection were recorded by each observer independently. Field data collected included: species, time, site number, distance to observed bird, whether detection was visible or audible, and weather conditions for that day. To prevent observer bias in detection probability, we avoided verbal and non-verbal cues between observers during surveys (Taulman 2013).

Pre-thinned stands reduced the range of visibility so we relied on estimations of distance from audible detections. Audio detections of birds during fixed radius point count sampling often overestimate distances to detected birds regardless of observer ability (Nichols et al. 2000, Alldredge et al. 2007, Taulman 2013). To reduce this source of error, a 25m logger's tape was stretched in each direction from each point center to mark point boundaries, allowing observers to visualize the boundary from the center of the point.

To detect medium mammal species and estimate richness and abundance, we used 30 Reconyx Hyper-fire motion game cameras (Reconyx Inc. Holmen, WI) at each site for 10 consecutive days (150 trap nights per site) with two cameras at each trap location (Sanderson and Trolle 2005). Cameras were programmed to take pictures continuously, with flash as needed, for each ten-day sampling period. Each motion detected by the cameras triggered a five-picture sequence. Cameras were placed randomly along sampling lanes to avoid bias. Cameras were placed on either side of each edge with five sets of cameras on even lanes on one side and five sets on odd lanes on the other. The remaining five camera sets were placed randomly on empty lanes on both sides of the edge.

After trimming back vegetation within the camera's flash range (5.5m), we placed cameras at appropriate heights (1-2m) and angles to focus on cleared

sampling lanes or obvious game trails and openings. The two cameras at each trap location were oriented to focus on the same focal point from different angles, to take pictures from both sides of the animal to facilitate individual identifications. Cameras were secured in a metal box screwed to trees and locked with a cable to prevent theft.

We sampled small mammals with 8 x 8 x 22 cm Sherman traps (H.B. Sherman Trap, Inc., Tallahassee Fla.) baited with pre-made peanut butter balls encased in wax paper. We deployed 200 traps per site, equaling 1,000 trap nights per survey per site. We set traps 10m from each other along 10 sampling lanes with 10 per side of edge. We marked captured small mammals via toe clipping (Umetsu et al. 2006) to identify unique individuals (SFA-IACUC Protocol # 2016-008). Sherman traps were sprayed with insect repellent prior to use to reduce the amount of fire ants attracted to baits, increase trapping success, and increase small mammal survival.

#### Measurements of Richness and Diversity

Calculations for richness and diversity were made with replacement, therefore we assumed that the wildlife communities sampled were “closed”, meaning that immigration, emigration, births, and deaths were not occurring during the sampling period and that no new species were colonizing or going extinct in the study area. Sampling with replacement means that sampled

individuals were recorded, but not removed from the assemblage. Thus, the abundance of each observed species affected how easily or how often they were detected.

Species richness was defined as the sum of vertebrate species observed on sampled edges within 200m x 200m blocks. Family richness was defined as the sum of invertebrate families observed on sampled edges. Diversity is defined as “an expression or index of some relation between the number of species and their corresponding abundances” (Spellerberg and Fedor 2003). There are two types of diversity indices (Itô 2007). Type 1 indices include the Shannon diversity index ( $H'$ , equation 1), which is most sensitive to the occurrence of rare species. Type 2 indices, like Simpson’s index ( $D$ , equation 3) and the Berger Parker index ( $d$ , equation 6), are most sensitive to changes in the abundance of the dominant species in each assemblage. Species dominance refers to which species contributes the most individuals to each assemblage. More than one dominant or rare species can exist at each site.

There are two kinds of data typically used in richness studies; incidence data, which treats each species as detected or undetected, and abundance data, where the number of each species is recorded in each sample (Gotelli and Colwell 2011). Due to logistical, temporal, and physical restraints that limit the

number samples that can be taken from wildlife communities, under-sampling bias can occur (Gotelli and Colwell 2011). To overcome this issue we utilized both incidence and abundance data from my samples to estimate diversity.

There are a few weaknesses with using diversity indices as a predictor of ecological diversity. It is difficult to interpret index values alone because species lose their identity when they are grouped together. This grouping assumes that all species are equal in value to the ecosystem, when in fact there are no two species who share identical abundances, life history traits, or habitat preferences (Barrantes and Sandoval 2009). Combining species into vertebrate groups does not fix the issue of combining species richness with abundance data into a single value; however if both Type 1 and Type 2 indices are used, a better understanding of the system can be formulated (Itô 2007). Finally, diversity indices lack a probabilistic basis, making it impossible to measure the accuracy of hypothesis using index values and thus compare them between communities (Barrantes and Sandoval 2009). For these reasons we elected to utilize two Type 2 indices (Simpson's, Berger-Parker), and one Type 1 (Shannon).

Species diversity indices along with their corresponding evenness (Shannon and Simpson indices only) were calculated for each edge type. Only vertebrate species were considered for estimates of species diversity. Shannon's index is a

measure of the character of the relationship between individual species' abundances ( $n_i$ ) and the total number of individuals observed ( $N$ ). Values for  $H'$  should fall between 1.5 and 3.5 for ecological data, but can equal zero if there is only one species in the dataset. Higher values of  $H'$  indicate communities that are more diverse.

Shannon's index ( $H'$ ) is affected more-so by less abundant species. The idea behind  $H'$  is that the more species there are, and the more equal their proportional abundances in the dataset, the more difficult it is to correctly predict which species will be the next one identified. Using the Shannon index quantifies the uncertainty associated with this prediction, and then it quantifies the uncertainty in predicting the species of a randomly selected individual taken from the dataset. The more unequal the abundances of the species types, the smaller the corresponding  $H'$ . If one species accounts for the majority of the total abundance, and the other species are very rare,  $H'$  declines. When there is only one species in the dataset,  $H'$  equals zero because there is no uncertainty in predicting the species of the next randomly chosen individual.

Shannon's Index of Diversity (equation 1)

$$H' = -\sum_{i=1}^S (P_i * \ln P_i)$$

Evenness is defined as the variability in species abundances amongst a sample (Magurran 2004). An “even” community would be one with an approximately equal number of individuals across species (Magurran 2004). Evenness for  $H'$  ( $E_{H'}$ , equation 2) was calculated by dividing  $H'$  by  $H'_{\max}$ .  $H'_{\max}$  is defined as the maximum diversity that could occur which would require all species to have equal abundances (Magurran 2004) and is calculated as the natural log of the total number of individuals amongst all species.

Evenness for the Shannon Index (equation 2)

$$E_{H'} = H' / H'_{\max}$$

where  $H'_{\max} = \ln(N)$

Values for Simpson’s reciprocal index ( $1/D$ ) begin at 1 and increase with increased diversity with the maximum value being less than or equal to the richness. Simpson’s index ( $D$ ) is known to work well with small sample sizes and represents the probability of picking two different individuals of the same species back to back. This index gives more attention to abundant species than rare or cryptic species. Simpson’s index is calculated by taking the sum of squares of the total number of individuals in each species, divided by the total number of individuals in all observed species (equation 3). We used the inverse of  $D$  to better illustrate and compare the indices (equation 4). This makes both  $H'$  and  $1/D$  positive integers with ascending values, indicating increased diversity.



Equation 3 is designed so that the smaller the sum of squares for  $n_i/N$ , the larger the reciprocal form of the index, making it more sensitive to changes in the number of individuals in the dominant species. Species that are more abundant raise the sum of squares, which ultimately lowers the reciprocal index value. Converting Simpson's index to its reciprocal form ( $1/D$ ) allowed for both  $H'$  and  $1/D$  to be translated with low index values indicating less diverse conditions and high index values indicating more diverse conditions.

Simpson's Index of Diversity (equation 3)

$$D = \sum(n_i/N)^2$$

Simpson's reciprocal index (equation 4)

$$1/D$$

Evenness for the Simpson's reciprocal index ( $E_{1/D}$ ) was calculated by dividing the index value by the total number of species observed ( $S$ ) (equation 5). Values for  $E_{1/D}$  range between 0-1.

Evenness for the Simpson's reciprocal index (equation 5)

$$E_{1/D} = (1/D) / S$$

The Berger-Parker index ( $d$ , equation 6) is commonly used to assess the dominance of the most abundant species in a community and is equal to the

highest value for  $n_i / N$ . This index has been used to compare differences in species abundances across varied communities within a similar ecosystem where species composition may remain similar but the number of individuals of each species may vary. The reciprocal form ( $1/d$ ) is used more often, so that an increase of  $1/d$  values represents an increase in diversity and a reduction in dominance (Magurran 2004). This is calculated by dividing the number of individuals in the most abundant species ( $n_i \text{ max}$ ) for each edge type and year by the total number of individuals in each sample ( $N_i$ ) and then converting to a reciprocal (equation 7). The greater the difference between the number of individuals in the most dominant species per edge and each edge's total number of individuals, the higher the corresponding value for  $1/d$ . Assemblages with the most dominant species, and lowest diversity, will therefore have the lowest value for  $1/d$ .

Berger-Parker Index of Dominance (equation 6)

$$d = (n_i \text{ max} / N)$$

Reciprocal form of Berger-Parker Index (equation 7)

$$1/d$$

Alpha, beta, and gamma diversity were calculated for each edge type and sampling season. Alpha diversity represents local richness per edge type (equation 8), gamma diversity represents richness across all sites (equation 9),

and beta diversity represents the dissimilarity between sites (equation 10). Beta values were calculated for each vertebrate group individually within each edge type and also for the sum of all vertebrate species found within each edge type.

Alpha Diversity ( $\alpha$ ) (equation 8)  
 $\alpha$  = Richness at edge A, B or C

Gamma Diversity ( $\gamma$ ) (equation 9)  
 $\gamma = S_{\text{edge A}} + S_{\text{edge B}} + S_{\text{edge C}}$

Beta Diversity ( $\beta$ ) (equation 10)  
 $\beta = \gamma / \alpha$

Looking into the composition of species may become a necessity if two edge types have similar biodiversity indices, richness, and/or evenness. For instance, the proportion of resident birds versus migrants observed, nuisance species versus game species, predator versus prey species, or the presence of rare, cryptic, threatened or endangered species may supersede richness as an indicator of edge habitat quality for wildlife.

Clustering of species detections amongst edges was graphed using a triangular coordinate system where each species' proportional abundance amongst edges created a profile of three numbers in decimal form that sum to 1 (Ex: 1,2,3=6  $1/6=0.17$ ,  $2/6=0.33$ ,  $3/6=0.5$ ). The abundance of each species per edge type was divided by the total number of individuals for each species among edges to create the triangular coordinate profiles (Ex: [0.17, 0.33, 0.50]). Profiles

represent individual species proportions amongst edges that are represented by each data point within the triangular coordinate graphs, which have three axes labeled from 0.0-1.0 (Greenacre 1993). Each apex point of the triangle represents a value of 1 for one edge and 0 for another. Data points located on triangle points indicate that the particular species was found exclusively within one edge type. These graphs allow the visualization of species detections and abundance between the three edge types (Figures 15-17).

Small sample sizes in wildlife studies result from logistic, spatial and temporal constraints that can limit replication. It is often advantageous in these situations to utilize tools like accumulation curves that allow for the extrapolation of some asymptotic measure of richness (Colwell et al. 2004, Willott 2001). Software EstimateS 9.1 is used to extrapolate species richness from small sample sizes using sample (Species accumulation curves, SAC) based incidence matrix (Colwell 2013). Each curve was created using binomial data sets from 2015 and 2016, where detection of a species was indicated with a 1 and non-detection with a 0. These two samples were then extrapolated out to six samples, and fitted to a curve, to compare estimated richness differences amongst animal groups and edge types (Colwell et al. 2004).

Problems associated with extrapolation via accumulation curves include the lack of data regarding relative abundances of species, detection probabilities, or occupancy rates. The species occurrence variation among samples and non-random patterns of co-occurrence of species are sources of heterogeneity, defined as “patchiness” among samples (Colwell et al. 2004). For patchy distributions, the individual based species accumulation curves overestimate richness (Ugland et al. 2003). For this reason, it is better to use sample based species/family accumulation curves (SBSAC, SBFAC) that will account for heterogeneity between samples (Ugland et al. 2003).

Another problem associated with extrapolation is that extending the number of samples in empirical data sets is only recommended up to triple the original dataset (Colwell et al 2004). Accumulation curves must have established an obvious plateau to provide reliable estimates of richness (Thompson and Thompson 2007, Willott 2001). For the assemblages being sampled, if their corresponding accumulation curves had not reached an obvious plateau, then we would have to assume that there was inadequate sampling effort to estimate richness (Thompson and Thompson 2007).

Seven curves (Figures 20-26) that illustrate the relationship between species/family richness and sampling effort were created using EstimateS 9.1

(Colwell 2013). Input for EstimateS required the construction of binomial incidence data for species (Colwell 2013). Estimated values for richness via EstimateS 9.1 were calculated as the mean of 100 randomized runs and 200 bootstraps. Outputs from EstimateS included the estimated number of species to be found at each edge type ( $S_{est}$ ) if six samples were taken based on extrapolation of the 2015-2016 samples. EstimateS also generated the upper and lower bounds of each SBRCs 95% confidence interval. EstimateS 9.1 generated three types of curves; cumulative vertebrate SBRCs for each edge type (3), SBFAC for the invertebrates with all three edges plotted together (1), and SBRCs for the invertebrates by edge type (3) (Figures 20-26). A Student's t-test and corresponding probability (p) values for each vertebrate group and invertebrates was calculated to identify any significant differences between edge types.

### Habitat Variables

We estimated vegetation variables along sampling lanes to account for differences in biodiversity values found between stands and edges. We selected three out of ten sampling lanes per side of each edge to sample vegetation. Vegetation sampling plots were placed at random distances inside each stand (10-100m), perpendicular to the edge (6 plots per site). Once plot center was established we selected a random azimuth to lay out the sampling transect.

Variables estimated included: over story density (ft<sup>2</sup>/ac), understory composition (%), vertical structural complexity (Nudd's board), stand height (ft.), and below canopy light conditions (DSF, ISF, GSF). Over-story density was sampled using three averaged 10 basal area factor (BAF) prism points; canopy total height was averaged using three site trees (tallest trees) per stand and a Suunto clinometer.

A Nudds' board (2m tall x 0.5 m wide) was used to identify mid-story structural complexity in each stand (Nudds, 1977). The board was randomly placed at each plot using three random azimuths and observations from a distance of 10m. The proportion of the board obstructed by vegetation was recorded as a single digit density score, which correspond to a mean value of a range of quintiles (1=0-20%, 2=21-40%, 3=41-60%, 4=61-80%, 5=81-100%) (Nudds, 1977). The three Nudd's board estimates at each plot were averaged.

CWD and understory composition was estimated using a modified version of the Brown method as described by Lutes and Keane (2006). The Brown method is typically used to monitor fuel loading for prescribed and natural fires. Only the CWD and understory composition estimates were utilized via this method, due to their direct relationship to avian and small mammal communities (Jones et al 2009). Duff, decay, litter height, and slope were not estimated. One notable difference in my methodology and Lutes and Keane's is that we used a

1m square plot on each transect to sample understory composition instead of the “sampling cylinder”.

Edge types were defined based on thinning regimes, thus the amount of light reaching the forest floor varied between stands and edge types. Digital hemispheric canopy photography (DHCP), as used in Stovall et al. (2009), was used to characterize the proportion of canopy and the amount of light penetrating the canopy. Twenty four DHCP images were taken, 4 pictures for each of the six sites with one picture 10m inside each stand and one 40m inside of each stand. The sampling lane chosen to take pictures was chosen randomly at each site. DHCP images were taken in the early morning hours on overcast days to reduce errors created by direct sunlight overhead. A Sigma-SD15 camera (Sigma Corp, Japan) with a Sigma DC HSM Circular Fish Eye 4.5mm: 2.8 lens (Sigma Corp, Japan) was placed on top of a 1m tripod to take pictures up from below the forest canopy.

Pictures were then thresholded on the gray channel using Hemi-View version 2.1 (Rich et al, 1999) to create binary images with the tree foliage and branches separated from the sky. Each image was thresholded three times and their means were used. The use of Hemi-View 2.1 canopy analysis software (Rich et al, 1999, Delta T Devices 1999) provided below-canopy light metrics, including the proportion of direct (DSF), indirect (ISF), and global (GSF) site



factors (Rich et al, 1999, and Stovall et al. 2009). Direct site factor indicates the ratio of direct light below the canopy to direct light above, indirect site factor indicates the proportion of diffuse light penetrating the canopy, and global site factor is the ratio of total light below the canopy to the total light above (Stovall et al. 2009).

## RESULTS

### Sample Size

A total of 339 individuals comprising 41 vertebrate species (26 birds, 10 medium mammals, and 5 small mammals) were identified within the six sites during 2015-2016 (Table 1 and 2). Fifty five invertebrate families were identified via pitfall trapping on the six sites during the summers of 2015-2016 (Table 3).

### Vertebrate Species and Invertebrate Families

The distributions and proportional abundances of vertebrate species amongst the three edge types for each year are displayed with triangular coordinate graphs (Figures 15-17). The Carolina wren (*Thryothorus*

*ludovicianus*), northern cardinal (*Cardinalis cardinalis*), and white-tailed deer (*Odocoileus virginianus*) were the only three vertebrate species found at all six sites (Table 1 and 2, Figures 9-11).

The Carolina chickadee (*Poecile carolinensis*), Carolina wren, Northern cardinal, and tufted titmouse (*Baeolophus bicolor*) were the only of the 21 bird species detected in 2015 found in all three edges, whereas 6 out of the 23 detected in 2016 were detected in all three edges (American crow (*Corvus brachyrhynchos*), Carolina wren, indigo bunting (*Passerina cyanea*), mourning dove (*Zenaida macroura*), Northern cardinal, and white-eyed vireo (*Vireo griseus*)) (Table 1). Overall, there were 12 resident bird species and 14 migratory species detected in the study area (Table 1). Resident avian species detected accounted for 67% of individuals and migrants accounted for 33% (Table 1). The abundance of resident species did not vary much between edge types (A=48, B=42, C=41), but the abundance of migrant species increased with edge stand ages (A=8, B=22, C=33) (Table 1).

Edge type A was the only edge with a detection of the migrant Kentucky warbler (*Geothlypis formosa*) and edge type B was the only edge type with a detection of the migrant summer tanager (*Piranga rubra*) and black and white warbler (*Mniotilta varia*) (Table 1). The American robin (*Turdus migratorius*), and

northern bobwhite, both resident species, along with the migrant blue-gray gnatcatcher (*Poliioptila caerulea*), ruby –throated hummingbird (*Archilochus colubris*), and eastern wood pee-wee (*Contopus virens*), were found exclusively in edge type C (Table 1).

Of the medium mammals 21 individuals were detected in edge type A, 34 in B and 33 in C (Table 2). The most abundant species detected was white-tailed deer (28) followed by feral hogs (*Sus scrofa*) (24) (Table 2). Detections of white-tailed deer were identical for edges A and B (8) with a slight increase in edge type C (12) (Table 2). Feral hog individuals were detected more in edge type C (14), than B (9) or A (1) (Table 2). Detections of bobcat (*Lynx rufus*) were exclusive to edge type A for both years (Table 2) and the only detection of a gray fox was within edge type C (2016) (Table 2).

Small mammal captures were more abundant in edge type A (30) than B (12) and C (17) combined (Table 2). Deer mice (*Peromyscus maniculatus*) captures accounted for more than the other four species combined (Table 2). The white-footed mouse (*Peromyscus leucopus*) was captured exclusively in edge type A (Table 2).

Of the 55 invertebrate families captured in 2015 and 2016, 21 of them were trapped exclusively in edge type B, including two families of spiders

(Pisaruidae and Theridiidae), two families of millipedes (Eurymerodesmidae and Spirobolidae), and seven families of beetles (Boridae, Caribidae, Cerambycidae, Pythidae, Staphylinidae, Tenbrionidae, and Trogossitidae) (Table 3). Seven families were found exclusively in edge type A, including three families of beetles (Lucanidae, Silphidae, and Synchronidae) (Table 3). Eight families were found exclusively in edge type C, including Scorpionidae (scorpions), and Ixodidae (ticks) (Table 3). Seven families were trapped in all edge types, including three cricket families (Gryllacridae, Tettigonidae, and Rhabdophoridae), two beetle families (Cucujidae and Scarabaeoidea), and one ant family (Formicidae) (Table 3).

### Richness

During 2015 the edge type with the highest vertebrate species richness was edge B ( $S=22$ ), followed by edge types A and C, which had equal values of richness ( $S=19$ ) (Table 5). In 2016 edge type C had the highest richness ( $S=28$ ), followed by edge type B ( $S=22$ ) and lastly edge type A ( $S=17$ ) (Table 5).

To determine which side of each edge contributed more vertebrate species and invertebrate families to their overall richness, the edges were separated and richness per side of each edge was graphed (Figures 9-14). With the exception of edge type B in 2015 (10 versus 10) and edge type A in 2016 (6

versus 7), each edge had more bird species in its older side, with the largest difference being edge type A in 2015 (9 vs 4) (Figures 9-14). Three sites had more medium mammals in their younger side (C-2015, A and B - 2016), two had equal ratios (A and B - 2015), and one (2016 - C) had more in its older side (Figures 9-14). Small mammals occurred at equal ratios for three sites (A and B-2015, and A for 2016), two sites had more species in their older sides (C-2015-16), and one had more in its younger side (B-2016) (Figures 9-14). Family richness in edge type B (35) for invertebrates was almost double that of A and C during 2015 (18) and was tied for the lowest by one family in 2016 (Figures 9-14). During 2015 each edge had more invertebrate families in their younger side (Figures 9-14), but in 2016 edges A and C were the same for the sides of each edge (Figures 12 and 14). Edge type B favored the older side by one family (Figure 13).

#### Proportional Abundances of Individuals Amongst Species and Edges

Of the small mammals detected, deer mice were found in the most equal proportions amongst edge types (Figure 9). Hispid cotton rats (*Sigmodon hispidus*) were only found in edges B and C, where they shared equal proportions of individuals (Figure 9). Two thirds of the northern pygmy mice (*Baiomys taylori*) were found in edge type A, none in B, and one third in C (Figure 9). Similarly, two thirds of southern short-tailed shrews (*Blarina*

*carolinensis*) were detected in edge A (Figure 9). White-footed mice were only detected in edge type A (Figure 9).

Of the medium sized mammals, the eastern grey squirrel (*Sciurus carolinensis*) and Virginia opossum (*Didelphis virginiana*) were detected in equal proportions amongst edge types (Figure 10). Bobcats were only detected in edge type A and the gray fox was only detected in edge type C (Figure 10). Half of all coyotes (*Canus latrans*) detected were within edge type A and a third were in edge type C (Figure 10). Two thirds of all eastern cottontail rabbits (*Sylvilagus floridanus*) and raccoons (*Procyon lotor*) were detected in edge type B (Figure 10). Half of all nine-banded armadillos (*Dasybus novemcinctus*) were detected within edge type B while edges A and C shared equal proportions of individuals (Figure 10). More white-tailed deer and feral hogs were found in edge type C than in A or B, however, deer shared equal proportions of individuals in edges A and B (Figure 10).

The American robin, blue-gray gnatcatcher, eastern wood pee-wee, northern bobwhite, and ruby-throated hummingbird were exclusively detected in edge type C (Figure 11). The black and white warbler and summer tanager were found exclusively in edge type B (Figure 11). The Kentucky warbler was exclusively found in edge A (Figure 11). The mourning dove and yellow-breasted

chat (*Icteria virens*) were found in equal proportions amongst the edge types (Figure 11). The hooded warbler and red-eyed vireo (*Vireo olivaceus*) shared the same profile, with two thirds of individuals (*Setophaga citrina*) being detected in edge C and one third in edge B (Figure 11). Blue jays (*Cyanocitta cristata*) and common yellowthroats (*Geothlypis trichas*) were detected disproportionately in edge type A (Figure 11). Half of all Northern cardinals, pine warblers (*Setophaga pinus*), and white-eyed vireos were detected in edge type B (Figure 11). Downy woodpeckers (*Picoides pubescens*) were found in equal proportions in edges A and B with zero detections in edge C (Figure 11). Half of all gray catbirds (*Dumetella carolinensis*) were found in edge type B and half in C (Figure 11). The majority of Carolina wrens, tufted titmice, and yellow-billed cuckoos (*Coccyzus americanus*) were found in edge type C (Figure 11). Most American crows were detected in edges A and C, indigo buntings in B and C, and red-bellied woodpeckers (*Melanerpes carolinus*) in A and B (Figure 11). One more Carolina chickadee was detected in edge type B than in edge types A and C (Figure 11).

### Diversity and Evenness

Cumulative vertebrate alpha diversity values reflect species richness for each edge type (Table 4). The highest alpha diversity for birds came from edge type C in 2016 ( $\alpha=19$ , Table 4). The highest alpha diversity for medium mammals

came from edge type A in 2016 ( $\alpha=9$ , Table 4). The highest alpha diversity for small mammals came from edge types A and C during 2015 ( $\alpha=4$ , Table 4).

Gamma diversity in 2015 for small mammals, medium mammals and birds was 5, 7, and 21 respectively (Table 4). Gamma diversity for all vertebrate groups combined during 2015 was 33 species (Table 4). Gamma diversity in 2016 for small mammals, medium mammals, and birds were 2, 10, and 23 respectively (Table 4). Gamma diversity for all vertebrate groups combined during 2016 was 35 species (Table 4).

Edges B-2015 and A-2016 had the lowest overall beta diversity amongst vertebrate groups, each contributing all but one of the medium mammals that were found amongst all sites (6/7-2015, 9/10-2016, Table 4). Beta diversity for birds was lowest amongst edge type C for both years ( $\beta =1.61$ -2015, 1.21-2016), while edge type B tied for lowest in 2015 (1.61) (Table 4). Edge type A was the least diverse for birds during both years ( $\beta=1.91$ -2015, 2.87-2016, Table 4). The lowest beta values for small mammals were equal for edges A and C during 2015 (1.25) and for edges B and C for 2016 (2.00) (Table 4). The least diverse beta value amongst vertebrate groups that had at least one detection was medium mammals, from edge type C in 2015 (3.50 Table 4). Edge type A



during 2016 had zero small mammal captures, so beta diversity was not calculated for them.

Shannon diversity was mathematically highest in edge type B during 2015 (2.77) and C in 2016 (2.99) (Table 5). During 2015 the difference between the least diverse edge (A-2.73) and the most diverse edge (B-2.77) was only 0.04  $H'$  units apart (Table 5). In 2016 the most diverse edge (C-2.99) was only 0.3  $H'$  units more than the least diverse edge (A-2.69), and only 0.03  $H'$  units more than the middle value (B-2.96) (Table 5). Evenness for  $H'$  was highest in edge type B for 2015 (0.65) and edge type A in 2016 (0.85) (Table 5).

In 2015 edge type B had the highest richness (22) as well as the highest proportion of species with only one individual (41%) and yet was still the most even ( $E_H = 0.65$ ) and diverse ( $H' = 2.77$ ,  $1/d = 7.8$ ) amongst edge types (Table 5). Edge type A for the same year exhibited the lowest diversity ( $H' = 2.73$ ) and evenness ( $E_H = 0.62$ ) despite having the lowest proportion of species with only one individual (0.11) (Table 5). Looking at the number of individuals amongst these two edge types and the function of equation 1 helps to illustrate how the less abundant species affect values of  $P_i (n_i/N)$  negatively more than the abundant species affect  $P_i$  positively. When the proportion of individuals from each species out of the entire sample ( $P_i$ ) is small, the less abundant species

create higher negative products of the natural log multiplied by  $P_i$ . The larger these negative products, the smaller the product of  $P_i$  times the natural log of  $P_i$ . These products are then summed and converted to a positive integer and the less abundant species drag the value of  $H'$  down farther than the abundant species raise it.

In 2016, edge types B and C shared similar values for  $H'$  (2.96 and 2.99 respectively) despite edge type C having six additional species than B (Table 5). Edge type C in 2016 had a higher proportion of species with only one individual than edge B (0.71 vs. 0.54) but the extra six species allowed edge type C to raise its  $H'$  value 0.03 units above edge type B (Table 5). Much of the variation observed between edge types come from the bird species that make up the majority of vertebrate species identified. They also make up the majority of species with only one individual for each edge type, except for edge type A during 2015 (Table 1).

Figure 18 illustrates the relationship between Shannon index values for each of the six sites and their corresponding vertebrate species richness. The most dramatic change in an edge type from 2015 to 2016 comes from edge type C, where richness increased by nine species and the sample size decreased by 24 individuals (Figure 18). Edge type C went from having four species with one

individual in 2015 to 20 species in 2016 (Table 5). Despite the increased ratio of species with 1 individual from 2015-2016, the new species added during 2016 raised the  $H'$  index value by 0.24 units (Figure 18).

Simpson's reciprocal index ( $1/D$ ) was mathematically highest in edge type C during 2015 (13.69) and B in 2016 (17.19), despite having three less species and four less individuals (Table 5). This is because edge type C was more even than edge type B ( $E_{1/D}=0.72$  and  $E_{1/D}=0.58$ , respectively), meaning the chances of randomly choosing two individuals of the same species from edge type B is greater than that of edge type C. Edge type C had 4 out of 19 species (ratio: 0.21) with only one individual, whereas edge type B had 9 out of 22 (ratio: 0.41) (Table 5). Low values of  $1/D$  came from edge type B during 2015 (12.83) and from A during 2016 (12.30) (Table 5). Edge type C was the most even ( $E_{1/D}$ ) during 2015 (0.72), but the least even during 2016 (0.47) (Table 5). Similarly, edge type B was the most even ( $E_{1/D}$ ) during 2016 (0.78) but the least even during 2015 (0.58) (Table 5).

Figure 26 illustrates the relationship between the Simpson's reciprocal index values for each of the six sites and their corresponding vertebrate species richness. This index shows a trend for edge type C that is different from the Shannon index (Figures 25-26). Instead of increasing from 2015 to 2016 like the

Shannon index did,  $1/D$  decreased from 2015 to 2016 (Figures 25-26).

Shannon's index is more sensitive to changes in less abundant species, whereas  $1/D$  is more sensitive to more abundant species, so the increase in species with only one individual from 2015-2016 (16 species) increased values for  $H'$  but lowered values for  $1/D$ .

Despite using identical sampling protocols for each season, over twice as many individuals were detected during 2015 than 2016 (Table 5). The individuals from 2016 surveys yielded the greatest difference from high to low values of  $1/d$  (Table 5). Each value of  $1/d$  from 2015 was within 0.8  $1/d$  units, whereas 2016 values varied as much as 4.5  $1/d$  units, suggesting that with increased detections of individuals, more of a detectable difference of  $1/d$  can be observed between edge types. This can be observed by considering  $1/d$  values from 2016 for edge types A and B, where during 2016 edge type A had a difference of 19 individuals between  $n_{i-max}$  and  $N_i$  ( $23-4=19$ ), which yielded a  $1/d$  value of 5.8, and edge type B for 2016 had a difference of 34 individuals between  $n_{i-max}$  and  $N_i$  ( $38-4=34$ ), which yielded a  $1/d$  value of 9.5 (Table 5). Berger-Parker index values ( $1/d$ ) for each year were least dominate in edge type B (7.8-2015, 9.5-2016) (Table 5). Dominate values for  $1/d$  were found in edge type A during 2015 (7.0) and C during 2016 (5.0) (Table 5).

Edge type C had less species with a more abundant assemblage of individuals than B, which lowered its sum of squares and increased the inverse value for D. In 2016 edge type B was more diverse ( $1/D$  and  $1/d$ ) than the other two edges, despite having six less species than edge type C (Table 5). This can be attributed to edge type B's low proportion of species with one individual ( $12/22=0.54$ ) and its evenness ( $E_{1/D}=0.78$ ), along with edge type C having 20 species with one individual ( $E_{1/D}=0.47$ ) (Table 5). Edge type C for 2016 exhibited the greatest richness (28) but was only 0.85  $1/D$  units away from the least diverse edge (A) that had 11 less species (Table 5).

The highest number of species with only one individual per edge comes from edge type C in 2016 (20); however, edge type A during 2016 had the highest proportion of species with only one individual ( $14/17=0.82$ ) (Table 5). The edge with the lowest proportion of species with one individual (0.11) came from edge type A during 2015 (Table 5).

#### Sample Based Species/Family Accumulation Curves

Extrapolated species richness means for all three vertebrate groups combined was highest in edge type A ( $41.22 \pm 15.14$ ), followed by C ( $38.94 \pm 8.25$ ), and lastly B ( $34.57 \pm 6.2$ ), however overlapping confidence intervals prevent the identification of the richest edge through extrapolation (Figures 20-

22). Student's t-test and p values for each vertebrate group did not find a significant difference between edge types. The highest estimated invertebrate extrapolated family richness means after six samples came from edge type B ( $154.15 \pm 68.32$ ), followed by A ( $109.87 \pm 58.42$ ), and lastly C ( $73.11 \pm 43.00$ ), however the means never reached an asymptote and overlapping confidence intervals prevented the identification of the richest assemblage of families through extrapolation (Figure 23). A significant difference was found between edge types B and C using the Student's t-test and p values, however failure of the curves to reach an asymptote negates this finding.

### Habitat Variables

The highest basal area ( $\text{ft}^2/\text{ac}$ ) in 2015 was found amongst the stands that comprise edge type C (83, 83, Table 6). The highest basal area in 2016 was found amongst the stands that comprise edge type A (93, 83, Table 6). The lowest basal area for 2015 was amongst the stands that comprise edge type B (50, 90, Table 6) and for 2016 it was edge type C (60, 70, Table 6). The greatest difference in diameter at breast height (2015 - 10" vs 5", 2016 - 11" vs 8") and total height (2015 - 62' vs 28', 2016 - 75' vs 52') within each edge's two stands come from edge type B each year (Table 6). Understory density (Nudd's board 1-

5) from each edge's two stands was highest in edge B during 2015 (5, 5), and edge A in 2016 (4, 5) (Table 6).

Individual stand age differences for each edge type between the 2 seasons were  $\leq 3$  years (Table 6). Stand heights varied as much as 30' (edge B's younger side) and as little as 6' (edge A's older side) between the 2 seasons (Table 6). Basal area averages varied as much as 23 ft<sup>2</sup>/ac (edge C's older sides) and as little as 3 ft<sup>2</sup>/ac (edge A's younger sides) (Table 6). Average DBH values varied as much as 3" (edge B's younger side) and as little as 0" (edge C's younger sides) (Table 6). Understory density (Nudd's board 1-5) was identical for edge type A's younger sides and edge type C's older sides (Table 6). The greatest dissimilarity for understory density was found in edge type A's older sides (3) (Table 6).

#### Digital Hemispheric Canopy Photography

During 2015 edge type A exhibited the highest averaged solar radiation values for each category (ISF=0.283, DSF=0.285, GSF=0.358, Table 7), whereas during 2016 edge type C had the highest averaged values for each category (ISF=0.282, DSF=0.295, GSF=0.294, Table 7). The highest DSF value estimated came from edge type B in 2016 (0.416) and the lowest came from edge type B in 2015 (0.149) (Table 7).

The most dramatic difference in DSF from 2015-2016's younger side of each edge occurred in edge type A and the least dramatic difference came from edge type B (Table 7, Figure 27). Amongst the older sides of each edge, the largest change in DSF between stands was also found in edge type A and the most similar DSF values were found in edge type B (Table 7, Figure 28). The largest difference in basal area (ft<sup>2</sup>/ac) came from edge type C for both sides of its edge (Table 6, Figures 27-28). It is important to note that amongst the three edge types the most dramatic changes in basal area (ft<sup>2</sup>/ac), between sampling seasons, did not account for the most dramatic changes in DSF. For both sides (older-younger) of each edge, stands with lower basal area (ft<sup>2</sup>/ac) had higher estimates of DSF.



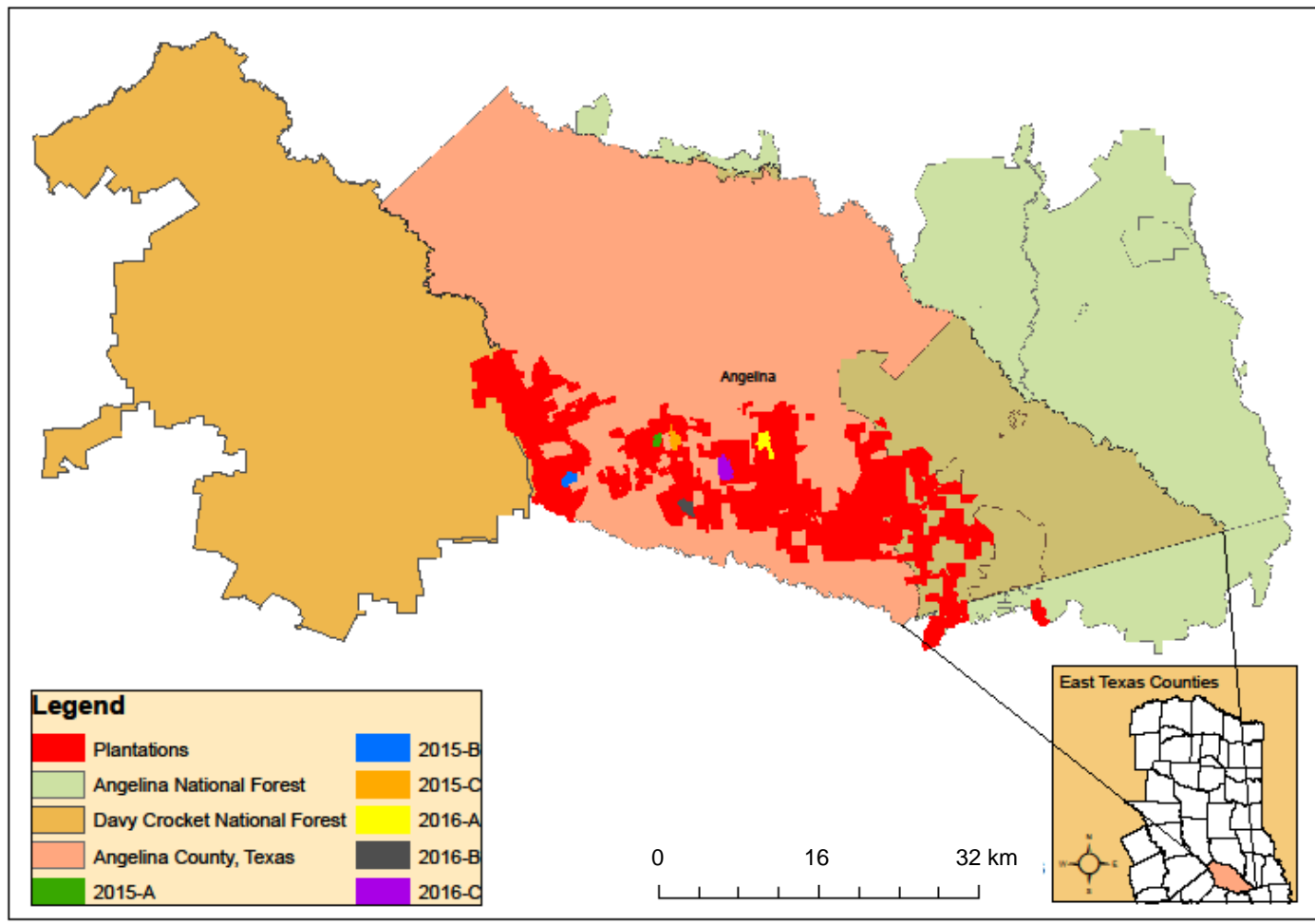


Figure 1: Plantation matrix of interest between two national forests in Angelina County, Texas.

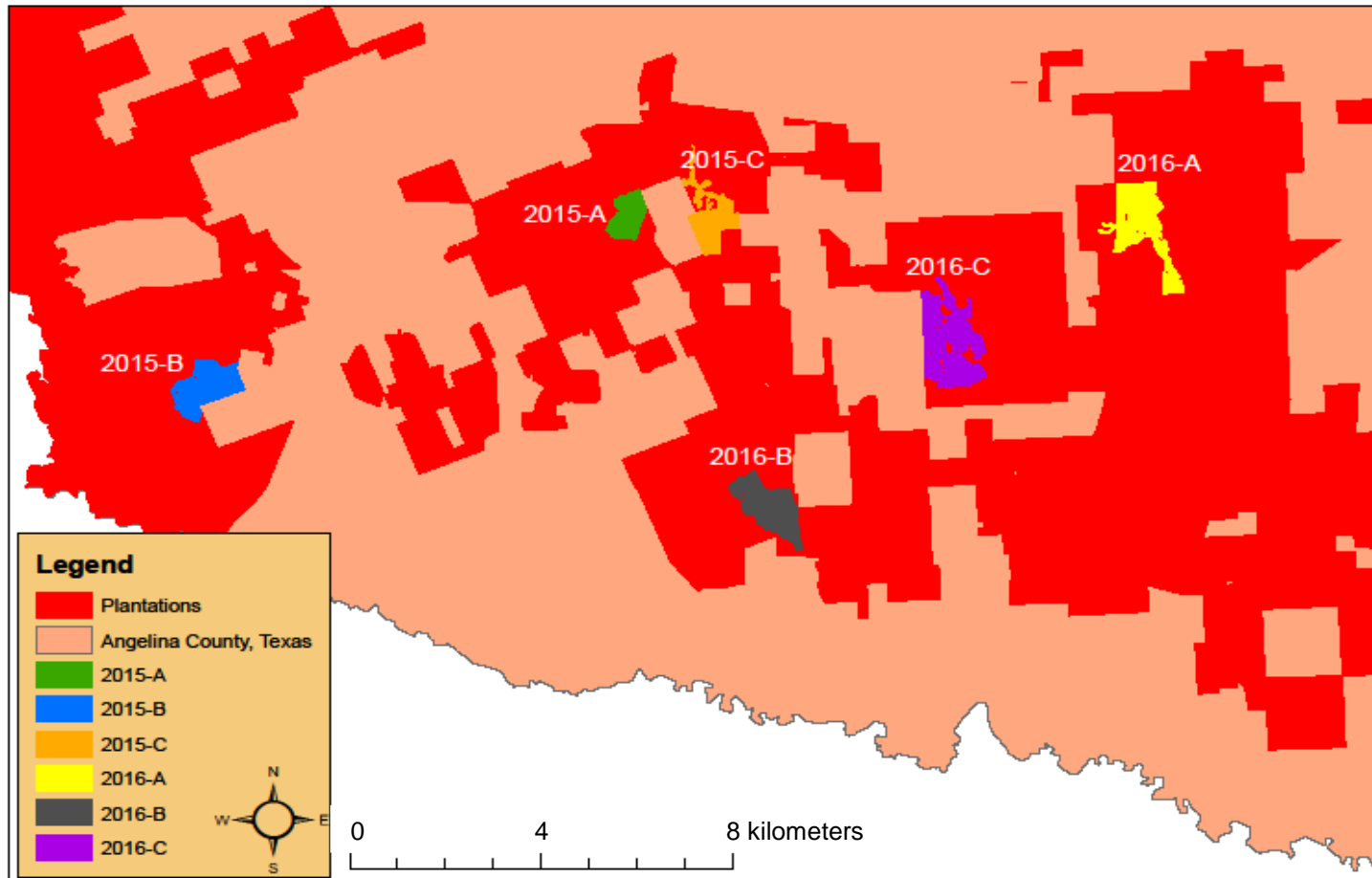


Figure 2: Map of 2015-2016 study sites near Diboll, Texas.

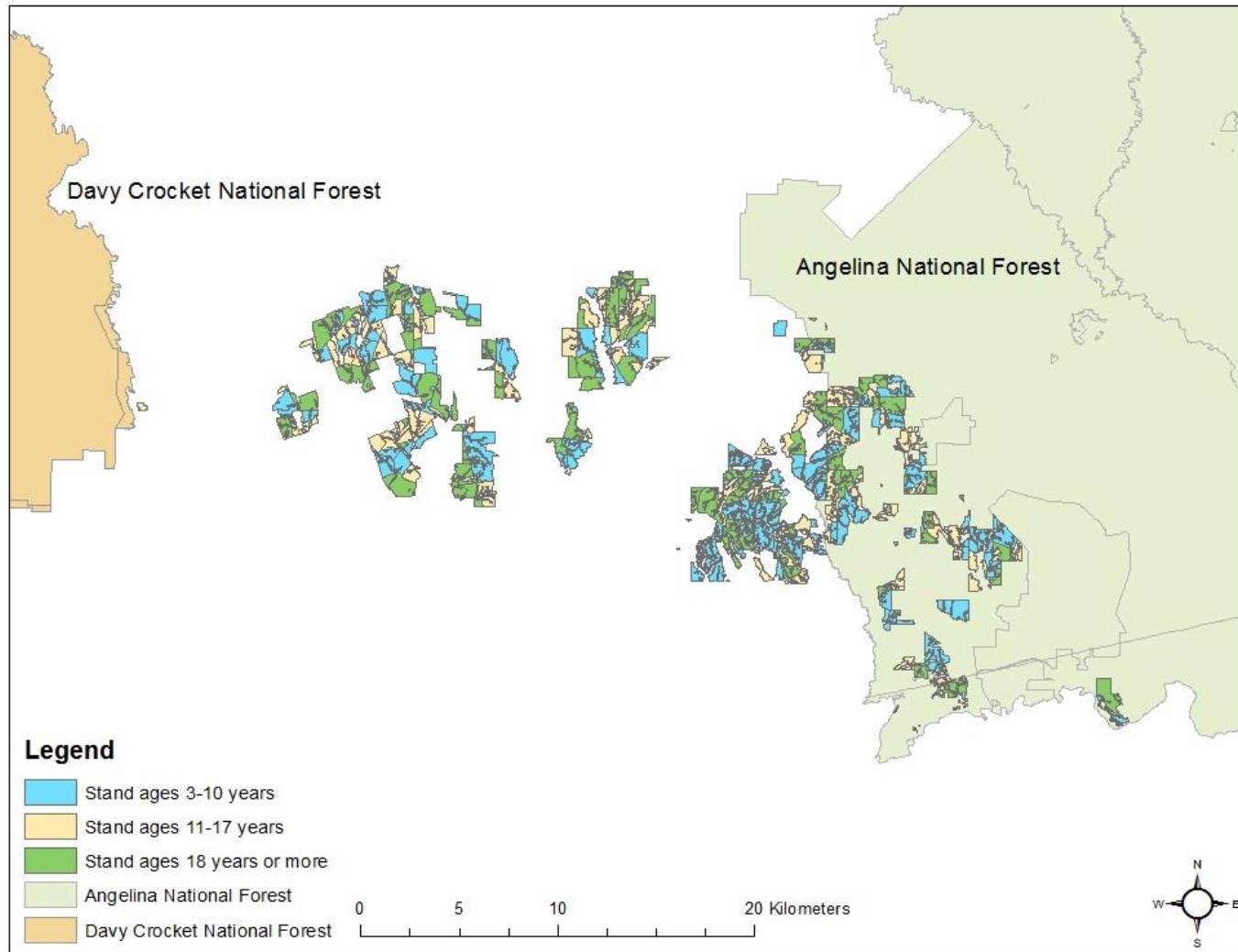


Figure 3: Map of available edges created by the combination of stand ages.

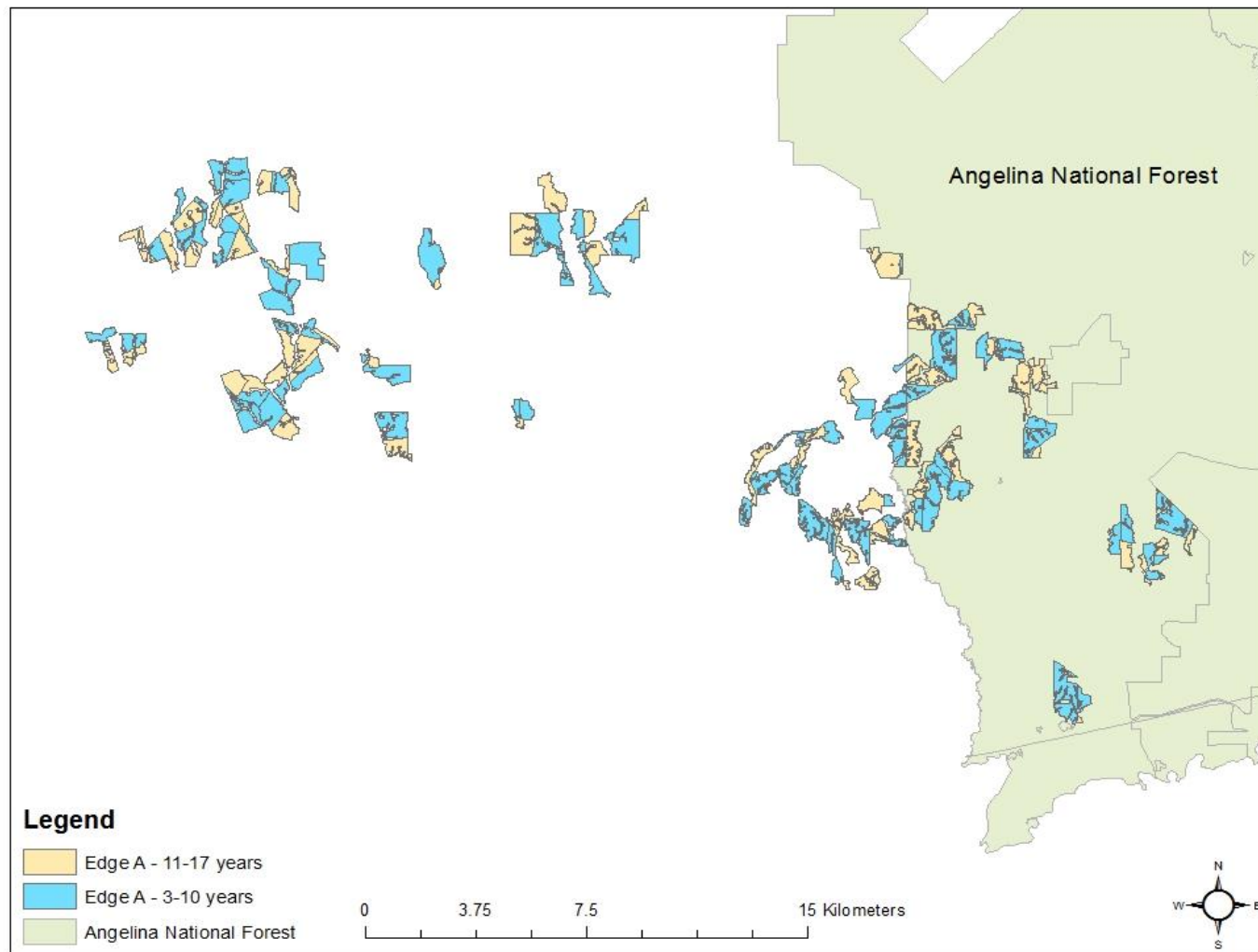


Figure 4: Map of stands that create edge type A within this study area from 2014.

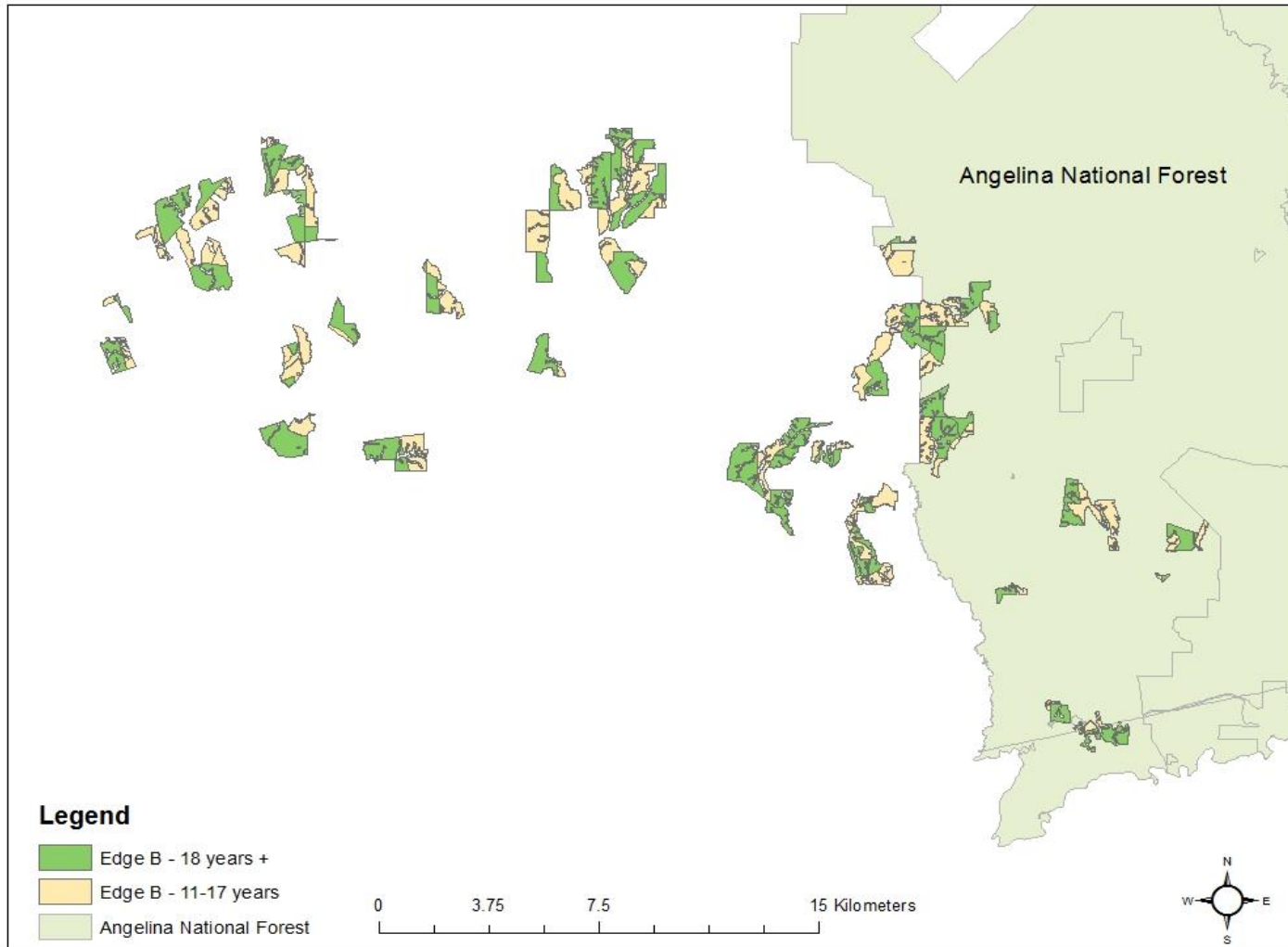


Figure 5: Map of stands that create edge type B within the study area from 2014.

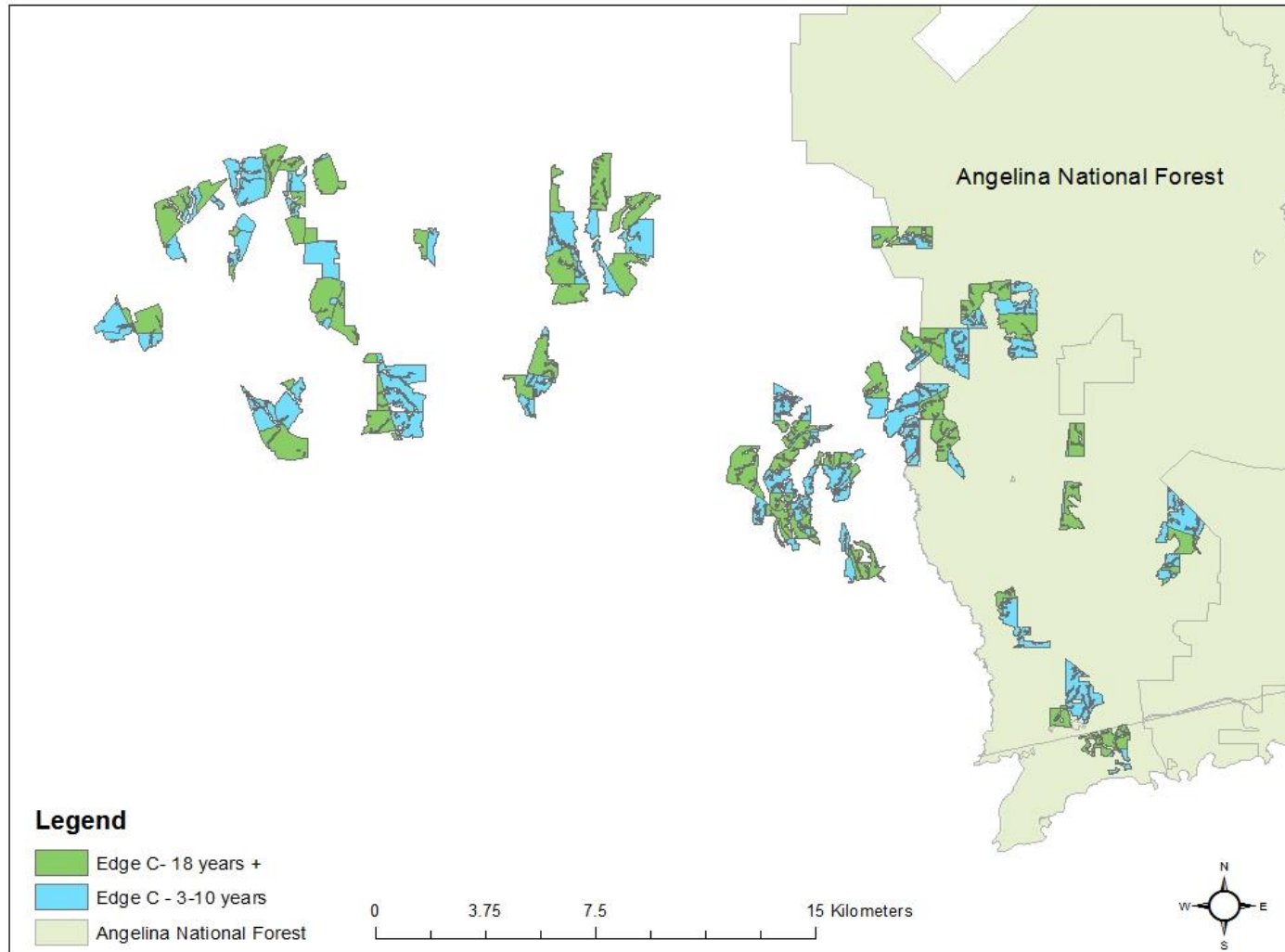


Figure 6: Map of stands that create edge type C within the study area from 2014.

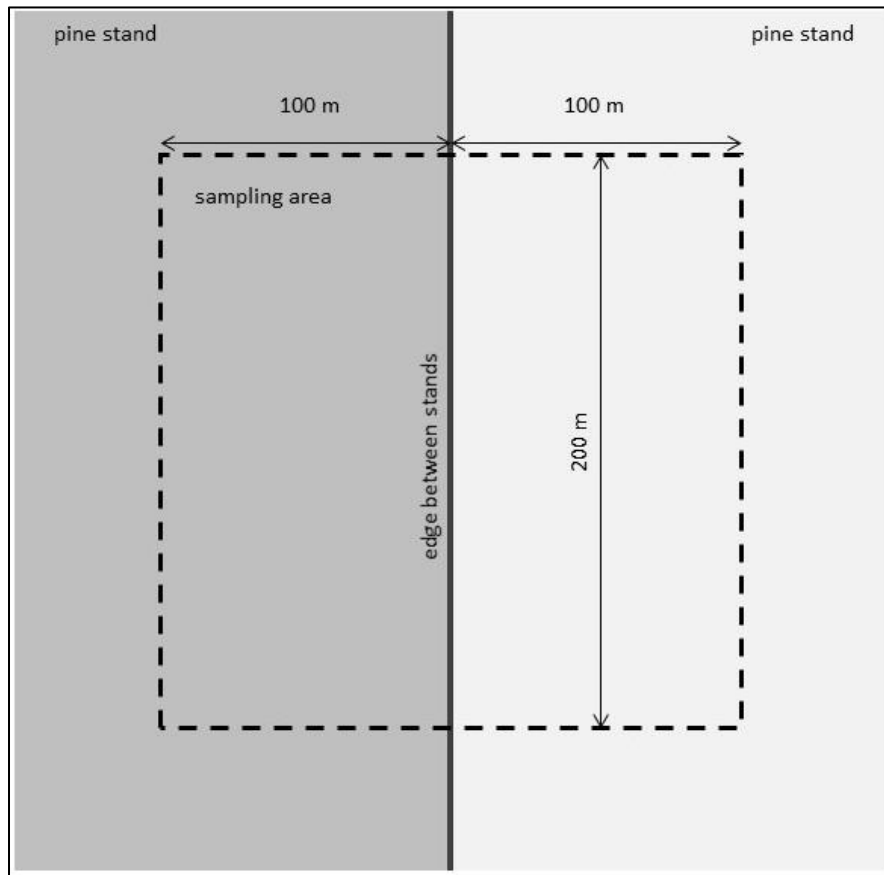


Figure 7: Detailed section of edge that was sampled for invertebrates, birds, small and medium-mammals.

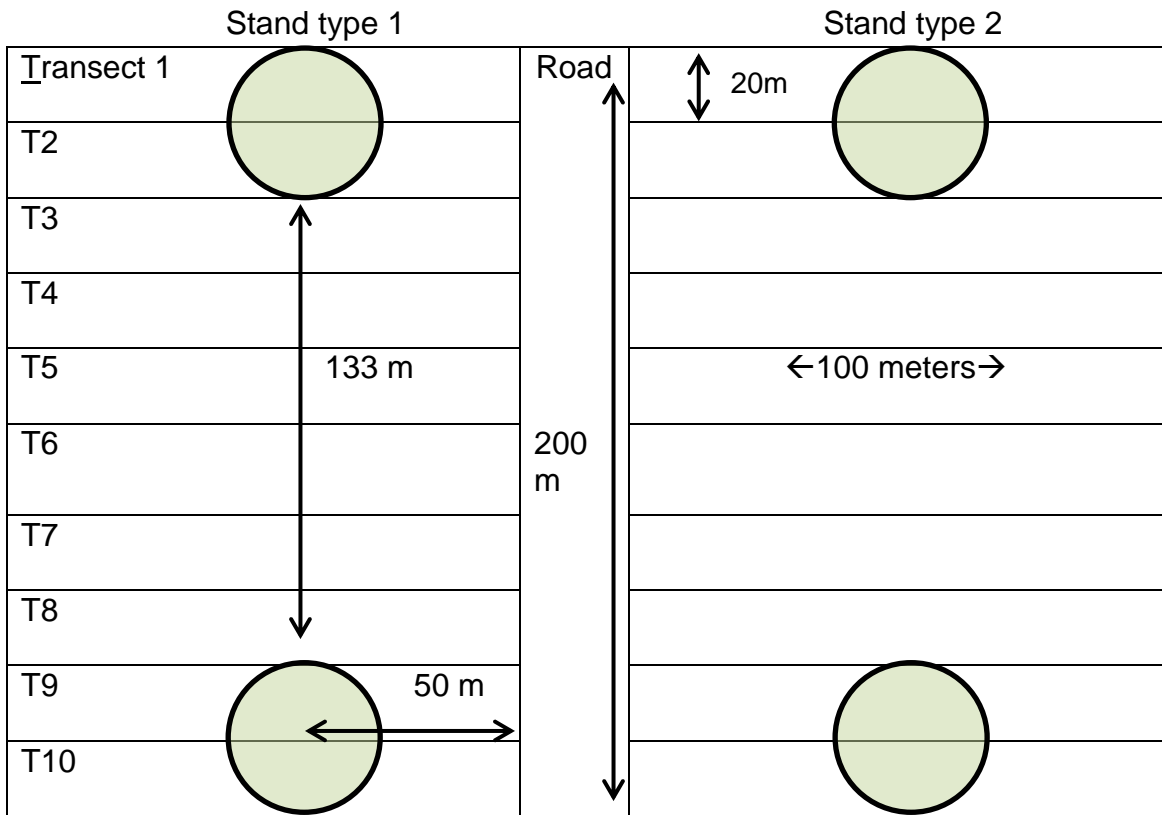


Figure 8: Orientation of double observer point counts for birds in 2015-16 near Diboll, TX. Four 25 m fixed radius plots were sampled for 10 minutes each per site/survey.

\*Points were located 50m from the tree line on either side. Road width varied between sites. Points were spaced as far apart as possible (133 m) along each stand type.



Small mammals

Species

- 1) Deer Mouse
- 2) Hispid Cotton Rat
- 3) Northern Pygmy Mouse
- 4) Southern Short Tailed Shrew
- 5) White Footed Mouse

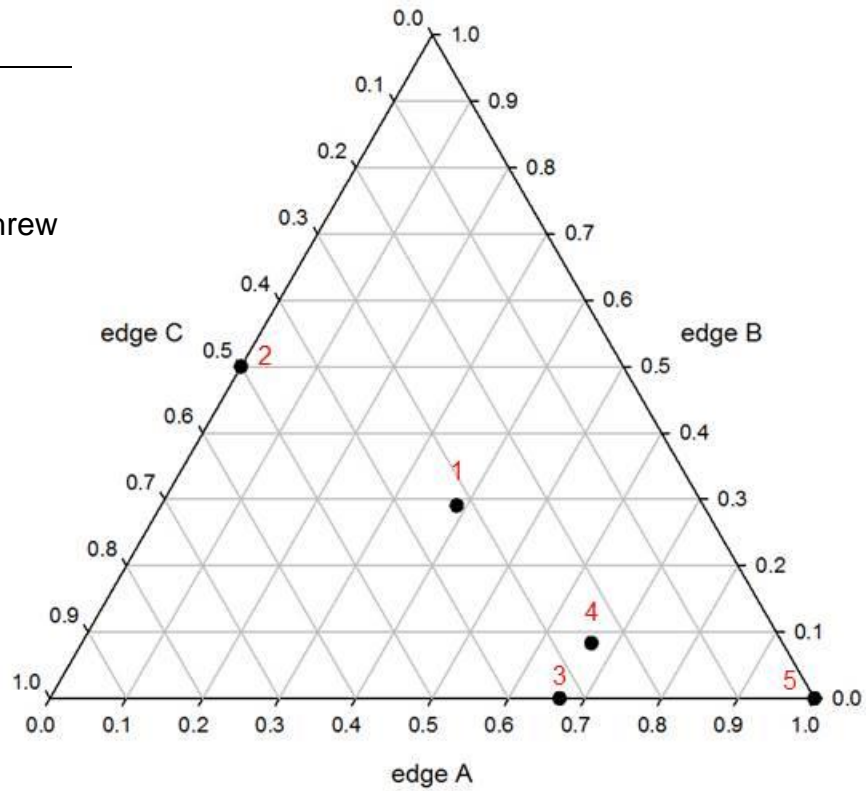


Figure 9: Triangular coordinate system graph of small mammal species captured during the summers of 2015-2016 near Diboll, TX

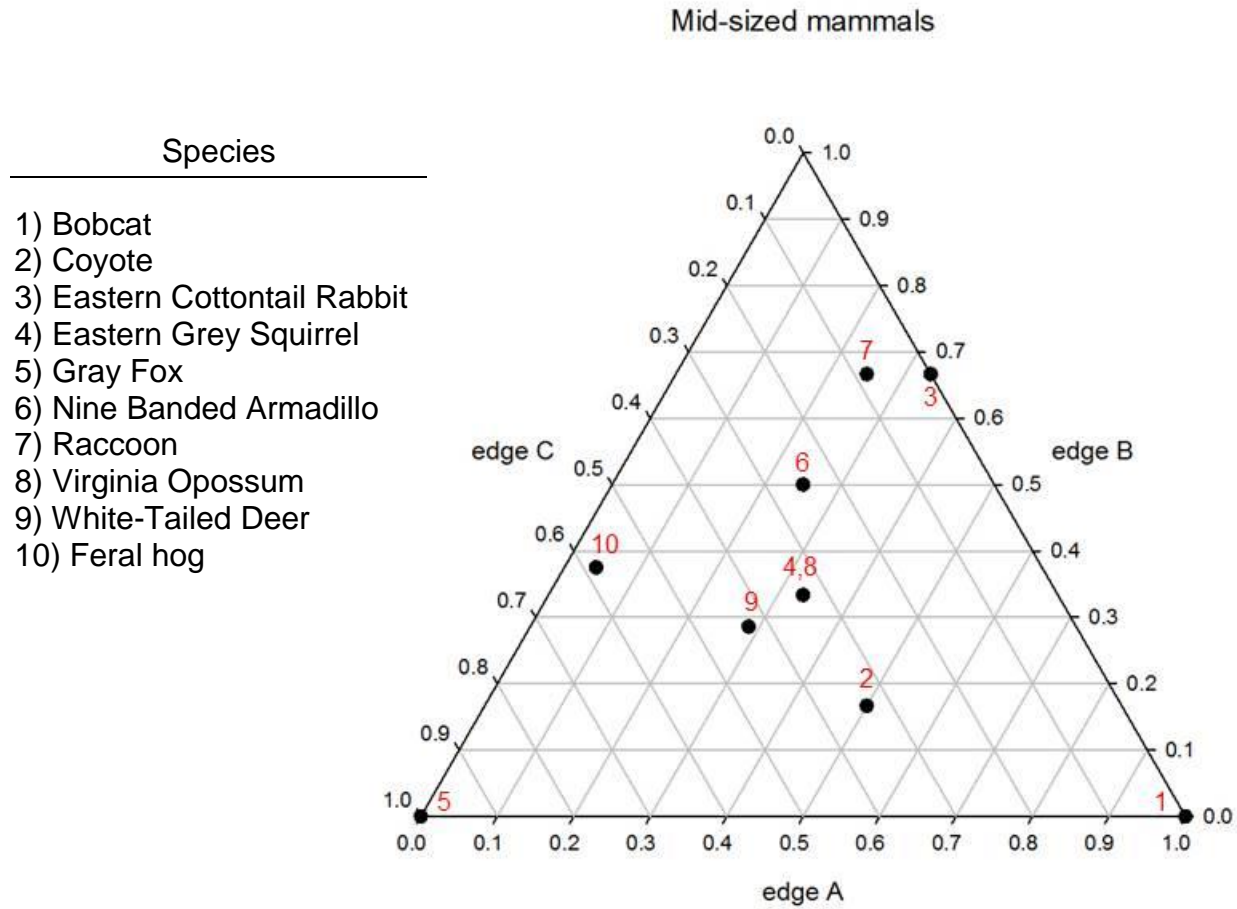


Figure 10: Triangular coordinate system graph of medium sized mammal species detected during the summers of 2015-2016 near Diboll, TX.

- Species
- 1) AMCR
  - 2) AMRO
  - 3) BGGN
  - 4) BLJA
  - 5) BLWA
  - 6) CACH
  - 7) CAWR
  - 8) COYE
  - 9) DOWO
  - 10) EWPE
  - 11) GRCA
  - 12) HOWA
  - 13) INBU
  - 14) KEWA
  - 15) MODO
  - 16) NOBO
  - 17) NOCA
  - 18) PIWA
  - 19) RBWO
  - 20) REVI
  - 21) RTHU
  - 22) SUTA
  - 23) TUTI
  - 24) WEVI
  - 25) YBCH
  - 26) YBCU

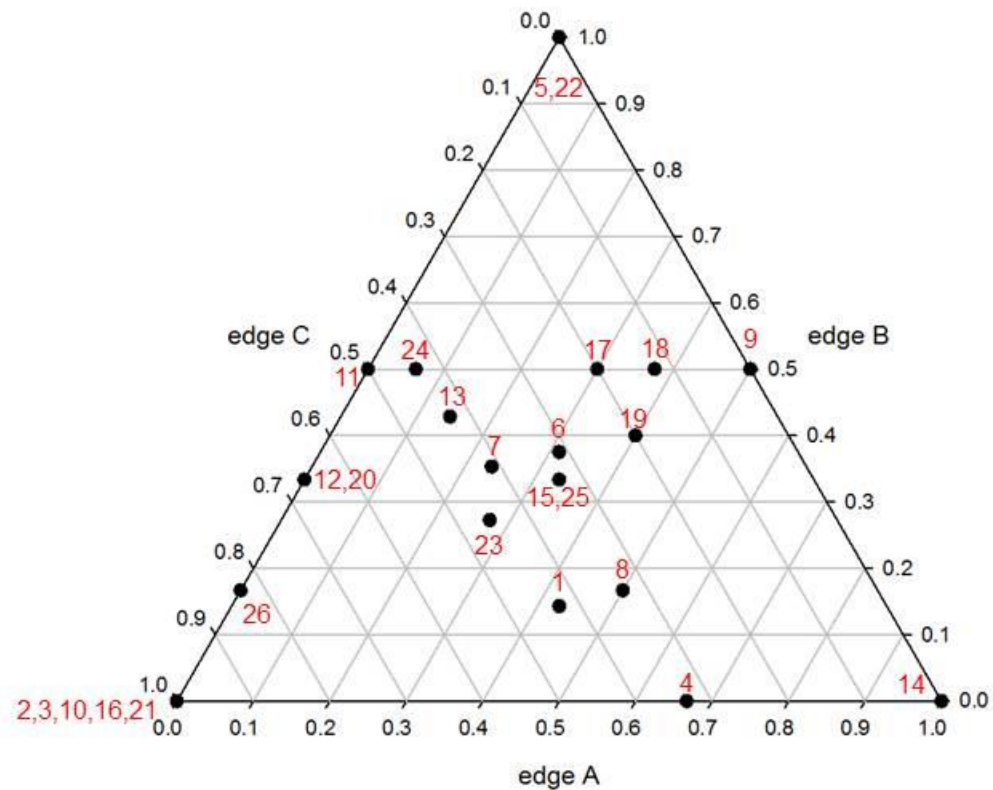


Figure 11: Triangular coordinate system graph of bird species found during the summers of 2015-2016 near Diboll, TX

Richness of edges by side

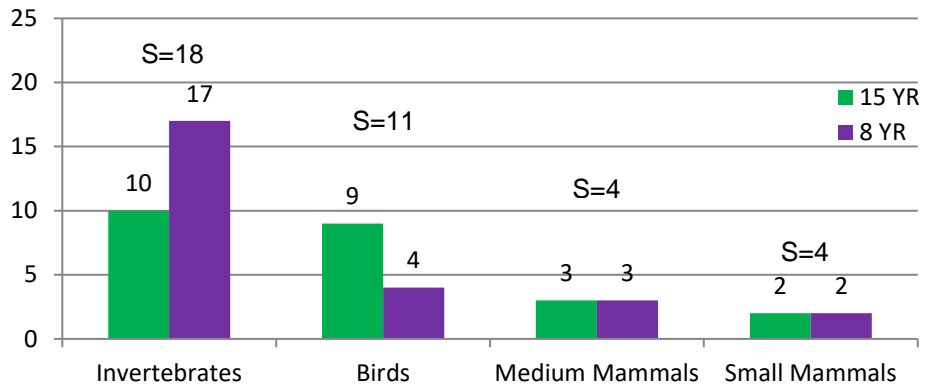


Figure 12: Edge type A species richness by side of edge for 2015 data. Invertebrates were identified to family.

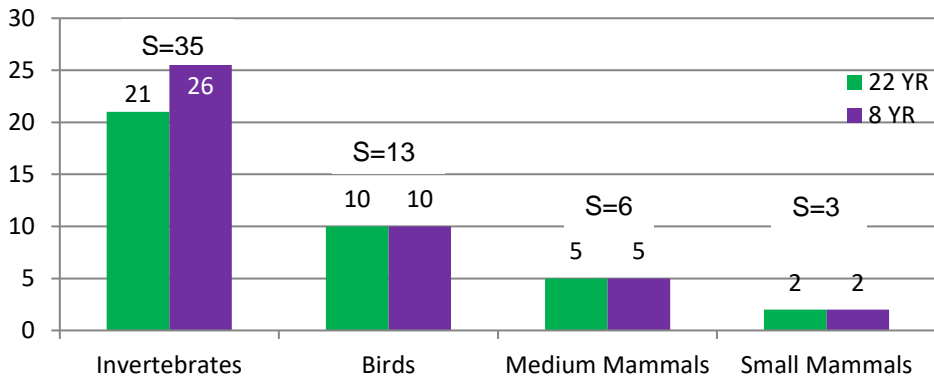


Figure 13: Edge type B species richness by side of edge for 2015 data. Invertebrates were identified to family.

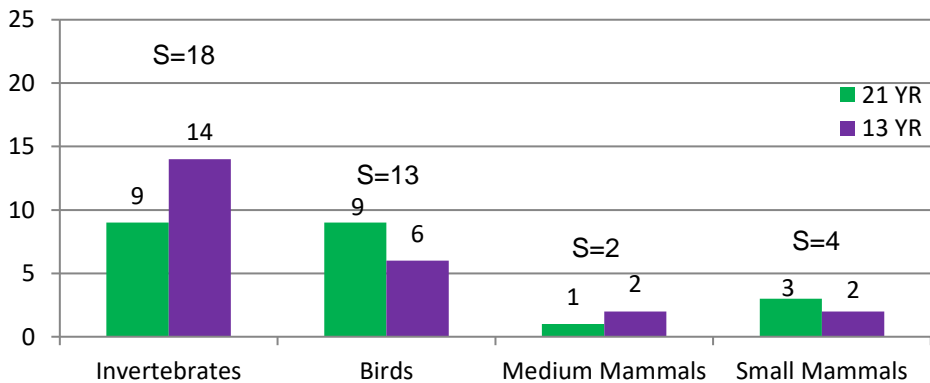


Figure 14: Edge type C species richness by side of edge for 2015 data. Invertebrates were identified to family.

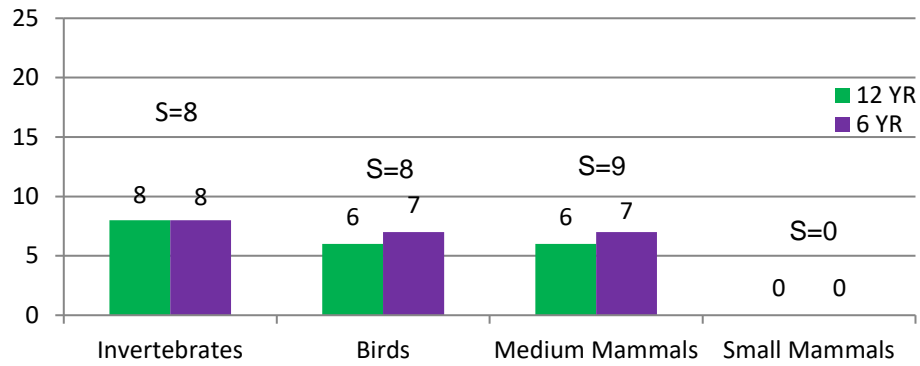


Figure 15: Edge type A species richness by side of edge for 2016 data. Invertebrates were identified to family.

Richness of edges by side

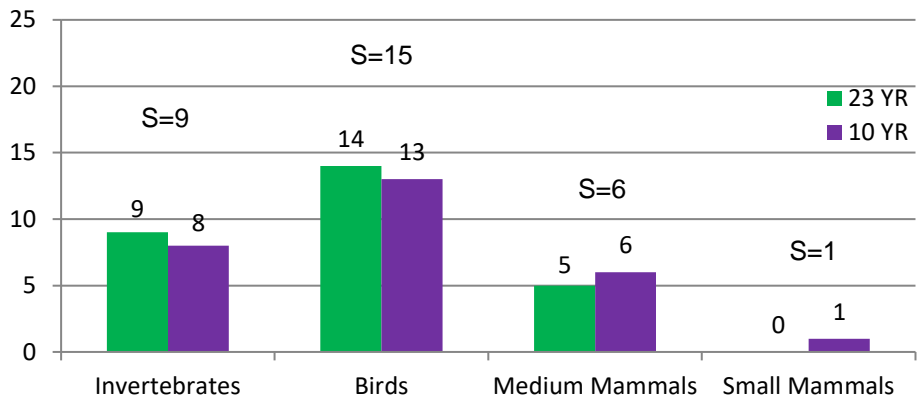


Figure 16: edge type B species richness by side of edge for 2016 data. Invertebrates were identified to family.

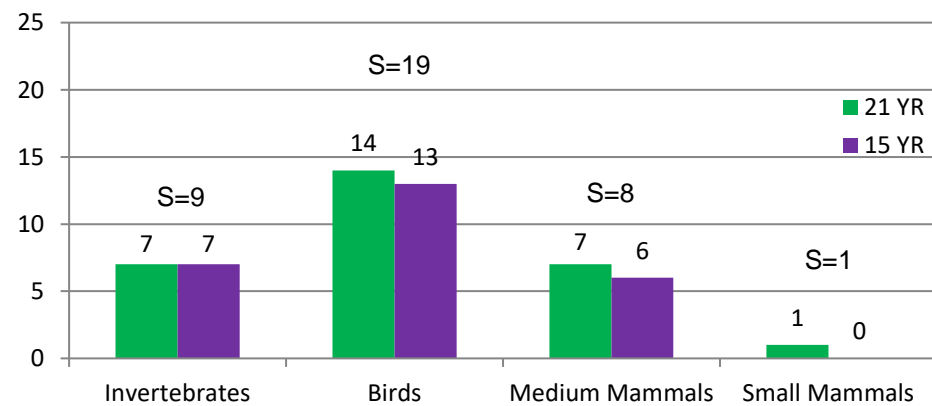


Figure 17: Edge type C species richness for 2016 data. Invertebrates were identified to family.

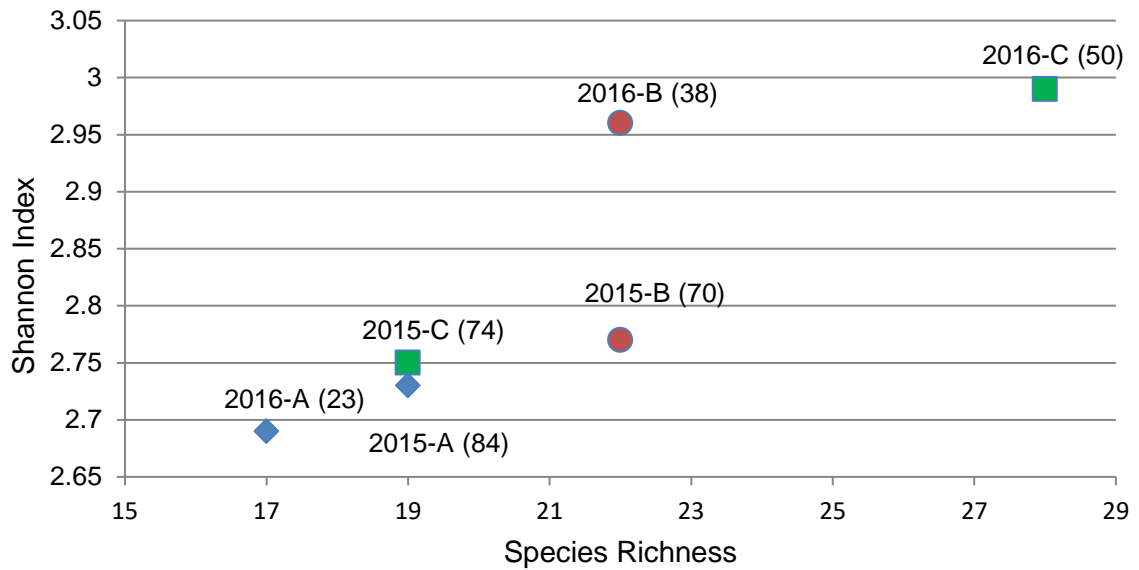


Figure 18: Comparison of Shannon Index values with each edge type's corresponding species richness. Abundance is in parenthesis. Data collected in the summers of 2015 and 2016 near Diboll, Texas.

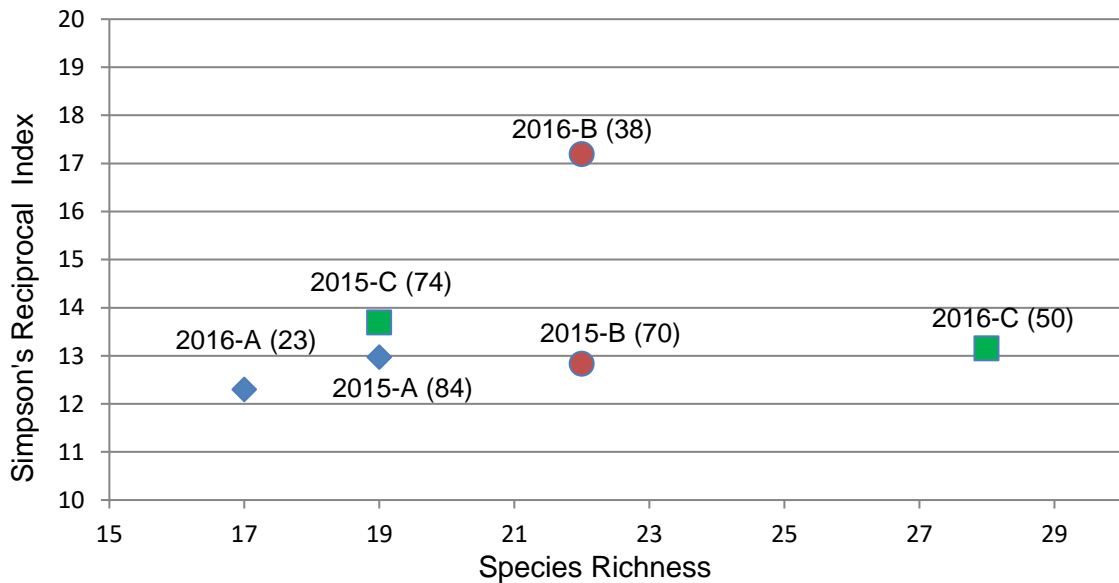


Figure 19: Comparison of Simpson's Reciprocal Index values with each edge type's corresponding species richness. Abundance is in parenthesis. Data collected in the summers of 2015- and 2016 near Diboll, Texas.

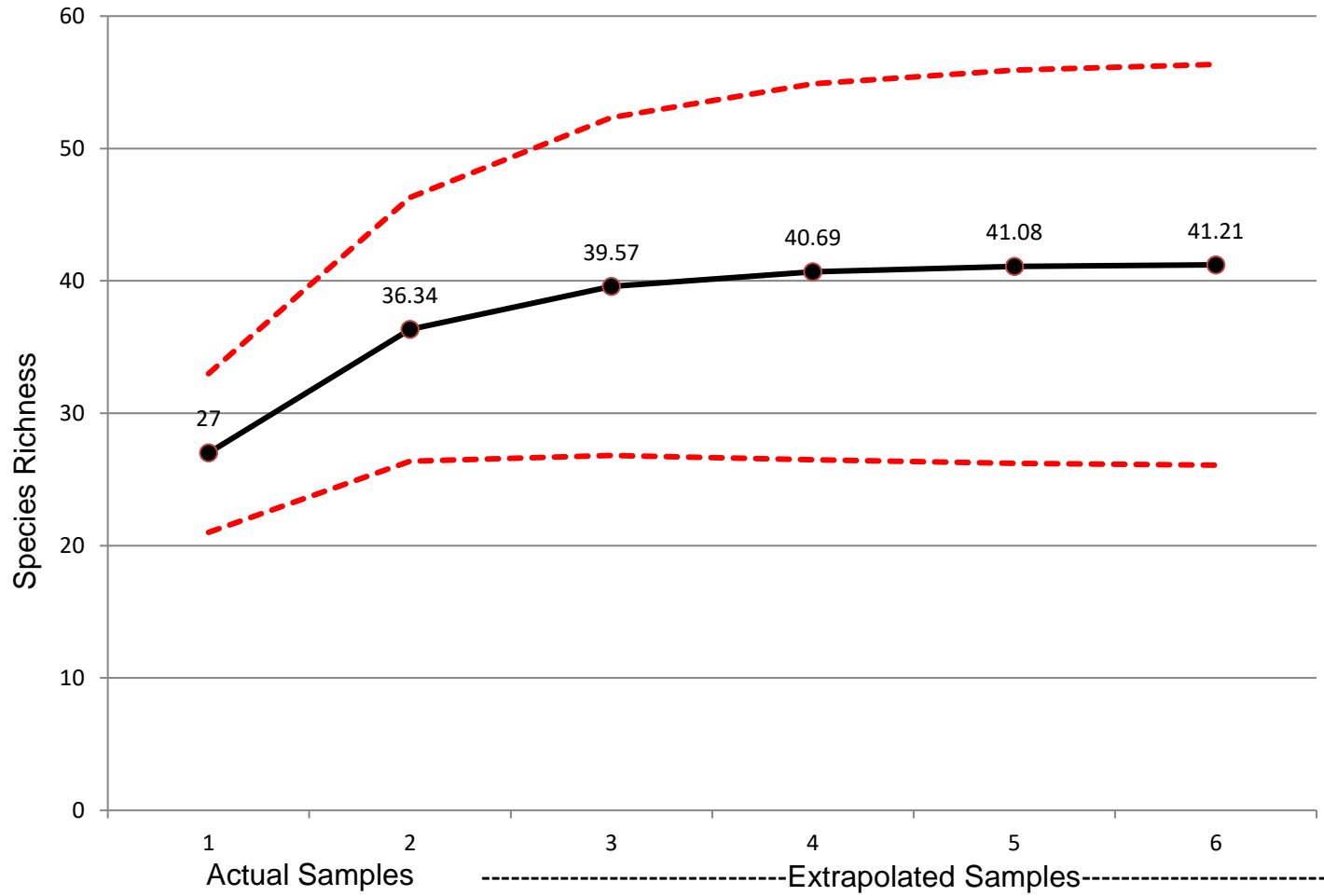


Figure 20: Sample based species accumulation curve with 95% confidence interval for edge type A observed from 2015-2016 in Diboll, TX. Samples 3-6 were generated using EstimateS Version 9.1.

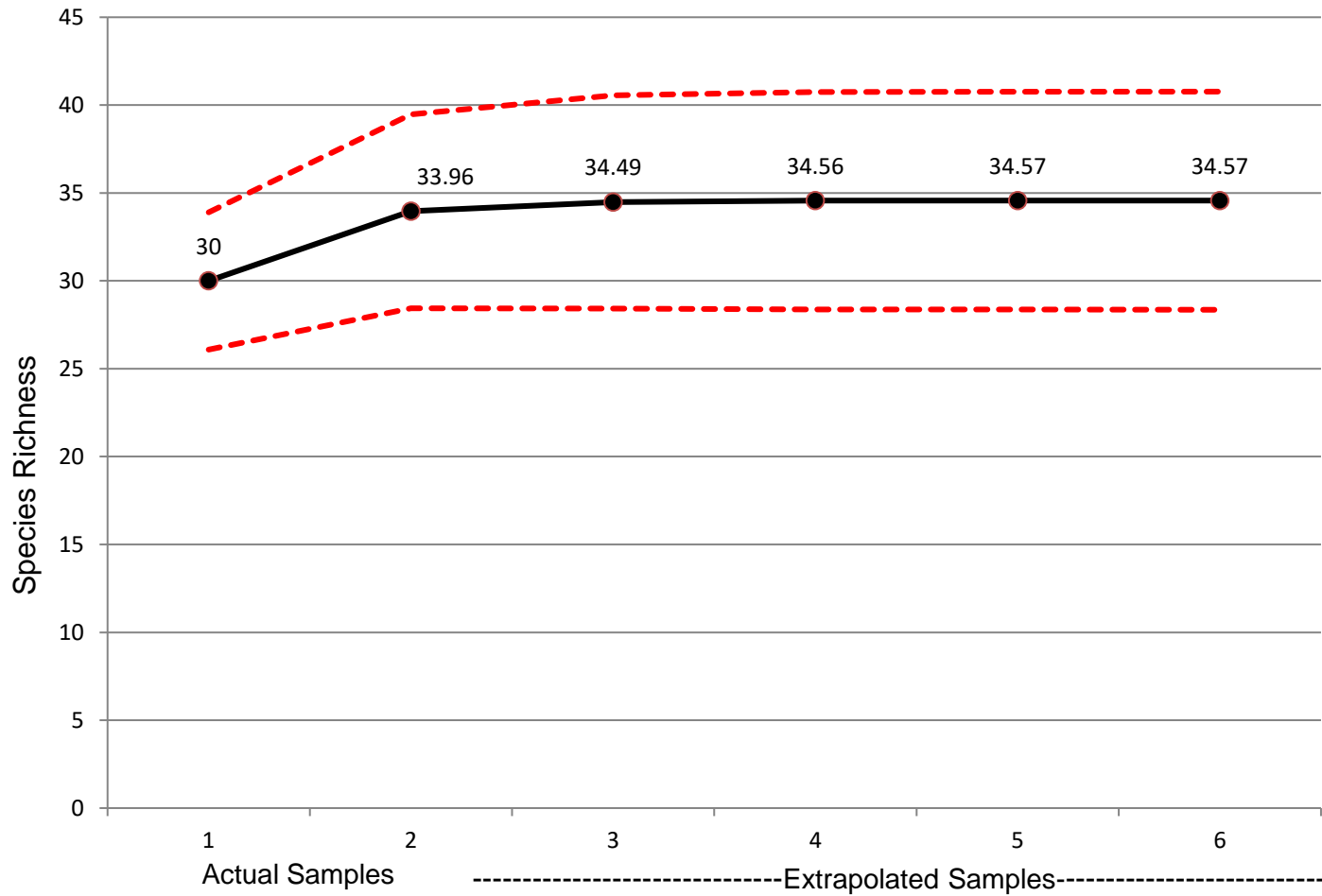


Figure 21: Sample based species accumulation curve with 95% confidence interval for edge type B observed from 2015-2016 in Diboll, TX. Samples 3-6 were generated using EstimateS Version 9.1.



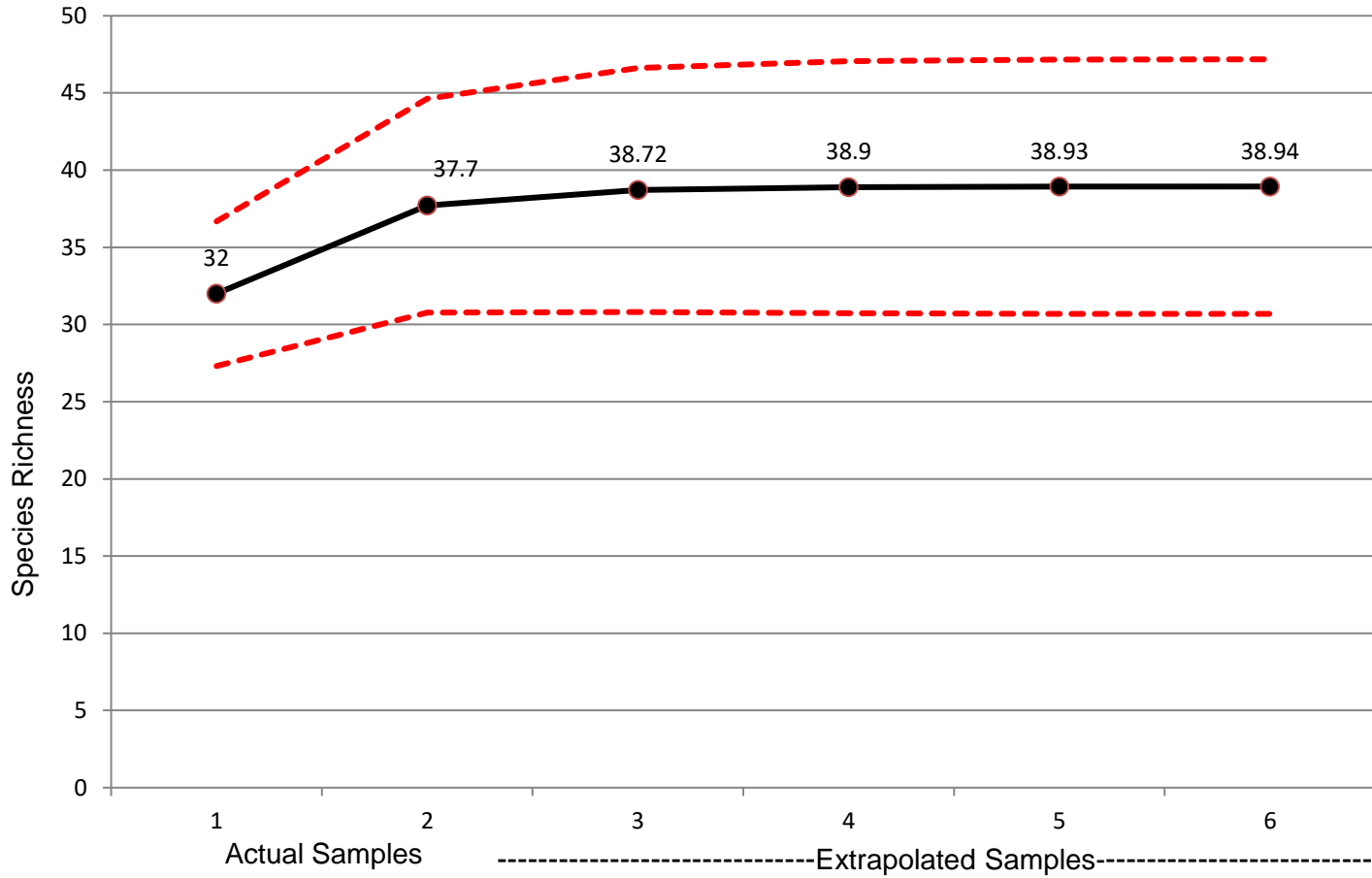


Figure 22: Sample based species accumulation curve with 95% confidence interval for edge type C observed from 2015-2016 in Diboll, TX. Samples 3-6 were generated using EstimateS Version 9.1.

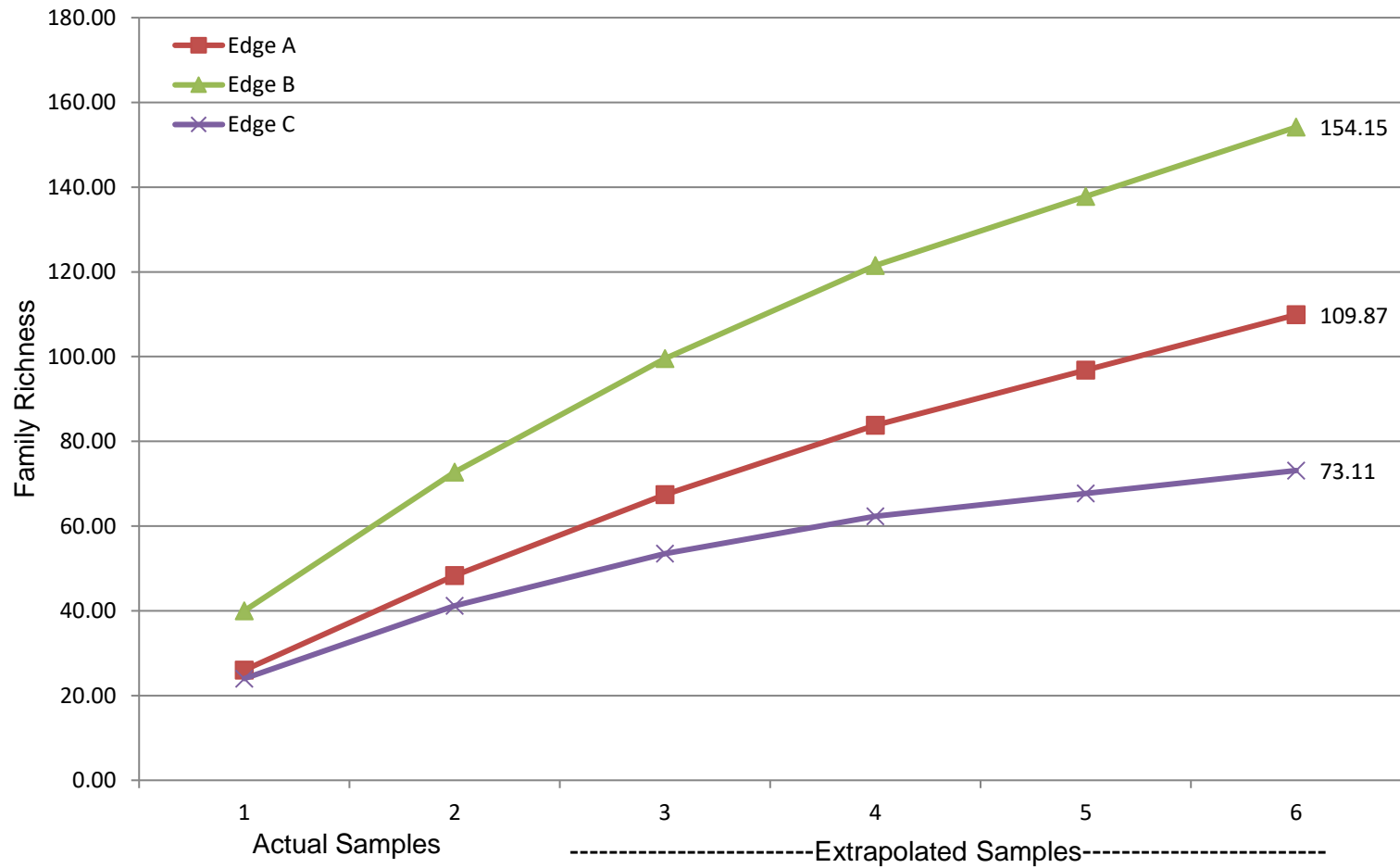


Figure 23: Sample based family accumulation curve for invertebrates captured during 2015-2016 in Diboll, TX. Samples 3-6 were generated using EstimateS Version 9.1.

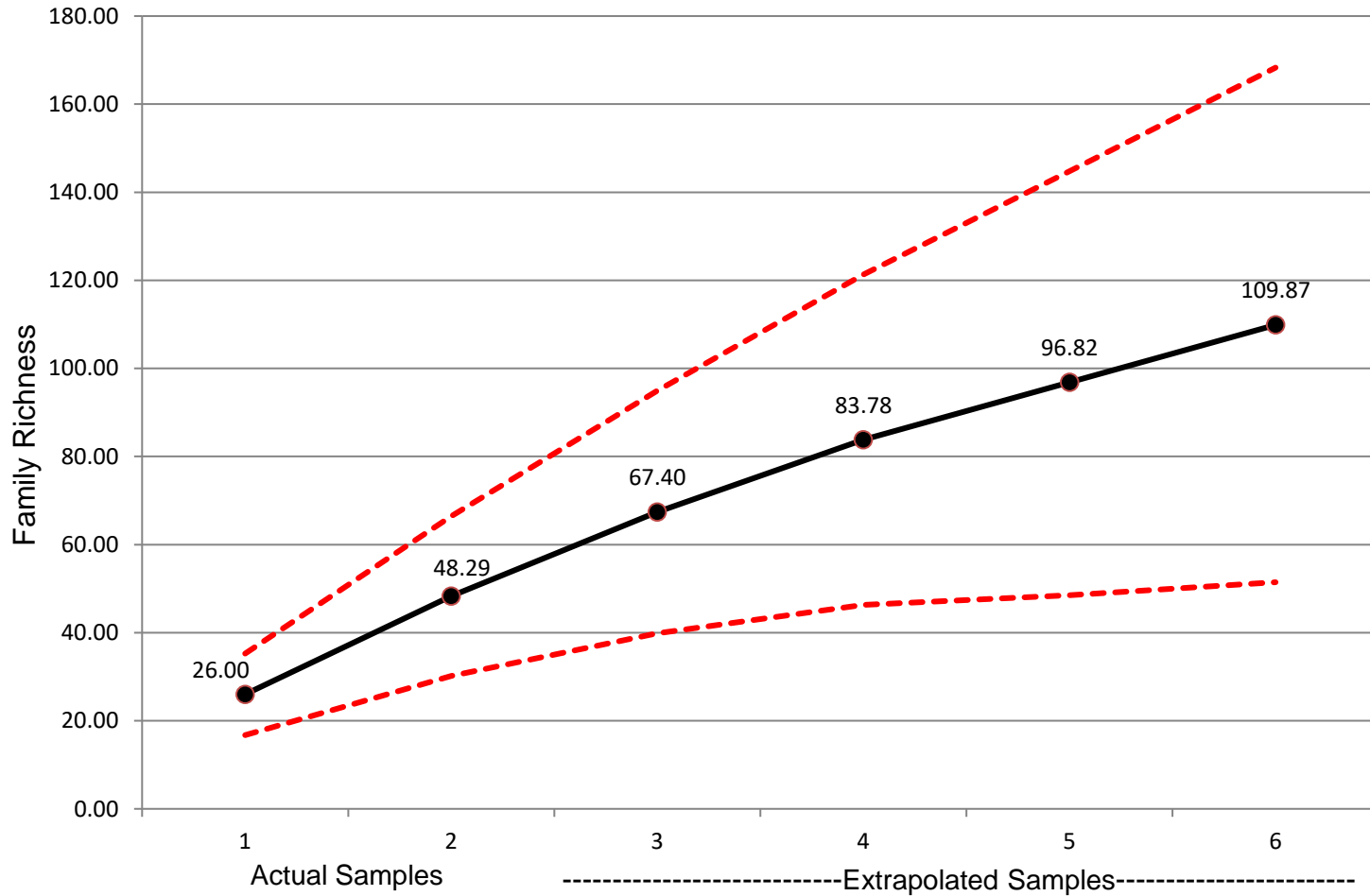


Figure 24: Sample based family accumulation curve with 95% confidence interval for invertebrate families captured in edge type A from 2015-2016 in Diboll, TX. Samples 3-6 were generated using EstimateS Version 9.1.

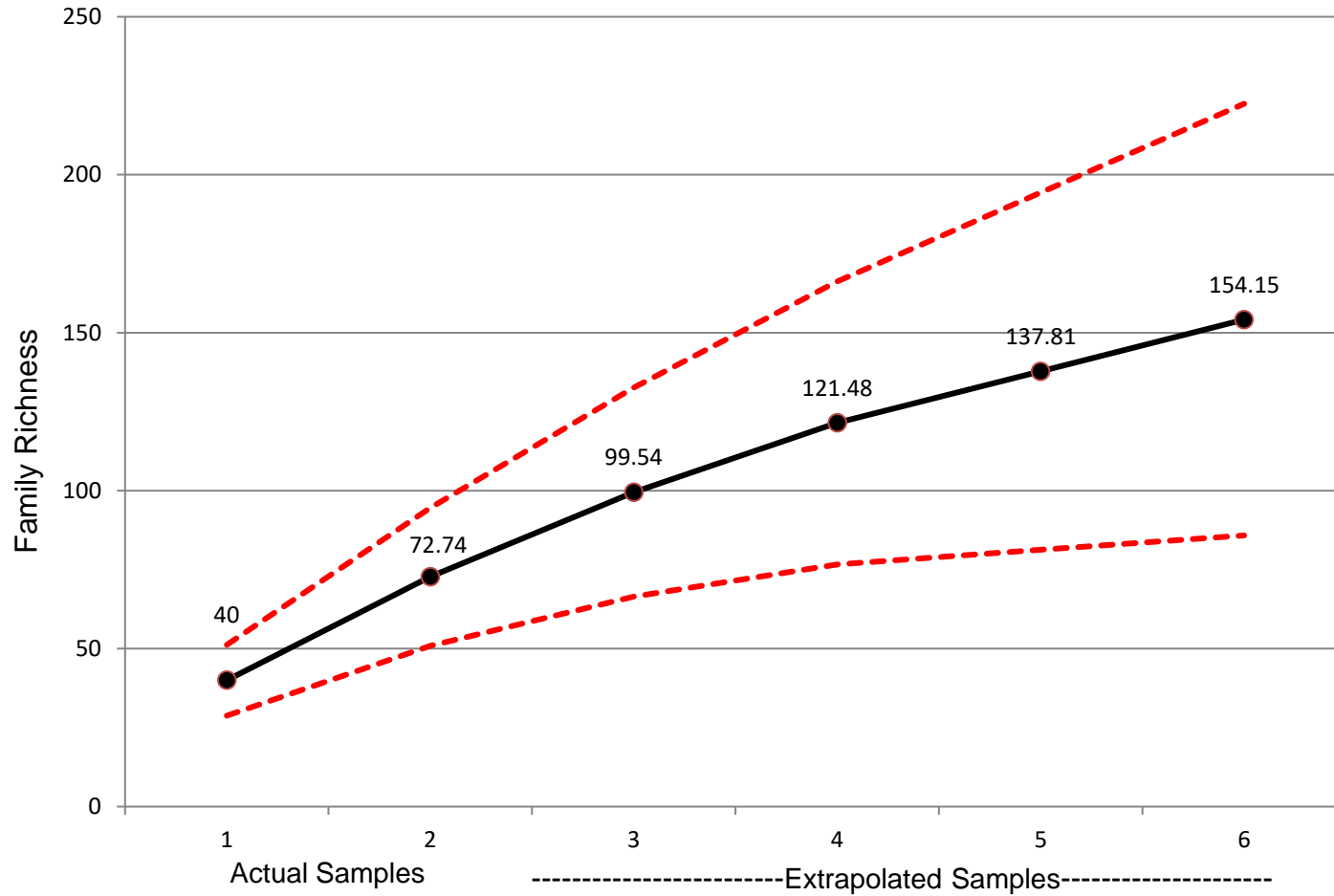


Figure 25: Sample based family accumulation curve with 95% confidence interval for invertebrate families captured in edge type B from 2015-2016 in Diboll, TX. Samples 3-12 were generated using EstimateS Version 9.1.

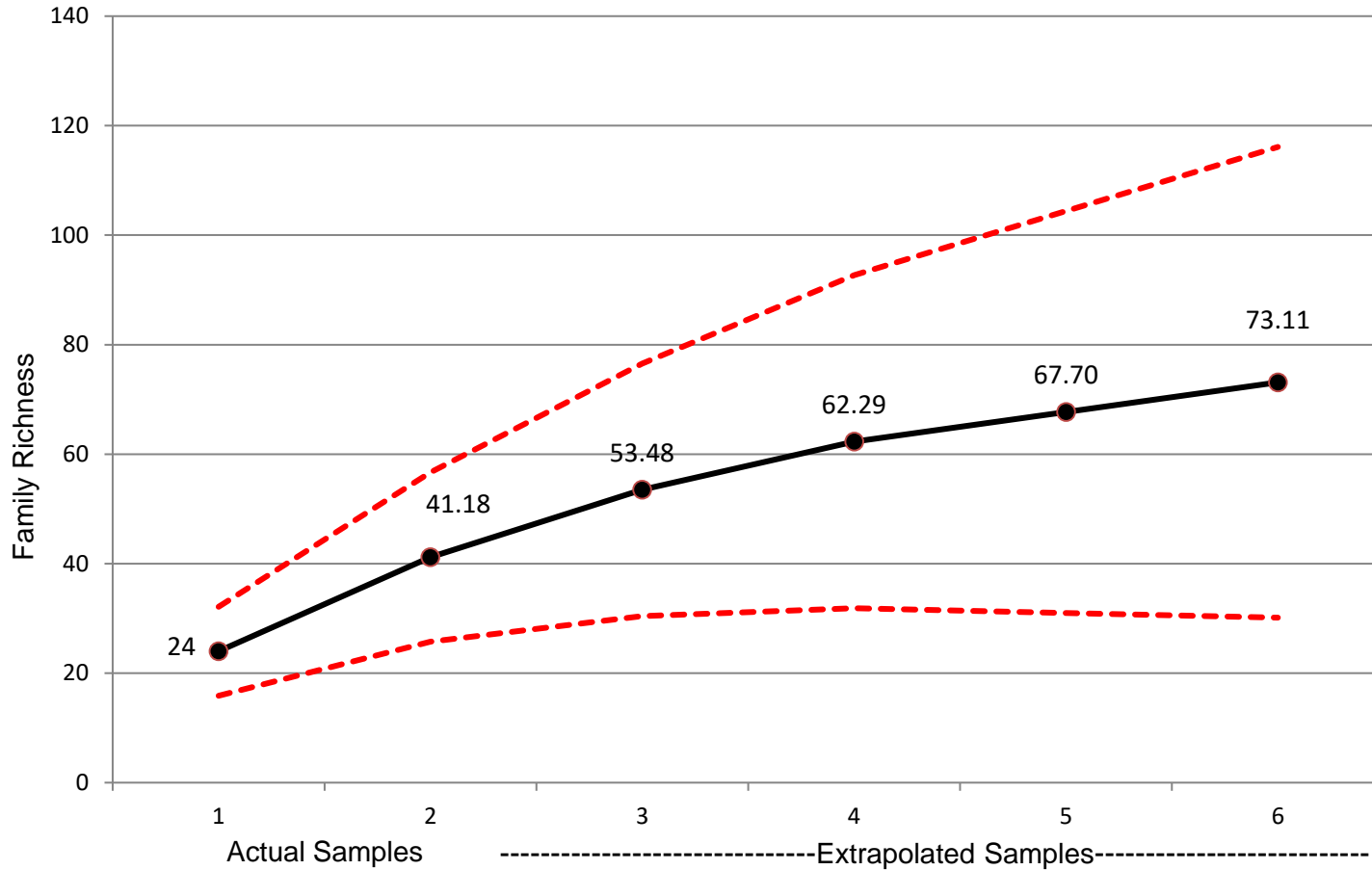


Figure 26: Sample based family accumulation curve with 95% confidence interval for invertebrate families captured in edge type C from 2015-2016 in Diboll, TX. Samples 3-6 were generated using EstimateS Version 9.1.

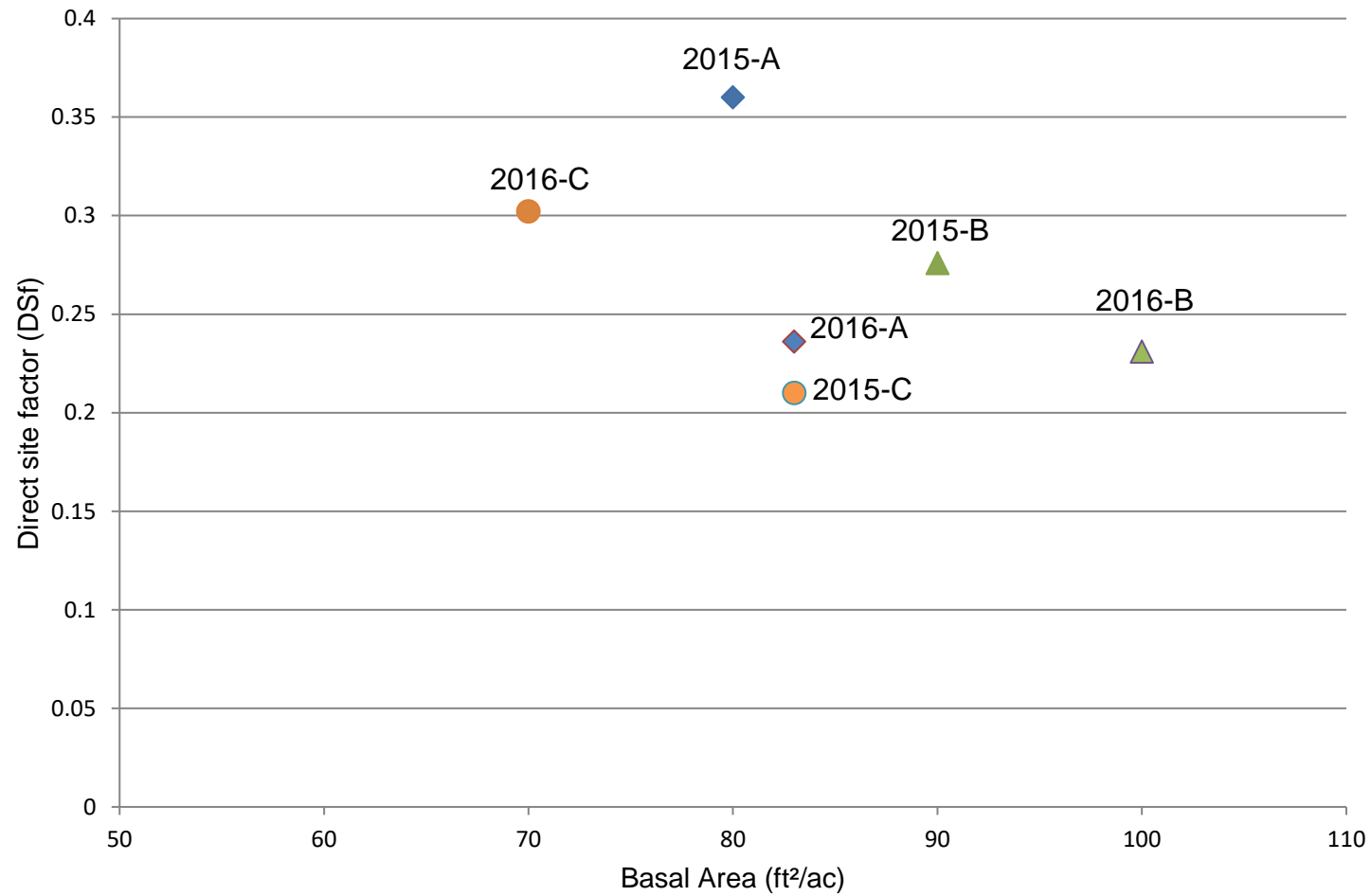


Figure 27: Comparison of direct site factor (DSF) and basal area (ft²/ac) of stands for the younger side of each edge type for 2015-2016.

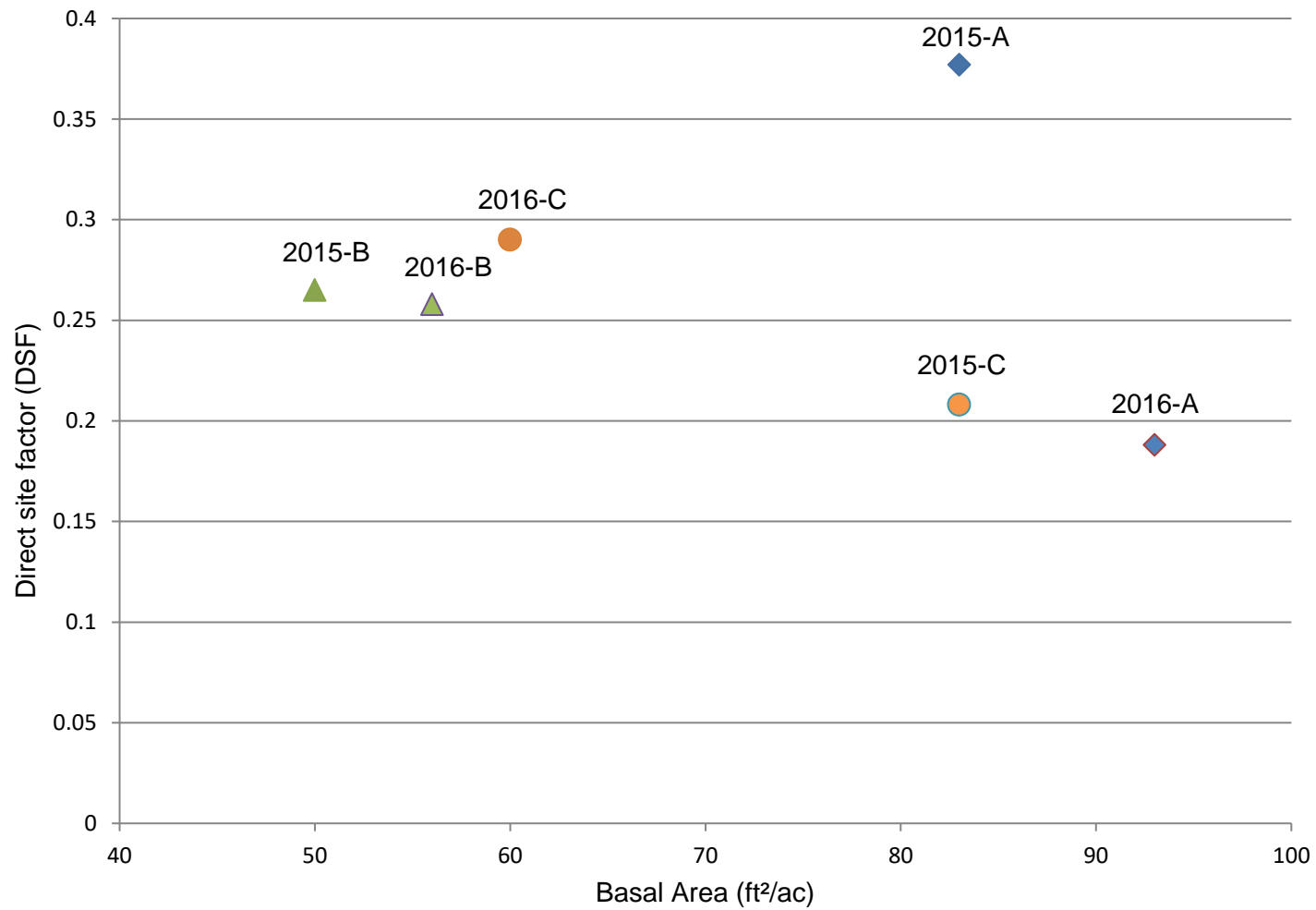


Figure 28: Comparison of direct site factor (DSF) and basal area (ft<sup>2</sup>/ac) of stands for the older side of each edge type for 2015-2016.

Table 1: List of bird species and number of individuals found in each edge type and season along with their abundances. Residents (R) and migrants (M) are indicated in parenthesis.

Species S=26	Edge A		Edge B		Edge C	
	2015	2016	2015	2016	2015	2016
American crow (R) ( <i>Corvus brachyrhynchos</i> )	8	1		3	8	1
American robin (R) ( <i>Turdus migratorius</i> )						1
Blue Jay (R) ( <i>Cyanocitta cristata</i> )	7	1			4	
Carolina chickadee (R) ( <i>Poecile carolinensis</i> )	5		4	2	4	1
Carolina Wren (R) ( <i>Thryothorus ludovicianus</i> )	3	1	4	2	6	1
Downy woodpecker (R) ( <i>Picooides pubescens</i> )	2		2			
Mourning dove (R) ( <i>Zenaida macroura</i> )		3		3	1	2
Northern bobwhite (R) ( <i>Colinus virginianus</i> )						1
Northern cardinal (R) ( <i>Cardinalis cardinalis</i> )	2	1	3	2	1	1
Pine warbler (R) ( <i>Setophaga pinus</i> )	9		9	3		3
Red bellied woodpecker (R) ( <i>Melanerpes carolinus</i> )	2		1	1		1
Tufted titmouse (R) ( <i>Baeolophus bicolor</i> )	3		2	1	3	2
Blue-gray Gnatcatcher (M) ( <i>Poliophtila caerulea</i> )						1
Black and white warbler (M) ( <i>Mniotilta varia</i> )				1		
Common yellowthroat (M) ( <i>Geothlypis trichas</i> )	3			1	2	
Eastern wood-pe-wee (M) ( <i>Contopus virens</i> )						1
Gray catbird (M) ( <i>Dumetella carolinensis</i> )			1			1
Hooded warbler (M) ( <i>Setophaga citrina</i> )				2	3	1
Indigo bunting (M) ( <i>Passerina cyanea</i> )		1	1	2		3
Kentucky warbler (M) ( <i>Geothlypis formosa</i> )	2					
Red-eyed vireo (M) ( <i>Vireo olivaceus</i> )			2	1	6	
Ruby-throated hummingbird (M) ( <i>Archilochus colubris</i> )					1	1
Summer tanager (M) ( <i>Piranga rubra</i> )			1			
White-eyed vireo (M) ( <i>Vireo griseus</i> )		1	5	3	5	2
Yellow-breasted chat (M) ( <i>Icteria virens</i> )		1	1			1
Yellow-billed cuckoo (M) ( <i>Coccyzus americanus</i> )				1	4	1



Table 2: List of medium (MM) and small (SM) mammal species found in each edge type and season along with their abundances.

Species MM S=10, SM S=5	Edge A		Edge B		Edge C	
	2015	2016	2015	2016	2015	2016
Bobcat ( <i>Lynx rufus</i> )	1	1				
Coyote ( <i>Canus latrans</i> )	2	1	1			2
Eastern cottontail ( <i>Sylvilagus floridanus</i> )		1	1	1		
Eastern grey squirrel ( <i>Sciurus carolinensis</i> )		1		1		1
Gray fox ( <i>Urocyon cinereoargenteus</i> )						1
Nine-banded armadillo ( <i>Dasypus novemcinctus</i> )		1	1	1		1
Raccoon ( <i>Procyon lotor</i> )	1	2	7	1		1
Virginia opossum ( <i>Didelphis virginiana</i> )		1		1		1
White-tailed deer ( <i>Odocoileus virginianus</i> )	4	4	4	4	6	6
Feral hog ( <i>Sus scrofa</i> )		1	9		4	10
Deer mouse ( <i>Peromyscus maniculatus</i> )	12		8	1	10	
Hispid cotton rat ( <i>Sigmodon hispidus</i> )			2		2	
Northern pygmy mouse ( <i>Baiomys taylori</i> )	4				1	1
Southern short-tailed shrew ( <i>Blarina carolinensis</i> )	8		1		3	
White-footed mouse ( <i>Peromyscus leucopus</i> )	6					

Table 3: List of invertebrate families captured during 2015-2016 near Diboll, Texas. Ratios of families found exclusively in one or more edge type are listed at the bottom.

Spiders/ scorpions	Beetles	Flies/Bees/ Gnats/wasps	Crickets	Moths/ Butterflies	Other
Agelenidae <sup>AB</sup> (spiders)	Boridae <sup>B</sup> (conifer bark beetles)	Apidae <sup>AB</sup> (bees)	Gryllidae <sup>AB</sup> (crickets)	Arctiidae <sup>A</sup> (moths)	Armadillidiidae <sup>B</sup> (woodlice)
Araneidae <sup>BC</sup> (orb weaver spiders)	Caribidae <sup>B</sup> (ground beetles)	Calliphoridae <sup>B</sup> (blow flies)	Gryllacridae <sup>ABC</sup> (leaf-rolling crickets)	Erebidae <sup>C</sup> (moths)	Blatellidae <sup>AB</sup> (cockroaches)
Buthidae <sup>B</sup> (scorpions)	Cantharidae <sup>C</sup> (soldier beetles)	Cephalidae <sup>B</sup> (stem sawflies)	Tettigoniidae <sup>ABC</sup> (bush crickets)	Nymphalidae <sup>AC</sup> (butterflies)	Curculionidae <sup>B</sup> (weevil)
Gnaphosidae <sup>AB</sup> (ground spiders)	Cerambycidae <sup>B</sup> (longhorn beetles)	Mantispidae <sup>C</sup> (mantidflies)	Rhaphidophoridae <sup>ABC</sup> (crickets)	Eurymerodesmidae <sup>B</sup> (millipedes)	
Lycosidae <sup>ABC</sup> (wolf spider)	Cucujidae <sup>ABC</sup> (flat bark beetles)	Muscidae <sup>B</sup> (house flies)			Forficulidae <sup>A</sup> (earwigs)
Phalangidae <sup>AC</sup> (harvestmen)	Lucanidae <sup>A</sup> (stag beetles)	Mycetophilidae <sup>C</sup> (fungus gnats)			Formicidae <sup>ABC</sup> (ants)
Pisauridae <sup>B</sup> (Nursery web spiders)	Melandryidae <sup>BC</sup> (false darkling beetles)	Sarcophagidae <sup>AB</sup> (flesh flies)			Helicidae <sup>AB</sup> (snails)
Scorpionidae <sup>C</sup> (scorpions)	Pythidae <sup>B</sup> (dead log bark beetles)	Scoliidae <sup>B</sup> (scoliid wasps)			Ixodidae <sup>C</sup> (ticks)
Theridiidae <sup>B</sup> (tangle web spiders)	Scarabaeoidea <sup>ABC</sup> (scarab beetles)				Labiidae <sup>B</sup> (little earwigs)
	Silphidae <sup>A</sup> (carrion beetles)				Lepismatidae <sup>A</sup> (silverfish)
	Staphylinidae <sup>B</sup> (rove beetle)				Lithobiidae <sup>A</sup> (centipedes)
	Synchroidea <sup>A</sup> (synchroa bark beetles)				Machilidae <sup>C</sup> (bristletails)
	Tenbrionidae <sup>B</sup> (darkling beetle)				Meinertellidae <sup>C</sup> (rock bristletails)
	Trogossitidae <sup>B</sup> (beetles)				Nabidae <sup>B</sup> (damselfly bugs)
A only=7/55	A and B=8/55	A, B and C=7/55			Polygyridae <sup>B</sup> (land snails)
B only=21/55	A and C=2/55	Total=55 families			Reduviidae <sup>AB</sup> (assassin bugs)
C only=8/55	B and C=2/55				Spirobolidae <sup>B</sup> (millipedes)

\*Superscript letters indicate in which edge(s) each invertebrate family was captured.

Table 4: Alpha ( $\alpha$ ), gamma ( $\gamma$ ), and beta ( $\beta$ ) diversity for vertebrate groups sampled summers of 2015 and 2016 near Diboll, TX.

Edge type	Vertebrate Group	2015			2016		
		$\alpha$	$\gamma$	$\beta$	$\alpha$	$\gamma$	$\beta$
A	SM	4	5	1.25	0	2	NA
	MM	4	7	1.75	9	10	1.11
	Birds	11	21	1.91	8	23	2.87
	Total-A	19	33	1.74	17	35	2.06
B	SM	3	5	1.66	1	2	2.00
	MM	6	7	1.16	6	10	1.66
	Birds	13	21	1.61	15	23	1.53
	Total-B	22	33	1.50	22	35	1.59
C	SM	4	5	1.25	1	2	2.00
	MM	2	7	3.50	8	10	1.25
	Birds	13	21	1.61	19	23	1.21
	Total-C	19	33	1.74	28	35	1.25

\* $\alpha$  = local richness per edge,  $\gamma$  = richness across all edges,  $\beta$  = dissimilarity between edges ( $\gamma/\alpha$ ).

Table 5: Number of species (S), total number of individuals (N) and values of species diversity indices of vertebrates observed in loblolly pine plantations during the summers of 2015-2016 near Diboll, Texas.

Edge Type	S	S (n = 1)	S(n=1)/S	N	n(i) max	H'	E <sub>H'</sub>	1/D	E <sub>1/D</sub>	1/d
A (2015)	19	2	0.11	84	12	2.73	0.62	12.97	0.68	7.0
B (2015)	22	9	0.41	70	9	2.77	0.65	12.83	0.58	7.8
C (2015)	19	4	0.21	74	10	2.75	0.64	13.69	0.72	7.4
A (2016)	17	14	0.82	23	4	2.69	0.85	12.30	0.72	5.8
B (2016)	22	12	0.55	38	4	2.96	0.81	17.19	0.78	9.5
C (2016)	28	20	0.71	50	10	2.99	0.76	13.15	0.47	5.0

\* S(N=1)= # of species with only 1 detected individual, N(i)max = # of individuals in the most abundant species, 1/D= Simpson's reciprocal index, H= Shannon Index, 1/d=Berger-Parker Index, E=evenness.

Table 6: Vegetation measurements for sampled pine plantations near Diboll, Texas from the summers of 2015 and 2016.

Edge types and ages	Basal area (ft <sup>2</sup> /ac)	Diameter at breast height (Inches)	Total height (feet)	Understory Density (Nudd's board 1-5)	Understory composition					
					Live woody (%)	Dead woody (%)	Live non-woody (%)	Dead non-woody (%)	Average woody height (feet)	Average non-woody height (inches)
<b>2015 Sites</b>										
Edge A -15 yr.	83	10	46	2	65	0	32	3	12	10
Edge A - 8 yr.	80	7	25	5	100	0	13	0	13	5
Edge B - 22 yr.	50	10	62	5	100	7	13	0	16	12
Edge B - 8 yr.	90	5	28	5	78	32	30	2	8	3
Edge C - 21 yr.	83	11	65	5	44	8	20	0	9	6
Edge C - 13 yr.	83	9	58	4	78	0	10	0	8	13
<b>2016 Sites</b>										
Edge A - 12 yr.	93	8	40	4	77	0	9	0	7	5
Edge A - 6 yr.	83	6	35	5	50	12	33	0	4	4
Edge B - 23 yr.	56	11	75	4	62	7	5	0	5	3
Edge B - 10 yr.	100	8	52	4	72	7	0	0	9	6
Edge C - 21 yr.	60	9	48	4	53	0	82	0	3	11
Edge C - 15 yr.	70	9	44	2	5	7	63	2	1	15

Table 7: Digital hemispheric canopy photography results from three edge types sampled in Diboll, TX August of 2016. Values for Indirect site factors (ISF), direct site factors (DSF) and global site factors (GSF) range from 0-1 with 0= no radiation reaching forest floor and 1= total radiation exposure. Analysis conducted using Hemi-View Canopy Analysis Software Version 2.1

Edge Type	Yards from edge	Stand Ages	2015			Stand ages	2016		
			ISF	DSF	GSF		ISF	DSF	GSF
A	40	8	0.288	0.361	0.352	6	0.250	0.264	0.263
	10	8	0.245	0.359	0.346	6	0.200	0.210	0.209
	10	15	0.288	0.354	0.346	12	0.165	0.186	0.184
	40	15	0.314	0.399	0.389	12	0.204	0.189	0.191
B	40	8	0.233	0.331	0.320	10	0.208	0.272	0.264
	10	8	0.225	0.221	0.222	10	0.180	0.189	0.188
	10	22	0.254	0.198	0.205	23	0.202	0.256	0.250
	40	22	0.264	0.331	0.323	23	0.211	0.259	0.254
C	40	13	0.259	0.270	0.269	15	0.271	0.321	0.315
	10	13	0.229	0.150	0.160	15	0.270	0.283	0.282
	10	21	0.181	0.149	0.153	21	0.241	0.163	0.173
	40	21	0.246	0.266	0.264	21	0.348	0.416	0.408
Averages			A = 0.283	0.285	0.358		0.204	0.212	0.211
			B = 0.244	0.270	0.267		0.200	0.244	0.239
			C = 0.228	0.208	0.211		0.282	0.295	0.294

## DISCUSSION

The goal of this study was to determine if biodiversity differed between plantation edges with stands of varied age ranges. Measuring biological features (richness and abundance) of the juxtaposition of structurally varied stand types within a plantation forest-dominated landscape, as proposed by Brokerhoff et al. (2008) and Smith et al. (2008), intended to identify similarities or differences amongst current forest management practices on sampled lands. The opportunity to better utilize the plantation edges in this study area as not only economic investments but as localized areas of higher diversity, or stepping stones for wildlife traveling between non-plantation forest remnants, was and is worth investigating. Careful consideration of the spatial and temporal patterns of plantation harvesting could create another tool for managers to improve biodiversity conservation in this and other plantation forest-dominated landscapes (Zobrist et al. 2005).

Managing individual timber stands for features of non-plantation forests including the retention of logging debris, snags, and legacy trees, increasing rotation lengths, maintaining understory plant diversity, and planting native crop species, can improve habitat conditions for some wildlife species, whereas

managing landscape characteristics such as the distribution and composition of edge types, increasing connectivity, targeting reforestation on former cutover lands, and retaining various sizes of protected natural forests can improve habitat for other, more wide-ranging species (Flaspohler and Webster 2011). No specific forest type or structure maximizes diversity; rather various species require various types of habitats to thrive (Zobrist et al. 2005). Likewise, even individual species require various habitats to survive and reproduce (Zobrist et al. 2005). That being so, it is not surprising that no difference was found amongst the three edge types, but rather each edge type benefits biodiversity in its own way.

The whole premise of this study is based on the notion that throughout plantation rotations, the thinning of sampled forests alters stand structure, which effects wildlife diversity in varied ways (Greene et al. 2016, Hartman et al. 2010, McWethy et al. 2009, Carnus et al. 2006, Hartley 2002, Hansen et al. 1991). Some of the subtle differences and similarities found for species richness, diversity, abundances, and assemblages for each edge could be partially explained by habitat variables found in sampled stands. For instance, productivity (McWethy et al. 2009, Carnus et al. 2006), the abundance of snags and CWD (Flaspohler and Webster 2009, Smith et al. 2008, Carnus et al. 2006, Hansen et al. 1991), canopy openness (Greene et al. 2016, Carnus et al. 2006, Hartley 2002), rotation length (Andreu et al. 2008, Carnus et al. 2006, Zobrist et al.

2005), and understory composition and structure (Hartley 2002) are all linked to forest biodiversity.

The microclimate conditions created beneath a forested canopy are typically cooler, moister, and more uniform than non-forested lands. This effect varies with the distance from the edge of the canopy (Murcia 1995). Light availability, air temperature, soil moisture and vapor pressure deficit vary between forest edges and interiors (Murcia 1995). This effect has been shown to disappear 50m into some forest fragments, while in others there is no change in these variables with varied distances from the edge (Murcia 1995). Research conducted on the effects of forested microhabitat post-logging determined that increased light from silvicultural disturbances lead to a denser understory composed of fast-growing, opportunistic plants (Kellner and Swihart 2014, Zobrist et al. 2005). Each sampled stand in this study exhibited more sunlight penetrating the canopy at 40m inside the stand than at 10m (Table 7), which could be due to differences in vegetation density resulting from increased sunlight closer to each edge.

One flaw in the methodology for sampling vegetation, was not measuring vegetation variables at the same locations as the light metrics to allow for adequate comparison of the two factors. These edges were bisected by primitive



logging roads, which created gaps between stands and allowed sunlight to reach the understory at varied levels, depending on the aspect. This increase in sunlight could allow woody and herbaceous plants to grow thick along edges, which could explain the decrease in light at the 10m interval versus 40m (Table 7).

This effect could offer more habitat structure and food for certain wildlife species, with the potential of making certain forest edges richer than the forest interior. For studies conducted on small mammals, researchers failed to detect edge effects within edges comprising young stands (0-5 years) (Constantine et al. 2005, Sekgororoane and Dilworth 1995); however, edge effects were detected in edges 6-10 years post clearcut (Sekgororoane and Dilworth 1995). The positive relationship that bird and small mammal abundance have with understory non-woody vegetation (Kellner and Swihart 2014) could possibly explain these findings for edge type A (8 years old, 2015), which had the highest percent of live non-woody plants (Table 6) and recorded the most bird (S=46, Table 1) detections and small mammal (S=30, Table 2) captures for any site.

A quantitative benefit of forest thinning for small mammals, invertebrates (Kellner and Swihart 2014), and birds (Owens et al. 2014) is the increase in CWD on the forest floor (Hinkleman et al. 2012, Jones et al. 2009). This debris includes fallen logs, treetops, limbs, and leaf litter substrate that provide ideal movement

pathways and habitat for small mammals and invertebrates (Kellner and Swihart 2014). Definitive information on use of each stand's CWD post-thinning or clearcut is unknown; however, observations during sampling suggest CWD is left on site post-thinning. Edge type B had the highest percentage of dead and live woody materials in the understory for both seasons (Table 7), which may partially explain why so many invertebrate families were exclusively found there (Table 3); however, it fails to explain why the two thinned stands of edge type C would not show elevated invertebrate, and small mammal abundance. A reduction in cover from predators in edge type C's two thinned stands may explain the lack of elevated small mammal abundance.

Constantine et al. (2005) found that small mammal captures did not demonstrate discrete peaks at southern pine plantation corridor edges but rather peaked within harvested stands with retained logging debris. Small mammal trapping was most successful during 2015 on edge type A (Table 2), which also had the most sunlight penetrating the canopy (Table 7), the highest percent of live non-woody growth, the highest average woody height, and tied with edge type B for the highest average non-woody height (Table 6). This increased understory growth exhibited by edge type A during 2015 may have facilitated its use by small mammals that benefited from better cover from predators, temperature regulation, movement pathways, and food sources.

Sites where CWD is left on site post-harvest have been shown to support as much as 45% more bird species at 50% higher densities than sites where CWD was shredded or removed (Owens et al. 2014). Resident bird species abundance between edges declined from A-C (48, 42, and 41) but not at a profound rate (Table 1), suggesting resident species utilize stand and edge types in equal proportions. Migrant avian species abundance increased from A-C (8, 22, and 33) (Table 1), which may suggest detected migrant avian species are seeking out older forest characteristics. Calladine et al. (2009) found that within thinned 18-32 year conifer plantations in Scotland no significant difference of avian species occurrence rates or abundance was found for any bird species, which may suggest that once stands reach canopy closure and are thinned, their value as bird habitat plateaus. While researching bird densities between clearcut forest edges in the Pacific Northwest, Hansen et al. (1991) found that avian density was significantly higher in forest and clearcut interiors rich with CWD than at edges, suggesting that forest patch size and fragmentation, not edge effects, are more responsible for avian abundance.

For the species assemblage sampled during 2015-2016, a few observations can be made in regards to the largest and most economically important species detected. The generalist white-tailed deer and pest feral hog

were the most abundant medium-sized mammals detected (Table 2). Not surprisingly, the white tailed deer was found in equal proportions amongst edges A and B and increased their abundance by one third in edge type C (Table 2). Feral hogs, on the other hand, were detected increasingly with edge stand ages (A=1, B=9, C=14) (Table 2). The overwhelmingly greater percentages of live non-woody vegetation recorded in edge type C during 2016 (older stand =82% and younger stand =63%, Table 6) may help explain these trends. Although no analysis was done on available browse, hard or soft mast amongst edges, several of the camera images of these two species recorded them eating blackberries (*Rubus repens* (L) Kuntze) growing in the understory. These two species are of the most economic value because they are game species for which hunters will pay a per acre fee to lease plantations, providing annual returns on long-term investments (Zobrist et al. 2005). In some cases, these funds help to pay for management actions that directly and indirectly benefit a wide range of species.

For each edge type, the year that had the higher basal area also had lower amounts of DSF (Figures 27 and 28). This relationship is intuitive considering basal area is a measure of tree density in each stand. Forest thinning reduces basal area and opens the canopy allowing more light to reach the forest floor and support herbaceous and woody growth from the understory.

Unfortunately, data on the time elapsed since the thinning on each sampled stand was not available, so interpreting woody and herbaceous responses from thinning operations is limited to conditions found during sampling.

Considering the two stand types that create edge type B are at opposite sides of their rotations, it is expected that edge type B rank second in variables (ISF, DSF, and GSF) for the proportion of light penetrating the canopy (Table 7). This variation creates an ecotone, with both older and younger forest characteristics that benefit both early successional species and species that require mature forest conditions. Edge type B, with the highest observed vertebrate richness for 2015, was also the only edge to have positive identifications of the insectivorous, forest edge-specialist gray catbirds and summer tanagers (Table 1). This could be partially explained by the elevated understory density (2015, Table 6) and large proportion of invertebrate families found exclusively in edge type B (Table 3). Richness of edge type B in 2015 can also be attributed to it being the only edge to have identifications of the eastern cottontail rabbit and nine-banded armadillo (Table 2).

In 2016 edge type C had the highest richness due to birds found exclusively there during the 2016 season, including the American robin, northern bobwhite, blue-gray gnatcatcher, the eastern wood-peewee, and the ruby-

throated hummingbird (Table 1). All of these species except the hummingbird prefer the open pine forest conditions created post-logging, with a thick grass understory (Kershner 2012, Brennan 1999, McCarthy 1999, and Sallabanks and James 1999). Blue-gray gnatcatchers and northern bobwhites in particular do not inhabit coniferous forests lacking in understory development (Kershner 2012, Brennan 1999). Due to the lowest basal areas (ft<sup>2</sup>/ac) and combined understory density score (Nudd's board) for 2016, edge type C exhibited the highest percentage of live non-woody vegetation, and the tallest average non-woody height (inches) (Table 6), which likely facilitated its use by these open pine forest specialist birds.

Edge type C may have elevated richness (2016) but this is likely a product of the positive relationship richness has with stand age (Hartmann et al., Carnus et al. 2006). Older timber stands benefit spatial and vertical heterogeneity, better developed soil layers, fungal floras, and increased large diameter trees and CWD (Jones et al. 2009) required by some indigenous species (Norton 1998). Two of the bird species in edge type C are forest interior specialists (blue-gray gnatcatchers, northern bobwhites) that require larger forested patch sizes and older structural characteristics (Kershner 2012, Brennan 1999). When stands that create edge type C are adjacent to other mature forests, they increase patch

sizes for the species that prefer forest interiors and, in turn, increase habitat availability and connectivity across differently managed forests.

Understory habitat (Nudd's board, live woody percent and average height, and live non-woody percent and height) variables estimated within edge type B with the lowest recorded basal areas amongst older stands (2015-2016), corroborate the notion that more severe thinnings lead to increased percentages of understory hardwoods and reduced percentages and average heights of non-woody vegetation (Table 6) (Andreu et al. 2008, Zobrist et al. 2005). This effect can also be supported using edges A (2015) and C (2016) where the averaged below canopy light metrics (DSF, ISF, GSF) were highest (Table 7). During 2015 edge A had the highest number of individuals (84), of which 12 were deer mice, whom may have been drawn to the edge by the elevated sunlight (Table 7), resulting in a higher percentage of live non-woody vegetation (Table 6). In these edges, the Nudd's board readings were the lowest (A-2015, C-2016), percent of live non-woody vegetation was the highest (A-2015, C-2016), average woody height was the lowest (C-2016), and average non-woody height was the highest (C-2016) (Table 6). Current management strategies on sampled lands did not include the use of mid-rotation prescribed fires or broadband herbicide

application to control hardwoods, which allowed for a less biased visualization of these vegetative effects post-thinning.

Previously mentioned limitations for the use of diversity indices, including the assumption that species are substitutable for each other, that the indices lack a probabilistic basis, and that they lack data regarding detection probabilities and false absences, limit their interpretive use in this study (Barrantes and Sandoval 2009). Lack of replication is another common problem with diversity studies utilizing indices that combine abundance and richness (Gotelli and Colwell 2011) and, with only two replicates; it is fair to assume that may be the case here. Furthermore, intra-specific differences among individuals such as age and sex could be potential sources of bias, if you consider that there are differences in habitat use by old and young, and male or female individuals (Barrantes and Sandoval 2009). Focusing indices on specific guilds does not alleviate the bias created by combining richness with abundance (Barrantes and Sandoval 2009). For these reasons, and for the lack of a detectable difference amongst edge types utilizing three indices (Shannon, Simpson's reciprocal and Berger Parker) interpretation of diversity amongst edges is limited. Barrantes and Sandoval (2009) suggest that richness may provide a better indication of value for each edge type than indices values.



Using richness as a measure of ecosystem health or stability can be an intuitive and cost effective means of monitoring ecosystem health; however, caution should be taken when doing so. Limiting analysis to the idea that higher richness is always better than lower richness fails to account for species composition. An over-abundance of invasive pest or predatory species could elevate richness, but hinder ecosystem functions. Managing an ecosystem for richness is very different from managing for diversity or evenness. Are edges with higher richness more valuable than edges with a more proportional assemblage of species? Are those extra species that make up the richest edge of a conservation concern? Having more species may be detrimental to an ecosystem if they are undesirable or destructive species, such as nest predators like the brown-headed cowbird (*Molothrus ater*). On the other hand, measuring diversity by the proportion of individuals found amongst the species is flawed, because the landscape does not need an equal proportion of bird species and mammalian predators. In such instances species being evenly distributed could be detrimental to ecosystem stability.

With these caveats in mind, richness results from the two seasons fail to single out one edge type over the others. The richness and abundance of species found in 2015 were very similar, despite edge B having over twice the number of species with only one individual than edge C and over four times that

of C (Table 5). In contrast to results from 2015, richness and abundance increased with edge stand ages during 2016 and edge type B had the lowest proportion of species with only one detected individual (Table 5). While 2016 data corroborates the hypothesis that richness and abundance increase with stand age (Hartmann et al., Carnus et al. 2006), 2015 data does not, which limits the interpretive value of this small dataset. One possible explanation for the variation between replicates is that they were sampled in different years that had different weather patterns.

An attempt was made to correct for any error caused by to limited replication using extrapolation and, while each vertebrate SBSAC generated reached a plateau around the sixth sample, captured invertebrate families extrapolated to six samples failed to reach an asymptote for any edge (Figures 20-26). Curves generated to illustrate extrapolated vertebrate richness of each edge type suggest that edge type A may harbor more vertebrate species ( $S=41.21$  at 6<sup>th</sup> sample) than edges C ( $S=38.94$  at 6<sup>th</sup> sample) and B ( $S=34.57$  at 6<sup>th</sup> sample), however, considering the confidence intervals for each edge type, one can see that each edge's extrapolated richness falls within the other edges 95% confidence interval (Figures 20-22). This means that, despite a six species difference from the low estimate (edge B,  $S= 34.57$ ) to the high estimate (edge A,

S=41.21), no real detectable statistical difference in extrapolated richness for vertebrates exists between the three edges (Figures 20-22). Student's t-test and p values for each vertebrate group corroborated the lack of statistical differences between edge types.

The estimates of invertebrate families may be attributed to the small sample size (Thompson and Thompson 2007); however, a study conducted in slash pine (*Pinus elliotii* Engelm.) and Camden white gum (*Eucalyptus benthamii* Maiden and Cambage) plantations in Louisiana found 127 invertebrate families using both pitfall trapping and insecticide knockdown methods (Messick et al. 2016). Using family richness estimates from all six EstimateS extrapolated samples, we found that there was an average richness of 112 families (A=110, B=154, C=73), which insinuates that our estimates may be a true representation of invertebrate family richness amongst these edge types given the sample size (Figures 23-26). Student's t-test and p values were calculated for invertebrate families found between edge types, and despite finding a significant difference between edges B and C with 6 extrapolated samples, we cannot know if the difference would still exist once curves reach an asymptote. More samples would be required to determine at which richness a true asymptote forms for invertebrates amongst each edge type.

The slope of each edge's increase in invertebrate family richness, from the second to the sixth sample, shows that edge type B had the greatest new number of families added to its assemblage with each additional sample (20 families / sample), edge type A added 15 new families per sample, and edge type C added 8 (Figures 24-26). Eventually these rates of increase should reduce with each additional sample until they reach an asymptote. Without additional samples all we can deduce is that edge type B, which was the exclusive host for 21/55 families, was advantageous for more invertebrate families than the other edge types. One explanation our habitat variables can offer regarding this is that edge type B had the highest percent of live and dead woody vegetation in its understory, both of which are positively correlated with invertebrate richness and abundance (Jones et al 2009).

Abiotic (microclimate alteration from edge to interior), biological (species richness and abundance), and indirect (predation, herbivory, pollination, and seed dispersal) edge effects may be more pronounced in sites of varying productivity (McWethy et al. 2009). The biomass accumulation hypothesis proposed by Hansen and Rotella (2000) suggests that edge effects for birds have the highest magnitude of influence in edges of higher biomass accumulation. Biomass accumulation, according to McWethy et al. (2009), "appears to represent a syndrome of ecosystem characteristics that increase the

magnitude of edge effects”. Comparison of productivity amongst the edge types is not possible with current data, however land managers on sampled lands should have long-term data on the productivity of their stands and could discern between sites of low and high biomass accumulation.

Currently the most productive lands are utilized for agriculture, while forestlands exist within marginal lands that are either of lower productivity or not geographically feasible for croplands (high slopes, unfavorable land fragmentation, proximity to water for irrigation etcetera.). Additionally, many forest managers of large land bases attempt to divest themselves of low productivity sites in favor of high productivity sites. Despite this, there is still variation amongst timber stand productivity and accessibility that could offer an alternative to edge management for landscape scale biodiversity management.

There is logic in the notion that sites that are more productive, better serve plantation managers in intensively managed timber production, and less productive sites, which may not be of high priority to managers, could be managed more for conservation (Pawson et al. 2013, Thompson et al. 2011, McWethy et al. 2009, Carnus et al. 2006, Lindenmayer 1999). Allowing less productive or accessible sites to grow on longer rotations, planting on otherwise degraded lands, planting mixed species stands, retaining CWD, legacy trees, and snags, and thinning early and heavier than normal would provide variety and

balance to an otherwise monoculture landscape. Doing so would also help meet many of the standards for conservation required by the many different forest certification groups.

What this all may mean regarding the current management strategies on sampled lands is that these considerations are already being addressed. The green up requirement held by the Sustainable Forestry Initiative for the Southern United States already ensures three years pass, or crop trees reach 5 feet in height, prior to adjacent stands being clearcut, which allows adjacent stands to vary in age and structure amongst SFI certified forests (SFI 2015-2019). This requirement promotes heterogeneity of stand ages and structures, which ultimately benefit wildlife through niche diversity. Re-evaluation of the minimum age and height requirements for SFI's green up requirement may reveal increased benefits for wildlife in further separating the age of adjacent stands. If increased heterogeneity of stand structure is desired, then using SFI's green up requirement may be the best current method to generate the desired result.

To better study the effects varied forest edges have on wildlife biodiversity, we recommend choosing a few vertebrate and invertebrate groups to use as indicators of diversity to focus long term monitoring efforts. Animal groups with increased sensitivity to disturbance or increased rarity are often the first to disappear from all but undisturbed areas, which limits their use as an

ecological disturbance indicator (Gardner 2010). Likewise, groups that are resilient and generalist in nature are also of little use as indicators (Gardner 2010). For these reasons, we recommend using an easily detectable, economically feasible, and diverse group like birds or invertebrates to compare responses to management 1) over time and 2) between managed and unmanaged (control) sites (Gardner 2010, and Lindenmayer et al 2008b). These groups are also important to ecosystem services, such as seed dispersal and pollination, which directly affect forest productivity and floral diversity (Thompson et al 2011). Identifying which vertebrate and invertebrate groups have the strongest interactions amongst species, and are area, dispersal, and resource limited, may be key to identifying suitable subjects for long-term surveys (Gardner 2010).

This research suggests that managing for wildlife biodiversity does not include the preference of one specific edge or stand rotation phase, but instead should focus on management for a diversity of stand and edge types with considerations for landscape scale and spacing. If diversity of wildlife within planted forests is the goal, then it is intuitive that a diversity of forest structures and ages would be required. Timberland managers whom oversee numerous planted tracts have the unique opportunity to have in rotation stands of varied

ages, structural features, and management strategies, which benefit a wider range of local wildlife species.



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