

**Wildlife in the Southern Blue Ridge Ecoregion: Assessing Management Impacts and
Establishing Regional Monitoring Efforts**

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EXECUTIVE SUMMARY

The Southern Blue Ridge (SBR), a region of the Southern Appalachians, is a key area of conservation value due to its high levels of wildlife diversity and endemism. Historically, regular occurrences of wildfire and prescribed fire have maintained this ecosystem and helped shape forest communities. The regular presence of fire in this system fostered oak- and hickory-dominated forests due to their relatively high tolerance to fire. These forests benefitted wildlife that relied on the food and shelter these tree species provided. Fire suppression policies lasting from the late 1800s through the mid 1900s essentially eliminated fire from these systems. These policies created conditions favorable for fire intolerant trees such as maples, and forest composition began to change. As forest managers realized that the removal of fire had changed the forest and wildlife communities of the SBR, they began to reintroduce prescribed fire during the past few decades. Forest managers want to reintroduce fire to restore historical communities to improve ecosystem health and resiliency, and want to better understand how their management actions are influencing wildlife populations in this region. The North Carolina Chapter of The Nature Conservancy sought to address this knowledge gap and highlight additional monitoring efforts needed to fully understand the effects of forest management on wildlife.

This document consists of two parts. The first is a systematic review that synthesizes current research on the impacts of prescribed fire and thinning treatments on wildlife. A systematic review is a literature review that follows strict guidelines and protocols to maximize rigor and objectivity. This systematic review includes a meta-analysis of effect sizes calculated from data reported in the literature, allowing for comparison among dissimilar studies. The results of this systematic review indicated that prescribed fire treatments in forests had an overall positive effect, generally leading to an increase in wildlife abundance. Conversely, mechanical and chemical thinning treatments tended to have no significant effects on wildlife abundance. The magnitude and direction of effects from different forest treatment types varied between wildlife taxa, however. Additionally, the review found that important factors, or covariates, influenced how forest management affects wildlife abundance differently between taxa. Most notably, forest type significantly influenced how birds, mammals, and reptiles were affected by forest management. For these taxa, treatments in oak and mixed oak forests tended to have no significant effects, while in pine and mixed mesophytic forests, they tended to have positive effects, suggesting wildlife preference for oak forests. Habitat use also emerged as an important variable for birds. Forest interior birds, which prefer undisturbed and continuous forest canopy, experienced negative effects due to forest treatments, while forest edge birds, which benefit from canopy gaps, experienced positive effects due to forest treatments.

The systematic review highlighted several gaps present in the literature and current monitoring efforts. While data on birds were readily available, the majority of these data were on one particular bird order, *Passeriformes*, while data on owls and raptor species were rare, despite their ecological importance. Research on mammals focused almost exclusively on rodents like mice and voles, while neglecting other important species such as bears, bats, foxes, and felines. Data on reptiles were especially scarce, with only two studies found with usable reptilian data.

Additionally, most of the studies found examined only short-term effects of single forest treatment applications, inadequately representing long-term forest management practices.

The second part of this document consists of a wildlife monitoring report, detailing existing monitoring carried out in the SBR in addition to highlighting potential indicator species forest managers could use to monitor overall ecosystem integrity. This report was meant as a reference tool for managers to help increase collaboration between partners. Data for this report were collected by contacting wildlife managers from throughout the region and from the relevant State Wildlife Action Plans.

To document existing wildlife monitoring, wildlife is broken down by taxa, and further by the type of organization performing the surveys (federal agency, state agency, NGO, or other). The report provides details about the type of monitoring, whether programs include citizen science, and ways to access monitoring data. The report also highlights monitoring programs in development for the SBR region to provide information for managers about future efforts that might be of interest to their organizations.

The monitoring report also documents potential indicator species for the SBR. Indicators are species whose abundance or survival rates can be used as a signal for other aspects of an ecosystem. For example, there are certain species known to require early successional habitats, so their presence or increase in abundance would indicate to managers that forest management techniques are successfully establishing those habitat types. Additionally, species known to be sensitive to particular types of disturbances could be indicators for the presence of that disturbance. Species or taxa identified in the SBR as potential indicators for the successful use of prescribed fire include northern bobwhite quail, the Appalachian cottontail, timber rattlesnakes, golden-winged warblers, and pollinators. Plethodontid salamanders are also highlighted as a potential indicator that could signal other types of ecological change.

The report ends by providing overarching recommendations for wildlife monitoring in the SBR ecoregion:

- There should be more coordination of monitoring efforts across the region using existing large regional networks (such as the Appalachian Mountain Joint Venture, the Avian Knowledge Network, or the Appalachian Landscape Conservation Cooperative) for leverage.
- Region-wide questions should be developed to help drive monitoring so it has a distinct purpose.
- Long-term data should be collected, and current data collection should be coordinated with historical datasets so that long-term trends can be detected.
- Central data repositories should be considered to make data organization and management more effective even when different partners are collecting data.

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1. INTRODUCTION

The Southern Blue Ridge Mountains are biologically important, harboring many rare and endangered species and high levels of biodiversity. However, a history of fire suppression in the region has led to loss of biodiversity through the decline of fire-reliant ecosystems, such as open pine and oak woodlands (Nowacki and Abrams 2008). Forest managers have accelerated the reintroduction of fire into the Southern Blue Ridge, but could benefit from more information about the positive and negative effects that prescribed fire, and related management activities, have on the region's wildlife. With a review of the relevant literature in addition to a synthesis of current monitoring activities and possible ways to move forward with collaborative regional monitoring, we provide Southern Blue Ridge Fire Learning Network (SBR FLN) partners with evidence-based knowledge to engage in more effective conservation and management to protect and restore the biodiversity of the Southern Appalachians.

Our project consists of two primary objectives: (1) Synthesize existing research on the effects of forest management techniques (fire and silviculture) on wildlife taxa in the Southern Blue Ridge using a literature review and meta-analysis; and (2) Develop recommendations for the implementation of a region-wide wildlife monitoring strategy using the meta-analysis results indicating significant effects or knowledge gaps to set priorities.

2. BACKGROUND

2.1 Biodiversity in the Southern Blue Ridge

The Southern Blue Ridge Ecoregion (SBR) is a globally outstanding center of biodiversity, with notably high endemism and species richness within its characteristic hardwood forests (Ricketts et al. 1999). It is particularly notable as the center of the world's salamander

diversity, particularly of family *Plethodontidae* (Petranka 1988). Efforts at an All Taxa Biodiversity Inventory (ATBI) of the Great Smoky Mountains National Park, a key landscape within the ecoregion and certainly the most well-known, recorded more than 5,500 species not previously known within the park (including 829 new to science) between 1998 and 2006 (Nichols and Langdon 2007). The U.S. National Vegetation Classification identified 136 different natural terrestrial vegetation communities, 90% of which are endemic to the SBR, that support the astounding levels of species diversity and endemism (Grossman et al. 1998, The Nature Conservancy 2000). In 2000, The Nature Conservancy produced the Southern Blue Ridge Ecoregional Conservation Plan which identified 89 animal species among the 188 species designated as conservation targets. This combination of remarkable biodiversity and numerous species of conservation concern cause the impacts of ecological changes, as well as the outcomes of management actions, to have potentially serious consequences for the ecology of the region.

2.2 Disturbance History of the Southern Appalachians

The Southern Appalachians have a long fire history, although the regime has varied over time (Welch 1999, Fowler and Konopik 2007, Fesenmyer and Christensen 2010, Falcon-Lang et al. 2015). Before human settlements by either Native Americans or Europeans, the Southern Blue Ridge regularly experienced wildfires. Multiple lines of evidence exist for the occurrence of these fires (Delcourt and Delcourt 1997, Delcourt and Delcourt 2004). Charcoal deposits in the area provide evidence of regularly occurring forest wildfires since at least 4000 years ago (Welch 1999, Fesenmyer and Christensen 2010). These fires affected not just oak and pine forests located on dry ridges, but also areas where wetter forest types such as mesic hardwood forests dominate today, suggesting the effects of fire in the Southern Appalachians were widespread (Fesenmyer and Christensen 2010). The frequency of these wildfires is not well understood, and

it is difficult to obtain from charcoal data due to their coarse temporal resolution. However, the charcoal data did show a marked increase in fire occurrence in the region about 1000 years ago, coinciding with the appearance of Native American tribes in the area.

When Europeans first arrived in the New World, they believed they had found an untouched wilderness. However, Native Americans had long modified the forests of North America to suit their own needs, using fire as a land management tool. Natives used fire to facilitate gathering and production of foods growing in forests, such as acorns and chestnuts from trees, and fruits and berries from shrubs (Delcourt and Delcourt 1997, Brose et al. 2001). Fire also helped improve hunting by creating more open forests and by concentrating game in predictable locations. Clearing land for agriculture and fire prevention around settlements were also methods of fire management used by these human communities (Delcourt and Delcourt 1997, Brose et al. 2001). During this time, Native Americans used lower-intensity fires at about five-year intervals to clear the forest understory. They used larger, high-intensity fires at about 16-year intervals to clear larger areas for agricultural fields (Aldrich et al. 2009). These anthropogenic fires, in addition to lightning-ignited fires, promoted fire-tolerant oak, pine, and chestnut trees. Following European settlement, fire practices remained largely similar as Europeans adopted Native American practices (Pyne et al. 1996). Fire intensity did increase during this time as heavy logging created conditions favorable for more intense fires, which further decreased forest cover. While these changes greatly decreased the overall forested area, oaks, chestnuts, and other sun-loving, fire-adapted trees gained competitive advantage compared to other species (Brose et al. 2001).

Due to concern from the widespread, intense fires caused by logging practices and a growing preservation movement in the United States, a strong push for fire prevention began in

the late 1800s and early 1900s. With an improvement in firefighting technology and a decline in logging, this push resulted in the near elimination of fires by the 1930s (Brose et al. 2001). This era of fire suppression has continued into the past few decades, and has strongly affected forest composition (Nowacki and Abrams 2008). When fire was more common on the landscape, chestnut, oak, hickory, and pine species dominated Southern Appalachian Forests. In the absence of fire, maple and shade-tolerant species have replaced the fire dependent oaks and pines, and the forest canopy has closed and become denser, a process termed, 'mesophication' (McClain et al. 2006, Nowacki and Abrams 2008). Forest managers from many organizations have attempted to reintroduce fire into the Southern Blue Ridge during the past few decades primarily for the purpose of maintaining or restoring native community types that were degraded or lost throughout the era of fire suppression. Management techniques include prescribed fires and combinations of prescribed fire with mechanical and herbicidal thinning treatments (The Nature Conservancy 2009).

While the effects of fire and fire suppression on forest vegetation composition are clear, their effects on various wildlife species that depend on this vegetation are variable and complicated. While many species clearly benefit from disturbances such as fire and treatments that mimic fire, many more species can be adversely affected. As such, there is no comprehensive overview of the effects of fire on wildlife of the Southern Appalachians, meaning that the future of wildlife in the SBR with the reintroduction of fire and thinning is unclear. The Nature Conservancy approached us with a proposal for this systematic review to amend this knowledge gap. We aimed to do this by summarizing known effects of forest management on wildlife, identifying species or taxa that require more research and monitoring, and proposing species that could potentially serve as good indicator species to enable managers in the Southern

Appalachians to engage in more informed and effective management. Since managers have only relatively recently reintroduced fire to many areas in the SBR or used fire in conjunction with mechanical and chemical thinning treatments, filling this knowledge gap will be valuable as forest managers will be better able to predict the effects of their management actions on the diverse wildlife in the region.

2.3 The Nature Conservancy and SBR Fire Learning Network

In recognition of the SBR's biological significance and high conservation value, The Nature Conservancy (TNC) has prioritized this landscape and worked actively for the conservation of SBR forests for more than 50 years. This long-term investment in the region placed TNC in a position to take a strong leadership role among both government agencies and other non-governmental organizations in the formation of the SBR Fire Learning Network (FLN) in 2007. Four states (Tennessee, North Carolina, South Carolina, and Georgia) have territory falling within the designated project area, an approximately 4.2 million-acre section of the Southern Appalachians (Rank 2012). The original partners of the SBR FLN, one of thirteen such regional networks across the United States as of 2016, collaborated to identify five primary goals at the outset of the partnership as a framework for the science-based restoration approach they sought to establish (Bucher et al. 2014):

1. Enhance landscape-level fire planning to help restore and maintain fire-adapted ecosystems;
2. Transfer lessons learned about fire effects among SBR FLN partners;
3. Develop outreach tools to explain the benefits of fire to public and agency staff;
4. Find opportunities to increase and share resources for implementing prescribed fire; and
5. Exchange information about fire ecology and fire management using a variety of outlets.

Since that time, the SBR FLN has been subdivided into eight focal landscapes run by place-based teams of local stakeholders from the nearly twenty network partners as of April 2015

(Buchanan et al. 2015). Landscape teams have further developed site-specific goals to facilitate restoration of the fire-adapted pine and oak forests of their focal areas and continue to share ideas and results through regular communication and workshops (Bucher et al. 2014).

The spirit of collaboration among agencies, partners, and private landowners that grew out of the activities of the SBR FLN has created a fertile environment to generate agreements and coordinated strategies to implement management, restoration, and monitoring goals at a regional scale. Within most of the SBR's eight landscapes, partnership burns across lands falling under multiple ownerships have begun to take place (Rank 2015). Vegetation modeling and mapping outputs resulting from collaborations within the FLN have also led to new enthusiasm for cross-boundary prescribed burning, with planning underway for a two-state, three-agency cooperative burn (Rank 2016) spanning the North Carolina-South Carolina state line (Rank 2015).

2.4 Project motivation and objectives

New cooperative partnerships and the establishment of a network of long-term monitoring plots across the SBR to observe the impacts of management actions on forests suggest there is currently an opportunity to develop a unified approach for monitoring the effects of fire reintroduction on wildlife as restoration efforts progress. This opportunity served as a motivation for our client, the North Carolina Chapter of The Nature Conservancy, to initiate this project as a way to both review the current knowledge of the effects of fire and forest management on wildlife taxa in central hardwood forests and use this information to develop a wildlife monitoring strategy for the landscapes within the SBR FLN territory.

The two distinct objectives for this project, as set forth by the client, are:

1. To synthesize existing research of the effects of forest management techniques (including fire) on wildlife taxa in the Southern Blue Ridge by:
 - a. conducting a rigorous literature review following established systematic review protocols, and
 - b. performing a meta-analysis on empirical data extracted from literature collected in the systematic review process.
2. To develop wildlife monitoring suggestions for implementation on TNC reserves and by other partners in the SBR FLN by:
 - a. using the results of the systematic review to identify both evidence of significant impacts on certain taxa (possible indicator species) as well as gaps in the research to help set priorities;
 - b. creating a monitoring report (Appendix III) which summarizes recent and current monitoring efforts undertaken by SBR partners and suggests strategies to standardize monitoring across the region

2.5 Systematic reviews

A systematic review is a synthesis of empirical evidence to answer a specific research question in a manner that is transparent, with well-defined *a priori* methods in order to minimize bias (Higgins and Green 2009). Systematic reviews are a well-established method in evidence-based medicine and health services, and researchers are increasingly adapting them to other fields (Higgins and Green 2009). The Collaboration for Environmental Evidence (CEE) has adapted the existing methods for systematic reviews specifically for environmental science. Systematic review methods call for a synthesis of evidence gained from data extracted from the relevant literature (CEE 2013). These reviews have well-defined steps: question-setting, protocol development, literature searching, data extraction, data synthesis, and final dissemination of results (Pullin and Stewart 2006). One way to synthesize data collected in a systematic review is by using a meta-analysis; however, not all meta-analyses are part of systematic reviews (Gates 2002). Perhaps the strongest use for systematic reviews is to identify gaps in research, and to determine the extent to which researchers have studied certain hypotheses and species (Lortie 2014).

Systematic reviews have several advantages over traditional narrative reviews and vote-counting synthesis methods (Gates 2002). The strict guidelines of a systematic review help ensure rigor and objectivity as well as transparency and independence, distinguishing them from traditional reviews (Pullin and Stewart 2006). The complexity of an ecological study, which looks for patterns across taxa and different environments, requires quantitative synthesis in order to draw conclusions (Gates 2002).

A systematic review is a good fit for our project for several reasons. Systematic reviews provide empirical evidence for the effects of wildlife management practices and can help inform managers to make decisions using evidence-based knowledge rather than experience-based knowledge (Pullin and Knight 2001). Further, systematic reviews are excellent at identifying gaps in the knowledge base, which can help inform and shape future monitoring strategies to address some of these gaps (Lortie 2014). Finally, a systematic review can help make sense of the various studies evaluated at different time scales with different treatments and focus species to draw some overall conclusions about wildlife response to fire and similar treatments in the SBR. Our main objective for this study is to use the results of the systematic review to develop a monitoring strategy that best reflects the state of current research and seeks to resolve some of the current gaps in knowledge.

3. METHODS

In this section we will discuss the methods for conducting the systematic review. The systematic review consists of several parts: question-setting and protocol development, data extraction, and finally, a meta-analysis.

3.1 Question-setting and protocol

Systematic reviews begin with a question, and that question must have a clearly defined subject, intervention, and outcome. The question should be relevant to practice or policy and be developed in collaboration with stakeholders (Pullin and Stewart 2006). We developed the following primary question and three secondary questions for our systematic review:

1. How does fire (and the application of silvicultural practices meant to have similar ecological effects) impact the abundance and diversity of wildlife taxa present within central hardwood forests?
 - a) How do wildlife abundances respond to varying fire intensities?
 - b) How does variation in initial forest conditions (including forest type) affect the outcomes of fires?
 - c) Do other management actions that imitate the effects of fire have similar effects on wildlife?

We formulated our questions with feedback from The Nature Conservancy and their SBR Fire Learning Network partners. Although our strategy will be for the SBR, we expanded our systematic review to include the entire central hardwoods region (Figure 1). An earlier review of the effects of disturbance on wildlife in the SBR struggled to build a sufficient dataset (Pitt et al. 2014), so we widened our study region to include more studies in order to discern detectable trends. After we determined our questions and defined our study area, we created a review protocol (Appendix I), which The Nature Conservancy also reviewed and approved. The review protocol is a document that outlines the methods of the systematic review *a priori* and ensures the review process is rigorous, transparent, and well-defined (Pullin and Stewart 2006).

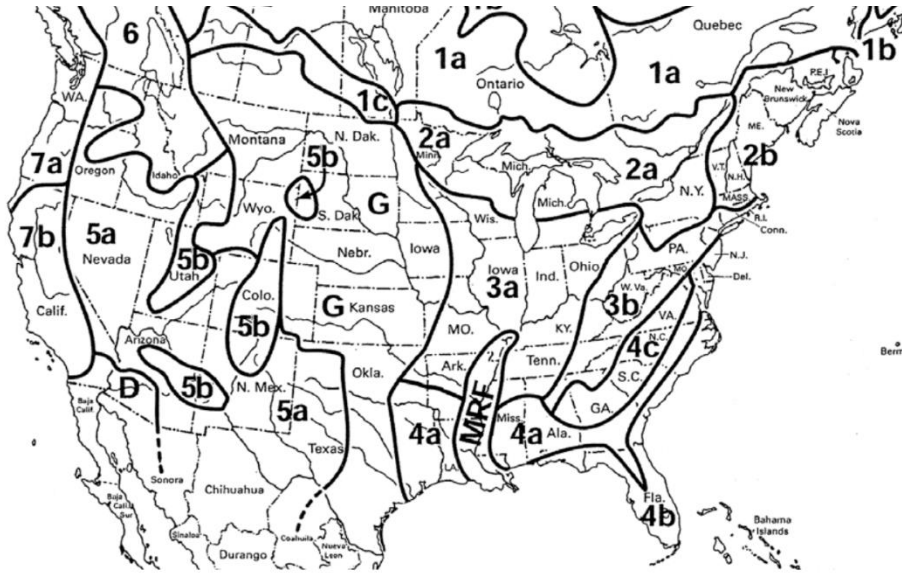


Figure 1. The map we used to define what areas fall within the central hardwoods. Any locations within the regions marked 3a or 3b we considered a part of our study area (map from Fralish 2003).

3.2 Data selection and extraction

We conducted our searches of the literature using the following four databases: Environment Complete, Forestry Abstracts, ProQuest, and Web of Science. We defined our searches using terms for the study subjects, treatments, and locations. Our searches contained a term from each column (Table 1). We limited it to combinations of these terms after reaching a saturation of results. We limited our searches to peer-reviewed articles only when using the ProQuest database due to the large volume of irrelevant results. We also accepted additional papers provided by our Southern Blue Ridge Fire Learning Network partners. Pullin and Stewart (2006) recommend ecological reviews use high sensitivity searches to reduce bias and increase repeatability. As a result, a large percentage of the studies found in the search must be culled. We also followed Pullin and Stewart's (2006) recommendation of culling papers based first on title,

then title and abstract, and then the full text, taking a conservative approach and retaining papers with uncertain relevance. We narrowed the papers down based on adherence to the following three criteria:

1. The treatments were either prescribed burning, wildfire, or a silvicultural treatment such as thinning or harvesting;
2. The dependent variable was either an abundance or diversity measurement of wildlife species;
3. The study was in the Central Hardwood region of North America.

Table 1. The search terms we used, with one column representing treatment, once column representing subject, and one column representing the geographic location.

Fire	Wildlife	South* Appalachia*
Prescribed Fire	Bird*	Central Hardwood*
Silvicultur*	Salamander*	Hardwood*
Burn*	Mammal*	Blue Ridge*
	Bat*	
	Insect*	
	Pollinator*	
	Reptile*	
	Amphibia*	
	Herp*	

For the data extraction process, we created a spreadsheet to record all pertinent information in a consistent manner to increase transparency and aid in future data synthesis. We recorded the species and taxa, and the corresponding abundance and/or diversity measures. We also recorded other characteristics such as forest type, treatment type, time since treatment, and

control age to examine as covariates in our analysis. We grouped the treatments into twelve different categories (Table 2). We partitioned our data based on site location and study year. We also considered the possible effects of varying study designs, and divided studies into three categories of study design: randomized, replicated treatment-control, before-after control impact, and age class comparison. We also considered the number of replications as an indicator of study quality. We could not account for any area effects due to an under-reporting of specific area dimensions. We also did not analyze the return interval of treatments due to a limited number of studies with repeated treatments.

Table 2. The various treatment types collected in the data extraction process.

Burn Treatments	Silviculture Treatments	Combination Treatments
Low intensity prescribed fire	Clearcut	Thin and burn
Mid intensity prescribed fire	Shelterwood cut	
High intensity prescribed fire	Two age cut	
Undefined intensity prescribed fire	Group selection cut	
	Herbicide	
	Understory removal	
	Thinning (other)	

3.3 *Meta-analysis*

The main metric used to compare studies in a meta-analysis is effect size, a measure of the magnitude of an effect based upon an experimental treatment. Traditional methods of calculating effect size are poorly suited for wildlife studies where replication may be lacking and variance is often not reported (Kalies et al. 2010). Using the recommendation of Hedges et al. 1999, we calculated effect sizes using a response ratio, $\ln(\text{experimental mean}/\text{control mean})$.

This is a suitable index of effect for ecological studies because it minimizes bias and has a relatively normal sampling distribution (Hedges et al. 1999). To prevent errors in our ratio calculations, no treatment or control mean could be equal to zero. We used the method of Kalies et al. 2010, who found that adding 0.001 to existing zero values had the smallest impact on overall effect size. Weighting of effect sizes typically incorporates the inverse of sample variance, but little to no reporting of standard deviation in the studies we analyzed meant we had to choose an alternative weighting scheme. We decided to weight studies based on the number of replicates, under the assumption that studies with greater replication are statistically superior (Johnson 2002). Because the impact of weighting varies based on weighting method and individual meta-analyses, we decided to analyze both unweighted and weighted effect sizes (Osenburg et al. 1999, Kalies et al. 2010, Marín-Martínez 2010).

To analyze these effect sizes we first selected predictor variables that had statistically significant impacts on effect size, with the assumption that predictor variables with strong correlation to the effect sizes are ecologically important to the wildlife in the system. We then examined the individual effect of each significant predictor variable. For categorical predictors, we accomplished this by calculating the mean effect size for each category along with a 95% confidence interval, and comparing them to 0 (with 0 indicating no effect). For continuous predictors, we examined the impact of predictor variables on effect sizes through regressions. We first performed this process for all data containing all of the wildlife species, and then repeated it for each individual taxon, to account for differences in importance and effect of predictor variables between different taxa.

We selected important predictor variables using generalized linear models (GLMs) and stepwise regression. We created GLMs for both the unweighted and weighted effect sizes. GLMs

are similar to simple linear regressions but use a link function (Neuhaus and McCulloch 2011). Link functions transform response variables so they are linearly related to the predictor variables. In our case, the response variables responded linearly to the predictor variables, so we used an identity link function. GLMs use maximum likelihood methods to find the best estimate of the model parameters. Our initial unweighted and weighted models included all covariates that we had complete information for across all studies.

We then used the stepwise regression “step” function from the base package in R Version 3.2.4 (R Core Team 2016) to determine the most parsimonious models. The stepwise regression uses bidirectional elimination, testing at each step for variable inclusion by comparing the Akaike information criterion (AIC) and removing variables that contribute to a higher AIC. AIC measures the quality of the model by computing a trade-off between goodness of fit and complexity. For all models, we calculated both the *P*-value to determine if the model performed significantly better than a null model and the percent of deviance explained by the model.

After building our final GLMs for both the all-taxa data and each individual taxon, we analyzed the effect sizes of the categorical variables shown to be important. We used bootstrapping to calculate 95% confidence intervals around the mean effect size for each variable, using 1000 replicates. To perform this analysis, we used the boot function from the boot package (Canty and Ripley 2016) in R Version 3.2.4 (R Core Team 2016). Bootstrapping is a nonparametric method of inference used when assumptions about distribution are not met, as is common in small sample sizes. However, due to inaccuracies that may result from samples that are too small, confidence intervals were only calculated when the sample size was at least 10 (Hesterberg 2011). Using bootstrapping, we were able to calculate mean effect size with confidence intervals to determine which categorical variables did not include zero, and therefore

indicated a positive or negative effect. For the continuous variables identified by the GLMs as important, we performed simple linear regressions to examine the relationship between effect size and the covariate.

4. RESULTS

After our initial 155 searches, we had 4,580 studies collected in our database. We removed all duplicate papers, leaving us with 2,048 studies. After culling by title and abstract as well as adding in relevant papers from partners, we had 149 studies. We culled studies that did not meet our three initial criteria laid out in the methods section, with the majority (76%) of papers being culled for being off-topic (Figure 2). Our data extraction process resulted in further culling due to papers lacking raw data or not meeting inclusion criteria, so that our final analysis included a total of 50 studies. Of these final papers, amphibians had the highest number of studies, and multiple taxa (herpetofauna) had just one study (Figure 3).

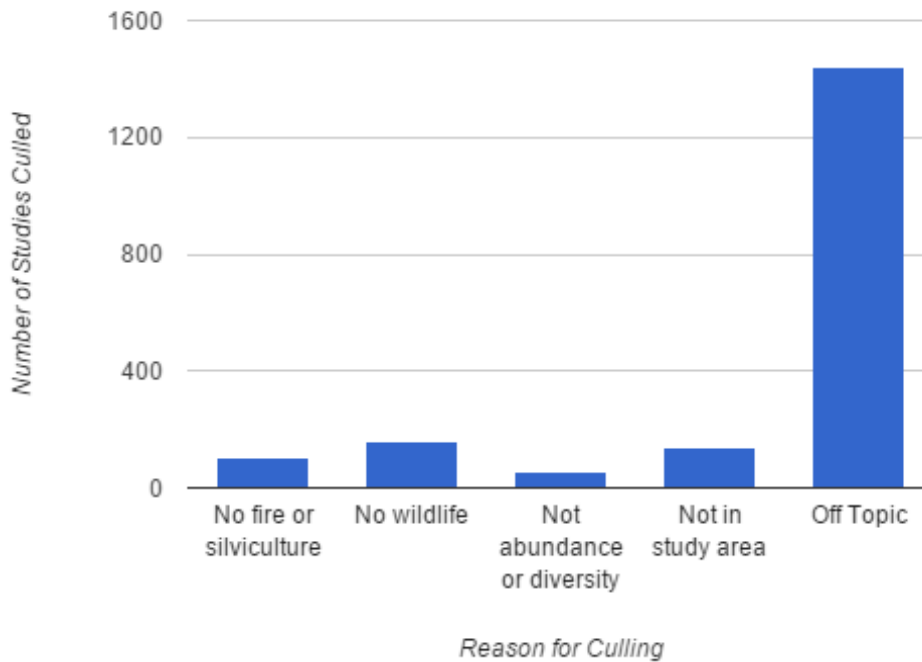


Figure 2. Number of papers culled by reason for elimination from analysis.

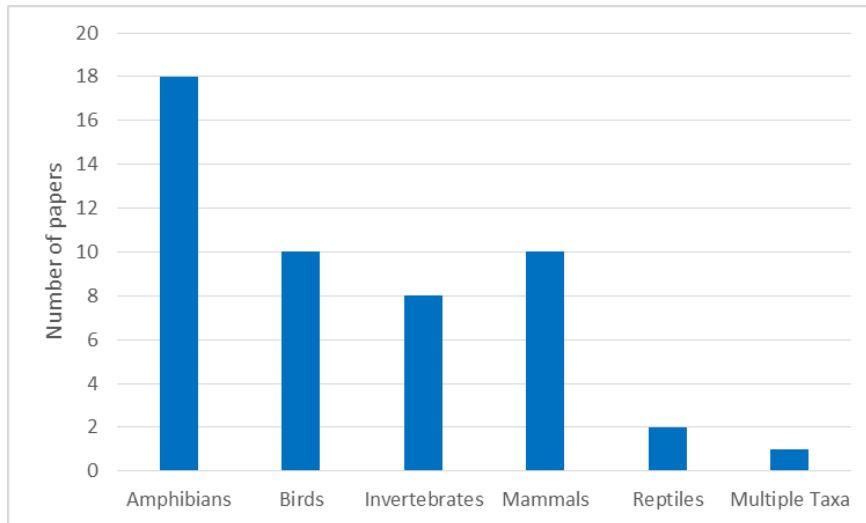


Figure 3. The number of papers used in the meta-analysis specific to each taxa.

The data we used consist not of each individual study, but of each individual observation. We recorded each observation as a separate line of data in our extraction spreadsheet. An observation was a record of abundance or diversity that is completely unique; that is, an observation that has at least one covariate (e.g. species, treatment type) that differs from another observation. Therefore, an individual study could potentially contain hundreds of observations. Hereafter, we define each “study” as a single publication, and each “observation” as a single line of data, or unique abundance or diversity measure. We had a total of 2,337 observations across 50 studies.

The studies were spread across ten different states, with North Carolina having the highest number of studies at 16 (Figure 4). We categorized the studies into six different forest types (oak-dominated, pine-dominated, pine-oak mix, mixed mesophytic, riparian, oak-hickory, pine-hardwood mix) and about a third of the studies took place in oak-dominated forests (Figure 5). We had three different study types included in our analysis: control-treatment (30), before-after control-impact (17), and age class comparisons (3). Of all the observations, 46% involved

burning, 41% involved silvicultural treatment, and 13% were a combination of the two. Just 0.05% of all observations were diversity measurements, while the majority (95.5%) were abundance measurements. Most observations measured wildlife response a relatively short time after treatment, with the average being 3.5 years. The average age of the control forest was approximately 67 years.

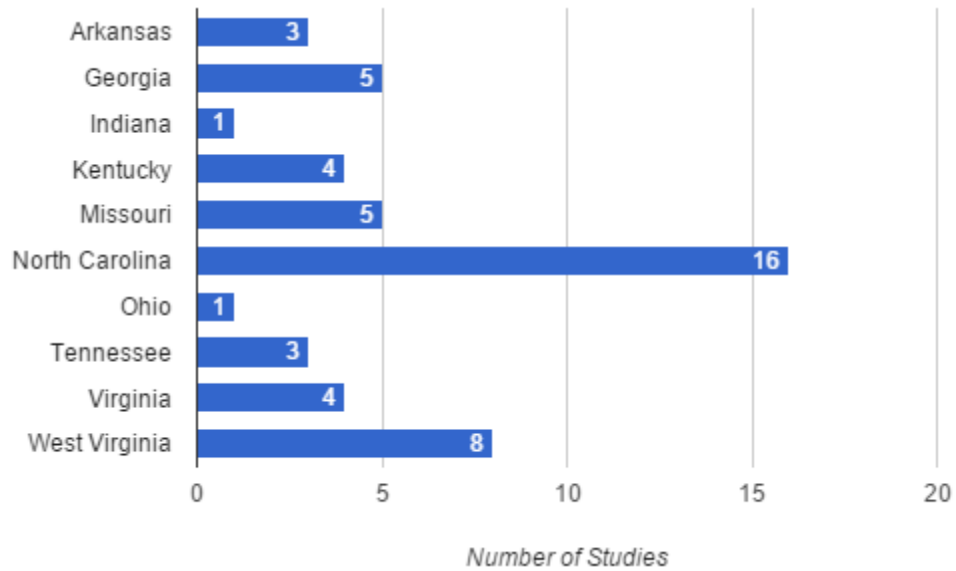


Figure 4. The distribution of studies across ten states.

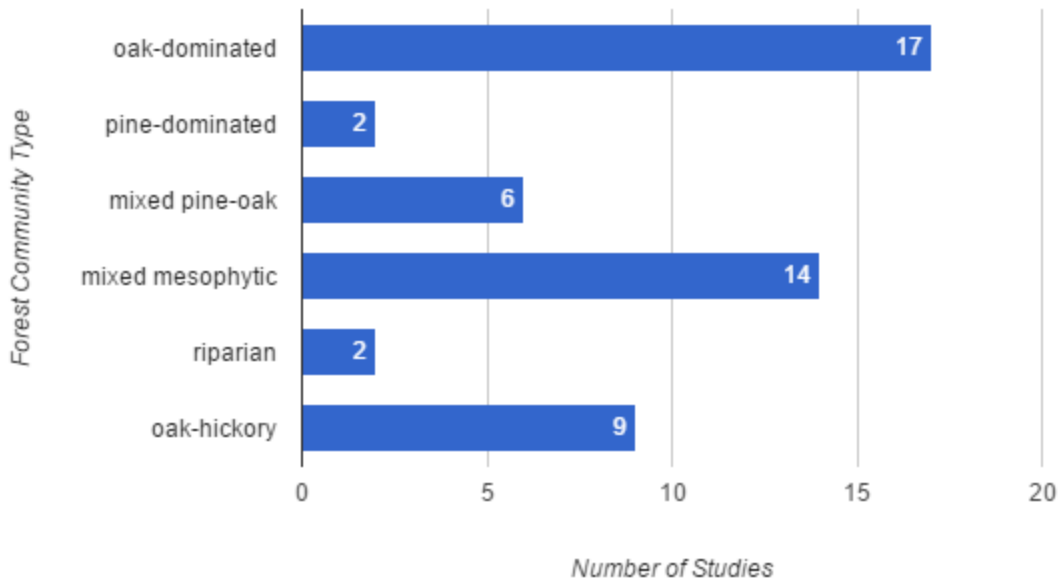


Figure 5. The distribution of forest types across studies.

After eliminating insignificant predictor variables via stepwise regression, our final GLMs for both the weighted and unweighted effect sizes included the variables taxa, treatment type, forest type, and study type, in order of decreasing importance. The results of our final GLMs including all of the taxa indicated very little difference between using weighted and unweighted effect sizes. The GLM for the weighted effect sizes had slightly greater explanatory power ($D^2=0.08$) compared to the GLM for the unweighted effect sizes ($D^2=0.06$). We decided to use unweighted effect size because the two models were similar, and we did not feel confident enough in our weighting method to justify its use. Large variation in the number of replicates, questions about pseudoreplication, and lack of a precedent in using number of replicates as a weighting scheme all contributed to this uncertainty. The final GLMs for each taxa varied in number of important covariates, which covariates were important, and the explanatory power of the models (Table 3).

Table 3. Important covariates for each GLM, listed in order of importance, and the explanatory power of the GLM.

Taxa	Important Covariates	Explanatory Power (D^2)	P-value
Amphibians	treatment, years since treatment	0.15	<0.001
Birds	order, forest type, control age	0.15	<0.001
Invertebrates	treatment, control age	0.09	<0.001
Mammals	forest type	0.03	<0.001
Reptiles	order, treatment, forest type, years since treatment	0.30	<0.001

4.1 All taxa

The confidence intervals for the mean effect size did not include zero for any taxa other than invertebrates, indicating an effect of treatment on abundance or diversity for mammals,

birds, reptiles, herpetofauna, and amphibians (Figure 6). For birds, mammals, herpetofauna, and reptiles, mean effect size was greater than zero, indicating a positive effect of treatment. For amphibians, however, mean effect size was less than zero, indicating a negative effect of treatment. All treatment effects were of a relatively low magnitude, with the absolute value of mean effect size (calculated as described in Methods Section 3.3) never exceeding 0.7.

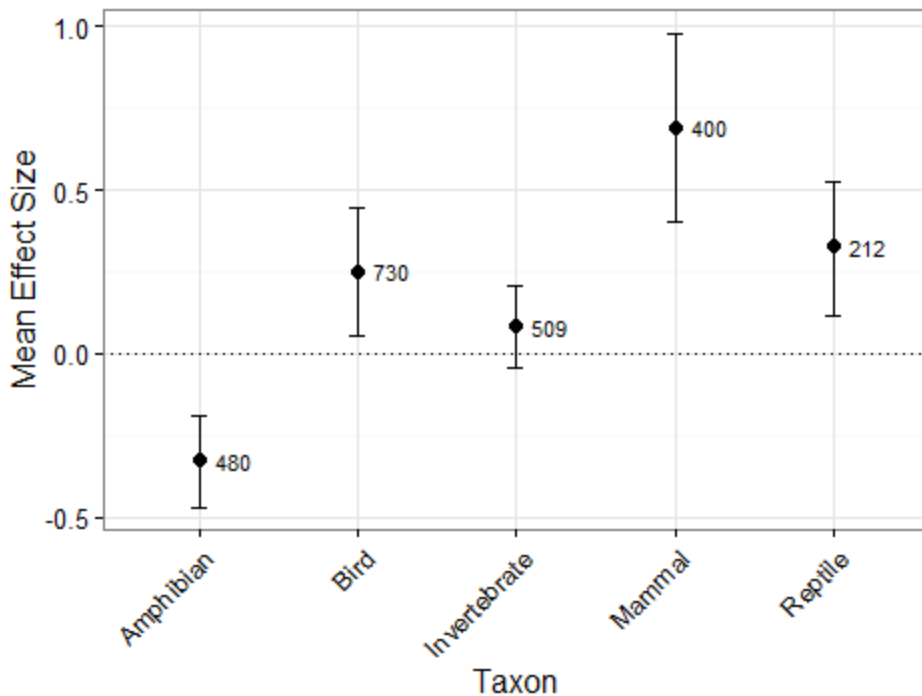


Figure 6. Mean effect sizes and 95% confidence intervals for each taxa. The number indicates the number of observations for each taxon.

When we examined mean effect sizes across treatment types, only four treatment types out of thirteen total treatment types had confidence intervals that did not include zero (Figure 7). Three types of burn treatment – mid-intensity prescribed burn, high-intensity prescribed burn and undefined-intensity prescribed burn – all had positive effects on wildlife abundance or diversity regardless of taxa. Only one silvicultural treatment had a confidence interval that did not include zero, which was group selection cut, which showed a negative effect on wildlife abundance or diversity. The magnitude of the effect was greater for all three burn treatments than the

silvicultural treatment (group selection cut). We also looked at treatment type by combining all fire treatments into one category, all thinning treatments into another category, all thin and burn treatments into another category, and herbicide in its own category. Analysis with these groupings showed only fire had an effect on wildlife abundance or diversity (Figure 8).

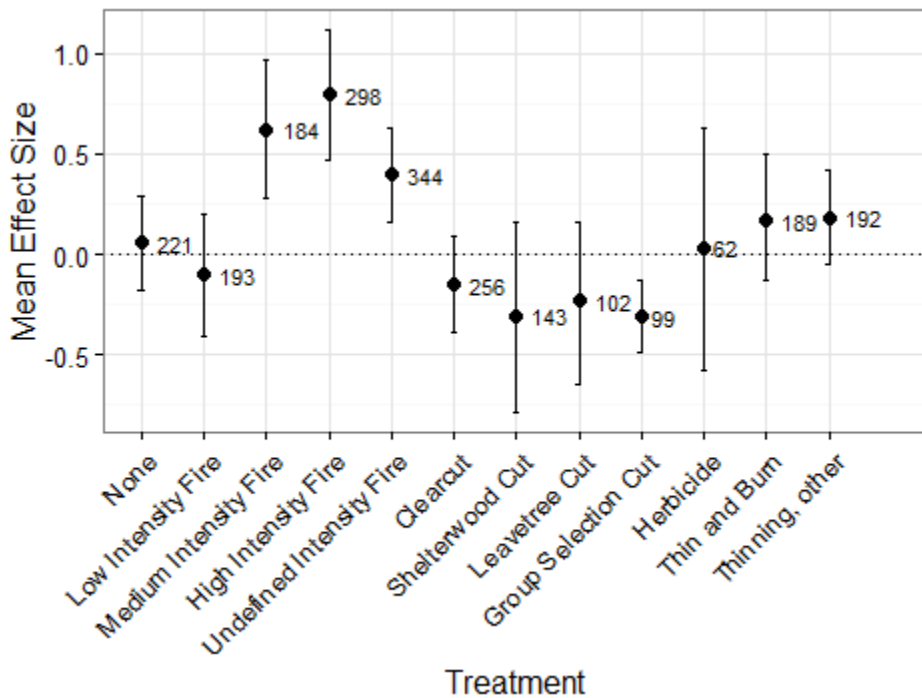


Figure 7. Mean effect sizes and 95% confidence intervals for each type of treatment across all taxa. The number indicates the number of observations for each treatment type.

For forest type, confidence intervals for three forest types did not include zero and showed a positive effect (Figure 9). These were pine-dominated forests, pine-oak mixed forests, and riparian forests. However, with the exception of pine-oak mixed forests, these forest types had considerably fewer observations. For study type, neither treatment-control nor before-after control impact studies had confidence intervals including zero and both indicated positive effects, but for age class comparison studies, the confidence interval did include zero (Figure 10). We did have far fewer observations for age class comparisons, just 54 compared to 556 for before-after control impact and 1,724 for treatment-control. The mean effect sizes for the

treatment-control and before-after control impact studies were small, with values of 0.11 and 0.44, respectively.

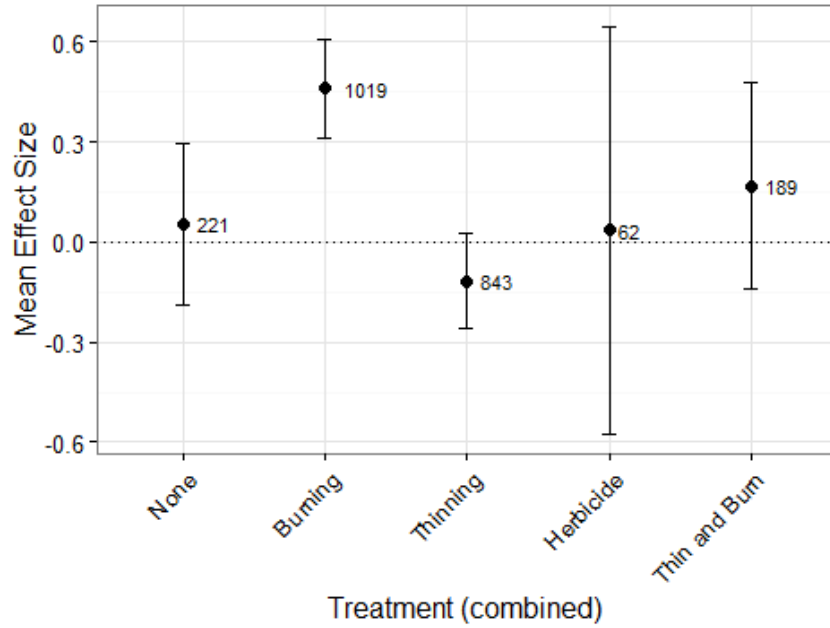


Figure 8. Mean effect sizes and 95% confidence intervals for each treatment group across all taxa. The number indicates the number of observations for each treatment group.

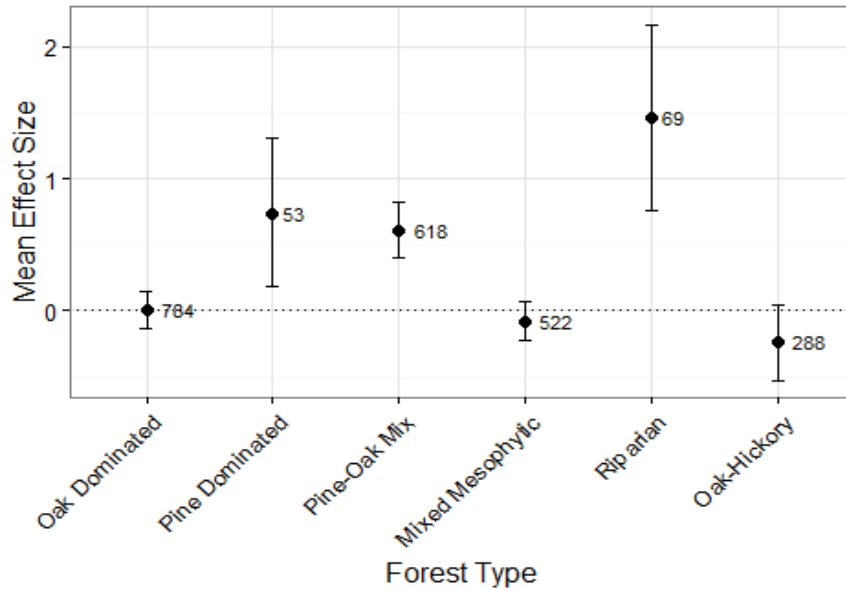


Figure 9. Mean effect sizes and 95% confidence intervals for each forest type across all taxa. The number indicates the number of observations for each forest type.

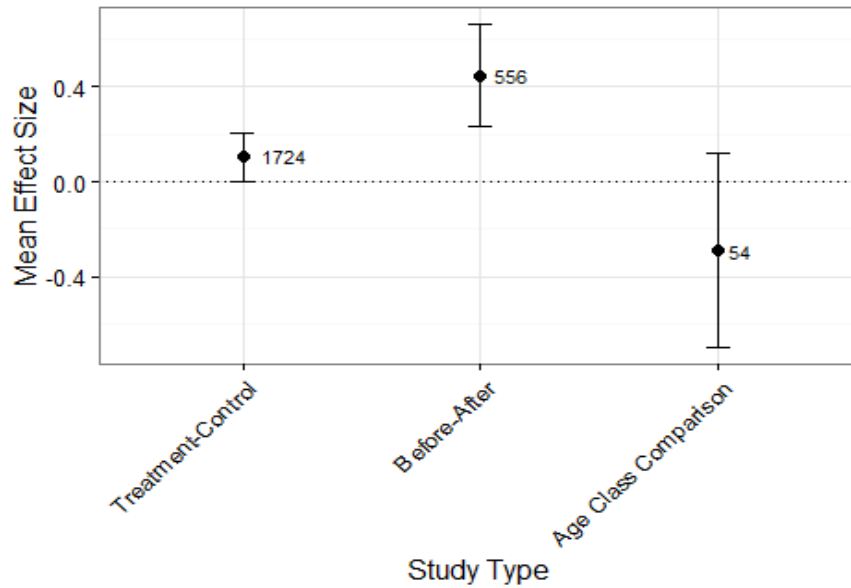


Figure 10. Mean effect sizes and 95% confidence intervals for each study type across all taxa. The number indicates the number of observations for each study type.

4.2 Amphibians

Although time since treatment was an important covariate according to the GLM, a simple linear regression of time since treatment against mean effect size did not reveal a significant relationship ($R^2=0.0000248$). Amphibians did show a response to treatment type, with nine out of the thirteen total treatment types having confidence intervals not containing zero (Figure 11). Only high intensity fire had a positive effect on amphibians, while low intensity fire, clearcut, shelterwood cut, two age cut, group selection cut, thin and burn, and thinning (other) treatments all had negative effects.

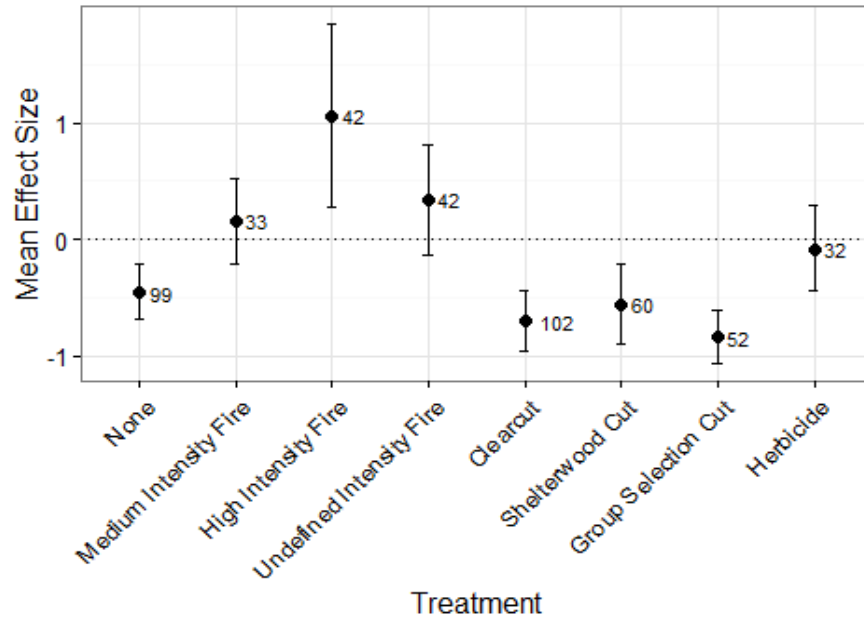


Figure 11. Mean effect sizes and 95% confidence intervals for each type of treatment for amphibians. The number indicates the number of observations for each treatment type.

4.3 Birds

Six of the nine orders of birds included in the meta analyses had mean effect sizes that differed from zero (Figure 12). These orders were Accipitriformes (falcons), Cathartiformes (buteos), Columbiformes (pigeons and doves), Cuculiformes (cuckoos), Galliformes (grouse, quail and turkeys), Piciformes (woodpeckers), and Strigiformes (owls). All orders except Strigiformes showed a positive effect. The magnitude of the response was quite high for some orders, such as Cuculiformes which had a mean effect size of 4.86, and Strigiformes which had a mean effect size of -4.61. However, the sample sizes for all the significant orders except Piciformes were less than 20. Passeriformes had by far the largest sample size (n=537 observations) but had a mean effect size of approximately zero.

Although forest type was an important covariate for birds, only pine-oak mixed forests and oak-hickory forests had non-zero responses (Figure 13). Pine-oak mixed forests showed a

positive response, while oak-hickory forests showed a negative response. Control age was also an important covariate according to the GLM, but a linear regression showed no significant relationship between the age of the control and the mean effect size ($R^2=0.032$).

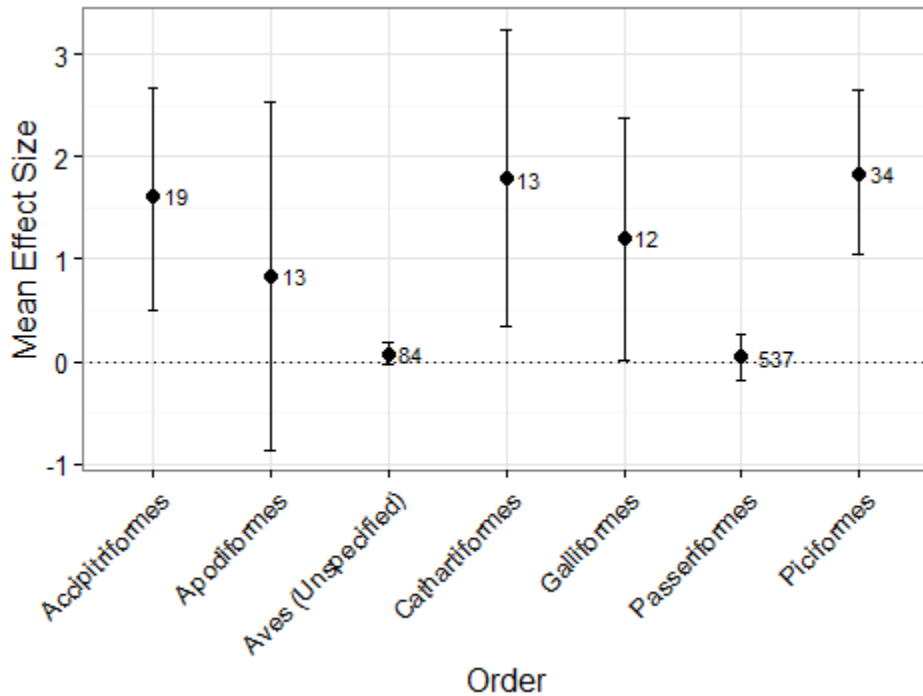


Figure 12. Mean effect sizes and 95% confidence intervals for each order of birds, as well as uncategorized birds. The number indicates the number of observations for each order.

Due to the large size of the passerine bird group (Passeriformes), we isolated the group for further analysis. We created GLMs including only passerine birds as described in Methods Section 3.3, but with the addition of habitat use and migratory behavior as predictor variables. These models again showed treatment type and forest type to be important covariates, with similar effects to the models including all bird orders. However, habitat use also emerged as an important predictor variable. While Passeriformes overall did not experience a significant effect due to forest treatments, dividing the Passeriformes into three groups based on habitat use showed significant effects. Treatments had a negative effect on passerine birds living in the

forest interior, a positive effect on those living both in the forest interior and the forest edge, and no effect on birds living in forest edges, shrubs, and fields (Figure 14).

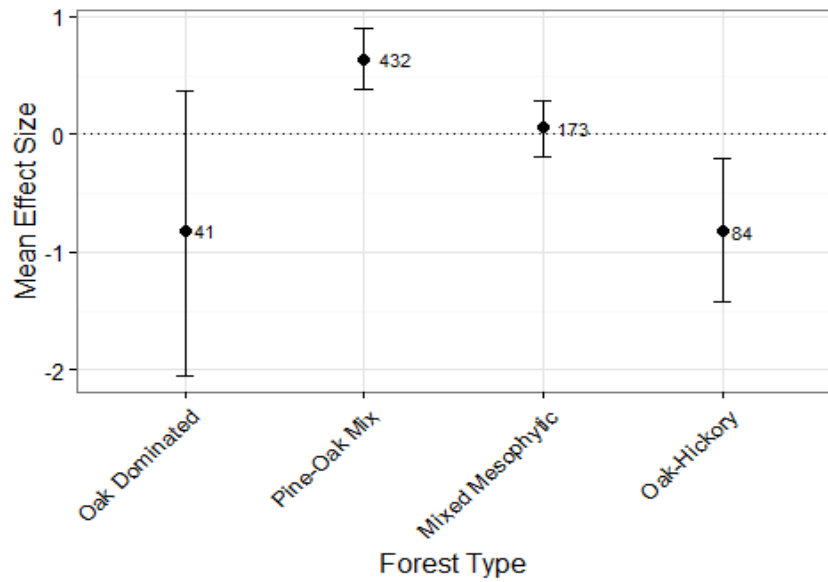


Figure 13. Mean effect sizes and 95% confidence intervals for each forest type for birds. The number indicates the number of observations for each forest type.

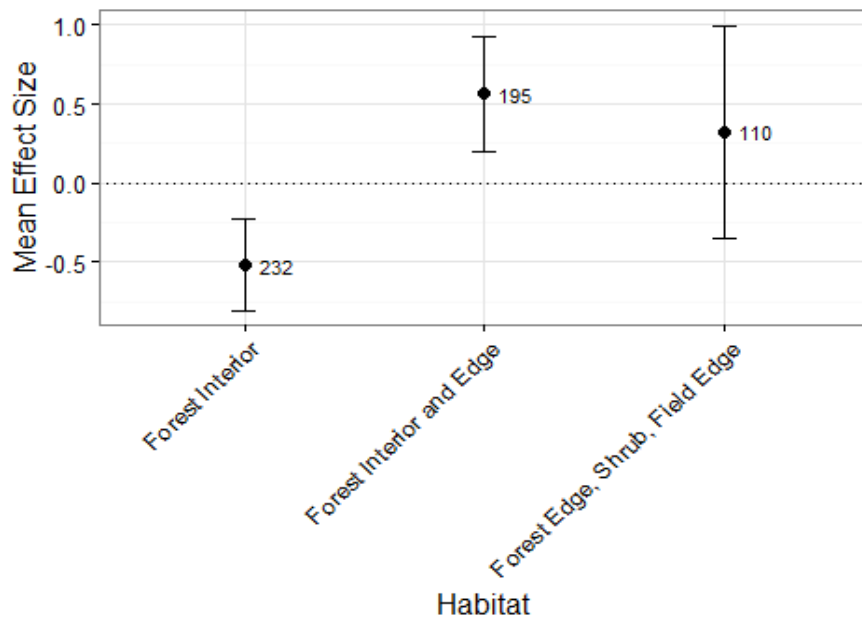


Figure 14. Mean effect sizes and 95% confidence intervals for each habitat type for passerine birds (Passeriformes). The number indicates the number of observations for each habitat type.

4.4 Invertebrates

Invertebrates showed a negative response to all three different burn intensities (low, mid, and high), but a small positive response to prescribed burns of undefined intensity (Figure 15). Mid and high intensity burns had very similar negative responses, but low intensity burns had a smaller negative response. Clearcut, thin and burn and thinning (other) treatments all showed no response. The GLM for invertebrates also indicated that control age was an important covariate, however a linear regression showed a very weak positive relationship between age of control treatment forest and effect size ($R^2=0.043$).

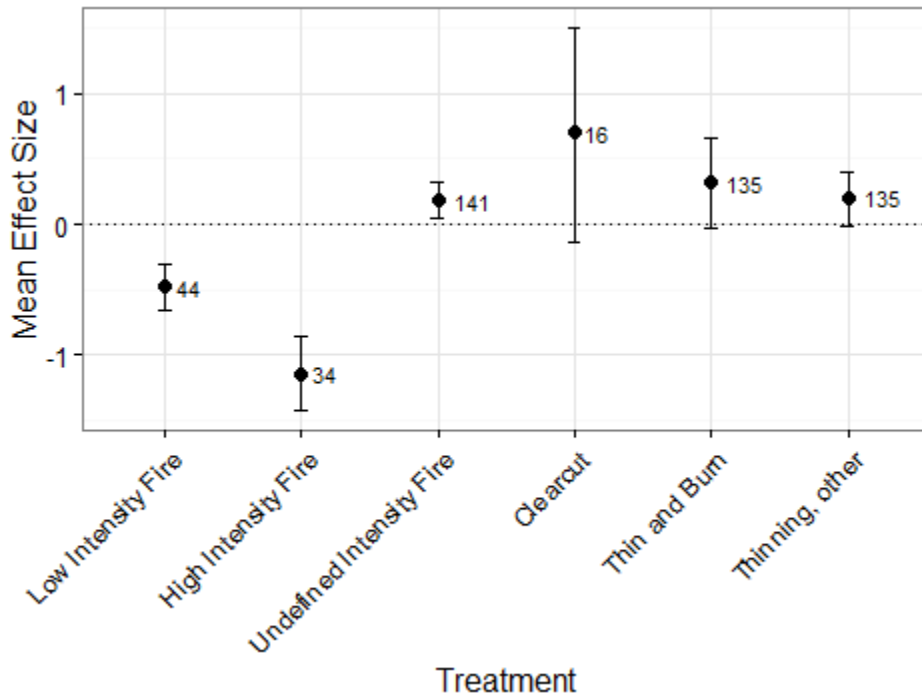


Figure 15. Mean effect sizes and 95% confidence intervals for each type of treatment for invertebrates. The number indicates the number of observations for each treatment type.

4.5 Mammals

Our GLM for mammals indicated that only forest type was an important variable. Pine-oak mixed forests, mixed mesophytic forests, and riparian forests all demonstrated positive

responses (Figure 16). Pine-oak mixed forests and mixed mesophytic forests had similar magnitudes of response, while riparian forests elicited a somewhat stronger response. Both oak-dominated forests and oak-hickory forests had confidence intervals that included zero, showing no response.

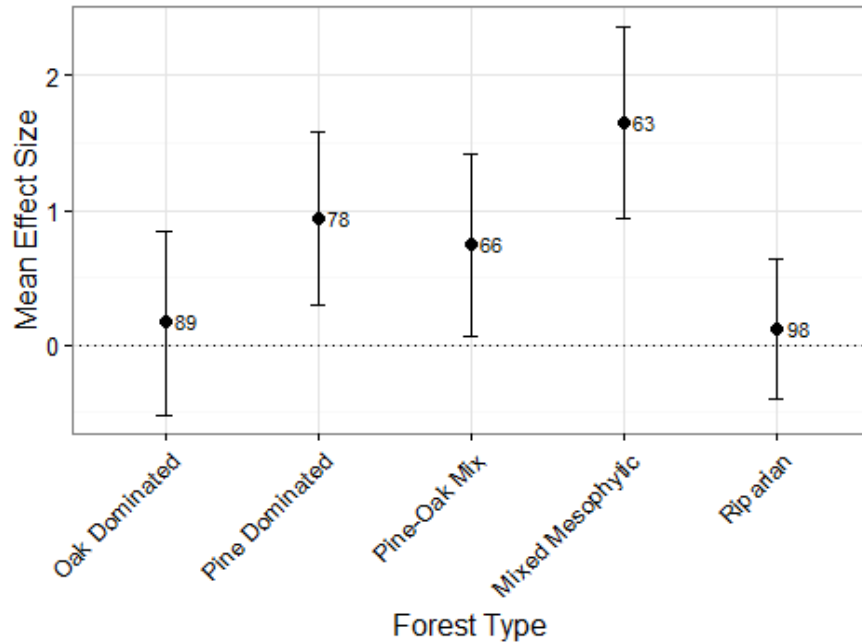


Figure 16. Mean effect sizes and 95% confidence intervals for each forest type for mammals. The number indicates the number of observations for each forest type.

4.6 Reptiles

For reptiles, both orders included in the meta-analysis, Squamata (lizards and snakes) and Testudines (turtles), showed a positive response (mean effect size = 0.22 and 4.13, respectively), however Testudines had a very small sample size ($n = 5$). With regards to treatment type, reptiles had positive responses to undefined intensity burning (the only type of burning recorded from reptile studies), shelterwood cuts, and group selection cuts (Figure 17). Reptiles did not show a response to clearcuts or herbicides. For various forest types, reptiles showed a positive response

to oak-dominated forests, pine-dominated forests, and mixed mesophytic forests. They showed a negative response to pine-oak mixed forests, and no response to riparian forests (Figure 18).

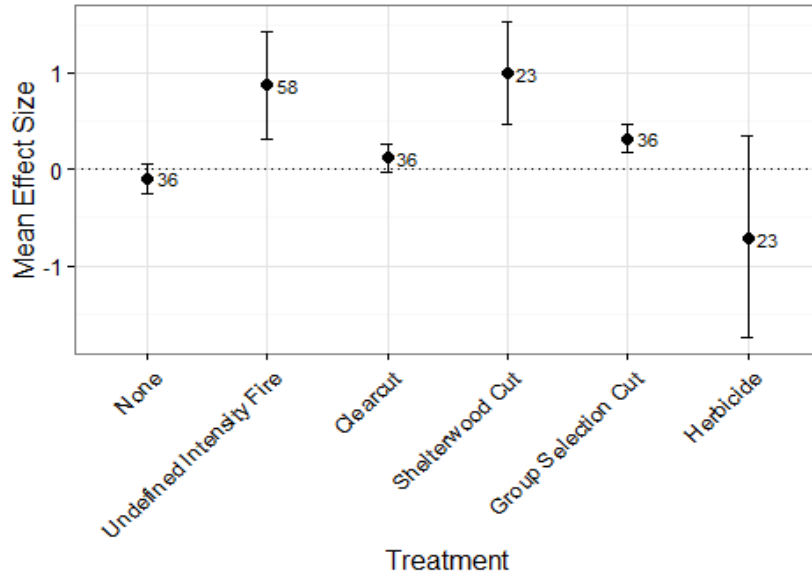


Figure 17. Mean effect sizes and 95% confidence intervals for each treatment type for reptiles. The number indicates the number of observations for each treatment type

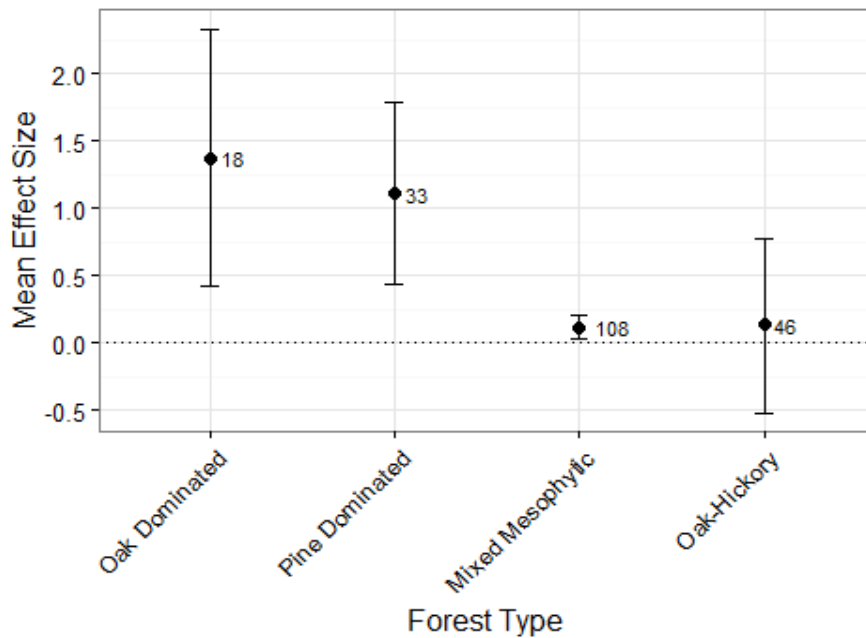


Figure 18. Mean effect sizes and 95% confidence intervals for each forest type for reptiles. The number indicates the number of observations for each forest type.

5. DISCUSSION

5.1 All taxa

When we combined all the taxa and looked at the effects across all treatments, we found that birds, mammals, and reptiles all had positive responses to treatment. Amphibians, however, had a negative response to treatment. Although these inferences are very generalized, it does affirm that fire and silvicultural treatments that emulate the effects of fire are having a mostly positive impact on wildlife. The main mechanism behind this positive effect is likely the restoration of a fire-dependent forest community that harbors rarer wildlife species (The Nature Conservancy 2009). However, it is difficult to parse out the details of the fire and wildlife interaction based solely on this generalized model.

After dividing the responses by treatment type, we see one major trend: wildlife is having a positive response to prescribed fire that is mid-intensity or higher. This is in contrast with a previous review, which found overall neutral effects of fire on wildlife (Pitt et al. 2014). However, that study only analyzed twenty-one studies, and did not employ the same rigor of a systematic review and meta-analysis. Like Pitt et al. (2014), our studies were mainly short-term, with almost all treatments occurring within five years of wildlife surveys, and many of those occurring within only two years. It is therefore possible that the positive effect of fire on most wildlife taxa is a short-term rather than a long-term effect. Future studies should examine the effects of fire at longer timescales. When looking at the effects of silvicultural treatments across all taxa, effects were mostly neutral, regardless of whether treatments were subdivided into groups or left as individual treatments. Therefore, it is possible that there is something unique about fire as a disturbance that positively affects wildlife. Again, we recommend long-term studies that examine the effects of these silvicultural treatments on wildlife.

Wildlife in three forest community types did have a positive response to treatment, while the other three community types showed a neutral response. Treatments in pine-dominated, pine-oak mixed, and riparian forests all resulted in a positive mean effect size for wildlife. This implies prior hypotheses suggesting that wildlife has a more positive response to fire-dependent oak-dominated forests rather than fire-suppressed pine-dominated or mesophytic forests is correct (McShea et al. 2007, The Nature Conservancy 2009). As these less-desirable forest community types receive treatment, they transition to more desirable oak-dominated forests, causing wildlife in these communities to show a positive response. Possible explanations for the positive response of wildlife to oak-dominated forests include an increase in food supply from acorns, changes in the abundance and composition of insects, and improved foraging for birds (Rodewald 2003).

The final important covariate of our all-taxa model, study type, can provide guidance for future research studies. Importantly, our analysis showed that age-class comparison studies show a net neutral effect, while both control-treatment and before-after control-impact studies show positive effects. This is in agreement with widespread statistical theory that manipulative experiments are superior to observational ones (Quinn and Keough 2002). This analysis also underscores the overall trend that wildlife generally seems to have a positive response to treatment. While the analyses that examine effect size across all taxa are informative, it is perhaps more useful to look at each taxon individually to further understand the impacts of treatment.

5.2 Amphibians

Many biologists consider amphibians to be ideal indicator species due to their central role in many ecosystems, high trophic level, complex life history, and declining worldwide numbers

(Wilbur et al. 1990, Wake et al. 1991). Amphibians are also of particular interest in the Southern Blue Ridge region because it is a global hotspot for plethodontid salamander diversity, and these species may be facing declines due to ongoing climate change (Milanovich et al. 2010). Despite being an important covariate, time since treatment showed no relationship with effect size. This is likely because the relationship is being dominated by a few outliers with longer times since treatment. Again, longer term studies may reveal an important relationship between time since treatment and abundance and/or diversity of amphibians, so more long-term research studies are needed. Prescribed burning had mixed effects on amphibians, with only high-intensity burns showing a non-neutral effect. According to Russell et al. (1999)'s review, most amphibian species have high survival rates after fires, which could explain why there was no clear negative effect of fire in the short-term. The positive response to high-intensity fire, but not to silvicultural treatments, is also in accordance with the review's findings, suggesting that only fire can successfully create the ideal frequency, intensity, and scale of disturbance for amphibians. Unlike our analysis, Pilliod et al. 2003 found a variety of different effects of fire on amphibians with no overarching signal or trend. However, Pilliod's review did not focus on a specific geographic area or community type, but looked at studies across North America, which may have led to confounding results.

There are even fewer reviews of the effects of silvicultural treatment on amphibians. A review of forest management effects on amphibians across North America also found negative effects of clearcutting on amphibian abundance (deMaynadier and Hunter 1995). The decrease in forest canopy from forest management practices causes increased light penetration to the forest floor, raising soil temperatures and increasing evaporative water loss. Along with decline in cover, these factors usually have a detrimental effect on amphibian abundance (Hunter 1990).

Another review found near-universal negative effects of clearcutting on amphibians (particularly salamanders) in the short-term, but more mixed or neutral results for uneven-aged harvesting (K.R. Russell et al. 2004). This is in contrast to our findings that all types of forest harvesting, both even- and uneven-aged, have a negative effect on amphibian abundance and diversity. Russell et al. (2004)'s review of the effects of herbicides are similar to our findings showing mixed or neutral effects on amphibians.

5.3 Birds

Although we found fewer studies on birds than salamanders during our search, we obtained more unique observations on birds than we did for salamanders. This is likely a product of the relative ease with which bird data are collected and the well-established birding community that is interested and invested in tracking bird populations. Unlike the other taxa in this study, bird data are relatively easy to collect, as data collection can use auditory cues, without relying on visually identifying or capturing specimens (Frommholt and Tauchert 2013, Sedláček et al. 2015). As a result, studies on birds tend to contain large amounts of data, and include many species, which has positive implications for bird monitoring efforts. However, this also causes vocal birds to be over-represented, as can be seen by the large amount of data obtained on passerine birds relative to other species in the study.

Nonetheless, the results from this meta-analysis provide important insights into the effects of forest management on birds. Treatment has either no effect or a negative effect on birds in oak dominated and oak-hickory forests, and positive effects in pine-oak forests, indicating that birds may prefer oak forests, and that treatments working to convert forests into oak forest are beneficial. Delving deeper and examining only passerine birds also reveals that birds living solely in the forest interior experience negative effects due to treatment, while birds

that live on the forest edge benefit. These results are logical as forest interior bird species are known to respond negatively to disturbance, while forest edge species benefit from activities that promote the creation of early successional forest patches (Goetz et al. 2010, McDermott et al. 2010, Boves et al. 2013). It is worth noting again, however, that most studies are short term, so conclusions about long-term effects remain unclear.

5.4 Invertebrates

Invertebrates as a whole had varied responses to fire treatments. Low and high intensity fires had significantly negative effects, while fires of undefined intensity had slightly positive effects. Many insects depend on the forest understory for food and shelter, so fire treatments could have negative impacts as they reduce it (Taki et al. 2010). However, it is also possible that insects prefer forest types, or forest gaps created by fire treatments, leading fires to also have a positive effect (Proctor et al. 2011). Examining the relationship between untreated forest age and effect size could offer a partial explanation. Treatments in younger forests tended to have negative effects, while treatments in older forests tended to have positive effects on insects. This implies that insects could prefer earlier forest succession stages, rather than old-growth oak forests.

5.5 Mammals

Mammals show similar trends to birds regarding effects of treatment in different forest types. Forest treatment tended to have positive effects on mammals in pine, mixed pine forests, and mixed mesophytic forests, regardless of treatment type, implying that mammals benefit as forest treatments work to convert pine forests into oak forests. However, as with birds, these results may not accurately reflect the effects of forest management on mammals as a whole, as most mammal data collected were on various types of rodents, such as voles and mice. This is

probably a product of how easy it is to collect data on rodents via various types of traps, due to rodents' small sizes (Umetsu et al. 2006, Stromgren and Sullivan 2013, Vieira et al. 2014). Data on larger mammals such as bears, foxes, and felines were not available for analysis, since no studies on these types of animals were found.

5.5 Reptiles

Of all the taxa in this study, reptiles had, by far, the fewest data available, with only two studies included in the systematic review. The data found on reptiles generally indicated that forest treatment tended to have positive effects, including fires, shelterwood cuts, and group selection cuts. Clearcuts and herbicide treatments did not have an effect however, suggesting that the removal of the entire canopy and chemical treatments do not carry the same benefits. These results differ from the results of the other taxa, as only reptiles experienced positive effects due to mechanical forest treatments. However, these results are logical, as reptiles are exotherms and thus rely on solar radiation to regulate their metabolism and body temperature. Therefore, treatments that decrease forest canopy density and help solar radiation reach the forest floor would benefit reptiles living on that forest floor (Greenberg 2001, Greenberg and Waldrop 2008, Pike et al. 2010). Treatments also had positive effects across a wide variety of forest types, including pine dominated, oak dominated, and mixed mesophytic forests. However, there were no significant effects of treatment in oak-hickory forests. This suggests a reptilian preference for oak-hickory forests, and treatments in other forest types that promote oak-hickory forests. Unfortunately, due to the small amount of data found on reptiles, more studies will be needed for more reliable results

5.6 Monitoring Implications

5.6.1 Study Design Considerations

As we have alluded throughout this discussion, it would be highly beneficial to gather and publish monitoring data that tracks wildlife populations in the long term in relation to forest management treatments. The average time since treatment in our study was only 3.5 years, and forest managers would benefit from having information that allows them to plan further in the future.

Similarly, we recommend that more studies collect data on wildlife species after repeated treatments; fewer than 25% of studies included wildlife measurements after repeated treatments. The dynamic effects of prescribed fire treatments can differ depending on return interval, and it would be valuable to have information on how the impacts of fire on wildlife might change depending on the prescribed fire regime. Managers could benefit from detailed studies that inform them of how to optimize their fire management based on how it might create benefits for certain wildlife species. This body of literature also lacks studies that examine combination treatments that test the effects of fire and silvicultural treatments used on one site. Fewer than 9% of our extracted data points included measurements after a combination treatment. Due to resource limitations or public pressures, it may not always be possible for forest managers to use certain forest management techniques, and so a combination of treatments might be required. Managers would benefit by knowing how silvicultural and fire treatments interact to impact wildlife populations.

5.6.2 Taxa knowledge gaps

As previously stated, reptiles were by far the least represented taxa in our study. They only represent 9% of our data points and only two out of fifty studies were dedicated solely to

reptile data collection. This taxon represents a wide array of ecologically important species, and includes species of conservation concern such as the eastern milk snake (*Lampropeltis triangulum triangulum*), timber rattlesnake (*Crotalus horridus*), coal skink (*Plestiodon anthracinus*), and the critically endangered bog turtle (*Glyptemys muhlenbergii*).

Though birds provide the largest taxa representation in our meta-analysis, data on non-passerine birds were lacking. Over 70% of our bird data represent passerine songbirds. This is likely due to the relative ease of collecting acoustic bird data, as described in section 5.3 of this discussion. State wildlife agencies are aware of this data collection bias, and have noted the importance of developing survey methods that better represent these other bird orders (NC Wildlife Resources Commission 2015).

We found no studies that provided usable information on bats for this systematic review. Bats are of special concern of late due to outbreaks of white-nose syndrome, as well as other threats to bat populations including wind energy development, habitat fragmentation, and climate change (Loeb et al. 2015). The potential for listing new bat species such as the Little Brown Bat, *Myotis lucifugus*, on the Endangered Species List would require that managers carefully document bat population levels. Having baseline data on bat populations would be extremely valuable in these circumstances. The U.S. Geological Survey (USGS) is attempting to address the lack of bat monitoring data nationwide by implementing the North American Bat Monitoring Program (NABat), which will tentatively launch in 2017 (Loeb et al. 2015) (See Appendix III for more information on NABat).

We also did not find any usable studies on large mammal populations to include in our systematic review. This is likely because of the relative difficulty and high expense related to surveying larger mammal species. However, information that indicates how some of these

species such as black bear (*Ursus americanus*), white-tailed deer (*Odocoileus virginianus*), and bobcats (*Lynx rufus*) respond to various forest treatments would be valuable, especially considering their high level in the food chain, and, in some cases, keystone or umbrella species status. Additionally, managers often must consider how forest treatments might impact game species, many of which are large mammals; any additional information that would aid management in this regard could have impacts on the hunting community.

6. CONCLUSIONS

Unlike previous reviews of fire effects in the SBR, the results of our systematic review suggest that prescribed fire in central hardwood forests has an overall positive effect on wildlife when all taxa are combined. Fire was unique in having a positive mean effect on wildlife, with application of thinning or herbicide treatments, or a combination of thinning and burning, having a neutral effect on wildlife abundance. When results were broken down by wildlife taxa, there was considerable variation in direction and magnitude of effect size of treatments. The vast majority of the studies contributing data to our review investigated treatment effects over a fairly short time scale, making more long-term studies to observe the change in these effects over time an important priority for research, as well as observation over repeated treatment cycles and combinations of multiple treatments. There is also a need for more research on several taxa that were underrepresented in the data, including reptiles, non-passerine birds, medium and large mammal species, and bats. Focusing on these gaps and the development of coordinated treatment and monitoring strategies over larger spatial scales at the landscape level are key considerations for a fuller understanding of forest management impacts on wildlife in the Southern Blue Ridge.

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APPENDIX I.

SYSTEMATIC REVIEW PROTOCOL

How do controlled burns and other forest management activities affect wildlife populations in the Southern Blue Ridge and the Central Hardwood Forests?

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Keywords: forest management, controlled burn, central hardwoods, Southern Blue Ridge, Southern Appalachians, wildlife populations, fire ecology

Background

The Southern Blue Ridge is both culturally and biologically significant, harboring a rich history, along with many rare and endangered species and high levels of biodiversity. Once the importance of this region was recognized, various management and conservation activities were initiated in the region to protect both its history and ecology. In the past, many conservation organizations achieved their goals by purchasing land or putting it under conservation easements to prevent it from being developed and then left the land to develop “naturally” over time. However, according to the best understood conservation practices of the past this “natural” state did not include fire. Fire was suppressed for many years in the Southern Blue Ridge, just as it was in other forests around the United States, and this practice led to numerous ecological shifts in the ecosystems of the region.

Due to the removal of fire from these systems, over time ecosystems that historically relied on forest fires were almost eliminated, such as the oak forests in the Southern Appalachians. Forest managers from many organizations have been attempting to reintroduce fire into the Southern Blue Ridge for the past few decades, primarily for the purposes of stimulating oak regeneration and restoring historic community types that have been degraded or lost throughout the era of fire suppression (The Nature Conservancy 2009). Many managers share this view; however, they want to be informed about the positive and negative effects that fires could have on the wildlife biodiversity of the region so beneficial management actions may be replicated, and any detrimental impacts can be anticipated and mitigated (M. Sutton, TNC Southern Blue Ridge Office, *personal communication*, March 20, 2015; Ford et al. 2010).

Land managers currently lack a formalized synthesis detailing the effects of fire on the wildlife of the Southern Blue Ridge. Because managers’ actions can have long-term consequences, we hope to provide a resource that details the current literature on this subject so that they can more fully understand and anticipate the outcomes of prescribed fires on a wide variety of wildlife taxa. This review can thus be used as a tool to help better conserve biodiversity of the Southern Appalachians.

Aim and Objectives of the Review

The aim of this systematic review is to compile a comprehensive database of the published research related to the impacts of prescribed burning and other forest management practices on wildlife abundances and diversity in central hardwood forests. The information assembled within this database will be used to answer the primary and secondary questions posed here.

Primary question

How does fire (and the application of other forestry practices meant to have similar ecological effects) impact the abundance and diversity of wildlife taxa present within central hardwood forests?

For additional detail and clarification, we present the following sub-questions as components of the primary question.

Secondary questions

- a) How do wildlife abundances respond to varying fire intensities?
- b) How does variation in initial forest conditions (including forest type) affect the outcomes of fires?
- c) Do other management actions that imitate the effects of fire have similar effects on wildlife?

Searches

For our searches, we will utilize the search terms indicated in Table 1. All searches will include one term or phrase from each column. We will consider all combinations of terms; however, we may eliminate some terms due to duplication of results. Some of the databases we plan to use have individual filtering systems that, if used, we will fully document along with the search term inputs. These filters can be geographical or keyword based. We intend for this search to be comprehensive for studies performed with the intent of examining the effects of fire and other similar management practices on wildlife taxa in our region of interest.

Table 1. Search terms that will be combined to create search strings for the systematic review.

Management technique/ Disturbance	Wildlife taxa	Regional Descriptor
Controlled burn(ing) Controlled fire Prescribed burn(ing) Prescribed fire Wildfire Fire Fire Management Fire Reintroduction Clearcut(ing) Thinning Understory removal	Wildlife Bird(s) Migratory Bird(s) Mammal(s) Small Mammal(s) Bat(s) Insect(s) Pollinator(s) Invertebrate(s) Reptile(s) Amphibian(s) Salamander(s)	Southern Blue Ridge Southern Appalachian(s) Southern Appalachian Forest(s) Central Hardwood(s) Central Hardwood Region Central Hardwood Forest(s) (Western) North Carolina Forest(s) Tennessee Forest(s) Kentucky Forest(s) Missouri Forest(s)

The databases we plan to search include: Web of Science, Forestry Abstracts, Environment Complete, Proquest Science and Technology, and we will utilize Google Scholar if we feel that additional data are needed. We do plan to include grey literature in our review, however we will limit these sources to those that pertain directly to the Southern Blue Ridge, rather than the entire Central Hardwoods region. Adam Warwick, a wildlife biologist with The Nature Conservancy North Carolina, has provided access to a resource library with literature that pertains to our review. We expect that this literature will emerge through our own search process, however if it does not we plan to include his resources in the review. This review is meant to be a resource to various partners within the Fire Learning Network, and if partners provide additional pertinent resources those could be included as well.

Study inclusion criteria

We propose the following guidelines for deciding whether to include or exclude articles based on relevancy. First, we must deem articles to have relevant subjects; the subject must include both a community type of central hardwood forests in addition to wildlife taxa of any sort, not limited to vertebrates. The relevant interventions include thinning, prescribed burning, harvesting, clear-cutting, wildfire, or some combination of these. The relevant comparator must be an untreated forest community of the same type that is unburned and not altered by forest management. We will be looking for relevant outcomes such as the effects of the intervention on density, abundance, diversity, and/or reproduction on specific wildlife taxa. Relevant studies will employ a treatment/control study design. After finishing our study inclusion analysis, we will conduct Kappa tests to check for consistency in deciding between inclusion and exclusion.

Potential effect modifiers and reasons for heterogeneity

This review is intended to primarily examine the effects of prescribed fire on various forms of wildlife taxa, however there are other forest management practices that can imitate the ecological effects of a prescribed burn or wildfire. With this in mind, our search terms include these management practices such as clear-cutting or understory removal. Additionally, because fire intensities can vary, the effects of a prescribed burn can also be varied. Through the review process we hope to be able to examine the effects of differing intensities along the spectrum. Additional variation could stem from a diversity of forest types being burned or managed. Initial forest conditions before treatment such as forest type, basal area, canopy cover, and understory cover could all be sources of heterogeneity in results. Because the literature on the SBR may not be extensive enough to provide adequate data for a comprehensive review, we have decided to include literature pertaining to the Central Hardwood Region/ the Southern Appalachians. Regional differences in forests throughout the study area could also provide heterogeneity in our results.

Study quality assessment

After we have narrowed down our list of studies using the inclusion criteria, we will then assess study quality. We will take note of the type of experimental design authors use in their studies, as well as the error rate, and whether or not the paper was peer-reviewed and/or published. We will also record any bias we note in the study. Furthermore, we will rank each individual study based on quality using Pullin and Knight's (2003) hierarchy (Table 2). Because we feel that our research question is broad enough to capture a large number of studies, we will only be including studies in our final meta-analysis in either category I or category II of this hierarchy.

Table 2. Pullin and Knight's hierarchy of quality of evidence.

Category	Quality of evidence
I	Strong evidence obtained from at least one properly designed randomized controlled trial of appropriate size.
II-1	Evidence obtained from well-designed controlled trials without randomization.
II-2	Evidence obtained from a comparison of differences between sites with and without (controls) a desired species or community.
II-3	Evidence obtained from multiple time series or from dramatic results in uncontrolled experiments.
III	Opinions of respected authorities based on qualitative field evidence, descriptive studies, or reports of expert committees.
IV	Evidence inadequate owing to problems of methodology (e.g., sample size, length or comprehensiveness of monitoring, or conflicts of evidence).

Data extraction strategy

For the data extraction portion of the systematic review, we will extract both qualitative and quantitative information about the subjects. We will record all our extracted data in a uniform spreadsheet that ensures the same data are collected across all studies.

Data synthesis and presentation

For the data synthesis, we plan to consult with Liz Kalies in order to conduct a meta-analysis. We plan on weighting based on study quality and taking into account the biases present in the studies. We will have recorded both study quality and biases during the data extraction step.

Sources

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APPENDIX II.

SYSTEMATIC REVIEW SPREADSHEET METADATA

Column A: Wildlife Species--Provide species name if applicable, or more detail on the taxa being examined in the paper

Column B: Common name (if applicable)

Column C: Taxa-- Input one of the following: Amphibian, reptile, mammal, invertebrate, pollinator, bird

Column D: Location (state)-- The state in which the study was conducted, if multiple states include all

Column E: Location (site)-- more detail on the site location including town, park, state forest etc.

Column F: Forest type-- general, use one of the following codes

- 1: oak dominated
- 2: pine dominated
- 3: pine oak mix
- 4: mixed mesophytic
- 5: riparian
- 6: oak-hickory
- 7: pine-hardwood mix

Column G: more detail on forest type as described in the paper

Column H: Silviculture or Fire treatment

Column I: Treatment type, use one of the following codes

- 1: low intensity prescribed fire
- 2: mid intensity prescribed fire
- 3: high intensity prescribed fire
- 4: undefined intensity prescribed fire
- 5: low intensity wildfire
- 6: high intensity wildfire
- 7: undefined intensity wildfire
- 8: Clearcut
- 9: Shelterwood cut
- 10: Leavetree cut (two age cut)
- 11: Group selection cut
- 12: Seed tree cut
- 13: Herbicide
- 14: thin and burn
- 15: thinning, other
- 16: understory removal/ fuel reduction
- 17: regeneration harvest
- 18: partial harvest

Column J: Treatment details-- add details about the treatment as provided by the paper

Column K: Diversity or abundance measure?

Column L: If it was diversity, what diversity measure did they use?

Column M: Study type, use one of the following codes

- 1: randomized, replicated treatment-control
- 2: before-after

- 3: age class comparison

- 4: treatment control (no replication)

Column N: Year of first treatment-- when did treatments for the study begin?

Column O: Year of last treatment-- when was the last treatment performed before wildlife data collection

Column P: Years since last treatment-- how many years passed between the last treatment and when wildlife data were collected

Column Q: Return interval of treatments-- how many years passed between treatment repetitions (if treatments were repeated)

Column R: Sampling method-- how were wildlife data collected, provide details from the paper

Column S: Number of replicates-- how many times was sampling replicated?

Column T: Number of visits to the sample site-- how many times was sampling performed at each site?

Column U: Treatment area-- the size of 1 treatment plot

Column V: Treatment area total-- the size of all treatment plots for that treatment (Calculation = # replicates * Treatment area for 1 plot) (Calculation = Column S * Column U)

Column W: Control Area-- size of control area

Column X: Control Age-- how old is the forest in the control plot

Column Y: Control Basal area-- what is the basal area of the control plot

Column Z: Total area-- (Calculation = Total Treatment area + Control area) (Calculation = Column V + Column W)

Column AA: Experimental mean-- the reported mean for treatments plots

Column AB: Control mean-- the reported mean for control plots

Column AC: Effect Size: $\ln(\text{experimental mean} / \text{control mean})$

Column AD: Weighted effect size-- replicates * $\ln(\text{experimental mean} / \text{control mean})$

Column AE: Reference-- basic reference from Refworks (author(s) and year)

Column AF: Refworks ID-- the RefID # found in our refworks account

Column AG: who extracted the data: ML, MW, MS, or SM

Passeriformes Only:

Habitat Codes

- FI: Forest Interior
- FIE: Forest Interior and Edge
- FES: Forest edge and scrub & Field Edge

Migration Codes

- PR: Permanent Residents
- NTM: Neotropical Migrants
- SDM: Short-Distance Migrants

APPENDIX III.

SOUTHERN BLUE RIDGE WILDLIFE MONITORING REPORT

As a supplement to our systematic review and meta-analysis, we wanted to provide a report detailing the state of current monitoring in the SBR and our suggestions for how it could move forward. The report includes the following information:

1. Background information
 - a. Adaptive management
 - b. The importance of monitoring and monitoring pitfalls
 - c. Elements of an effective monitoring program
 - d. Prioritization and indicators
 - e. Citizen science and monitoring
2. Data collection methods
3. Documentation of existing SBR wildlife monitoring
 - a. Important future monitoring planned for the SBR
4. Potential indicator species
5. Monitoring gaps
6. Monitoring goals and suggestions

1. BACKGROUND

1.1 Monitoring

Wildlife monitoring can take on many forms and can be carried out in many different ways. Good monitoring is performed in a systematic, robust, and statistically significant manner (see section 1.4). Collecting data on the existence, abundance, or diversity of wildlife species is considered a key piece of successful management. Without monitoring data there is no way to determine whether conservation plans are truly meeting their goals (Franklin et al. 2011). Monitoring thus becomes an essential component of the Adaptive Management cycle.

1.2 Adaptive management

Adaptive management (AM) is an integral part of natural resource management. It includes iterative planning, implementation, analysis, and adaptation. It is widely understood that there is an inherent level of uncertainty regarding ecosystem processes and the complex interactions that occur in these systems (Holling 1978, Walters 1986, Walters and Holling 1990,

Haney and Power 1996, McClain and Lee 1996). AM allows managers to use that uncertainty in a productive manner, whereby management actions serve as pseudo-treatments in an experiment, during which they continue to learn about the workings of the managed ecosystem (Walters and Holling 1990). AM has been termed a ‘learning-by-doing’ process, in which management not only achieves objectives, but also provides insight about the system being managed (Johnson 1999, Lee 2001). The true adaptive phase of AM arises when ecologists and managers know enough about a system to identify clear hypotheses about the impacts of their activities and adjust these activities accordingly (Walters 1986).

For a management program to be considered adaptive, it should include the identification of goals and objectives, alternative strategies, implementation, monitoring, and the adjustment of goals and objectives as needed (Moir and Block 2001, Schreiber et al. 2004) (Figure 1).



Figure 1. Diagram showing cyclical stages of the adaptive management process (Comendant et al. 2006).

1.3 The importance of monitoring and monitoring pitfalls

AM is a means of implementing best-management practices and learning by carrying them out. However, the cycle is often broken or stunted by a lack of proper monitoring that adequately informs managers about how to alter their current management activities based on system responses. Without monitoring, AM cannot function because there is no way to measure changes and provide feedback for an updated planning or implementation stage (Waldrop 2014). Effective ecosystem monitoring following management actions is generally a weak point in AM

(Moir and Block 2001, Franklin et al. 2011). This lack of monitoring is not seen as the fault of managers themselves, but instead a combined effect of many interconnected issues (Table 1).

Increased collaboration between researchers, conservation managers, politicians, and policy-makers can facilitate multi-party monitoring, which can increase the size of datasets, exchange ideas and information, build trust, and strengthen relationships between organizations working towards similar goals (Pitt et al. 2014).

Table 1. The reasons why monitoring strategies are often ineffective.

Reason Monitoring Fails	Details	Source
Current/ popular politics and policies	Funding for monitoring goes to current issues/ concerns, but is not constant over the length of time needed to fully understand a problem	Moir and Block 2001
Limited resources/ agencies and other resource-managing organizations being stretched too thin	Funding must be available and long term so that sufficient trends can be examined; sufficient personnel and training are often not available or affordable	Moir and Block 2001, Field et al. 2007
Lack of accountability	Who is ultimately responsible for monitoring? Especially in landscapes managed by multiple agencies/ organizations	Moir and Block 2001
Monitoring without clear objectives	Monitoring for monitoring's sake: without specific goals in mind there is the risk of collecting lots of data that is statistically or functionally unimportant or unusable.	Vos et al. 1999, Legg and Nagy 2006, Field et al. 2007
Difficulty of collaborating monitoring efforts across a landscape or ecosystem	Data is lost or never used and little attention is paid to information management. Cohesiveness of monitoring by multiple groups is often lacking	Moir and Block 2001, Legg and Nagy 2006
Inadequate sampling design	Sampling design does not have the capability of detecting change and/ or statistical validity	Field et al. 2007
Lack of analysis	Data remains un-analyzed or un-interpreted; without analysis data does not add to an understanding of the system.	Field et al. 2007

1.4 Important elements of an effective monitoring program

There are four elements to an effective monitoring program: objectives, sampling strategy, data collection, and data handling (Vos et al. 1999). Each element consists of component parts that should be planned before monitoring begins (Table 2).

Table 2. The four main elements of a monitoring program, the component parts that make up each element, and examples of how components could be defined in the context of the SBR.

Monitoring plan elements	Component parts/ decisions to be made	Example
1. Objectives	What do we want to understand about the system?	How is our prescribed burning regime affecting woodland salamanders? How is our timber management regime affecting songbirds?
	What do we want to measure? Is it a resource of concern or an indicator?	Plethodontid salamander population trends
2. Sampling Strategy	Site selection: what sites will be representative of the system you are managing How many sites, how many replications?	
	Sampling design built with analyses in mind: how will data collected be translated into meaningful statistical analyses?	
	Monitoring technique: what technique will provide the data you require?	Pitfall Traps, point counts, coverboards, sherman traps, mist nets
	Sampling frequency: how often must monitoring be carried out	Once/year, once/season
3. Data Collection	Who performs sampling? How will they be trained?	
	Uniformity: how can uniform sampling be ensured across all sites and through many years of monitoring	Training manuals, training protocols
4. Data handling	Data storage: how will data be kept organized and in what format/ location will it be kept	The AKN data repository for the AMJV bird monitoring collaborative (see section 3.7.1)
	Data analysis: who has the ability to analyze and interpret data	
	Distribution: how will analysis results be shared	Publication, white paper, partner websites

(Adapted from Vos et al. 1999 and Manley et al. 2006)

1.5 Monitoring prioritization and the use of indicator species or taxa

It is not possible to monitor each component of an ecosystem. Managers must establish monitoring priorities at the beginning of a monitoring plan, which should be based on the ecology of the system and related to the goals and objectives of the overall conservation plan (Regan et al. 2008). Additional criteria that can help serve as the basis for prioritization include at-risk species, or identification as a keystone, umbrella or indicator species (Vos et al. 1999, Regan et al. 2008, Franklin et al. 2011).

Using indicators for monitoring is a means of assessing the status of an ecosystem by monitoring only a certain species or taxa. While the relationship between indicators and target

variables should be well understood and previously studied, indicators are an efficient way to gather data on other variables that are harder, more expensive, or impossible to measure (Vos et al. 1999). These surrogate measures of ecosystem status can indicate toxicity levels, resource abundance, biodiversity levels, and other aspects of system health (Hilty and Merenlender 1999). While no one species or taxa can reveal everything about ecosystem health, the correct questions and collection of appropriate data can reveal trends and help reformulate hypotheses (Hilty and Merenlender 1999, Franklin et al. 2011).

1.6 Use of citizen science in monitoring

There is potential for monitoring programs throughout the SBR to begin to incorporate citizen science (publicly sourced data) to try and increase their scope. Citizen science refers to any form of the scientific process that involves the public (Kobori et al. 2016). Ecologists have realized that utilizing the public for monitoring allows for data collection on much larger spatial and/or temporal scales than could be possible with most traditional research or monitoring methods (Cohn 2008, Sullivan et al. 2009, Kobori et al. 2016). Many managers working on monitoring have limited time, manpower, and money, so utilizing the public for data collection on a grand scale can be very appealing (Kobori et al. 2016). It is becoming easier to include the public in scientific research as new technologies and the internet allow information dissemination, data sharing, and data collection far more easily and faster than was previously possible (Silvertown 2009). Smart phones can serve as a GPS, document photographic evidence, connect to databases, and provide guidance for data collection.

Of course, using the public to collect data does involve certain risks and biases that must be considered at the outset of any monitoring program. Protocols must be relatively simple to accommodate varying skills and levels of understanding and to ensure data collection is uniform (Hochachka et al. 2012). Even with careful design, some readily cited biases include issues with species detectability (only noting easily detected species), misidentifications, uneven distribution of sampling effort, and geographic bias in sample collection (collecting in locations where participants expect to find species) (Sullivan et al. 2009). Good monitoring programs will often incorporate a verification process that uses specialist knowledge to “check” unlikely data entries made by the public, but it is impossible to catch every incorrect entry (Sullivan et al. 2009).

However, it is still possible to collect meaningful data if participants are trained correctly and protocols are easy to follow. Due to the benefits of crowd-sourced data, scientists have been learning how to use those data in truly meaningful analyses, despite some of their biases and drawbacks (Hochachka et al. 2012).

National or state level citizen science platforms are already being utilized to some extent in the SBR. Partners of the SBR FLN could tap into and/or promote the use of eBird (already used by NC Audubon, see section 3.3), iNaturalist, eMammal (see section 3.4), the Carolina Herp Atlas (see sections 3.2 and 3.5), or Moths and Butterflies of North America (see section 3.6). Alternatively, partners could develop their own protocols and partner with local schools, community groups, civil societies, or clubs to find volunteers for citizen science monitoring. It should be noted that citizen science is likely not applicable to every monitoring project, but in certain cases it could prove very useful.

2. METHODS

SBR wildlife monitoring suggestions were derived from information collected from SBR FLN partners, literature research, and results of the systematic review.

The first step in the development of the monitoring strategy was to engage SBR FLN partners to inform them of project goals and receive feedback and suggestions. A webinar was held in December 2015 and professionals from 10 different resource management or research institutions were invited to participate and share how these organizations view ongoing monitoring and visions for how it could be improved.

Information about existing monitoring activities was collected from SBR partners. One or more individuals from the following organizations was contacted: NC Wildlife Resources Commission, NC Forest Service, GA Forest Service, NC Audubon, GA Department of Natural Resources, the Orianne Society, US Fish and Wildlife Service, and Appalachian Mountain Joint Venture. These organizations were asked to share:

1. What species they monitor
2. Where they monitor and the extent of their monitoring
3. What monitoring techniques they used
4. How long data have been collected

5. The primary purpose for monitoring
6. Whether data were public information
7. If they had produced any publications or gray literature based upon this monitoring.

To discover any national or regional monitoring projects that partners in the SBR could participate in, we performed literature searches and followed leads given to us during our partners webinar.

Primary sources of monitoring information were the four SBR FLN member state Wildlife Action Plans (North Carolina, South Carolina, Tennessee, and Georgia). In 2005, Congress mandated the creation of these Wildlife Action Plans (WAPs) for each US state and territory. These plans were meant to identify species of greatest conservation concern, assess wildlife and habitat health, identify major threats, and urge state wildlife agencies to plan for long-term conservation (Association of Fish and Wildlife Agencies 2014). These plans form the basis of the monitoring suggestions in this report, combined with results from the meta-analysis and guidance from existing monitoring prioritization schemes (Hilty and Merenlender 1999, Regan et al. 2008, Franklin et al. 2011). Using this information along with the input of wildlife managers, suggestions for priority monitoring within the SBR region are provided.

3. EXISTING MONITORING

3.1 Existing Monitoring for All Taxa

While there are no all-taxa monitoring programs in the SBR, the Global Biodiversity Information Facility (GBIF) is a data source that collects monitoring data from multiple open-source repositories and presents it in an accessible way (Table 3).

Table 3. Existing monitoring data available for all taxa groups in the SBR.

Organization	Includes Citizen Science?	Monitoring what?	Survey Locations	Is data public?	Contact(s)/ Resources/ Notes
Global Biodiversity Information Facility	Yes	All taxa	Global	Downloadable	Collects occurrence records from multiple public sources including eBird and iNaturalist. Good for species specific data queries. Includes many filters for finding appropriate data; (http://www.gbif.org/species)

3.2 Existing Monitoring for Amphibians

We summarized the existing amphibian monitoring efforts in the SBR ecoregion, which include both region-specific and wider-scale datasets (Table 4).

Table 4. Existing amphibian monitoring efforts in the Southern Blue Ridge ecoregion. Data listed as “downloadable” can be found at the website links in the “Resources” column.

Organization	Includes Citizen Science?	Monitoring what?	Survey Locations	Is data public?	Contact(s)/ Resources/ Notes
Federal Monitoring					
USGS North American Amphibian Monitoring Program	Yes	Taxa wide surveys	North America	Downloadable	Volunteer auditory surveys along specific, pre-determined routes across North America. Organized by local wildlife agencies, overseen by USGS. (https://www.pwrc.usgs.gov/naamp/index.cfm?fuseaction=app.dataDownload)
USFS (with SC DNR as a partner)	No	<i>Plethodon websteri</i> (Webster's salamander)	Sumter National Forest	Upon request	SC Wildlife Action Plan
State Agency Monitoring					
NC Wildlife Resources Commission	No	<i>Cryptobranchus alleganiensis</i> (Hellbender)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Necturus maculosus</i> (Mudpuppy)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Pseudacris brachyphona</i> (Mountain chorus frog)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Plethodon welleri</i> (Wellers salamander)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Plethodon longicus</i> (Yonahlossee salamander)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Desmognathus wrighti</i> (Pygmy salamander)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Aneides aeneus</i> (Green salamander)	Western NC	Upon request	Kendrick Weeks (NCWRC)
TN Wildlife Resources Agency	Yes	Frogs and Toads (TN Amphibian Monitoring Program)	TN (statewide)	Upon request	
NGO/ Other Monitoring					
Oriante Society	No	<i>Cryptobranchus alleganiensis</i> (Hellbenders)	Little Tennessee Watershed	Upon request	Chris Jenkins (Oriante Society)
Carolina Herp Atlas (Davidson College)	Yes	Taxa wide occurrence records	Carolinas (not much currently for SBR, but as usership grows could be a valuable resource)	Downloadable	Volunteers enter occurrence data as they encounter herp species (http://www.carolinaherpatlas.org/Data)

3.3 Existing Monitoring for Birds

We summarized the existing bird-monitoring efforts in the SBR ecoregion, which include both region-specific and wider-scale datasets (Table 5).

Table 5. Existing bird monitoring efforts in the Southern Blue Ridge ecoregion. Data listed as “downloadable” can be found at the website links in the “Resources” column.

Organization	Includes Citizen Science?	Monitoring what?	Survey Locations	Is data public?	Contact(s)/ Resources/ Notes
Federal Monitoring					
USGS Breeding Bird Survey	Yes	General taxa survey efforts	North America	Downloadable	Volunteer surveys along specific, pre-determined routes across North America (https://www.pwrc.usgs.gov/bbs/RawData/Choose-Method.cfm)
USFWS, USGS	No	<i>Haliaeetus leucocephalus</i> (Bald eagle)	Statewide in SC and TN	Upon request	SC Wildlife Action Plan; TN Wildlife Action Plan
USFWS, (with help of other federal agencies)	No	<i>Leucotopicus borealis</i> (Red-cockaded woodpecker)	Federal lands in SC, NC, and GA	Upon request	SC Wildlife Action Plan
USFS	No	<i>Aegolius acadicus</i> (Northern saw-whet owl)	Cherokee National Forest	Upon request	TN Wildlife Action Plan
State Agency Monitoring					
NC Wildlife Resources Commission	No	<i>Haliaeetus leucocephalus</i> (Bald eagle)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Falco peregrinus</i> (Peregrine falcon)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Falco sparverius</i> (American kestrel)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	Songbird general surveys	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Vermivora chrysoptera</i> (Golden-winged warbler)	Western NC	Upon request	Kendrick Weeks (NCWRC)
TN Wildlife Resources Agency	No	<i>Vermivora chrysoptera</i> (Golden-winged warbler)	Statewide in TN	Upon request	TN Wildlife Action Plan
NC Wildlife Resources Commission	No	<i>Setophaga cerulea</i> (Cerulean warbler)	Western NC	Upon request	Kendrick Weeks (NCWRC)
TN Wildlife Resources Agency	No	<i>Setophaga cerulea</i> (Cerulean warbler)	Statewide in TN	Upon request	TN Wildlife Action Plan
NC Wildlife Resources Commission	No	<i>Aegolius acadicus</i> (Northern saw-whet owl)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Tyto alba</i> (barn owl)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Meleagris gallopavo</i> (Turkey)	Western NC, specifically game lands	Upon request	Gordon Warburton (NCWRC)
NC Wildlife Resources Commission	No	Grouse (as game species)	Western NC, specifically game lands	Upon request	Gordon Warburton (NCWRC)
NC Wildlife Resources Commission	No	Quail (as game species)	Sandy Mush Game Land, NC	Upon request	Sandy Mush Game Land Management Plan
NC Wildlife Resources Commission	No	Dove (as game species)	Western NC, specifically game lands	Upon request	Gordon Warburton (NCWRC)
NC Wildlife Resources Commission	No	Duck/ Waterfowl (as game species)	Western NC, specifically game lands	Upon request	Gordon Warburton (NCWRC)
NC Wildlife Resources Commission	No	Nightjars (Birds in the <i>Caprimulgidae</i> family)	Sandy Mush Game Land, NC	Upon request	Sandy Mush Game Land Management Plan
SC Department of Natural Resources	No	Bluebirds and other cavity-nesting birds	Statewide in SC	Upon request	SC Wildlife Action Plan
TN Wildlife Resources Agency	No	General taxa (Regional bird banding stations)	Statewide in TN	Upon request	TN Wildlife Action Plan
TN Dep't of Env't and Conservation	No	All taxa inventory	Statewide in TN	Upon request	TN Wildlife Action Plan
NGO/ Other Monitoring					
North Carolina Audubon Society	No	General taxa survey efforts	Mainly within important bird areas in NC	Upon request	Curtis Smalling (NC Audubon)
North Carolina Audubon Society	No	<i>Vermivora chrysoptera</i> (Golden-winged warbler)	Mainly within important bird areas in NC	Upon request	Curtis Smalling (NC Audubon)
Nightjar Survey Network	Yes	Nightjars (Birds in the <i>Caprimulgidae</i> family)	Nationwide	Some downloadable, more by request	Volunteer surveys along pre-determined routes. (http://www.nightjars.org/survey_data)
eBird (Cornell Lab of Ornithology)	Yes	General taxa survey efforts	Global	Downloadable	Volunteer checklists documenting presence/absence and abundance. (http://ebird.org/ebird/data/download); (http://ebird.org/ebird/eBirdReports?cmd=Start)
Christmas Bird Count (Audubon Society)	Yes	General taxa survey efforts	Nationwide	Downloadable	In December and January volunteers can sign up through local Audubon groups to collect data; (http://netapp.audubon.org/cbcobservation/#)
TN Ornithological Society	No	Spring bird counts (taxa wide survey)	Statewide in TN	Upon request	TN Wildlife Action Plan

3.4 Existing Monitoring for Mammals

We summarized the existing mammal monitoring efforts in the SBR ecoregion, which include both region-specific and wider-scale datasets (Table 6).

Table 6. Existing mammal monitoring efforts in the Southern Blue Ridge ecoregion. Data listed as “downloadable” can be found at the website links in the “Resources” column.

Organization	Includes Citizen Science?	Monitoring what?	Survey Locations	Is data public?	Contact(s)/ Resources/ Notes
Federal Monitoring					
USGS NABat (North American Bat Monitoring)	Yes	All bat species monitoring	North America	Pilot projects running; program planned for full start in 2017	Some data to be collected by volunteers. The program plans to include 4 survey types: winter hibernaculum counts, maternity colony counts, mobile acoustic surveys along road transects, and acoustic surveys at stationary points; (https://www.fort.usgs.gov/science-tasks/2457)
State Agency Monitoring					
NC Wildlife Resources Commission	No	All bat species monitoring	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Glaucomys sabrinus</i> (Northern flying squirrel)	Western NC	Upon request	Kendrick Weeks (NCWRC)
NC Wildlife Resources Commission	No	<i>Odocoileus virginianus</i> (White-tailed deer) (as game species)	Western NC, specifically game lands	Upon request	Gordon Warburton (NCWRC)
NC Wildlife Resources Commission	No	<i>Ursus americanus</i> (Black bear)	Western NC, bait station indexes taken at Green River and Sandy Mush Game Lands	Upon request	Gordon Warburton (NCWRC)
NGO/ Other Monitoring					
eMammal (Smithsonian and NC Museum of Life and Science)	Yes	Taxa-wide surveys	Global	Downloadable	System for collecting, storing, and sharing camera trap data--scientists or citizens can create online "projects" and recruit other users to contribute camera trap data (https://emammal.si.edu/projects); (https://emammal.si.edu/analysis/data-download)

3.5 Existing Monitoring for Reptiles

We summarized the existing reptile monitoring efforts in the SBR ecoregion, which include both region-specific and wider-scale datasets (Table 7).

Table 7. Existing reptile monitoring efforts in the Southern Blue Ridge ecoregion. Data listed as “downloadable” can be found at the website links in the “Resources” column.

Organization	Includes Citizen Science?	Monitoring what?	Survey Locations	Is data public?	Contact(s)/ Resources/ Notes
State Agency Monitoring					
NC Wildlife Resources Commission (partnering with USFWS)	No	<i>Glyptemys muhlenbergii</i> (Bog turtle)	Western NC	Upon request	Kendrick Weeks (NCWRC); Susan Cameron (USFWS)
TN Wildlife Resources Agency (partnering with Knoxville Zoo and TNC)	No	<i>Glyptemys muhlenbergii</i> (Bog turtle)	Eastern TN	Upon request	TN Wildlife Action Plan
TN Wildlife Resources Agency	No	Turtles	Statewide in TN	Upon request	TN Wildlife Action Plan
NGO/ Other Monitoring					
Orianne Society	No	<i>Crotalus horridus</i> (Timber rattlesnake)	Rabun County GA and Macon County NC	Upon request	Chris Jenkins (Orianne Society)
Carolina Herp Atlas (Davidson College)	Yes	Taxa wide occurrence records	Carolinas (not much currently for SBR, but as usership grows could be a valuable resource)	Downloadable	Volunteers enter occurrence data as they encounter herp species; (http://www.carolinaherpatlas.org/Data)

3.6 Existing Monitoring for Invertebrates

There are few existing invertebrate monitoring efforts in the SBR ecoregion, and with the exception of butterflies and moths, this monitoring focuses primarily on rare species (Table 8).

Table 8. Existing reptile monitoring efforts in the Southern Blue Ridge ecoregion. Data listed as “downloadable” can be found at the website links in the “Resources” column.

Organization	Includes Citizen Science?	Monitoring what?	Survey Locations	Is data public?	Contact(s)/ Resources/ Notes
Federal Monitoring					
USFWS	No	<i>Microhexura montivaga</i> (Spruce Fir Moss Spider)	Western NC, Eastern TN	Upon request	Susan Cameron USFWS
State Agency Monitoring					
NC Natural Heritage Program	No	Rare insect/ arachnid species	Statewide NC	Downloadable (upon request for sensitive information)	Occurrence data by county (http://ncnhp.org/web/nhp/database-search)
NGO/ Other Monitoring					
Butterflies and Moths of N. America	Yes	Butterflies and moths (<i>Lepidoptera</i>)	Nationwide	Downloadable	Search by species to get occurrence points or a map of occurrence data (http://www.butterfliesandmoths.org/species_search)

3.7 Future Monitoring Programs of Note

Two monitoring program initiatives noteworthy to SBR wildlife monitoring programs are *The Appalachian Mountain Joint Venture regional bird monitoring collaborative* and *The North American Bat Monitoring Program*. These programs could provide important future datasets as well as opportunities for SBR wildlife monitoring organizations to engage in these initiatives.

3.7.1 The Appalachian Mountain Joint Venture regional bird monitoring collaborative

The Appalachian Mountain Joint Venture has established a technical committee to oversee the creation of a bird monitoring collaborative for the Appalachian region with the primary goal of establishing a standardized, region-wide protocol for bird sampling. Data collected by various partners would then be directly comparable and broad-scale analyses could be made more easily. The eventual protocol for bird surveys will be based on common survey methods so that new data can be combined with historical data. New data protocols will also provide for additional data collection that will allow for more sophisticated population estimates.

The plan identifies the Avian Knowledge Network (AKN) as the central hub for data storage. Individual monitoring agencies or organizations can follow the standardized bird monitoring protocol and will then upload data to a central repository hosted by the AKN. This compilation of information will then provide region-wide datasets that scientists or managers can download to do their own analyses.

The draft protocols are being tested during the 2016 field season, and final protocols will likely be published and distributed in time for data collection for the 2017 field season. (C. Smalling, personal communication, March 10, 2016).

3.7.2 The North American Bat Monitoring Program (NABat)

Scientists across the United States have lamented the fact that no national or continental scale bat monitoring programs are in place. This has especially been a concern in recent years due to outbreaks of white-nose syndrome as well as other threats to bat populations including wind energy development, habitat fragmentation, and climate change (Loeb et al. 2015). The U.S. Geological Survey (USGS) has initiated the North American Bat Monitoring Program (NABat) to address the lack of broad scale data on bats in North America.

NABat has identified four survey approaches that will be the basis for NABat data collection: 1) winter hibernaculum counts, 2) maternity colony counts, 3) mobile acoustic

surveys along road transects, and 4) acoustic surveys at stationary points. While pilot projects currently test the survey protocols created by NABat, the full program will likely not be operational until 2017 or later (Loeb et al. 2015).

4. INDICATOR SPECIES FOR FUTURE MONITORING

4.1 Indicator species criteria and considerations

The term indicator species refers to organisms that are associated with a particular environmental trait or whose presence, absence, or change in abundance may signal a change in conditions within their environment. In practice, it will be inferences from the status of indicator species that will take the observations from monitoring efforts as discussed above and use them to inform future management actions. Lindenmayer et al. (2000) assembled a list of seven alternative definitions for indicators, and within the context of monitoring in the SBR we will focus on the seventh definition. This definition specifies a species that “reflects the effects of a disturbance regime or the efficacy of efforts to mitigate disturbance effects.” These indicators are known as management indicator species. The term has in the past been criticized for its vague application, imprecise definitions, and lack of clear criteria and selection procedures (Landres et al. 1988). Several recent works have attempted to provide guidelines for more transparent and rigorous selection of indicators (Hilty and Merenlender 2000, Carignan and Villard 2002, Caro 2010). Caro’s volume *Conservation by Proxy* (2010) is particularly thorough, with an informative and instructive chapter on ecological-disturbance indicator species. Drawing heavily from previous literature, Caro identified four broad criteria (each comprised of several sub-criteria) which we will touch on briefly in this work.

Measurement attributes. Effective indicator species should be easy to locate and identify and relatively cheap to monitor to make monitoring feasible with a good return of useful data relative to effort. Species with a wide geographic distribution allow for comparison among sites.

Life history characteristics. The literature recommends species with a small body size and home range that is resource limited. Conventional wisdom supports using habitat specialists that will be sensitive to habitat perturbation and show a clear response to change. A good strategy in selecting indicators, particularly in the context of the SBR, is to start with habitat

types of interest and concern, and select indicators that are specialists for that habitat type. However, recent work on insects and birds (McGeoch 2007, Morelli 2015) suggest using a combination of specialist and generalist species in monitoring. McGeoch argues that characteristic species (specialists) may decline rapidly due to changing conditions and become more difficult to sample or even disappear completely and lose monitoring value. Meanwhile, detector species (more generalist) could provide more useful information on the direction of environmental change (2007).

Population considerations. Population should be relatively stable under regular conditions to allow for disturbance induced changes to be noticed quickly. Furthermore, past research should have informed a known cause and effect relationship between the species and a particular environmental variable, with a predictable response.

Other variables. These include factors that make a species of special conservation concern, such as threatened or endangered status or economic importance. This criteria can help attract interest and focus the public's attention on the outcome for a certain species.

Hilty and Merenlender (2000) point out that many of the suggested criteria can contradict each other and it may be that no single species of potential monitoring value meets all the criteria. They suggest monitoring several species simultaneously (but still keeping the number quite limited) to better document the consequences of environmental change. These authors furthermore propose a decision making framework that could help balance different criteria to make choices among potential indicators (Hilty and Merenlender 2000).

In the remainder of this section we present examples of possible indicator species for the different taxa included in our monitoring investigation based on the criteria above as well as contextual knowledge of ecological history and current conditions in the SBR.

4.2 Amphibians

4.2.1 Salamanders

Experts consider the Southern Appalachian region to be a biodiversity hotspot for amphibians; this region contains the highest diversity of amphibians in the United States and hosts the richest salamander diversity in the world (Gibbons and Buhlmann 2001). Not only is this salamander diversity inherently valuable, but measures of diversity and abundance of these animals could act as indicators for various types of ecological change. Salamanders are

numerous and relatively easy/cheap to sample, occur in middle levels of the food web, and are sensitive to many stressors and could thus act as an early warning sign of ecological change (Welsh and Droege 2001).

Specifically, Plethodontid salamanders could be used as indicators of forest biodiversity and integrity (Welsh and Droege 2001). Many of the SBR salamanders are Plethodontids and respire through the skin, which requires a moist environment (Ash 1997). SBR terrestrial salamanders also forage primarily in leaf litter (Ash 1997). Thus, management activities that reduce surface moisture or temporarily reduce or remove the litter layer (e.g., prescribed burning) affect salamander habitat structure (Ford et al. 2010). Thus, monitoring of salamander populations or specific species could be an indicator of these habitat shifts.

In our meta-analysis, amphibians were the taxa most negatively impacted by mechanical treatment types (all represented mechanical treatments resulted in a negative effect size). This is not to say all management actions have a negative impact, but that amphibians are very sensitive to changes in their habitats. They could be monitored as indicators, but also to more fully understand how their populations are being impacted by management actions.

4.3 Birds

4.3.1 Northern Bobwhite Quail

The Northern Bobwhite Quail, *Colinus virginianus*, could be used as a potential indicator for the success of prescribed burns or thinning mechanical treatments. Northern Bobwhites are highly dependent on disturbance; they are habitat specialists that require early successional habitat (Stoddard 1931, Brennan 1991, Johnson and Hale 2002, Warburton et al. 2011). Much of the literature on the Northern Bobwhite as it relates to fire refers to the work of Herbert Stoddard in the 1930s. His book on the Northern Bobwhite documented for the first time the importance of fire for maintaining quail populations. Further, he identified that the Northern Bobwhite is so dependent on early successional habitat that to maintain quail populations fire frequency should be on a 1-2 year cycle (Stoddard 1931, Van Lear and Waldrop 1989). These burns should create a mosaic of early successional patches interspersed throughout denser forested areas, allowing quail to find good nesting areas and cover from predators (Stoddard 1931).

Work since then has only corroborated Stoddard's findings. Since the 1980s there has been a severe population decline in the Northern Bobwhite throughout its habitat range,

especially in the Appalachians (Brennan 1991, Dimmick et al. 2002). This is likely linked to canopy closure and loss of the early successional habitat that this species depends upon (Brennan 1991). A closed canopy does not allow for growth of plants in the herbaceous layer that make up quail's diets. More frequent burning would open up the canopy and allow for the quail's food to grow (Brennan 1991). Similarly, research shows that litter depth in a forest is negatively correlated with Northern Bobwhite survival rates, indicating that in forests where fires occur more frequently and therefore the litter layer is thinner, quail tend to survive better (Peters et al. 2015).

Because the Northern Bobwhite is so dependent on early successional habitat and a relatively open canopy, changes in quail abundance levels could be used to indicate the success of prescribed burning (or other treatments) for creating this habitat type. Not only is this species relatively easy to survey, but multiple stakeholder groups have an interest in the Northern Bobwhite. It is a game species, but also a species of conservation concern. Conservation NGOs, state agencies, hunting organizations, and already established groups like the National Bobwhite Conservation Initiative could be leveraged to provide resources for monitoring the Northern Bobwhite.

4.3.2 American Woodcock

Scolopax minor, the American Woodcock, is a potential indicator species for areas of high bird diversity (Masse et al 2015). At woodcock singing grounds bird diversity is on average 1.5x higher than at other random forest sites. Woodcock depend on a matrix of forest types including 30-year old stands and early successional forest openings (Kelley et al. 2008). This could make woodcock a good indicator species because it could be assumed that where they are seen, there would inherently be a diverse array of habitats that could support a diversity of bird species (and potentially other wildlife taxa). Additionally, because the habitat matrix this species requires includes early successional habitat, the presence of woodcock could be an indicator for the success of forest management actions that aim to create this habitat type.

Woodcock is also a popular game bird (Cooper and Rau 2012). A wide array of stakeholders, including state or federal wildlife agencies, NGOs, and private hunters, are thus interested in tracking this species' population levels and would potentially be willing to contribute monitoring resources.

It should be noted that forest interior bird species are prone to avoid areas of forest mosaic made up of early and mid-successional patches (Welsh and Healy 1993) where woodcock are likely to thrive, and woodcock should not be considered an indicator for this particular suite of bird species.

4.3.3 *Golden-winged warbler*

The Golden-winged warbler, *Vermivora chrysoptera*, is another bird species associated with a diverse forest matrix including early successional patches (Bakermans et al. 2013). This neo-tropical migrant chooses early successional nest sites with available grass and forb cover (Bulluck and Buehler 2008). Many other species of concern or interest such as American woodcock, Appalachian cottontail, black bear, and a variety of other songbirds are also commonly found in these forest edge areas (Bakermans et al. 2013). Again, due to the habitat diversity requirements of the golden-winged warbler managers can infer that where this species is found that forest type diversity is relatively high. This would then indicate an area which would support other wildlife diversity as well. Because the habitat matrix the golden-winged warbler requires includes early successional habitat, the presence of this species could be an indicator for the success of forest management actions that aim to create this habitat type.

The golden-winged warbler has gone through a severe population decline in the past decades (Bakermans et al. 2013), making it a species of high conservation concern. Managers and scientists assume these declines are due to a loss of early-successional habitat and the recent hybridization between golden-winged warblers and blue-winged warblers (Bakermans et al. 2013). Golden-winged warblers are thus a convenient indicator species because they already receive a lot of attention, and there are existing monitoring efforts to track their populations (see Section 3.3, Table 5). The existence of the golden-winged warbler working group (<http://www.gwwa.org/>) provides evidence for the dedication to conserving and monitoring these birds, which could be utilized to leverage further monitoring resources.

Similar to the woodcock, golden-winged warblers should not be used as an indicator for all birds, as forest interior birds are unlikely to share habitat with this species (Welsh and Healy 1993).

4.4 Mammals

4.4.1 Appalachian Cottontail

Scientists first described the Appalachian cottontail (*Sylvilagus obscurus*) as a unique species less than 25 years ago, distinguishing it from the New England cottontail (*Sylvilagus transitionalis*) (Chapman et al. 1992). There is relatively little knowledge about the species, which is rare or uncommon in all four states within the SBR FLN (Bunch et al. n.d.). Found only in fragmented habitat patches within its range, researchers think the Appalachian cottontail is in decline, but largely believe this due to a lack of available data (Barry and Lazell 2008). Heath-like plants (ericaceous cover) including mountain laurel, blueberries, blackberry vines, greenbriar, and cane characterize the sites the species occupy. (Chapman et al. 1992, Bunch et al. 1997). They have been noted in young pine plantations and recent clearcuts, as well as mature pine and mixed pine hardwood stands (Bunch et al. 1997, Bunch and Dye 1999). While ideal habitat is not thoroughly understood, they do require dense understory vegetation (Laseter 1999) and consume more forbs, while being less dependent on grasses than eastern cottontails, *Sylvilagus floridanus* (Spencer and Chapman 1986).

Habitat types used by the Appalachian cottontail suggest that they may benefit from moderate tree harvesting or thinning that allows sunlight to reach the forest floor (Virginia DGIF 2016). Further evaluation of the benefits of prescribed burning in managing for Appalachian cottontail habitat has been recommended (Bunch et al. n.d.). One study found that after cutting and burning a mature pine-hardwood stand, eastern cottontails used it during a regeneration period before Appalachian cottontails moved back into the area after about seven years (Bunch and Dye 1999). This implies that monitoring for the Appalachian cottontail as an indicator species following forest management would require long-term surveys, with inter-specific dynamics among the eastern and Appalachian species potentially being a useful method of tracking habitat changes through succession. Though the relative lack of knowledge on this species perhaps makes them less than ideal as an indicator species according to the published guidelines, their clear relationship to the type of habitat being managed for in the SBR and likely declining numbers makes them an important species to consider monitoring directly

4.5 Reptiles

4.5.1 Timber Rattlesnake

A potential reptilian indicator species is the timber rattlesnake, *Crotalus horridus*. Beaupre and Douglas (2012) have suggested that this species would be a good indicator for large-scale habitat manipulations such as fire. By monitoring a high trophic level predator such as the Timber Rattlesnake, managers could make assumptions about other aspects of the ecosystem such as small mammal abundance and the availability of food for granivores (Beaupre and Douglas 2012). With forest manipulations that increase canopy gaps, associated habitat changes often include increases in seed producing early successional plants such as sun grasses, blackberry, early annuals and perennials, and shade perennials (Beaupre and Douglas 2012). One study found that at manipulated sites where small mammal food availability increased there was a subsequent increase in small mammal abundances, and a corresponding increase in growth rate and body condition of timber rattlesnakes (Beaupre and Douglas 2012). Additionally, it is known that timber rattlesnakes prefer a habitat matrix consisting of both open and closed canopy patches, so where timber rattlesnakes are found it can be assumed that both of these habitat types exist (Ulev 2008). In a basic sense, our systematic review corroborates these results and shows that reptile abundances and/or diversity increase with both fire and mechanical forest management treatments (see systematic review section 4.6 and Figure 17).

C. horridus meets multiple qualifications for good indicators including: small territory size, relative ease of detection, and well studied natural history (Hilty and Merenlender 1999). However, Vos et al. (1999) point out that the relationship between any indicator and target variables should be well understood and studied. It would be valuable for future studies to reinforce Beaupre and Douglas' (2012) findings before implementing any monitoring plan that uses timber rattlesnakes as indicators.

Another argument for using a species like the timber rattlesnake as an indicator is the relative lack of data on reptiles in the literature. Our systematic review found a paucity of studies that investigated the relationship between reptiles and forest manipulations in the Central Hardwood region. Only two out of fifty studies collected data solely on reptiles. Specifically, it has been noted that data documenting the effects of prescribed fire on timber rattlesnakes is lacking (Ulev 2008). Monitoring plans that measure *C. horridus* population levels and/or body condition would thus help address an important knowledge gap in the literature.

4.6 Invertebrates

4.6.1 Bumblebees

Among invertebrate species, pollinating insects are a readily apparent group from which to choose candidate indicator species. They are both crucially important in forest ecosystems for the pollination services they provide plants from trees down to herbaceous understory species (Hanula et al. 2015) and have had a well-documented decline in recent years (Kremen and Ricketts 2000). Bumble bees (*Bombus spp.*), a high-profile species with a great deal of past research, would be an appropriate choice to designate as indicators from this group. They are generalist pollinators, providing services to a wide range of plants, and have been singled out as deserving of focused conservation for their importance to wild plant populations (Hatfield et al. 2012). Recent research has focused on how forest changes resulting from past management and fire suppression have led to a decline in bees and other pollinators in southeastern forests, with bees favoring younger forests with presumed greater light availability and flower abundance (Hanula et al. 2015; Jackson et al. 2014). Hanula et al. (2015) found that bee communities had higher species richnesses and abundances in habitats consistent with areas marked by frequent disturbance, and recommend frequent fire and periodic thinning to maintain habitat for pollinators in the long term.

The studies cited here used pan trapping over short periods as a fairly simple and cost-effective means of monitoring abundance and species richness, and recent efforts used netting by volunteers to do the same as a part of the Blue Ridge Bumble Bee Megatransect of July 2015. Bumble bees fulfill several important criteria that distinguish them as effective indicators in that they play an important role in ecosystem function, are currently of notable conservation concern, have a demonstrated sensitivity to forest habitat changes and disturbance, and (at the genus level) are easy to identify. They would therefore be a logical choice to begin filling the noted monitoring gap that exists for invertebrates within the SBR region.

5. MONITORING GAPS

Reptiles were by far the least represented taxon in our systematic review. They only represent 9% of our data points and only two out of fifty studies were dedicated solely to reptile data collection. This taxon represents a wide array of ecologically important species that are important to manage for, and includes species of conservation concern such as the eastern milk

snake (*Lampropeltis triangulum triangulum*), timber rattlesnake (*Crotalus horridus*), coal skink (*Plestiodon anthracinus*), and the critically endangered bog turtle (*Glyptemys muhlenbergii*).

Though birds provide the largest taxon representation in our meta-analysis, data on non-passerine birds are lacking. Over 70% of our bird data represent passerine songbirds. Passerine birds encompass all birds within the order *Passeriformes*, and make up more than half of all known bird species. This overrepresentation in our data is likely due to the relative ease of collecting acoustic bird data, as described in section 5.3 of the main systematic review document. State wildlife agencies are aware of this data collection bias, and have noted the importance of developing survey methods that better represent these other bird orders (NC Wildlife Resources Commission 2015).

We found no studies that provided usable information on bats for our systematic review, indicating that little bat data is being published even in the few places where it is collected. Bats are of special concern of late due to outbreaks of white-nose syndrome, as well as other threats to bat populations including wind energy development, habitat fragmentation, and climate change (Loeb et al. 2015). The potential for listing new bat species such as the little brown bat, *Myotis lucifugus*, on the Endangered Species List would require that managers carefully document bat population levels. Having baseline data on bat populations would be extremely valuable in these circumstances. The U.S. Geological Survey (USGS) is attempting to address the lack of bat monitoring data nationwide by implementing the North American Bat Monitoring Program (NABat), which will tentatively launch in 2017 (Loeb et al. 2015) (See section 3.7.2 of this report for more information on NABat).

We also did not find any usable studies on large mammal populations to include in our systematic review. This is likely because of the relative difficulty and high expense related to surveying larger mammal species. However, information that indicates how some of these species such as black bear (*Ursus americanus*), white-tailed deer (*Odocoileus virginianus*), and bobcats (*Lynx rufus*) respond to various forest treatments would be valuable, especially considering their high level in the food chain, and, in some cases, keystone or umbrella species status. Additionally, managers often must consider how forest treatments might impact game species, many of which are large mammals; any additional information that would aid management in this regard could have impacts on the hunting community. Through interviews with members of state wildlife agencies, we did find that there is some monitoring of these larger

game species by state agencies, but usually within a specific park or game land (see section 3.4). Coordinating this data across multiple agencies or groups would be beneficial to examine how these species respond on a landscape scale.

6. MONITORING GOALS AND RECOMMENDATIONS

6.1 Suggestions compiled from state Wildlife Action Plans

The new North Carolina WAP highlights monitoring recommendations that can be applied to all taxa, and nicely encompasses generalized goals for future monitoring in the following excerpt:

Long-term monitoring is critical to assessing species and ecosystem health and gauging the resilience of organisms to a changing climate. Studies should include identification of population trends, as well as assessment of impacts from conservation or development activities [...] Long-term monitoring sites need to be identified and monitoring protocols developed for all priority species. Monitoring plans should be coordinated with other existing monitoring programs where feasible (NC Wildlife Resources Commission 2015).

6.1.1 All taxa

All WAPs examined for this study similarly recommend an intensification in wildlife monitoring. While this may not always be possible, it is important to acknowledge the large-scale vision of wildlife monitoring agencies and organizations across the SBR region.

6.1.2 Amphibians

The state WAPs provide the following recommendations with regard to amphibian monitoring that could be applicable in the SBR.

1. Develop and continue to refine monitoring protocols (SC Department of Natural Resources 2005).
2. Track population trends for species of concern with particular attention to four-toed salamanders (NC Wildlife Resources Commission 2015).
3. Continue existing annual inventories to build up long-term datasets (NC Wildlife Resources Commission 2015).

6.1.3 Birds

The state WAPs provide the following specific recommendations with regard to bird monitoring.

1. Continue to develop monitoring coordination and to support national and regional bird-monitoring coordination bodies (South Carolina Department of Natural Resources 2005).
2. Continue long-term monitoring of bald eagles (NC Wildlife Resources Commission 2015).
3. Continue long-term monitoring of birds that use early successional habitats (NC Wildlife Resources Commission 2015).
4. Continue montane bird population monitoring (NC Wildlife Resources Commission 2015).
5. Expand monitoring frameworks so that populations of species unsuited for traditional monitoring techniques can be tracked (e.g. hawks, nightjars, owls) (NC Wildlife Resources Commission 2015).
6. Begin long-term monitoring of birds that depend on snags and on cavity-nesting species (NC Wildlife Resources Commission 2015).

6.1.4 Mammals

The state WAPs provide the following specific recommendations with regard to mammal monitoring.

1. Standardized monitoring protocols should be developed for small mammals and bats (SC Department of Natural Resources 2005).
2. Data needs are most pressing for all bat species (SC Department of Natural Resources 2005).
3. Continue existing bat monitoring and expand it to a wider area (NC Wildlife Resources Commission 2015).
4. Continue monitoring Carolina Northern Flying Squirrel populations (NC Wildlife Resources Commission 2015).

6.1.5 Reptiles

The state WAPs provide the following specific recommendations with regard to reptile monitoring.

1. Develop standardized monitoring protocols (SC Department of Natural Resources 2005).
2. Monitor priority reptile species that are perceived as declining or rare (e.g. Northern Pine Snake and Timber Rattlesnake) (NC Wildlife Resources Commission 2015).
3. Continue bog-turtle monitoring (NC Wildlife Resources Commission 2015).

4. Monitor snake populations for emerging diseases (NC Wildlife Resources Commission 2015).

6.1.6 Invertebrates

The WAPs provide relatively little information on existing monitoring or monitoring goals for invertebrates. Much of the information is either about invertebrates in relation to other species that rely on them as a food source, or about invertebrates' status as pests. The NC WAP (NCWRC 2015) notes that data availability for this taxonomic group is remarkably low. Specific invertebrate species are often only monitored if they are federally listed under the Endangered Species Act.

Only the new NC WAP provides recommendations specific to invertebrate/ insect monitoring, and they can be summarized as the following.

1. Basic monitoring is needed to understand these species and their habitat requirements (NC Wildlife Resources Commission 2015).
2. Surveys are needed for species believed to be in decline or dependent on at-risk ecosystems (NC Wildlife Resources Commission 2015).

6.2 Overarching monitoring suggestions

In summary, there are many opportunities to coordinate monitoring of management impacts on wildlife populations for an effective strategy across the landscapes of the SBR FLN. The results from our systematic review and meta-analysis of past research in central hardwood forests offer empirical data on responses of wildlife taxa to forest management to inform comparisons and hypotheses for future monitoring efforts. A key consideration for moving regional monitoring forward is the definition of specific research questions among collaborators within the FLN. Identifying a purpose behind monitoring at this scale will allow partners to move beyond simply taking stock of species presence and compiling population numbers and work toward documenting ecological change and more fully understanding the wildlife community of the SBR.

The relative lack of long-term data on wildlife responses to forest management should be another key concern moving forward, with monitoring designed in a way that can be maintained over periods of time through succession and repeated disturbance. Where appropriate, new monitoring could be designed to coordinate with the design and methods of past research to detect long term trends over the intervening time period. Implementing ways to share methods

and data effectively between partners as monitoring is carried out will be key for such a strategy at a regional scale to have the desired outcomes, which could involve making standardized protocols for surveys and data collection (created by taxa experts among FLN partners) available, as well as centralized repositories for spatial and survey data. These steps would help to facilitate cohesive data management and enable planning for monitoring across the landscape by documenting distribution of survey efforts.

Though not yet fully operational, *the Appalachian Mountain Joint Venture Bird Monitoring Collaborative* (see section 3.7.1) could be used as a template for future monitoring collaborations. This bird monitoring collaborative aims to combine partner efforts efficiently and effectively by establishing uniform protocols, making comparisons with historical data possible, incorporating new monitoring techniques so that more sophisticated analyses can be performed, and creating a central data repository to organize and store all partner data. Other taxa experts across the SBR could come together in this way to formulate cohesive, systematic monitoring networks. Already established regional organizations like the Appalachian Mountain Joint Venture or the Appalachian Landscape Conservation Cooperative could act as leverage points for beginning these cooperative monitoring efforts.

While we lacked the field experience and on-the-ground knowledge of the region and its ecology to make exhaustive recommendations for indicator species that could make up the most informative and cost effective monitoring program, we did identify some key resources to help guide regional partners in making logical and practical choices. This included a discussion of several possible examples of indicators based on species ecology, conservation concerns, and gaps in existing monitoring, followed by a summary of major recommendations from the available Wildlife Action Plans for states with territory in the SBR FLN. We hope this compiled information will help provide a foundation for crafting a successful regional wildlife monitoring strategy.

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APPENDIX IV.

PAPERS INCLUDED IN SYSTEMATIC REVIEW AND META-ANALYSIS:

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APPENDIX V.

```
# Analysis of SBR Systematic Review Data
#R code
# 25 Feb 2016

#####
library(boot)
library(ggplot2)
# Read in data
# Rename columns
SR.dat <- read.csv("SR_data_20160225.csv", header = T)
SR.header <- c("Order", "Common_Name", "Taxa", "Location", "Site", "Forest_Type",
"Forest_descr", "Silv_Fire", "Treatment", "Treatment_descr", "Div_Abund",
              "Div_Metric", "Study_Type", "Tmt_Yr_First",
" Tmt_Yr_Last", "Yrs_Since_Tmt", "Return_Int", "Samp_Meth", "Reps", "Site_Visits",
" Tmt_Area_1",
              "Tmt_Area_All", "Ctrl_Area", "Ctrl_Age", "Ctrl_descr", "Total_Area",
"Exp_Mean", "Ctrl_Mean", "Eff_Size", "Eff_Size_Wtd", "Ref", "Ref_ID",
              "Extractor")
names(SR.dat) <- SR.header

# Force correct data format
SR.dat$Order <- as.factor(SR.dat$Order)
SR.dat$Common_Name <- as.character(SR.dat$Common_Name)
SR.dat$Site <- as.character(SR.dat$Site)
SR.dat$Forest_Type <- as.factor(SR.dat$Forest_Type)
SR.dat$Forest_descr <- as.character(SR.dat$Forest_descr)
SR.dat$Silv_Fire <- as.factor(SR.dat$Silv_Fire)
SR.dat$Treatment <- as.factor(SR.dat$Treatment)
SR.dat$Treatment_descr <- as.character(SR.dat$Treatment_descr)
SR.dat$Study_Type <- as.factor(SR.dat$Study_Type)
SR.dat$Tmt_Yr_First <- as.character(SR.dat$Tmt_Yr_First)
SR.dat$Tmt_Yr_Last <- as.character(SR.dat$Tmt_Yr_Last)
SR.dat$Return_Int <- as.character(SR.dat$Return_Int)
SR.dat$Samp_Meth <- as.character(SR.dat$Samp_Meth)
SR.dat$Site_Visits <- as.character(SR.dat$Site_Visits)
SR.dat$Tmt_Area_1 <- as.character(SR.dat$Tmt_Area_1)
SR.dat$Tmt_Area_All <- as.character(SR.dat$Tmt_Area_All)
SR.dat$Ctrl_Area <- as.character(SR.dat$Ctrl_Area)
SR.dat$Ctrl_descr <- as.character(SR.dat$Ctrl_descr)
SR.dat$Total_Area <- as.character(SR.dat$Total_Area)
SR.dat$Exp_Mean <- as.numeric(as.character(SR.dat$Exp_Mean))
SR.dat$Ctrl_Mean <- as.numeric(as.character(SR.dat$Ctrl_Mean))
SR.dat$Ref <- as.character(SR.dat$Ref)
SR.dat$Ref_ID <- as.factor(SR.dat$Ref_ID)

# Create column for reference year
substrRight <- function(x, n){
  substr(x, nchar(x)-n+1, nchar(x))
}

Ref_Yr <- c()
for(i in 1:nrow(SR.dat)) {
```

```

  Ref_Yr[i] <- substrRight(SR.dat$Ref[i], 4)
}
SR.dat$Ref_Yr <- Ref_Yr
SR.dat$Ref_Yr <- as.numeric(SR.dat$Ref_Yr)

# Correct Columns where control or experimental mean is 0
SR.dat$Exp_Mean[SR.dat$Exp_Mean == 0] <- 0.001
SR.dat$Ctrl_Mean[SR.dat$Ctrl_Mean == 0] <- 0.001

# Calculate effect sizes (weighted & unweighted)
SR.dat$Eff_Size <- log(SR.dat$Exp_Mean/SR.dat$Ctrl_Mean)
SR.dat$Eff_Size_Wtd <- log(SR.dat$Reps + 1)*log(SR.dat$Exp_Mean/SR.dat$Ctrl_Mean) #
This doesn't seem right?
SR.dat <- SR.dat[-1112,]

# Trim data sheet
SR.dat.trim <- SR.dat[, -c(2, 5, 7, 10, 12, 14, 15, 17, 18, 20, 21, 22, 23, 25, 26)]

# Separate data from different taxa into separate sheets
SR.amph <- SR.dat.trim[SR.dat.trim$Taxa=="Amphibian",]
SR.bird <- SR.dat.trim[SR.dat.trim$Taxa=="Bird",]
SR.invt <- SR.dat.trim[SR.dat.trim$Taxa=="Invertebrate",]
SR.mamm <- SR.dat.trim[SR.dat.trim$Taxa=="Mammal",]
SR.rept <- SR.dat.trim[SR.dat.trim$Taxa=="Reptile",]
SR.mult <- SR.dat.trim[SR.dat.trim$Taxa=="Multiple",]
SR.amph <- SR.amph[ , -2]
SR.bird <- SR.bird[ , -2]
SR.invt <- SR.invt[ , -2]
SR.mamm <- SR.mamm[ , -2]
SR.rept <- SR.rept[ , -2]
SR.mult <- SR.mult[ , -2]

#####
# Examine year distribution
hist(SR.amph$Ref_Yr)
hist(SR.bird$Ref_Yr)
hist(SR.invt$Ref_Yr)
hist(SR.mamm$Ref_Yr)
hist(SR.rept$Ref_Yr)

# Boxplots
boxplot(SR.amph$Eff_Size ~ SR.amph$Treatment, ylim = c(-10, 10))
boxplot(SR.bird$Eff_Size ~ SR.bird$Treatment, ylim = c(-10, 10))
boxplot(SR.invt$Eff_Size ~ SR.invt$Treatment, ylim = c(-10, 10))
boxplot(SR.mamm$Eff_Size ~ SR.mamm$Treatment, ylim = c(-10, 10))
boxplot(SR.rept$Eff_Size ~ SR.rept$Treatment, ylim = c(-10, 10))
# Some of the boxes and whiskers look weird. Not sure what that's about.
boxplot(SR.amph$Eff_Size_Wtd ~ SR.amph$Treatment, ylim = c(-10, 10))
boxplot(SR.bird$Eff_Size_Wtd ~ SR.bird$Treatment, ylim = c(-10, 10))
boxplot(SR.invt$Eff_Size_Wtd ~ SR.invt$Treatment, ylim = c(-10, 10))
boxplot(SR.mamm$Eff_Size_Wtd ~ SR.mamm$Treatment, ylim = c(-10, 10))
boxplot(SR.rept$Eff_Size_Wtd ~ SR.rept$Treatment, ylim = c(-10, 10))

#####

```

```

# GLM for all species combined
all.glm01 <- glm(SR.dat.trim$Eff_Size ~ ., data = SR.dat.trim)
summary(all.glm01)

all.glm02 <- glm(SR.dat.trim$Eff_Size ~ SR.dat.trim$Taxa + SR.dat.trim$Treatment +
SR.dat.trim$Forest_Type + SR.dat.trim$Yrs_Since_Tmt + SR.dat.trim$Study_Type, data =
SR.dat.trim)
summary(all.glm02)
all.glm02.step <- step(all.glm02)
summary(all.glm02.step)
# Taxa, treatment, forest type, study type
all.glm02.r2 <- 1 - (all.glm02.step$deviance/all.glm02.step$null)
all.glm02.r2
# R2 = 0.06088406
all.glm02.p <- 1 - pchisq(all.glm02.step$null - all.glm02.step$deviance, 6)
all.glm02.p
# p = 0

#####
# Weighted GLM
all.glm02.wtd <- glm(SR.dat.trim$Eff_Size_Wtd ~ SR.dat.trim$Taxa +
SR.dat.trim$Treatment + SR.dat.trim$Forest_Type + SR.dat.trim$Yrs_Since_Tmt +
SR.dat.trim$Study_Type, data = SR.dat.trim)
summary(all.glm02.wtd)
all.glm02.wtd.step <- step(all.glm02.wtd)
summary(all.glm02.wtd.step)
# Taxa, treatment, forest type, study type
all.glm02.wtd.r2 <- 1 - (all.glm02.wtd.step$deviance/all.glm02.wtd.step$null)
all.glm02.wtd.r2
# R2 = 0.08208443
all.glm02.wtd.p <- 1 - pchisq(all.glm02.wtd.step$null - all.glm02.wtd.step$deviance,
6)
all.glm02.wtd.p
# p = 0.006829774

#####
# GLM for amphibians
amph.glm01 <- glm(SR.amph$Eff_Size ~ ., data = SR.amph[, -c(11, 12, 13, 14, 15)])
summary(amph.glm01)
amph.glm01.step <- step(amph.glm01)
summary(amph.glm01.step)
# treatment, years since treatment
amph.glm01.step.r2 <- 1 - (amph.glm01.step$deviance/amph.glm01.step$null)
amph.glm01.step.r2
# R2 = 0.1502103
amph.glm01.step.p <- 1 - pchisq(amph.glm01.step$null - amph.glm01.step$deviance, 3)
amph.glm01.step.p
# P = 0

# try glm without Order, ref id, study type
amph.glm02 <- glm(SR.amph$Eff_Size ~ SR.amph$Treatment + SR.amph$Forest_Type +
SR.amph$Yrs_Since_Tmt + SR.amph$Ctrl_Age, data = SR.amph)
summary(amph.glm02)
amph.glm02.step <- step(amph.glm02)

```

```

summary(amph.glm02.step)
# treatment & years since treatment
amph.glm02.step.r2 <- 1 - (amph.glm02.step$deviance/amph.glm02.step$null)
amph.glm02.step.r2
# R2 = 0.1502103
amph.glm02.step.p <- 1 - pchisq(amph.glm02.step$null - amph.glm02.step$deviance, 3)
amph.glm02.step.p
# P = 0

# try glm without, ref id, study type
amph.glm03 <- glm(SR.amph$Eff_Size ~ SR.amph$Order + SR.amph$Treatment +
SR.amph$Forest_Type + SR.amph$Yrs_Since_Tmt + SR.amph$Ctrl_Age, data = SR.amph)
summary(amph.glm03)
amph.glm03.step <- step(amph.glm03)
summary(amph.glm03.step)
# treatment, years since treatment
amph.glm03.step.r2 <- 1 - (amph.glm03.step$deviance/amph.glm03.step$null)
amph.glm03.step.r2
# R2 = 0.1502103
amph.glm03.step.p <- 1 - pchisq(amph.glm03.step$null - amph.glm02.step$deviance, 3)
amph.glm03.step.p
# P = 0

#####
# Weighted GLM for amphibians
amph.glm01.wtd <- glm(SR.amph$Eff_Size_Wtd ~ ., data = SR.amph[, -c(11, 12, 13, 14,
15)])
summary(amph.glm01.wtd)
amph.glm01.wtd.step <- step(amph.glm01.wtd)
summary(amph.glm01.wtd.step)
# Treatment
amph.glm01.wtd.step.r2 <- 1 - (amph.glm01.wtd.step$deviance/amph.glm01.wtd.step$null)
amph.glm01.wtd.step.r2
# R2 = 0.1470497
amph.glm01.wtd.step.p <- 1 - pchisq(amph.glm01.wtd.step$null -
amph.glm01.wtd.step$deviance, 2)
amph.glm01.wtd.step.p
# P = 0

# try glm without Order, ref id, study type
amph.glm02.wtd <- glm(SR.amph$Eff_Size_Wtd ~ SR.amph$Treatment + SR.amph$Forest_Type
+ SR.amph$Yrs_Since_Tmt + SR.amph$Silv_Fire + SR.amph$Location + SR.amph$Ctrl_Age,
data = SR.amph)
summary(amph.glm02.wtd)
amph.glm02.wtd.step <- step(amph.glm02.wtd)
summary(amph.glm02.wtd.step)
# treatment
amph.glm02.wtd.step.r2 <- 1 - (amph.glm02.wtd.step$deviance/amph.glm02.wtd.step$null)
amph.glm02.wtd.step.r2
# R2 = 0.1470497
amph.glm02.wtd.step.p <- 1 - pchisq(amph.glm02.wtd.step$null -
amph.glm02.wtd.step$deviance, 2)
amph.glm02.wtd.step.p
# P = 0

```

```

# try glm without ref id, study type
amph.glm03.wtd <- glm(SR.amph$Eff_Size_Wtd ~ SR.amph$Order + SR.amph$Treatment +
SR.amph$Forest_Type + SR.amph$Yrs_Since_Tmt + SR.amph$Silv_Fire + SR.amph$Location +
SR.amph$Ctrl_Age, data = SR.amph)
summary(amph.glm03.wtd)
amph.glm03.wtd.step <- step(amph.glm03.wtd)
summary(amph.glm03.wtd.step)
# Order, forest type, location
amph.glm03.wtd.step.r2 <- 1 - (amph.glm03.wtd.step$deviance/amph.glm03.wtd.step$null)
amph.glm03.wtd.step.r2
# R2 = 0.1470497
amph.glm03.wtd.step.p <- 1 - pchisq(amph.glm03.wtd.step$null -
amph.glm03.wtd.step$deviance, 3)
amph.glm03.wtd.step.p
# P = 0

#####
# GLM for birds
bird.glm01 <- glm(SR.bird$Eff_Size ~ ., data = SR.bird[, -c(11, 12, 13, 14, 15)])
summary(bird.glm01)
bird.glm01.step <- step(bird.glm01)
summary(bird.glm01.step)
# Order, ref_id
bird.glm01.step.r2 <- 1 - (bird.glm01.step$deviance/bird.glm01.step$null)
bird.glm01.step.r2
# R2 = 0.1674894
bird.glm01.step.p <- 1 - pchisq(bird.glm01.step$null - bird.glm01.step$deviance, 3)
bird.glm01.step.p
# P = 0

# try glm without Order, ref id, study type
bird.glm02 <- glm(SR.bird$Eff_Size ~ SR.bird$Treatment + SR.bird$Forest_Type +
SR.bird$Yrs_Since_Tmt + SR.bird$Ctrl_Age, data = SR.bird)
summary(bird.glm02)
bird.glm02.step <- step(bird.glm02)
summary(bird.glm02.step)
# forest type, control age
bird.glm02.step.r2 <- 1 - (bird.glm02.step$deviance/bird.glm02.step$null)
bird.glm02.step.r2
# R2 = 0.05222427
bird.glm02.step.p <- 1 - pchisq(bird.glm02.step$null - bird.glm02.step$deviance, 3)
bird.glm02.step.p
# P = 0

# try glm without ref id, study type
bird.glm03 <- glm(SR.bird$Eff_Size ~ SR.bird$Order + SR.bird$Treatment +
SR.bird$Forest_Type + SR.bird$Yrs_Since_Tmt + SR.bird$Ctrl_Age, data = SR.bird)
summary(bird.glm03)
bird.glm03.step <- step(bird.glm03)
summary(bird.glm03.step)
# Order, Forest type, Control age
bird.glm03.step.r2 <- 1 - (bird.glm03.step$deviance/bird.glm03.step$null)
bird.glm03.step.r2

```

```

# R2 = 0.1493108
bird.glm03.step.p <- 1 - pchisq(bird.glm03.step$null - bird.glm03.step$deviance, 3)
bird.glm03.step.p
# P = 0

#####
# Weighted GLM for birds
bird.glm01.wtd <- glm(SR.bird$Eff_Size_Wtd ~ ., data = SR.bird[, -c(11, 12, 13, 14,
15)])
summary(bird.glm01.wtd)
bird.glm01.wtd.step <- step(bird.glm01.wtd)
summary(bird.glm01.wtd.step)
# Order, ref id
bird.glm01.wtd.step.r2 <- 1 - (bird.glm01.wtd.step$deviance/bird.glm01.wtd.step$null)
bird.glm01.wtd.step.r2
# R2 = 0.1617378
bird.glm01.wtd.step.p <- 1 - pchisq(bird.glm01.wtd.step$null -
bird.glm01.wtd.step$deviance, 3)
bird.glm01.wtd.step.p
# P = 0

# try glm without Order, ref id, study type
bird.glm02.wtd <- glm(SR.bird$Eff_Size_Wtd ~ SR.bird$Treatment + SR.bird$Forest_Type
+ SR.bird$Yrs_Since_Tmt + SR.bird$Silv_Fire + SR.bird$Location + SR.bird$Ctrl_Age,
data = SR.bird)
summary(bird.glm02.wtd)
bird.glm02.wtd.step <- step(bird.glm02.wtd)
summary(bird.glm02.wtd.step)
# forest type, years since treatment, fire/silv
bird.glm02.wtd.step.r2 <- 1 - (bird.glm02.wtd.step$deviance/bird.glm02.wtd.step$null)
bird.glm02.wtd.step.r2
# R2 = 0.06977039
bird.glm02.wtd.step.p <- 1 - pchisq(bird.glm02.wtd.step$null -
bird.glm02.wtd.step$deviance, 4)
bird.glm02.wtd.step.p
# P = 0

# try glm without ref id, study type
bird.glm03.wtd <- glm(SR.bird$Eff_Size_Wtd ~ SR.bird$Treatment + SR.bird$Forest_Type
+ SR.bird$Yrs_Since_Tmt + SR.bird$Silv_Fire + SR.bird$Location + SR.bird$Ctrl_Age,
data = SR.bird)
summary(bird.glm03.wtd)
bird.glm03.wtd.step <- step(bird.glm03.wtd)
summary(bird.glm03.wtd.step)
# forest type, years since treatment, fire/silv
bird.glm03.wtd.step.r2 <- 1 - (bird.glm03.wtd.step$deviance/bird.glm03.wtd.step$null)
bird.glm03.wtd.step.r2
# R2 = 0.06977039
bird.glm03.wtd.step.p <- 1 - pchisq(bird.glm03.wtd.step$null -
bird.glm03.wtd.step$deviance, 4)
bird.glm03.wtd.step.p
# P = 0

#####

```

```

# GLM for invertebrates
inv.t.glm01 <- glm(SR.invt$Eff_Size ~ ., data = SR.invt[, -c(11, 12, 13, 14, 15)])
summary(inv.t.glm01)
inv.t.glm01.step <- step(inv.t.glm01)
summary(inv.t.glm01.step)
# study type, ref id
inv.t.glm01.step.r2 <- 1 - (inv.t.glm01.step$deviance/inv.t.glm01.step$null)
inv.t.glm01.step.r2
# R2 = 0.1046794
inv.t.glm01.step.p <- 1 - pchisq(inv.t.glm01.step$null - inv.t.glm01.step$deviance, 3)
inv.t.glm01.step.p
# P = 0

# try glm without Order, ref id, study type
inv.t.glm02 <- glm(SR.invt$Eff_Size ~ SR.invt$Treatment + SR.invt$Forest_Type +
SR.invt$Yrs_Since_Tmt + SR.invt$Ctrl_Age, data = SR.invt)
summary(inv.t.glm02)
inv.t.glm02.step <- step(inv.t.glm02)
summary(inv.t.glm02.step)
# treatment, control age
inv.t.glm02.step.r2 <- 1 - (inv.t.glm02.step$deviance/inv.t.glm02.step$null)
inv.t.glm02.step.r2
# R2 = 0.09272203
inv.t.glm02.step.p <- 1 - pchisq(inv.t.glm02.step$null - inv.t.glm02.step$deviance, 3)
inv.t.glm02.step.p
# P = 0

# try glm without ref id, study type
inv.t.glm03 <- glm(SR.invt$Eff_Size ~ SR.invt$Order + SR.invt$Treatment +
SR.invt$Forest_Type + SR.invt$Yrs_Since_Tmt + SR.invt$Ctrl_Age, data = SR.invt)
summary(inv.t.glm03)
inv.t.glm03.step <- step(inv.t.glm03)
summary(inv.t.glm03.step)
# treatment, control age
inv.t.glm03.step.r2 <- 1 - (inv.t.glm03.step$deviance/inv.t.glm03.step$null)
inv.t.glm03.step.r2
# R2 = 0.09272203
inv.t.glm03.step.p <- 1 - pchisq(inv.t.glm03.step$null - inv.t.glm03.step$deviance, 3)
inv.t.glm03.step.p
# P = 0

#####
# Weighted GLM for invertebrates
inv.t.glm01.wtd <- glm(SR.invt$Eff_Size_Wtd ~ ., data = SR.invt[, -c(11, 12, 13, 14,
15)])
summary(inv.t.glm01.wtd)
inv.t.glm01.wtd.step <- step(inv.t.glm01.wtd)
summary(inv.t.glm01.wtd.step)
# Order, treatment, div/ab, study type, ref id
inv.t.glm01.wtd.step.r2 <- 1 - (inv.t.glm01.wtd.step$deviance/inv.t.glm01.wtd.step$null)
inv.t.glm01.wtd.step.r2
# R2 = 0.4036755
inv.t.glm01.wtd.step.p <- 1 - pchisq(inv.t.glm01.wtd.step$null -
inv.t.glm01.wtd.step$deviance, 6)

```

```

invt.glm01.wtd.step.p
# P = 0

# try glm without Order, ref id, study type
invt.glm02.wtd <- glm(SR.invt$Eff_Size_Wtd ~ SR.invt$Treatment + SR.invt$Forest_Type
+ SR.invt$Yrs_Since_Tmt + SR.invt$Silv_Fire + SR.invt$Location + SR.invt$Ctrl_Age,
data = SR.invt)
summary(invt.glm02.wtd)
invt.glm02.wtd.step <- step(invt.glm02.wtd)
summary(invt.glm02.wtd.step)
# treatment, location
invt.glm02.wtd.step.r2 <- 1 - (invt.glm02.wtd.step$deviance/invt.glm02.wtd.step$null)
invt.glm02.wtd.step.r2
# R2 = 0.3597741
invt.glm02.wtd.step.p <- 1 - pchisq(invt.glm02.wtd.step$null -
invt.glm02.wtd.step$deviance, 3)
invt.glm02.wtd.step.p
# P = 0

# try glm without Order, ref id, study type
invt.glm03.wtd <- glm(SR.invt$Eff_Size_Wtd ~ SR.invt$Order + SR.invt$Treatment +
SR.invt$Forest_Type + SR.invt$Yrs_Since_Tmt + SR.invt$Silv_Fire + SR.invt$Location +
SR.invt$Ctrl_Age, data = SR.invt)
summary(invt.glm03.wtd)
invt.glm03.wtd.step <- step(invt.glm03.wtd)
summary(invt.glm03.wtd.step)
# treatment, location
invt.glm03.wtd.step.r2 <- 1 - (invt.glm03.wtd.step$deviance/invt.glm03.wtd.step$null)
invt.glm03.wtd.step.r2
# R2 = 0.3597741
invt.glm03.wtd.step.p <- 1 - pchisq(invt.glm03.wtd.step$null -
invt.glm03.wtd.step$deviance, 3)
invt.glm03.wtd.step.p
# P = 0

#####
# GLM for mammals
SR.mamm <- na.omit(SR.mamm)
mamm.glm01 <- glm(SR.mamm$Eff_Size ~ ., data = SR.mamm[, -c(11, 12, 13, 14, 15)])
summary(mamm.glm01)
mamm.glm01.step <- step(mamm.glm01)
summary(mamm.glm01.step)
# Order, div/ab, ref id
mamm.glm01.step.r2 <- 1 - (mamm.glm01.step$deviance/mamm.glm01.step$null)
mamm.glm01.step.r2
# R2 = 0.1574203
mamm.glm01.step.p <- 1 - pchisq(mamm.glm01.step$null - mamm.glm01.step$deviance, 4)
mamm.glm01.step.p
# P = 0

# try glm without Order, ref id, study type
mamm.glm02 <- glm(SR.mamm$Eff_Size ~ SR.mamm$Treatment + SR.mamm$Forest_Type +
SR.mamm$Yrs_Since_Tmt + SR.mamm$Ctrl_Age, data = SR.mamm)
summary(mamm.glm02)

```



```

mamm.glm02.step <- step(mamm.glm02)
summary(mamm.glm02.step)
# forest type
mamm.glm02.step.r2 <- 1 - (mamm.glm02.step$deviance/mamm.glm02.step$null)
mamm.glm02.step.r2
# R2 = 0.03311335
mamm.glm02.step.p <- 1 - pchisq(mamm.glm02.step$null - mamm.glm02.step$deviance, 2)
mamm.glm02.step.p
# P = 0

# try glm without ref id, study type
mamm.glm03 <- glm(SR.mamm$Eff_Size ~ SR.mamm$Order + SR.mamm$Treatment +
SR.mamm$Forest_Type + SR.mamm$Yrs_Since_Tmt + SR.mamm$Ctrl_Age, data = SR.mamm)
summary(mamm.glm03)
mamm.glm03.step <- step(mamm.glm03)
summary(mamm.glm03.step)
# forest type
mamm.glm03.step.r2 <- 1 - (mamm.glm03.step$deviance/mamm.glm03.step$null)
mamm.glm03.step.r2
# R2 = 0.03311335
mamm.glm03.step.p <- 1 - pchisq(mamm.glm03.step$null - mamm.glm03.step$deviance, 2)
mamm.glm03.step.p
# P = 0

#####
# Weighted GLM for mammals
mamm.glm01.wtd <- glm(SR.mamm$Eff_Size_Wtd ~ ., data = SR.mamm[, -c(11, 12, 13, 14,
15)])
summary(mamm.glm01.wtd)
mamm.glm01.wtd.step <- step(mamm.glm01.wtd)
summary(mamm.glm01.wtd.step)
# Order, div/ab, reps, ref id
mamm.glm01.wtd.step.r2 <- 1 - (mamm.glm01.wtd.step$deviance/mamm.glm01.wtd.step$null)
mamm.glm01.wtd.step.r2
# R2 = 0.1688733
mamm.glm01.wtd.step.p <- 1 - pchisq(mamm.glm01.wtd.step$null -
mamm.glm01.wtd.step$deviance, 5)
mamm.glm01.wtd.step.p
# P = 0

# try glm without Order, ref id, study type
mamm.glm02.wtd <- glm(SR.mamm$Eff_Size_Wtd ~ SR.mamm$Treatment + SR.mamm$Forest_Type
+ SR.mamm$Yrs_Since_Tmt + SR.mamm$Silv_Fire + SR.mamm$Location + SR.mamm$Ctrl_Age,
data = SR.mamm)
summary(mamm.glm02.wtd)
mamm.glm02.wtd.step <- step(mamm.glm02.wtd)
summary(mamm.glm02.wtd.step)
# forest type, location, control age
mamm.glm02.wtd.step.r2 <- 1 - (mamm.glm02.wtd.step$deviance/mamm.glm02.wtd.step$null)
mamm.glm02.wtd.step.r2
# R2 = .09797343
mamm.glm02.wtd.step.p <- 1 - pchisq(mamm.glm02.wtd.step$null -
mamm.glm02.wtd.step$deviance, 4)
mamm.glm02.wtd.step.p

```

```

# P = 0

# try glm without Order, ref id, study type
mamm.glm03.wtd <- glm(SR.mamm$Eff_Size_Wtd ~ SR.mamm$Order + SR.mamm$Treatment +
SR.mamm$Forest_Type + SR.mamm$Yrs_Since_Tmt + SR.mamm$Silv_Fire + SR.mamm$Location +
SR.mamm$Ctrl_Age, data = SR.mamm)
summary(mamm.glm03.wtd)
mamm.glm03.wtd.step <- step(mamm.glm03.wtd)
summary(mamm.glm03.wtd.step)
# forest type, location, control age
mamm.glm03.wtd.step.r2 <- 1 - (mamm.glm03.wtd.step$deviance/mamm.glm03.wtd.step$null)
mamm.glm03.wtd.step.r2
# R2 = .09797343
mamm.glm03.wtd.step.p <- 1 - pchisq(mamm.glm03.wtd.step$null -
mamm.glm03.wtd.step$deviance, 4)
mamm.glm03.wtd.step.p
# P = 0

#####
# GLM for reptiles
SR.rept <- na.omit(SR.rept)
rept.glm01 <- glm(SR.rept$Eff_Size ~ ., data = SR.rept[, -c(11, 12, 13, 14, 15)])
summary(rept.glm01)
rept.glm01.step <- step(rept.glm01)
summary(rept.glm01.step)
# Order, treatment, ref id
rept.glm01.step.r2 <- 1 - (rept.glm01.step$deviance/rept.glm01.step$null)
rept.glm01.step.r2
# R2 = 0.341145
rept.glm01.step.p <- 1 - pchisq(rept.glm01.step$null - rept.glm01.step$deviance, 4)
rept.glm01.step.p
# P = 0

# try glm without Order, ref id, study type
rept.glm02 <- glm(SR.rept$Eff_Size ~ SR.rept$Treatment + SR.rept$Forest_Type +
SR.rept$Yrs_Since_Tmt + SR.rept$Ctrl_Age, data = SR.rept)
summary(rept.glm02)
rept.glm02.step <- step(rept.glm02)
summary(rept.glm02.step)
# treatment, forest type
rept.glm02.step.r2 <- 1 - (rept.glm02.step$deviance/rept.glm02.step$null)
rept.glm02.step.r2
# R2 = 0.2044481
rept.glm02.step.p <- 1 - pchisq(rept.glm02.step$null - rept.glm02.step$deviance, 3)
rept.glm02.step.p
# P = 0

# try glm without ref id, study type
rept.glm03 <- glm(SR.rept$Eff_Size ~ SR.rept$Order + SR.rept$Treatment +
SR.rept$Forest_Type + SR.rept$Yrs_Since_Tmt + SR.rept$Ctrl_Age, data = SR.rept)
summary(rept.glm03)
rept.glm03.step <- step(rept.glm03)
summary(rept.glm03.step)
# Order, treatment, forest type, Yrs since treatment

```

```

rept.glm03.step.r2 <- 1 - (rept.glm03.step$deviance/rept.glm03.step$null)
rept.glm03.step.r2
# R2 = 0.3011766
rept.glm03.step.p <- 1 - pchisq(rept.glm03.step$null - rept.glm03.step$deviance, 4)
rept.glm03.step.p
# P = 0

#####
# Weighted GLM for reptiles
rept.glm01.wtd <- glm(SR.rept$Eff_Size_Wtd ~ ., data = SR.rept[, -c(11, 12, 13, 14,
15)])
summary(rept.glm01.wtd)
rept.glm01.wtd.step <- step(rept.glm01.wtd)
summary(rept.glm01.wtd.step)
# Order, treatment, ref id
rept.glm01.wtd.step.r2 <- 1 - (rept.glm01.wtd.step$deviance/rept.glm01.wtd.step$null)
rept.glm01.wtd.step.r2
# R2 = 0.2815876
rept.glm01.wtd.step.p <- 1 - pchisq(rept.glm01.wtd.step$null -
rept.glm01.wtd.step$deviance, 4)
rept.glm01.wtd.step.p
# P = 0

# try glm without Order, ref id, study type
rept.glm02.wtd <- glm(SR.rept$Eff_Size_Wtd ~ SR.rept$Treatment + SR.rept$Forest_Type
+ SR.rept$Yrs_Since_Tmt + SR.rept$Silv_Fire + SR.rept$Location + SR.rept$Ctrl_Age,
data = SR.rept)
summary(rept.glm02.wtd)
rept.glm02.wtd.step <- step(rept.glm02.wtd)
summary(rept.glm02.wtd.step)
# treatment, forest type
rept.glm02.wtd.step.r2 <- 1 - (rept.glm02.wtd.step$deviance/rept.glm02.wtd.step$null)
rept.glm02.wtd.step.r2
# R2 = 0.1694398
rept.glm02.wtd.step.p <- 1 - pchisq(rept.glm02.wtd.step$null -
rept.glm02.wtd.step$deviance, 3)
rept.glm02.wtd.step.p
# P = 0

# try glm without Order, ref id, study type
rept.glm03.wtd <- glm(SR.rept$Eff_Size_Wtd ~ SR.rept$Order + SR.rept$Treatment +
SR.rept$Forest_Type + SR.rept$Yrs_Since_Tmt + SR.rept$Silv_Fire + SR.rept$Location +
SR.rept$Ctrl_Age, data = SR.rept)
summary(rept.glm03.wtd)
rept.glm03.wtd.step <- step(rept.glm03.wtd)
summary(rept.glm03.wtd.step)
# Order, treatment, forest type
rept.glm03.wtd.step.r2 <- 1 - (rept.glm03.wtd.step$deviance/rept.glm03.wtd.step$null)
rept.glm03.wtd.step.r2
# R2 = 0.235403
rept.glm03.wtd.step.p <- 1 - pchisq(rept.glm03.wtd.step$null -
rept.glm03.wtd.step$deviance, 4)
rept.glm03.wtd.step.p
# P = 0

```

```

#####
# Calculate mean effect sizes and confidence intervals
meanfun <- function(x, ind) {
  mean(x[ind])
}
#####
# Set minimum sample size
min.samp <- 10

# Overall Model
# for taxa
all.boot.taxa <- as.data.frame(c())
for (i in c(1:length(unique(SR.dat.trim$Taxa)))) {
  vars <- unique(SR.dat.trim$Taxa)[i]
  mean <- mean(SR.dat.trim$Eff_Size[SR.dat.trim$Taxa == vars])
  boot <- boot(SR.dat.trim$Eff_Size[SR.dat.trim$Taxa == vars], statistic = meanfun, R
= 1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.dat.trim$Eff_Size[SR.dat.trim$Taxa == vars])
  all.boot.taxa[i,1] <- as.character(vars)
  all.boot.taxa[i,2] <- mean
  all.boot.taxa[i,3] <- conf$normal[2]
  all.boot.taxa[i,4] <- conf$normal[3]
  all.boot.taxa[i,5] <- samp
  names(all.boot.taxa) <- c("var", "mean", "lower95", "upper95", "samp")
}
all.boot.taxa <- all.boot.taxa[all.boot.taxa$samp >= 10,]

# treatment
all.boot.tmnt <- as.data.frame(c())
for (i in c(1:length(unique(SR.dat.trim$Treatment)))) {
  vars <- unique(SR.dat.trim$Treatment)[i]
  mean <- mean(SR.dat.trim$Eff_Size[SR.dat.trim$Treatment == vars])
  boot <- boot(SR.dat.trim$Eff_Size[SR.dat.trim$Treatment == vars], statistic =
meanfun, R = 1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.dat.trim$Eff_Size[SR.dat.trim$Treatment == vars])
  all.boot.tmnt[i,1] <- as.character(vars)
  all.boot.tmnt[i,2] <- mean
  all.boot.tmnt[i,3] <- conf$normal[2]
  all.boot.tmnt[i,4] <- conf$normal[3]
  all.boot.tmnt[i,5] <- samp
  names(all.boot.tmnt) <- c("var", "mean", "lower95", "upper95", "samp")
}
all.boot.tmnt <- all.boot.tmnt[all.boot.tmnt$samp >= 10,]

# forest type
all.boot.fort <- as.data.frame(c())
for (i in c(1:length(unique(SR.dat.trim$Forest_Type)))) {
  vars <- unique(SR.dat.trim$Forest_Type)[i]
  mean <- mean(SR.dat.trim$Eff_Size[SR.dat.trim$Forest_Type == vars])
  boot <- boot(SR.dat.trim$Eff_Size[SR.dat.trim$Forest_Type == vars], statistic =
meanfun, R = 1000)

```

```

conf <- boot.ci(boot, conf = 0.95, type = "norm")
samp <- length(SR.dat.trim$Eff_Size[SR.dat.trim$Forest_Type == vars])
all.boot.fort[i,1] <- as.character(vars)
all.boot.fort[i,2] <- mean
all.boot.fort[i,3] <- conf$normal[2]
all.boot.fort[i,4] <- conf$normal[3]
all.boot.fort[i,5] <- samp
names(all.boot.fort) <- c("var", "mean", "lower95", "upper95", "samp")
}
all.boot.fort <- all.boot.fort[all.boot.fort$samp >= 10,]

# study type
all.boot.stdt <- as.data.frame(c())
for (i in c(1:length(unique(SR.dat.trim$Study_Type)))) {
  vars <- unique(SR.dat.trim$Study_Type)[i]
  mean <- mean(SR.dat.trim$Eff_Size[SR.dat.trim$Study_Type == vars])
  boot <- boot(SR.dat.trim$Eff_Size[SR.dat.trim$Study_Type == vars], statistic =
meanfun, R = 1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.dat.trim$Eff_Size[SR.dat.trim$Study_Type == vars])
  all.boot.stdt[i,1] <- as.character(vars)
  all.boot.stdt[i,2] <- mean
  all.boot.stdt[i,3] <- conf$normal[2]
  all.boot.stdt[i,4] <- conf$normal[3]
  all.boot.stdt[i,5] <- samp
  names(all.boot.stdt) <- c("var", "mean", "lower95", "upper95", "samp")
}
all.boot.stdt <- all.boot.stdt[all.boot.stdt$samp >= 10,]

# combine treatments
# 1-4 in one group
# 9-11, 15, 16 in one group
# other separate
combofun <- function(dat) {
  if(dat[6] %in% c("1", "2", "3", "4")) {
    return("burn")
  }
  else if (dat[6] %in% c("8", "9", "10", "11", "12", "15", "16")) {
    return("thinning")
  }
  else if (dat[6] == "13") {
    return("herb")
  }
  else if (dat[6] == "14") {
    return("thinburn")
  }
  else if (dat[6] == "0") {
    return("control")
  }
}
}
tcom <- apply(SR.dat.trim, 1, combofun)
SR.dat.temp <- cbind(SR.dat.trim, tcom)
SR.dat.temp$tcom <- as.factor(SR.dat.temp$tcom)

```

```

all.boot.tcom <- as.data.frame(c())
for (i in c(1:length(unique(SR.dat.temp$tcom)))) {
  vars <- unique(SR.dat.temp$tcom)[i]
  mean <- mean(SR.dat.temp$Eff_Size[SR.dat.temp$tcom == vars])
  boot <- boot(SR.dat.temp$Eff_Size[SR.dat.temp$tcom == vars], statistic = meanfun, R
= 1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.dat.temp$Eff_Size[SR.dat.temp$tcom == vars])
  all.boot.tcom[i,1] <- as.character(vars)
  all.boot.tcom[i,2] <- mean
  all.boot.tcom[i,3] <- conf$normal[2]
  all.boot.tcom[i,4] <- conf$normal[3]
  all.boot.tcom[i,5] <- samp
  names(all.boot.tcom) <- c("var", "mean", "lower95", "upper95", "samp")
}
all.boot.tcom <- all.boot.tcom[all.boot.tcom$samp >= 10,]

#####
# Amphibians
# Time since treatment
amph.lm.yrssinc <- lm(formula = SR.amph$Eff_Size ~ SR.amph$Yrs_Since_Tmt)
summary(amph.lm.yrssinc)
# R2 = 2.48e-05
# P = 0.9133

# Treatment
amph.boot.tmnt <- as.data.frame(c())
for (i in c(1:length(unique(SR.amph$Treatment)))) {
  vars <- unique(SR.amph$Treatment)[i]
  mean <- mean(SR.amph$Eff_Size[SR.amph$Treatment == vars])
  boot <- boot(SR.amph$Eff_Size[SR.amph$Treatment == vars], statistic = meanfun, R =
1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.amph$Eff_Size[SR.amph$Treatment == vars])
  amph.boot.tmnt[i,1] <- as.character(vars)
  amph.boot.tmnt[i,2] <- mean
  amph.boot.tmnt[i,3] <- conf$normal[2]
  amph.boot.tmnt[i,4] <- conf$normal[3]
  amph.boot.tmnt[i,5] <- samp
  names(amph.boot.tmnt) <- c("var", "mean", "lower95", "upper95", "samp")
}
amph.boot.tmnt <- amph.boot.tmnt[amph.boot.tmnt$samp >= 10,]

#####
# Birds
# Order
bird.boot.ordr <- as.data.frame(c())
for (i in c(1:length(unique(SR.bird$Order)))) {
  vars <- unique(SR.bird$Order)[i]
  mean <- mean(SR.bird$Eff_Size[SR.bird$Order == vars])
  boot <- boot(SR.bird$Eff_Size[SR.bird$Order == vars], statistic = meanfun, R =
1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.bird$Eff_Size[SR.bird$Order == vars])

```

```

bird.boot.ordr[i,1] <- as.character(vars)
bird.boot.ordr[i,2] <- mean
bird.boot.ordr[i,3] <- conf$normal[2]
bird.boot.ordr[i,4] <- conf$normal[3]
bird.boot.ordr[i,5] <- samp
names(bird.boot.ordr) <- c("var", "mean", "lower95", "upper95", "samp")
}
bird.boot.ordr <- bird.boot.ordr[bird.boot.ordr$samp >= 10,]

# Forest Type
bird.boot.fort <- as.data.frame(c())
for (i in c(1:length(unique(SR.bird$Forest_Type)))) {
  vars <- unique(SR.bird$Forest_Type)[i]
  mean <- mean(SR.bird$Eff_Size[SR.bird$Forest_Type == vars])
  boot <- boot(SR.bird$Eff_Size[SR.bird$Forest_Type == vars], statistic = meanfun, R
= 1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.bird$Eff_Size[SR.bird$Forest_Type == vars])
  bird.boot.fort[i,1] <- as.character(vars)
  bird.boot.fort[i,2] <- mean
  bird.boot.fort[i,3] <- conf$normal[2]
  bird.boot.fort[i,4] <- conf$normal[3]
  bird.boot.fort[i,5] <- samp
  names(bird.boot.fort) <- c("var", "mean", "lower95", "upper95", "samp")
}
bird.boot.fort <- bird.boot.fort[bird.boot.fort$samp >= 10,]

# Control Age
bird.lm.ctrlage <- lm(formula = SR.bird$Eff_Size ~ SR.bird$Ctrl_Age)
summary(bird.lm.ctrlage)
# R2 = 0.03165
# P = 1.316e-06

#####
# Invertebrates
# Treatment
inv.boot.tmnt <- as.data.frame(c())
for (i in c(1:length(unique(SR.invnt$Treatment)))) {
  vars <- unique(SR.invnt$Treatment)[i]
  mean <- mean(SR.invnt$Eff_Size[SR.invnt$Treatment == vars])
  boot <- boot(SR.invnt$Eff_Size[SR.invnt$Treatment == vars], statistic = meanfun, R =
1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.invnt$Eff_Size[SR.invnt$Treatment == vars])
  inv.boot.tmnt[i,1] <- as.character(vars)
  inv.boot.tmnt[i,2] <- mean
  inv.boot.tmnt[i,3] <- conf$normal[2]
  inv.boot.tmnt[i,4] <- conf$normal[3]
  inv.boot.tmnt[i,5] <- samp
  names(inv.boot.tmnt) <- c("var", "mean", "lower95", "upper95", "samp")
}
inv.boot.tmnt <- inv.boot.tmnt[inv.boot.tmnt$samp >= 10,]

# Control Age

```

```

inv.t.lm.ctrlage <- lm(formula = SR.inv.t$Eff_Size ~ SR.inv.t$Ctrl_Age)
summary(inv.t.lm.ctrlage)
# R2 = 0.0432
# P = 2.25e-06

#####
# Mammals
# Forest Type
mamm.boot.fort <- as.data.frame(c())
for (i in c(1:length(unique(SR.mamm$Forest_Type)))) {
  vars <- unique(SR.mamm$Forest_Type)[i]
  mean <- mean(SR.mamm$Eff_Size[SR.mamm$Forest_Type == vars])
  boot <- boot(SR.mamm$Eff_Size[SR.mamm$Forest_Type == vars], statistic = meanfun, R
= 1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.mamm$Eff_Size[SR.mamm$Forest_Type == vars])
  mamm.boot.fort[i,1] <- as.character(vars)
  mamm.boot.fort[i,2] <- mean
  mamm.boot.fort[i,3] <- conf$normal[2]
  mamm.boot.fort[i,4] <- conf$normal[3]
  mamm.boot.fort[i,5] <- samp
  names(mamm.boot.fort) <- c("var", "mean", "lower95", "upper95", "samp")
}
mamm.boot.fort <- mamm.boot.fort[mamm.boot.fort$samp >= 10,]

#####
# Reptiles
# Order
# some salamanders need to be moved out of this category
rept.boot.ordr <- as.data.frame(c())
for (i in c(1:length(unique(SR.rept$Order)))) {
  vars <- unique(SR.rept$Order)[i]
  mean <- mean(SR.rept$Eff_Size[SR.rept$Order == vars])
  boot <- boot(SR.rept$Eff_Size[SR.rept$Order == vars], statistic = meanfun, R =
1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.rept$Eff_Size[SR.rept$Order == vars])
  rept.boot.ordr[i,1] <- as.character(vars)
  rept.boot.ordr[i,2] <- mean
  rept.boot.ordr[i,3] <- conf$normal[2]
  rept.boot.ordr[i,4] <- conf$normal[3]
  rept.boot.ordr[i,5] <- samp
  names(rept.boot.ordr) <- c("var", "mean", "lower95", "upper95", "samp")
}
rept.boot.ordr <- rept.boot.ordr[rept.boot.ordr$samp >= 10,]

# Treatment
rept.boot.tmnt <- as.data.frame(c())
for (i in c(1:length(unique(SR.rept$Treatment)))) {
  vars <- unique(SR.rept$Treatment)[i]
  mean <- mean(SR.rept$Eff_Size[SR.rept$Treatment == vars])
  boot <- boot(SR.rept$Eff_Size[SR.rept$Treatment == vars], statistic = meanfun, R =
1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")

```



```

samp <- length(SR.rept$Eff_Size[SR.rept$Treatment == vars])
rept.boot.tmnt[i,1] <- as.character(vars)
rept.boot.tmnt[i,2] <- mean
rept.boot.tmnt[i,3] <- conf$normal[2]
rept.boot.tmnt[i,4] <- conf$normal[3]
rept.boot.tmnt[i,5] <- samp
names(rept.boot.tmnt) <- c("var", "mean", "lower95", "upper95", "samp")
}
rept.boot.tmnt <- rept.boot.tmnt[rept.boot.tmnt$samp >= 10,]

# Forest_Type
rept.boot.fort <- as.data.frame(c())
for (i in c(1:length(unique(SR.rept$Forest_Type)))) {
  vars <- unique(SR.rept$Forest_Type)[i]
  mean <- mean(SR.rept$Eff_Size[SR.rept$Forest_Type == vars])
  boot <- boot(SR.rept$Eff_Size[SR.rept$Forest_Type == vars], statistic = meanfun, R
= 1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.rept$Eff_Size[SR.rept$Forest_Type == vars])
  rept.boot.fort[i,1] <- as.character(vars)
  rept.boot.fort[i,2] <- mean
  rept.boot.fort[i,3] <- conf$normal[2]
  rept.boot.fort[i,4] <- conf$normal[3]
  rept.boot.fort[i,5] <- samp
  names(rept.boot.fort) <- c("var", "mean", "lower95", "upper95", "samp")
}
rept.boot.fort <- rept.boot.fort[rept.boot.fort$samp >= 10,]

# Years since treatment
rept.lm.yrssinc <- lm(formula = SR.rept$Eff_Size ~ SR.rept$Yrs_Since_Tmt)
summary(rept.lm.yrssinc)
# R2 = 0.00178
# P = 0.5412

#####
# Plots
wt <- 3.0

#####
# All Taxa
# Taxa
ggplot(all.boot.taxa, aes(x = var, y = mean)) +
  labs(x = "Taxon", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = all.boot.taxa$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_all_taxa.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Treatment

```

```

ggplot(all.boot.tmnt, aes(x = var, y = mean)) +
  labs(x = "Treatment", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  scale_x_discrete(limits=c("0", "1", "2", "3", "4", "8", "9", "10", "11", "13",
"14", "15"), labels=c("None", "Low Intensity Fire", "Medium Intensity Fire", "High
Intensity Fire", "Undefined Intensity Fire", "Clearcut", "Shelterwood Cut",
"Leavetree Cut", "Group Selection Cut", "Herbicide", "Thin and Burn", "Thinning,
other")) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = all.boot.tmnt$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_all_tmnt.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Forest Type
ggplot(all.boot.fort, aes(x = var, y = mean)) +
  labs(x = "Forest Type", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  scale_x_discrete(labels=c("Oak Dominated", "Pine Dominated", "Pine-Oak Mix", "Mixed
Mesophytic", "Riparian", "Oak-Hickory")) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = all.boot.fort$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_all_fort.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Study Type
ggplot(all.boot.stdt, aes(x = var, y = mean)) +
  labs(x = "Study Type", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  scale_x_discrete(labels=c("Treatment-Control", "Before-After", "Age Class
Comparison")) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = all.boot.stdt$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_all_stdt.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Combined Treatments
ggplot(all.boot.tcom, aes(x = var, y = mean)) +
  labs(x = "Treatment (combined)", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  scale_x_discrete(limits=c("control", "burn", "thinning", "herb", "thinburn"),
labels=c("None", "Burning", "Thinning", "Herbicide", "Thin and Burn")) +

```

```

    geom_point(size=2) +
    geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
    geom_hline(yintercept = 0, lty=3) +
    geom_text(aes(label = all.boot.tcom$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_all_tcom.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

#####
# Amphibians
# Time since treatment
ggplot(SR.amph, aes(x = Yrs_Since_Tmt, y = Eff_Size)) +
  labs(x = "Years Since Treatment", y = "Effect Size") +
  theme_bw() +
  geom_point(size=0.7) +
  geom_smooth(method=lm, se=FALSE, fullrange=TRUE)
ggsave("SR_HR_amph_yrssl.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Treatment
ggplot(amph.boot.tmnt, aes(x = var, y = mean)) +
  labs(x = "Treatment", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  scale_x_discrete(limits=c("0", "2", "3", "4", "8", "9", "11", "13"),
labels=c("None", "Medium Intensity Fire", "High Intensity Fire", "Undefined Intensity
Fire", "Clearcut", "Shelterwood Cut", "Group Selection Cut", "Herbicide")) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = amph.boot.tmnt$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_amph_tmnt.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

#####
# Birds
# Order
ggplot(bird.boot.ordr, aes(x = var, y = mean)) +
  labs(x = "Order", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  scale_x_discrete(labels=c("Accipitriformes", "Apodiformes", "Aves (Unspecified)",
"Cathartiformes", "Galliformes", "Passeriformes", "Piciformes")) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = bird.boot.ordr$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_bird_ordr.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Forest Type
ggplot(bird.boot.fort, aes(x = var, y = mean)) +

```

```

labs(x = "Forest Type", y = "Mean Effect Size") +
theme_bw() +
theme(axis.text.x = element_text(hjust = 1, angle=45)) +
scale_x_discrete(labels=c("Oak Dominated", "Pine-Oak Mix", "Mixed Mesophytic",
"Oak-Hickory")) +
geom_point(size=2) +
geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
geom_hline(yintercept = 0, lty=3) +
geom_text(aes(label = bird.boot.fort$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_bird_fort.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

```

```

# Control Age
ggplot(SR.bird, aes(x = Ctrl_Age, y = Eff_Size)) +
labs(x = "Control Forest Age", y = "Effect Size") +
theme_bw() +
geom_point(size=0.7) +
geom_smooth(method=lm, se=FALSE, fullrange=TRUE)
ggsave("SR_HR_bird_ctra.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

```

#####

```

# Invertebrates
ggplot(invt.boot.tmnt, aes(x = var, y = mean)) +
labs(x = "Treatment", y = "Mean Effect Size") +
theme_bw() +
theme(axis.text.x = element_text(hjust = 1, angle=45)) +
scale_x_discrete(limits=c("1", "3", "4", "8", "14", "15"), labels = c("Low
Intensity Fire", "High Intensity Fire", "Undefined Intensity Fire", "Clearcut", "Thin
and Burn", "Thinning, other")) +
geom_point(size=2) +
geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
geom_hline(yintercept = 0, lty=3) +
geom_text(aes(label = invt.boot.tmnt$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_invt_tmnt.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

```

```

# Control Age
ggplot(SR.invt, aes(x = Ctrl_Age, y = Eff_Size)) +
labs(x = "Control Forest Age", y = "Effect Size") +
theme_bw() +
geom_point(size=0.7) +
geom_smooth(method=lm, se=FALSE, fullrange=TRUE)
ggsave("SR_HR_invt_ctra.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

```

#####

```

# Mammals
# Forest Type
ggplot(mamm.boot.fort, aes(x = var, y = mean)) +
labs(x = "Forest Type", y = "Mean Effect Size") +
theme_bw() +

```

```

    theme(axis.text.x = element_text(hjust = 1, angle=45)) +
    scale_x_discrete(labels=c("Oak Dominated", "Pine Dominated", "Pine-Oak Mix", "Mixed
Mesophytic", "Riparian", "Oak-Hickory")) +
    geom_point(size=2) +
    geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
    geom_hline(yintercept = 0, lty=3) +
    geom_text(aes(label = mamm.boot.fort$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_mamm_fort.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

#####
# Reptiles
# Order
ggplot(rept.boot.ordr, aes(x = var, y = mean)) +
  labs(x = "Order", y = "Mean Effect Size") +
  theme_bw() +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = rept.boot.ordr$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_rept_ordr.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Treatment
ggplot(rept.boot.tmnt, aes(x = var, y = mean)) +
  labs(x = "Treatment", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  scale_x_discrete(limits=c("0", "4", "8", "9", "11", "13"), labels = c("None",
"Undefined Intensity Fire", "Clearcut", "Shelterwood Cut", "Group Selection Cut",
"Herbicide")) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = rept.boot.tmnt$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_rept_tmnt.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Forest Type
ggplot(rept.boot.fort, aes(x = var, y = mean)) +
  labs(x = "Forest Type", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  scale_x_discrete(labels=c("Oak Dominated", "Pine Dominated", "Mixed Mesophytic",
"Oak-Hickory")) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = rept.boot.fort$samp, hjust = -0.35), size = wt, show.legend =
FALSE)

```

```

ggsave("SR_HR_rept_fort.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Time Since Treatment
ggplot(SR.rept, aes(x = Yrs_Since_Tmt, y = Eff_Size)) +
  labs(x = "Years Since Treatment", y = "Effect Size") +
  theme_bw() +
  geom_point(size=0.7) +
  geom_smooth(method=lm, se=FALSE, fullrange=TRUE)
ggsave("SR_HR_rept_yrss.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

#####
# Additional Analysis for Passeriformes
# Read in data
# Rename columns
SR.pass <- read.csv("SR_data_Pass_20160319.csv", header = T)
SR.pass.header <- c("Spp", "Hab", "Mig", "Hab_Mig", "Common_Name", "Taxa",
"Location", "Site", "Forest_Type", "Forest_descr", "Silv_Fire", "Treatment",
"Treatment_descr", "Div_Abund",
"Div_Metric", "Study_Type", "Tmt_Yr_First",
"Tmt_Yr_Last", "Yrs_Since_Tmt", "Return_Int", "Samp_Meth", "Reps", "Site_Visits",
"Tmt_Area_1",
"Tmt_Area_All", "Ctrl_Area", "Ctrl_Age", "Ctrl_descr", "Total_Area",
"Exp_Mean", "Ctrl_Mean", "Eff_Size", "Eff_Size_Wtd", "Ref", "Ref_ID",
"Extractor")
names(SR.pass) <- SR.pass.header

# Force correct data format
SR.pass$Spp <- as.factor(SR.pass$Spp)
SR.pass$Hab <- as.factor(SR.pass$Hab)
SR.pass$Mig <- as.factor(SR.pass$Mig)
SR.pass$Hab_Mig <- as.factor(SR.pass$Hab_Mig)
SR.pass$Common_Name <- as.character(SR.pass$Common_Name)
SR.pass$Site <- as.character(SR.pass$Site)
SR.pass$Forest_Type <- as.factor(SR.pass$Forest_Type)
SR.pass$Forest_descr <- as.character(SR.pass$Forest_descr)
SR.pass$Silv_Fire <- as.factor(SR.pass$Silv_Fire)
SR.pass$Treatment <- as.factor(SR.pass$Treatment)
SR.pass$Treatment_descr <- as.character(SR.pass$Treatment_descr)
SR.pass$Study_Type <- as.factor(SR.pass$Study_Type)
SR.pass$Tmt_Yr_First <- as.character(SR.pass$Tmt_Yr_First)
SR.pass$Tmt_Yr_Last <- as.character(SR.pass$Tmt_Yr_Last)
SR.pass$Return_Int <- as.character(SR.pass$Return_Int)
SR.pass$Samp_Meth <- as.character(SR.pass$Samp_Meth)
SR.pass$Site_Visits <- as.character(SR.pass$Site_Visits)
SR.pass$Tmt_Area_1 <- as.character(SR.pass$Tmt_Area_1)
SR.pass$Tmt_Area_All <- as.character(SR.pass$Tmt_Area_All)
SR.pass$Ctrl_Area <- as.character(SR.pass$Ctrl_Area)
SR.pass$Ctrl_descr <- as.character(SR.pass$Ctrl_descr)
SR.pass$Total_Area <- as.character(SR.pass$Total_Area)
SR.pass$Exp_Mean <- as.numeric(as.character(SR.pass$Exp_Mean))
SR.pass$Ctrl_Mean <- as.numeric(as.character(SR.pass$Ctrl_Mean))
SR.pass$Ref <- as.character(SR.pass$Ref)

```

```

SR.pass$Ref_ID <- as.factor(SR.pass$Ref_ID)

# Create column for reference year
substrRight <- function(x, n){
  substr(x, nchar(x)-n+1, nchar(x))
}

Ref_Yr <- c()
for(i in 1:nrow(SR.pass)) {
  Ref_Yr[i] <- substrRight(SR.pass$Ref[i], 4)
}
SR.pass$Ref_Yr <- Ref_Yr
SR.pass$Ref_Yr <- as.numeric(SR.pass$Ref_Yr)

# Correct Columns where control or experimental mean is 0
SR.pass$Exp_Mean[SR.pass$Exp_Mean == 0] <- 0.001
SR.pass$Ctrl_Mean[SR.pass$Ctrl_Mean == 0] <- 0.001

# Calculate effect sizes (weighted & unweighted)
SR.pass$Eff_Size <- log(SR.pass$Exp_Mean/SR.pass$Ctrl_Mean)
SR.pass$Eff_Size_Wtd <- log(SR.pass$Reps + 1)*log(SR.pass$Exp_Mean/SR.pass$Ctrl_Mean)

# Trim data sheet
SR.pass.trim <- SR.pass[, -c(1, 5, 6, 8, 10, 13, 14, 15, 17, 18, 20, 21, 23, 24, 25,
26, 28, 29)]

#####
# GLM for all Passerines
pass.glm01 <- glm(SR.pass.trim$Eff_Size ~ ., data = SR.pass.trim)
summary(pass.glm01)

pass.glm02 <- glm(SR.pass.trim$Eff_Size ~ SR.pass.trim$Hab + SR.pass.trim$Mig +
SR.pass.trim$Treatment + SR.pass.trim$Forest_Type + SR.pass.trim$Yrs_Since_Tmt +
SR.pass.trim$Study_Type, data = SR.pass.trim)
summary(pass.glm02)
pass.glm02.step <- step(pass.glm02)
summary(pass.glm02.step)
# Habitat, treatment, forest type
pass.glm02.r2 <- 1 - (pass.glm02.step$deviance/pass.glm02.step$null)
pass.glm02.r2
# R2 = 0.1342779
pass.glm02.p <- 1 - pchisq(pass.glm02.step$null - pass.glm02.step$deviance, 6)
pass.glm02.p
# p = 0

#####
# Bootstrap confidence intervals for Passerines
# Habitat
pass.boot.habt <- as.data.frame(c())
for (i in c(1:length(unique(SR.pass.trim$Hab)))) {
  vars <- unique(SR.pass.trim$Hab)[i]
  mean <- mean(SR.pass.trim$Eff_Size[SR.pass.trim$Hab == vars])
  boot <- boot(SR.pass.trim$Eff_Size[SR.pass.trim$Hab == vars], statistic = meanfun,
R = 1000)

```

```

conf <- boot.ci(boot, conf = 0.95, type = "norm")
samp <- length(SR.pass.trim$Eff_Size[SR.pass.trim$Hab == vars])
pass.boot.habt[i,1] <- as.character(vars)
pass.boot.habt[i,2] <- mean
pass.boot.habt[i,3] <- conf$normal[2]
pass.boot.habt[i,4] <- conf$normal[3]
pass.boot.habt[i,5] <- samp
names(pass.boot.habt) <- c("var", "mean", "lower95", "upper95", "samp")
}
pass.boot.habt <- pass.boot.habt[pass.boot.habt$samp >= 10,]

# Treatment
pass.boot.tmnt <- as.data.frame(c())
for (i in c(1:length(unique(SR.pass.trim$Treatment)))) {
  vars <- unique(SR.pass.trim$Treatment)[i]
  mean <- mean(SR.pass.trim$Eff_Size[SR.pass.trim$Treatment == vars])
  boot <- boot(SR.pass.trim$Eff_Size[SR.pass.trim$Treatment == vars], statistic =
meanfun, R = 1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.pass.trim$Eff_Size[SR.pass.trim$Treatment == vars])
  pass.boot.tmnt[i,1] <- as.character(vars)
  pass.boot.tmnt[i,2] <- mean
  pass.boot.tmnt[i,3] <- conf$normal[2]
  pass.boot.tmnt[i,4] <- conf$normal[3]
  pass.boot.tmnt[i,5] <- samp
  names(pass.boot.tmnt) <- c("var", "mean", "lower95", "upper95", "samp")
}
pass.boot.tmnt <- pass.boot.tmnt[pass.boot.tmnt$samp >= 10,]

# Forest_Type
pass.boot.fort <- as.data.frame(c())
for (i in c(1:length(unique(SR.pass.trim$Forest_Type)))) {
  vars <- unique(SR.pass.trim$Forest_Type)[i]
  mean <- mean(SR.pass.trim$Eff_Size[SR.pass.trim$Forest_Type == vars])
  boot <- boot(SR.pass.trim$Eff_Size[SR.pass.trim$Forest_Type == vars], statistic =
meanfun, R = 1000)
  conf <- boot.ci(boot, conf = 0.95, type = "norm")
  samp <- length(SR.pass.trim$Eff_Size[SR.pass.trim$Forest_Type == vars])
  pass.boot.fort[i,1] <- as.character(vars)
  pass.boot.fort[i,2] <- mean
  pass.boot.fort[i,3] <- conf$normal[2]
  pass.boot.fort[i,4] <- conf$normal[3]
  pass.boot.fort[i,5] <- samp
  names(pass.boot.fort) <- c("var", "mean", "lower95", "upper95", "samp")
}
pass.boot.fort <- pass.boot.fort[pass.boot.fort$samp >= 10,]

#####
# Plots for Passerines
# Habitat
ggplot(pass.boot.habt, aes(x = var, y = mean)) +
  labs(x = "Habitat", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +

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    scale_x_discrete(limits=c("FI", "FIE", "FES"), labels = c("Forest Interior",
"Forest Interior and Edge", "Forest Edge, Shrub, Field Edge")) +
    geom_point(size=2) +
    geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
    geom_hline(yintercept = 0, lty=3) +
    geom_text(aes(label = pass.boot.habt$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_pass_habt.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Treatment
ggplot(pass.boot.tmnt, aes(x = var, y = mean)) +
  labs(x = "Treatment", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  scale_x_discrete(limits=c("0", "1", "2", "3", "8", "9", "10", "15"), labels =
c("None", "Low Intensity Fire", "Medium Intensity Fire", "High Intensity Fire",
"Clearcut", "Shelterwood Cut", "Leavetree Cut", "Thinning, other")) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = pass.boot.tmnt$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_pass_tmnt.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

# Forest Type
ggplot(pass.boot.fort, aes(x = var, y = mean)) +
  labs(x = "Forest Type", y = "Mean Effect Size") +
  theme_bw() +
  theme(axis.text.x = element_text(hjust = 1, angle=45)) +
  scale_x_discrete(limits=c("1", "3", "4", "6"), labels=c("Oak Dominated", "Pine Oak
Mix", "Mixed Mesophytic", "Oak-Hickory")) +
  geom_point(size=2) +
  geom_errorbar(aes(ymin=lower95, ymax=upper95), width=.1) +
  geom_hline(yintercept = 0, lty=3) +
  geom_text(aes(label = pass.boot.fort$samp, hjust = -0.35), size = wt, show.legend =
FALSE)
ggsave("SR_HR_pass_fort.png", scale = 1.2, width = 4, height = 3, units = "in", dpi =
300)

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