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Past, Current, and Future Potential Distributions of Red Spruce and Fraser Fir Forests in the Southern Appalachians: Interpreting Possible Impacts of Climate Change

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Past, Current, and Future Potential Distributions of Red Spruce and Fraser Fir Forests in the Southern Appalachians: Interpreting Possible Impacts of Climate Change

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by

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ABSTRACT

Past, Current, and Future Potential Distributions of Red Spruce and Fraser Fir Forests in the Southern Appalachians: Interpreting Possible Impacts of Climate Change

by

Danika Leigh Mosher

Spruce-Fir forests are relicts from the Pleistocene and can only be found within the Southern Appalachians. Analyzing the relationships between species distribution, climatic parameters, topography, and biotic interactions through ecological niche modeling creates prediction maps for conservation efforts. Maxent, Boosted Regression, and Random Forest were utilized to compare which model and variable combinations best approximate the unique mountain forest environment. Maxent with a bias file produced optimal results and was used to examine distributional changes that may occur in the future and how these changes compare to paleo-environmental distributions. Fraser fir has shown evidence of being influenced by changing climates based on historical data and in future predictions. These findings show areas of decline in 2050 and 2070. When combined with weather, climate, genetics, and ecological studies, this is a useful tool for resource allocation to areas that are predicted to be resilient in the face of climate change.

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CHAPTER 1. INTRODUCTION

Sky Islands

Climate, topography, and geography together drive interactions that heavily influence the patterns and long-term trends of species distributions and biodiversity (Badgley et al. 2017; Gundogdu 2017). Previous research examined fossil records in relation to changes in climate to deduce the connection between climate change, composition of communities, and extinction of species (Peters 1990). Habitats that reside in high altitude and latitude locations are one of the most responsive ecosystems to climate change (Aitken et al. 2008). High altitude environments are especially sensitive and vulnerable to changes in climate, which may cause usually small and fragmented suitable environments to disappear completely (Potter et al. 2010). In addition to geographic restraints, high altitude forests heavily rely on precipitation to shape their biomes (Palmate et al. 2014). Factors such as annual precipitation, precipitation during the warmest month, or even coldest month, may be altered due to climate change. When combined with geographic constraints, it is detrimental to forest ecosystems such as the Southern Appalachian Spruce-Fir forest.

The Southern Appalachian Mountains (SAM) are considered to be the only temperate rainforest in the United States east of the Mississippi River (Aldy et al. 1999). The Spruce Fir (SF) forest occurs in Tennessee, Virginia, and primarily North Carolina on seven of the ten mountain tops that are higher than 1,680 m in elevation (Cogbill and White 1991; Aldy et al. 1999; Hayes et al. 2006). The SF name is derived from red spruce (*Picea rubens*) and Fraser fir (*Abies fraseri*). Due to the limited habitat space, this ecosystem is considered refugial and harbors numerous disjunct, isolated, and endangered species (Berry and Smith 2012). There are 17 species of plants and animals and 20 species of invertebrates that are endemic to these forests

(Jenkins et al. 2002; NC Wildlife). The Great Smoky Mountains in particular contain upper and lower limit environments for 125 species (Shanks 1954). Rare species include the moss spider (*Microhexura montivaga*), ground beetles (Coleoptera: Carabidae), Weller's salamander (*Plethodon welleri*), Carolina northern flying squirrel (*Glaucomys sabrinus*), Virginia big-eared bat (*Plecotus townsendii*), northern saw-whet owl (*Aegolius acadicus*), blue ridge goldenrod (*Solidago spithamaea*), and Heller's blazing star (*Liatris helleri*) with the rarest being the rock gnome lichen (*Gymnoderma lineare*) (Evans et al. 2013; Evans et al. 2014; Ford et al. 2015; USDA; NC Wildlife).

The geographic distribution of this ecosystem is primarily explained by climate parameters. Fog immersion, which results in low cloud ceilings, not only provides ample precipitation, but also regulates temperatures by reducing radiative forcing (Richardson et al. 2003; Berry et al. 2013). Average levels of cloud bases in this region are associated with the distribution and health of SF forests, especially since these habitats are immersed in clouds 70 percent of the year (Berry et al. 2013; Cory et al. 2017). Decreased evapotranspiration and increased precipitation with altitude in conjunction with moist southwesterly winds aid in mean annual precipitation ranges from 127 to 200 cm (Shanks 1954, Wiser et al. 1996). The majority of precipitation falls during the summer and winter months with wind speeds around 18.5 km/hr to 33 km/hr, creating harsh winters and limiting what species can survive at the highest elevations (Wiser et al. 1996). Mean July temperatures differ based on elevation with 17°C at 1,618 m and 15°C at 1,990 m, with the highest tolerable temperature at 22°C (Cogbill and White 1991; Wiser et al. 1996). With these specific parameters, the sensitivity of these species to climate is observed in ecotones, the transitional treeline between SF forests and deciduous hardwood forests (Peteet 2000). Southern-facing slope ecotones are higher in elevation due to historic logging and additional radiative forcing compared to northern slopes (Busing et al. 1993; Hayes et al. 2006; White et al. 2014).

Previous Impacts

Human disturbance is the primary driver altering the SF ecosystem dating back to 19th century extensive logging that increased the occurrence of fires (Hayes et al. 2006; Berry et al. 2013; Mitchell et al. 2014; White et al. 2014; NC Wildlife). In the 1950s, balsam woolly adelgid (*Adelges piceae*) was introduced to central Virginia and spread to the Appalachians, killing between 40 and 90 percent of mature Fraser fir (Berry and Smith 2012, Cory et al. 2017; Kaylor et al. 2017). The three fates a species encounters when faced with stress is adaptation, migration, or extirpation (Aitken et al. 2008). Due to the longevity of trees and times between generations that can span from 100 to 1,000 years, adaptation and evolution occurs more slowly than the rate of current climate change (Petit et al. 2008; Potter et al. 2010;). The SF forests are boreal relicts from the late Pleistocene (~22,000 years ago) during the last glacial maximum and are typical of temperate and higher latitude populations that inhabited this region during this time (Hampe and Jump 2011; Berry et al. 2013). As temperatures warmed, migration occurred either altitudinally or poleward, eventually separating balsam fir (*Abies balsamea*) and the southern extreme extent that formed into Fraser fir (Potter et al. 2009; Hampe and Jump 2011). Isolation of these SAM ‘sky islands’ has been exacerbated by fragmentation, which can aid in species extinction by preventing distribution changes (Pitelka et al. 1997; Thomas 2011). Even if these habitats could migrate without the threat of inhospitable landscapes due to fragmentation and differences in climate, migration rates would need to be 1 km per year under twice the amount of carbon dioxide climate forcing they have experienced in the past, which is the fastest that has been observed for trees in general (Pitelka et al. 1997; Aitken et al. 2008). Even though the required migration rate is equivalent to extreme past rates, the projected change for climate is a higher rate than observed, thus it will be difficult for trees in particular to respond effectively (Peters 1990). This type of isolation makes SF forests more susceptible to catastrophic events and ultimately one of the most threatened ecosystems (Hayes et al. 2006; NC Wildlife).

Threat of Climate Change

Southern Appalachian Spruce-Fir forests are listed as the second-most endangered ecosystem within the United States and this ecosystem is listed as a priority habitat in the 2005 Wildlife Action Plan (NC Wildlife). If certain tolerance thresholds are passed for this habitat, such as reduced cloud cover or higher average temperatures in July, then the replacement of native species with exotic invasives will become more likely (Delcourt and Delcourt 1998). Red spruce and especially Fraser fir are considered foundation, or keystone, species. There are many species that rely on these trees to regulate their habitat and generate stability, such as nutrient and water availability (Hayes et al. 2006; Aitken et al. 2008; White et al. 2014). Fraser fir is better suited for the harsh winters and thrives on natural disturbances such as ice and high winds (White et al. 1985; Busing et al. 1993; Busing and Pauley 1994; USDA). Red spruce relies on Fraser fir for protection and it has been observed that the death of Fraser fir not only influences the magnitude of spruce deaths, but also impacts the community composition and understory regeneration (Busing et al. 1993; Busing and Pauley 1994; Busing 2004; NC Wildlife). With cloud ceilings rising and cloud immersion being less frequent with warmer temperatures, it is only natural for the baseline of this ecosystem to follow the base of clouds (Berry et al. 2013). Previous research examined the extinction of keystone mutualists, like Fraser fir, and suggested that on average 10 to 30 other species relied on them (Ehlrich and Mooney 1983).

Despite the morbid outlook for this endangered habitat, ecological niche models (ENM) help with understanding how a species may react to climate change and can be used to inform mitigation and conservation planning (Guisan and Thuiller 2005). ENM primarily evaluates the relationship between the presence of a species and its environment based on geographic and climate information to form hypothetical fundamental niche boundaries (Guisan and Thuiller 2005; Araújo and Guisan 2006; Naimi et al. 2011). These models can confirm field observations, such as SF requiring ample precipitation and low average temperatures, and also point out gaps in understanding parameter requirements that are important (Busing and Mailly 2004; Bastow et al. 2005). Understanding the biological process of certain species is still necessary to evaluate the effectiveness of a model and understand what is important versus what is noise or repetitive. This is particularly pertinent to rare species, such as Fraser fir, to know if the model is over or under predicting based on the variable inputs (Delcourt and Delcourt 1998; Wiser et al. 1998; Arújo and Guisan 2006; Merow et al. 2014; Breiner et al. 2015). For example, the explanatory variables for extreme areas, like those representatives of alpine or arctic environments, will more likely be climatic rather than topographic (Arújo and Guisan 2006).

Modeling for Change

There are multiple types of models that can help answer these specific types of questions, but the majority of them are mechanistic and derive maps based on statistics and species physiology (Guisan and Thuiller 2005; Hijmans and Graham 2006; Aitken et al. 2008; Merow et al. 2014). Some of the different types include: 1) generalized linear and additive models (e.g., GLM, GAM), 2) maximum entropy (Maxent), or 3) decision tree-based models (e.g., random forest (RF), boosted regression (BR)). These models are often grouped as artificial intelligence or machine learning approaches where they ‘learn’ the patterns of the presence of a species in correlation with physiological or behavioral characteristics that are associated with climatic and geographic variables, generating a prediction on where a species may exist, or at least where its fundamental niche occurs (i.e., maximum suitable (Guisan and Thuiller 2005; Aitken et al. 2008). The outputs show which variables have the most explanatory power and percent contribution to the model, which not only help with verification on known field observations, but aid in identifying possible gaps in ecological theories (Elith et al. 2008; He et al. 2015; Yuan et al. 2015).

Analyzing the relationship between a species and its environment is complex and complicated, as there may be many influential direct and indirect variables (Griesbauer et al. 2011). The primary limitation of ENMs is the lack of biological inclusion, such as interspecific and intraspecific competition, mutualism, predation, symbiosis, commensalism, and parasitism (Guisan and Thuiller 2005; Araújo and Guisan 2006; Hijmans and Graham 2006; Bahn and McGill 2012). An additional issue with modeling that has ties to the ecological processes is spatial bias resulting from the sampling process. Difficulties arise when sampling in mountainous areas with steep gradients such as the SAM, making the samples heterogeneous. Information to complete the niche description can be neglected in models that include these environmental gradients (Williams et al. 2009; He et al. 2015). With a restricted species like Fraser fir that may have low sample size after spatial rarefication, model robustness is compromised unless alternative methods such as model ensembles or inclusion of bias files are applied (Araújo and Guisan 2006; Williams et al. 2009; Breiner et al. 2015). It is important to understand the assumptions inherent to ENMs such as a species being in pseudo-equilibrium with the environment, degrees of overlap between abiotic, biotic, and geographic variables, and the level of uncertainty from lack of information (Guisan and Thuiller 2005; Soberón and

Peterson 2005; Griesbauer et al. 2011). Additional assumptions can include variation based on the spatial scale and selected model that is used to perform ENM (Delcourt and Delcourt 1998; Naimi et al. 2011). The outputs of these models primarily predict the broader fundamental niche based on numerous assumptions, but when combined with field observations and other post-hoc testing and modification procedures, model predictions can be successful in identifying unexplored suitable habitats (Busing and Mailly 2004).

Modeling the Southern Appalachians

The purpose of this study is to understand which variables impact the potential distribution of Fraser fir and red spruce. This information is then added to predictive models of historic climate change and different future anthropogenic forcings to properly understand how these species responded to change in the past and how they may respond to future expected changes. With North Carolina declaring SF forests priority habitat, this type of information is imperative for policy decisions, budget priorities, management strategies, and biodiversity conservation (Jenkins et al. 2002; Hijmans and Graham 2006; Griesbauer et al. 2011). While the future is uncertain, data are assimilated to include socio-economic change, technological change, energy land use, and air pollutants such as greenhouse gases in the form of representative concentration pathways (RCPs) that are published in the Intergovernmental Panel on Climate Change (IPCC) assessment reports. Different RCP levels account for the degree of emissions that are the result of changes in policies such as the switch to using mostly renewable energy and changing population patterns (van Vuuren et al. 2011). It is pertinent to understand historic species distributions prior to human interference, but conservation should not use them as baselines. Instead, conservation efforts must account for future prospects that include a range of ‘best’ and ‘worst’ scenarios (Hampe and Jump 2011; Wang et al. 2012). ENMs that project into the future to generate predictive maps aid in understanding how a species may be successful in certain locations with, for example, warmer temperatures, sunnier exposures, and lower humidity, while other areas may experience habitat loss (Berry and Smith 2012). This helps with allocation of efforts, also called triage, to protect and strengthen conservation efforts for more than just one species. Plants traditionally garner the least amount of funding because they are less charismatic, but are incredibly important for shaping the habitat for other rare or endangered flora and fauna (Cornwall 2018).

Inclusion of ENMs during the policy-making process can also benefit the economy. The Great Smoky Mountains National Park (GRSM) is the most highly visited national park in the country with 12.5 million visitors in 2019, primarily attracting those from the eastern states. It is an incredibly unique environment within the southern United States, making it attractive because of its varied landscape compared to the surrounding foothills and coasts (Aldy et al. 1999). The Appalachians are known for having poor local economies due to the demographics of the area, but businesses such as Dollywood in Gatlinburg, Tennessee help bring tourism to these areas, creating revenue for these economies. Based on a survey for those attending GRSM during 1999 by Aldy et al, it was predominantly wealthy households that were tourists visiting the parks and towns in the surrounding area, increasing revenue at local businesses that aid in combating poverty in rural Appalachia. The survey also indicated that households with lower income held a higher value for these forests rather than wealthier families. This could be in relation to the local population being predominantly poor and relying on tourism, while the wealthy explore these areas for aesthetic satisfaction and educational experiences. Christmas tree farms, another regional economic driver, rely on the success of Fraser firs since they make up 90 percent of trees sold for the season. In North Carolina alone, over 50 million trees are grown each year to meet the demand, covering over 30,000 hectares of land and valued at $100 million per year (Cory et al. 2017). Fraser firs are preferred for their structure and conical shape, which protects them well during storm events. Because of their valued aesthetic, high demand calls for them to be grown in naturally unfavorable areas that require significant upkeep such as weeding and pesticides. Understanding how the Fraser fir responds to and possibly adapts to climate change may even improve farm management practices (Cory et al. 2017).

Objectives and Research Questions

Federal, state, and non-profit agencies rely on the diversity of the SAM for economic and research purposes. Anticipating the fate of the SF habitat under different climate scenarios and understanding historic changes aids in forest management and planning. This study contributes to the decision-making process for these agencies and brings awareness to the potential disappearance not only of a unique habitat, but several species that is instrumental to the cultural identity of the Southern Appalachians. Comparing different ENMs based on statistics and known distributions will inform past and future projections for these species. Changes such as expansion, contraction, and continued presence and absence between time periods will be used to characterize how red spruce and Fraser fir will fare with a changing climate.

CHAPTER 2. WHERE DID THEY COME FROM, WHERE DO THEY GO: USING ECOLOGICAL NICHE MODELS TO ASSESS HOW SOUTHERN APPALACHIAN SPRUCE-FIR FORESTS RESPOND TO CHANGING CLIMATES

Danika L. Mosher, T. Andrew Joyner, Josh X. Samuels, Eileen G. Ernenwein

Keywords: Habitat Suitability, Biogeography, Rare Species, Mountains, Maxent, Random Forest, Boosted Regression

Abstract

The Southern Appalachian Mountains harbor a unique habitat with numerous disjunct, isolated, and endangered species residing under a Spruce-Fir forest canopy. While red spruce (*Picea rubens*) has a distribution that travels up the Appalachians into Canada, Fraser fir (*Abies fraseri*) is endemic and is genetically different from northern balsams. The combination of these two species provide unique habitats that reside on the highest peaks in North Carolina, Tennessee, and Virginia. These refugial forests require certain climatic parameters in order to stay viable such as significant precipitation, cool summer temperatures, and predominant cloud cover. Due to limited immigration for the majority of the species on these mountains, a significant number of organisms are at risk of being endangered or extinct. Ecological niche models help with conservation management by determining what factors influence species' distribution and how they would react in a historical or future context. Models like boosted regression, random forest, and Maxent provide such a service because of their computational power. Boosted regression and random forest were used in the R package biomod2 and statistically performed well, but Maxent through a graphical user interface was used for model comparisons. With a rare species like Fraser fir, a bias file was needed to reduce overpredicting.

Precipitation dominated how Fraser fir responded to the model inputs for the past and future where projections exhibited significant decline. Red spruce also significantly contracted within the Southern Appalachians, but show resilience at higher elevations. Representative concentration pathway 4.5 holds more hope for the survival of Spruce-Fir forests whereas 8.5 shows near extinction for Fraser fir and would generate metapopulations on peaks for red spruce, potentially reducing gene flow.

Introduction

Anticipating how a species may respond to a changing climate is often complicated, with unknown and poorly understood ecological impacts and co-dependencies. The use of models, particularly ecological niche models (ENMs), provides a quantitative glance at the estimated environmental requirements and parameters of a species (Araújo and Guisan 2006). These models help reveal what influences the distribution of a species by analyzing relationships and patterns between the presence of a species and the concurrent geography and climate where it is most suitable (Bastow et al. 2005; Guisan and Thuiller 2005; Naimi et al. 2011; Gundogdu 2017). Because of the limited amount of information that can be included in a model, ENMs primarily depict some variation of the fundamental niche (maximum realized niche space) rather than the realized niche (actual inhabited niche space) (Guisan and Thuiller 2005; Soberón and Peterson 2005; Phillips and Dudík 2008). Although this can be a limitation, models fill in knowledge gaps for a species and its interaction with the environment and help to confirm field observations (Busing and Mailly 2004).

Certain ENMs utilize artificial intelligence that combines statistics and machine-learning to generate predictions based on what the model learns from inputs (Aitken et al. 2008). The models use the inputs (occurrences and variables) in an iterative training process that results in distribution predictions that may increase understanding of physiological, biological, ecological, climatic, and geographic barriers and parameters for suitability (Guisan and Thuiller 2005). The types of models used, also called mechanistic models, can be generalized linear or additive models, maximum entropy, regression, or tree-based, as examples (Hijmans and Graham 2006; Elith et al. 2008; Merow et al. 2014). The majority of these are presence-only models, as presence-absence indicates that a species is truly absent from (or does not maintain a population within) a certain environment, which is more difficult to determine compared to presence (Phillips and Dudik 2008). Since absence data are often not available and difficult to confirm when they are available, there is some uncertainty inherent to presence-only models (Griesbauer et al. 2011). This may result in variable model outputs depending on the algorithm, parameters, and variables chosen (Naimi et al. 2011).

The primary assumption with ENMs is that a species is in pseudo-equilibrium with its environment (Iverson and Prasad 2001; Guisan and Thuiller 2005; Soberón and Peterson 2005). Because of the complexity of ecological interactions, it is hard to know every single influence on a species' distribution in addition to acquiring adequate occurrence data (Wiser et al. 1998; Koo et al. 2014). Variables used as inputs may also be highly spatially autocorrelated, impacting their interpretive ability. Spatial autocorrelation also happens when occurrence points (sample locations) are too close together, possibly leading to overestimation in some areas and underestimation in other areas (Bahn and McGill 2012). Sampling should be conducted across a gradient of geographical or environmental space to adequately show the relationship between temperature, precipitation, and radiative forcing, as examples (Araújo and Guisan 2006; Williams et al. 2009; Berry and Smith 2012; Franklin et al. 2012). This is particularly important with rare species that occupy relatively small niche spaces (Breiner et al. 2015).

Another common issue inherent to modeling is the exclusion of biotic interactions. This is partly due to the complexity of biotic interactions and the difficulty of including such interactions as 'variable' inputs, but inclusion of biotic interactions can be critical in better understanding the distribution of a species (Soberón and Peterson 2005; Araújo and Guisan 2006; Bahn and McGill 2012; Clark et al. 2014). A useful suggestion is to examine specific species, such as keystone species, foundation species, or those that impact biogeochemistry such as trees (Brodie et al. 2018). While ENMs are essential tools used to model broadly defined distributions, additional information (included within a model or during model post-processing) can elucidate a species' ecology, population dynamics, and sensitivities to extremes, such as moisture content, to determine what variables are important and to observe if the model is representative (Delcourt and Delcourt 1998; Araújo and Guisan 2006; Merow et al. 2014). Spatial scale of the model is also important. Even when small 'sub-habitat' areas are examined, it may be best to include all possible locations of the species to incorporate a variety of environmental conditions that may occur in the smaller area (Hijmans and Graham 2006; Clark et al. 2014).

ENMs have multiple uses depending on the question, but are particularly useful for management and conservation efforts (Hijmans and Graham 2006; Hampe and Jump 2011). The goals of conservation typically address issues such as mitigating anthropogenic forcings impacting an endangered habitat so that the area not only is sustained, but could potentially expand its boundaries and corridors for migration (Delcourt and Delcourt 1998). While it is desired to focus conservation efforts on every single species facing impacts to their habitat, it is difficult to discern how species will react to these efforts and the degree of effort required. ENMs can project into the past to see how a species historically reacted to a changing climate and how it may react under different forcings in the future (Davis 1978; Peteet 2000; Aitken et al. 2008; Petit et al. 2008; Hu et al. 2009; French and Millar 2013). Relict populations in particular are essential in understanding how a species may react to climate change, establishing a natural laboratory (Hampe and Jump 2011). Current relict populations, along with paleoecology and fossil records, can lead to locating refuge populations and colonization routes, aiding in the characterization of a species' response to a changing climate (Hu et al. 2009). The characteristics are then compared with future models to test validity of future shifts and vegetation change (Overpeck et al. 1992; Clark et al. 2014).

These predictions help feed into decisions, such as allocations of effort, also known as triage, to strengthen conservation efforts for a specific species or areas and to admit when these endeavors may be inconsequential (Jenkins et al. 2002; Cornwall 2018). Funding tends to follow charismatic organisms, resulting in minimal conservation efforts for most flora and fauna (Cornwall 2018). Being able to understand habitat composition and cross-species interactions can help save more than just one group. For example, trees help shape habitats. When focusing on an endangered or threatened rodent, it may be beneficial to allocate efforts in conserving the trees it uses for housing to ensure the preservation of its habitat. Of course, triage is not for every situation, but can help guide decision-making (Cornwall 2018). While historical data can provide a window for several millennia, future predictions use temporal scales measured in decades because of a high amount of uncertainty and variance. However, models help by providing a glimpse into what may happen based on different scenarios. While the past provides useful information, conservation cannot rely on traditional management in restoring historical biota (Thomas 2011). Instead, comprehension of a changing climate and the degree of uncertainty surrounding what may happen should be integrated more into a science-based approach to conservation management, including the use of ENMs (Delcourt and Delcourt 1998; Griesbauer et al. 2011; Thomas 2011; Wang et al. 2012; Seidl and Lexer 2013).

Climate change is a natural phenomenon that is constant and expected (Petit et al. 2008). Fossil records expose this phenomenon by recording its impacts on large-scale shifts in the distribution, adaptation, or extinction of species correlated to changes in temperature and moisture (Peters 1990; Griesbauer et al. 2011). Changes in vegetative compositions have been observed on a continental-scale since the end of the last glacial maximum (~20,000 years ago) to reveal a responsive pattern that lags around 1,500 years (Prentice et al. 1993). However, because anthropogenic forcings are increasing the rate of the current changing climate, the response of species migration and adaptation will need to be quicker than ever before to avoid extirpation (Peters 1990; Aitken et al. 2008). Other changes to anticipate may include altered levels of albedo, canopy, water vapor, and carbon dioxide exchange as vegetation composition within habitats changes (Pitelka et al. 1997).

Organisms modify their environments to varying degrees, but controllers play a significant role by impacting structure, species composition, and trophic relationships (Ehlrich and Mooney 1983; Bastow et al. 2005). Trees in particular influence the trophic levels by fixing solar energy, controlling water, and maintaining microclimates (Ehlrich and Mooney 1983). Many trees are regarded as keystone species - not only is half of terrestrial Earth covered by forests, three-fourths of land biomass is contained within these forests (Aitken et al. 2008). Depletion of this mass in the form of canopy mortality can impact an ecosystem's resilience to invasive species or climate change, ultimately transforming a habitat. The importance of having these keystone mutualist species of trees is observable. When one plant species goes extinct, an average of 10 to 30 other species that relied on plants for shaping habitats and primarily trophic levels may even go extinct themselves (Raven 1976).

The fastest migration rate recorded for trees was one kilometer per year, which is the required average rate to keep up with current climate forcings (Pitelka et al. 1997; Aitken et al. 2008). While ecotones are the best areas to initiate migration, expansion requires the population to not fall under a minimum value to succeed in at least a fraction of the new habitat (Pitelka et al. 1997; Hampe and Jump 2011). However, species near ecotone boundaries are often more climatically sensitive because they inhabit the edge of their dispersal zones (White et al. 2014). The geographic distribution of metapopulations aids in the exchange of genetics to ensure a population does not reach that minimum threshold, but fragmentation, most often caused by human development and natural resource extraction, threatens this ability (Pitelka et al. 1997; Potter et al. 2008; Thomas 2011). If migration is not feasible, adaptation can help a species survive a changing climate, especially when combined with migration (Aitken et al. 2008). However, the process of adaptation and evolution for a species is conservative and may take longer than the current rate of change, particularly with trees that have long life histories (Peters 1990; Petit et al. 2008; Seidl and Lexer 2013). Phenotypic variation, strength of selection, fecundity, and interspecific competition are all biotic factors that dictate adaptation ability but are difficult to predict (Aitken et al. 2008). When inbreeding and genetic drift occurs, a species can easily succumb to the loss of genetic variation and become more susceptible to pathogens as an example. With energy being allocated for survival, the ability to adapt is lessened, ensuing a positive feedback and eventually extinction (Potter et al. 2010). This type of path is more common among species that are endemic with restricted populations and may also impact keystone species (Peters 1990). Generalists in this situation may be more adaptable to a changing niche, but the same cannot be said for specialists because of their specific requirements that contribute to their ecosystem function (Ehlrich and Mooney 1983).

Locations at high altitudes and latitudes experience warming at a greater rate, impacting them more significantly than most other types of ecosystems (Peters 1990; Aitken et al. 2008; Palmate et al. 2014). Species at high elevations also have limited space to which they can migrate or have additional suitable habitat and may even compete with species at higher altitudes that add new environmental pressures (Peters 1990; Potter et al. 2010). Most species that reside in these elevated habitats are relicts from the last glacial maximum and commonly have cooler preferences (Hampe and Jump 2011). As temperatures warmed, these populations that reside in low-latitude high-altitude regions encroached on the tolerance limits for that species. Because of this, extreme events such as increases in fires or an abnormally warm summer, can impact reproduction and regeneration along with limited migration (Delcourt and Delcourt 1998; Hampe and Jump 2011). When considering the rate of the current changing climate, the outcomes of many relict, endemic, and disjunct species that reside on mountaintops, particularly in low-latitude areas, may be dire (Potter et al. 2010). Change is expected to have repercussions for biodiversity that will even trickle down into local and regional economies (Peters 1990; Díaz et al. 2006).

The Spruce-Fir (SF) forests in the Southern Appalachian Mountains (SAM), which primarily consist of red spruce (*Picea rubens*) and Fraser fir (*Abies fraseri*), is an ecosystem that is threatened by the impacts of a changing climate. The SAM is unique because it is the only temperate rainforest east of the Mississippi in the United States and harbors one of the most threatened and rarest ecosystems, the SF forest (Aldy et al. 1999; Hays et al. 2006; NC Wildlife). According to the 2005 Wildlife Action Plan in North Carolina, the Southern Blue Ridge Mountain SF forests are a priority habitat (NC Wildlife). These areas occur in Tennessee, Virginia, and primarily North Carolina on seven mountaintops (Aldy et al. 1999; Berry and Smith 2012) (Figure 2.1). The geological environment from juxtaposed rocks and metamorphosed sandstone outcrops and cliffs aided in the diversity of habitats that harbor rare plants and animals (Clark 2001). Habitats south of Asheville, North Carolina primarily face northeast and are close to streams within low-base metamorphic rocks on broad ridges. North of Asheville they typically reside away from low-base sedimentary and metamorphic rocks while being near streamheads with substantial rainfall during the growing season (Simon et al. 2005). SF forests typically exist above 1,370 meters, but do not reside on all mountaintops, some of which even reach 1,680 meters such as Beech Mountain (Cogbill and White 1991; Aldy et al. 1999; Hayes et al. 2006). The mountains draw in crowds from surrounding areas, and recreational opportunities are prominent in the Jefferson, Pisgah, and Cherokee National Forests, the Blue Ridge Parkway, Appalachian Trail, the North Carolina State Park System, and the Great Smoky Mountains National Park (GRSM) (Jenkins et al. 2002). The GRSM is the most visited national park and brings in residents from states along the coast to provide a unique experience. The SF forest covers over 34,000 hectares with around 75 percent of the habitat residing in the park, which also hosts the most virgin and oldest SF stands (Oosting and Billings 1951; Aldy et al. 1999; Hayes et al. 2006; Koo et al. 2014). Fraser firs are popular to use as Christmas trees and over 50 million trees are grown in North Carolina alone, but typically require pesticides and herbicides if grown out of their natural habitat (Cory et al. 2017).

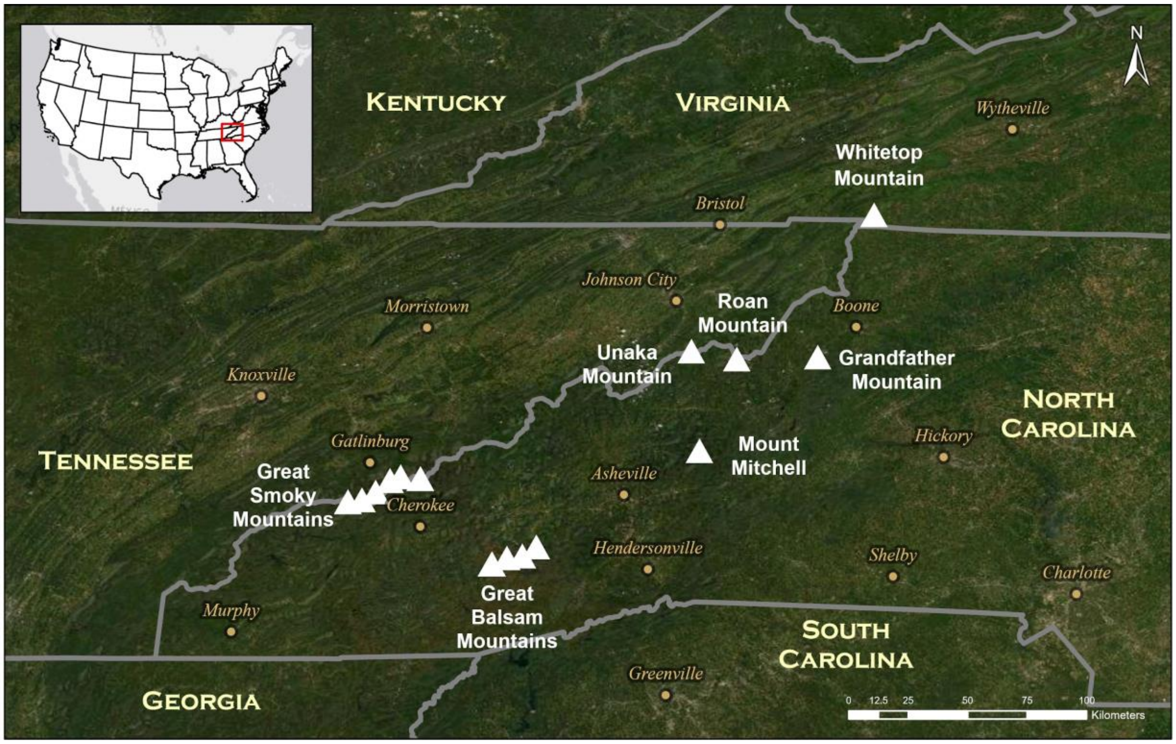

Figure 2.1. Mountaintop locations that harbor Spruce-Fir forests

The SF ecosystem is a remnant of the late Pleistocene boreal forest that primarily consisted of balsam fir (*Abies balsamea*) rather than Fraser fir (Berry et al. 2013). The southern extent of balsam fir reached its tolerance limit and either receded to the north or stayed within the mountains when temperatures warmed. Because of the length of separation and the southern extent being able to be plastic enough genetically to have different characteristics, Fraser fir came to be (Oostings and Billings, 1951). SF forests are still similar to their balsam relatives such as the Acadian forest rather than other habitats that are closer in areas like Knoxville, Tennessee (Shanks 1954). The primary difference in habitat preferences is that the North Carolina mountains are warmer and wetter. Mountains in New Hampshire are colder in the winter and receive more snow, but mountains in North Carolina have a cooler climate during the summer (Oosting and Billings 1951). Forest composition also differs where SAM SF forests are mixed conifer with a deciduous shrub understory in addition to the presence of balds (Cogbill and White 1991; Wilds et al. 2000). Balds are located in areas where there is poor nutrient availability because of the rock type, such as granite domes and fine-textured bedrock such as the Anakeesta slate. Fire, logging, and acid deposition also influence the distribution of balds (Wilds et al. 2000; Clark 2001). SF habitats typically have long fire intervals on the order of decades due to the moisture content, attracting species that are fire sensitive (Mitchell et al. 2014). The extents of ecotones differ based on aspect and are relatively narrow, residing primarily on steep, north-facing slopes because of lower solar radiation and cooler temperatures (Cogbill and White 1991; Busing et al. 1993).

Average temperatures at these seven habitat peaks are 5-8℃ cooler than the surrounding foothills during the growing season (Shanks 1954). Average July temperatures are 11.8℃ at the treeline, 17 ℃ at 1,618 m, and 15 ℃ at 1,991 m with maximum temperatures getting to 22 ℃

(Cogbill and White 1991; Wiser et al. 1996; Cory et al. 2017). The northern distribution around Roan Mountain and Mount Rodgers are cooler (Simon et al. 2005). Winds are dominant from the southwest, with speeds from 18.5 kilometers per hour up to 33 kilometers per hour. Most precipitation arrives during the summer and winter resulting in 1270 to 2000 mm of rainfall (Wiser et al. 1996). The amount received is dependent on elevation and is higher closer to the Georgia and South Carolina border (Shanks 1954; Simon et al. 2005). Potential evaporation is also dependent on elevation and decreases with altitude (Shanks 1954). Low cloud ceilings that lead to immersion are vital for these habitats since they experience fog 70 percent of the year (Cory et al. 2017). Cloud immersion is important to improve carbon gain and water conservation and helps delineate ecotones (Busing et al. 1993; Richardson et al. 2003; Berry et al. 2013). Harsh winters, particularly ice and high winds, also determine the extent of the habitat of primarily Fraser fir (White et al. 1985; Cogbill and White 1991; Hayes et al. 2006; NC Wildlife; USDA).

The biodiversity in the SAM is renowned among researchers and attracts many visitors (Clark 2001; White et al. 2014). Rare species such as the moss spider (*Microhexura montivaga*), ground beetles (Coleoptera: Carabidae), Weller's salamander (*Plethodon welleri*), Carolina northern flying squirrel (*Glaucomys sabrinus*), Virginia big-eared bat (*Plecotus townsendii*), blue ridge goldenrod (*Solidago spithamaea*), Heller's blazing star (*Liatris helleri*), and the very rare rock gnome lichen (*Gymnoderma lineare*) can be spotted within these habitats (NC Wildlife; USDA). Up to 125 other species reach their upper or lower limits, attributing to their behavior and degree of sensitivity to changes in the climate (Shanks 1954; Aldy 1999). There are 17 species or subspecies of both plants and animals that are endemic in addition to 20 species or subspecies of invertebrates (Aldy et al. 1999; Jenkins et al. 2002; NC Wildlife). Total plant count is 185 species where there are 22 trees, 34 shrubs, 126 herbs, and 3 vines (Simon et al. 2005). Yellow birch (*Betula alleghaniensis*) and red spruce are dominant along the ecotone (Cogbill and White 1991). The habitat these plants comprise is critical for the breeding of numerous landbirds that are of high concerns such as the brown creeper (*Certhia americana*), northern saw-whet owl (*Aegolius acadicus*), and black-capped chickadee (*Poecile atricapillus*) (NC Wildlife). Weller's salamander is the most at risk of extirpation and the moss spider and ground beetles are also susceptible to desiccation (NC Wildlife).

Both red spruce and Fraser fir are considered to be foundation, keystone, or controller species. They impact numerous species and even their own regeneration (Hayes et al. 2006). They are both shade tolerant and require the other for understory growth (White et al. 1985). Red spruce habitat starts around 1,190 meters with its most southern extent being in the SAM and its northern extent extending into Canada (Cogbill and White 1991). Spruce domination occurs above 1,400 meters and can go as high as 1,900 meters, but can only exist at sheltered areas due to high winds (Busing et al. 1993). The transition to dominant fir occurs around 1,620 to 1,689 meters (Cogbill and White 1991). Spruce has high economic value and was logged in the early 19th century and into the beginning of the 20th century (Hayes et al. 2006). Spruce is a long-lived species where the average age of death is 225 years (White et al. 1985; McLaughlin et al. 1987). Their preferences include metal-rich layers that are acidic and regenerate well in yellow birch gaps (White et al. 1985; Clark 2001). While red spruce itself is not globally threatened, it is within the SAM due to it being closest to the temperature optimum for summer (Prentice et al. 1993; Pearson 2016).

Fraser fir are abundant in shallow rocky soils to deeper mineral soils with an organic layer (USDA). Cloud immersion is more important to water balance for fir than spruce by supplying a third of water intake (Berry et al. 2013). Fir covers around 18,000 hectares and dominates above 1,800 meters (Cogbill and White 1991; Busing et al. 1993; Cory et al. 2017). Ice storms and large-scale windfalls are important factors that make these peaks more favorable to fir than spruce (Busing and Pauley 1994). Despite separation, gene exchange between metapopulations still occurs from wind-dispersed pollen and populations are still genetically well-mixed (Potter et al. 2009). The mean age of death is 137 years and it is the most important successor in all gaps, particularly within spruce gaps (White et al. 1985). Fir has dense understories which provide a higher chance of dominating regeneration since it has short canopy time and high turnover rate from withstanding intense ice and wind (White et al. 1985; Busing et al. 1993; USDA).

Even though fir relies on natural disturbances to promote rapid colonization, the SF forest has endured human disturbances that have altered the ecosystem (Hayes et al. 2006). Issues started with intense logging in the 19th century, but increased fires, introduction of exotic insects, historic grazing, and even recreational development exacerbated the decline into the 21st century (Jenkins et al. 2002; Berry et al. 2013; White et al. 2014; NC Wildlife). Intense mortality rates were predominantly experienced between 1840 and 1950 (McLaughlin et al. 1987). Logging eventually led to clear cutting of most areas aside from those on cliffs and high slopes. The lack of management meant there was no replanting or soil rework to reduce solar radiation that would destroy the soil and its ability to recover (Hayes et al. 2006). Even though these habitats experience abundant moisture, the lack of trees made it more susceptible to fires. More intense logging led to more fires in the region and severely disturbed or eliminated the organic soil layer (Hayes et al. 2006; Mitchell et al. 2014; NC Wildlife). Once forest regrowth occurred, there was less spruce and the species became more influenced by aspect (Cogbill and White

1991; Hayes et al. 2006). This becomes evident when comparing stands in North Carolina and Tennessee since logging primarily took place in the eastern state. Elevation of the ecotone is higher on the southern slopes compared to the northern due to increased solar radiation exposure and potentially more soil erosion (Hayes et al. 2006). This ecosystem is used to natural disturbances that cause gap regeneration, but logging was exceptional. Soon after recovery was underway, an invasive species was introduced in the middle of the 20th century that stunted adequate restoration (Hayes et al. 2006).

As many as 40 percent of nearly all documented species-level extinctions are attributed to invasive species (Thomas 2011). The balsam woolly adelgid (*Adelges piceae*) was introduced to the United States in the 1950s in central Virginia and made its way to the Appalachians later in the century. Their impact was felt in the decline of basal area and canopy cover that impacted both fauna and flora (Allen and Kupfer 2001). Prior to the 1930s, fir stands were described as uniform across peaks, had a higher basal area compared to present, and the canopies were denser which prevented significant radiational energy from reaching the forest floor (White et al. 2014; Kaylor et al. 2017). Once balsam woolly adelgid was introduced, between 40 to 90 percent of firs were killed and it has permanently impacted regeneration capabilities (Berry and Smith 2012; Kaylor et al. 2017; Cory et al. 2017). In regards to fir, there was a 78 percent decrease in basal area and 28 percent decrease in total basal area (Busing and Pauley 1994). While the link between balsam woolly adelgid activity and climate change has not been extensively studied, the presence of plant diseases is correlated with climate change impacting both host and pathogen (Bosso et al. 2017). However, these populations are experiencing deterioration from both an invasive species and climate change individually (Jenkins et al. 2002).

Mortality has increased while canopy size has decreased in these forest environments since 1985 (Busing 2004). During this time, a regional drought from 1983 to 1993 was linked with the loss of forest canopy (Busing 2004). The percent of recent decrease of spruce being 4 percent per year (1993-2004) is higher than noted in the 1960s through 1986 (0.5 percent per year). Wind deaths have also increased during this time, expanding spruce gaps (Busing 2004). The death of fir influences the death of spruce because firs protect spruce from wind damage (Busing and Pauley 1994; Busing 2004). This habitat helps with community stability and has gone through numerous threats, but is now encroaching, or going beyond, the critical threshold for recovery. This can be observed with what has happened on the south-facing slopes where the composition and ecosystem dynamics in those old ecotones have changed (Busing et al. 1993; Hayes et al. 2006; NC Wildlife). The ecotone for fir specifically has been undergoing change as they compete with encroaching herbaceous and deciduous woody species beneath dead fir canopy (Allen and Kupfer 2001). Low cloud ceilings aid in controlling the boundary between them, but with rising ceilings due to climate change, it is more difficult for firs to withstand the invasion (Richardson et al. 2003). SF forests are not able to migrate altitudinally because of a lack of available land. Human activity has induced fragmentation further disrupting patterns of migration and expanding loss of potential habitat (Peters 1990; Pitelka et al. 1997). Repercussions to the SF ecosystem will continue due to ongoing climate change and human impact. Past studies show effects already experienced in addition to what may happen through models.

Recovery from majority of historical disturbances is already underway at Roan Mountain and the Black Mountains as observed by increase in Fraser fir overstory, but most models anticipate significant change during the next few decades (Hampe and Jump 2011; Kaylor et al.

2017). On a regional scale, future projections indicate that even though areas east of the Mississippi will see an increase of precipitation by six percent, the fire season will be around two to three months longer (Mitchell et al. 2014). Other models predict shifts in forest compositions (Aitken et al. 2008). Clouds will not only become less frequent, but the lifting condensation level, or the cloud ceiling, will be higher with warmer air temperatures (Berry and Smith; Berry et al. 2013). Less precipitation from loss of cloud immersion pairs with changed times of snowmelt and the arrival of spring and summer rains, impacting growing days, lack of nutrient reserves, and delay of frost hardening required to reduce tissue damage (White et al. 2014). Some models predict that cloud heights may lower over the next several decades, but there is a consensus that cloud heights will rise back up higher than the current level towards the latter half of the 21st century (Richardson 2003; Berry and Smith 2012; Berry et al. 2013; Koo et al. 2014). SF habitats lowest in elevation are anticipated to decline (Kaylor et al. 2017). There could be temporary recovery by 2050, similar to the lowered cloud ceilings, but certain contraction by 2100 (Potter et al. 2010; Kaylor et al. 2017). Areas where fir may recover are around mature overstories that have remained steady within the past two decades (Kaylor et al. 2017). Another study indicates that spruce will experience growth from 2080 to 2099 and that the degree of air pollution in the model impacts the availability of suitable habitat (Koo et al. 2015). Additional parameters that influenced models used in these studies were elevation, geofertility, and average annual precipitation (Simon et al. 2005). The impact of solar radiation diminished at high elevations, and so both spruce and fir did not show a strong response (Busing et al. 1993).

The purpose of this study is to observe which parameters influence red spruce and Fraser fir distributions through the use of ENMs at all seven mountaintop locations. The selected variables will then be used for historic and future projections to better understand how these species have been influenced by historic climate change and how they may fare in the future. Findings can be used by organizations such as the Southern Appalachian Spruce Restoration Initiative, Grandfather Mountain Stewardship Foundation, Southern Appalachian Highland Conservancy, Appalachian Trail Conservancy, US Fish and Wildlife Services, National Park Services, US Forest Services, and Highlands of Roan Stewardship to inform conservation and management plans. While past studies indicate decline in most areas, this study can provide quantitative support for targeted conservation and resource allocation efforts for areas that may be more likely to withstand the various impacts of climate change.

Methods

The incorporation of biotic interactions as recommended for both red spruce and Fraser fir was done by observing interspecific competition, parasitic relationships, and symbiosis within primarily hardwoods (Guisan and Thuiller 2005; Soberón and Peterson 2005; Araújo and Guisan, 2006; Hijmans and Graham 2006; Griesbauer et al. 2011). This aids in obtaining overall dynamics of the forest by simulating multiple trees (Busing and Mailly 2004). Occurrence data for red spruce, Fraser fir, yellow birch (*Betula alleghaniensis*), North American beech (*Fagus grandifolia*), Catawba rhododendron (*Rhododendron catawbiense*), water molds (*Phytophthora*), balsam woolly adelgid (*Adelges piceae*), American mountain ash (*Sorbus americana*), and mountain maple (*Acer spicatum*) were obtained from the Global Biodiversity Information Facility (GBIF). Balsam fir (*Abies balsamea*) was combined with Fraser fir and used for late historic data. Points were compared with known distribution to eliminate major outliers (Phillips and Dudík 2008).

Points were spatially rarefied by 1 kilometer to fit the spatial resolution of climate data and to reduce over-sampling bias (Bahn and McGill 2012; He et al. 2015; Shabani et al. 2017).

Data were then split between training (80 percent) and testing (20 percent) (Bahn and McGill 2012; Liu et al. 2015). Fraser fir and red spruce locality data are mapped in figure 2.2. Climate data and elevation were obtained from WorldClim.org at 30 arc seconds (~1 x 1 kilometer) for higher sensitivity, particularly in mountainous regions (Hijmans et al. 2005; Bahn and McGill 2012). Data were retrieved for the time periods of the Last Glacial Maximum (LGM, ~22,000 years ago), the Middle Holocene (Mid-Holo, ~6,000 years ago), the present (1960 - 1990 climatic data), 2050, and 2070. Future data were based on representative concentration pathways (RCPs) which anticipate socio-economic changes, technological change, energy land use, and air pollutants. The numbers represent radiative forcing levels ($\frac{W}{m^2}$) at increments of 2.6, 4.5, 6.0, and 8.5 (van Vuuren et al. 2011). Selected forcings were 4.5 as a moderate best-case scenario and 8.5 as worst-case. The Complete Coupled System Model (CCSM4) was used as the global circulation model (GCM) because of its reliability and availability across time periods in the study (Bosso et al. 2017; Shabani et al. 2017). Slope, aspect cosine, roughness, profile curvature, and terrain ruggedness index were obtained from EarthEnv.org at a 1 kilometer resolution (Amatulli et al. 2018). The environmental data were extracted to the occurrence points of each species. A Pearson’s correlation in SPSS produced coefficients to determine the selection of variables where correlation was less than 0.85 for each tree species (Williams et al. 2009; Elith et al. 2011; Clark et al. 2014; Hill et al. 2017; Shabani et al. 2017). This is to reduce variables that may have similar explanation power (Simon et al. 2005; Phillips and Dudíc 2008; Koo et al. 2015). Even though the focus area is in the southern Appalachians, the extent of the data included the continental US and the lower Canadian provinces (Newfoundland, Prince Edward Island, Nova Scotia, New Brunswick, Quebec, Ontario, Manitoba, Saskatchewan, Alberta, and

British Columbia). Inclusion of a larger area improves explanatory power for the variables by covering the full ranges of species.

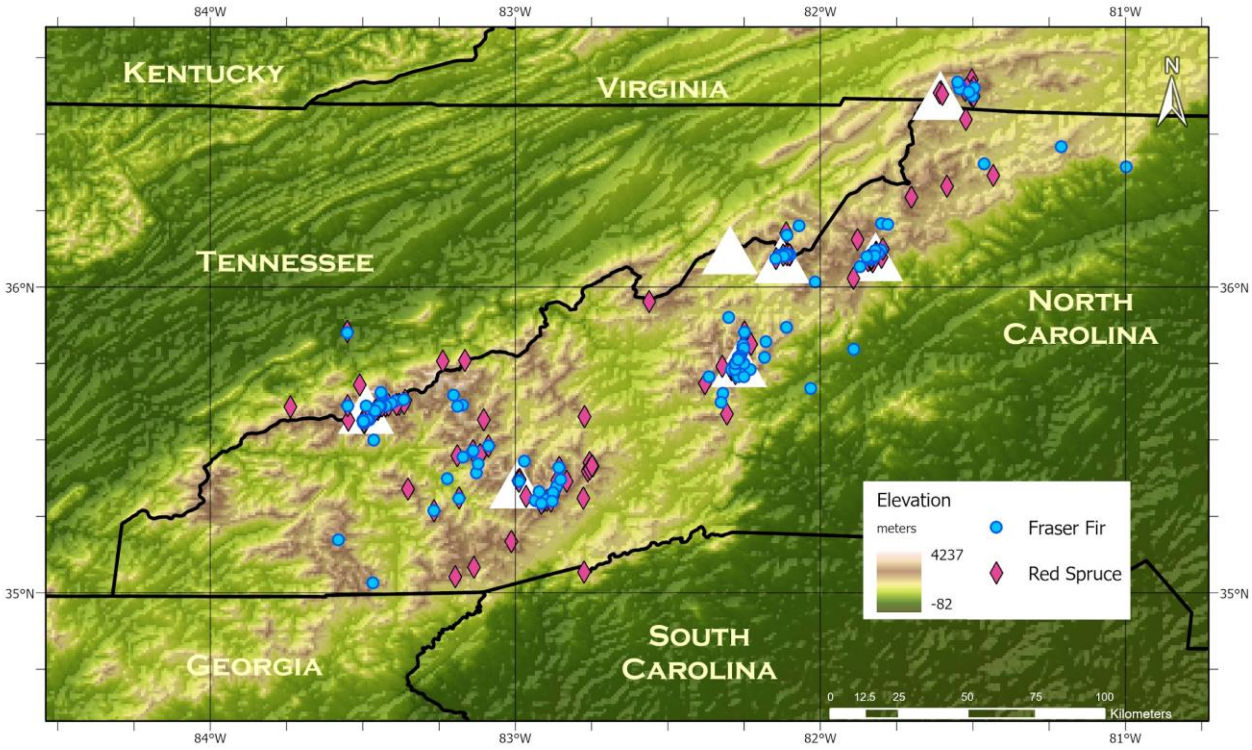

Figure 2.2. Species occurrence points from GBIF for Fraser fir (blue dots) and red spruce (pink diamonds). The white triangles are in reference to Figure 2.1 of the labeled mountains and ranges. Highest point is at Mount Mitchell at 2,037 meters. Unaka Mountain is the lowest in elevation with the peak at 1,584 meters.

Generalized Boosted Regression (GBM) and Random Forest (RF) were used in the biomod2 package within R following the methods outlined by Georges and Thuiller (2014). While biomod2 has the capability to perform Maximum Entropy (Maxent), the model was run through its stand-alone graphical user interface (GUI) (Phillips et al. 2020). Models were compared based on true skill statistic (TSS) and receiver operating characteristic (ROC) area under the curve (AUC). TSS is a range of sensitive and specific values where its range is from -1 to 1 and AUC has a range from 0 to 1 that details a model’s ability to predict the presence of a species. Values closer to 1 for both TSS and AUC indicate good model performance, 0.5 is random, and anything less is worse than random (Williams et al. 2009; Clark et al. 2014; Liu et al. 2015; Mi et al. 2017). Because rare species tend to be over-predicted through usual modeling means from a limited and homogenous sample size (Wilds et al. 2000; Evans et al. 2010; Liu et al. 2015), the inclusion of a bias density file helps inform pseudo-absence data (Williams et al. 2009; Elith et al. 2011; Merow et al. 2013; Rej and Joyner 2019). This also reduces the number of explanatory variables to prevent overprediction (Breiner et al. 2015). The Maxent GUI is able to incorporate a bias file made through the SDMtoolbox (Brown et al. 2014; Brown et al. 2017), so this model was chosen over GBM and RF for all species and time periods to address the overfitting issue with Fraser fir. The bias file was made using Gaussian density with a distance of 10 kilometers for only Fraser fir.

The selected variables for Fraser fir were precipitation of driest month (Bio 14), Catawba rhododendron, red spruce, beech, temperature seasonality (Bio 4), mean diurnal range (Bio 2), and precipitation seasonality (Bio 15). The variables for red spruce were mountain ash, annual precipitation (Bio 12), minimum temperature of coldest month (Bio 6), mean temperature of wettest quarter (Bio 8), maximum temperature of warmest month (Bio 5), slope, and mean temperature of driest quarter (Bio 9). Probability maps of occurrence were generated using the 10-percentile training threshold to reclassify into binary maps of projected presence-absence of a species (Clark et al. 2014; Norris 2014; Liu et al. 2015). The binary maps were then compared for red spruce and Fraser fir through each time period to detect any expansion, contraction, and absence or presence in both scenarios.

Table 2.1. Total variables placed in initial models. Species Model Output Variables were generated from modeling each individual species with the WorldClim and EarthEnv variables. Variables included in the final red spruce model are indicated with * whereas Fraser fir are indicated with ⸙.

WorldClim Bioclimatic Variables	**Species Model Output Variables**	**EarthEnv Additional Abiotic Variables**
Annual Mean Temperature	Fraser fir (*Abies fraseri*)	Elevation
Mean Diurnal Range⸙	Mountain Maple (*Acer spicatum*)	Slope*
Isothermality	Balsam Woolly Adelgid (*Adelges piceae*)	Aspect Cosine
Temperature Seasonality⸙	Yellow Birch (*Betula alleghaniensis*)	Roughness
Max. Temp. of Warmest Month*	American Beech⸙ (*Fagus grandifolia*)	Terrain Ruggedness Index
Min. Temp. of Coldest Month*	Red Spruce⸙ (*Picea rubens)*	Profile Curvature
Temp. Annual Range	Water Mold (*Phytophthora*)	Mean Annual Cloud Cover
Mean Temp. of Wettest Quarter*	Catawba Rhododendron⸙ (*Rhododendron catawbiense*)	Seasonality Concentration Cloud Cover
Mean Temp. of Driest Quarter*	Mountain Ash* (*Sorbus americana*)	Cloud Cover Mean for July
Mean Temp. of Warmest Quarter		
Mean Temp. of Coldest Quarter		
Annual Precipitation*		
Precip. Of Wettest Month		
Precip. Of Driest Month		
Precipitation Seasonality⸙		
Precip. Of Wettest Quarter		
Precip. Of Driest Quarter⸙		
Precip. Of Warmest Quarter		
Precip. Of Coldest Quarter		

Results

Maxent, GBM, and RF produced unique results for both red spruce (Figure 2.3) and Fraser fir (Figure 2.4). Of the three comparing models, statistically RF was the best performing for both red spruce (Figure 2.3c) and Fraser fir (Figure 2.4c). Maxent had the lowest values, but was still a well performing model due to its AUC proximity to 1.0 (Figures 2.3b and 2.4b). Minimal visual difference was detected between all three models for red spruce (Figure 2.3b-d), indicating the selected model for time comparisons would be RF. However, significant visual change is evident for Fraser fir when a bias file was included for Maxent (Figure 2.4b-d). When compared to the GBIF locations (Figure 2.4a) and habitat maps for SF forests provided by both the US Forest Service (USFS) and North Carolina Wildlife Resources Commission (NC Wildlife), Maxent was able to predict a slightly more accurate prediction map.

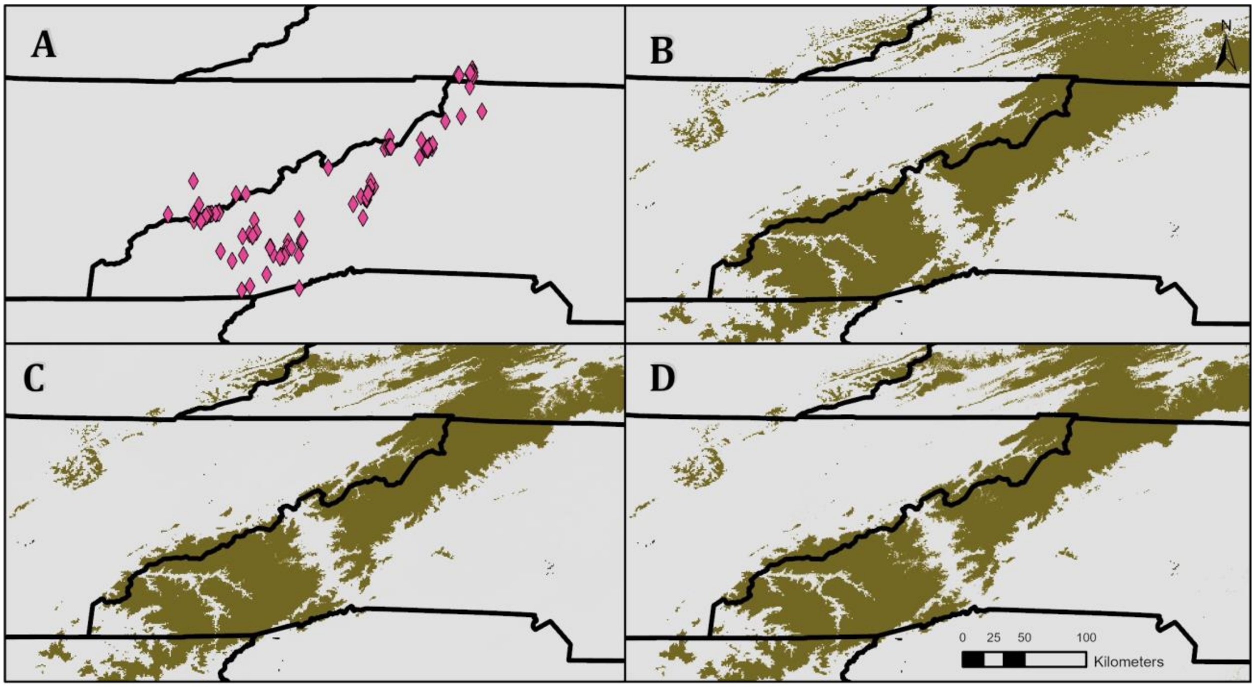

Figure 2.3. GBIF locations for red spruce (A) that informed the models for Maxent with an AUC of 0.959 (B), random forest with an AUC of 1 and a TSS of 0.986 (C), and boosted regression with an AUC of 0.996 and a TSS of 0.951 (D).

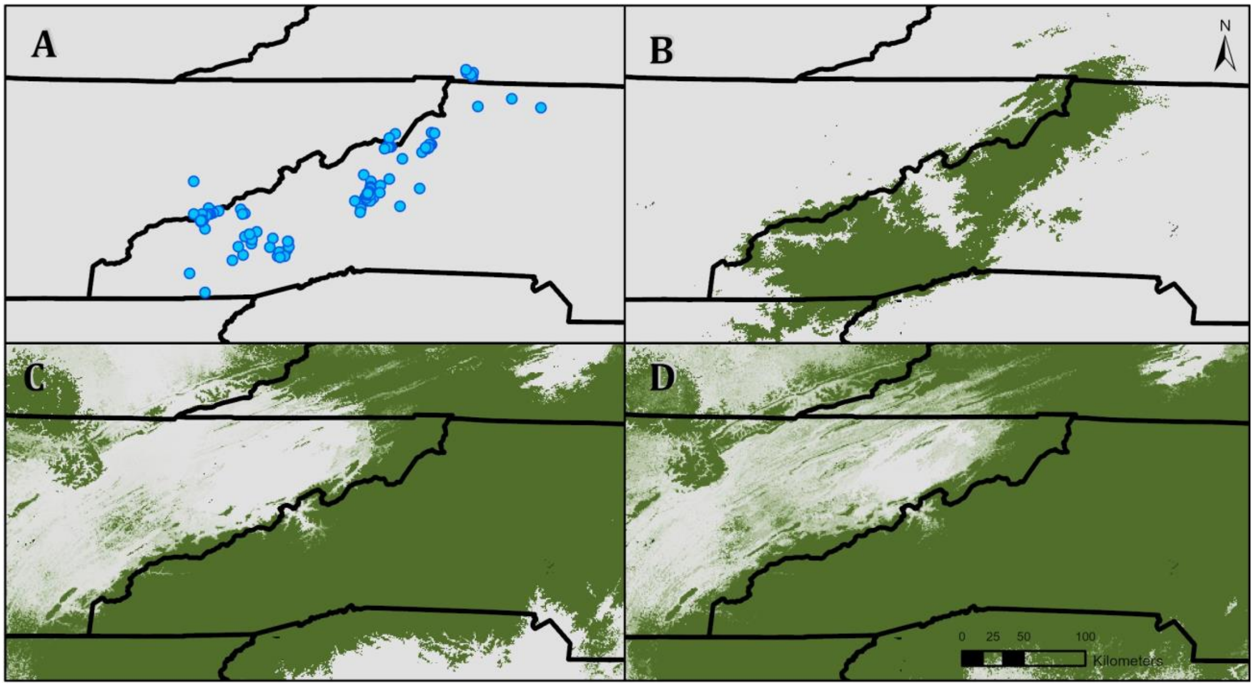

Figure 2.4. GBIF locations for Fraser fir (A) that informed the models for Maxent with an AUC of 0.991 (B), random forest with an AUC of 1.0 and a TSS of 0.994 (C), and boosted regression with an AUC of 1.0 and a TSS of 0.996 (D).

During the LGM and Mid-Holo, both red spruce and Fraser fir (with balsam fir) were predicted to occupy the coasts along the Carolinas and Virginia in addition to the Piedmont regions of Georgia and Alabama (Figure 2.5a,c). Within the preceeding ~14,000 years to the Mid-Holo, significant contraction and expansion was observed to where there was no overlap of extent (Table 2.1). Red spruce spread through the Appalachian Mountains (Figure 2.5a) while Fraser fir/balsam fir was restricted to the lower SAM stretching from Hendersonville, NC into the GRSM and dipping down into the Chattahoochee National Forest in Georgia (Figure 2.5c). The next ~6,000 years to the present was nearly the same for red spruce (Figure 2.5b), but Fraser fir experienced an upward shift through the SAM to where it has the near same extent as red spruce (Figure 2.5d). Out of all time comparisons, this represented the highest percentage of expansion (Table 2.1).

Table 2.2. Percent contribution of each classification to the map outputs of Figures 2.5 through 2.8.

Figure	Description	% Contraction	% Absent Both	% Present Both	% Expansion
2.5 a	RS Mid-Holo - LGM	1.159	96.535	0.0	2.305
2.5 b	RS Pres - Mid-Holo	0.553	96.864	1.752	0.831
2.5 c	FF Mid-Holo - LGM	1.542	98.424	0.0	0.034
2.5 d	FF Pres - Mid-Holo	0.013	97.426	0.0	2.561
2.6 a	RS 2050 4.5 - Present	1.749	96.036	0.834	1.381
2.6 b	RS 2050 8.5 - Present	1.969	95.932	0.614	1.485
2.6 c	RS 2070 4.5 - Present	1.870	96.082	0.712	1.335
2.6 d	RS 2070 8.5 - Present	2.318	95.384	0.264	2.034
2.7 a	FF 2050 4.5 - Present	0.045	99.863	0.079	0.013
2.7 b	FF 2050 8.5 - Present	0.088	99.876	0.036	0.001
2.7 c	FF 2070 4.5 - Present	0.085	99.852	0.039	0.024
2.7 d	FF 2070 8.5 - Present	0.123	99.858	0.001	0.018
2.8 a	RS 2070 4.5 - 2050 4.5	0.516	97.437	1.699	0.348
2.8 b	RS 2070 8.5 - 2050 8.5	0.937	96.765	1.161	1.137
2.8 c	FF 2070 4.5 - 2050 4.5	0.046	99.890	0.045	0.018
2.8 d	FF 2070 8.5 - 2050 8.5	0.036	99.946	0.001	0.018

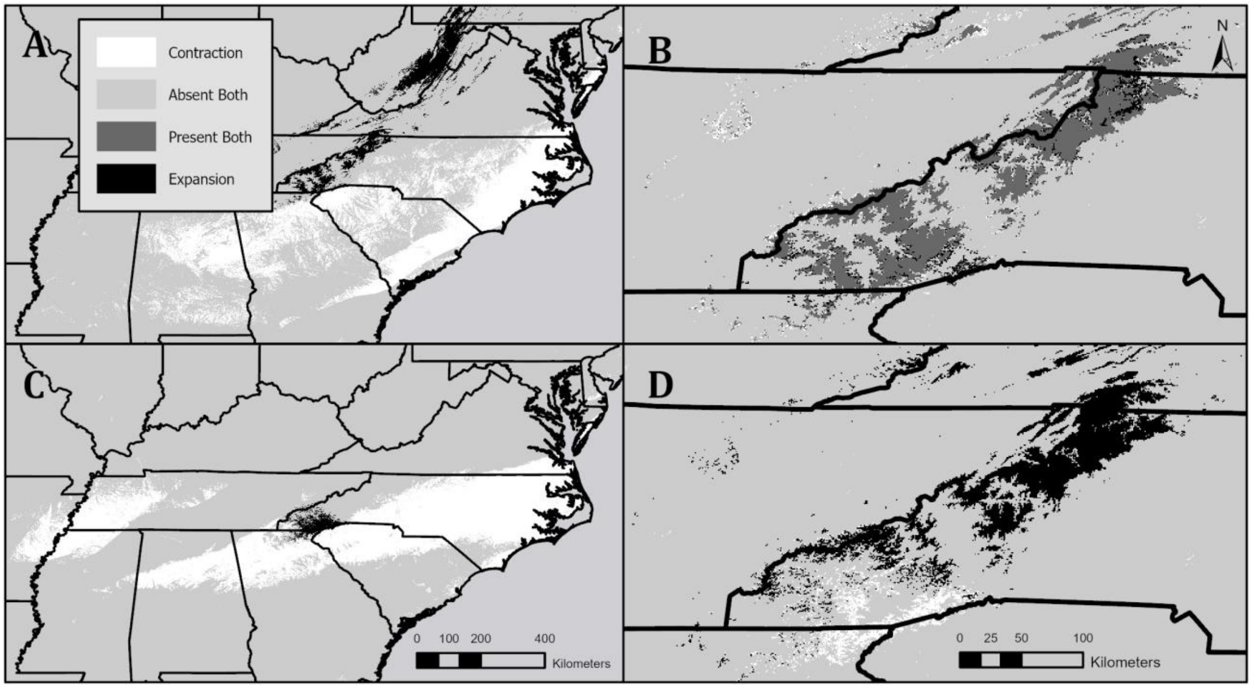

Figure 2.5. Historical comparisons for red spruce between LGM and Mid-Holo (A) and between Mid-Holo and the present (B). Fraser fir comparisons between LGM and Mid-Holo (C) and between Mid-Holo and the present (D).

All future projections for red spruce indicate contraction with RCP 4.5 (Figure 2.6a,c) having more standing habitat than 8.5 (Figure 2.6b,d). RCP 8.5 for 2050 most adequately resembles the habitat maps by USFS and NC Wildlife. Mount Mitchell is the prominent stand that withstands all future climates. The next best safe haven according to RCP 8.5 in 2070 is the GRSM with Roan Mountain coming in as a close third. The Great Balsam Mountains have a few peaks that will be viable as well as Mount Rogers, but not Whitetop Mountain. Unaka Mountain has no areas for ‘present both’ and Grandfather Mountain only has one small area. Figure 2.6d has the highest percent contraction because of the SAM, but also the highest expansion because of predicted migration in northern New England and primarily southeastern Canada (Table 2.1). Majority of the contraction occurred between the present and 2050 for both RCPs in addition to expansion, but to a lesser degree (Figure 2.8 a,b).

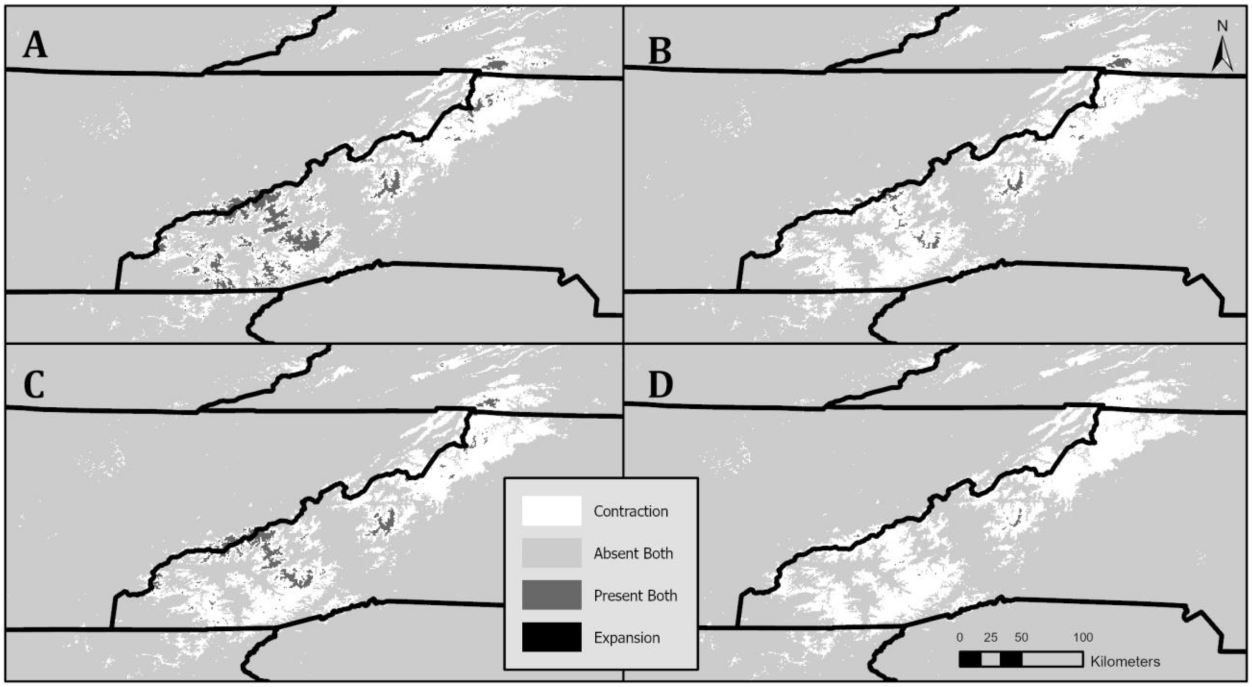

Figure 2.6. Future projection comparisons for red spruce from the present to 2050 using RCPs 4.5 (A) and 8.5 (B) along with 2070 projections from the present with RCPs 4.5 (C) and 8.5 (D).

Fraser fir experiences the least amount of expansion out of any time comparison and species for the future with a slightly higher degree of contraction in 2070 than 2050 (Table 2.1). Expansion is also higher in 2070 than 2050. RCP 8.5 in 2050 (Figure 2.7b) is visually similar to RCP 4.5 2070 (Figure 2.7c), but there is slightly more expansion in 2070 (Table 2.1). According to the worst-case scenario of RCP 8.5 in 2070, the only safe havens for Fraser fir are scattered along the Great Balsam Mountains, GRSM, and into Nantahala National Forest (Figure 2.7d). None of the northern refugial peaks have areas of ‘present both.’ The majority of contraction occurred between the present and 2050 for RCP 8.5, whereas expansion primarily occurred between 2050 and 2070 for RCP 8.5 (Figure 2.8d). RCP 4.5 had nearly the same metrics for expansion and contraction for both time periods (Figure 2.8c, Table 2.1).

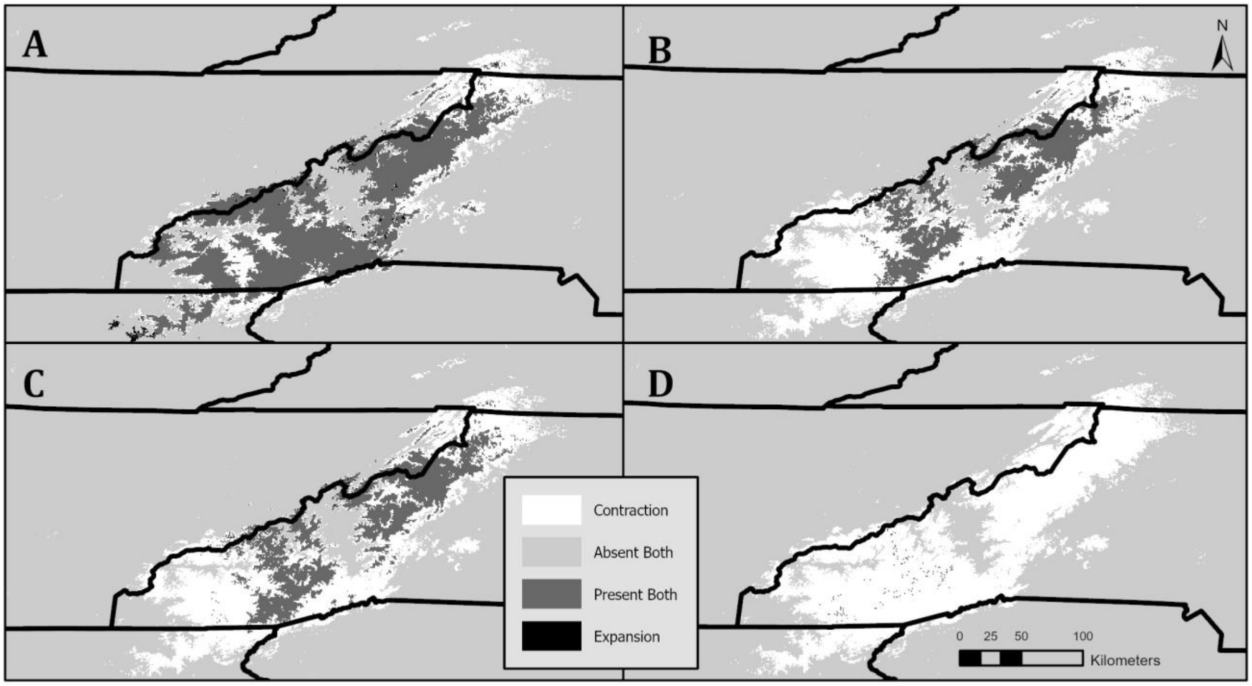

Figure 2.7. Future projection comparisons for Fraser fir from the present to 2050 using RCPs 4.5 (A) and 8.5 (B) along with 2070 projections from the present with RCPs 4.5 (C) and 8.5 (D).

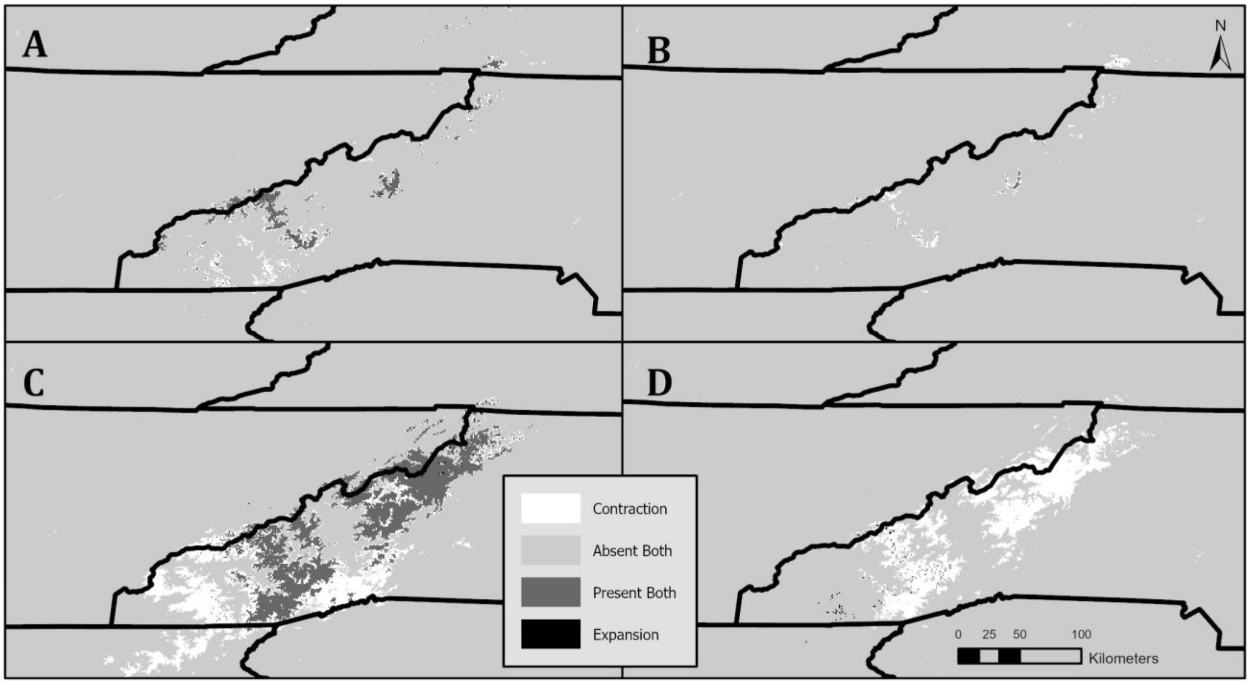

Figure 2.8. Changes between projected 2050 and 2070 for red spruce RCP 4.5 (A) and 8.5 (B) and Fraser fir 4.5 (C) and 8.5 (D).

Discussion

Precipitation plays an important role for both Fraser fir and red spruce when it comes to influencing their delineation and the model. Elevation may play an important role because of the difference in altitude between the SAM and New England red spruce, but could actually be a surrogate for precipitation or temperature (Simon et al. 2005; Soberón and Peterson 2005; Koo et al. 2015). Precipitation of the driest month (Bio 14) for Fraser fir needs to be higher than the surrounding area at a median of 129 mm, indicating that precipitation is an important factor for sustaining this species since it was the variable that contributed the most to the models. Fraser fir also prefer lower precipitation seasonality (Bio 15) at around 9 percent, alluding to the need for consistent precipitation around 1270 to 2000 mm (Wiser et al. 1996). This suggests that the drought from 1983 to 1993, an extreme derivation, was a major factor in the loss of Fraser fir forest canopy (Busing 2004). The primary difference between the SAM and New England is that the summers are cooler and the winters are warmer (Oosting and Billings 1951). This is reflected in the annual mean diurnal range (Bio 2) being lower than the surrounding area of around 10.4℃ in addition to lower temperature seasonality (Bio 4).

Red spruce prefers the maximum temperature of the warmest month to be lower than the surrounding area at around 25℃, which holds close to an observed maximum threshold of 22℃ (Cory et al. 2017). Overall annual precipitation for red spruce is around 1084 mm, but within the SAM is around 1981 mm, also reflecting the mean annual precipitation range and the need of water availability (Wiser et al. 1996). The mean temperature experienced during the wettest quarter is close but cooler than the July mean temperature (Cogbill and White 1991). On the opposite end of the spectrum for the driest quarter, it is during the winter months.

Model outputs differ between models and should be chosen based on the questions that are being asked (Hijmans and Graham 2006; Naimi et al. 2011). Statistical assessments reveal the better performing model, but are limited based on the provided parameters that may negate variables that may be important, but difficult to capture (Williams et al. 2009). Visually comparing models based on the known extent of a species from other studies is essential to understand the biases observed in a model (Mi et al. 2017). Rare species pose a particular difficulty because not only are the sample sizes small, the distribution of these samples to adequately understand their true range creates power issues and ultimately stifles the model's robustness and lead to overprediction (Figure 2.4 c,d) (Wilds et al. 2000; Williams et al. 2009). It is suggested that the sample size should be 10 times larger than the number of variables used in the model (Breiner et al. 2015). Fraser fir originally had 14 after performing a stepwise variable selection, requiring 140 points. After rarefication, Fraser fir only had 80 points that then had to be split into training and testing data for the models. With the introduction of a bias file, the environmental variables went down to seven.

There will always be a level of uncertainty when choosing and interpreting a model due to the multitude of factors that are not possible to enter into a model, such as biotic factors like dispersal limitation, competition, and random events (Wiser et al. 1998; Griesbauer et al. 2011; Soberón and Peterson 2005). There is also the limitation of acquiring adequate samples along mountains, which is reflected with Unaka Mountain having no location points due to limited and difficult access to the peak (Figure 2.2) (Araújo and Guisan 2006; Clark et al. 2014). When observing a model, it is pertinent to understand that they assume tree species occur wherever possible based on the aligning variables and that the species are in equilibrium with the environment and may not be sustained outside of that environment (Iverson and Prasad 2001).

Most models are not able to incorporate human impacts, such as logging. Red spruce was historically widespread above 910 m in west-central VA, but now is only observed at higher elevations due to logging. This may explain why red spruce looks to cover more area within all of the models compared to maps by the USFS and NC Wildlife (Figure 2.3c-d) (Cogbill and White 1991). The lack of adequate explanatory variables for Fraser fir can also explain why both RF and GBM performed poorly for Fraser fir (Figure 2.4c,d), whereas Maxent performed better with a bias file (Figure 2.4b). RF nearly always has a better statistical performance with TSS and AUC and tends to do well in undersampled areas (Williams et al. 2009; Mi et al. 2017). However, there are multiple implementations to use RF such as the R packages randomForest and biomod2, Python, and a GUI which may lead to differences in performance based on computation power and options (Mi et al. 2017).

When comparing historic projections, it should be noted that climate change within the past 18,000 years has been responsible for the changing distribution of trees that can be observed in late Quaternary pollen records (Prentice et al. 1993). During the Wisconsinian glacial period, which started 110,000 years ago and ended with the LGM, balsam fir was in a mixed boreal forest that spread from the coast of Virginia and North Carolina into the Piedmont region (Figure 2.5c) (Potter et al. 2009). When observing pollen core data sites (Figure 2.9), Rockyhound Bay, Quicksand Pond, Chesapeake Bay, Browns Pond, Cranberry Glades, Anderson Pond, and Jackson Pond had the presence of *Abies* and *Picea* pollen prior to 20,000 years BP. Because of the intense coldness and dryness during this period, fir presence was minimal (Prentice et al. 1993). Based on what influences the current models, precipitation plays an important role for both species by residing near the Atlantic coast to withstand reduced precipitation near the LGM alpine permafrost (north of 38° N) and tundra (north of 34° N) (Delcourt 1979; French and

Millar 2013). Fraser fir, intermediate fir (Canaan fir, *Abies balsamea* var. *pahnerolepis*), and maritime balsam fir are genetically similar, so it is suggested that during this time they shared a Pleistocene glacial refuge that stemmed from balsam fir (Potter et al. 2009). SAM red spruce was also very similar to the current northern extent (Delcourt 1979).

Significant change occurred between the LGM and Mid-Holo that influenced the drastic expansion and contraction with no overlap (Figure 2.5a,c). Between 18,000 to 16,300 years before present (BP), red spruce declined where balsam fir had trace amounts, from consistent low precipitation, while only amounting to 1,000 m in elevation at 35°N (Delcourt 1979; Prentice et al. 1993; Hayes et al. 2006). Presence of pollen was prominent at Anderson Pond and Brown Pond during this period (Figure 2.9). Temperatures increased suddenly 16,000 years BP, signaling retreat from both species either latitudinally or altitudinally (Potter et al. 2009).

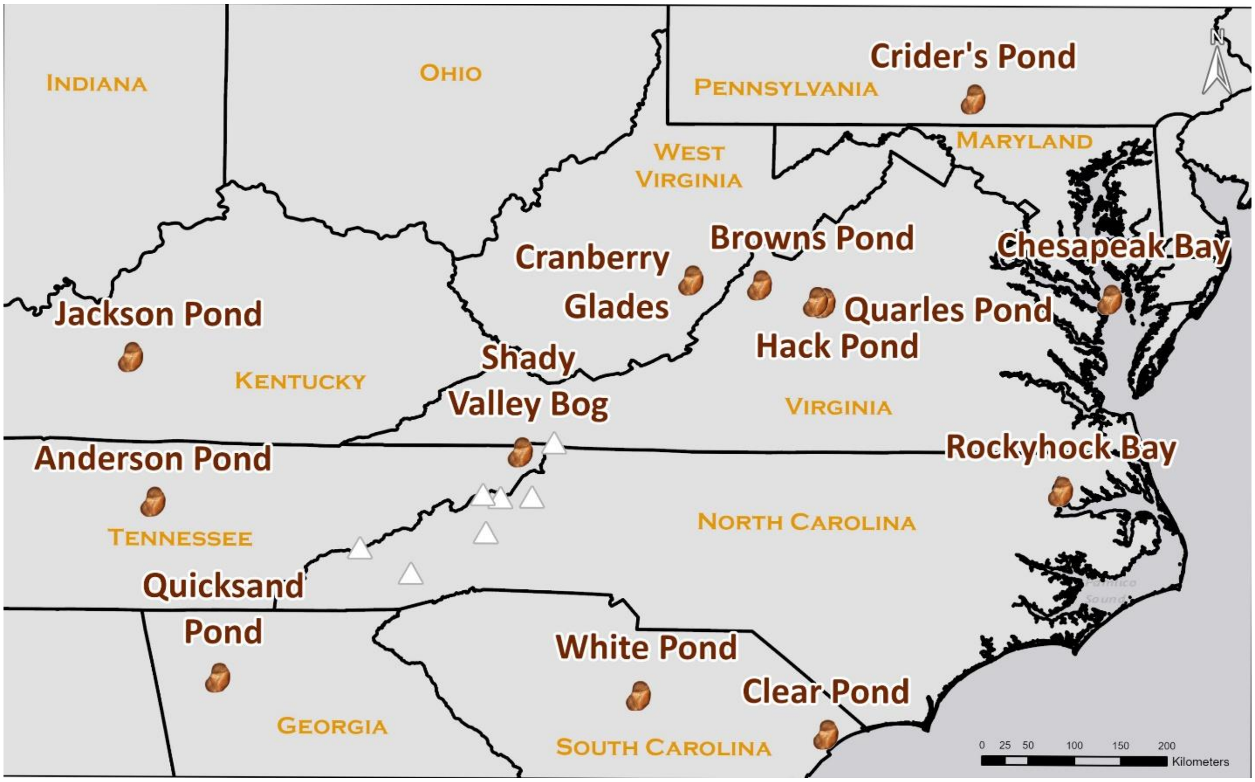

Figure 2.9. Locations of pollen core data containing genus *Abies* and *Picea* derived from Neotoma data.

The tundra that resided in the Piedmont foothills and mountains north of 34° latitude infers why it was easier for species to migrate on the eastern side of the Appalachians since minimal species resided there during the LGM and there were less fires compared to areas inland (Cwynar 1990; French and Millar 2013). Both red spruce and fir were able to populate the SAM more between 16,300 and 12,500 years BP while the Laurentide ice sheet decreased (Delcourt 1979). Neotoma pollen core data show high consistency of red spruce at Rockyhound Bay, Hack Pond, Cranberry Glades, Anderson Pond, Jackson Pond, and Crider's Pond. Anderson Pond and Browns Pond sees a fair amount of Fraser fir during this period with very minimal numbers at Rockyhound Bay, Cranberry Glades, and Jackson Pond. Crider's Pond saw a significant increase of Fraser fir pollen around 13,255. During this period by 14,180 years BP, it is recognized that SF forests were established (Kneller and Peteet 1999). Warming and deglaciation continued into the Bølling-Allerød period that led to the rise of oak, hickory, beech, ash, and hornbeam (Peteet 2000). Increase in precipitation during this period also allowed for the establishment and northeastward expansion of fir (Prentice et al. 1993). The Younger Dryas Cold Snap that began around 13,000 to 11,600 years BP witnessed the most abrupt climate change where temperature declined between 6° and 20°C (Peteet 2000). Warming occurred again, bringing the temperatures back up by 6°C that helped define the Pleistocene-Holocene boundary along with ecosystem and landscape instability (Delcourt 1979; Peteet 2000). This boundary experienced an increase in deciduous trees, a decrease in fir, and the continued migration of fir to the north and primarily on the eastern side of the Appalachians (Overpeck et al. 1992; Prentice et al. 1993; Kneller and Peteet 1999; Potter et al. 2009). A cold reversal 11,300 years BP in the northern North Atlantic caused an increase in warmth, moisture, and storms that contributed to the present coastline free of ice (Cwynar 1990; Kneller and Peteet 1999). Around 10,000 years BP, balsam fir in the

Northeast and SAM were separated long enough to be genetically different based on chloroplast DNA (cpDNA) markers, thus creating a new species of Fraser fir (Potter et al. 2009). The separation of species after the LGM is the reason why balsam fir was combined with Fraser fir for the LGM model. The exclusion of other species in the model was also influenced by the fact that there are non analog forests prior to 9,000 years BP that currently exist since 40 percent of these forest compositions were lost between 16,000 and 11,000 years BP (Overpeck et al. 1992). Shady Valley Bog still has minimal amounts of Fraser fir pollen with more red spruce (Figure 2.9). Hack Pond and Crider's Pond see a significant decline in red spruce while Cranberry Glades experiences an increase. Warming and drying occurred from 8,000 until 4,000 with a peak 7,000 years BP. Drought completed the separation between northern and southern species for Fraser fir where only those at high elevations withstood this hypsithermal period (Delcourt 1979; Oosting and Billings 1951; Kneller and Peteet 1999).

The most virgin SF forest resides in the GRSM, which was identified well in the Mid-Holo model for Fraser fir (Figure 2.5c,d) (Oosting and Billings 1951; Hayes et al. 2006). The migration from the LGM to the Mid-Holo also indicates that not all species migrate northward during a changing climate (Davis 1978). The SAM provided a refuge for SF forests from unfavorable temperature and precipitation conditions, observing fast tree migrations to shift with the climate (Figure 2.5d) (Iverson and Prasad 2001; Petit et al. 2008). This warming influenced the elimination of SF forests from lower elevations and created a bottleneck effect for Fraser firs due to higher warmth and aridity compared to the present (Potter et al. 2008). A thousand years after the Mid-Holo, an increased tropical maritime air mass from the Gulf of Mexico increased precipitation and decreased temperature, lowering the ecotone from 1,700 meters to the current 1,370 meters (Delcourt 1979; Aldy et al. 1999; Hayes et al. 2006). Since then, populations on the refuge mountaintops have had no contact with each other aside from winds carrying pollen to nearby, leading to some degree of genetic isolation (Wiser et al. 1998). Mount Rogers and Whitetop Mountain—the northernmost peaks—are considered to be genetic outliers for Fraser fir, contain the most private alleles, and are the most inbred (Potter et al. 2008; 2009). The Balsam Mountains fall in the same category for alleles in addition to having the greatest allelic richness alongside Grandfather Mountain. The GRSM and Grandfather Mountain both have the most alleles per locus (Potter et al. 2008). Mount Mitchell is the least inbred. Grandfather Mountain has the highest genetic variation despite it being one of the smaller populations due to its proximity to Mount Mitchell and Roan (Potter et al. 2008). While Fraser fir may be genetically impoverished compared to other conifers, high winds contribute to adequate dispersal for pollen to create genetically well-mixed populations (Potter et al. 2008; 2009).

Assumptions can be made as to which peaks will progress in the future based on genetics, but changes in climate and extremes are more urgent to comprehend for future habitats. All futures exhibit a decline for both species within the SAM, particularly in the lower elevations (Figures 2.6 and 2.7) (Kaylor et al. 2017). This is also observed in two other studies where the next few decades exhibit a reduction in habitat, but one of them expressed a recovery in mature overstory during this period (Potter et al. 2010; Kaylor et al. 2017). The GRSM shows a promising location, even if only at the highest peaks, for both species. This may be due to the GRSM having the largest block of old growth and containing the most virgin forest (Oosting and Billings 1951, Hayes et al. 2006). For red spruce, all other locations bode well for both RCPs in 2050 including Big Bald, Beech Mountain, Plott Balsam Mountains, Sugar Mountain, and Elk Knob.

It may be speculated that the development of the current climate dataset attributes to why red spruce's model output for 2050 RCP 8.5 is the closest visually to the USFS and NC Wildlife's SF delineation maps. WorldClim produces the current environmental data based on climate data from 1960 to 1990. Areas high in latitude and altitude are impacted by climate change to a higher degree than most surrounding areas, especially where trees exist near the limit of their range (Araújo and Guisan 2006; Aitken et al. 2008; Hampe and Jump 2011; Palmate et al. 2014; White et al. 2014). Since this study has been conducted, the WorldClim data has been updated to contain climate data from 1970 to 2000, but not for the global circulation model (GCM) CCSM4 (Fick and Hijmans 2020). It could also be due to the extent of logging and impact of balsam woolly adelgid severely stunting the regeneration of SF forests to occupy its full fundamental niche, equating the severity of reduction to RCP 8.5 in 2050 for the fundamental niche.

The projections for 2070 RCP 4.5 for both species still see some reduction, but to a significantly lesser degree compared to RCP 8.5. The red spruce projection of 2070 RCP 4.5 (Figure 2.6c) shows more habitat withstanding contraction than 2050 RCP 8.5 (Figure 2.6b). There is no expansion in the SAM for red spruce, only into Canada. One study anticipates the decline in lower elevations (Kaylor et al. 2017), but two more studies agree that overall SF habitat will expand toward the end of the century (Potter et al. 2010; Koo et al. 2015). Fraser fir has a similar prediction in contradiction to the projected models here (Potter et al. 2010; Kaylor et al 2017). However, with the importance of precipitation and cloud immersion, one study suggests the lowering of cloud height and the eventual rise to where it is higher than current (Berry and Smith 2012; Berry et al. 2013; Richardson et al. 2003). Fraser fir may be following the pattern of reduced precipitation for its contraction particularly in 2070 RCP 8.5 since the lower peaks receive more rain (Simon et al. 2005).

Conclusion

Temperature and precipitation parameters act as surrogates for geographical variables that contribute to interpreting the delineation of species within ENMs (Soberón and Peterson 2005). It is evident in the models that Fraser fir responds significantly to precipitation to ensure it receives adequate amounts. This is observed in its historical distribution near the coasts and the southernmost peaks withstanding worst-case scenario futures since they receive more moisture from the Gulf (Shanks 1954; Delcourt 1979; Simon et al. 2005). This is also reflected in temperature seasonality and mean diurnal range being important since cloud covers provide a blanket of protection during the summer's heat. Reduction of precipitation and rise to a cloud ceiling will give way to more extreme events, to which Fraser firs are ill-suited (Oosting and Billings 1951; Peters 1990). Red spruce followed similar patterns of previous studies where they experience reduction in future climates, but are still able to find refuge on the higher peaks (Potter et al. 2010; Kaylor et al. 2017).

Future research calls for employing more models and better data to ensure that the statistics match with the visual outputs. The recent update of WorldClim data to bring climate data closer to the present will improve model outputs (Fick and Hijmans 2017). Future projections are also made at 20-year intervals so it is easier to outline which periods will experience the most decline. Rare species, particularly those along complex topography, require larger resolution to pick up environmental gradients, so it is recommended to wait until the 30 arc second data is available (Franklin 2012). Additional variables should also be considered to better represent anthropogenic influences like fragmentation or other disturbances such as wind, ice, and extreme weather events (Mi et al. 2017). While models perform better with less overlapping variables, ensembling models to generate weight input for the overall model mitigate this issue. Additional GCMs can also be added into these models to provide a better summarization of what may happen (Breiner et al. 2015; Shabani et al. 2017). The future of conservation is about managing change and being able to incorporate finer temporal scale data in addition to more information within models that can provide the quality of information needed to mitigate climate change (Delcourt and Delcourt 1998; Thomas 2011).

A relict habitat like SF forests are conservation hotspots and should bring together multiple fields of study to comprehend where a habitat has been and where it may go based on a changing climate (Hampe and Jump 2011). Collaborative efforts with genetics, remote sensing, field biology, and statistical modeling bring together information to provide exceptional explanatory power to models and ultimately conservation efforts (Pitelka 1997; Allen and Kupfer 2001; Aitkin et al. 2008; Hu et al. 2009; Cord et al. 2013; He et al. 2015). There will always be room for improvements, such as increased occurrence points along gradients and better spatial distribution (Simon et al. 2005; Araújo and Guisan 2006; Shibani et al. 2017). There will always be a level of uncertainty with ENMs, but with internal and external validation from adequate presence data, fossil records, and other models, ENMs provide an essential and necessary service for conservation management (Griesbauer et al. 2011; Thomas 2011; Wang et al. 2012; Seidl and Lexer 2013).

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CHAPTER 3. CONCLUSIONS AND FUTURE WORK

A clear upward trend in global and regional temperatures are apparent and will continue into subsequent decades, making it pertinent to understand how species will survive in this type of environment where it will be sunnier and lower humidity, both which may negatively impact the SF forests (Berry and Smith 2012). ENMs are helpful in understanding possible impacts, but some improvements need to be implemented for this habitat in particular. While red spruce has adequate samples in regard to quantity and quality, Fraser fir is severely lacking. Because of the difficult terrain, many occurrence points are overlapping or within 1 kilometer of each other, increasing spatial autocorrelation and overestimation (Bahn and McGill 2012). Fraser firs need more samples that are spatially distributed and along gradients (Simon et al. 2005; Araújo and Guisan 2006). This can be done by employing volunteers for field efforts or through the use of unmanned aerial vehicles (UAVs) (Wilds et al. 2000; Mi et al. 2017). Purposefully selecting outliers to observe the presence of Fraser firs generates better validation for models (Shabani et al. 2017). Though limited through available data, increased resolution can significantly help with rare species that reside in small niches and complex topography (Simon et al. 2005). Large spatial resolution results in loss of occurrence points for explanatory power within models that impacts rare species the most (Franklin et al. 2012). One method is to spatially correct climate data down to 90 meters using ancillary data, improving the correlation with plant distributions and the selected climate variables (Franklin et al. 2012).

Model accuracy will always be questioned, especially since outputs can vary depending on the approach and the GCM used (Wang et al. 2012). It is also admissible to understand all that may influence a species such as population dynamics, sensitivity to disturbances, and of course climate, leading to a multitude of predictors that can impact the model’s performance (Araújo and Guisan 2006). Both of these issues can be simultaneously combatted through the use of ensembles, or model averaging (Iverson and Prasad 2001; Araújo and Guisan 2006; Breiner et al. 2015; Shabani et al. 2017). Since rare species tend to include more variables than most, this can allow them to include more explanatory power by using small bivariate models using two predictors. The models are then combined by using weights inferred from the model performances so as not to lose explanatory power, to stabilize inference, and generate better predictions (Breiner et al. 2015).

Ensembles allow additional variables to be considered for models at least in the current projections. Weather studies that include cloud regimes, teleconnections, and anomalies can be influential to a species like Fraser fir (Peters 1990; Hampe and Jump 2011; Berry et al. 2013). While this study attempted to include biotic interactions, more research is needed to better understand forest structure and composition through interspecific interactions and metapopulation dynamics (Busing and Mailly 2004; Soberón and Peterson 2005). Scale also plays an important role. As a whole for red spruce, Fraser fir is not important to their distribution; however, in the SAM Fraser fir provides shelter allowing them to reach higher elevations (Busing et al. 1993; Busing and Pauley 1994; Busing 2004). The same can be said for the importance of yellow birch along ecotones and in regeneration gaps (White et al. 1985; Cogbill and White, 1991). Other disturbances aside from ice and wind that need to be included in models are roads, railroads, rivers, lakes, coastline, and settlement maps as a way to include anthropogenic influences that are not pollution-based, but rather near the realm of fragmentation (Mi et al. 2017).

The use of remote sensing can be useful for acquiring occurrence points where UAVs are not permitted due to protection laws of national and state forests and parks (Allen and Kupfer

2001). Remote sensing has been slowly introduced into the realm of ENMs to infer more about known absences, abiotic influence, dispersal barriers, and even biotic interactions (Cord et al. 2013). Additional variables can be included in models such as normalized difference vegetation index (NDVI), leaf area index, biophysical, biochemical, and physiological predictors, or spectral signature of specific species (He et al. 2015; Cord et al. 2013). Accuracy can vary between 76.5 to 93.2 percent when combined with hyperspectral imagery and light detection and ranging (Lidar) due to geographical biases and lack of interpolation (He et al. 2015). It can also be used to acquire ecotone position and data (Hayes et al. 2006).

Model accuracy can also be acquired through using paleo data as a natural lab. Projected models should be compared with the fossil record such as pollen cores or even cpDNA (Aitkin et al. 2008). Reproductive rates, maturity, lag times, and life histories help inform historical and future migrations to generate a better picture as to how a species will react to climate change (Pitelka et al. 1997). One way this can be done is to observe the maternally inherited markers to track historic geographic locations. This is possible with trees because few generations have passed, causing less genetic drift and essentially “fossilizing” and “carrying over” the genes (Hu et al. 2009). This genetic data can track postglacial migration and dispersal patterns of a species. Rare species that are also controllers require attention from all fields to mitigate the impacts of climate change. Utilizing ENMs in combination with fossil records, genetics, and remote sensing can improve the quality of information provided to conservation management agencies and effectively triage the potential loss of so many species and biodiversity.

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APPENDIX: R CODE

```
install.packages(c('dismo', 'rgdal', 'maptools', 'biomod2'))
library(dismo)
library(biomod2)
library(rgdal)
library(maptools)

#Input species data
Balsam_Test <-
read.csv("C:\\Temp\\Thesis\\\Species\\BalsamWoollyAdelgid\\train_test\\balsamwoolly_all_test.
csv")
Balsam_Train <-
read.csv("C:\\Temp\\Thesis\\Species\\BalsamWoollyAdelgid\\train_test\\balsamwoolly_all_train.
csv")

Fraser_Test <- read.csv("C:\\Temp\\Thesis\\Species\\FraserFir\\train_test\\fraserfir_test.csv")
Fraser_Train <- read.csv("C:\\Temp\\Thesis\\Species\\FraserFir\\train_test\\fraserfir_train.csv")

Mash_Test <- read.csv("C:\\Temp\\Thesis\\Species\\MountainAsh\\train_test\\mash_test.csv")
Mash_Train <- read.csv("C:\\Temp\\Thesis\\Species\\MountainAsh\\train_test\\mash_train.csv")

Maple_Test <-
read.csv("C:\\Temp\\Thesis\\Species\\MountainMaple\\train_test\\mmaple_test.csv")
Maple_Train <-
read.csv("C:\\Temp\\Thesis\\Species\\MountainMaple\\train_test\\mmaple_train.csv")

Beech_Test <-
read.csv("C:\\Temp\\Thesis\\Species\\NAmBeech\\train_test\\nambeech_test.csv")
Beech_Train <-
read.csv("C:\\Temp\\Thesis\\Species\\NAmBeech\\train_test\\nambeech_train.csv")

Phytoph_Test <-
read.csv("C:\\Temp\\Thesis\\Species\\Phytophthora\\train_test\\phytoph_test.csv")
Phytoph_Train <-
read.csv("C:\\Temp\\Thesis\\Species\\Phytophthora\\train_test\\phytoph_train.csv")

Spruce_Test <- read.csv("C:\\Temp\\Thesis\\Species\\RedSpruce\\train_test\\redspruce_test.csv")
Spruce_Train <-
read.csv("C:\\Temp\\Thesis\\Species\\RedSpruce\\train_test\\redspruce_train.csv")
```

```
Rhodo_Test <- read.csv("C:\\Temp\\Thesis\\Species\\Rhododendron\\train_test\\rhodo_test.csv")
Rhodo_Train <-
read.csv("C:\\Temp\\Thesis\\Species\\Rhododendron\\train_test\\rhodo_train.csv")

Birch_Test <- read.csv("C:\\Temp\\Thesis\\Species\\YellowBirch\\train_test\\ylwbirch_test.csv")
Birch_Train <-
read.csv("C:\\Temp\\Thesis\\Species\\YellowBirch\\train_test\\ylwbirch_train.csv")

#Input predictor data
Current_vars_path <- file.path("C:\\Temp\\Thesis\\AndrewVars\\Test\\Current")
Current_vars <- list.files(Current_vars_path, pattern = 'asc$', full.names = TRUE)
predictors <- stack(Current_vars)
names(predictors)

#Models for each species

#################################################
#Balsam
#################################################

BalsamName <- "species"
BalsamXY <- Balsam_Train[,c("Longitude","Latitude")]
RespBalsam <- as.numeric(Balsam_Train[,BalsamName])

BalsamBiomodData <- BIOMOD_FormatingData(resp.var = RespBalsam,
                                         expl.var = predictors,
                                         resp.xy = BalsamXY,
                                         resp.name = BalsamName,
                                         PA.nb.rep = 1,
                                         PA.nb.absences = 200,
                                         PA.strategy = 'random')
plot(BalsamBiomodData)


BiomodOption <- BIOMOD_ModelingOptions()
BalsamModelOut <- BIOMOD_Modeling(BalsamBiomodData,
                                  models = c("GBM", "RF"),
                                  models.options = BiomodOption,
                                  NbRunEval = 1,
```

```
                              Prevalence = 0.5,
                              VarImport = 3,
                              models.eval.meth = c('TSS', 'ROC'),
                              SaveObj = TRUE,
                              rescal.all.models = TRUE,
                              do.full.models = FALSE,
                              modeling.id = paste(BalsamName, "BalsamModeling", sep=""))

BalsamModelOut

#Get test metrics for GBM
BalsamModelEval <- get_evaluations(BalsamModelOut)
dimnames(BalsamModelEval)
BalsamModelEval["TSS", "Testing.data", "GBM",,]
BalsamModelEval["TSS", "Testing.data", "RF",,]
BalsamModelEval["ROC", "Testing.data", "GBM",,]
BalsamModelEval["ROC", "Testing.data", "RF",,]
get_variables_importance(BalsamModelOut)

#Project
BalsamProj <- BIOMOD_Projection(modeling.output = BalsamModelOut,
                             new.env = predictors,
                             proj.name = 'balsam',
                             selected.models = 'all',
                             binary.meth = 'TSS',
                             compress = 'xz',
                             clamping.mask=F,
                             do.stack=F,
                             output.format='.img')

#Display
plot(BalsamProj,str.grep='GBM')
plot(BalsamProj,str.grep='RF')

proj.Balsam <- get_predictions(BalsamProj)

#ID which laer correspond to which projection
names(proj.Balsam)

#choose which layer you want to export
```

```
writeRaster(subset(proj.Balsam, "species_PA1_Full_GBM"), filename = "balsamGBM.asc")
writeRaster(subset(proj.Balsam, "species_PA1_Full_RF"), filename = "balsamRF.asc")




################################################################
#FraserFir
################################################################

FraserName <- "species"
FraserXY <- Fraser_Train[,c("Longitude","Latitude")]
RespFraser <- as.numeric(Fraser_Train[,FraserName])

FraserBiomodData <- BIOMOD_FormatingData(resp.var = RespFraser,
                                         expl.var = predictors,
                                         resp.xy = FraserXY,
                                         resp.name = FraserName,
                                         PA.nb.rep = 1,
                                         PA.nb.absences = 500,
                                         PA.strategy = 'random')
plot(FraserBiomodData)

BiomodOption <- BIOMOD_ModelingOptions()
FraserModelOut <- BIOMOD_Modeling(FraserBiomodData,
                                  models = c("GBM", "RF"),
                                  models.options = BiomodOption,
                                  NbRunEval = 1,
                                  Prevalence = 0.5,
                                  VarImport = 3,
                                  models.eval.meth = c('TSS', 'ROC'),
                                  SaveObj = TRUE,
                                  rescal.all.models = TRUE,
                                  do.full.models = FALSE,
                                  modeling.id = paste(FraserName, "FraserModeling", sep=""))
FraserModelOut

#Get test metrics for GBM
FraserModelEval <- get_evaluations(FraserModelOut)
dimnames(FraserModelEval)
```

```
FraserModelEval["TSS", "Testing.data", "GBM",,]
FraserModelEval["TSS", "Testing.data", "RF",,]
FraserModelEval["ROC", "Testing.data", "GBM",,]
FraserModelEval["ROC", "Testing.data", "RF",,]
get_variables_importance(FraserModelOut)

#Project
FraserProj <- BIOMOD_Projection(modeling.output = FraserModelOut,
                        new.env = predictors,
                        proj.name = 'fraser',
                        selected.models = 'all',
                        binary.meth = 'TSS',
                        compress = 'xz',
                        clamping.mask=F,
                        do.stack=F,
                        output.format='.img')

#Display
plot(FraserProj,str.grep='GBM')
plot(FraserProj,str.grep='RF')

proj.Fraser <- get_predictions(FraserProj)

#ID which laer correspond to which projection
names(proj.Fraser)

#choose which layer you want to export
writeRaster(subset(proj.Fraser, "species_PA1_Full_GBM"), filename = "fraserGBM.asc")
writeRaster(subset(proj.Fraser, "species_PA1_Full_RF"), filename = "fraserRF.asc")



##############################################################################
############
#Mountain Ash
##############################################################################
############

MashName <- "species"
MashXY <- Mash_Train[,c("Longitude","Latitude")]
```

```
RespMash <- as.numeric(Mash_Train[,MashName])

MashBiomodData <- BIOMOD_FormatingData(resp.var = RespMash,
                              expl.var = predictors,
                              resp.xy = MashXY,
                              resp.name = MashName,
                              PA.nb.rep = 1,
                              PA.nb.absences = 500,
                              PA.strategy = 'random')
plot(MashBiomodData)

BiomodOption <- BIOMOD_ModelingOptions()
MashModelOut <- BIOMOD_Modeling(MashBiomodData,
                            models = c("RF"),
                            models.options = BiomodOption,
                            NbRunEval = 1,
                            Prevalence = 0.5,
                            VarImport = 3,
                            models.eval.meth = c('TSS', 'ROC'),
                            SaveObj = TRUE,
                            rescal.all.models = TRUE,
                            do.full.models = FALSE,
                            modeling.id = paste(MashName, "MashModeling", sep=""))
MashModelOut

#Get test metrics for GBM
MashModelEval <- get_evaluations(MashModelOut)
dimnames(MashModelEval)
MashModelEval["TSS", "Testing.data", "GBM",,]
MashModelEval["TSS", "Testing.data", "RF",,]
MashModelEval["ROC", "Testing.data", "GBM",,]
MashModelEval["ROC", "Testing.data", "RF",,]
get_variables_importance(MashModelOut)

#Project
MashProj <- BIOMOD_Projection(modeling.output = MashModelOut,
                          new.env = predictors,
                          proj.name = 'ash',
                          selected.models = 'all',
                          binary.meth = 'TSS',
```

```
                          compress = 'xz',
                          clamping.mask=F,
                          do.stack=F,
                          output.format='.img')

#Display
plot(MashProj,str.grep='GBM')
plot(MashProj,str.grep='RF')

proj.Mash <- get_predictions(MashProj)

#ID which laer correspond to which projection
names(proj.Mash)

#choose which layer you want to export
writeRaster(subset(proj.Mash, "species_PA1_Full_GBM"), filename = "ashGBM.asc")
writeRaster(subset(proj.Mash, "species_PA1_Full_RF"), filename = "ashRF.asc")


################################################################################
###############
#Mountain Maple
################################################################################
###############

MapleName <- "species"
MapleXY <- Maple_Train[,c("Longitude","Latitude")]
RespMaple <- as.numeric(Maple_Train[,MapleName])

MapleBiomodData <- BIOMOD_FormatingData(resp.var = RespMaple,
                              expl.var = predictors,
                              resp.xy = MapleXY,
                              resp.name = MapleName,
                              PA.nb.rep = 1,
                              PA.nb.absences = 500,
                              PA.strategy = 'random')
plot(MapleBiomodData)

BiomodOption <- BIOMOD_ModelingOptions()
MapleModelOut <- BIOMOD_Modeling(MapleBiomodData,
```

```
                              models = c("RF"),
                              models.options = BiomodOption,
                              NbRunEval = 1,
                              Prevalence = 0.5,
                              VarImport = 3,
                              models.eval.meth = c('TSS', 'ROC'),
                              SaveObj = TRUE,
                              rescal.all.models = TRUE,
                              do.full.models = FALSE,
                              modeling.id = paste(MapleName, "MapleModeling", sep=""))
MapleModelOut

#Get test metrics for GBM
MapleModelEval <- get_evaluations(MapleModelOut)
dimnames(MapleModelEval)
MapleModelEval["TSS", "Testing.data", "GBM",,]
MapleModelEval["TSS", "Testing.data", "RF",,]
MapleModelEval["ROC", "Testing.data", "GBM",,]
MapleModelEval["ROC", "Testing.data", "RF",,]
get_variables_importance(MapleModelOut)

#Project
MapleProj <- BIOMOD_Projection(modeling.output = MapleModelOut,
                             new.env = predictors,
                             proj.name = 'maple',
                             selected.models = 'all',
                             binary.meth = 'TSS',
                             compress = 'xz',
                             clamping.mask=F,
                             do.stack=F,
                             output.format='.img')

#Display
plot(MapleProj,str.grep='GBM')
plot(MapleProj,str.grep='RF')

proj.Maple <- get_predictions(MapleProj)

#ID which laer correspond to which projection
names(proj.Maple)
```

```
#choose which layer you want to export
writeRaster(subset(proj.Maple, "species_PA1_Full_GBM"), filename = "mapleGBM.asc")
writeRaster(subset(proj.Maple, "species_PA1_Full_RF"), filename = "mapleRF.asc")


###############################################################################
################
#N. Am. Beech
###############################################################################
################

BeechName <- "species"
BeechXY <- Beech_Train[,c("Longitude","Latitude")]
RespBeech <- as.numeric(Beech_Train[,BeechName])

BeechBiomodData <- BIOMOD_FormatingData(resp.var = RespBeech,
                              expl.var = predictors,
                              resp.xy = BeechXY,
                              resp.name = BeechName,
                              PA.nb.rep = 1,
                              PA.nb.absences = 500,
                              PA.strategy = 'random')
plot(BeechBiomodData)

BiomodOption <- BIOMOD_ModelingOptions()
BeechModelOut <- BIOMOD_Modeling(BeechBiomodData,
                            models = c("RF"),
                            models.options = BiomodOption,
                            NbRunEval = 1,
                            Prevalence = 0.5,
                            VarImport = 3,
                            models.eval.meth = c('TSS', 'ROC'),
                            SaveObj = TRUE,
                            rescal.all.models = TRUE,
                            do.full.models = FALSE,
                            modeling.id = paste(BeechName, "BeechModeling", sep=""))
BeechModelOut

#Get test metrics for GBM
```

```
BeechModelEval <- get_evaluations(BeechModelOut)
dimnames(BeechModelEval)
BeechModelEval["TSS", "Testing.data", "GBM",,]
BeechModelEval["TSS", "Testing.data", "RF",,]
BeechModelEval["ROC", "Testing.data", "GBM",,]
BeechModelEval["ROC", "Testing.data", "RF",,]
get_variables_importance(BeechModelOut)

#Project
BeechProj <- BIOMOD_Projection(modeling.output = BeechModelOut,
                               new.env = predictors,
                               proj.name = 'beech',
                               selected.models = 'all',
                               binary.meth = 'TSS',
                               compress = 'xz',
                               clamping.mask=F,
                               do.stack=F,
                               output.format='.img')

#Display
plot(BeechProj,str.grep='GBM')
plot(BeechProj,str.grep='RF')

proj.Beech <- get_predictions(BeechProj)

#ID which laer correspond to which projection
names(proj.Beech)

#choose which layer you want to export
writeRaster(subset(proj.Beech, "species_PA1_Full_GBM"), filename = "beechGBM.asc")
writeRaster(subset(proj.Beech, "species_PA1_Full_RF"), filename = "beechRF.asc")



###################################################################################
##############
#Phytophthora
###################################################################################
##############
```

```
PhytophName <- "species"
PhytophXY <- Phytoph_Train[,c("Longitude","Latitude")]
RespPhytoph <- as.numeric(Phytoph_Train[,PhytophName])

PhytophBiomodData <- BIOMOD_FormatingData(resp.var = RespPhytoph,
                                expl.var = predictors,
                                resp.xy = PhytophXY,
                                resp.name = PhytophName,
                                PA.nb.rep = 1,
                                PA.nb.absences = 500,
                                PA.strategy = 'random')
plot(PhytophBiomodData)

BiomodOption <- BIOMOD_ModelingOptions()
PhytophModelOut <- BIOMOD_Modeling(PhytophBiomodData,
                              models = c("RF"),
                              models.options = BiomodOption,
                              NbRunEval = 1,
                              Prevalence = 0.5,
                              VarImport = 3,
                              models.eval.meth = c('TSS', 'ROC'),
                              SaveObj = TRUE,
                              rescal.all.models = TRUE,
                              do.full.models = FALSE,
                              modeling.id = paste(PhytophName, "PhytophModeling", sep=""))
PhytophModelOut

#Get test metrics for GBM
PhytophModelEval <- get_evaluations(PhytophModelOut)
dimnames(PhytophModelEval)
PhytophModelEval["TSS", "Testing.data", "GBM",,]
PhytophModelEval["TSS", "Testing.data", "RF",,]
PhytophModelEval["ROC", "Testing.data", "GBM",,]
PhytophModelEval["ROC", "Testing.data", "RF",,]
get_variables_importance(PhytophModelOut)

#Project
PhytophProj <- BIOMOD_Projection(modeling.output = PhytophModelOut,
                            new.env = predictors,
                            proj.name = 'phytophthora',
```

```
                        selected.models = 'all',
                        binary.meth = 'TSS',
                        compress = 'xz',
                        clamping.mask=F,
                        do.stack=F,
                        output.format='.img')

#Display
plot(PhytophProj,str.grep='GBM')
plot(PhytophProj,str.grep='RF')

proj.Phytoph <- get_predictions(PhytophProj)

#ID which laer correspond to which projection
names(proj.Phytoph)

#choose which layer you want to export
writeRaster(subset(proj.Phytoph, "species_PA1_Full_GBM"), filename = "phytophGBM.asc")
writeRaster(subset(proj.Phytoph, "species_PA1_Full_RF"), filename = "phytophRF.asc")


###################################################################################################
#Red Spruce
###################################################################################################

SpruceName <- "species"
SpruceXY <- Spruce_Train[,c("Longitude","Latitude")]
RespSpruce <- as.numeric(Spruce_Train[,SpruceName])

SpruceBiomodData <- BIOMOD_FormatingData(resp.var = RespSpruce,
                                expl.var = predictors,
                                resp.xy = SpruceXY,
                                resp.name = SpruceName,
                                PA.nb.rep = 1,
                                PA.nb.absences = 500,
                                PA.strategy = 'random')
plot(SpruceBiomodData)
```

```
BiomodOption <- BIOMOD_ModelingOptions()
SpruceModelOut <- BIOMOD_Modeling(SpruceBiomodData,
                                  models = c("RF"),
                                  models.options = BiomodOption,
                                  NbRunEval = 1,
                                  Prevalence = 0.5,
                                  VarImport = 3,
                                  models.eval.meth = c('TSS', 'ROC'),
                                  SaveObj = TRUE,
                                  rescal.all.models = TRUE,
                                  do.full.models = FALSE,
                                  modeling.id = paste(SpruceName, "SpruceModeling", sep=""))
SpruceModelOut

#Get test metrics for GBM
SpruceModelEval <- get_evaluations(SpruceModelOut)
dimnames(SpruceModelEval)
SpruceModelEval["TSS", "Testing.data", "GBM",,]
SpruceModelEval["TSS", "Testing.data", "RF",,]
SpruceModelEval["ROC", "Testing.data", "GBM",,]
SpruceModelEval["ROC", "Testing.data", "RF",,]
get_variables_importance(SpruceModelOut)

#Project
SpruceProj <- BIOMOD_Projection(modeling.output = SpruceModelOut,
                                new.env = predictors,
                                proj.name = 'spruce',
                                selected.models = 'all',
                                binary.meth = 'TSS',
                                compress = 'xz',
                                clamping.mask=F,
                                do.stack=F,
                                output.format='.img')

#Display
plot(SpruceProj,str.grep='GBM')
plot(SpruceProj,str.grep='RF')

proj.Spruce <- get_predictions(SpruceProj)
```

```
#ID which laer correspond to which projection
names(proj.Spruce)

#choose which layer you want to export
writeRaster(subset(proj.Spruce, "species_PA1_Full_GBM"), filename = "spruceGBM.asc")
writeRaster(subset(proj.Spruce, "species_PA1_Full_RF"), filename = "spruceRF.asc")


###############################################################################
####################
#Rhododendron
###############################################################################
####################

RhodoName <- "species"
RhodoXY <- Rhodo_Train[,c("Longitude","Latitude")]
RespRhodo <- as.numeric(Rhodo_Train[,RhodoName])

RhodoBiomodData <- BIOMOD_FormatingData(resp.var = RespRhodo,
                                        expl.var = predictors,
                                        resp.xy = RhodoXY,
                                        resp.name = RhodoName,
                                        PA.nb.rep = 1,
                                        PA.nb.absences = 500,
                                        PA.strategy = 'random')
plot(RhodoBiomodData)

BiomodOption <- BIOMOD_ModelingOptions()
RhodoModelOut <- BIOMOD_Modeling(RhodoBiomodData,
                                  models = c("RF"),
                                  models.options = BiomodOption,
                                  NbRunEval = 1,
                                  Prevalence = 0.5,
                                  VarImport = 3,
                                  models.eval.meth = c('TSS', 'ROC'),
                                  SaveObj = TRUE,
                                  rescal.all.models = TRUE,
                                  do.full.models = FALSE,
                                  modeling.id = paste(RhodoName, "RhodoModeling", sep=""))
RhodoModelOut
```

```
#Get test metrics for GBM
RhodoModelEval <- get_evaluations(RhodoModelOut)
dimnames(RhodoModelEval)
RhodoModelEval["TSS", "Testing.data", "GBM",,]
RhodoModelEval["TSS", "Testing.data", "RF",,]
RhodoModelEval["ROC", "Testing.data", "GBM",,]
RhodoModelEval["ROC", "Testing.data", "RF",,]
get_variables_importance(RhodoModelOut)

#Project
RhodoProj <- BIOMOD_Projection(modeling.output = RhodoModelOut,
                              new.env = predictors,
                              proj.name = 'rhododendron',
                              selected.models = 'all',
                              binary.meth = 'TSS',
                              compress = 'xz',
                              clamping.mask=F,
                              do.stack=F,
                              output.format='.img')

#Display
plot(RhodoProj,str.grep='GBM')
plot(RhodoProj,str.grep='RF')

proj.Rhodo <- get_predictions(RhodoProj)

#ID which laer correspond to which projection
names(proj.Rhodo)

#choose which layer you want to export
writeRaster(subset(proj.Rhodo, "species_PA1_Full_GBM"), filename = "rhodoGBM.asc")
writeRaster(subset(proj.Rhodo, "species_PA1_Full_RF"), filename = "rhodoRF.asc")



##########################################################################################
#################
#Yellow Birch
```

```
##############################################################################
#################

BirchName <- "species"
BirchXY <- Birch_Train[,c("Longitude","Latitude")]
RespBirch <- as.numeric(Birch_Train[,BirchName])

BirchBiomodData <- BIOMOD_FormatingData(resp.var = RespBirch,
                        expl.var = predictors,
                        resp.xy = BirchXY,
                        resp.name = BirchName,
                        PA.nb.rep = 1,
                        PA.nb.absences = 500,
                        PA.strategy = 'random')
plot(BirchBiomodData)

BiomodOption <- BIOMOD_ModelingOptions()
BirchModelOut <- BIOMOD_Modeling(BirchBiomodData,
                      models = c("GBM", "RF"),
                      models.options = BiomodOption,
                      NbRunEval = 1,
                      Prevalence = 0.5,
                      VarImport = 3,
                      models.eval.meth = c('TSS', 'ROC'),
                      SaveObj = TRUE,
                      rescal.all.models = TRUE,
                      do.full.models = FALSE,
                      modeling.id = paste(BirchName, "BirchModeling", sep=""))
BirchModelOut

#Project
BirchProj <- BIOMOD_Projection(modeling.output = BirchModelOut,
                     new.env = predictors,
                     proj.name = 'birch',
                     selected.models = 'all',
                     binary.meth = 'TSS',
                     compress = 'xz',
                     clamping.mask=F,
                     do.stack=F,
                     output.format='.img')
```

```
#Display
plot(BirchProj,str.grep='GBM')
plot(BirchProj,str.grep='RF')

proj.Birch <- get_predictions(BirchProj)

#ID which laer correspond to which projection
names(proj.Birch)

#choose which layer you want to export
writeRaster(subset(proj.Birch, "species_PA1_Full_GBM"), filename = "birchGBM.asc")
writeRaster(subset(proj.Birch, "species_PA1_Full_RF"), filename = "birchRF.asc")


#moved files to respective folders without code cause i can do it easier manually


################################################################
#FraserFir2.0 (I'm you but better)
################################################################

#Input predictor data
FF_RF_vars_path <- file.path("C:\\Temp\\Thesis\\GBM_RF\\FF_vars\\RF")
FF_GBM_vars_path <- file.path("C:\\Temp\\Thesis\\GBM_RF\\FF_vars\\GBM")
FF_RF_vars <- list.files(FF_RF_vars_path, pattern = 'asc$', full.names = TRUE)
FF_GBM_vars <- list.files(FF_GBM_vars_path, pattern = 'asc$', full.names = TRUE)
FF_RF_predictors <- stack(FF_RF_vars)
FF_GBM_predictors <- stack(FF_GBM_vars)

FraserName <- "species"
FraserXY <- Fraser_Train[,c("Longitude","Latitude")]
RespFraser <- as.numeric(Fraser_Train[,FraserName])

FF_RF_BiomodData <- BIOMOD_FormatingData(resp.var = RespFraser,
                                         expl.var = FF_RF_predictors,
                                         resp.xy = FraserXY,
                                         resp.name = FraserName,
                                         PA.nb.rep = 1,
                                         PA.nb.absences = 500,
```

```
                              PA.strategy = 'random')

FF_GBM_BiomodData <- BIOMOD_FormatingData(resp.var = RespFraser,
                              expl.var = FF_GBM_predictors,
                              resp.xy = FraserXY,
                              resp.name = FraserName,
                              PA.nb.rep = 1,
                              PA.nb.absences = 500,
                              PA.strategy = 'random')
plot(FF_RF_BiomodData)
plot(FF_GBM_BiomodData)

BiomodOption <- BIOMOD_ModelingOptions()

FF_RF_ModelOut <- BIOMOD_Modeling(FF_RF_BiomodData,
                          models = ("RF"),
                          models.options = BiomodOption,
                          NbRunEval = 1,
                          Prevalence = 0.5,
                          VarImport = 3,
                          models.eval.meth = c('TSS', 'ROC', 'ACCURACY', 'BIAS', 'KAPPA'),
                          SaveObj = TRUE,
                          rescal.all.models = TRUE,
                          do.full.models = FALSE,
                          modeling.id = paste(FraserName, "FraserModeling_RF", sep=""))

FF_GBM_ModelOut <- BIOMOD_Modeling(FF_GBM_BiomodData,
                          models = ("GBM"),
                          models.options = BiomodOption,
                          NbRunEval = 1,
                          Prevalence = 0.5,
                          VarImport = 3,
                          models.eval.meth = c('TSS', 'ROC', 'ACCURACY', 'BIAS', 'KAPPA'),
                          SaveObj = TRUE,
                          rescal.all.models = TRUE,
                          do.full.models = FALSE,
                          modeling.id = paste(FraserName, "FraserModeling_GBM", sep=""))
FF_RF_ModelOut
```

```
#Get test metrics for GBM
FF_RF_ModelEval <- get_evaluations(FF_RF_ModelOut)
FF_GBM_ModelEval <- get_evaluations(FF_GBM_ModelOut)

dimnames(FF_RF_ModelEval)
dimnames(FF_GBM_ModelEval)



FF_GBM_ModelEval["TSS", "Testing.data", "GBM",,]
FF_RF_ModelEval["TSS", "Testing.data", "RF",,]
FF_GBM_ModelEval["ROC", "Testing.data", "GBM",,]
FF_RF_ModelEval["ROC", "Testing.data", "RF",,]
FF_GBM_ModelEval["ACCURACY", "Testing.data", "GBM",,]
FF_RF_ModelEval["ACCURACY", "Testing.data", "RF",,]
FF_GBM_ModelEval["BIAS", "Testing.data", "GBM",,]
FF_RF_ModelEval["BIAS", "Testing.data", "RF",,]
FF_GBM_ModelEval["KAPPA", "Testing.data", "GBM",,]
FF_RF_ModelEval["KAPPA", "Testing.data", "RF",,]

calculate.stat(FF_RF_ModelOut, stat='KAPPA')

get_variables_importance(FF_RF_ModelOut)
get_variables_importance(FF_GBM_ModelOut)

#Project
FF_RF_Proj <- BIOMOD_Projection(modeling.output = FF_RF_ModelOut,
                        new.env = FF_RF_predictors,
                        proj.name = 'fraser_RF',
                        selected.models = 'all',
                        binary.meth = 'TSS',
                        compress = 'xz',
                        clamping.mask=F,
                        do.stack=F,
                        output.format='.img')
FF_GBM_Proj <- BIOMOD_Projection(modeling.output = FF_GBM_ModelOut,
                        new.env = FF_GBM_predictors,
                        proj.name = 'fraser_GBM',
                        selected.models = 'all',
                        binary.meth = 'TSS',
                        compress = 'xz',
```

```
                    clamping.mask=F,
                    do.stack=F,
                    output.format='.img')


#Display
plot(FF_GBM_Proj,str.grep='GBM')
plot(FF_RF_Proj,str.grep='RF')

proj.FF_RF <- get_predictions(FF_RF_Proj)
proj.FF_GBM <- get_predictions(FF_GBM_Proj)

#ID which laer correspond to which projection
names(proj.FF_RF)
names(proj.FF_GBM)

#choose which layer you want to export
writeRaster(subset(proj.FF_RF, "species_PA1_Full_RF"), filename = "fraserGBM2.0.asc")
writeRaster(subset(proj.FF_GBM, "species_PA1_Full_GBM"), filename = "fraserRF2.0.asc")

FilteringTransformation(proj.FF_RF,0.5)



################################################################################
#####################
#Red Spruce 2: Electric Boogaloo
################################################################################
#####################
#Input predictor data
RS_RF_vars_path <- file.path("C:\\Temp\\Thesis\\GBM_RF\\RS_vars\\RF")
RS_GBM_vars_path <- file.path("C:\\Temp\\Thesis\\GBM_RF\\RS_vars\\GBM")
RS_RF_vars <- list.files(RS_RF_vars_path, pattern = 'asc$', full.names = TRUE)
RS_GBM_vars <- list.files(RS_GBM_vars_path, pattern = 'asc$', full.names = TRUE)
RS_RF_predictors <- stack(RS_RF_vars)
RS_GBM_predictors <- stack(RS_GBM_vars)
names(RS_GBM_predictors)

SpruceName <- "species"
SpruceXY <- Spruce_Train[,c("Longitude","Latitude")]
```

```
RespSpruce <- as.numeric(Spruce_Train[,SpruceName])

RS_RF_BiomodData <- BIOMOD_FormatingData(resp.var = RespSpruce,
                                   expl.var = RS_RF_predictors,
                                   resp.xy = SpruceXY,
                                   resp.name = SpruceName,
                                   PA.nb.rep = 1,
                                   PA.nb.absences = 500,
                                   PA.strategy = 'random')

RS_GBM_BiomodData <- BIOMOD_FormatingData(resp.var = RespSpruce,
                                    expl.var = RS_GBM_predictors,
                                    resp.xy = SpruceXY,
                                    resp.name = SpruceName,
                                    PA.nb.rep = 1,
                                    PA.nb.absences = 500,
                                    PA.strategy = 'random')
plot(RS_RF_BiomodData)
plot(RS_GBM_BiomodData)

BiomodOption <- BIOMOD_ModelingOptions()

RS_RF_ModelOut <- BIOMOD_Modeling(RS_RF_BiomodData,
                             models = ("RF"),
                             models.options = BiomodOption,
                             NbRunEval = 1,
                             Prevalence = 0.5,
                             VarImport = 3,
                             models.eval.meth = c('TSS', 'ROC', 'ACCURACY', 'BIAS', 'KAPPA'),
                             SaveObj = TRUE,
                             rescal.all.models = TRUE,
                             do.full.models = FALSE,
                             modeling.id = paste(SpruceName, "RS_RF_Modeling", sep=""))


RS_GBM_ModelOut <- BIOMOD_Modeling(RS_GBM_BiomodData,
                             models = ("GBM"),
                             models.options = BiomodOption,
                             NbRunEval = 1,
                             Prevalence = 0.5,
```

```
                              VarImport = 3,
                              models.eval.meth = c('TSS', 'ROC', 'ACCURACY', 'BIAS', 'KAPPA'),
                              SaveObj = TRUE,
                              rescal.all.models = TRUE,
                              do.full.models = FALSE,
                              modeling.id = paste(SpruceName, "RS_GBM_Modeling", sep=""))

#Get test metrics for GBM
RS_RF_ModelEval <- get_evaluations(RS_RF_ModelOut)
RS_GBM_ModelEval <- get_evaluations(RS_GBM_ModelOut)


dimnames(RS_RF_ModelEval)
dimnames(RS_GBM_ModelEval)


RS_GBM_ModelEval["TSS", "Testing.data", "GBM",,]
RS_RF_ModelEval["TSS", "Testing.data", "RF",,]
RS_GBM_ModelEval["ROC", "Testing.data", "GBM",,]
RS_RF_ModelEval["ROC", "Testing.data", "RF",,]

get_variables_importance(RS_RF_ModelOut)
get_variables_importance(RS_GBM_ModelOut)

#Project
RS_RF_Proj <- BIOMOD_Projection(modeling.output = RS_RF_ModelOut,
                             new.env = RS_RF_predictors,
                             proj.name = 'spruce_RF',
                             selected.models = 'all',
                             binary.meth = 'TSS',
                             compress = 'xz',
                             clamping.mask=F,
                             do.stack=F,
                             output.format='.img')
RS_GBM_Proj <- BIOMOD_Projection(modeling.output = RS_GBM_ModelOut,
                              new.env = RS_GBM_predictors,
                              proj.name = 'spruce_GBM',
                              selected.models = 'all',
                              binary.meth = 'TSS',
                              compress = 'xz',
```

```
                    clamping.mask=F,
                    do.stack=F,
                    output.format='.img')


#Display
plot(RS_GBM_Proj,str.grep='GBM')
plot(RS_RF_Proj,str.grep='RF')

proj.RS_RF <- get_predictions(RS_RF_Proj)
proj.RS_GBM <- get_predictions(RS_GBM_Proj)

#ID which laer correspond to which projection
names(proj.RS_RF)
names(proj.RS_GBM)

#choose which layer you want to export
writeRaster(subset(proj.RS_RF, "species_PA1_Full_RF"), filename = "spruceGBM2.0.asc")
writeRaster(subset(proj.RS_GBM, "species_PA1_Full_GBM"), filename = "spruceRF2.0.asc")

threshold(RS_GBM_Proj)

setwd("C:\\Temp\\Thesis\\GBM_RF")


###This is an example of a time period. Names and data were switched out based on the time
observed


##############################################################
#Mid-Holocene
##############################################################

#holocene variables
seven8.five_vars_path <- file.path("E:\\ThesisTake2\\AndrewVars\\Test\\7085")
seven8.five_vars <- list.files(seven8.five_vars_path, pattern = 'asc$', full.names = TRUE)
seven8.five_predictors <- stack(seven8.five_vars)

seven4.five_vars_path <- file.path("E:\\ThesisTake2\\AndrewVars\\Test\\7045")
seven4.five_vars <- list.files(seven4.five_vars_path, pattern = 'asc$', full.names = TRUE)
```

```
seven4.five_predictors <- stack(seven4.five_vars)

five8.five_vars_path <- file.path("E:\\ThesisTake2\\AndrewVars\\Test\\5085")
five8.five_vars <- list.files(five8.five_vars_path, pattern = 'asc$', full.names = TRUE)
five8.five_predictors <- stack(five8.five_vars)

five4.five_vars_path <- file.path("E:\\ThesisTake2\\AndrewVars\\Test\\5045")
five4.five_vars <- list.files(five4.five_vars_path, pattern = 'asc$', full.names = TRUE)
five4.five_predictors <- stack(five4.five_vars)



#Mountain Ash
Mash_Projseven8.five <- BIOMOD_Projection(modeling.output = MashModelOut,
                                new.env = seven8.five_predictors,
                                proj.name = 'Mash_7085',
                                selected.models = 'all',
                                binary.meth = 'TSS',
                                compress = 'xz',
                                clamping.mask = T,
                                output.format = '.img')

Mash_Projseven4.five <- BIOMOD_Projection(modeling.output = MashModelOut,
                                new.env = seven4.five_predictors,
                                proj.name = 'Mash_7045',
                                selected.models = 'all',
                                binary.meth = 'TSS',
                                compress = 'xz',
                                clamping.mask = T,
                                output.format = '.img')

Mash_Projfive8.five <- BIOMOD_Projection(modeling.output = MashModelOut,
                                new.env = five8.five_predictors,
                                proj.name = 'Mash_5085',
                                selected.models = 'all',
                                binary.meth = 'TSS',
                                compress = 'xz',
                                clamping.mask = T,
                                output.format = '.img')

Mash_Projfive4.five <- BIOMOD_Projection(modeling.output = MashModelOut,
```

```
                        new.env = five4.five_predictors,
                        proj.name = 'Mash_8045',
                        selected.models = 'all',
                        binary.meth = 'TSS',
                        compress = 'xz',
                        clamping.mask = T,
                        output.format = '.img')

proj.Mash.seven8.five <- get_predictions(Mash_Projseven8.five)

proj.Mash.seven4.five <- get_predictions(Mash_Projseven4.five)

proj.Mash.five8.five <- get_predictions(Mash_Projfive8.five)

proj.Mash.five4.five <- get_predictions(Mash_Projfive4.five)


writeRaster(subset(proj.Mash.seven8.five, "species_PA1_Full_RF"), filename =
"mash_7085.asc")

writeRaster(subset(proj.Mash.seven4.five, "species_PA1_Full_RF"), filename =
"mash_7045.asc")

writeRaster(subset(proj.Mash.five8.five, "species_PA1_Full_RF"), filename = "mash_5085.asc")

writeRaster(subset(proj.Mash.five4.five, "species_PA1_Full_RF"), filename = "mash_5045.asc")


#Beech
Beech_Projseven8.five <- BIOMOD_Projection(modeling.output = BeechModelOut,
                           new.env = seven8.five_predictors,
                           proj.name = 'Beech_7085',
                           selected.models = 'all',
                           binary.meth = 'TSS',
                           compress = 'xz',
                           clamping.mask = T,
                           output.format = '.img')

Beech_Projseven4.five <- BIOMOD_Projection(modeling.output = BeechModelOut,
                           new.env = seven4.five_predictors,
```

```
                                           proj.name = 'Beech_7045',
                                           selected.models = 'all',
                                           binary.meth = 'TSS',
                                           compress = 'xz',
                                           clamping.mask = T,
                                           output.format = '.img')

Beech_Projfive8.five <- BIOMOD_Projection(modeling.output = BeechModelOut,
                                          new.env = five8.five_predictors,
                                          proj.name = 'Beech_5085',
                                          selected.models = 'all',
                                          binary.meth = 'TSS',
                                          compress = 'xz',
                                          clamping.mask = T,
                                          output.format = '.img')

Beech_Projfive4.five <- BIOMOD_Projection(modeling.output = BeechModelOut,
                                          new.env = five4.five_predictors,
                                          proj.name = 'Beech_8045',
                                          selected.models = 'all',
                                          binary.meth = 'TSS',
                                          compress = 'xz',
                                          clamping.mask = T,
                                          output.format = '.img')

proj.Beech.seven8.five <- get_predictions(Beech_Projseven8.five)

proj.Beech.seven4.five <- get_predictions(Beech_Projseven4.five)

proj.Beech.five8.five <- get_predictions(Beech_Projfive8.five)

proj.Beech.five4.five <- get_predictions(Beech_Projfive4.five)


writeRaster(subset(proj.Beech.seven8.five, "species_PA1_Full_RF"), filename =
"beech_7085.asc")

writeRaster(subset(proj.Beech.seven4.five, "species_PA1_Full_RF"), filename =
"beech_7045.asc")
```

```
writeRaster(subset(proj.Beech.five8.five, "species_PA1_Full_RF"), filename =
"beech_5085.asc")

writeRaster(subset(proj.Beech.five4.five, "species_PA1_Full_RF"), filename =
"beech_5045.asc")


#Phytophthora
Phytoph_Projseven8.five <- BIOMOD_Projection(modeling.output = PhytophModelOut,
                                  new.env = seven8.five_predictors,
                                  proj.name = 'Phytoph_7085',
                                  selected.models = 'all',
                                  binary.meth = 'TSS',
                                  compress = 'xz',
                                  clamping.mask = T,
                                  output.format = '.img')

Phytoph_Projseven4.five <- BIOMOD_Projection(modeling.output = PhytophModelOut,
                                  new.env = seven4.five_predictors,
                                  proj.name = 'Phytoph_7045',
                                  selected.models = 'all',
                                  binary.meth = 'TSS',
                                  compress = 'xz',
                                  clamping.mask = T,
                                  output.format = '.img')

Phytoph_Projfive8.five <- BIOMOD_Projection(modeling.output = PhytophModelOut,
                                 new.env = five8.five_predictors,
                                 proj.name = 'Phytoph_5085',
                                 selected.models = 'all',
                                 binary.meth = 'TSS',
                                 compress = 'xz',
                                 clamping.mask = T,
                                 output.format = '.img')

Phytoph_Projfive4.five <- BIOMOD_Projection(modeling.output = PhytophModelOut,
                                 new.env = five4.five_predictors,
                                 proj.name = 'Phytoph_8045',
                                 selected.models = 'all',
                                 binary.meth = 'TSS',
```

```
                              compress = 'xz',
                              clamping.mask = T,
                              output.format = '.img')

proj.Phytoph.seven8.five <- get_predictions(Phytoph_Projseven8.five)

proj.Phytoph.seven4.five <- get_predictions(Phytoph_Projseven4.five)

proj.Phytoph.five8.five <- get_predictions(Phytoph_Projfive8.five)

proj.Phytoph.five4.five <- get_predictions(Phytoph_Projfive4.five)


writeRaster(subset(proj.Phytoph.seven8.five, "species_PA1_Full_RF"), filename =
"phytoph_7085.asc")

writeRaster(subset(proj.Phytoph.seven4.five, "species_PA1_Full_RF"), filename =
"phytoph_7045.asc")

writeRaster(subset(proj.Phytoph.five8.five, "species_PA1_Full_RF"), filename =
"phytoph_5085.asc")

writeRaster(subset(proj.Phytoph.five4.five, "species_PA1_Full_RF"), filename =
"phytoph_5045.asc")

#Red Spruce
Spruce_Projseven8.five <- BIOMOD_Projection(modeling.output = SpruceModelOut,
                              new.env = seven8.five_predictors,
                              proj.name = 'Spruce_7085',
                              selected.models = 'all',
                              binary.meth = 'TSS',
                              compress = 'xz',
                              clamping.mask = T,
                              output.format = '.img')

Spruce_Projseven4.five <- BIOMOD_Projection(modeling.output = SpruceModelOut,
                              new.env = seven4.five_predictors,
                              proj.name = 'Spruce_7045',
                              selected.models = 'all',
                              binary.meth = 'TSS',
```

```
                                            compress = 'xz',
                                            clamping.mask = T,
                                            output.format = '.img')

Spruce_Projfive8.five <- BIOMOD_Projection(modeling.output = SpruceModelOut,
                                           new.env = five8.five_predictors,
                                           proj.name = 'Spruce_5085',
                                           selected.models = 'all',
                                           binary.meth = 'TSS',
                                           compress = 'xz',
                                           clamping.mask = T,
                                           output.format = '.img')

Spruce_Projfive4.five <- BIOMOD_Projection(modeling.output = SpruceModelOut,
                                           new.env = five4.five_predictors,
                                           proj.name = 'Spruce_8045',
                                           selected.models = 'all',
                                           binary.meth = 'TSS',
                                           compress = 'xz',
                                           clamping.mask = T,
                                           output.format = '.img')

proj.Spruce.seven8.five <- get_predictions(Spruce_Projseven8.five)

proj.Spruce.seven4.five <- get_predictions(Spruce_Projseven4.five)

proj.Spruce.five8.five <- get_predictions(Spruce_Projfive8.five)

proj.Spruce.five4.five <- get_predictions(Spruce_Projfive4.five)


writeRaster(subset(proj.Spruce.seven8.five, "species_PA1_Full_RF"), filename =
"spruce_7085.asc")

writeRaster(subset(proj.Spruce.seven4.five, "species_PA1_Full_RF"), filename =
"spruce_7045.asc")

writeRaster(subset(proj.Spruce.five8.five, "species_PA1_Full_RF"), filename =
"spruce_5085.asc")
```

```
writeRaster(subset(proj.Spruce.five4.five, "species_PA1_Full_RF"), filename =
"spruce_5045.asc")

#Rhododendron
Rhodo_Projseven8.five <- BIOMOD_Projection(modeling.output = RhodoModelOut,
                         new.env = seven8.five_predictors,
                         proj.name = 'Rhodo_7085',
                         selected.models = 'all',
                         binary.meth = 'TSS',
                         compress = 'xz',
                         clamping.mask = T,
                         output.format = '.img')

Rhodo_Projseven4.five <- BIOMOD_Projection(modeling.output = RhodoModelOut,
                         new.env = seven4.five_predictors,
                         proj.name = 'Rhodo_7045',
                         selected.models = 'all',
                         binary.meth = 'TSS',
                         compress = 'xz',
                         clamping.mask = T,
                         output.format = '.img')

Rhodo_Projfive8.five <- BIOMOD_Projection(modeling.output = RhodoModelOut,
                        new.env = five8.five_predictors,
                        proj.name = 'Rhodo_5085',
                        selected.models = 'all',
                        binary.meth = 'TSS',
                        compress = 'xz',
                        clamping.mask = T,
                        output.format = '.img')

Rhodo_Projfive4.five <- BIOMOD_Projection(modeling.output = RhodoModelOut,
                        new.env = five4.five_predictors,
                        proj.name = 'Rhodo_8045',
                        selected.models = 'all',
                        binary.meth = 'TSS',
                        compress = 'xz',
                        clamping.mask = T,
                        output.format = '.img')
```

```
proj.Rhodo.seven8.five <- get_predictions(Rhodo_Projseven8.five)

proj.Rhodo.seven4.five <- get_predictions(Rhodo_Projseven4.five)

proj.Rhodo.five8.five <- get_predictions(Rhodo_Projfive8.five)

proj.Rhodo.five4.five <- get_predictions(Rhodo_Projfive4.five)


writeRaster(subset(proj.Rhodo.seven8.five, "species_PA1_Full_RF"), filename =
"rhodo_7085.asc")

writeRaster(subset(proj.Rhodo.seven4.five, "species_PA1_Full_RF"), filename =
"rhodo_7045.asc")

writeRaster(subset(proj.Rhodo.five8.five, "species_PA1_Full_RF"), filename =
"rhodo_5085.asc")

writeRaster(subset(proj.Rhodo.five4.five, "species_PA1_Full_RF"), filename =
"rhodo_5045.asc")

#Fraser Fir 2.0
FF_RF_vars_path <- file.path("C:\\Temp\\Thesis\\GBM_RF\\FF_vars\\RF")
FF_RF_vars <- list.files(FF_RF_vars_path, pattern = 'asc$', full.names = TRUE)
FF_RF_predictors <- stack(FF_RF_vars)

FraserName <- "species"
FraserXY <- Fraser_Train[,c("Longitude","Latitude")]
RespFraser <- as.numeric(Fraser_Train[,FraserName])

FFseven8.five_vars_path <- file.path("E:\\ThesisTake2\\GBM_RF\\FF_7085")
FFseven8.five_vars <- list.files(FFseven8.five_vars_path, pattern = 'asc$', full.names = TRUE)
FFseven8.five_predictors <- stack(FFseven8.five_vars)

FFseven4.five_vars_path <- file.path("E:\\ThesisTake2\\GBM_RF\\FF_7045")
FFseven4.five_vars <- list.files(FFseven4.five_vars_path, pattern = 'asc$', full.names = TRUE)
FFseven4.five_predictors <- stack(FFseven4.five_vars)

FFfive8.five_vars_path <- file.path("E:\\ThesisTake2\\GBM_RF\\FF_5085")
FFfive8.five_vars <- list.files(FFfive8.five_vars_path, pattern = 'asc$', full.names = TRUE)
```

```
FFfive8.five_predictors <- stack(FFfive8.five_vars)

FFfive4.five_vars_path <- file.path("E:\\ThesisTake2\\GBM_RF\\FF_5045")
FFfive4.five_vars <- list.files(FFfive4.five_vars_path, pattern = 'asc$', full.names = TRUE)
FFfive4.five_predictors <- stack(FFfive4.five_vars)

Fraser2_Projseven8.five <- BIOMOD_Projection(modeling.output = FF_RF_ModelOut,
                            new.env = FFseven8.five_predictors,
                            proj.name = 'FF2_7085',
                            selected.models = 'all',
                            binary.meth = 'TSS',
                            compress = 'xz',
                            clamping.mask = T,
                            output.format = '.img')

Fraser2_Projseven4.five <- BIOMOD_Projection(modeling.output = FF_RF_ModelOut,
                            new.env = FFseven4.five_predictors,
                            proj.name = 'FF2_7045',
                            selected.models = 'all',
                            binary.meth = 'TSS',
                            compress = 'xz',
                            clamping.mask = T,
                            output.format = '.img')

Fraser2_Projfive8.five <- BIOMOD_Projection(modeling.output = FF_RF_ModelOut,
                           new.env = FFfive8.five_predictors,
                           proj.name = 'FF2_5085',
                           selected.models = 'all',
                           binary.meth = 'TSS',
                           compress = 'xz',
                           clamping.mask = T,
                           output.format = '.img')

Fraser2_Projfive4.five <- BIOMOD_Projection(modeling.output = FF_RF_ModelOut,
                           new.env = FFfive4.five_predictors,
                           proj.name = 'FF2_8045',
                           selected.models = 'all',
                           binary.meth = 'TSS',
                           compress = 'xz',
                           clamping.mask = T,
```

```
                                    output.format = '.img')

proj.Fraser2.seven8.five <- get_predictions(Fraser2_Projseven8.five)

proj.Fraser2.seven4.five <- get_predictions(Fraser2_Projseven4.five)

proj.Fraser2.five8.five <- get_predictions(Fraser2_Projfive8.five)

proj.Fraser2.five4.five <- get_predictions(Fraser2_Projfive4.five)


writeRaster(subset(proj.Fraser2.seven8.five, "species_PA1_Full_RF"), filename =
"fraser2_7085.asc")

writeRaster(subset(proj.Fraser2.seven4.five, "species_PA1_Full_RF"), filename =
"fraser2_7045.asc")

writeRaster(subset(proj.Fraser2.five8.five, "species_PA1_Full_RF"), filename =
"fraser2_5085.asc")

writeRaster(subset(proj.Fraser2.five4.five, "species_PA1_Full_RF"), filename =
"fraser2_5045.asc")

#Red Spruce 2.0
RS_RF_vars_path <- file.path("C:\\Temp\\Thesis\\GBM_RF\\RS_vars\\RF")
RS_RF_vars <- list.files(RS_RF_vars_path, pattern = 'asc$', full.names = TRUE)
RS_RF_predictors <- stack(RS_RF_vars)

RSseven8.five_vars_path <- file.path("E:\\ThesisTake2\\GBM_RF\\RS_7085")
RSseven8.five_vars <- list.files(RSseven8.five_vars_path, pattern = 'asc$', full.names = TRUE)
RSseven8.five_predictors <- stack(RSseven8.five_vars)

RSseven4.five_vars_path <- file.path("E:\\ThesisTake2\\GBM_RF\\RS_7045")
RSseven4.five_vars <- list.files(RSseven4.five_vars_path, pattern = 'asc$', full.names = TRUE)
RSseven4.five_predictors <- stack(RSseven4.five_vars)

RSfive8.five_vars_path <- file.path("E:\\ThesisTake2\\GBM_RF\\RS_5085")
RSfive8.five_vars <- list.files(RSfive8.five_vars_path, pattern = 'asc$', full.names = TRUE)
RSfive8.five_predictors <- stack(RSfive8.five_vars)
```

```
RSfive4.five_vars_path <- file.path("E:\\ThesisTake2\\GBM_RF\\RS_5045")
RSfive4.five_vars <- list.files(RSfive4.five_vars_path, pattern = 'asc$', full.names = TRUE)
RSfive4.five_predictors <- stack(RSfive4.five_vars)

Spruce2_Projseven8.five <- BIOMOD_Projection(modeling.output = RS_RF_ModelOut,
                                             new.env = RSseven8.five_predictors,
                                             proj.name = 'Spruce2_7085',
                                             selected.models = 'all',
                                             binary.meth = 'TSS',
                                             compress = 'xz',
                                             clamping.mask = T,
                                             output.format = '.img')

Spruce2_Projseven4.five <- BIOMOD_Projection(modeling.output = RS_RF_ModelOut,
                                             new.env = RSseven4.five_predictors,
                                             proj.name = 'Spruce2_7045',
                                             selected.models = 'all',
                                             binary.meth = 'TSS',
                                             compress = 'xz',
                                             clamping.mask = T,
                                             output.format = '.img')

Spruce2_Projfive8.five <- BIOMOD_Projection(modeling.output = RS_RF_ModelOut,
                                            new.env = RSfive8.five_predictors,
                                            proj.name = 'Spruce2_5085',
                                            selected.models = 'all',
                                            binary.meth = 'TSS',
                                            compress = 'xz',
                                            clamping.mask = T,
                                            output.format = '.img')

Spruce2_Projfive4.five <- BIOMOD_Projection(modeling.output = RS_RF_ModelOut,
                                            new.env = RSfive4.five_predictors,
                                            proj.name = 'Spruce2_8045',
                                            selected.models = 'all',
                                            binary.meth = 'TSS',
                                            compress = 'xz',
                                            clamping.mask = T,
                                            output.format = '.img')
```

```
proj.Spruce2.seven8.five <- get_predictions(Spruce2_Projseven8.five)

proj.Spruce2.seven4.five <- get_predictions(Spruce2_Projseven4.five)

proj.Spruce2.five8.five <- get_predictions(Spruce2_Projfive8.five)

proj.Spruce2.five4.five <- get_predictions(Spruce2_Projfive4.five)


writeRaster(subset(proj.Spruce2.seven8.five, "species_PA1_Full_RF"), filename =
"spruce2_7085.asc")

writeRaster(subset(proj.Spruce2.seven4.five, "species_PA1_Full_RF"), filename =
"spruce2_7045.asc")

writeRaster(subset(proj.Spruce2.five8.five, "species_PA1_Full_RF"), filename =
"spruce2_5085.asc")

writeRaster(subset(proj.Spruce2.five4.five, "species_PA1_Full_RF"), filename =
"spruce2_5045.asc")
```

VITA

DANIKA LEIGH MOSHER

Education:	M.S. Geosciences (Geospatial Analysis Concentration) East Tennessee State University, Johnson City, Tennessee, December 2020 B.S. Environmental Science Appalachian State University, Boone, North Carolina, May 2018
Professional Experience:	National Park Service Contracted Research Assistant, United States Geological Survey, North Central Climate Adaptation Science Center, Sept. 2020 - Present Ecological Forecasting Committee Intern, American Meteorological Society, July 2019 - Present Lab Instructor and Coordinator, East Tennessee State University, Department of Geosciences, Aug. 2018 - May 2020 Project Lead, NASA DEVELOP National Program, NOAA-National Centers for Environmental Information, Jun. - Aug. 2019 GIS Intern, City of Johnson City Government, Streets Division, May - Aug. 2019 Naturalist Intern, Grandfather Mountain Stewardship Foundation, June - Sept. 2017
Publications:	Mosher, D. L. (2020) Grandfather Mountain, North Carolina - A Sky Island Wonder. *Southeastern Geographer*. 2:60-4.
Academic Awards:	Mountain Geography Specialty Group Mauna Kea Student Presentation Award, American Association of Geographers, Virtual, May 2020

American Meteorological Student Travel Grant, Jan. 2020

Weather Analysis and Forecasting/Numerical Weather Predictions Student Travel Grant, Jan. 2020

Highest Scoring Female at SouthEastern Division of the American Association of Geographers Geography Bowl, Wilmington, North Carolina, Nov. 2019

Southeastern Geographer Cover Art Contest Winner, Wilmington, NC, Nov. 2019

First Place in Master’s Natural Resources, Agriculture, and Environmental Sciences Poster Presentation, East Tennessee State University Appalachian Student Research Forum, April 2019

Paleoenvironmental Change Specialty Group Thesis Proposal Award, American Association of Geographers, Washington D.C., April 2019

First Place Group for Extreme Temperature Development Model, CCx:Hack, The Collider, Asheville, NC, March 2019

Professional Membership: Earth Science Women’s Network

American Meteorological Society (AMS)

Ecological Forecasting Committee of AMS

Asheville Chapter of AMS

The American Association of Geographers (AAG)

Paleoenvironmental Specialty Group of AAG

Mountain Geography Specialty Group of AAG

SouthEastern Division of AAG

Southern Appalachian Spruce Restoration Initiative