

Forest Tree Genetic Risk Assessment System:
A Tool for Conservation Decision-Making in Changing Times

User Guide Version 1.2

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Overview

Changing climate conditions and increasing pest and pathogen infestations will increase the likelihood that forest trees could experience population-level extirpation or species-level extinction during the next century. Funds, however, will be limited for management and gene conservation efforts to preserve forest tree genetic diversity. The Forest Tree Genetic Risk Assessment System provides a framework for users to rank the relative risk of genetic degradation for multiple forest tree species. We have applied this framework for the species-rich forests of the Southern Appalachian Mountains of the southeastern United States.

Species differ in their physiological tolerances, life-history strategies, probabilities of population extinctions and colonizations, and dispersal abilities; these individualistic traits likely underlie the high variability in strength of climate response across wild species, even among those subjected to similar climatic trends (Parmesan 2006, Parmesan and Yohe 2003). In the face of these changes, an important goal will be to safeguard existing adaptedness and create conducive conditions for future evolution, with a focus on the conservation of variability in adaptive traits (Myking 2002).

In the absence of good information about the genetic composition of species, or even an understanding of the relevant adaptive traits, several researchers have suggested using ecological and life-history traits to rank the predisposition of species to climate change and other threats, for conservation planning, for the evaluation of species' genetic resources, and for the early detection of vulnerability (Aitken and others 2008, Bradshaw and others 2008, Myking 2002, Sjostrom and Gross 2006).

The Forest Tree Genetic Risk Assessment System gives each species a rating for risk factors relating to **(1)** its intrinsic attributes, such as population structure, fecundity and seed dispersal mechanism, that may increase its vulnerability in the face of change, and **(2)** the external threats to its genetic integrity, including changing climate and insect and disease threats. Species may be additionally rated for a set of conservation modifiers, such as listed status and endemism. The factor index values are weighted and summed to give risk ratings for the species within a given region, which are ranked according to their overall susceptibility to genetic degradation.

This system has the advantage of accounting for the interactions among threats that may result in the most severe impacts associated with climate change (Thomas and others 2004). Only by considering extinction as a synergistic process of external threats and intrinsic biological traits will it be possible to make predictions of risk that approximate reality for most species, and therefore to increase the likelihood that conservation efforts will be effective (Brook and others 2008). Additionally, the flexibility of the Forest Tree Genetic Risk Assessment System allows for its application at multiple scales and across any area for which the relevant data exist for the species of interest.

How to Use the Risk Assessment System

This framework is designed to be flexible in terms of the area the risk assessment encompasses, the species characteristics included in the assessment, and the weighting of those characteristics. Information about most species characteristics is available from public sources.

This document provides details on each of the 10 indices proposed for inclusion in a risk ranking, and the steps taken to complete the ranking process. The indices are divided into six intrinsic risk factors, which describe characteristics of tree species and their distributions; two external risk factors, which describe external threats to tree species; and two conservation modifiers, which describe conservation value associated with species (Table 1). Users can decide which of these risk factors and modifiers to include in their assessments, and how to assign the appropriate relative weights placed on each.

Table 1: The intrinsic risk factors, external risk factors and conservation modifiers included in the Forest Tree Genetic Risk Assessment System for the assessment of the 131 tree species of the Southern Appalachians.

Intrinsic Risk Factors	External Risk Factors	Conservation Modifiers
A1) Population Structure	B1) Pest and Pathogen Threats	C1) Endemism
A2) Rarity/Density	B2) Habitat Shift Pressure	C2) Conservation Status
A3) Regeneration Capacity		
A4) Dispersal Ability		
A5) Habitat Affinities		
A6) Genetic Variation		

We used the Forest Tree Genetic Risk Assessment System to conduct a risk assessment for 131 native forest tree species encompassed by the Southern Appalachian region. In this document, we will describe the steps we have taken in this process, referring to the associated Excel file “SoApps_Risk_Ranking_Final.xlsx.”

The genetic risk assessment is completed in four major steps: **(1)** determining the area of interest and the species encompassed by that region, **(2)** selecting risk factors and conservation modifiers to include in the assessment, **(3)** collecting relevant data for each species and calculating risk factor and conservation modifier index values, and **(4)** weighting these index values, calculating a final risk rating score for each species, and ranking the species based on their final scores.

Step 1: Determining the area of interest and the associated forest tree species

The area encompassed by a given assessment will depend on the needs of the user. For our purposes, we defined the Southern Appalachians as seven high-elevation ecoregion sections south of the Mason-Dixon line (the border between Pennsylvania and Maryland) (Figure 1). Our goal was to define the Southern Appalachians from an ecological perspective, but regions could also encompass states, groups of states, or within-state regions. Users may have a pre-existing list of the species to include in their assessment, or they may need to use publicly available data sources to

determine which species exist within the region. For our Southern Appalachian assessment, we included all the species that occurred on Forest Inventory and Analysis (FIA) plots (United States Department of Agriculture Forest Service 2008a) within the region (Figure 2). Because the FIA plot sample does not typically inventory tree species that occur only rarely, we added additional species known to exist in the region, based on Little’s distribution maps (United States Geological Survey 1999) and other sources. Additionally, in some cases, we combined multiple FIA species codes into a single species when doing so was taxonomically justified (e.g., combining all hawthorn species, which are difficult to differentiate even by experts, into a single “*Crataegus* spp.” category).

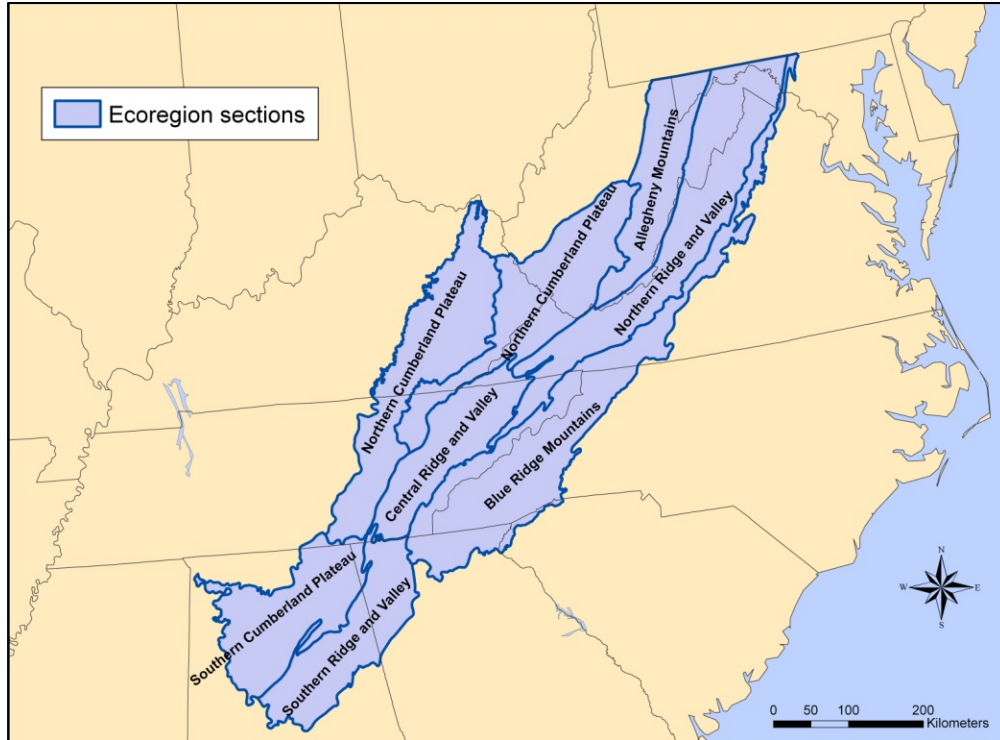


Figure 1: The Southern Appalachian region, as defined for this regional genetic risk assessment.

Step 2: Selecting the risk factors and conservation modifiers to include

A key feature of the framework is its flexibility to suit the needs of users. This includes the selection of the risk factors and conservation modifiers that are important in an assessment of the genetic vulnerability of forest tree species in a given region. We have suggested a set of eight risk factors and two conservation modifiers from our assessment of Southern Appalachian tree species (Table 1). Six of these are intrinsic risk factors that can be further divided into 20 variables (Figure 3), two are external risk factors divided into five variables (Figure 4) and two are conservation modifiers each consisting of a single variable (Figure 5).

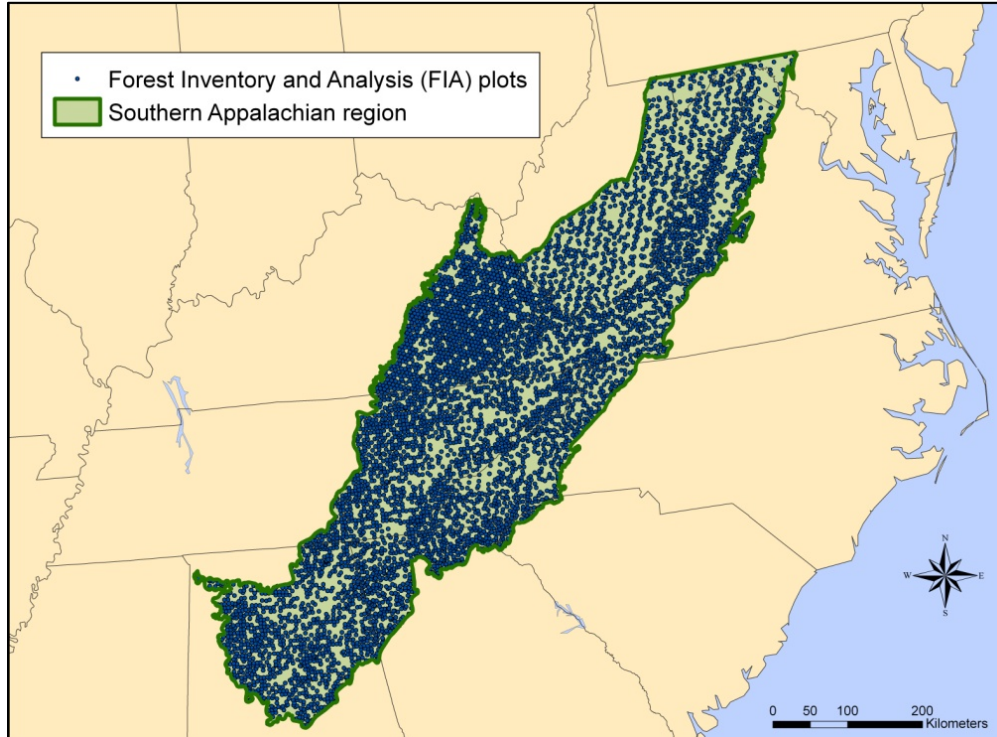


Figure 2: Forest Inventory and Analysis (FIA) plots occurring within the Southern Appalachian region.

Any of these risk factors or variables could be dropped, and new risk factors or variables added. For example, “forest fragmentation” could be elevated from a variable as part of the Climate Change Pressure external risk factor (B2) to a separate risk factor in its own right. “Number of disjunct populations” could be moved from the Population Structure intrinsic risk factor (A1) to the Genetic Variation intrinsic risk factor (A6). “Mean elevation” could be dropped from the Habitat Affinities intrinsic risk factor (A5). A new conservation modifier could be created to quantify the phylogenetic distinctiveness of each species in the region (e.g., the mean evolutionary distance between it and all the other species in the region).

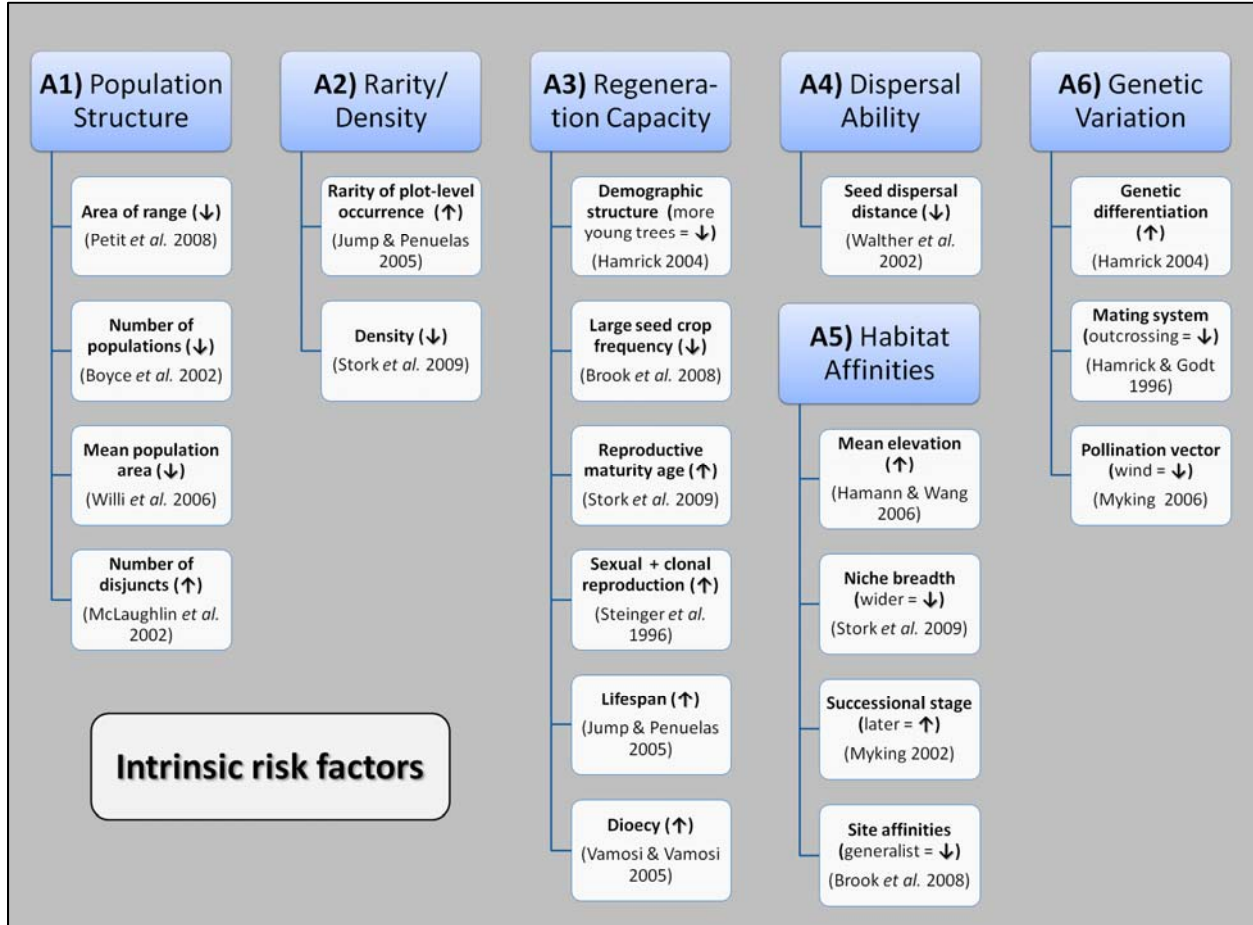


Figure 3: Six species-intrinsic risk factors for genetic vulnerability are included in this assessment. Variables for each factor are noted here, along with whether higher values are expected to be associated with greater genetic vulnerability (↑) or less genetic vulnerability (↓), as outlined in the listed reference.

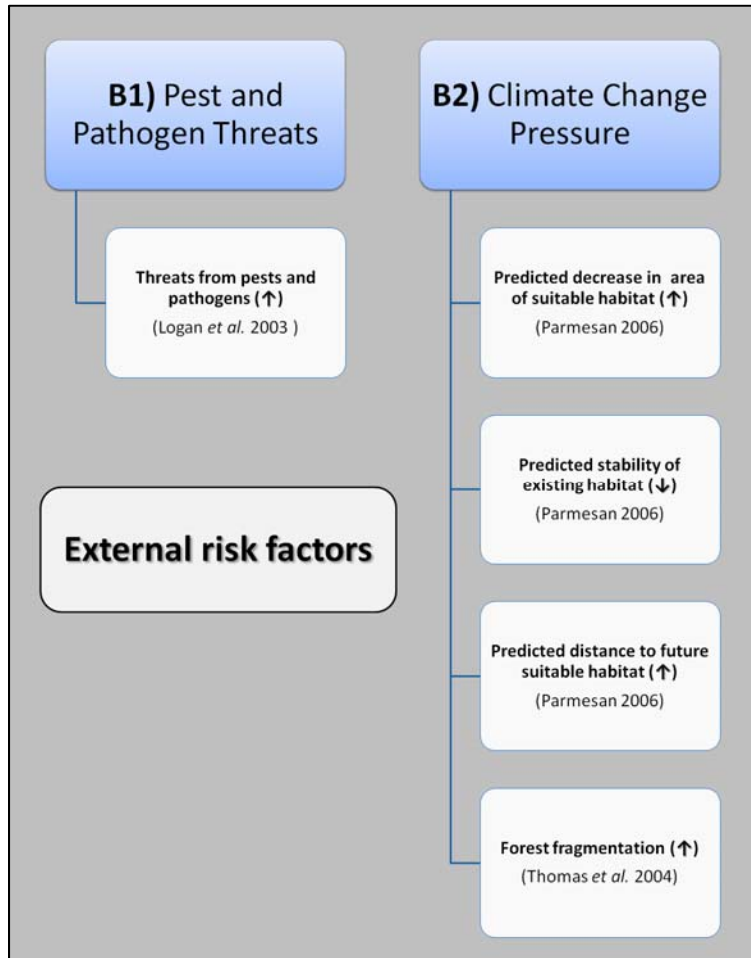


Figure 4: Two species-external risk factors for genetic vulnerability are included in this assessment. Variables for each factor are noted here, along with whether higher values are expected to be associated with greater genetic vulnerability (↑) or less genetic vulnerability (↓), as outlined in the listed reference.

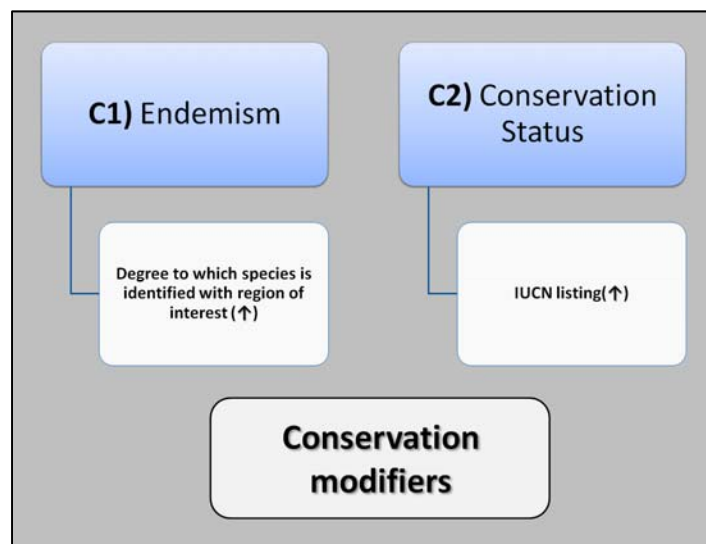


Figure 5: Two conservation modifiers are included in this assessment. The variable associated with each modifier is noted here. Species with higher modifier values (↑) are weighted higher in the overall risk vulnerability scores.

Step 3: Collecting relevant data and calculating index values

Detailed descriptions are provided below for how risk factors and conservation modifier values were calculated for Southern Appalachian forest tree species. The calculation of each risk factor or modifier was done on a separate worksheet within the “SoApps_Risk_Ranking_Final.xlsx” Excel file (“A1) Population Structure,” “B1) Pests & Pathogens”, etc.). The tabs of these worksheets are color coded green for intrinsic risk factors, blue for external risk factors, and orange for conservation modifiers.

Most of the data were available from a handful of publicly available sources, including the FIA database, Little’s species distribution maps, the Silvics of North America manual (Burns and Honkala 1990), Woody Plant Seed Manual (Bonner and Karrfalt 2008), the Flora of North America North of Mexico (Flora of North America Editorial Committee 1993+), the NatureServe online data explorer (NatureServe 2010), a national 30-m resolution forest cover map using the 2001 National Land Cover Database (Homer and others 2007), and a 1-km digital elevation model (United States Geological Survey 1996). Other sources may be necessary to compile information about population genetic differentiation within species, and to list the most serious insect and disease threats to species.

Step 4: Calculating final rankings

Within the worksheet titled “Ranking” in the Excel file, with a purple tab, the indices associated with each risk factor or conservation modifier were combined for a final set of risk scores. From each of the index values, a score was calculated (e.g. “**Population Score**” and “**Pest Score**”) by multiplying the index value by a weight. The sum of these weights, across the factors included in the analysis, need to sum to 1.0 for the final risk score to generate a risk score for each species on a scale of 0 to 100, with higher scores reflecting higher vulnerability. These factor weights should reflect the importance of each factor relative to the other factors. For example, if the Pests and Pathogens risk factor is considered twice as important as Population Structure, the former could be assigned a weight of 0.2 and the latter 0.1 (assuming that all the other risk factors together sum to 0.7).

The scores were then added across the factors (“**Risk Sum**”), divided by the highest possible score to generate a “**Risk Total**” score from 0 to 100. These risk totals were then ranked for all the species in the assessment (“**Risk Rank**”). Species ranked in the top third for “**Risk Rank**” were designated with a red icon, those in the middle third with a yellow icon, and those in the bottom third with a green icon.

Table 2: The 25 tree species of the Southern Appalachians with the highest overall vulnerability scores using the Forest Tree Genetic Risk Assessment System. (See text for an explanation of the risk factor weightings.)

Rank	Species	Score
1	Carolina hemlock (<i>Tsuga caroliniana</i>)	63.14
2	September elm (<i>Ulmus serotina</i>)	62.53
3	Fraser fir (<i>Abies fraseri</i>)	54.97
4	blue ash (<i>Fraxinus quadrangulata</i>)	54.61
5	butternut (<i>Juglans cinerea</i>)	54.53
6	Shumard oak (<i>Quercus shumardii</i>)	53.84
7	Table Mountain pine (<i>Pinus pungens</i>)	52.77
8	Carolina silverbell (<i>Halesia carolina</i>)	52.59
9	American chestnut (<i>Castanea dentata</i>)	52.49
10	black ash (<i>Fraxinus nigra</i>)	52.21
11	Ohio buckeye (<i>Aesculus glabra</i>)	52.20
12	eastern hemlock (<i>Tsuga canadensis</i>)	52.13
13	swamp white oak (<i>Quercus bicolor</i>)	51.43
14	red pine (<i>Pinus resinosa</i>)	50.28
15	Carolina ash (<i>Fraxinus caroliniana</i>)	49.76
16	Virginia roundleaf birch (<i>Betula uber</i>)	49.31
17	spruce pine (<i>Pinus glabra</i>)	48.93
18	rock elm (<i>Ulmus thomasii</i>)	48.72
19	red spruce (<i>Picea rubens</i>)	48.70
20	chalk maple (<i>Acer leucoderme</i>)	48.49
21	painted buckeye (<i>Aesculus sylvatica</i>)	48.45
22	balsam fir (<i>Abies balsamea</i>)	48.14
23	black maple (<i>Acer nigrum</i>)	47.65
24	nutmeg hickory (<i>Carya myristiciformis</i>)	47.59
24	yellow buckeye (<i>Aesculus flava</i>)	47.59

Again, the assessment system is flexible in the assignment of weights for each of the indices. We here assigned a weight of 0.1 to all six of the intrinsic risk factors, 0.15 to the two external risk factors (Pest and Pathogen Threats and Habitat Shift Pressure external risk factor), and a weight of 0.05 to the two conservation modifiers. (These weights sum to 1.) Dividing the actual total score for each species by the total possible value results in a standardized score across species, regardless of whether a species is lacking some index values. The 25 species with the highest overall vulnerability scores for the Southern Appalachians region are shown in Table 2.

Intrinsic Factor A1: Population Structure

Description: Index quantifying the size of each species range within the area of interest, the total number of populations, and the number of disjunct populations. Index values will be higher for species with smaller ranges, a greater number of overall populations, and a greater number of disjunct populations.

Justification: Population size and isolation are likely to represent highly important risk factors for forest tree species facing changing climate conditions. Small populations are expected to have a reduced ability to adapt to environmental change because genetic variation and response to selection are thought to be positively correlated with population size (Hamrick and Godt 1996, Hamrick and others 1992, Willi and others 2006), and because individuals in small populations have lower fitness as a result of environmental stress and inbreeding, which can substantially increase the probability of population extinction in changing environments (Willi et al. 2006). The extent of a species' native range is an expression of its geographic, altitudinal and habitat tolerance, so widespread species tend to have a higher capacity to tolerate new environments given that they have already encountered a variety of climatic and habitat conditions in their evolutionary history and acquired a relatively higher phenotypic plasticity (Bradshaw and others 2008, Sax and Brown 2000). In fact, small geographic range is one of the best-supported empirical correlates of extinction (Brook and others 2008, Stork and others 2009), and range-restricted species are among the first in which entire species have gone extinct due to recent climate change (Parmesan 2006). Extinction vulnerability in forest tree species is expected to increase with decreasing distribution size, as species with small range sizes are more likely to have future distributions that are largely or wholly disjunct from current distributions (Petit and others 2008, Schwartz and others 2006). On the other hand, widespread species in large populations will likely be able to adapt to climate change in a relatively few generations, and will likely survive in the interim as their major competitors face the same short-term maladaptation (Aitken and others 2008).

The extent to which the populations of a forest tree species are peripheral, that is, distant and isolated from large continuous areas of distribution, could influence their risk of genetic degradation. Neutral marker studies have, on average, found a decline in diversity and an increase in differentiation among peripheral populations of plants (Eckert and others 2008), although species with naturally disjunct ranges are likely to have higher genetic diversity among populations than those with continuous ranges (Hamrick 2004). Strong and continuous directional selection in extreme environments might reduce genetic variability for traits related to fitness in peripheral populations, compared to central populations, which are expected to experience a much larger component of stabilizing selection. On the other hand, fluctuating

environmental conditions at the range edge may maintain more genetic variation in peripheral populations (Eckert et al. 2008).

Finally, species with multiple populations may be at decreased risk of severe genetic degradation. Having multiple populations strongly decreases the probability of extinction, because additional populations cause a geometric decline in extinction risk (Boyce and others 2002). The interaction between a small number of isolated populations and climate change has been demonstrated to result in population extinctions (McLaughlin and others 2002).

Data source(s):

- Little’s tree species distribution maps for North America (United States Geological Survey 1999) (<http://esp.cr.usgs.gov/data/atlas/little/>).
- Shapefile encompassing boundary of the region of interest.

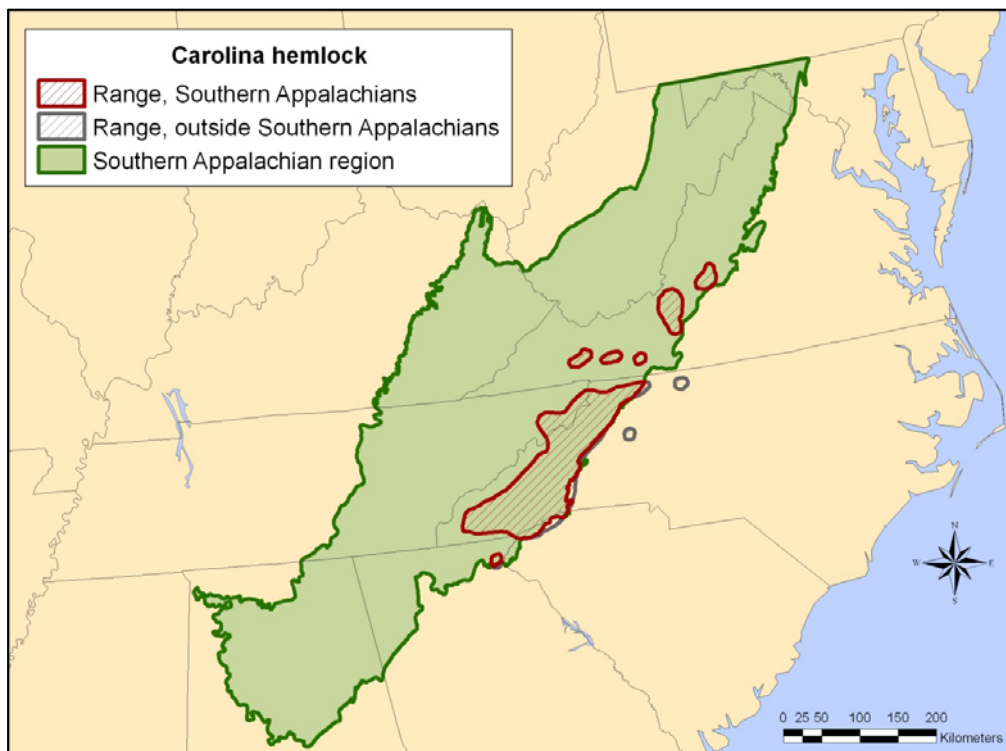


Figure 6: The intersection of the range of Carolina hemlock (*Tsuga caroliniana*) and the Southern Appalachian region. The distribution of this species covers 1.9 million hectares in the region across seven populations, two of which were classified as disjunct.

Data processing:

A) Area of species range in region of interest (Figure 6)

- 1) Clip each species’ range boundary to the area of interest.

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- 2) For each species, calculate total area of distribution within the region of interest, in hectares (**Range Area**).
- 3) Calculate the reverse relative percent for range size, on a scale of 0 to 100, for each species compared to the species with the largest and smallest ranges within the area of interest, with higher percentages reflecting smaller range sizes (**Range Score**).

B) Number of populations within the region of interest (Figure 6)

- 1) For each species, count the number of populations that intersect the area of interest (**N Pops**).
- 2) Calculate the relative percent for the number of populations, on a scale of 0 to 100, for each species compared to the species with the most and fewest populations within the area of interest, with higher percentages reflecting more populations (**Pops Score**).

C) Mean area of the populations within the region of interest (Figure 6)

- 1) For each species, count the number of populations that intersect the area of interest (**Mean Pop Area**).
- 2) Calculate the reverse relative percent for mean range size, on a scale of 0 to 100, for each species compared to the species with the largest and smallest mean range sizes within the area of interest, with higher percentages reflecting smaller mean range sizes (**Pop Area Score**).

D) Number of disjunct populations in the region of interest (Figure 6)

- 1) For each species, count the number of disjunct populations that intersect the area of interest. Disjunct populations are those that are smaller than 250,000 hectares, and are at least 50 kilometers from the nearest population that is more than 250,000 hectares in extent (**N Disjuncts**).
- 2) Calculate the relative percent for the number of disjunct populations, on a scale of 0 to 100, for each species compared to the species with the most and fewest disjunct populations within the area of interest, with higher percentages reflecting more disjunct populations (**Disjuncts Score**).

E) Index calculation

- 1) Sum these four values (each on a scale of 0 to 100), and divide by four, for an overall index value between 0 and 100 (**Population Index**).

Status for Southern Appalachians: Completed. See Table 3 for the Southern Appalachians tree species with the highest unweighted vulnerability index values for the Population Structure intrinsic factor.

Table 3: The 10 tree species of the Southern Appalachians with the highest unweighted vulnerability index values for the Population Structure intrinsic factor. Index values are on a scale of 0 to 100.

Rank	Species	Index
1	sweet crabapple (<i>Malus coronaria</i>)	96.04
2	red spruce (<i>Picea rubens</i>)	88.21
3	northern white-cedar (<i>Thuja occidentalis</i>)	82.51
4	shingle oak (<i>Quercus imbricaria</i>)	78.69
5	yellowwood (<i>Cladrastis kentukea</i>)	73.25
6	paper birch (<i>Betula papyrifera</i>)	71.84
7	quaking aspen (<i>Populus tremuloides</i>)	71.62
8	September elm (<i>Ulmus serotina</i>)	70.10
9	shellbark hickory (<i>Carya laciniosa</i>)	69.64
10	chokecherry (<i>Prunus virginiana</i>)	68.12

Intrinsic Factor A2: Rarity/Density

Description: Index quantifying the commonness of plot-level occurrences of each species within the area of interest (rarity), and the relative number of trees of each species occurring within its range within the area of interest (density). Index values will be higher for species that occur less commonly overall, and that occur at a low density across the area in which they occur.

Justification: The consequences of climate change for rare species and those occurring in isolated habitats may be severe, because their populations are likely to be less numerous and may be less well-connected or occur over narrow geographical regions (Jump and Penuelas 2005).

In general, low population density is a strong empirical predictor of extinction risk, particularly following large-scale disturbances (Stork et al. 2009). Forest tree species with low density are assumed to have less gene flow and thus lower diversity and more coarse genetic structure than high-density species (Hamrick et al. 1992, Myking 2002).

The risk factor variables quantifying forest tree species rarity and density are based on Forest Inventory and Analysis data, which are collected from standardized plots arranged across the landscape in a systematic fashion and from all land ownerships (U.S. Department of Agriculture Forest Service 2008a). As such, they should provide unbiased measures of frequency of occurrence across the range of each species.

Data source(s):

- Forest Inventory and Analysis data for the area of interest (U.S. Department of Agriculture Forest Service 2008a) (<http://www.fia.fs.fed.us/>).
- Little's tree species distribution maps for North America (United States Geological Survey 1999) (<http://esp.cr.usgs.gov/data/atlas/little/>).
- Shapefile encompassing boundary of the region of interest.

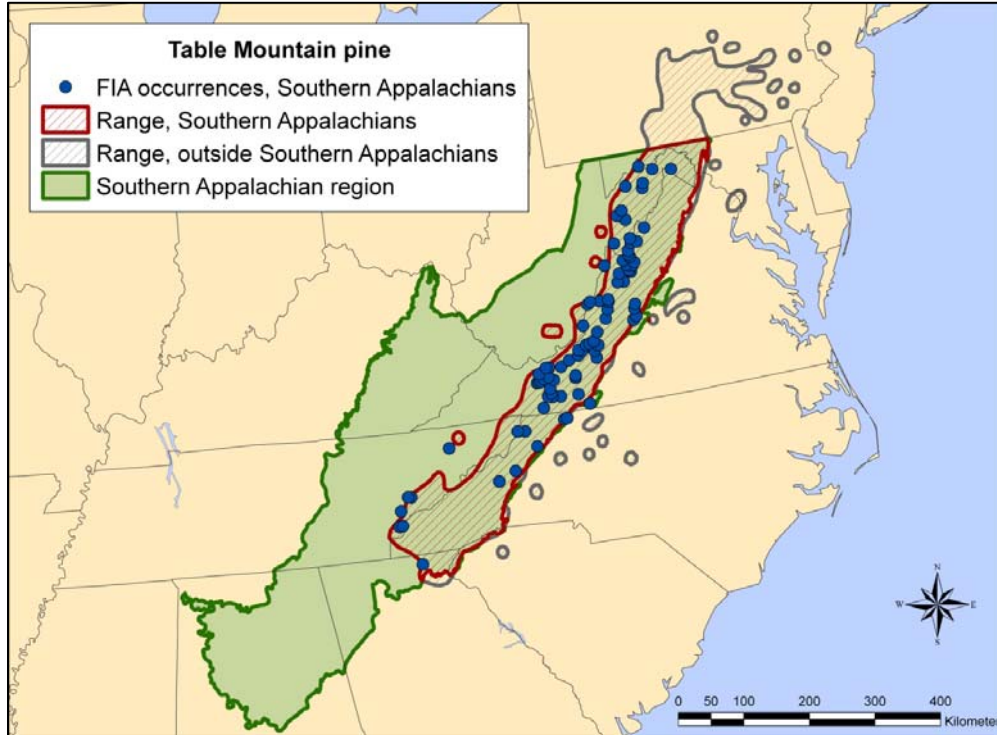


Figure 7: For Table Mountain pine, rarity and density were calculated using FIA occurrences of the species within in the Southern Appalachian region.

Data processing:

A) Rarity of plot-level occurrence within the region of interest (Figure 7)

- 1) Determine the total number of FIA plots within the area of interest.
- 2) Determine the number of FIA plots within the area of interest containing at least one tree (dbh > 2.54 cm) of each species (*N Plots*).
(Notes: If a species is known to occur within the area of interest but does not occur on an FIA plot, enter this value as 0. There were 6,211 plots in the Southern Appalachian region).
- 3) Calculate the percent of FIA plots within the area that contain each species (*Percent Plots*).
- 4) Calculate the reverse relative percent for the percent of FIA plots containing a species, on a scale of 0 to 100, for each species compared to the species with the largest and smallest ranges within the area of interest, with higher percentages reflecting fewer plots (*Plots Score*).

B) Tree density within the species range within region of interest

- 1) For each species, count the number of trees (dbh > 2.54 cm) inventoried in the FIA database within the area of interest (*N Trees*).

(Note: If a species is known to occur within the area of interest but does not occur on an FIA plot, enter this value as 0).

- 2) For each species, calculate total area of distribution within the region of interest, in hectares (**Range Area**). (Note: This was also done for factor A1).
- 3) Calculate the number of trees occurring per hectare within each species' range within the area of interest (**Trees/1000ha**).
- 4) Calculate the reverse relative percent for trees per hectare, on a scale of 0 to 100, for each species compared to the species with the largest and smallest numbers of trees per acre, with higher percentages reflecting fewer trees (**Density Score**).

C) Index calculation

- 1) Sum these two values (each on a scale of 0 to 100), and divide by two, for an overall index value between 0 and 100 (**Rarity Index**).

Status for Southern Appalachians: Completed. See Table 4 for the Southern Appalachian tree species with the highest unweighted vulnerability index values for the Rarity/Density intrinsic factor.

Table 4: The 12 Southern Appalachian tree species with the highest unweighted vulnerability index values for the Rarity/Density intrinsic factor. Index values are on a scale of 0 to 100.

Rank	Species	Index
1	paper birch (<i>Betula papyrifera</i>)	100.00
2	quaking aspen (<i>Populus tremuloides</i>)	100.00
3	Kentucky coffeetree (<i>Gymnocladus dioicus</i>)	100.00
4	roundleaf serviceberry (<i>Amelanchier sanguinea</i>)	100.00
5	tamarack (<i>Larix laricina</i>)	100.00
6	Virginia roundleaf birch (<i>Betula uber</i>)	100.00
7	Boynton oak (<i>Quercus boyntonii</i>)	100.00
8	Arkansas oak (<i>Quercus arkansana</i>)	100.00
9	painted buckeye (<i>Aesculus sylvatica</i>)	99.98
10	yellowwood (<i>Cladrastis kentukea</i>)	99.97
10	rock elm (<i>Ulmus thomasi</i>)	99.97
10	northern white-cedar (<i>Thuja occidentalis</i>)	99.97

Intrinsic Factor A3: Regeneration Capacity

Description: Index quantifying, for each species within the area of interest, the percent of trees per acre across plots that are saplings, as a measurement of the current reproductive success of each species, as well as the relative reproductive potential of each species based on several species-specific characteristics. Index values will be higher for species with a smaller proportion of saplings versus larger trees, and for species with lower reproductive capacity.

Justification: Genetic risk to changing climate condition in forest trees is likely to be influenced by several factors associated with species' ability to successfully regenerate.

First, it's important to know not only whether tree species can survive in a given location; they must also be able to germinate, grow, compete and reproduce effectively to maintain a population in a given area under a new environmental regime (Hamrick 2004). A species' existing demographic structure is a crucial indicator of whether it is able to maintain its existence even under current environmental conditions.

Second, reproductive rate, or fecundity, will be critical. Among the best-supported empirical correlates of extinction includes low fecundity (Brook et al. 2008), and low reproductive rate also increases risk following large-scale disturbance (Stork et al. 2009). In response to changing climate conditions, species with low fecundity, or late stage of reproductive maturity, will likely suffer greater adaptational lag (Aitken and others 2008).

Third, maturation age will influence the ability of tree species to either adapt to changing conditions, or to successfully shift their distributions in response. Specifically, delayed reproductive maturity will reduce the number of generations that can establish during any period of time (Jump and Penuelas 2005, Savolainen and others 2004), and increases extinction risk following large-scale disturbance (Stork et al. 2009). Based on the paleorecord, taxa displaying to most rapid spread as a result of long-term climate changes were those that matured early, had high reproductive capacity, and were able to disperse seeds long distances (Clark 1998).

Fourth, the potential for a population to adapt to changes in climate will in part be governed by the average lifespan of individuals. The lag of adaptation in those species with a long generation time and long lifespan will be significantly larger for several reasons (Jump and Penuelas 2005), including the fact that long lifespan (and hence low turnover) of individuals will reduce the opportunities for establishment of new genotypes within existing populations (Jump and Penuelas 2005, Savolainen et al. 2004). Given their longevity, tree populations may be able to persist in a given spot much longer than many short-lived plant species, though with reduced numbers and with

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increases in the intervals between successful recruitment events (Hamrick 2004). It's unclear, however, whether all species would be able to continue to successfully reproduce, given the potential degree of climate change.

Similarly, tree species that have the capacity for clonal reproduction can, such as in the case of aspen (*Populus tremuloides*), persist in the absence of sexual reproduction for centuries or even millennia (Ally and others 2008). This could be either an advantage or a disadvantage: some clonal species have been found to persist in a single location for long periods despite climatic changes (Steinger and others 1996), but such a situation probably reduces the establishment of new genotypes that could be better adapted to new conditions, as is the expectation with long-lived trees. The most advantageous strategy for tree species is therefore perhaps a combination of sexual and vegetative reproduction, with vegetative reproduction occurring after topkill or other disturbance.

Finally, dioecy, the breeding system in which there are separate male and female individuals, is a factor associated with a higher risk of extinction, suggesting that dioecious plants may warrant special attention in conservation practices (Vamosi and Vamosi 2005). The cause is not entirely clear, but hypotheses include reduced mate assurance, a "seed-shadow handicap" (only have the female trees produce seed), and a reliance on large pollinator pools.

Data source(s):

- Eastern Oldlist (Pederson 2010)
(<http://www.ldeo.columbia.edu/~adk/oldlisteast/>).
- Fire Effects Information System (United States Department of Agriculture Forest Service 2010) (<http://www.fs.fed.us/database/feis/>).
- Flora of North America North of Mexico (Flora of North America Editorial Committee 1993+) (<http://www.fna.org/>).
- Forest Inventory and Analysis data for the area of interest (U.S. Department of Agriculture Forest Service 2008a)
(<http://www.fia.fs.fed.us/>).
- North American Trees, Fifth Edition (Preston and Braham 2002).
- Silvics of North America (Burns and Honkala 1990)
(http://www.na.fs.fed.us/spfo/pubs/silvics_manual/table_of_contents.htm).
- Woody Plant Seed Manual (Bonner and Karrfalt 2008)
(<http://www.nsl.fs.fed.us/wpsm/>).

Data processing:

A) Demographic structure within the region of interest

- 1) For each species, determine the mean trees per acre of large trees (dbh > 12.7 cm) across FIA plots within the area of interest (**Mean TPA/plot**). (Note: If a species is known to occur within the area of interest but does not occur on an FIA plot, either as a large tree or a sapling, enter "0", but do not count this category when calculating the regeneration index [see below]. If a species does not occur as a large tree on at least one FIA plot, but does occur as a sapling, also enter this value as "0", and include this value in the final calculation of the regeneration index).
- 2) For each species, determine the mean trees per acre of large trees (dbh 2.54 - 12.7 cm) across FIA plots within the area of interest (**Sapling Mean TPA/Plot**). (Note: If a species is known to occur within the area of interest but does not occur on an FIA plot, either as a large tree or a sapling, enter "0", but do not count this category when calculating the regeneration index [see below]. If a species does not occur as a sapling on at least one FIA plot, but does occur as a larger tree, also enter this value as "0", and include this value in the final calculation of the regeneration index).
- 3) Calculate the percent of trees per acre occurring on FIA plots that are saplings (**Percent Saplings**).
- 4) Calculate the reverse relative percent saplings, on a scale of 0 to 100, for each species compared to the species with the largest and smallest percent of saplings, with higher percentages reflecting fewer saplings (**Demographic Score**).

B) Large seed crop frequency

- 1) Search the Silvics Manual, Woody Plant Seed Manual, North American Trees and the Fire Effects Information System for information on fecundity for each species (**Large Seed Crop Frequency, Seed Crop Source**).
- 2) Assign each species a **Seed Crop Score** based on the interval between large seed crops.
 - Long (4 or more years between large seed crops, or erratic/irregular) = 100
 - Moderate (large seed crop every 2-3 years) = 50
 - Short (large seed crop more or less annually) = 0

C) Reproductive maturity age

- 1) Search the Silvics Manual, Woody Plant Seed Manual, and the Fire Effects Information System for information on maturation age for each species (*Maturation, Maturation Source*).
- 2) Assign each species a *Maturation Score* based on its fecundity level.
 - Very late (40 or more years) = 100
 - Late (30-39 years) = 75
 - Moderate (20-29 years) = 50
 - Early (10-19 years) = 25
 - Very early (<10 years) = 0

D) Combination of sexual and vegetative reproduction strategies

- 1) Search the Silvics Manual, Woody Plant Seed Manual, and the Fire Effects Information System for information on the vegetative reproduction ability of each species (*Cloning Ability, Cloning Source*).
- 2) Assign each species a *Cloning Score* based on its ability to reproduce vegetatively.
 - Cloning (through root suckering, etc.) more important regeneration strategy than sexual reproduction = 100
 - Does not reproduce vegetatively (or no vegetative reproduction known) = 100
 - Vegetative reproduction possible, but rare = 75
 - Stump sprouting common after topkill of smaller trees = 25
 - Prolific vegetative reproduction (stump sprouting, root suckering) after topkill or disturbance, or vegetative reproduction possible from living stems = 0

E) Lifespan

- 1) Search the Silvics Manual, Woody Plant Seed Manual, North American trees, the Fire Effects Information System, and Eastern Oldlist for information on lifespan for each species (*Lifespan, Lifespan Source*).
- 2) Assign each species a *Lifespan Score* based on its longevity.
 - Very old (>200 years) = 100
 - Old (150-199 years) = 75
 - Moderate (100-149 years) = 50

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- Young (50-99 years) = 25
- Very young (<50 years) = 0

F) Dioecy

- 1) Search the Silvics Manual, Woody Plant Seed Manual, North American Trees and the Fire Effects Information System for information on whether each species is dioecious (*Dioecy*, *Dioecy Source*).
- 2) Assign each species a *Dioecy Score* based on its fecundity level.
 - Dioecious = 100
 - Mostly dioecious, some monoecious; polygamous or dioecious = 50
 - Polygamodioecious = 25
 - Monoecious, polygamonoecious, hermaphroditic (perfect flowers) = 0

G) Index calculation

- 1) Sum these six values (each on a scale of 0 to 100) (*Regen Total*).
- 2) Count the number of scores calculated for each species (*Regen Number*). (Note: A species which occurred on no FIA plots would have a value of 5, while species for which all data were collected would have a 6).
- 3) Calculate the *Regeneration Index* by dividing *Regen Total* by *Regen Number*.

Status for Southern Appalachians: Completed. See Table 5 for the Southern Appalachians tree species with the highest unweighted vulnerability index values for the Regeneration Capacity intrinsic factor.

Table 5: The 10 Southern Appalachian tree species with the highest unweighted vulnerability index values for the Regeneration Capacity intrinsic factor. Index values are on a scale of 0 to 100.

Rank	Species	Index
1	smoketree (<i>Cotinus obovatus</i>)	75.00
1	Carolina ash (<i>Fraxinus caroliniana</i>)	75.00
3	red pine (<i>Pinus resinosa</i>)	75.00
4	black ash (<i>Fraxinus nigra</i>)	70.83
5	red spruce (<i>Picea rubens</i>)	69.13
6	quaking aspen (<i>Populus tremuloides</i>)	65.00
6	baldcypress (<i>Taxodium distichum</i>)	65.00
8	eastern redcedar (<i>Juniperus virginiana</i>)	64.88
9	swamp white oak (<i>Quercus bicolor</i>)	62.50
10	white ash (<i>Fraxinus americana</i>)	60.15

Intrinsic Factor A4: Dispersal Ability

Description: Index quantifying the relative ability to disperse the seed for each species within the area of interest. Index values will be higher for species that on average disperse seed shorter distances.

Justification: A major concern for forest tree species in the face of climate change is whether they will be able to disperse into newly available habitats quickly enough to match the rate of environmental change (Cain and others 2000, Clark 1998). Consequently, species with low adaptability and/or dispersal capacity will be caught by the dilemma of climate-forced range change and low likelihood of finding distant habitats to colonize, ultimately resulting in increased extinction rates (Walther and others 2002). Therefore, the ability of plants to disperse seeds may be critical for their survival under the current constraints of landscape fragmentation and climate change (Vittoz and Engler 2007), and data on long-distance seed dispersal can be used on a species-by-species basis to assess likelihood of survival (Cain et al. 2000).

In fact, within some species, long-distance seed dispersal has appeared, following Pleistocene warming, to have restored extirpated populations with populations containing a full complement of genetic variation (Hamrick 2004). On the other hand, low dispersal ability is a strong empirical predictor of extinction risk (Brook et al. 2008, Stork et al. 2009).

Additionally, adaptation to changing conditions may be more possible depending on a suite of species traits, including the extent of gene flow among populations through dispersal of both pollen and seeds (Davis and others 2005). High rates and distances of seed and pollen dispersal will contribute positively to tree species' capacity both to adapt and to migrate (Aitken and others 2008). Also, species with effective dispersal of pollen and seeds maintain high gene flow and hence high variability within species and populations, while those with isolated populations tend to have low genetic variation (Hamrick et al. 1992, Hamrick and Godt 1996).

Data source(s):

- Vittoz and Engler (2007) estimate seed dispersal distance for temperate region plants. They identified seven “dispersal types” with similar dispersal distances, and for each type calculated the upper limits (80th percentile for the plants within a given dispersal type) for the distance within which 99% of a species' seeds will disperse.
- Fire Effects Information System (United States Department of Agriculture Forest Service 2010) (<http://www.fs.fed.us/database/feis/>).
- Flora of North America North of Mexico (Flora of North America Editorial Committee 1993+) (<http://www.fna.org/>).

- Silvics of North America (Burns and Honkala 1990) (http://www.na.fs.fed.us/spfo/pubs/silvics_manual/table_of_contents.htm).
- Woody Plant Seed Manual (Bonner and Karrfalt 2008) (<http://www.nsl.fs.fed.us/wpsm/>).

Data processing:

A) Seed dispersal distance

- 1) For each species, compile seed dispersal mechanism information from the Silvics Manual, the Woody Plant Seed Manual, Flora of North America and the Fire Effects Information System (*Seed Dispersal Description, Seed Dispersal Source*).
- 2) Assign each seed dispersal type to one of the seven described by Vittoz and Engler (2007) (*Seed Dispersal Type*), and determine the appropriate 99% seed dispersal distance (*Seed Dispersal Distance*).
 - Type 2 – gravity dispersed, small-animal dispersed = 5 meters
 - Type 4 – winged, wind-dispersed = 150 meters
 - Type 6 – bird-dispersed, water-dispersed = 1,500 meters
- 3) Assign each species a *Dispersal Index* based on its seed dispersal distance (scaled from 0 to 100 from longest to shortest distance).
 - Type 2 – gravity dispersed, small-animal dispersed = 100
 - Type 4 – winged, wind-dispersed = 90
 - Type 6 – bird-dispersed, water-dispersed = 0

Status for Southern Appalachians: Completed. See Table 6 for the Southern Appalachian tree species with the highest unweighted vulnerability index values for the Regeneration Capacity intrinsic factor.

Table 6: The eight Southern Appalachian tree species with the highest unweighted vulnerability index values for the Dispersal Ability intrinsic factor. (Several species were tied for the ninth highest vulnerability index value). Index values are on a scale of 0 to 100.

Rank	Species	Index
1	Kentucky coffeetree (<i>Gymnocladus dioicus</i>)	100
1	Ohio buckeye (<i>Aesculus glabra</i>)	100
1	painted buckeye (<i>Aesculus sylvatica</i>)	100
1	yellow buckeye (<i>Aesculus flava</i>)	100
1	sourwood (<i>Oxydendrum arboreum</i>)	100
1	bitternut hickory (<i>Carya cordiformis</i>)	100
1	Carolina hemlock (<i>Tsuga caroliniana</i>)	100
1	eastern hemlock (<i>Tsuga canadensis</i>)	100

Intrinsic Factor A5: Habitat Affinities

Description: Index quantifying the relative risk of climate change on tree species as a result of habitat specifications, including niche breadth, site affinities, and associations with higher elevations and later forest successional stages. Index values will be higher for species that exist at higher elevations, tend toward later forest successional stages, and have narrower niche breadth and more specific site affinities.

Justification: Ecosystems in mountainous areas appear to be particularly vulnerable to the effects of climate change (Hamann and Wang 2006). Montane species, including trees, are at risk of the “summit trap phenomenon,” in which species inhabiting mountain summits are forced to move to higher altitudes when temperatures increase: They have no escape route and may become locally extinct, with the restriction of the suitable habitat reducing the carrying capacity and depressing the overall effective population size (Pertoldi and Bach 2007). In fact, mountaintop species have been among the first groups in which entire species have gone extinct due to recent climate change (Parmesan 2006).

Species associated with late stages of forest succession display more variation within populations than pioneer species (Hamrick et al. 1992), and have been considered at higher risk of vulnerability (Myking 2002).

One response to modest climate change may be for trees to migrate within local areas among microsites or aspects. However, for species that inhabit a small range of aspects, slopes and microsites, this is not a likely mechanism for maintaining high levels of adaptive diversity (Bower and Aitken 2008). Additionally, narrow niche breadth is, in general, a strong predictor of extinction risk (Stork et al. 2009, Brook et al. 2008).

Data source(s):

- Fire Effects Information System (United States Department of Agriculture Forest Service 2010) (<http://www.fs.fed.us/database/feis/>).
- Flora of North America North of Mexico (Flora of North America Editorial Committee 1993+) (<http://www.fna.org/>).
- Forest Inventory and Analysis data for the area of interest (U.S. Department of Agriculture Forest Service 2008a) (<http://www.fia.fs.fed.us/>).
- Global 1-km digital elevation model (U.S. Geological Survey 1996) (http://eros.usgs.gov/#/Find_Data/Products_and_Data_Available/gtopo30_info).

- Quantitative niche breadth determinations (Hargrove and Hoffman 2005) (http://www.geobabble.org/~hnw/global/treeranges2/climate_change/index.html).
- Silvics of North America (Burns and Honkala 1990) (http://www.na.fs.fed.us/spfo/pubs/silvics_manual/table_of_contents.htm).
- Woody Plant Seed Manual (Bonner and Karrfalt 2008) (<http://www.nsl.fs.fed.us/wpsm/>).

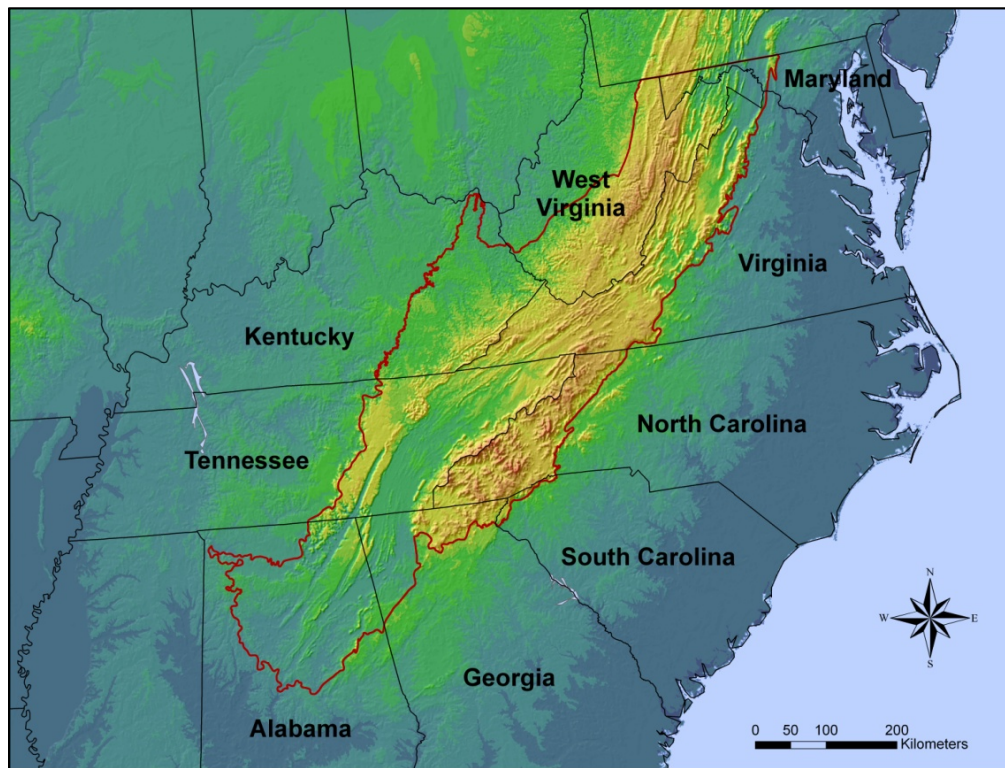


Figure 8: Digital elevation model (DEM) for the Southern Appalachian region.

Data processing:

A) Mean elevation of species occurrences within region of interest (Figure 8)

- 1) Intersect a point file of the FIA plots within the region of interest with the DEM.
- 2) Calculate the mean elevation of the plots on which each species occurs (**Mean Elevation**). (Note: If a species is known to occur within the area of interest but does not occur on an FIA plot, it will be necessary to calculate mean elevation another way. We clipped the

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DEM to the range of each of these species within the area of interest, then calculated the mean elevation of the pixels within that range area).

- 3) Calculate the relative percent for mean elevation population, on a scale of 0 to 100, for each species compared to the species with the highest and lowest mean elevations within the area of interest, with higher percentages reflecting higher elevations (*Elevation Score*).

B) Niche breadth

- 1) Find quantitative niche breadth determinations for each species (*Niche Breadth*) at http://www.geobabble.org/~hnw/global/treeranges2/climate_change/index.html. Go to “Species Atlas” and click on the name of the species. The column at the right reports “# of Unique Ecoregions Containing 2 or More Occurrences (Niche Breadth)”. This is the number of quantitatively defined ecoregions in which fall at least two Forest Inventory and Analysis plots containing the species. The ecoregions are defined using the Multivariate Spatio-Temporal Clustering (MSTC) method.
- 2) Calculate the reverse relative percent for number of quantitative ecoregions for each species, on a scale of 0 to 100, for each species compared to the species present in the most and fewest quantitative ecoregions, with higher percentages reflecting fewer ecoregions, and thus narrower ecological niche (*Niche Score*). Species without two or more FIA occurrences on any ecoregion are assigned a score of 0.

C) Successional stage affinity

- 1) Search the Silvics Manual, Woody Plant Seed Manual, and the Flora of North America for information on successional stage affinity for each species (*Successional Stage, Stage Source*).
- 2) Assign each species a *Stage Score* based on its affinity to a successional stage.
 - Climax = 100
 - Late = 75
 - Intermediate = 50
 - Early = 25
 - Pioneer = 0

D) Site affinities

- 1) Search the Silvics Manual, Woody Plant Seed Manual, and the Flora of North America for information on niche breadth for each species (*Site Affinities, Site Source*).
- 2) Assign each species a *Site Score* based on its affinity to a site affinity.
 - Narrow breadth/specialist = 100
 - Moderate to narrow breadth = 75
 - Moderate breadth = 50
 - Wide to moderate breadth = 25
 - Wide breadth/generalist = 0

E) Index calculation

- 4) Sum these four values (each on a scale of 0 to 100) (*Habitat Total*).
- 5) Count the number of scores calculated for each species (*Habitat Number*).
- 6) Calculate the *Habitat Index* by dividing *Habitat Total* by *Habitat Number*.

Status for Southern Appalachians: Completed. See Table 7 for the Southern Appalachian tree species with the highest unweighted vulnerability index values for the Habitat Affinities intrinsic factor.

Table 7: The 10 Southern Appalachian tree species with the highest unweighted vulnerability index values for the Habitat Affinities intrinsic factor. Index values are on a scale of 0 to 100.

Rank	Species	Index
1	Carolina silverbell (<i>Halesia caroliniana</i>)	78.68
2	Carolina hemlock (<i>Tsuga caroliniana</i>)	76.48
3	sand hickory (<i>Carya pallida</i>)	75.64
4	mountain magnolia (<i>Magnolia fraseri</i>)	74.90
5	striped maple (<i>Acer pensylvanicum</i>)	74.53
6	red spruce (<i>Picea rubens</i>)	73.64
7	baldcypress (<i>Taxodium distichum</i>)	72.24
8	painted buckeye (<i>Aesculus sylvatica</i>)	71.64
9	sand hickory (<i>Carya pallida</i>)	70.17
10	redbay (<i>Persea borbonia</i>)	69.85

Intrinsic Factor A6: Genetic Variation

Description: Index quantifying the relative amount of between-population variation that exists within the species. Index values will be higher for species that have higher levels of genetic differentiation among populations.

Justification: Low levels of between-population genetic differentiation may be a strong indicator of genetic vulnerability within forest tree species in the face of climate change. Species with high population-level variation in fitness-related traits run the least risk of losing adaptedness, which is necessary for future evolution in response to changing conditions (Myking 2002). Plant species with greater genetic diversity have been found to have greater variation in phenological responses to temperature, indicating the importance of maintaining genetic diversity within populations to alleviate changes in phenology due to future climate change (Doi and others 2010). Although the consequences of reduced genetic diversity will vary, decreased climate-related diversity is likely to reduce a population's ability to withstand and recover from future climatic perturbations (Jump and Penuelas 2005). At the same time, the magnitude of genetic variation in natural populations for traits likely to be critical to survival and reproduction in future climates is largely unknown (Davis and Shaw 2001), although initial evidence suggests that sufficient genetic variation resides within tree populations to allow them to adapt to changing environmental conditions (Hamrick 2004). Tree species maintain significantly more genetic variation within their populations than other groups of plants, but the distribution of genetic diversity among tree populations is probably more important in the context of global climate change (Hamrick 2004). Specifically, a greater liability of loss of genetic variation might be expected in tree species in which a greater proportion of the variation exists between populations (Myking 2002).

Mating system, too, may play a role in the ability of forest tree populations to survive climate change. Generally, outcrossing species with large continuous geographic ranges, and effective dispersal of pollen and seeds, maintain high gene flow and hence high variability within species and populations. Selfing species, meanwhile, have particularly low genetic variation (Hamrick et al. 1992, Hamrick and Godt 1996, Myking 2002). Tree species with mixed-mating systems have significantly more genetic diversity among populations than predominantly outcrossing trees (Hamrick 2004).

Finally, the vector for pollination of forest trees is an important consideration, given that within-population variation in allozyme diversity and adaptive traits is associated with species in which pollen is dispersed by wind, indicating that wind is a more effective vector for dispersal than insects (Govindaraju 1988, Myking 2002). Additionally, disrupted synchrony between the availability of insect pollinators and the timing of flowering

could affect the successful reproduction of insect-pollinated angiosperm tree species.

Data source(s):

- Fire Effects Information System (United States Department of Agriculture Forest Service 2010) (<http://www.fs.fed.us/database/feis/>).
- Flora of North America North of Mexico (Flora of North America Editorial Committee 1993+) (<http://www.fna.org/>).
- North American Trees, Fifth Edition (Preston and Braham 2002).
- Population genetics literature.
- Silvics of North America (Burns and Honkala 1990) (http://www.na.fs.fed.us/spfo/pubs/silvics_manual/table_of_contents.htm).
- Synthesis of the North American Flora (Kartesz 2009) (**fee**; <http://www.bonap.org/synth.html>).
- USDA Plants Database (<http://plants.usda.gov/>).
- Woody Plant Seed Manual (Bonner and Karrfalt 2008) (<http://www.nsl.fs.fed.us/wpsm/>).

Data processing:

A) Genetic differentiation among populations within the region of interest

- 1) Search the USDA Plants Database, Floristic Synthesis, the Silvics Manual, Woody Plant Seed Manual, North American Trees, the Fire Effects Information System and the population genetic literature for information about population differentiation of species within the region of interest (**Population Differentiation, Differentiation Source**). For example, species encompassing more than one recognized taxonomic variety or having a high level of morphological or molecular marker (F_{ST}) variation would be classified as having “high variation.” Species having several recognized ecotypes or moderate F_{ST} values would be classified as having “moderate variation.” Species with very little or no variation among populations would have “low variation.”
- 2) Assign each species a **Differentiation Score** based on its level of population differentiation. (*Note: If no information is available about*

a given species, enter “0”, but do not count this category when calculating the variation index [see below].)

- High variation (two or more nontypic varieties) = 100
- Moderate to high variation (one nontypic variety) = 75
- Moderate variation (ecotypes or races and/or high trait or marker variation) = 50
- Low to moderate variation (no nontypic varieties and some trait or marker variation) = 25
- Low variation (no nontypic varieties and little trait or marker variation) = 0

B) Mating system

- 1) Search the Silvics Manual, Woody Plant Seed Manual, the Flora of North America, the Fire Effects Information System and the population genetics literature for information on mating system for each species (*Mating System, Mating Source*).
- 2) Assign each species a *Mating Score* based on its mating system.
 - Selfing (or apomixis) possible and common; outcrossing rate (t_m) < 0.75 = 100
 - Selfing possible, and somewhat common; outcrossing rate (t_m) between 0.75 and 0.9 = 66
 - Selfing possible, but unlikely (including via male and female flower asynchrony); outcrossing rate (t_m) > 0.9 = 33
 - Obligate outcrossing (including dioecy) or outcrossing rate (t_m) not significantly different from 1.0 = 0

C) Pollination vector

- 1) Search the Silvics Manual, Woody Plant Seed Manual, the Flora of North America, North American Trees, the Fire Effects Information System and other sources for information on pollination vector for each species (*Pollination Vector, Pollination Source*).
- 2) Assign each species a *Pollination Score* based on its pollination vector or vectors.
 - Insects only = 100
 - Mostly insects, also wind = 66
 - Mostly wind, also insects = 33
 - Wind only = 0

D) Index calculation

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- 1) Sum these three values (each on a scale of 0 to 100) (***Variation Total***).
- 2) Count the number of scores calculated for each species (***Variation Number***).
- 3) Calculate the ***Variation Index*** by dividing ***Variation Total*** by ***Variation Number***.

Status for Southern Appalachians: Completed. See Table 8 for the Southern Appalachian tree species with the highest unweighted vulnerability index values for the Genetic Variation intrinsic factor.

Table 8: The 10 Southern Appalachian tree species with the highest unweighted vulnerability index values for the Genetic Variation intrinsic factor. Index values are on a scale of 0 to 100.

Rank	Species	Index
1	Carolina silverbell (<i>Halesia caroliniana</i>)	100.00
1	hawthorn species (<i>Crataegus</i> spp.)	100.00
1	black cherry (<i>Prunus serotina</i>)	100.00
1	gum bumelia (<i>Sideroxylon lanuginosum</i>)	100.00
1	chokecherry (<i>Prunus virginiana</i>)	100.00
6	pin cherry (<i>Prunus pensylvanica</i>)	91.67
6	eastern redbud (<i>Cercis canadensis</i>)	91.67
8	Ohio buckeye (<i>Aesculus glabra</i>)	87.50
9	black locust (<i>Robinia pseudoacacia</i>)	83.33
9	yellow-poplar (<i>Liriodendron tulipifera</i>)	83.33

External Factor B1: Pest and Pathogen Threats

Description: Index quantifying, for each species within the area of interest, the relative threat posed by pests and pathogens. Index values will be higher for species facing more serious and more immediate insect and disease threats.

Justification: A long and growing list of invasive and native insects and pathogens threaten North American forest tree species in the absence of climate change, and represent the most pervasive and important disturbance agents in North American forests (Logan and others 2003). Several pest and pathogen species are likely to have stronger or more widespread effects on forest composition and structure under the projected climate (Dukes and others 2009, Logan and others 2003), and the ability of native species to persist in appropriate climates is likely to be affected by new invasive species (Thomas et al. 2004). For tree species threatened by pests and diseases in addition to climate change, minimizing maladaptation may mean the difference between establishing or maintaining viable populations and local extirpation (Bower and Aitken 2008).

Data source(s):

- For the Eastern United States: List of major insect and disease threats to North American forest tree species at the U.S. Forest Service Eastern Forest Environmental Threat Assessment Center (EFETAC) Web site (<http://www.threatsummary.forestthreats.org/>).
- Information from experts from USDA Forest Service Forest Health Protection and/or state departments of forestry.

Data processing:

A) Relative degree of insect and disease threat to populations within the region of interest

- 1) Determine the major insect and disease threats to each of the species within the area of interest. List these (up to 5) under “**Threat 1,**” “**Threat 2,**” etc.
- 2) For each threat, assign a threat severity rating (**Threat 1 Severity, Threat 2 Severity,** etc.).

- Complete mortality of all mature trees = 10
- Significant mortality of mature trees = 8
- Significant/complete mortality in related species = 6
- Moderate mortality of mature trees = 5
- Moderate mortality in association with other threats = 3
- Minor mortality, usually of already-stressed trees = 1

- 3) For each threat, assign a threat immediacy rating (*Threat 1 Immediacy*, *Threat 2 Immediacy*, etc.).
 - Present in region of interest = 3
 - Approaching region of interest = 2
 - Potential to reach region of interest = 1
- 4) For each threat, multiply the severity and immediacy scores to generate a threat score (*Threat 1 Score*, *Threat 2 Score*, etc.).
- 5) Sum the threat scores for each species (*Pest Total*).
- 6) Calculate the relative percent for total pest and pathogen threat score, on a scale of 0 to 100, for each species compared to the species with the highest and lowest total threat scores, with higher percentages reflecting higher threat scores (*Pest Index*).

Status for Southern Appalachians: Completed. See Table 9 for the Southern Appalachian tree species with the highest unweighted vulnerability index values for the Pests and Pathogen Threats external factor.

Table 9: The 10 Southern Appalachian tree species with the highest unweighted vulnerability index values for the Pests and Pathogen Threats external factor. Index values are on a scale of 0 to 100.

Rank	Species	Index
1	American elm (<i>Ulmus americana</i>)	100.00
2	winged elm (<i>Ulmus alata</i>)	89.09
2	September elm (<i>Ulmus serotina</i>)	89.09
2	slippery elm (<i>Ulmus rubra</i>)	89.09
2	rock elm (<i>Ulmus thomasii</i>)	89.09
6	butternut (<i>Juglans cinerea</i>)	87.27
7	eastern hemlock (<i>Tsuga canadensis</i>)	74.55
7	Carolina hemlock (<i>Tsuga caroliniana</i>)	74.55
9	shortleaf pine (<i>Pinus echinata</i>)	67.27
10	American chestnut (<i>Castanea dentata</i>)	60.00

External Factor B2: Climate Change Pressure

Description: Index quantifying the relative risk of climate change on tree species as a result of the expected impact of climate change on the future area and location of their suitable habitat, and the degree to which their existing distribution is fragmented. Index values will be higher for species that are expected to have less suitable habitat in the future, that have less current habitat overlapping with expected future habitat, that have current habitat farther distances from expected future habitat, and that exist in more highly fragmented landscapes.

Justification: Different areas within the distributions of forest tree species are likely to experience different degrees of climate change pressure. For example, the paleorecord suggests that populations at the trailing edge of the shifting distribution were often extirpated, resulting in a latitudinal displacement of range rather than a simple expansion into newly favorable region (Davis and Shaw 2001). Already, a disproportionate number of population extinctions have been documented along southern and low-elevation range edges in response to recent climate warming, resulting in contraction of species' ranges at these warm boundaries (Parmesan 2006). At the same time, these trailing edge populations appear to have played a key role for the maintenance of biodiversity through the Quaternary, and Hampe and Petit (2005) argue that rear-edge populations are disproportionately important for the long-term conservation of genetic diversity, phylogenetic history and evolutionary potential of species and that, therefore, their investigation and conservation deserve high priority.

The widespread conversion of forest land to other uses may present an impediment to the shifting of forest tree populations to more suitable habitats as the climate changes (Thomas et al. 2004). For plant species to migrate across a landscape, its habitat patches must be sufficiently well connected to allow gene flow (by pollen and propagule dispersal) between populations, but this may not be possible in heavily fragmented landscapes (Jump and Penuelas 2005, Walther and others 2002). This is both a considerable and a novel obstruction to range shifts and to gene flow among populations (Davis and Shaw 2001). In concert with large-scale disturbances caused by extreme weather events, this inhabitation of range shift could result in an overall contraction of the distribution ranges of species (Opdam and Wascher 2004). In addition, fragmentation of once continuous tree populations potentially could disrupt natural ecological and evolutionary processes and could adversely modify their genetic composition (Hamrick 2004, Young and others 1996). For many species, gene flow between populations may be critically low because of the effects of habitat fragmentation; in these species, adaptation to the changing climate may be even more restricted (Jump and Penuelas 2005, Savolainen et al. 2004).

Data source(s):

- Climate change projection maps (such as Bill Hargrove’s Multivariate Spatio-Temporal Clustering maps) for each of the species of interest (Hargrove and Hoffman 2005) (http://www.geobabble.org/~hnw/global/treeranges2/climate_change/index.html).
- A forest cover map (1 km² resolution), derived from Moderate Resolution Imaging Spectroradiometer (MODIS) imagery by the U.S. Forest Service Remote Sensing Applications Center (United States Department of Agriculture Forest Service 2008b) (http://fsgeodata.fs.fed.us/rastergateway/forest_type/).
- Little’s tree species distribution maps for North America (United States Geological Survey 1999) (<http://esp.cr.usgs.gov/data/atlas/little/>).
- Shapefile encompassing boundary of the region of interest.

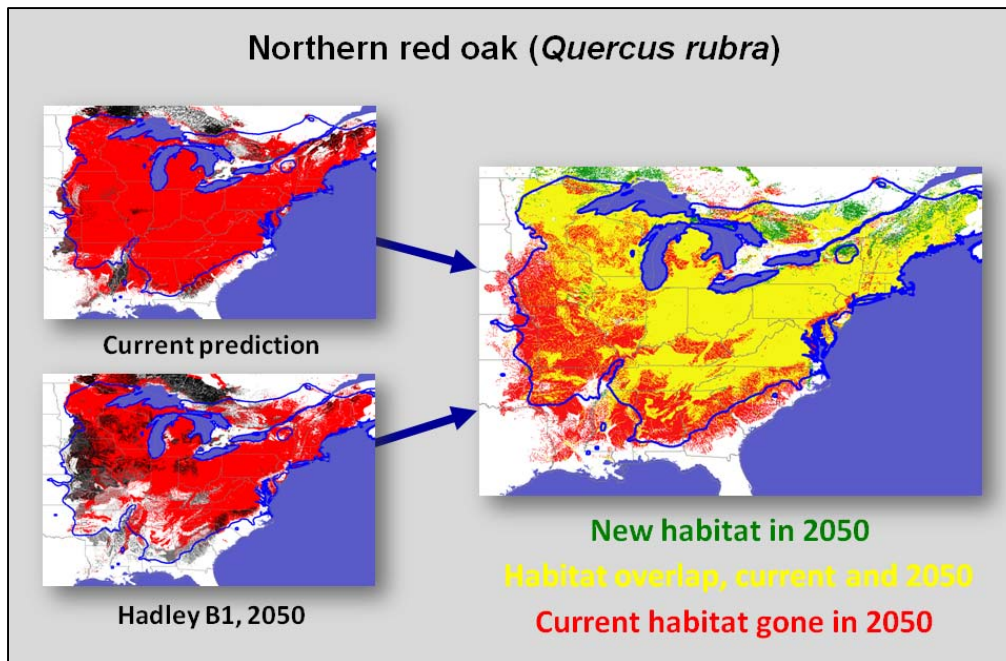


Figure 9: Multivariate Spatio-Clustering (MSTC) map comparing suitable habitat for northern red oak (*Quercus rubra*) over time. The future prediction is for 2050 under the Hadley global climate model, B1 (lower emissions) scenario.

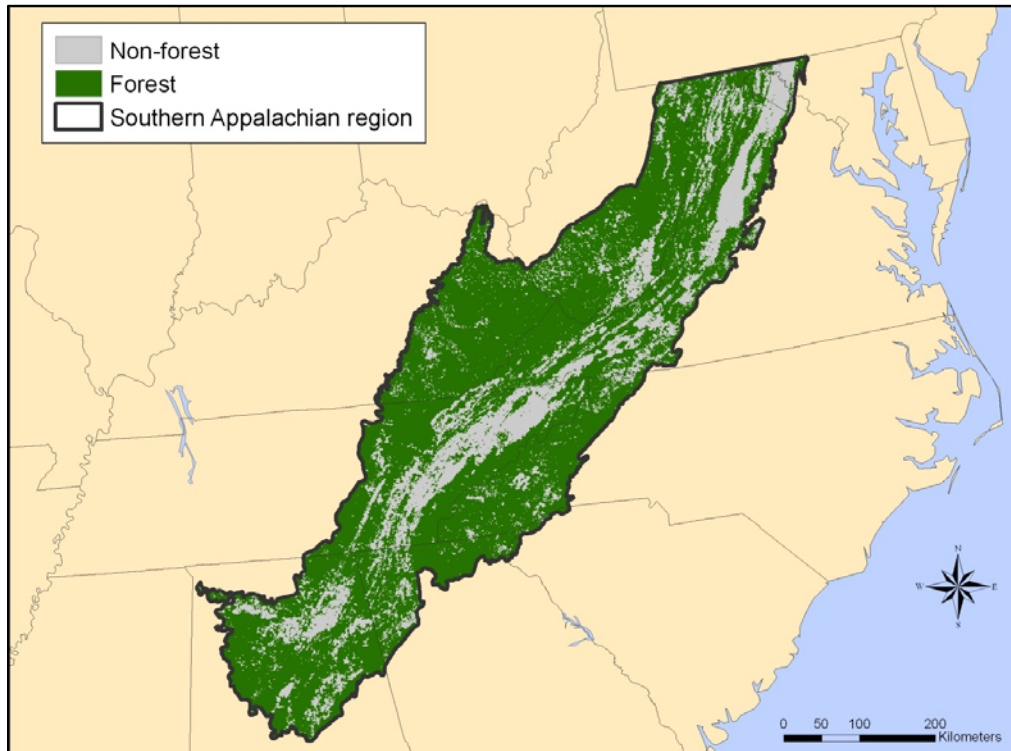


Figure 10: Forest land cover for the Southern Appalachian region.

Data processing:

A) Measure of change over time in species range area: Percent change between area of current suitable habitat and area of future suitable habitat expected under climate change (Figure 9)

- 1) For each species, find area in present suitable range, in square kilometers, (*Current Suitable*) and projected future suitable habitat area (under the Hadley global climate model, B1 [lower emissions] scenario, for 2050) (*Future Suitable*). Go to http://www.geobabble.org/~hnw/global/treeranges2/climate_change/index.html, click on “Species Atlas” and select the name of the species. The column at the right contains the relevant information. The habitat projections are defined using the Multivariate Spatio-Temporal Clustering (MSTC) method.
- 2) Calculate the percent change in suitable habitat over time ($-100 * ((\textit{Future Suitable} - \textit{Current Suitable}) / \textit{Current Suitable})$). Negative values equate to expected loss in suitable habitat over time, and positive values equate to gain in suitable habitat over time (*Area Change*).
- 3) Calculate the relative percent of expected suitable habitat percent change, on a scale of 0 to 100, for each species compared to the

species with the greatest increases and decreases in percent of suitable habitat, with higher percentages reflecting greater expected losses of suitable habitat (**Area Change Score**). Species for which climate change habitat maps have not been generated are assigned a value of 50 percent.

B) Measure of range stability over time: Percent of currently suitable habitat that overlaps with future suitable habitat expected under climate change (Figure 9)

- 1) For each species, find area in present suitable range, in square kilometers, (**Current Suitable**) and area of habitat that is expected to be suitable in both current time and in 2050 under the Hadley global climate model, B1 (lower emissions) scenario, for 2050 (**Suitable Overlap**). Go to http://www.geobabble.org/~hnw/global/treeranges2/climate_change/index.html, click on “Species Atlas” and click on the name of the species. The column at the right contains the relevant information. The habitat projections are defined using the Multivariate Spatio-Temporal Clustering (MSTC) method.
- 2) Calculate the percent of currently suitable habitat that is expected to remain suitable into the future ($100 * (\text{Suitable Overlap} / \text{Current Suitable})$). A species expected to maintain all of its current suitable habitat into the future would have a stability score of 100, and one expected to lose all of its current suitable habitat would have a stability score of 0 (**Stability Percent**).
- 3) Reverse the **Stability Percent** value ($100 - \text{Stability Percent}$) so that species expected to lose more of their current suitable habitat have higher scores (**Stability Score**). Species for which climate change habitat maps have not been generated are assigned a value of 50 percent.

C) Measure of shift pressure over time: Mean distance of each cell of currently acceptable habitat to the nearest cell of suitable habitat in 2050 (Figure 9)

- 1) For each species, the predicted mean non-zero minimum required movement distance, in map cells, between cells of habitat in current time that are expected to become unsuitable, to the nearest expected suitable habitat cell (**Movement Distance**). These values are based on habitat projections from the Hadley global climate model, B1 (lower emissions) scenario, for 2050. Go to http://www.geobabble.org/~hnw/global/treeranges2/climate_change/index.html, click on “Species Atlas” and click on the name of the species. The column at the right contains

the relevant information. The habitat projections are defined using the Multivariate Spatio-Temporal Clustering (MSTC) method.

- 2) Calculate the mean required movement distance for all current habitat cells, regardless of whether they are expected to become unsuitable (**Shift Pressure**) ($((\text{Current Suitable} - \text{Suitable Habitat}) * \text{Movement Distance}) / \text{Current Suitable}$).
- 3) Calculate the relative percent of the **Shift Pressure** score, on a scale of 0 to 100, for each species compared to the species with the lowest and greatest shift pressure values, with higher percentages reflecting greater expected shift pressure (**Shift Score**). Species for which climate change habitat maps have not been generated are assigned a value of 50 percent.

D) Forest fragmentation of species distribution within region of interest (Figure 10)

- 1) For each species, calculate total area of distribution within the region of interest, in square kilometers, using the raster forest cover data (**Range Area**).
- 2) Clip the land cover data to the species range maps within the region of interest.
- 3) Calculate the area of forest within the range area of interest for each species (**Forest Area**).
- 4) Calculate the percentage of each species range area that is unforested (**Nonforest Score**).

E) Index calculation

- 1) Sum the score values (each on a scale of 0 to 100) and divide by three, for an overall index value between 0 and 100 (**Climate Index**).

Status for Southern Appalachians: Completed. See Table 10 for the Southern Appalachian tree species with the highest unweighted vulnerability index values for the Climate Change Pressure external factor.

Table 10: The 10 Southern Appalachian tree species with the highest unweighted vulnerability index values for the Climate Change Pressure external factor. Index values are on a scale of 0 to 100.

Rank	Species	Index
1	September elm (<i>Ulmus serotina</i>)	78.32
2	Boynton oak (<i>Quercus boyntonii</i>)	73.14
3	nutmeg hickory (<i>Carya myristiciformis</i>)	69.97
4	Delta post oak (<i>Quercus similis</i>)	68.82
5	Arkansas oak (<i>Quercus arkansana</i>)	67.65
6	Kentucky coffeetree (<i>Gymnocladus dioicus</i>)	64.39
7	chalk maple (<i>Acer leucoderme</i>)	63.88
8	smoketree (<i>Cotinus obovatus</i>)	63.54
9	rock elm (<i>Ulmus thomasii</i>)	60.24
10	blue ash (<i>Fraxinus quadrangulata</i>)	56.74

Conservation Modifier C1: Endemism

Description: Percent of a given species' range encompassed by the area of interest. A species endemic to a region would have an index value of 100 percent.

Justification: The endemism index quantifies the degree to which a given species is associated with the region of interest. More conservation effort may be justified for a species that is endemic or nearly endemic to a given region.

Data source(s):

- Little's tree species distribution maps for North America (United States Geological Survey 1999) (<http://esp.cr.usgs.gov/data/atlas/little/>).
- Shapefile encompassing boundary of the region of interest.

Data processing:

A) Degree of endemism for each species associated with the region of interest

- 1) For each species, calculate total area of distribution, in hectares (**Range Area Total**).
- 2) Clip each species' range boundary to the area of interest.
- 3) For each species, calculate total area of distribution within the region of interest, in hectares (**Range Area in Region**).
- 4) Calculate the percent of total species range that occurs within the region of interest, by dividing the species distribution within the region by the total distribution area (**Endemism Index**).

Status for Southern Appalachians: Completed. See Table 11 for the Southern Appalachian tree species with the highest unweighted Endemism modifier index values.

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Table 11: The 10 Southern Appalachian tree species with the highest unweighted Endemism modifier index values. Index values are on a scale of 0 to 100.

Rank	Species	Index
1	Virginia roundleaf birch (<i>Betula uber</i>)	100.00
1	Fraser fir (<i>Abies fraseri</i>)	100.00
3	Boynton oak (<i>Quercus boyntonii</i>)	95.30
4	Carolina hemlock (<i>Tsuga caroliniana</i>)	93.42
5	mountain magnolia (<i>Magnolia fraseri</i>)	88.14
6	Table Mountain pine (<i>Pinus pungens</i>)	74.27
7	yellow buckeye (<i>Aesculus flava</i>)	53.58
8	umbrella magnolia (<i>Magnolia tripetala</i>)	49.79
9	black locust (<i>Robinia pseudoacacia</i>)	45.00
10	Virginia pine (<i>Pinus virginiana</i>)	40.25

Conservation Modifier C2: Conservation Status

Description: Index quantifying, for each species within the area of interest, conservation status as assessed by NatureServe. Index values will be higher for species with more imperiled conservation status. (Note: For the Southern Appalachians, the index values were determined based on global conservation status, but information on state-level conservation status could also be used.)

Justification: More conservation effort may be justified for species that have been determined to be imperiled, and therefore at greater risk of extinction.

Data source(s):

- NatureServe conservation status (NatureServe 2010) (<http://www.natureserve.org/explorer>).

Data processing:

A) Conservation status

- 1) Search the NatureServe database for the global conservation status of each species within the area of interest (***Global Conservation Status***).
- 2) Assign a conservation index value (between 0 and 100) for each global conservation status ranking (***Conservation Index***). (Note: *Modifiers, such as “Q” for “questionable taxonomy” are included for informational purposes, but not used in assigning a conservation index value.*)
 - G1 – critically imperiled = 100
 - G2 – imperiled = 75
 - G3 – vulnerable = 50
 - G4 – apparently secure = 25
 - G4G5 – secure to apparently secure = 12.5
 - G5 – secure = 0

Status for Southern Appalachians: Completed. See Table 12 for the Southern Appalachian tree species with the highest unweighted Conservation Status modifier index values.

Table 12: The 15 Southern Appalachian tree species with the highest unweighted Conservation Status modifier index values. Index values are on a scale of 0 to 100.

Rank	Species	Index
1	Virginia roundleaf birch (<i>Betula uber</i>)	100.00
1	Boynton oak (<i>Quercus boyntonii</i>)	100.00
3	Fraser fir (<i>Abies fraseri</i>)	75.00
4	Carolina hemlock (<i>Tsuga caroliniana</i>)	50.00
4	Arkansas oak (<i>Quercus arkansana</i>)	50.00
5	Table Mountain pine (<i>Pinus pungens</i>)	25.00
5	yellowwood (<i>Cladrastis kentukea</i>)	25.00
5	American chestnut (<i>Castanea dentata</i>)	25.00
5	smoketree (<i>Cotinus obovatus</i>)	25.00
5	September elm (<i>Ulmus serotina</i>)	25.00
5	butternut (<i>Juglans cinerea</i>)	25.00
5	hawthorn species (<i>Crataegus</i> spp.)	25.00
5	Florida maple (<i>Acer barbatum</i>)	25.00
5	Delta post oak (<i>Quercus similis</i>)	25.00
5	nutmeg hickory (<i>Carya myristiciformis</i>)	25.00

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