Sawtimber potential proportion dynamics for loblolly pine in the Southeastern U.S.

by

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(Under the Direction of Nicole Lazar)

Abstract

The stand timber monetary value is a function of merchantable volume and timber price. Finding the proportions of timber in each of the commercial pine product classes (i.e., sawtimber, chip-n-saw, and pulpwood) is a critical component in calculating the stand timber value. The objective of this research is to predict the sawtimber potential (STP) proportion over time as a function of tree and stand characteristics: the management intensity, planting density, thinning, tree diameter distribution percentile at year six, and defects and fungus infection incidence at year six. Data from a designed research trial evaluating the impacts of density and management over years 6 to 21 were used. This research has direct timber management application since a forestland owner can predict the STP when the forest plantation is still young and decide the suitable management regime. Furthermore, STP can be used to optimize financial returns by performing marginal analysis.

Index words: Timber product class proportions, Generalized linear mixed effects models, Blended price.

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Dedication

To my lovely wife and daughter, Adriana and Sofia, and my family who were supportive in difficult moments and cheering me on during the good times of my studies.

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Chapter 1

Introduction and literature review

Loblolly pine (*Pinus taeda* L.), with a forest plantation area estimated at 14.4 million hectares, is the most commercially important forest species in the Southeastern United States (South and Harper 2016). The timber production in this region has been enhanced using genetically improved seedlings, and a wide range of silvicultural treatments such as mechanical site preparation, competing vegetation control, fertilization, and thinning[1] (Allen et al. 2005). These intensive forest management practices, in conjunction with planting density, age, and environmental conditions, are the main drivers of forest stand dynamics[2] (Clutter et al. 1992).

Timber production analysis requires an accurate estimation of the merchantable[3] timber volume as a vital input for forest financial return calculations. Merchantable volume estimations can be performed by i) modeling forest growth and yield, and ii) finding the quantity of timber in each commercial timber product class:

- Sawtimber: trees or logs that meet the minimum required dimensions and quality specifications for conversion to lumber.

- Chip-n-saw: tree or logs that can be commercialized for small dimensional lumber and obtaining the byproduct chips, small pieces of wood used for paper pulp, firewood, or for making wood composites.

[1]A cultural treatment made to reduce the number of trees in a tract of land, primarily to improve growth, and enhance forest health (Helms 1998).

[2]Stand: a contiguous group of trees sufficiently uniform in age-class distribution, composition, and structure, and growing on a site of sufficient uniform quality, to be a distinguishable unit. Stand dynamic or stand development: changes in forest stand structure over time (Helms 1998).

[3]Trees and stands having the size, quality, and condition suitable for marketing under a given economic condition, even if not immediately accessible for logging.

- Pulpwood: roundwood, whole-tree chips, or wood residues that are used for paper production and allied products.

Two primary forest growth and yield modeling approaches are usually utilized in the Southeastern U.S.: size-class and whole-stand models (Burkhart et al. 2018). The size-class cohort model, a type of the stand-table[4] projection method, recognizes the stand structure[5] and growth dynamics (Poudel and Cao 2013). A present or current stand table is projected to the future by using per class annual increments and mortality rates. Present and future stand tables are converted to stock tables[6] by using local height-diameter relationships and individual-tree volume equations. Such a disaggregation of stand characteristics and structure by diameter classes allows for quantifying the volume in commercial timber product classes (Burkhart 1979; Pienaar and Harrison 1988). Although size-class cohort models allow for the estimation of volume in the commercial timber product classes, the method has some caveats. Assuming that past per-diameter-class growth rate will remain invariant in the future, and the difficulty in obtaining accurate mortality rate estimates are the two evident shortcomings of the stand-table projection method (Burkhart and Tomé 2012).

Conversely, whole-stand models, which corresponds to most existing forest growth and yield models for loblolly pine, allow for estimating total volume or weight at a given age as a function of site index[7] and stand characteristics (Burkhart et al. 2018). Whole-stand models make the differentiation of volume into the commercial timber product classes somewhat cumbersome. This problem has been traditionally addressed by finding the proportions to split the total volume into timber product classes. Binomial and multinomial response models

[4]Stand table: a list of the number of trees by diameter classes, generally per unit area. The data may be presented in the form of frequency distribution of diameter classes (Helms 1998).

[5]Stand structure: the horizontal and vertical distribution of components of a forest stand including the diameter, height, crown layers, and stand density (Helms 1998).

[6]Stock table: a list showing the proportions of total volume within a stand by diameter classes (Helms 1998).

[7]Site index: a species-specific measure of actual or potential forest productivity, expressed in terms of the average height of trees included in a specified stand component (defined as a certain number of the largest and tallest trees per unit area) at a specified based age (Helms 1998).

typify statistical approaches in which theoretical probabilities, or in this case, parameters of the proportion of classes, are mathematically expressed as a function of covariates.

The proportion of timber product classes has traditionally been modeled as a function of environmental conditions, soil type, culture intensity, planting or stand density, thinning, genetics, size, age, forest health, and stem quality assessments. Strub et al. (1986) estimated the individual-tree probability of merchantability as a function of tree diameter at breast height (DBH) in old-field[8] loblolly pine plantations. Burkhart and Bredenkamp (1989) estimated the proportion of trees in pulpwood, sawtimber, and peelers[9] by DBH classes using an extension of Strub et al. (1986) modeling approach. Buford and Burkhart (1987) found that the proportion of stems with defects was not significantly different between stands of unimproved and improved genetic stocks. Teeter and Zhou (1998) estimated multinomial models to predict timber product proportions to distribute per-acre total volume within four categories, i.e., softwood pulpwood, softwood sawtimber, hardwood pulpwood, and hardwood sawtimber as a function of DBH and volume. Prestemon and Buongiorno (2000) estimated an ordered-probit model to predict the lumber grade as a function of DBH and height. Green et al. (2018) estimated the proportion of solid wood, the aggregation of sawtimber and chip-n-saw classes, as a function of two management regimes and six planting densities. Choi et al. (2008) found that the stem quality dynamics during 15 years of measurements is a function of the DBH, total height, crown[10] class, relative height, age, site index, and stand density. Likewise, stem quality assessments such as fork[11], broken top, sweep[12], and incidence of diseases have been used to improve the estimation of timber product class proportions (Choi et al. 2008; Buford and Burkhart 1987; Green et al. 2018; Cumbie et al. 2012).

[8] Late successional or climax stage of a forest.

[9] A high-grade log from which veneer is peeled on a lathe or sliced for the production of plywood (Helms 1998).

[10] The part of a tree or woody plant bearing live branches and foliage (Helms 1998).

[11] A tree's stem that is naturally divided into two or more stems.

[12] The extent to which the lower portion of a tree's stem diverges from straight.

Most of the monetary value of timber in intensively managed pine plantations in the Southeastern United States corresponds to solid wood (Amateis and Burkhart 2005; Green et al. 2018). Depending on local markets and forest management objectives, silviculturist and forestland owners attempt to increase the amount of solid wood as a strategy to maximize financial returns. Since collecting data for aforementioned commercial timber product classes is expensive, most of the stem quality assessments have primarily been focused on sawtimber, the most valuable commercial timber product class.

Consider a binary response variable, $y_i \sim^{iid} Bernoulli(\theta)$, taking the value of one if the ith tree has been assessed to have sawtimber potential or the value zero otherwise (non-sawtimber). An extension of this model allows for $y_i \sim^{id} Bernoulli(\theta_i)$ with covariates accounting for the variation among trees in the generalized linear model (GLM) (McCullagh and Nelder 1989). Consider a model with p covariates, $\mathbf{x_i}^\top = (1, x_{i1}, x_{i2}, ..., x_{ip})$, and $p+1$ parameters, $\boldsymbol{\beta}^\top = (\beta_0, \beta_1, \beta_2, ..., \beta_p)$, as follows (Rencher and Schaalje 2008; Zhang et al. 2011):

$$y_i|\mathbf{x_i} \sim^{id} Bernoulli(\theta_i), \quad \theta_i = \mathsf{E}(y_i|\mathbf{x_i}), \quad \text{logit}(\theta_i) = \mathbf{x_i}^\top \boldsymbol{\beta}, \quad i = 1, 2, ..., n \tag{1.1}$$

where n is the number of trees. The model usually embodies assumptions that should not be taken for granted, such as zero correlation or independence, lack of interaction or additivity, and linearity (McCullagh and Nelder 1989). Because trees in forestry studies are usually measured several times, the assumption of independence between (among) observations is violated. Thus, serial correlation is present when a time-varying stochastic process is operating on the units, and the units are repeatedly measured (Rencher and Schaalje 2008). Besides, a hierarchical arrangement is present because the studies are conducted in regions with contrasting climatic characteristics, on a variety of soil types, and in measurement plots. An extension of the GLM, the generalized linear mixed model (GLMM) is used to cope with the error structure issue in forestry datasets (Zhang et al. 2011):

$$y_{it}|\mathbf{x_{it}}, \mathbf{z_i}, \mathbf{b} \sim^{id} Bernoulli(\theta_{it}), \quad \mathsf{E}(y_{it}|\mathbf{x_{it}}, \mathbf{z_i}, \mathbf{b}) = \theta_{it}, \quad \text{logit}(\theta_{it}) = \mathbf{x_{it}}^\top \boldsymbol{\beta} + \mathbf{z_i}^\top \mathbf{b} \tag{1.2}$$

$$\mathbf{b} \sim \mathcal{N}(0, \boldsymbol{\Sigma}_b), \quad i = 1, 2, ..., n, \quad t = 1, 2, ..., M \tag{1.3}$$

where $\mathbf{z_i}^\top = (\mathbf{z_{i1}}^\top, \mathbf{z_{i2}}^\top, ..., \mathbf{z_{ik}}^\top)$ is the partitioned vector of covariates within k random effects; $\mathbf{b}^\top = (\mathbf{b_1}^\top, \mathbf{b_2}^\top, ..., \mathbf{b_k}^\top)$ represents the partitioned vector of k random effects; each pair $\mathbf{z_{i1}}$ and $\mathbf{b_1}$, $\mathbf{z_{i2}}$ and $\mathbf{b_2}$, and $\mathbf{z_{ik}}$ and $\mathbf{b_k}$ is conformable for multiplication; $\mathcal{N}(0, \boldsymbol{\Sigma}_b)$ is the multivariate normal distribution with mean zero and variance-covariance matrix equal to $\boldsymbol{\Sigma}_b$; and M is the number of periods.

The objective of this research is to predict the sawtimber potential (STP) proportion over time for loblolly pine trees in the Southeastern U.S. as a function of tree and stand characteristics, management regimes, planting density, thinning, and early assessments of the relative tree size, a fungus disease incidence and severity of damage. This research can be directly applied by forestland owners in predicting STP at a juvenile stage, as forest geneticists have suggested (Cumbie et al. 2012), to decide the suitable silvicultral practices and remedy measures to maximize the stand timber value.

Chapter 2

Methods

2.1 Data

The Plantation Management Research Cooperative (PMRC) at the University of Georgia, Athens, Georgia, established 40 sites across the Southeastern United States with the purpose of testing the effect of management intensity and planting density, named Culture / Density studies, on loblolly pine (*Pinus taeda*) growth and yield. Two management intensities, operational and intensive, were applied to the sites; planting densities in all study sites were 300, 600, 900, 1200, 1500, and 1800 trees per acre (TPA).

The first study, named Coastal Plain (CP) Culture / Density, composed of 17 study sites, was installed in the Lower Coastal Plain of Georgia, Florida, and South Carolina during the 1995/1996 dormant season. All installations were planted with loblolly pine first generation, open-pollinated[1] family 7-56, an exceptionally fast grower. At the time of age 21 measurement, 11 installations remained (Figure 2.1). The second study, named South Atlantic Gulf Slope (SAGS) Culture / Density, composed of 23 study sites, was installed in the Piedmont and Upper Coastal Plain regions of Georgia, Alabama, Florida, Mississippi, and South Carolina. The genetic material, considered as good quality at the time of planting, most likely a combination of first-generation open-pollinated families, was selected by the PMRC cooperator. After 18 growing seasons, 7 and 9 installations remained being measured in the Piedmont and Upper Coastal Plain regions, respectively (Figure 2.1).

[1]Offspring from a mating where pollination was not controlled. The mother is known because seeds are collected from that individual, but the father is unknown because pollinization was not controlled.

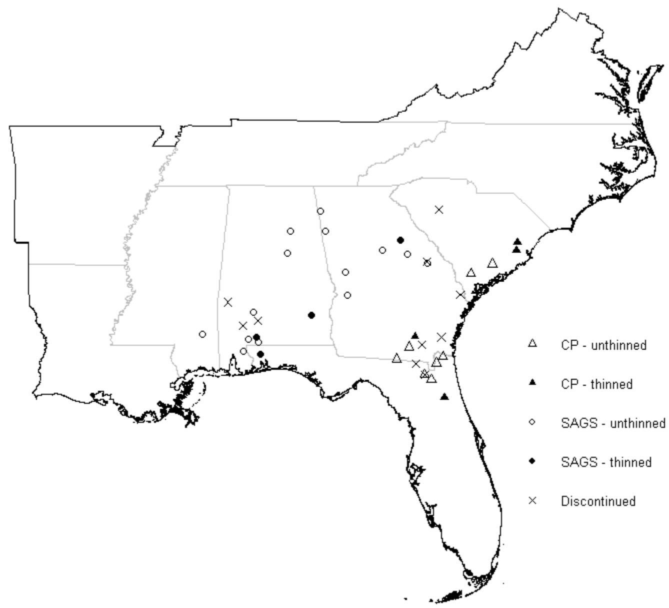

Figure 2.1: Location of the Culture / Density studies: Coastal Plain (CP) in the Lower Coastal Plain physiographic region, and South Atlantic Gulf Slope (SAGS) in the Piedmont and Upper Coastal Plain physiographic regions.

The experimental design for each study, CP and SAGS, corresponded to a split-split plot design. The study was at the highest hierarchy level of the experimental design and accounted for the effect of the physiographic region. The levels within the second level were associated with soil classes of the Cooperative Research in Forest Fertilization (CRIFF) system. The soil classes, eight in total, coded from A to H, are defined using soil drainage, and texture and depth of the surface soil layers (Jokela and Long 2012) (Figure 2.2). CRIFF classes can be subdivided into subgroups, coded by Arabic numbers, to account for differences of depth within the same class. For example, the depth of the argillic horizon of B1 CRIFF class is in the range 20-40 in, whereas the depth of the argillic horizon of B2 CRIFF class is greater than 40 in or the argillic horizon is absent (Zhao et al. 2014). In CP, at least three installations were established on each of the five CRIFF soil groups A, B1, B2, C, and D.

CRIFF classes in SAGS were E, F, and G, without any arrangement of the minimum number of installations assigned to CRIFF soil classes. The third and last level was installation, in which plots were split for management, operational and intensive, and then the six planting densities were established within each of the management plots (Harrison and Shiver 1999).

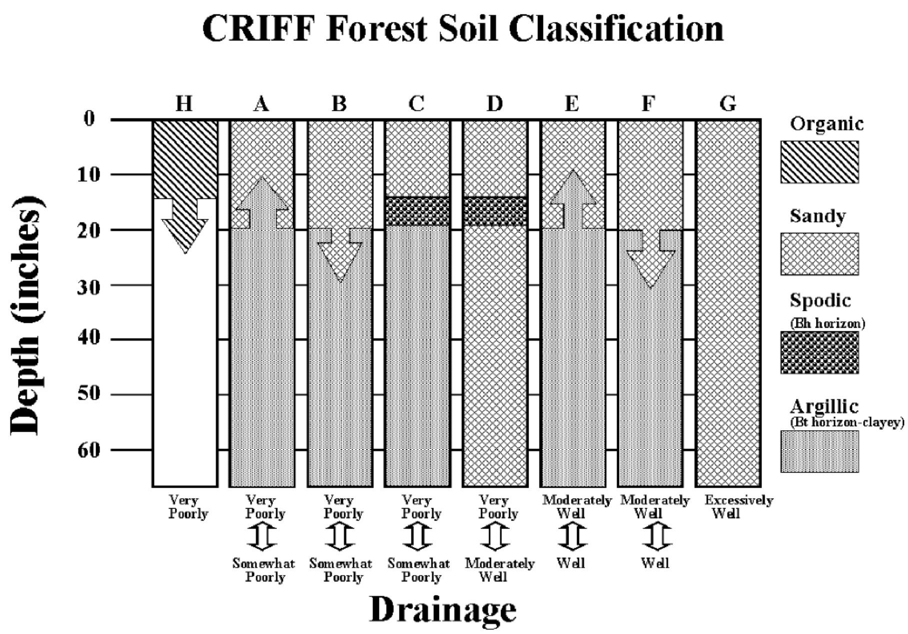

Figure 2.2: The CRIFF (Cooperative Research in Forest Fertilization) forest soil classification system. Source: (Jokela and Long 2012).

The operational management consisted of bedding (only in CP) in the spring followed by a fall herbicide treatment. The herbicide treatment consisted of 12 oz. Arsenal plus 1 qt. Garlon 4 per acre if the competition was waxy-leafed species or 12 oz. Arsenal plus 1 qt. Accord per acre if the competition consisted mainly of grass. Herbicide was applied in a 5-foot band over the rows. At planting, 500 lbs. of N-P-K 10-10-10 fertilizer was applied. In the spring of the eight, twelfth and sixteenth growing seasons, operational treatment plots were fertilized with the equivalent of 200 lbs. of N and 25 lbs. of P per acre.

The intensive management consisted of bedding (only in CP) in the spring followed by a fall herbicide application. The herbicide treatment was a broadcast application of 16 oz. Arsenal, 2 quarts Garlon 4 and 2 quarts Accord per acre. At planting, 500 lbs. of N-P-K 10-10-10 fertilizer was applied on all plots. Fertilizer treatments, including the addition of micronutrients, were repeated every three years. The intensive cultural treatment plots received additional herbicide treatments to keep them as completely free of competing vegetation as possible throughout their rotation. Beginning in the spring of the first growing season, the plots were sprayed with 4 oz. Oust (sulfometuron methyl) per acre along with directed sprays of Accord. Insecticides like Pounce were applied as often as necessary to maintain tip moth controlled through the first two growing seasons. In the spring of the third growing season, the plots received 600 lbs/ac of N-P-K 10-10-10 plus micronutrients and 117 lbs/ac of NH4NO3. An additional 117 lbs/ac of NH4NO3 was applied in the spring of the fourth growing season, 300 lbs/ac of NH4NO3 was added in the spring of the sixth growing season, and 200 lbs of elemental N and 25 lbs of elemental P were applied in the spring of the eighth, tenth, twelfth, fourteenth, sixteenth and eighteenth growing seasons.

At each installation, there was a random allocation of management intensity to each of the main plots. Within a management intensity, the density treatment subplots with 300, 600, 900, 1200, 1500 and 1800 TPA were randomly assigned. A third row thinning with low thinning on leave rows was implemented on four installations in each CP and SAGS to 600, 900, and 1200 TPA plots to the current stand density on their 300-TPA planting density - management counterparts.

Forest measurements were taken at years 2, 4, 6, 8, 10, 12, 15, and 18 for both CP and SAGS; and an additional measurement at age 21 for CP was taken. At each measurement, trees taller than 4.4 ft were measured for diameter at breast height (DBH), and after the fourth growing season, total heights (Ht) were measured or estimated with site-specific height-diameter allometric models. Stem quality assessments (sawtimber potential started at year 12), evaluations of forest health, and evaluations of damage were also taken at each measurement.

2.2 Model building

2.2.1 Response variable

The binary response variable STP takes the value of one if the tree has sawtimber potential (STP=1), or zero otherwise (STP=0) (Figure 2.3):

$$\text{STP} = \begin{cases} 1 & \text{Sawtimber potential: no defects, good sawtimber potential} \\ 0 & \text{Non-sawtimber potential: sawtimber reject for stem fork in first log,} \\ & \text{crook or sweep, fungus disease in first log, or ugly tree} \end{cases}$$

In total, 115138 observations from 38508 trees measured from year 12 to 21 on 429 plots within 36 installations were used to model the STP proportion (Table 2.1). Data from discontinued installations were also included in the database as long as they had at least one STP evaluation.

Figure 2.3: Sawtimber potential assessment. Tree with a good form and without defects, classified as sawtimber potential tree (left); and tree with fork in the first log, classified as a non-sawtimber tree (right).

Table 2.1: Location, soil information, site index, year of thinning, and last growing season measured for installations of the Coastal Plain (CP) Culture / Density study located in the Lower Coastal Plain, and South Atlantic Gulf Slope (SAGS) Culture / Density study located in the Upper Coastal Plain and Piedmont of the Southeastern United States.

Installation	State	County	CRIFF soil	NRCS soil series	SI	Thinned at year	Measured at year
Coastal Plain (CP)							
1	FL	Baker	C	Sapelo	97		21
2*	FL	Baker	D	Leon	86		4
3	FL	Columbia	C	Sapelo	78		15
4	FL	Columbia	B1	Leon	90		21
6	SC	Hampton	C	Pelham	93		21
7	SC	Georgetown	A	Cape Fear	79	12	21
8	SC	Williams	A	Cape Fear	89	12	21
9	FL	Nassau	B1	Yamassee	91		21
10*	GA	Charlton	C		86		12
11	FL	Nassau	D	Ocila	61		21
12	GA	Ware	B2		79	12	18
13	FL	Putnam	C	Albany/Leefield	93	12	21
14	SC	Dorchester	A	Pomona	95		21
15	GA	Lowndes	B2	Mouzon	86		21
16	GA	Clinch	B2	Albany	83		18
17	GA	Effingha	B1		78		21
18*	GA	Brantley	D		86		10
South Altantic Gulf Slope (SAGS)							
1	GA	Hancock	F	Bonifay/Cowarts	72		15
2	AL	Baldwin	G	Lakeland	74		18
3	AL	Escambia	F	Freemanville	79	12	18
4	AL	Escambia	E	Orangeburg	85		18
5	GA	Talbot	F	Lloyd	89		18
6	GA	Marion	G	Lakeland	69		18
7	FL	Santa Rosa	F	Troup	79	10	18
8	SC	Laurens	E	Cecil	77		12
9	AL	Monroe	E	Bama/Malbis	83		18
10	AL	Monroe	F	Lucy	85		12
11	GA	Greene	F	Cecil	82	12	18
12	AL	Barbour	E	Orangeburg-Springhill	86	12	18
13	GA	Jasper	E	Lloyd/Pacolet	84		18
15	AL	Shelby	F	Decatur/Tupelo	77		18
16	AL	St. Clair	E	Conasauga/Firestone	71		18
17	GA	Harolson	F	Grover	84		18
18	GA	Chatooga	F	Fullerton	75		18
19	MS	Perry	F	Susquehanna/Freest	92		18
20	AL	Escambia	E	Benndale	85		15
21	GA	Burke	E	Tifton	86		16
22	GA	Burke	E	Tifton	80		14
23	AL	Clarke	F	Okeelala/Brantley	81		12
24*	AL	Choctaw	E	Luverne	92		10

*Not available stem quality evaluation of sawtimber. SI: site index (ft @ 25 years).

2.2.2 Covariates

The covariates used in the model were:

- *Age*, stand-level continuous variable (years)

- *Management*, stand-level dichotomous variable, takes the value of one for installations with intensive silvicultural management, zero otherwise

- *Site index* (SI), stand-level continuous variable (ft @ 25 yrs), calculated using the following functions (Borders et al. 2014):

$$\mathrm{SI} = \exp(5.4185 + (\ln(Hd) - 5.4185)(Age/25)^{0.5235}), \text{ for CP} \quad (2.1)$$

$$\mathrm{SI} = \exp(5.6065 + (\ln(Hd) - 5.6065)(Age/25)^{0.4837}), \text{ for SAGS} \quad (2.2)$$

  where Hd is the average height (ft) of dominant and codominant trees[2] at the oldest available measurement Age (years)

- *Planting density*, stand-level continuous variable (TPA)

- *Thinning*, stand-level dichotomous variable, takes the value of one for stands that have been thinned, zero otherwise

- *DBH percentile at year six*, tree-level continuous variable in the range 0-1

- *Rust at year six*, tree-level ordinal variable, corresponding to the percentage of the stem circumference infected with the rust fungus *Cronartium quercuum* at year six:

  - Level 0: No infection
  - Level 1: Circumference infected between 1 and 25%
  - Level 2: Circumference infected between 26 and 50%

[2] A dominant or codominant tree is one that its crown extends above, or helps to form, the general level of the main canopy, and receives full light from above and partial or little light from the sides (Helms 1998).

  - Level 3: Circumference infected between 51 and 75%
  - Level 4: Circumference infected between 76 and 100%

- *Damage at year six*, tree-level factor, each level of the factor works as a dichotomous variable. Tree bole defects as a result of diseases, soil nutrient deficiencies, silvicultural malpractices, and catastrophic events and natural disasters such as hurricanes, tornadoes, ice storms, droughts, wildfires, and floods. The factor levels are described as follows:

  - *Yellow needles*, tree-level dichotomous variable, takes the value of one if the tree had yellow needles, zero otherwise
  - *Dead needles*, tree-level dichotomous variable, takes the value of one if the tree had dead needles, zero otherwise
  - *Tip dieback*, tree-level dichotomous variable, takes the value of one if the tree was progressive dying from the top, zero otherwise
  - *Leaning tree*, tree-level dichotomous variable, takes the value of one if the tree was inclined, zero otherwise
  - *Broken top*, tree-level dichotomous variable, takes the value of one if the tip of stem and significant part of crown were missing, zero otherwise

Therefore, there were 12 covariates to be used in the model building: *Age*, *Management*, *Site index*, *Planting density*, *Thinning*, *DBH percentile at year six*, *Rust at year six*, and *Damage at year six* (five levels). Information of the study sites regarding the physiographic region, CRIFF soil classification, USDA Natural Resources Conservation Service (NRCS) soil series, site index, thinning age if practiced, and the last growing season measured was also included in Table 2.1.

2.2.3 Model

Consider the full GLM:

$$E(\mathbf{y}|\mathbf{X}) = \frac{\exp(\mathbf{X}\boldsymbol{\beta})}{1+\exp(\mathbf{X}\boldsymbol{\beta})} \quad (2.3)$$

$$\text{logit}(\boldsymbol{\theta}) = \mathbf{X}\boldsymbol{\beta} \quad (2.4)$$

where $\boldsymbol{\theta}$ is the vector of dimension n of the STP at tree level, $\mathbf{y}$ is the vector of dimension n of observed binary responses, $\boldsymbol{\beta}$ is the vector of parameters of dimension 13, 12 covariates and an intercept, and $\mathbf{X}$ is the matrix of covariates of dimension $n \times 13$, associated with the fixed effects, composed of a vector of ones in the first column and covariates in the remaining columns.

Consider now the full GLMM:

$$E(\mathbf{y}|\mathbf{X}, \mathbf{Z}, \mathbf{b}) = \frac{\exp(\mathbf{X}\boldsymbol{\beta}+\mathbf{Z}\mathbf{b})}{1+\exp(\mathbf{X}\boldsymbol{\beta}+\mathbf{Z}\mathbf{b})} \quad (2.5)$$

$$\text{logit}(\boldsymbol{\theta}) = \mathbf{X}\boldsymbol{\beta}+\mathbf{Z}\mathbf{b} \quad (2.6)$$

$$\mathbf{b} \sim \mathcal{N}(\mathbf{0}_3, \boldsymbol{\Sigma}_b)$$

where $\mathbf{Z}$ is the matrix of covariates associated with the random effects, partitioned as $\mathbf{Z} = [\mathbf{Z_1}, \mathbf{Z_2}, \mathbf{Z_3}]$ where $\mathbf{Z_1}$ is the $n \times 3$ matrix of physiographic region (i.e., Lower Coastal Plain, Upper Coastal Plain, and Piedmont), $\mathbf{Z_2}$ is the $n \times 10$ matrix of the CRIFF soil groups within physiographic region (i.e., CRIFF soil A within Lower Coastal Plain, CRIFF soil B1 within Lower Coastal Plain,..., CRIFF soil F within Piedmont), and $\mathbf{Z_3}$ is the $n \times 429$ matrix of the plots within CRIFF soil group (e.i., CP installation 1 within CRIFF soil C, CP installation 3 within CRIFF soil C, ..., SAGS installation 23 within CRIFF soil F); $\mathbf{b}$ is the vector of random effects, partitioned as $\mathbf{b}^\top = (\mathbf{b_1}^\top, \mathbf{b_2}^\top, \mathbf{b_3}^\top)$, vectors with dimensions 3, 10, and 429, respectively; $\mathbf{0}_3$ is the vector of the means of the random effects of dimension 3, assumed equal to zero; and $\boldsymbol{\Sigma}_b$ is the 3×3 variance-covariance matrix of the random effects with diagonal composed of the individual variances of the random effects $\sigma^2_{b_1}$, $\sigma^2_{b_2}$, and $\sigma^2_{b_3}$.

We estimated and evaluated nested models using the likelihood ratio test (LRT). For a large number of observations, $-2\ln(LRT)$ has approximately a χ^2 distribution with degrees of freedom equal to the difference of degrees of freedom of the models, the full and reduced model, and rejection region defined as RR:$\{-2\ln(LRT) > -2\ln(c) = c^*\}$ (Rencher and Schaalje 2008; Wackerly et al. 2008; Kutner et al. 2005). For $\chi^2_{(1)}$, $c^* = 3.8415$. We evaluated two approaches when a factor level within *Damage at year six* was not statistically significant, but the remaining factor levels were statistically significant: i) collapsing the factor level into the intercept, and ii) collapsing the factor level into the most biological similar factor level. We used the R function *glmer* in the package *lme4* to estimate GLMMs (R Development Core Team 2018).

2.2.4 Model diagnostics

Consider the residuals of the binary response model:

$$\mathbf{e} = \mathbf{y} - \hat{\boldsymbol{\theta}} \tag{2.7}$$

where $\mathbf{e}$ is the vector of residuals, $\mathbf{y}$ is the vector of the observed binary responses (zeros and ones), and $\hat{\boldsymbol{\theta}}$ is the vector of fitted values of probabilities. Residual analysis for logistic regression is more complicated than for linear regression models because the responses y_i take only the values of zero and one. Hence, residuals will not be normally distributed, and, indeed, their distribution under the assumption that the fitted model is correct is unknown (Kutner et al. 2005). Using Equation (2.7), Pearson's residuals can be calculated as:

$$\mathbf{e_p} = \mathbf{SE} \times \mathbf{e} \tag{2.8}$$

where $\mathbf{SE} = Diag\left(\frac{1}{\sqrt{\hat{\theta}_1(1-\hat{\theta}_1)}}, \frac{1}{\sqrt{\hat{\theta}_2(1-\hat{\theta}_2)}}, ..., \frac{1}{\sqrt{\hat{\theta}_n(1-\hat{\theta}_n)}}\right)$ is the diagonal matrix of the standard errors of $\mathbf{y}$ (Kutner et al. 2005). If logistic regression model is correct, $\mathsf{E}(\mathbf{y}|\mathbf{X}, \mathbf{Z}, \mathbf{b}) = \boldsymbol{\theta}$, and it follows asymptotically that $\mathsf{E}(\mathbf{e}) = \mathsf{E}(\mathbf{e_p}) = \mathbf{0}$. This suggests that a lowess smooth of the plot of the Pearson's residuals ($\mathbf{e_p}$), against the estimated probability $\hat{\boldsymbol{\theta}}$, should result approximately in a horizontal line with zero intercept. Likewise, a mean of the observed and estimated STP were used to calculate stand-level residuals. A plot of the aggregated SPT at stand level was used to assess for the model performance.

Chapter 3

Results

3.1 Exploratory analysis

The STP proportion at year 12 ranged from 3 to 52%, with mean and standard deviation (SD) equal to 32 and 15%. At year 18, the STP ranged from 33 to 75%, with mean and SD at 56 and 12%. At year 21, when only 11 installations remained in CP out of 17, STP ranged from 44 to 77%, with mean and SD at 65 and 9% (Table 3.1). Conversely, 62, 36, and 26% of the trees were marked to be rejected for crook and sweep at years 12, 18, and 21, respectively. Trees with forking in the first log represent approximately 5% during all measurements (Table 3.1).

Most of the trees were healthy, 90 and 85% of the trees remained free of rust infection at years 18 and 21, respectively (Table 3.1). The incidence of rust infection in the range 1-25% was about 2% at all ages, and the infection in the range 26-50% slightly increased over time up to 7% at year 21. The percentage of trees with incidence of rust infection in the range 51-75% was relatively constant over time at about 2%; whereas only 1% of trees presented the most severe level of rust infection in the range 76-100% (Table 3.1).

There was a reduction in the proportion of non-damaged trees from 88% at year 12 to 74% at year 21; whereas the percentage of forking double folded during the analysis period, from 8% at year 12 to 16% at year 21 (Table 3.1). Percentage for broken top and leaning trees were relatively constant around 4% (Table 3.1). No trees exhibited damage in the remaining categories of tip and stem damage during the analysis period (i.e., yellow needles, dead needles, and tip dieback, which were relatively important at a juvenile stage of growth).

Table 3.1: Summary statistics of sawtimber potential (STP), rust infection incidence, tip and stem damage, management, thinning, diameter at breast height (DBH), total height, and site index over age in the Southeaster U.S.

VARIABLE	AGE							
	12	13	14	15	16	17	18	21
CATEGORICAL								
Sawtimber potential (%)								
No defects (STP=1)	32	21	46	39	51	54	56	65
Crook or sweep	62	72	40	48	38	37	36	26
Fork in the first log	5	6	5	5	5	5	4	5
Rust in the first log	1	1	1	2	2	3	3	4
Ugly tree	0	0	8	6	4	1	1	0
Rust infection incidence (%)								
No infection	95	94	93	91	93	91	90	85
Infection at 1-25%	1	2	2	2	2	2	2	3
Infection at 26-50%	3	3	4	5	4	6	5	7
Infection at 51-75%	1	1	1	2	1	1	2	4
Infection at 76-100%	0	0	0	0	0	0	1	1
Tip and stem damage (%)								
No damage	88	82	78	79	75	75	78	74
Forked stem	8	12	17	14	17	19	16	16
Leaning tree	3	4	1	4	4	2	3	6
Broken top	1	1	4	3	4	4	3	4
Management (%)								
Operational	52	52	52	54	55	55	56	59
Intensive	48	48	48	46	45	45	44	41
Thinning (%)								
Non-thinned	99	92	92	95	95	88	94	93
Thinned	1	8	8	5	5	12	6	7
CONTINUOUS								
Number of installations	22	7	7	31	12	8	28	11
Number of plots	264	84	84	371	142	92	329	128
Number of trees	25635	7038	6668	29546	10921	5841	22367	7122
DBH (in)	6.05 (1.80)	6.39 (1.82)	6.67 (1.89)	6.83 (2.08)	7.12 (2.14)	7.61 (2.24)	7.69 (2.27)	8.59 (2.51)
Height (ft)	46.50 (6.69)	50.46 (5.99)	53.39 (5.77)	57.25 (8.32)	60.64 (8.34)	64.46 (8.52)	66.37 (9.56)	76.48 (10.47)
Site index (ft @ 25 yr)	80.15 (6.97)	80.18 (5.72)	80.14 (5.79)	81.53 (8.02)	81.83 (7.86)	82.73 (7.93)	81.85 (8.33)	85.14 (8.36)

Values in parentheses represent the standard deviation. Damage associated with yellow or dead needles, and tip dieback was absent or negligible between years 12 to 21.

More than half of the trees were under operational management at the beginning of the analysis period, a percentage that increased up to 59% at year 21. The percentage of trees under the thinning regime started at 1% at year 12 and ended up at 7% at year 21 (Table 3.1)

Regarding the continuous variables, diameter and height increased over time (Table 3.1). The DBH at age 12 ranged from 0.2 to 14 in with mean and SD at 6.05 and 1.80 in; the DBH at year 21 ranged from 1.8 to 18.7 in with mean and SD at 8.59 and 2.51 in. Similarly, total height at year 12 ranged from 5 to 68 ft with mean and SD at 46.5 and 6.69 ft; the height at year 21 ranged from 34 to 100 ft with mean 76.48 and 10.47 ft. Site index was around 80 ft @ 25 yr up to year 18; whereas at year 21 was 85 ft @ 25 yr mainly because all available data at this age corresponds to CP. Summary information for CP and SAGS is presented in Tables 3.2 and 3.3.

Table 3.2: Summary statistics of sawtimber potential (STP), rust infection incidence, tip and stem damage, management, thinning, diameter at breast height (DBH), total height, and site index over age in Coastal Plain Culture / Density study.

VARIABLE	AGE				
	15	16	17	18	21
		CATEGORICAL			
Sawtimber potential (%)					
No defects (STP=1)	34	45	59	47	65
Crook or sweep	58	35	32	44	26
Fork in the first log	6	7	7	7	5
Rust in the first log	2	1	2	2	4
Ugly tree	0	12	0	0	0
Rust infection incidence (%)					
No infection	87	92	93	86	85
Infection at 1-25%	3	3	2	3	3
Infection at 26-50%	6	4	4	6	7
Infection at 51-75%	3	1	1	4	4
Infection at 76-100%	1	0	0	1	1
Tip and stem damage (%)					
No damage	79	74	74	76	74
Forked stem	13	18	18	17	16
Leaning tree	5	4	3	3	6
Broken top	3	4	5	4	4
Management (%)					
Operational	56	57	55	58	59
Intensive	44	43	45	42	41
Thinning (%)					
Non-thinned	94	100	94	93	93
Thinned	6	0	6	7	7
		CONTINUOUS			
Number of installations	13	4	4	13	11
Number of plots	155	46	44	153	128
Number of trees	11774	3641	2810	10219	7122
DBH (in)	6.80 (2.17)	6.93 (2.14)	7.50 (2.30)	7.62 (2.35)	8.58 (8.59)
Height (ft)	60.29 (8.41)	61.13 (10.43)	65.64 (10.71)	68.91 (9.70)	76.48 (10.74)
Site index (ft @ 25 yr)	84.19 (7.96)	82.36 (9.87)	83.55 (10.11)	84.16 (8.15)	85.14 (8.36)

Values in parentheses represent the standard deviation. Damage associated with yellow or dead needles, and tip dieback was absent or negligible between years 12 to 21.

Table 3.3: Summary statistics of sawtimber potential (STP), rust infection incidence, tip and stem damage, management, thinning, diameter at breast height (DBH), total height, and site index over age in the South Atlantic Gulf Slope Culture / Density study.

VARIABLE	AGE						
	12	13	14	15	16	17	18
			CATEGORICAL				
Sawtimber potential (%)							
No defects (STP=1)	32	21	46	42	54	50	64
Crook or sweep	62	72	40	42	39	42	29
Fork in the first log	5	6	5	4	3	3	3
Rust in the first log	1	1	1	2	3	5	3
Ugly tree	0	0	8	10	1	0	1
Rust infection incidence (%)							
No infection	95	94	93	94	93	89	93
Infection at 1-25%	1	2	2	2	2	2	2
Infection at 26-50%	3	3	4	3	4	7	5
Infection at 51-75%	1	1	1	1	1	2	0
Infection at 76-100%	0	0	0	0	0	0	0
Tip and stem damage (%)							
No damage	88	82	78	79	75	77	80
Forked stem	8	13	17	15	17	19	15
Leaning tree	3	3	2	3	4	1	3
Broken top	1	2	3	3	4	3	2
Management (%)							
Operational	52	52	52	53	54	54	54
Intensive	48	48	48	47	46	46	46
Thinning (%)							
Non-thinned	99	92	92	96	92	82	94
Thinned	1	8	8	4	8	18	6
			CONTINUOUS				
Number of installations	22	7	7	18	8	4	15
Number of plots	264	84	84	216	96	48	176
Number of trees	25635	7038	6668	17772	7280	3031	12148
DBH (in)	6.05 (1.80)	6.39 (1.82)	6.67 (1.89)	6.85 (2.02)	7.21 (2.14)	7.70 (2.17)	7.74 (2.20)
Height (ft)	46.50 (6.69)	50.46 (5.99)	53.39 (5.77)	55.22 (7.61)	60.40 (7.08)	63.42 (5.77)	64.25 (8.91)
Site index (ft @ 25 yr)	80.15 (6.97)	80.18 (5.72)	80.14 (5.79)	79.76 (7.56)	81.56 (6.61)	81.96 (5.03)	80.00 (7.98)

Values in parentheses represent the standard deviation. Damage associated with yellow or dead needles, and tip dieback was absent or negligible between years 12 to 21.

3.2 Variable selection and model building

Three models are presented in this section, the full GLM (Equation 2.4), the full GLMM (Equation 2.6), and the best GLMM achieved. The first model estimated, the full GLM, had 12 of its parameter estimates highly significant (p-value < 0.0001), and one parameter estimate statistically significant (p-value < 0.05) (Table 3.4). The parameter estimate of

Damage at year six: Yellow needles is more negative than the parameter estimate of *Damage at year six: Dead needles*, which seems contraintuitive. However, there is more uncertainty associated with the effect of *Damage at year six: Yellow needles* than with the effect of *Damage at year six: Dead needles.* Thus, *Damage at year six: Yellow needles* may have a very similar effect that *Damage at year six: Dead needles.*

Table 3.4: Parameter estimates for the full GLM.

	Estimate	Std. Error	z value	Pr(>|z|)
Intercept	-1.9733	0.0821	-24.02	<0.0001
Age	0.1811	2.54×10^{-3}	71.16	<0.0001
Management (intensive)	-0.3252	0.0130	-25.10	<0.0001
Site index	-0.0122	8.97×10^{-4}	-13.58	<0.0001
Planting density	-2.39×10^{-4}	1.28×10^{-5}	-18.66	<0.0001
Thinning	0.1194	9.28×10^{-3}	12.86	<0.0001
DBH percentile at year six	0.6338	0.0236	26.85	<0.0001
Rust at year six	-0.5224	0.0219	-23.90	<0.0001
Damage at year six:				
Dead needles	-0.6700	0.1370	-4.89	<0.0001
Yellow needles	-0.9758	0.4361	-2.24	0.0252
Tip dieback	-1.0463	0.1119	-9.35	<0.0001
Leaning tree	-1.4239	0.1953	-7.29	<0.0001
Broken top	-1.7941	0.2214	-8.10	<0.0001

The estimated full GLMM had 10 highly statistically significant fixed effects (p-value < 0.0001), one statistically significant fixed effect (p-value < 0.05), and two non-significant fixed effects (p-value > 0.05), *Thinning* and *Damage at year six: Yellow needles* (Table 3.5). The parameter estimate of *Thinning* was reduced by four times, and its associated standard error double folded with the inclusion of random effects. The absolute value of the parameter estimate of *Damage at year six: Yellow needles* was slightly reduced and its standard error was slightly increased with the inclusion of the random effects. The parameter estimate, in absolute value, and standard error of *Damage at year six: Yellow needles* were larger than the corresponding for *Damage at year six: Dead needles*, suggesting a higher impact.

The change in the statistical significance of the fixed effects, especially for *Thinning*, suggests that the random effects were essential to explaining the hierarchical structure of the

Table 3.5: Parameter estimates for the full GLMM.

Fixed effects				
	Estimate	Std. Error	z value	Pr(>|z|)
Intercept	-4.8410	0.4702	-10.2940	<0.0001
Age	0.2138	3.20×10^{-3}	66.8960	<0.0001
Management (intensive)	-0.5084	0.05917	-8.5930	<0.0001
Site index	0.0152	5.21×10^{-3}	2.9160	0.0035
Planting density	-1.49×10^{-4}	5.76×10^{-5}	-2.5900	0.0096
Thinning	0.0322	0.0189	1.7020	0.0888
DBH percentile at year six	0.6971	0.0245	28.4320	<0.0001
Rust at year six	-0.4788	0.0228	-21.0080	<0.0001
Damage at year six:				
Dead needles	-0.4593	0.1510	-3.0420	0.0023
Yellow needles	-0.8006	0.4663	-1.7170	0.0860
Tip dieback	-0.7464	0.1223	-6.1010	<0.0001
Leaning tree	-1.3540	0.2012	-6.7330	<0.0001
Broken top	-1.9840	0.2309	-8.5940	<0.0001
Random effects				
	$\hat{\sigma}^2_{b_1} = 0.0621$	$\hat{\sigma}^2_{b_2} = 0.0950$	$\hat{\sigma}^2_{b_3} = 0.2908$	

DBH is the diameter at breast height. Random effects: $\hat{\sigma}^2_{b_1}$, $\hat{\sigma}^2_{b_2}$, and $\hat{\sigma}^2_{b_1}$ represent the variance of the random effects of physiographic region, CRIFF soil within physiographic region, and installation withing CRIFF soil, respectively.

data and the autocorrelation associated with the repeated measures (Figure 3.1). Although keeping *Thinning* in the model was considered given its importance for a potential silvicultural explanation, it was dropped because of its large standard error. The thinning effect was dropped without a significant loss in the statistical explanation in the model (p-value > 0.05) (Model 3, Table 3.6).

Collapsing *Damage at year six: Yellow needles* into its closest biological factor level, *Damage at year six: Dead needles*, resulted in a better fit than collapsing *Damage at year six: Yellow needles* into the intercept (Model 5, Table 3.6). Using the best model achieved in the fixed effects selection (Model 5, Table 3.6), the random effects were also selected following the two approaches of elimination, from top to bottom hierarchal selection and from bottom to top hierarchal selection. Neither of these two elimination paths was suitable because

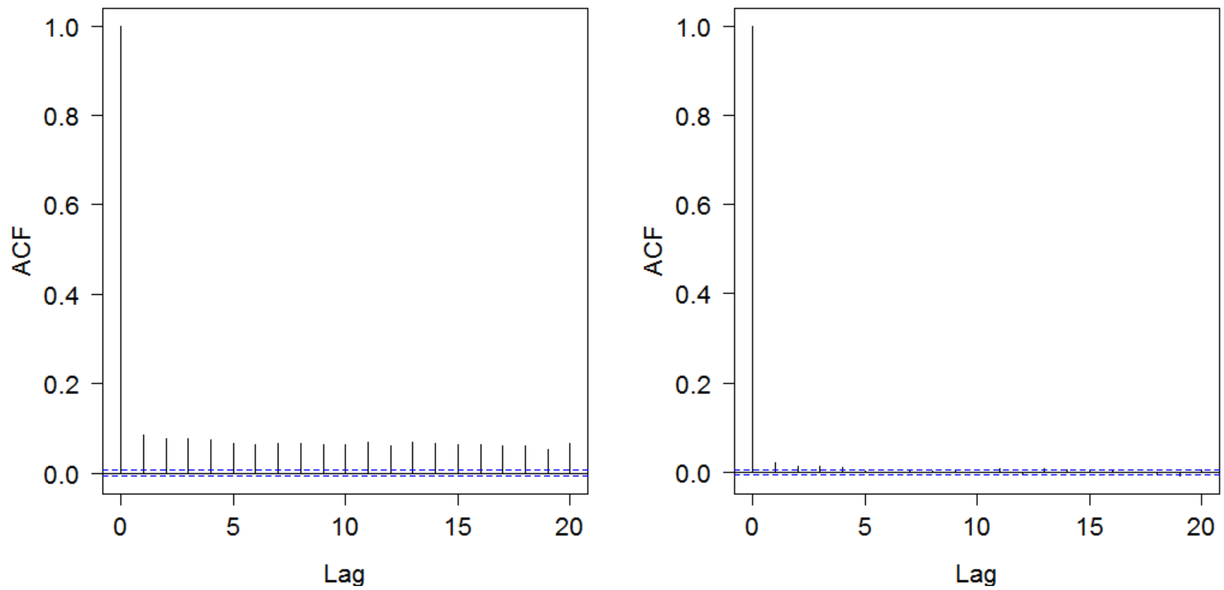

Figure 3.1: Autocorrelation function (ACF) of residuals of the full GLM (left) and the full GLMM (right).

Table 3.6: Model building using the likelihood ratio test considering fixed and random effects selection.

Model	Df	AIC	logLik	Best	χ^2	χ^2 df	Pr($> \chi^2$)
1 Full GLM	13	148137.95	-74055.98				
2 Full GLMM	16	142300.27	-71134.13	1	5843.69	3	<0.0001
3 *Thinning* dropped	15	142301.16	-71135.58	2	2.89	1	0.0892
4 *Yellow needles* **ci** intercept	14	142302.56	-71137.28	2	3.40	1	0.0650
5 *Yellow needles* **ci** *Dead needles*	14	142299.69	-71135.85	2	0.54	1	0.4634
6 without $\mathbf{b_1}$	13	142328.78	-71151.39	5	31.08	1	<0.0001
7 without $\mathbf{b_2}$	13	142323.24	-71148.62	5	25.55	1	<0.0001
8 without $\mathbf{b_3}$	13	146763.24	-73368.62	5	4465.54	1	<0.0001
9 without both $\mathbf{b_1}$ and $\mathbf{b_2}$	12	142384.64	-71180.32	5	88.95	2	<0.0001
10 without both $\mathbf{b_1}$ and $\mathbf{b_3}$	12	146762.69	-73369.34	5	4466.99	2	<0.0001
11 without both $\mathbf{b_2}$ and $\mathbf{b_3}$	12	147480.97	-73728.48	5	5185.27	2	<0.0001
12 GLM	11	148301.30	-74139.65	5	6007.61	3	<0.0001

Yellow needles and *Dead needles* are levels within the factor *Damage at year six*; df: degrees of freedom; **ci**: collapsed into. $\mathbf{b_1}$ is the random effect associated with physiographic region, $\mathbf{b_2}$ is the random effect of CRIFF soil within physiographic region, and $\mathbf{b_3}$ is the random effect of installation within CRIFF soil.

Table 3.7: Parameter estimates for the best model achieved in the model building and variable selection process.

Fixed effects				
	Estimate	Std. Error	z value	Pr(>|z|)
Intercept	-4.8290	0.4981	-9.6936	<0.0001
Age	0.2146	3.17×10^{-3}	67.6928	<0.0001
Management (intensive)	-0.5078	0.0600	-8.4611	<0.0001
Site index	0.0151	5.48×10^{-3}	2.7499	0.0060
Planting density	-1.56×10^{-4}	5.86×10^{-5}	-2.6594	0.0078
DBH percentile at year six	0.6990	0.0245	28.5334	<0.0001
Rust at year six	-0.4791	0.0228	-21.0176	<0.0001
Damage at year six				
Yellow and Dead needles	-0.4919	0.1434	-3.4306	<0.0001
Tip dieback	-0.7457	0.1222	-6.1026	<0.0001
Leaning tree	-1.3541	0.2003	-6.7602	<0.0001
Broken top	-1.9866	0.2308	-8.6075	<0.0001
Random effects				
	$\sigma^2_{b_1} = 0.0638$	$\sigma^2_{b_2} = 0.0913$	$\sigma^2_{b_3} = 0.2970$	

DBH is the diameter at breast height. Random effects: $\hat{\sigma}^2_{b_1}$, $\hat{\sigma}^2_{b_2}$, and $\hat{\sigma}^2_{b_1}$ represent the variance of the random effects of physiographic region, CRIFF soil within physiographic region, and installation withing CRIFF soil, respectively.

the reduction in the statistical explanation of the phenomenon was statistically significant (p-value<0.0001) compared to the best model achieved in the fixed effects selection step (Model 5, Table 3.6). The final comparison between Model 10 (GLM without *Thinning* and with *Damage at year six: Yellow needles* collapsed into *Damage at year six: Dead needles*) and Model 5 was significant (p-value < 0.001, Table 3.6). Therefore, random effects were necessary for the model. The best model achieved through the fixed and random effects selection process (Model 5 in Table 3.6) has nine highly statistically significant fixed effects (p-value < 0.0001), and two statistically significant fixed effects (p-value < 0.05) (Table 3.7).

3.3 Model diagnostics for the best model

The smooth line of the Pearson's residuals exhibits an approximately horizontal trend (no evident slope) with an intercept slightly higher than zero, at approximately 0.5 (Figure 3.2). The residuals of the stand-level STP do not show any trend (Figure 3.3). The autocorrelation function (ACF) of the residuals from Model 5 (Table 3.7) looks identical to the ACF of the full GLMM (Figure 3.1).

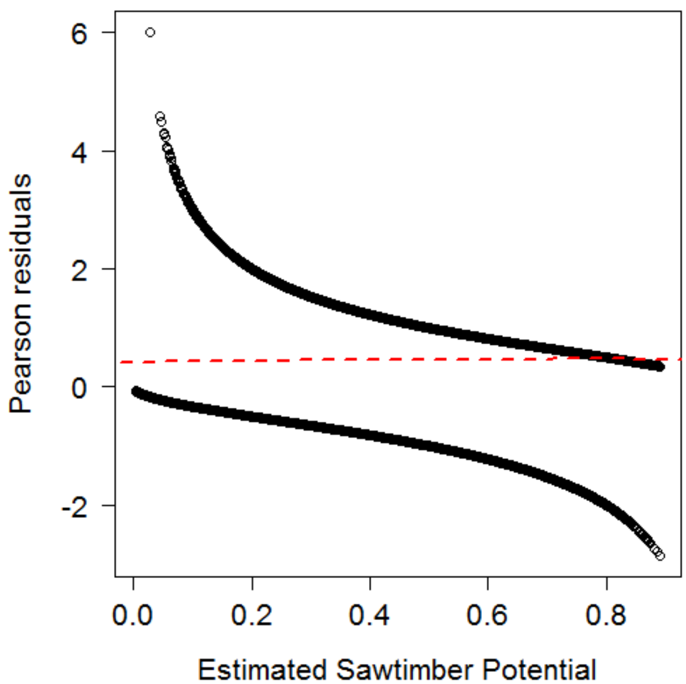

Figure 3.2: Pearson's residuals of the best-estimated model, Model 5. The dashed line represents the lowess smooth.

3.4 Logistic mean response curves

STP increases as *Age*, *Site index*, and the *DBH percentile at year six* increase; whereas there is a reduction in the STP due to *Management* (intensive), incidence of *Rust at year six*, and severity of *Damage at year six* (Table 3.7). The mean response of STP for operational *Management* over stand *Age* presented higher STP than intensive *Management*; an increase

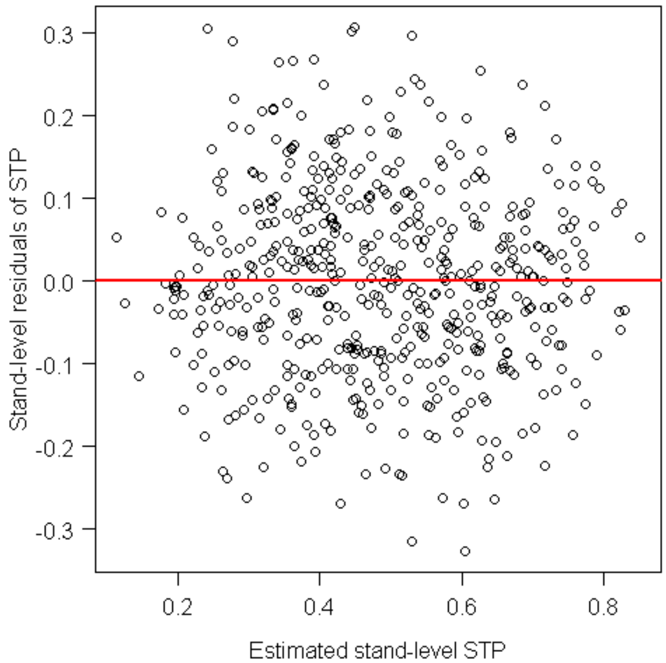

Figure 3.3: Stand-level residuals of STP of the best-estimated model, Model 5.

of *Site index* from 60 to 100 ft @ 25 yr makes the STP mean response curve shift upwards; the higher the *Planting density*, the lower the STP; and STP mean response curves shift upwards as the *DBH percentile at age six* increases. However, there were no statistical differences over *Age* among aforementioned categories within *Management*, *Site index*, *Planting density*, and *DBH percentile at year six* since their 95% confidence intervals (CI) overlap. Conversely, There were statistical differences over *Age* between (among) some of the aforementioned categories of the incidence of *Rust at year six*, and severity of *Damage at year six*.

The mean response of STP decreases as the incidence of *Rust at year six* increases (Figure 3.5). A tree under operational *Management* over the incidence of *Rust at year six* presented higher STP than an intensively managed tree. The STP over *Rust at year six* shifts upwards as the *Site index* increases or the *DBH percentile at year six* increases. There were no

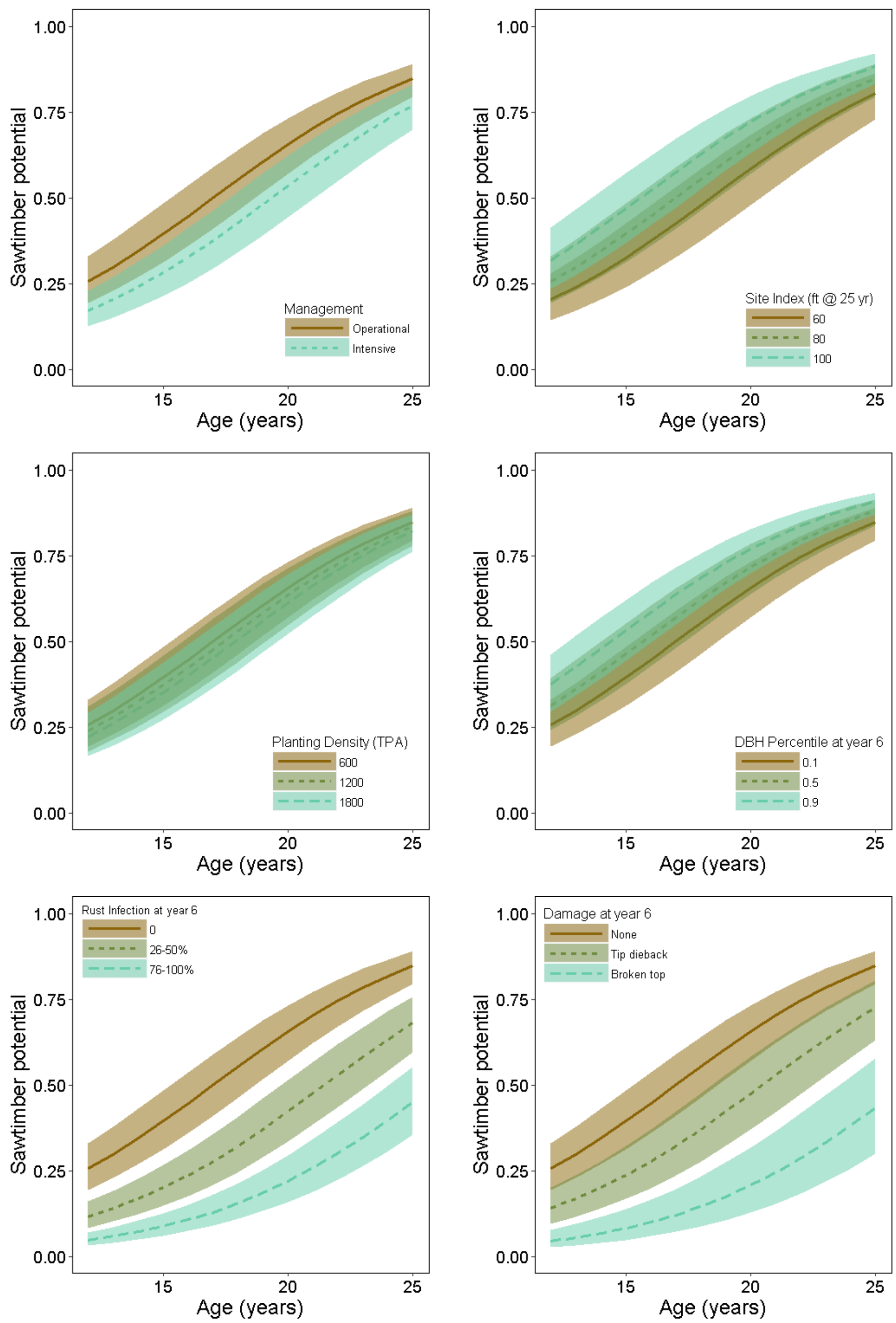

Figure 3.4: Sawtimber potential (STP) for an individual tree over age by *Management*, *Site index*, *Planting density*, *DBH percentile at year six*, incidence of *Rust at year six*, and *Damage at year six*. The solid line, and its 95% CI, represents a tree in a stand managed operationally, of *Site index* at 80 ft @ 25 yr, planted with 600 TPA, of *DBH percentile at year six* at the median, not infected with *Rust at year six*, and without any *Damage at age six*. Levels of *Rust at year six* at 1-25% and 51-75%, and *Damage at year six* caused by *Yellow and dead needles*, and *Leaning trees* were not shown to facilitate the graph visualization and interpretation.

statistical differences over *Rust at year six* among mentioned categories within the covariates *Management*, *Site index*, and *DBH percentile at year six* since the 95% CI overlap (Figure 3.5).

There was a dramatic reduction of the STP over *Rust at year six* as the *Damage at year six* increases in severity from *No damage* to *Tip dieback*, and from *Tip dieback* to *Broken top* (Figure 3.5). The 95% CI of *No damage* and *Tip dieback* barely overlap, suggesting that more samples are required to draw firm conclusions regarding these two factor levels. However, there were statistical differences between *No damage* and *Broken top*, and between *Tip dieback* and *Broken top* since their 95% CI do not overlap (Figure 3.5). Consider the following example of the combination of the incidence of *Rust at year six* and severity of *Damage at year six*. A 25-year old perfectly healthy tree under operational *Management*, in a stand with initial *Planting density* of 600 TPA, on a *Site index* 80 ft @ 25 yr, without *Rust infection* or *Damage at year six* had a STP at 88%. If the tree were prone to be completely infected with rust at year six but without any damage, the estimated STP dropped to 52%. However, if the tree were also prone to suffer from *Broken top*, the resulting STP dramatically dropped to 13%. The effect of *Site index*, *Planting density*, and *DBH percentile at year six* on STP were not as strong as presented effects of *Age*, *Rust at year six*, and *Damage at year six* a reason why they were not depicted.

Predicted values of the first random effect suggest that the STP in Lower Coastal Plain and Piedmont were reduced by 0.15 and 0.13 logits (0.86 and 0.88 odds), respectively, in comparison with the mean response; whereas the STP in the Upper Coastal Plain was increased by 0.29 logits (1.33 odds) in comparison with the mean response (Figure 3.6, Appendix). Predicted values of the second random effect suggest the largest reduction in the STP compared to the mean response curve occurred on CRIFF soil classes C, E, and E, within Lower Coastal Plain, Upper Coastal Plain, and Piedmont respectively; whereas the largest increment occurred on CRIFF soil classes D, G, and F within Lower Coastal Plain, Upper Coastal Plain, and Piedmont respectively (Appendix).

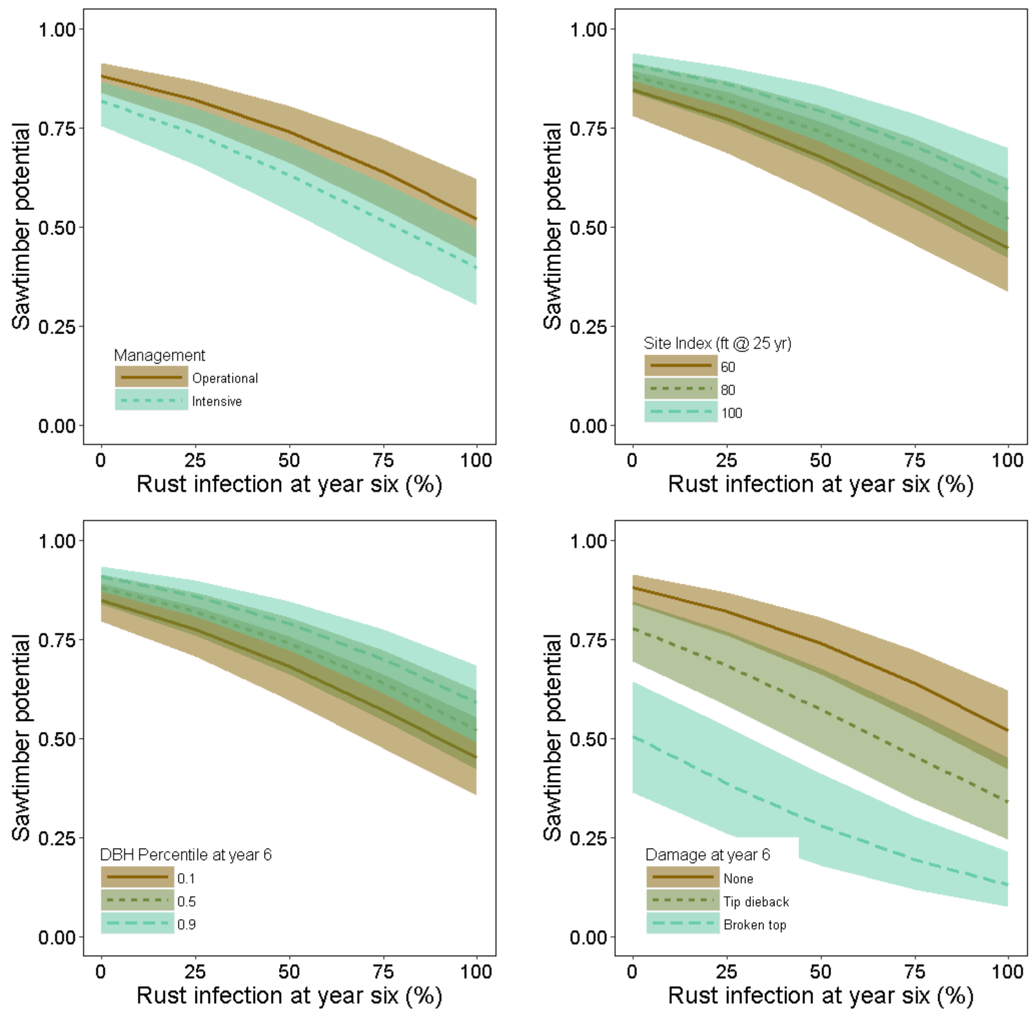

Figure 3.5: Sawtimber potential (STP) for an individual tree over the incidence of *Rust at year six* by *Management*, *Site index*, *DBH percentile at year six*, and *Damage at year six*. The solid line, and its 95% CI, represents a 25-year old tree in a stand managed operationally, of *Site index* 80 ft @ 25 yr, planted with 600 TPA, of *DBH percentile at age six* at the median, not infected with *Rust at year six*, and without any *Damage at age six*. *Damage at year six* caused by *Yellow and dead needles*, and *Leaning trees* were not shown to facilitate the graph visualization and interpretation.

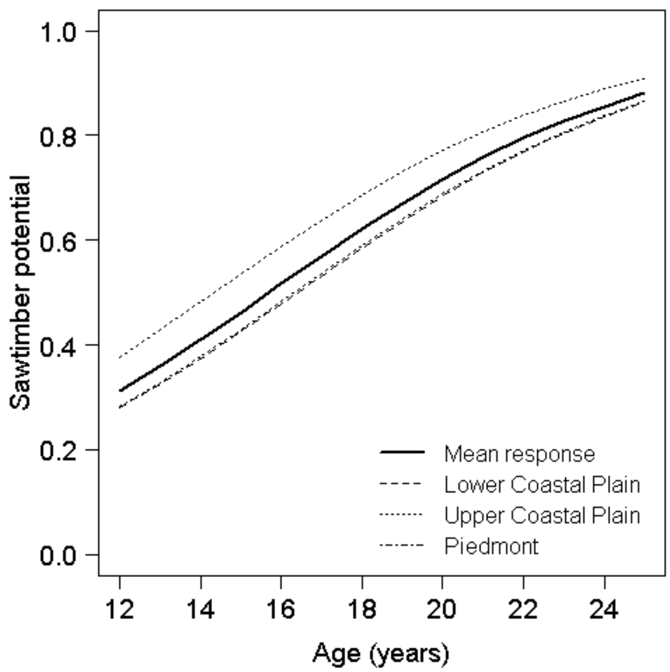

Figure 3.6: The effect physiographic region (random) on the sawtimber potential of loblolly pine in the Southeastern U.S. The mean response curve represents a tree in a stand managed operationally, of *Site index* at 80 ft @ 25 yr, planted with 600 TPA, of *DBH percentile at year six* at the median, not infected with *Rust at year six*, and without any *Damage at age six*. The curves of Lower Coastal Plain and Piedmont overlap.

Chapter 4

Discussion and conclusions

Although studies with the same definition of STP for loblolly pine were not found, the STP proportion criterion is similar to the proportion of solid wood and similar merchantability criteria reported in the literature. We found that 56 and 65% of the trees had STP at years 18 and 21, respectively. Likewise, 85-90% of the trees were not infected with rust, and 74-78% of the trees were free of damage between years 18 and 21. These percentages of healthy STP trees are similar to the proportions reported in the literature. On average, 94% of loblolly pine stem volume is merchantable, which includes sawtimber, chip-n-saw, and pulpwood (Sherrill et al. 2011). The percentage of solid wood at year 16 in six installations of SAGS was in the range 79-90% (Green et al. 2018). The percentage of high-grade lumber volume production at year 27 in plantations was in the range 73-84% (Amateis and Burkhart 2013); whereas the percentage of high-grade lumber volume in uneven-aged loblolly-shortleaf pine mixed stands was estimated at 40% (Prestemon and Buongiorno 2000). The percentage of trees classified in high-value timber product classes, sawtimber and peeler, was estimated in the range 61-65%, and 7-11%, respectively (Burkhart and Bredenkamp 1989). The percentage of trees with STP in mature stands (about 30 years) ranged 50-90% (Strub et al. 1986). Half of the trees in mature loblolly pine stands across 12 states in the Southeastern U.S. were non-diseased or insect-damaged, single-straight stem, normal top trees (Choi et al. 2008).

We found the incidence of *Rust at year six* in the range 6-13%, value relatively small compared to 23-56% found by Cumbie et al. (2012) at the same age. At older ages, between years 12 and 21, the percentage of trees with rust infection was in the range 5-15%, similar to 12% reported by Choi et al. (2008), but lower compared to the rust incidence rate in the range 25-29% at year 14 found by Gräns et al. (2017).

The percentage of trees with any *Damage at year six* was about 2%, whereas the percentage only for fork at year six was reported in the range 7-32% by Cumbie et al. (2012). We found that 8-19% of the trees in the analysis period from 12 to 21 years had a forked stem, similar to 19-34% at year 14 found by Gräns et al. (2017), but relatively high compared to 4% reported by Choi et al. (2008). The rate of recovery from forked stem to single stem was reported at 37% (Choi et al. 2008), evaluation that we did not include in our analysis. We found that less than 4% of the trees between years 12 and 21 presented broken tops, a similar value was reported by Choi et al. (2008) at 5%. Choi et al. (2008) suggested that 83% of the trees with broken top recovered the stem and crown to a normal top, trend that we did not evaluate.

Estimated logistic regression models consider the statistical contribution of fixed (GLM, GLMM) and random effects (GLMM) for the tree-level loblolly pine STP in the Southeastern U.S. The initial full GLM (Equation 2.4) suggested that all covariates were statistically significant (p-value < 0.05). However, the original arrangement of the database, with such a hierarchical structure and repeated measure dependence, results in a mixed model (Harrison and Shiver 1999). Omitting random effects poses a serious statistical problem in the fixed effects estimation (McCulloch and Searle 2001). Thus, the inclusion of the random effects made the fixed effects *Thinning* and *Damage at year six: Yellow needles* not statistically significant in the GLMM.

The best-estimated model captures the tree-level STP dynamics taking into account the effect of *Age*, *Management* intensity, *Planting density*, *Site index*, *DBH percentile at year six*, incidence of *Rust at year six*, and the severity of *Damage at year six*. Overall, covariates selected to explain STP proportion were consistent with previous research. Proportions of timber product classes have been estimated as a function of age, height, and stand density (Strub et al. 1986). While DBH explained the variability in the product-class allocation-probability model, the statistical contribution of tree height, stand density, site index, and degree of thinning was negligible (Burkhart and Bredenkamp 1989). Timber product proportions to distribute per-acre total volume were predicted as a function of DBH and volume (Teeter and Zhou 1998). Choi et al. (2008) found that the stem quality dynamics in mature loblolly pine stands over a 15-year period was a function of the DBH, total height, crown class, relative height, age, site index, stand density, and stem quality assessments: forking, top damage, interaction top damage and short crook, bole characteristics (form such as straight or sweep), damage after disease or insect outbreaks, and undamaged and healthy trees.

There is no direct explanation with regard to the unexpected adverse effect of the intensive *Management* regime on the STP proportion. A similar result was found in six installations of SAGS (Green et al. 2018). Intensive forest management, particularly fertilization, has been found to induce mortality in loblolly pine through an increment of the competing vegetation, mainly hardwood. In uneven-aged loblolly-shortleaf pine mixed stands, low fertile soils produced a slightly larger proportion of high-grade lumber than more fertile soils (Prestemon and Buongiorno 2000). Taking the soil fertility effect on lumber production proportion as a reference, and depending on the soils conditions, an excess of a nutrient after fertilization can induce a disbalance in the soil nutrient budget, which turns out in a bad expression of tree form. The intensive management regime practiced on the locations in this research corresponds to a very high level of inputs. Thus, high nitrogen to calcium ratio in soils may result in a stem sinuosity of loblolly pine trees (Espinoza et al. 2012), affecting STP and stand timber value. The reduction of STP proportion by intensive management has direct implications for the forestland owner. The effect of intensive management on tree form and STP (Green et al. 2018) may negate volume gains from silvicultural practices (Restrepo et al. 2018). Forestland owners should evaluate the overall effect of intensive management on the stand timber monetary value (Green et al. 2018).

The higher the *Planting density*, the lower the STP, which is in accordance with models previously estimated describing stem quality proportions (Choi et al. 2008; Strub et al. 1986). However, different levels of discretized categories of *Planting density* did not affect the proportion of trees with STP over *Age*, which is also consistent with results previously reported (Green et al. 2018; Burkhart and Bredenkamp 1989; Amateis and Burkhart 2013; Prestemon and Buongiorno 2000). Although trees in highly dense stands have small branches (Borders and Volfovicz 2010), which may increase the tree STP, the effect of high stand density on tree size (Restrepo et al. 2019) may diminish the stand timber monetary value. The actual stand timber monetary value increased significantly as the planting density decreased as a consequence of the high-grade lumber production (Amateis and Burkhart 2013). *Thinning* was not significant in the best GLMM (Model 5, Table 3.7). This finding is also consistent with results previously reported (Burkhart and Bredenkamp 1989).

Site index was significant in explaining the variation of STP in the best-estimated model, although differences among discretized categories of *Site index* over *Age* were not significant. Site index, as the typical metric to assess for the overall environmental effect on forest productivity, is not a good descriptor of the timber product class distribution and timber merchantability potential (Burkhart and Bredenkamp 1989).

Geneticists have proposed the use of early assessments at year six of forest stands as predictors of the future forest plantation performance (Cumbie et al. 2012). We proposed the use of *DBH percentile at year six*, *Rust at year six*, and *Damage at year six* as covariates in the STP model. Given the different management intensities and planting densities in the studies, we considered unfair to directly compare trees using DBH or any other tree size variable. For that reason we proposed and successfully tested the *DBH percentile at year six*, a measure of the relative size of a tree, comparing to the neighboring trees in the plot. No previous relative tree size index based on DBH or based on early assessment of the tree size was found in the literature as a covariate to explain timber volume merchantability. Based on absolute measures of tree size, our results are consistent with the literature evaluating the effect of DBH on tree merchantability, and sawtimber proportion (Strub et al. 1986; Burkhart and Bredenkamp 1989; Teeter and Zhou 1998). However, other measures of tree size like total height, may not explain volume merchantability (Burkhart and Bredenkamp 1989). Realistically, only trees with DBH greater to 11.6 inches would be in the sawtimber category at the rotation age. For that reason, although the stem quality and form may be good, small trees will be considered in the non-sawtimber category. Therefore, the total realized proportion of sawtimber trees over the diameter distribution may be lower than estimated in this analysis.

Increasing levels of the incidence of *Rust at year six* and severity of *Damage at year six* diminished the STP proportion. Studies with similar predictors regarding early evaluations of forest health were not found to compare our results. Research in mature loblolly pine stands suggests that stem quality in terms of sweep, forking, broken top, and incidence of diseases was stable over time (Choi et al. 2008), which is consistent with what we found. Moreover, typically some stem defects near to the stump can be removed at harvest, and the remaining stem might be sold without downgrading of the timber quality at the mill (Green et al. 2018).

Three random effects accounting for the hierarchical structure and temporal dependence were included in the model. Random effects in the GLMM explained an additional portion of the STP variability compared with the full GLM. The first random effect in the hierarchical structure of the GLMM is the study level, accounting for the effect of physiographic region. Differences in STP can be found between physiographic regions as a result of the frequency and magnitude of wind-throw[1] caused by tornadoes, hurricanes, and tropical storms. Although the effect of genetics was not directly tested in the model due to the unknown planting material in SAGS, we can expect a similar trend in both studies since the genetic material was first-generation of open-pollinated families. Research has found that the proportion of stem with defects is not significantly different between stands of unimproved and

[1] Tree felled or broken off by wind (Helms 1998).

improved genetic stock (Buford and Burkhart 1987). Amateis and Burkhart (1987) found significant differences in volume, height-diameter, tree form, and taper relationships in stands from loblolly pine old-field plantations, cut-over[2] plantations, and natural stands. Cumbie et al. (2012) found that 48 first- and second-generation families presented different STP to individual-tree volume ratios. Therefore, genetics may be an important factor if the study consider different generations of genetic material.

The second random effect was CRIFF soil classes within study. Although this soil classification system is based primarily on physical properties, this classification method reflects the overall soil conditions. Although slower growing trees in low fertile soils my have time to occlude branch scars, develop a clear log, and produce higher proportion of lumber (Prestemon and Buongiorno 2000), deficiencies or excesses of macro, secondary, and micronutrients may also induce an expression of bad tree form (Espinoza et al. 2012; Lehto et al. 2010); therefore affecting the tree sawtimber potential and stand timber value. For instance, pines on slightly boron-deficient soils may have a thick stem base, and a low branch and needle mass to stem ratio; whereas a dramatic deficiency in boron results in the loss of the apical dominance[3] (Lehto et al. 2010), which has severe consequences on stem quality and tree form.

The third and last random effect was installation within CRIFF soil class. This random effect had the highest variance of the three random effects. Therefore, differences among plots within the same CRIFF soil class are larger than the overall variability among CRIFF soil classes or between studies, suggesting a markedly micro-site effect on STP.

Assuming that the average tree is representative of the stand, estimated STP proportion given the covariates can be used to weigh either the total volume or timber prices of the timber product classes to obtain merchantable volume (Choi et al. 2008; Amateis and Burkhart 2005) or blended price (Klemperer 2003), respectively. The STP proportion allows

[2] Land that has previously been logged (Helms 1998).

[3] The upward gorwth of terminal shoot tissues at the expense of lateral shoots below them (Helms 1998).

for utilizing whole-stand yield models given the tree and stand characteristics and simplifying financial calculations of timber production. This research helps forestland owners in making informed decisions regarding the allocation of resources to simultaneously optimize growth and STP proportion as a strategy to maximize financial returns. Likewise, to the best of our knowledge, this is the first time that the dynamics of a measure of stem quality like STP proportion is depicted over *Age* with its associated uncertainty. The confidence intervals in the figures of STP proportion allow forestland owners for a better-informed decision making.

Conclusions

An accurate estimation of merchantable volume is a vital input for forest financial return calculations. This goal can be achieved by i) modeling forest growth and yield using the whole-stand approach, and ii) finding the quantity (proportion) of timber in each of commercial timber product classes (i.e., sawtimber, chip-n-saw, and pulpwood). Although these two topics are closely related, research rarely considers the proportions or weights as a way to split the forest yield into product classes.

The stand timber monetary value is a function of merchantable volume and timber price. Finding the proportions of timber in each of the commercial pine product classes is a vital step in calculating the stand timber monetary value when using whole-stand models, the most widely used forest growth and yield modeling approach in the Southeastern U.S. The proportions can weigh either the total volume or timber prices of the timber product classes to obtain merchantable volume or blended price (Klemperer 2003), respectively, which result in a simplification of financial calculations. Most of the stand timber monetary value corresponds to the sawtimber product class. For that reason, depending on local markets and forest management goals, most of the effort in timber production is focused on increasing the amount of sawtimber as a strategy to maximize financial returns.

Although the parameter estimates in the full GLM were significant, the inclusion of the random effects, accounting for the hierarchical structure and repeated measure dependence, improved the model fit. Random effects (study, CRIFF soil classes withing study, and plots within CRIFF soil classes) were crucial to handle such error structure. The estimated model can be used to predict the sawtimber potential proportion dynamics as a function of *Age*, *Management* intensity, *Planting density*, *Site index*, *DBH percentile at year six*, the incidence of *Rust at year six*, and the severity of *Damage at year six*.

Forest yield has been found double fold by applying intensive forest management practices (Restrepo et al. 2019; Restrepo et al. 2018). However, the effect of intensive management on tree form (sawtimber potential) (Green et al. 2018; Choi et al. 2008), may negate volume gains from silvicultural practices, a reason why forestland owners should evaluate the overall effect of intensive management on the stand timber value (Green et al. 2018).

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Appendix

Random effects

PHYSIOGRAPHIC REGION

Lower Coastal Plain	-0.1513
Upper Coastal Plain	0.2911
Piedmont	-0.1344

CRIFF SOIL CLASS WITHIN PHYSIOGRAPHIC REGION

Lower Coastal Plain:A	-0.2007
Lower Coastal Plain:B1	-0.1199
Lower Coastal Plain:B2	0.0003
Lower Coastal Plain:C	-0.2811
Lower Coastal Plain:D	0.3849
Upper Coastal Plain:E	-0.1685
Upper Coastal Plain:F	0.0678
Upper Coastal Plain:G	0.5172
Piedmont:E	-0.2610
Piedmont:F	0.0687

Note: Random effects of the installations within soil classes (429) are not shown.

R script

```
#LIBRARIES------------------
library(sas7bdat)
library(lme4)
library(ggplot2)
library(glmm)
library(car)
library(maptools)
library(raster)
library(rgdal)
library(rgeos)
library(mosaic)
library(mvtnorm)
library(nlme)
library(xtable)
library(texreg)
library(grDevices)

setwd("./Dropbox/Chapter 2 Form and taper")

#METHODS*********************************

#MAP--------------
points<-readShapePoints('loc.shp')
map_US1 <-getData(name="GADM",country='USA',level=1)

States.name<-c('Alabama','Arkansas','Florida','Georgia','Louisiana','Mississippi',
'North Carolina','South Carolina', 'Tennessee','Virginia')
SE<-subset(map_US1,subset=map_US1$NAME_1 %in% States.name)
SE.border<-unionSpatialPolygons(SE,SE$ISO)

par(mar=c(1,2,1,1))
plot(SE,border='grey')
plot(SE.border,border='black',add=T)

pc<-c(17,4,4,17,17,2,2,17,4,17,2,2,17,17,17,4,4,1,1,19,1,1,1,19,4,1,4,19,19,rep(1,8),4,4,4)
plot(points,pch=pc,col='black',add=T)
llgridlines(SE,col='gray60',offset = 0.05)
legend('topleft',c('','','CP - unthinned','CP - thinned','SAGS - unthinned','SAGS - thinned','Discontinued'),
pc=c(1,1,17,2,19,1,4),col=c(0,0,rep(1,40)),cex=0.8,box.col='white')

#RESULTS**************************

#READING DATA AND CREATING ONE DATA FRAME-----------------
#Reading the two datasets
CP<-read.sas7bdat("CPCD96Tree2016e_2.sas7bdat")[,2:18]
SAGS<-read.sas7bdat("SAGCD98Tree2016e.sas7bdat")
summary(CP)
summary(SAGS)
head(CP)
head(SAGS)
data<-rbind(CP,SAGS)
STUDY<-c(rep('CP',nrow(CP)),rep('SAGS',nrow(SAGS)))
ID<-paste(STUDY,data$INST,data$MAN,data$PLTPA,data$AGE,sep='_')
ID2<-paste(STUDY,data$INST,data$MAN,data$PLTPA,sep='_')
ID3<-paste(STUDY,data$INST,sep='_')
data<-data.frame(ID=ID,ID2=ID2,ID3=ID3,STUDY=STUDY,data)
summary(data)
str(data)
nrow(data)


#Reading the soil, physiographic region, and state info
criff<-read.csv('CRIFF&Region.csv',head=T)
str(criff)

#Making the sawtimber potential variable
data$SAW01<-(data$SAW!=0)*0+(data$SAW==0)*1

#Merging dataset of CPCD and SAGSCD data
data1<-merge(data,criff,by="ID3")

table(data$AGE, data$SAW,data$STUDY)
table(data$SAW,data$CR)
table(data$SAW,data$DAM)

#Relevant ages and excluding death trees
data1<-data[data$DBH!='99.9',]
data1CP<-data1[data1$STUDY=='CP' & data1$AGE>=15,]
data1SAGS<-data1[data1$STUDY=='SAGS' & data1$AGE>=12,]
data1<-rbind(data1CP,data1SAGS)

summary(data1)
nrow(data1)

table(data1$AGE, data1$SAW,data1$STUDY)
table(data1$SAW,data1$CR)
```

```
#Adding stand characteristics of rust infection and damage from age 6 to the database at tree level
z<-0
data1$CR6<-integer(nrow(data1))
data1$DAM6<-integer(nrow(data1))
for(i in 1:nrow(data1)){
if(length(data$CR[data$ID2==data1$ID2[i] & as.integer(data$TAG)==as.integer(data1$TAG[i]) & data$AGE==6] |
data$DAM[data$ID2==data1$ID2[i] & as.integer(data$TAG)==as.integer(data1$TAG[i]) & data$AGE==6])>0) {
data1$CR6[i]<-data$CR[data$ID2==data1$ID2[i] & as.integer(data$TAG)==as.integer(data1$TAG[i]) & data$AGE==6]
data1$DAM6[i]<-data$DAM[data$ID2==data1$ID2[i] & as.integer(data$TAG)==as.integer(data1$TAG[i]) & data$AGE==6]
} else {
data1$CR6[i]<-data$CR[data$ID2==data1$ID2[i] & as.integer(data$TAG)==as.integer(data1$TAG[i]) & data$AGE==8]
data1$DAM6[i]<-data$DAM[data$ID2==data1$ID2[i] & as.integer(data$TAG)==as.integer(data1$TAG[i]) & data$AGE==8]
z<-z+1
}
}
z
i

write.csv(x=data1,file='treelevel.csv',col.names = TRUE)

table(data1$SAW,data1$CR6);sum(table(data1$SAW,data1$CR6))
table(data1$AGE,data1$SAW,data1$STUDY);sum(table(data1$AGE,data1$SAW,data1$STUDY))
table(data1$SAW,data1$DAM6)
nrow(data1)

#error i=21434
#TOtal z=17, i reach 115134, nrow is 115138, there are 4 missing.


# Getting the dominant height and Dq
com.ID2<-as.character(unlist(unique(data1$ID2)))
length(com.ID2)


#Function to extract Dq and Hd at age 18

HdDq18.f<-function(combo=com.ID2[1],data=data1){
ID<-paste(combo,'_18',sep='')
Dq<-sqrt(mean(data$DBH[data$ID==ID & data$DBH!=99.9],na.rm=TRUE)^2+var(data$DBH[data$ID==ID & data$DBH!=99.9],na.rm=TRUE))
Hd<-mean(data$HT[data$ID==ID & data$CC=='1'], na.rm=TRUE)
out<-c(combo,Dq,Hd)
return(out)
}

HdDq18.f(data=data1,combo=com.ID2[1])


#Making a summary dataset of Dq and Hd for age 18
t<-Sys.time()
my.HdDq18<-matrix(ncol=3,nrow=length(com.ID2),
dimnames = list(1:length(com.ID2),
c('ID3','Dq18','Hd18')))
for(i in 1:length(com.ID2)){
my.HdDq18[i,]<-HdDq18.f(combo=com.ID2[i],data=data1)
}
Sys.time()-t
class(my.HdDq18)

my.HdDq18<-data.frame(ID=my.HdDq18[,1],Dq=as.numeric(my.HdDq18[,2]),Hd=as.numeric(my.HdDq18[,3]))
head(my.HdDq18)
write.csv(my.HdDq18,file='my.HdDq18.csv')
summary(my.HdDq18)


my.HdDq18<-data.frame(ID=my.HdDq18[,1],Dq=as.numeric(my.HdDq18[,2]),Hd=as.numeric(my.HdDq18[,3]))
head(my.HdDq18)
write.csv(my.HdDq18,file='my.HdDq18.csv')
summary(my.HdDq18)

#Marging the dataset with CPCD and SAGSCD, criff, phyregion, location with the Dq and Hd
data2<-merge(data1,my.HdDq18,by.x='ID2',by.y='ID')
summary(data2)
head(data2)
nrow(data2)

write.csv(x=data2,file='treelevel2.csv')

table(data2$SAW,data2$CR6);sum(table(data2$SAW,data1$CR6))
table(data2$SAW,data2$DAM6)

#PER6: percentil of the diameter at age 6

per.f<-function(combo,age=6,data=data){
trees<-data$TAG[data$ID==paste(combo,age,sep='_') & !is.na(data$DBH) & data$DBH!='99.9']
y<-data$DBH[data$ID==paste(combo,age,sep='_') & !is.na(data$DBH) & data$DBH!='99.9' & data$TAG%in%trees]
f<-ecdf(y)
f.dbh<-f(y)
id2<-rep(combo,length(trees))
out<-data.frame(ID2_TAG=paste(id2,trees,sep='_'),PER6=f.dbh)
return(out)
}
```

```
per.f(combo='CD_1_I_1200',age=21,data=saw)

com.ID2<-as.character(unlist(unique(data2$ID2)))
per6.d<-NULL
for(i in 1:length(com.ID2)){
per<-per.f(data=data,combo=com.ID2[i])
per6.d<-rbind(per6.d,per)
}
write.csv(x=per6.d,file='per6.csv')


data2$ID2_TAG<-paste(data2$ID2,data2$TAG,sep='_')
data3<-data2
#data3$PER6<-merge(data2,per6.d,by='ID2_TAG',all.x=TRUE) I COULD NOT MAKE IT TO WORK
#write.csv(x=data3,file='treelevel3.csv')

mi<-read.csv('missing.csv',header = TRUE,as.is=TRUE)[,1]
mi

per8.d<-NULL
for(i in 1:length(mi)){
per<-per.f(data=data,age=8,combo=mi[i])
per8.d<-rbind(per8.d,per)
}
write.csv(x=per8.d,file='per8.csv')

#Making a summary dataset with site index accordingly with the physiographic region
#Function
data4<-data
com.ID3<-as.character(unlist(unique(data$ID3)))
length(com.ID3)

SI.f<-function(combo=com.ID3[9],data=data4){
age<-max(data$AGE[data$ID3==combo])
#hd<-mean(data$HT[data$ID3==combo & data$CC=='1' & data$AGE==age], na.rm=TRUE)
hd=50
study<-substr(combo,1,2)
si<-(study=='CP')*(exp(5.4185+(log(hd)-5.4185)*(age/25)^(0.5235)))+
(study!='CP')*(exp(5.606524+(log(hd)-5.606524)*(age/25)^(0.48372)))
out<-c(ID3=combo,SI=si)
return(out)
}

SI.f(combo=com.ID3[40],data=data4)

t<-Sys.time()
SI.d<-matrix(ncol=2,nrow=length(com.ID3),
dimnames = list(1:length(com.ID3),
c('ID3','SI')))

for(i in 1:length(com.ID3)){
SI.d[i,]<-SI.f(combo=com.ID3[i],data=data4)
}

Sys.time()-t
class(SI.d)
str(SI.d)

SI<-data.frame(ID3=as.factor(SI.d[,1]),SI=as.numeric(SI.d[,2]))
str(SI)
summary(SI)

write.csv(x=SI,file='./Dropbox/SI20190604.csv')

data5<-merge(saw,SI,by='ID2')
head(data5)

write.csv(x=data5,file='treelevel4_20180919.csv')

#ESTIMATING A MODEL FOR HEIGHT---------------------------------------------
data1$ID_TAG<-paste(data1$ID,data1$TAG,sep="_")
data4Ht<-cbind(ID_TAG=data1$ID_TAG,HT=data1$HT)
saw$ID_TAG<-paste(saw$ID,saw$TAG,sep="_")

saw4Ht<-merge(saw,data4Ht,by="ID_TAG")
saw4Ht<-data.frame(DBH=saw4Ht$DBH,HT=saw4Ht$HT,PROV=saw4Ht$PROV)
head(saw4Ht)
str(saw4Ht)
saw4Ht$HT<-as.numeric(saw4Ht$HT)
str(saw4Ht)

ModHt<-lmer(I(log(HT))~I(1/DBH)+(1|PROV),saw4Ht)
summary(ModHt)

ranef(ModHt)

saw4Ht$HTe<-((exp(4.2907-0.8056/saw$DBH+0.08749759*(saw$PROV=='LCP')-0.03418520*(saw$PROV=='PIE')-0.05331242*(saw$PROV=='UCP'))))
head(saw4Ht)
plot(saw4Ht$HT,saw4Ht$HTe)
abline(0,1)
```

```
#PREDICTING THE SAWTIMBER POTENTIAL BASED ON PAST TREE CHARACTERISTICS--------------------------------

#****************************************************************

saw<-read.csv('saw20180920.csv',header=TRUE)
saw$MAN<-factor(saw$MAN,levels=c('O','I'))
str(saw)
summary(saw)

#Exploratory analysis----------

STP.d<-read.csv('Prop.csv',header=TRUE)
STP.d$ID3<-as.factor(STP.d$ID3)
STP.d$`Study & Installation`<-STP.d$ID3
str(STP.d)

ggplot(STP.d, aes(AGE, STP))+
geom_point(size = 2)+
geom_point(aes(colour = factor(`Study & Installation`)), size = 2)+
theme(legend.title = element_text())

ggplot(STP.d, aes(x=AGE)) +
geom_line(aes(y=STP, colour=`Study & Installation`), size=0.8) +
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.1),color = 'black'),
axis.title = element_text( size = 14),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
legend.title = element_text(),
legend.position = "none")+
labs(x="Age (years)",
y="Sawtimber potential")

#summary statistics

#STP
aggregate(SAW01~AGE,data=saw,function(x) c(mean=mean(x),sd=sd(x)))

#DBH
aggregate(DBH~AGE,data=saw,function(x) c(mean=mean(x),sd=sd(x),max=max(x),min=min(x)))


#PER6
aggregate(PER6~AGE,data=saw,function(x) c(mean=mean(x),sd=sd(x)))

#HT
aggregate(HT~AGE,data=data1,function(x) c(mean=mean(x),sd=sd(x),max=max(x),min=min(x)))

#Man
MAN.sum<-apply(as.data.frame.matrix(table(saw$MAN,saw$AGE)),2,sum)
matrix(rep(MAN.sum,2),nrow=2,byrow = T)
round(as.data.frame.matrix(table(saw$MAN,saw$AGE))/matrix(rep(MAN.sum,2),nrow=2,byrow = T),2)

#THIN
THIN.sum<-apply(as.data.frame.matrix(table(saw$THIN,saw$AGE)),2,sum)
matrix(rep(THIN.sum,2),nrow=2,byrow = T)
round(as.data.frame.matrix(table(saw$THIN,saw$AGE))/matrix(rep(THIN.sum,2),nrow=2,byrow = T),2)

#SI
aggregate(SI~AGE,data=saw,function(x) c(mean=mean(x),sd=sd(x)))


#CR
CR.sum<-apply(as.data.frame.matrix(table(data1$CR,data1$AGE)),2,sum)
matrix(rep(CR.sum,5),nrow=5,byrow = T)
round(as.data.frame.matrix(table(data1$CR,data1$AGE))/matrix(rep(CR.sum,5),nrow=5,byrow = T),2)

#CR6
CR6.sum<-apply(as.data.frame.matrix(table(saw$CR6,saw$STUDY)),2,sum)
matrix(rep(CR6.sum,5),nrow=5,byrow = T)
round(as.data.frame.matrix(table(saw$CR,saw$STUDY))/matrix(rep(CR6.sum,5),nrow=5,byrow = T),2)

#DAM
DAM.sum<-apply(as.data.frame.matrix(table(data1$DAM,data1$AGE)),2,sum)
matrix(rep(DAM.sum,8),nrow=8,byrow = T)
round(as.data.frame.matrix(table(data1$DAM,data1$AGE))/matrix(rep(DAM.sum,8),nrow=8,byrow = T),2)

#DAM6
DAM6.sum<-apply(as.data.frame.matrix(table(saw$DAM6,saw$STUDY)),2,sum)
matrix(rep(DAM6.sum,6),nrow=6,byrow = T)
round(as.data.frame.matrix(table(saw$DAM6,saw$STUDY))/matrix(rep(DAM6.sum,6),nrow=6,byrow = T),3)


#SAW
SAW.sum<-apply(as.data.frame.matrix(table(data1$SAW,data1$AGE)),2,sum)
matrix(rep(SAW.sum,5),nrow=5,byrow = T)
round(as.data.frame.matrix(table(data1$SAW,data1$AGE))/matrix(rep(SAW.sum,5),nrow=5,byrow = T),2)

#SAW at year six
```

```
SAW6.sum<-apply(as.data.frame.matrix(table(data$SAW,data$AGE)),2,sum)
matrix(rep(SAW.sum,5),nrow=5,byrow = T)
round(as.data.frame.matrix(table(data1$SAW,data1$AGE))/matrix(rep(SAW.sum,5),nrow=5,byrow = T),2)

#CC
CC.sum<-apply(as.data.frame.matrix(table(saw$CC,saw$AGE)),2,sum)
matrix(rep(CC.sum,4),nrow=4,byrow = T)
round(as.data.frame.matrix(table(saw$CC,saw$AGE))/matrix(rep(CC.sum,4),nrow=4,byrow = T),2)

#G L M ---------------------------------------------------------
tl.glm.1<-glm(SAW01~AGE+MAN+SI+PLTPA+THIN+CR6+asfDAM6+PER6,data=saw,family=binomial(link='logit'))
summary(tl.glm.1)

tl.glm.2<-glm(SAW01~AGE+MAN+SI+PLTPA+PLTPA:THIN+CR6+as.factor(DAM6)+PER6,data=saw,family=binomial(link='logit'))
summary(tl.glm.2)

anova(tl.glm.1,tl.glm.2,test="Chisq")

#Collapsing levels
saw$ColDAM6<-as.factor(ifelse(saw$DAM6==1,0,saw$DAM6))

tl.glm.3<-glm(SAW01~AGE+MAN+SI+PLTPA+PLTPA:THIN+CR6+ColDAM6+PER6,data=saw,family=binomial(link='logit'))
summary(tl.glm.3)

anova(tl.glm.2,tl.glm.3,test="Chisq")
acf(tl.glm.3$res,lag.max=20)

#Figures

#Figure of rust infection

#Data frame for prediction
man='I'
pltpa=600
thin=0 #other level is 3
newCR6<-data.frame(MAN=factor((rep(man,20))),
PLTPA=rep(pltpa,20),
THIN=rep(thin,20),
CR6=rep(0:4,each=4),
DAM6=rep(c(0,3,5,6),5))

newCR6$ColDAM6<-as.factor(newCR6$DAM6)

head(newCR6)
str(newCR6)
summary(newCR6$ColDAM6)

#Prediciton of the new observations
PRED.CR6<-predict(tl.glm.2,newdata=newCR6,type='link',se.fit=TRUE)
ub.CR6<-exp(PRED.CR6$fit+1.96*PRED.CR6$se.fit)/(1+exp(PRED.CR6$fit+1.96*PRED.CR6$se.fit))
lb.CR6<-exp(PRED.CR6$fit-1.96*PRED.CR6$se.fit)/(1+exp(PRED.CR6$fit-1.96*PRED.CR6$se.fit))
PRED.CR6<-predict(tl.glm.2,newdata=newCR6,type='response',se.fit=TRUE)
ad<-rep(c(-0.075,-0.025,0.025,0.075),5)
co<-c('darkseagreen4','gold','darkgoldenrod4','brown3')
plot(newCR6$CR6[1:20]+ad,PRED.CR6$fit[1:20],col=co,pch=19,xaxt='n',ylim=c(min(lb.CR6)*0.95,max(ub.CR6)*1.05),cex.lab=1.2,cex.axis=1.2,cex.main=1.2,
xlab='Rust infection (%)',ylab='Sawtimber proportion',main='Sawtimber potential at age 18 years')
mtext(paste('MAN=',man,'    PLPTA=',pltpa,'    THIN=',thin,sep=''),cex=0.7)
CR.names<-c('0','1-25','26-50','51-75','76-100')
for(i in 1:6) mtext(paste(CR.names[i]),side=1,at=i-1,line=0.5,cex=1.2)
arrows(newCR6$CR6[1:20]+ad, PRED.CR6$fit[1:20], newCR6$CR6[1:20]+ad, ub.CR6[1:20], length = 0.05, angle = 90,col=co)
arrows(newCR6$CR6[1:20]+ad, PRED.CR6$fit[1:20], newCR6$CR6[1:20]+ad,  lb.CR6[1:20], length = 0.05, angle = 90,col=co)
legend('topright',c('None damage in tree or \n minimum damage in needles','Tip dieback','Leaning tree','Broken top'),
y.intersp = 0.7, col=co,bty='n',cex=0.8,pch=19)

#Figure of trees per hectare

#Data frame for prediction of trees per hectare
man<-'O'
pltpa<-unique(data18$PLTPA)
thin<-0 #other level is 3
cr6<-0
newPLTPA<-data.frame(MAN=factor((rep(man,24))),
PLTPA=rep(pltpa,each=4),
THIN=rep(thin,24),
CR6=rep(cr6,24),
DAM6=rep(c(0,3,5,6),6))

newPLTPA$ColDAM6<-as.factor(newPLTPA$DAM6)

head(newPLTPA)
str(newPLTPA)



#*********************************************************************
# G L M M ---------------------------------------------------------
saw$asfDAM6<-as.factor(saw$DAM6)

tl.glm.1<-glm(SAW01~AGE+MAN+SI+PLTPA+THIN+CR6+asfDAM6+PER6,data=saw,family=binomial(link='logit'))
summary(tl.glm.1)

tl.glmm.1<-glmer(SAW01~AGE+MAN+SI+PLTPA+THIN+CR6+asfDAM6+PER6+(1|PROV)+(1|PROV:CRIFF)+(1|CRIFF:ID2),
```

```
data=saw,family=binomial)
summary(tl.glmm.1)
anova(tl.glmm.1,tl.glm.1)
beepr::beep(4)
xtable(anova(tl.glmm.1,tl.glm.1))

#Testing fixed effects
#Dropping SI
tl.glmm.2<-glmer(SAW01~AGE+MAN+PLTPA+THIN+CR6+asfDAM6+PER6+(1|PROV)+(1|PROV:CRIFF)+(1+AGE|CRIFF:ID2),
data=saw,family=binomial)
summary(tl.glmm.2)
beepr::beep(4)

xtable(anova(tl.glmm.1,tl.glmm.2))

#Dropping THIN
tl.glmm.3<-glmer(SAW01~AGE+MAN+PLTPA+CR6+asfDAM6+PER6+(1|PROV)+(1|PROV:CRIFF)+(1+AGE|CRIFF:ID2),
data=saw,family=binomial)
summary(tl.glmm.3)
beepr::beep(4)

xtable(anova(tl.glmm.1,tl.glmm.3))
xtable(anova(tl.glmm.2,tl.glmm.3))


#Collapsing yellow needles into the intercept
saw$asfDAM6<-as.factor(ifelse(saw$DAM6==1,0,saw$DAM6))
tl.glmm.4<-glmer(SAW01~AGE+MAN+PLTPA+CR6+asfDAM6+PER6+(1|PROV)+(1|PROV:CRIFF)+(1+AGE|CRIFF:ID2),
data=saw,family=binomial)
summary(tl.glmm.4)
xtable(anova(tl.glmm.3,tl.glmm.4))
beepr::beep(4)

#Collapsing yellow needles into the dead needles.
saw$asfDAM6<-as.factor(ifelse(saw$DAM6==1,2,saw$DAM6))
tl.glmm.5<-glmer(SAW01~AGE+MAN+PLTPA+CR6+asfDAM6+PER6+(1|PROV)+(1|PROV:CRIFF)+(1+AGE|CRIFF:ID2),
data=saw,family=binomial)
summary(tl.glmm.5)
xtable(anova(tl.glmm.3,tl.glmm.5))
beepr::beep(4)


#Testing for random effects
#Reducing random effects starting from the low hierarchy to compare it with model 5 (fixed effect accepted)
tl.glmm.6<-glmer(SAW01~AGE+MAN+SI+PLTPA+CR6+asfDAM6+PER6+(1|PROV)+(1|PROV:CRIFF)+(1|CRIFF:ID2),
data=saw,family=binomial)
summary(tl.glmm.6)
xtable(anova(tl.glmm.5,tl.glmm.6))
beepr::beep(4)


tl.glmm.7<-glmer(SAW01~AGE+MAN+PLTPA+CR6+asfDAM6+PER6+(1|PROV)+(1|PROV:CRIFF),
data=saw,family=binomial)
summary(tl.glmm.7)
xtable(anova(tl.glmm.5,tl.glmm.7))
beepr::beep(4)

tl.glmm.8<-glmer(SAW01~AGE+MAN+PLTPA+CR6+asfDAM6+PER6+(1|PROV),
data=saw,family=binomial)
summary(tl.glmm.8)
xtable(anova(tl.glmm.5,tl.glmm.8))
beepr::beep(4)

#Reducing random effects starting from the high hierarchy to compare it with model 5 (fixed effect accepted)
tl.glmm.9<-glmer(SAW01~AGE+MAN+PLTPA+CR6+asfDAM6+PER6+(1|CRIFF)+(1+AGE|CRIFF:ID2),
data=saw,family=binomial)
summary(tl.glmm.9)
xtable(anova(tl.glmm.5,tl.glmm.9))
beepr::beep(4)

tl.glmm.10<-glmer(SAW01~AGE+MAN+PLTPA+CR6+asfDAM6+PER6+(1+AGE|ID2),
data=saw,family=binomial)
summary(tl.glmm.10)
xtable(anova(tl.glmm.5,tl.glmm.10))
beepr::beep(4)

tl.glmm.11<-glmer(SAW01~AGE+MAN+PLTPA+CR6+asfDAM6+PER6+(AGE-1|ID2),
data=saw,family=binomial)
summary(tl.glmm.11)
xtable(anova(tl.glmm.5,tl.glmm.11))
beepr::beep(4)

#GLM
tl.glm.2<-glm(SAW01~AGE+MAN+PLTPA+CR6+asfDAM6+PER6,data=saw,family=binomial(link='logit'))
summary(tl.glm.2)

xtable(anova(tl.glmm.5,tl.glm.2))

#Best model tl.glmm.5
#Printing the full model
xtable(summary(tl.glmm.1)$coe)
```

```
#Printing anovas comparing the models
#Comparing fixed effects
xtable(anova(tl.glmm.2,tl.glmm.3))
xtable(anova(tl.glmm.3,tl.glmm.4))
xtable(anova(tl.glmm.3,tl.glmm.5))

#Comparing random effects
xtable(anova(tl.glmm.5,tl.glmm.6))
xtable(anova(tl.glmm.5,tl.glmm.7))
xtable(anova(tl.glmm.5,tl.glmm.8))
xtable(anova(tl.glmm.5,tl.glmm.9))
xtable(anova(tl.glmm.5,tl.glm.2))

#Best model achieved
xtable(summary(tl.glmm.5)$coe)

#Diagnostics
summary(tl.glmm.5)$optin$derivs
hes<-summary(tl.glmm.5)$optin$derivs[[2]]
cov2cor(hes[1:3,1:3])
round(solve(hes),3)
round(summary(tl.glmm.2)$vcov,3)
round(cov2cor(summary(tl.glmm.2)$vcov),3)
co<-summary(tl.glmm.2)$vcov
round(solve(co),3)
round(hes,3)

car::vif(tl.glmm.5)

xtable(summary(tl.glmm.5)$vcov)


#RESIDUALS
par(mar=c(4,4,1,1))
pred<-predict(tl.glmm.6,type='response')#,re.form=~0)

#Ordinary
or<-saw$SAW01[!is.na(saw$PER6)]-pred
plot(pred,or,las=1,ylab='Ordinary residuals',xlab='Estimated Sawtimber Potential',cex.axis=1.3,cex.lab=1.3)
lines(smooth.spline(or,pred,df=3), col='red',lwd=2,lty=2)

plot(fitted(tl.glmm.6),residuals(tl.glmm.6))
lines(smooth.spline(residuals(tl.glmm.6),fitted(tl.glmm.6),df=3), col='red',lwd=2,lty=2)

#abline(h=0.5,lty=2,col='gray')
#abline(v=0.5,lty=2,col='gray')

#Pearson
rp<-(saw$SAW01[!is.na(saw$PER6)]-pred)/sqrt(pred*(1-pred))
plot(pred,rp,las=1,ylab='Pearson residuals',xlab='Estimated Sawtimber Potential',cex.axis=1.3,cex.lab=1.3)
lines(smooth.spline(rp,pred,df=3),col='red',lwd=2,lty=2)

#ACF
acf(tl.glm.1$residuals,lag.max=20,las=1,main='',cex.axis=1.4,cex.lab=1.4, ylab='Autocorrelation Function of Residuals')
acf(summary(tl.glmm.1)$residuals,lag.max=20,las=1,main='',cex.axis=1.3,cex.lab=1.3)
acf(summary(tl.glmm.6)$residuals,lag.max=20,las=1,main='',cex.axis=1.4,cex.lab=1.4, ylab='Autocorrelation Function of Residuals')

acf(tl.glm.2$residuals,lag.max=20,las=1,main='',cex.axis=1.3,cex.lab=1.3)

acf(residuals(tl.glm.1))


#Trying with function glmm to compare results

sl.pro.glmm.age<-glmm(cbind(SAW1,SAW0)~AGE+MAN+PLTPA+THIN,random=~ID2,
varcomps.names = c('S'),data=my.data,family.glmm=binomial.glmm(),m=10^4,debug=TRUE)

Val.glmm<-glmm(SAW01~AGE+MAN+SI+PLTPA+CR6+asfDAM6+PER6+(1|PROV)+(1|PROV:CRIFF)+(1|CRIFF:ID2),
data=saw,family=binomial)

tl.glmm.6<-glmer(SAW01~AGE+MAN+SI+PLTPA+CR6+asfDAM6+PER6+(1|PROV)+(1|PROV:CRIFF)+(1|CRIFF:ID2),
data=saw,family=binomial)
summary(tl.glmm.6)

ranef(tl.glmm.6)

#FUNCTION FOR CREATING THE NEW DATA FRAME --------------------------------------------

#Data frame
newDat.f<-function(AGE=25,MAN='O',SI=80,PLTPA=600,CR6=0,DAM6=0,PER6=0.5){
new<-expand.grid(AGE=AGE,MAN=MAN,SI=SI,PLTPA=PLTPA,CR6=CR6,DAM6=DAM6,PER6=PER6)
new$asfDAM6<-as.factor(ifelse(new$DAM6==1,2,new$DAM6))
return(new)
}

#Non empirical (no simulation) CI function
ci.f<-function(obj=tl.glmm.6,newdata){
Xh<-as.matrix(cbind(rep(1,nrow(newdata)),newdata$AGE,(newdata$MAN=='I')*1,newdata$SI,newdata$PLTPA,
newdata$CR6,(newdata$DAM6==2)*1,(newdata$DAM6==3)*1,(newdata$DAM6==5)*1,(newdata$DAM6==6)*1,
newdata$PER6))
S2b<-summary(obj)$vcov
mean<-predict(obj,newdata=newdata,re.form=NA,type='link')
```

```
ci<-matrix(ncol=2,nrow=nrow(newdata),dimnames=list(1:nrow(newdata),c('lb','ub')))
for(i in 1:nrow(newdata)){
s<-sqrt(as.numeric(t(Xh[i,])%*%S2b%*%Xh[i,]))
lb<-mean[i]-1.96*s
ub<-mean[i]+1.96*s
ci[i,]<-c(exp(lb)/(1+exp(lb)),exp(ub)/(1+exp(ub)))
}
fit<-predict(obj,newdata=newdata,re.form=NA,type='response')
out<-data.frame(newdata,fit,ci)
return(out)

}


#FIGURES OF RESPONSE ---------------------------------

if (Sys.info()[6]=='HR') setwd("C:/Users/HR/Dropbox/Chapter 2 Form and taper/MS Stat Thesis")

#FIGURES OF AGE-------------------------------------

#oooooooooooooooooooooooooooooooooooooo
#Figure of AGE effect and MANAGEMENT
#oooooooooooooooooooooooooooooooooooooo

#WITHOUT PREDICTION INTERVALS
AgeMan<-ci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),MAN=c('O','I')))
AgeMan$Management<-factor(ifelse(AgeMan$MAN=='O','Operational','Intensive'),levels=c('Operational','Intensive'))
AgeMan$lb<-AgeMan$ub<-AgeMan$fit

ggplot(AgeMan, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=Management, colour=Management), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=Management), alpha=0.0)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_text(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.77,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','aquamarine3'))

#WITH ONE PREDICTION INTERVALS FOR MANAGEMENT OPERATIONAL
AgeMan<-ci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),MAN=c('O','I')))
AgeMan$Management<-factor(ifelse(AgeMan$MAN=='O','Operational','Intensive'),levels=c('Operational','Intensive'))
AgeMan$lb[AgeMan$Management=='Intensive']<-AgeMan$ub[AgeMan$Management=='Intensive']<-AgeMan$fit[AgeMan$Management=='Intensive']

ggplot(AgeMan, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=Management, colour=Management), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=Management), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_text(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.77,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','aquamarine3'))

#WITH TWO PREDICTION INTERVALS FOR MANAGEMENT OPERATIONAL
AgeMan<-ci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),MAN=c('O','I')))
AgeMan$Management<-factor(ifelse(AgeMan$MAN=='O','Operational','Intensive'),levels=c('Operational','Intensive'))

#png(filename = "MANtwoCI.png",
#    width = 480, height = 480, units = "px", pointsize = 12, bg = "white")

ggplot(AgeMan, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=Management, colour=Management), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=Management), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
```

```
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_text(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.77,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','aquamarine3'))

#dev.off()

#Figure of AGE effect and SI
AgeSI<-ci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),SI=c(60,80,100)))
AgeSI$`Site Index (ft @ 25 yr)`<-factor(AgeSI$SI)

#png(filename = "SItwoCI.png",
#    width = 480, height = 480, units = "px", pointsize = 12,
#    bg = "white")


ggplot(AgeSI, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`Site Index (ft @ 25 yr)`, colour=`Site Index (ft @ 25 yr)`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Site Index (ft @ 25 yr)`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_text(text='Site Index'),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.77,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  'darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#dev.off()

#Figure of AGE effect and planting density
AgePLTPA<-ci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),PLTPA=c(600,1200,1800)))
AgePLTPA$`Planting Density (TPA)`<-factor(AgePLTPA$PLTPA)

#png(filename = "PLTPAthreeCI.png",
#    width = 480, height = 480, units = "px", pointsize = 12,
#    bg = "white")


ggplot(AgePLTPA, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`Planting Density (TPA)`, colour=`Planting Density (TPA)`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Planting Density (TPA)`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.75,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#dev.off()

#Figure of AGE effect and rust infection at age 6

#WITHOUT PREDICTION INTERVALS
AgeCR6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),CR6=c(0,2,4)))
```

```
AgeCR6$`Rust Infection at year 6`<-ifelse(AgeCR6$CR6==0,0,ifelse(AgeCR6$CR6==2,'26-50%','76-100%'))
AgeCR6$lb<-AgeCR6$ub<-AgeCR6$fit

ggplot(AgeCR6, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`Rust Infection at year 6`, colour=`Rust Infection at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Rust Infection at year 6`), alpha=0)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 10),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.19,.88), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))


#WITH ONE PREDICTION INTERVAL
AgeCR6<-eci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),CR6=c(0,2,4)))
AgeCR6$`Rust Infection at year 6`<-ifelse(AgeCR6$CR6==0,0,ifelse(AgeCR6$CR6==2,'26-50%','76-100%'))
AgeCR6$lb[AgeCR6$`Rust Infection at year 6`!='0']<-AgeCR6$ub[AgeCR6$`Rust Infection at year 6`!='0']<-AgeCR6$fit[AgeCR6$`Rust Infection at year 6`!='0']

ggplot(AgeCR6, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`Rust Infection at year 6`, colour=`Rust Infection at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Rust Infection at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 10),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.19,.88), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#WITH TWO PREDICTION INTERVALS
AgeCR6<-eci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),CR6=c(0,2,4)))
AgeCR6$`Rust Infection at year 6`<-ifelse(AgeCR6$CR6==0,0,ifelse(AgeCR6$CR6==2,'26-50%','76-100%'))
AgeCR6$lb[AgeCR6$`Rust Infection at year 6`=='76-100%']<-AgeCR6$ub[AgeCR6$`Rust Infection at year 6`=='76-100%']
<-AgeCR6$fit[AgeCR6$`Rust Infection at year 6`=='76-100%']


ggplot(AgeCR6, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`Rust Infection at year 6`, colour=`Rust Infection at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Rust Infection at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 10),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.19,.88), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#WITH THREE PREDICTION INTERVALS
AgeCR6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),CR6=c(0,2,4)))
AgeCR6$`Rust Infection at year 6`<-ifelse(AgeCR6$CR6==0,0,ifelse(AgeCR6$CR6==2,'26-50%','76-100%'))

#png(filename = "CR6threeCI.png",
#    width = 480, height = 480, units = "px", pointsize = 12,
#    bg = "white")
```

```
ggplot(AgeCR6, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`Rust Infection at year 6`, colour=`Rust Infection at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Rust Infection at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 10),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.19,.88), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#dev.off()

#Figure of AGE effect and damage at age 6, three level factors

#WITHOUT PREDICTION INTERVALS
AgeDAM6<-eci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),DAM6=c(0,3,5)))
AgeDAM6$`Damage at year 6`<-factor(ifelse(AgeDAM6$DAM6==0,'None',ifelse(AgeDAM6$DAM6==3,'Tip dieback','Broken top')),
levels=c('None','Tip dieback','Broken top'))
AgeDAM6$lb<-AgeDAM6$ub<-AgeDAM6$fit

ggplot(AgeDAM6, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`Damage at year 6`, colour=`Damage at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Damage at year 6`), alpha=0)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 10),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.2,.88), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))


#WITH ONE PREDICTION INTERVALS
AgeDAM6<-eci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),DAM6=c(0,3,5)))
AgeDAM6$`Damage at year 6`<-factor(ifelse(AgeDAM6$DAM6==0,'None',ifelse(AgeDAM6$DAM6==3,'Tip dieback','Broken top')),
levels=c('None','Tip dieback','Broken top'))
AgeDAM6$lb[AgeDAM6$`Damage at year 6`!='None']<-AgeDAM6$ub[AgeDAM6$`Damage at year 6`!='None']<-AgeDAM6$fit[AgeDAM6$`Damage at year 6`!='None']

ggplot(AgeDAM6, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`Damage at year 6`, colour=`Damage at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Damage at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 10),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.2,.88), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#WITH TWO PREDICTION INTERVALS
AgeDAM6<-eci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),DAM6=c(0,3,5)))
AgeDAM6$`Damage at year 6`<-factor(ifelse(AgeDAM6$DAM6==0,'None',ifelse(AgeDAM6$DAM6==3,'Tip dieback','Broken top')),
levels=c('None','Tip dieback','Broken top'))
```

```
AgeDAM6$lb[AgeDAM6$`Damage at year 6`=='Broken top']<-AgeDAM6$ub[AgeDAM6$`Damage at year 6`=='Broken top']
<-AgeDAM6$fit[AgeDAM6$`Damage at year 6`=='Broken top']

ggplot(AgeDAM6, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`Damage at year 6`, colour=`Damage at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Damage at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 10),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.2,.88), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#WITH THREE PREDICTION INTERVALS
AgeDAM6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),DAM6=c(0,3,5)))
AgeDAM6$`Damage at year 6`<-factor(ifelse(AgeDAM6$DAM6==0,'None',ifelse(AgeDAM6$DAM6==3,'Tip dieback','Broken top')),
levels=c('None','Tip dieback','Broken top'))

#png(filename = "DAM6threeCI.png",
#    width = 480, height = 480, units = "px", pointsize = 12,
#    bg = "white")

ggplot(AgeDAM6, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`Damage at year 6`, colour=`Damage at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Damage at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.2,.87), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#dev.off()


#Other color combinations
#'chocolate4','chartreuse4','antiquewhite3'
#'forestgreen','darkolivegreen4','darkslategray4'


#Figure of AGE effect and percentile at age 6, three level factors
AgePER6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(AGE=seq(12,25),PER6=c(0.1,0.5,0.9)))
AgePER6$`DBH Percentile at year 6`<-factor(AgePER6$PER6)

#png(filename = "PER6threeCI.png",
#    width = 480, height = 480, units = "px", pointsize = 12,
#    bg = "white")


ggplot(AgePER6, aes(x=AGE)) +
geom_line(aes(y=fit, linetype=`DBH Percentile at year 6`, colour=`DBH Percentile at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`DBH Percentile at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.77,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
```

```
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Age (years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#dev.off()

#FIGURES OF SITE INDEX ------------------------------------

#Figure of SI and Management
SIMAN<-ci.f(obj=tl.glmm.6,newdata=newDat.f(SI=seq(60,100),MAN=c('O','I')))
SIMAN$Management<-factor(ifelse(SIMAN$MAN=='O','Operational','Intensive'),levels=c('Operational','Intensive'))


ggplot(SIMAN, aes(x=SI)) +
geom_line(aes(y=fit, linetype=Management, colour=Management), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=Management), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(0.25,0.25), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','aquamarine3'))+
labs(x="Site index (ft/25 years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','aquamarine3'))


#Figure of SI and PLTPA
SIPLTPA<-ci.f(obj=tl.glmm.6,newdata=newDat.f(SI=seq(60,100),PLTPA=c(600,1200,1800)))
SIPLTPA$`Planting Density (TPA)`<-factor(SIPLTPA$PLTPA)

ggplot(SIPLTPA, aes(x=SI)) +
geom_line(aes(y=fit, linetype=`Planting Density (TPA)`, colour=`Planting Density (TPA)`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Planting Density (TPA)`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(0.25,0.25), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  'darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Site index (ft/25 years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))



#Figure of SI effect and rust infection at age 6
SICR6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(SI=seq(60,100),CR6=c(0,2,4)))
SICR6$`Rust Infection at year 6`<-ifelse(SICR6$CR6==0,0,ifelse(SICR6$CR6==2,'26-50%','76-100%'))


ggplot(SICR6, aes(x=SI)) +
geom_line(aes(y=fit, linetype=`Rust Infection at year 6`, colour=`Rust Infection at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Rust Infection at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(0.25,0.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  'darkgoldenrod4','darkolivegreen4','aquamarine3'))+
```

```
labs(x="Site index (ft/25 years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))


#Figure of SI effect and damage at age 6, three level factors
SIDAM6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(SI=seq(60,100),DAM6=c(0,3,5)))
SIDAM6$`Damage at year 6`<-factor(ifelse(SIDAM6$DAM6==0,'None',ifelse(SIDAM6$DAM6==3,'Tip dieback','Broken top')),
levels=c('None','Tip dieback','Broken top'))


ggplot(SIDAM6, aes(x=SI)) +
geom_line(aes(y=fit, linetype=`Damage at year 6`, colour=`Damage at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Damage at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.25,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  'darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Site index (ft/25 years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#Figure of SI effect and percentile at age 6, three level factors
SIPER6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(SI=seq(60,100),PER6=c(0.1,0.5,0.9)))
SIPER6$`DBH Percentile at year 6`<-factor(SIPER6$PER6)

ggplot(SIPER6, aes(x=SI)) +
geom_line(aes(y=fit, linetype=`DBH Percentile at year 6`, colour=`DBH Percentile at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`DBH Percentile at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.25,.25), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  'darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Site index (ft/25 years)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))


#FIGURES OF PLANTING DENSITY --------------------------------------------------

PLTPAMAN<-eci.f(obj=tl.glmm.6,newdata=newDat.f(PLTPA=seq(300,1800,by=300),MAN=c('O','I')))
PLTPAMAN$Management<-factor(ifelse(PLTPAMAN$MAN=='O','Operational','Intensive'),levels=c('Operational','Intensive'))

ggplot(PLTPAMAN, aes(x=PLTPA)) +
geom_line(aes(y=fit, linetype=Management, colour=Management), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=Management), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(0.25,0.2), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','aquamarine3'))+   scale_color_manual(values=c('black','grey40'))+
labs(x="Planting density (TPA)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','aquamarine3'))


#Figure of PLTPA effect and SI
```

```
PLTPASI<-ci.f(obj=tl.glmm.6,newdata=newDat.f(PLTPA=seq(300,1800,by=300),SI=c(60,80,100)))
PLTPASI$‘Site Index (ft/25 yr)‘<-factor(PLTPASI$SI)


ggplot(PLTPASI, aes(x=PLTPA)) +
geom_line(aes(y=fit, linetype=‘Site Index (ft/25 yr)‘, colour=‘Site Index (ft/25 yr)‘), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=‘Site Index (ft/25 yr)‘), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = ’black’),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = ’white’, colour = ’white’),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_text(text=’Site Index’),
legend.text = element_text(size = 10),
legend.key.width = unit(2, ’cm’),
legend.position=c(.25,0.2), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  ’darkgoldenrod4’,’darkolivegreen4’,’aquamarine3’))+
labs(x="Planting density (TPA)",
y="Sawtimber potential")+
scale_fill_manual(values=c(’darkgoldenrod4’,’darkolivegreen4’,’aquamarine3’))

#Figure of PLTPA effect and percentile at age 6, three level factors
PLTPAPER6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(PLTPA=seq(300,1800,by=300),PER6=c(0.1,0.5,0.9)))
PLTPAPER6$‘DBH Percentile at year 6‘<-factor(PLTPAPER6$PER6)

ggplot(PLTPAPER6, aes(x=PLTPA)) +
geom_line(aes(y=fit, linetype=‘DBH Percentile at year 6‘, colour=‘DBH Percentile at year 6‘), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=‘DBH Percentile at year 6‘), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = ’black’),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = ’white’, colour = ’white’),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, ’cm’),
legend.position=c(.25,.2), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  ’darkgoldenrod4’,’darkolivegreen4’,’aquamarine3’))+
labs(x="Planting density (TPA)",
y="Sawtimber potential")+
scale_fill_manual(values=c(’darkgoldenrod4’,’darkolivegreen4’,’aquamarine3’))

#Figure of PLTPA effect and rust infection at age 6
PLTPACR6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(PLTPA=seq(300,1800,by=300),CR6=c(0,2,4)))
PLTPACR6$‘Rust Infection at year 6‘<-ifelse(PLTPACR6$CR6==0,0,ifelse(PLTPACR6$CR6==2,’26-50%’,’76-100%’))

ggplot(PLTPACR6, aes(x=PLTPA)) +
geom_line(aes(y=fit, linetype=‘Rust Infection at year 6‘, colour=‘Rust Infection at year 6‘), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=‘Rust Infection at year 6‘), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = ’black’),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = ’white’, colour = ’white’),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, ’cm’),
legend.position=c(0.25,0.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  ’darkgoldenrod4’,’darkolivegreen4’,’aquamarine3’))+
labs(x="Planting density (TPA)",
y="Sawtimber potential")+
scale_fill_manual(values=c(’darkgoldenrod4’,’darkolivegreen4’,’aquamarine3’))

#Figure of PLTPA effect and damage at age 6, three level factors
PLTPADAM6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(PLTPA=seq(300,1800,by=300),DAM6=c(0,3,5)))
PLTPADAM6$‘Damage at year 6‘<-factor(ifelse(PLTPADAM6$DAM6==0,’None’,ifelse(PLTPADAM6$DAM6==3,’Tip dieback’,’Broken top’)),
levels=c(’None’,’Tip dieback’,’Broken top’))


ggplot(PLTPADAM6, aes(x=PLTPA)) +
geom_line(aes(y=fit, linetype=‘Damage at year 6‘, colour=‘Damage at year 6‘), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=‘Damage at year 6‘), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
```

```
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.25,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  'darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Planting density (TPA)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))


#FIGURES OF RUST INFECTION ------------------------------------

CR6MAN<-ci.f(obj=tl.glmm.6,newdata=newDat.f(CR6=seq(0,4),MAN=c('O','I')))
CR6MAN$Management<-factor(ifelse(CR6MAN$MAN=='O','Operational','Intensive'),levels=c('Operational','Intensive'))
CR6MAN$CR6p<-CR6MAN$CR6*25

ggplot(CR6MAN, aes(x=CR6p)) +
geom_line(aes(y=fit, linetype=Management, colour=Management), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=Management), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(0.25,0.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c('darkgoldenrod4','aquamarine3'))+
labs(x="Rust infection at year six (%)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','aquamarine3'))

#Figure of CR6 effect and SI
CR6SI<-ci.f(obj=tl.glmm.6,newdata=newDat.f(CR6=seq(0,4),SI=c(60,80,100)))
CR6SI$`Site Index (ft @ 25 yr)`<-factor(CR6SI$SI)
CR6SI$CR6p<-CR6SI$CR6*25

ggplot(CR6SI, aes(x=CR6p)) +
geom_line(aes(y=fit, linetype=`Site Index (ft @ 25 yr)`, colour=`Site Index (ft @ 25 yr)`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Site Index (ft @ 25 yr)`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_text(text='Site Index'),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.25,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  'darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Rust infection at year six (%)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#Figure of CR6 effect and damage at age 6, three level factors
CR6DAM6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(CR6=seq(0,4),DAM6=c(0,3,5)))
CR6DAM6$`Damage at year 6`<-factor(ifelse(CR6DAM6$DAM6==0,'None',ifelse(CR6DAM6$DAM6==3,'Tip dieback','Broken top')),
levels=c('None','Tip dieback','Broken top'))
CR6DAM6$CR6p<-CR6DAM6$CR6*25

ggplot(CR6DAM6, aes(x=CR6p)) +
geom_line(aes(y=fit, linetype=`Damage at year 6`, colour=`Damage at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`Damage at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
```

```
#legend.title = element_text(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.25,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  'darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Rust infection at year six (%)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))

#Figure of cr6 effect and percentile at age 6, three level factors
CR6PER6<-ci.f(obj=tl.glmm.6,newdata=newDat.f(CR6=seq(0,4),PER6=c(0.1,0.5,0.9)))
CR6PER6$`DBH Percentile at year 6`<-factor(CR6PER6$PER6)
CR6PER6$CR6p<-CR6PER6$CR6*25


ggplot(CR6PER6, aes(x=CR6p)) +
geom_line(aes(y=fit, linetype=`DBH Percentile at year 6`, colour=`DBH Percentile at year 6`), size=1.1) +
geom_ribbon(show.legend=T,aes(ymin=lb, ymax=ub, fill=`DBH Percentile at year 6`), alpha=0.5)+
scale_y_continuous(limits=c(0,1))+
theme(axis.text.x = element_text(angle=0), #legend elements
axis.text = element_text(size = rel(1.3),color = 'black'),
axis.title = element_text( size = 18),
title = element_text(size = 12),
panel.background = element_rect(fill = 'white', colour = 'white'),
panel.border=element_rect(colour = "black", fill=NA, size=0.5),
#legend.title = element_blank(),
legend.text = element_text(size = 10),
legend.key.width = unit(2, 'cm'),
legend.position=c(.25,.15), #positioning the legend INSIDE the plot
legend.background = element_rect(color = "white",
fill = "white",
size = 1,
linetype = "solid"))+ #you can take linetype, size, and color to have no border
scale_color_manual(values=c(  'darkgoldenrod4','darkolivegreen4','aquamarine3'))+
labs(x="Rust infection at year six (%)",
y="Sawtimber potential")+
scale_fill_manual(values=c('darkgoldenrod4','darkolivegreen4','aquamarine3'))
```