A GROWTH AND YIELD SYSTEM OF DIFFERENTIAL EQUATIONS FOR SLASH PINE PLANTATIONS INCLUDING RESPONSE TO SILVICULTURAL TREATMENTS

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ABSTRACT

Slash pine (*Pinus elliottii*) is the second most important commercial species in the Southeastern United States and is usually established in poorly drained flatwoods where it outperforms other common pines. Modeling slash pine growth and how it responds to silvicultural treatments is of interest to forest managers wanting to maximize growth and profits. In this research, a growth and yield system of differential equations is proposed to model slash pine growth, including the effects of some silvicultural treatments (i.e., bedding and vegetation control). Data for this model came from a long-term study (30 years) established by the Plantation Management Research Cooperative (PMRC) of the University of Georgia across Georgia, Florida, and South Carolina. The model system describes the trajectory of three state variables: dominant height, mortality, and basal area. Treatment effects were incorporated into the dominant height and basal area models by using parameter modifiers and dummy variables associated with each of the treatments. Survival was not affected by the studied treatments, but the presence of fusiform rust (*Cronartium quercuum*) was found to be essential to determine the stand density trajectories for the evaluated stands. The three models were estimated simultaneously using maximum likelihood and the variance-covariance was modeled within the system.

INTRODUCTION

Differential equations have been used in forestry to construct growth and yield models and analyze how growth is both generated and constrained (Zeide 1993). Some of the most commonly used models, such as the Schumacher and the Chapman-Richards model (Pienaar and Turnbull 1972) when expressed in the differential form, rely on theories based on assumptions about how organisms grow (e.g., growth proportional to surface area) and how this growth is limited (e.g., maximum carrying capacity). Therefore, parameters in models constructed from differential equations have a biological interpretation which helps researchers to understand the underlying processes. Having interpretable parameters also facilitates the modification or construction of these models when the growth dynamic is changed by factors like silvicultural treatments or external pathogens.

Different strategies have been used in forestry to include silvicultural treatment effects into forest growth models. These usually consist of either including additional factors to the (integrated) model to account for the treatment effect (Pienaar and Rheney 1995), modifying the parameters of the model according to the treatment applied (Mason and Milne 1999), adding other covariables related to the treatment (Hynynen 1995), or using an age-shift approach in which the basic structure of the model is not modified (Snowdon 2002). Using models in the differential equation form facilitates the way treatment effects are incorporated into the growth model because the parameters that should be modified become more

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intuitive. Thus, treatments that aim to increase growth rate (e.g., fertilization) can be modeled by modifying parameters that describe growth in the model, while parameters that describe the decline or limiting factors within the model can be modified if a treatment targets the reduction of limiting factors (e.g., vegetation control).

We used this strategy to model the response to bedding and vegetation control for slash pine (*Pinus elliottii*) plantations in the Southern United States. The technique of using parameter modifiers is a flexible methodology that allows for the inclusion of multiple treatments and their interactions (Ramirez and others 2022); therefore, this technique was tested to include the mentioned response. Survival was not affected by the treatments evaluated, but the presence of fusiform rust (*Cronartium quercuum*) was evaluated as a potential predictor to help describe mortality for the evaluated stands. Fusiform rust is the most common pathogen affecting slash pine in the Southern United States, and is associated with higher mortality rates and losses in product quality (Bailey and others 1989, Devine and Clutter 1985, Nance and others 1981, Susaeta 2020).

MATERIALS AND METHODS

Data

Data from the three variables of interest were available from a slash pine site preparation trial established in 1979 by the Plantation Management Research Cooperative (PMRC) of the University of Georgia. For this research, the treatments evaluated were bedding, competing vegetation control, and the combination of these two treatments. Measurements of diameter at breast height (d.b.h.), dominant height, stand density, and average fusiform rust infection rates per plot were available every 3 years from age 5 to age 31.

Growth responses were evaluated on three state variables (dominant height, survival, and basal area) and the growth and yield system constructed in this research incorporated the effect of bedding and vegetation control on dominant height and basal area growth. The three models composing the system were fitted simultaneously using maximum likelihood. All models were fitted using the differential equation form and the initial value for solving the differential equation was taken as an additional parameter to be estimated on each one of the models (i.e., local parameters per plot). These models were fitted using the Julia programming language (Bezanson and others 2017). More details about the study are provided by Zhao and others (2007, 2009) and Ramirez and others (2022).

Dominant Height Model

A model form that had previously been used to model dominant height with the inclusion of bedding and vegetation control treatment effects was used (Ramirez and others 2023). This model is based on the Gompertz equation [equation (1)], and with the inclusion of the two silvicultural treatments of interest has the form of equation (2). For the construction of the growth and yield system, parameters of the model [equation (2)], were not taken directly from the Ramirez and others (2023) publication but were estimated following the methodology explained below.

$$\frac{dH}{dt} = \mu_0 H e^{-Kt} \tag{1}$$

$$\frac{dH}{dt} = \mu_0 b_1^{Z_1} H e^{-K b_2^{Z_2} t} \tag{2}$$

where

H is dominant height (m)

t is time in years

μ_0, K, b_1, and b_2 are parameters to be estimated

Z_1 and Z_2 are dummy variables equal to 1 if bedding or vegetation control was applied, respectively, and zero if otherwise.

Mortality Model

Mortality rates in slash pine plantations in the Southeastern United States have been demonstrated to be influenced by the presence of fusiform rust infection (Jones 1972, Sluder 1977, Wells and Dinus 1978). Recently, Ramirez and others (2023) developed a mortality model in which the rate of mortality depended on the proportion of fusiform rust infection at year 5. This model form [equation (3)] was used in this research as part of the growth and yield system:

$$\frac{dN}{dt} = (\alpha_0 + \alpha_1 * FR)\, N t^{\delta} \tag{3}$$

where

N is trees per hectare

t is time in years

α_0, α_1, and δ are parameters to be estimated

FR is the proportion of trees affected by fusiform rust on a given plot at age 5.

Similar to the dominant height component, parameters for this model were estimated as part of the system and not taken directly from Ramirez and others (2023). The effect of bedding and vegetation control on survival of slash pine plantations was found to be nonsignificant by Ramirez and others (2023), and therefore, this model was not further modified to include treatment effects.

Basal Area Model

Model from equation (4) was proposed to describe basal area trajectories. This model is based on the Korf growth model (Korf 1939, Zarnovican 1979) although modified to include dominant height and mortality as covariables, similar to the basal area model proposed by Pienaar and Shiver (1986) for slash pine plantations:

$$\frac{dB}{dt} = [\beta_1 + \beta_2 H + \beta_3 N] \frac{B}{t^{\beta_4}} \qquad (4)$$

where

B is basal area (m^2 ha^{-1})

H , N, and t are as defined before

β_1..β_4 are parameters to be estimated.

An analysis of variance showed that there were significant differences in basal area for the treatments evaluated at every age. Therefore, the model from equation (4) was modified similarly to the dominant height model to include treatment effects as follows:

$$\frac{dB}{dt} = [\beta_1 + \beta_2 H + \beta_3 N] \frac{B}{t^{\beta_4}} \ \delta_1^{Z_1} \delta_2^{Z_2} \qquad (5)$$

where Z_1 and Z_2 are the same dummy variables related to the treatments and defined for the dominant height model and δ_1 and δ_2 are additional parameters to be estimated.

In order to determine if the proposed modifications to the dominant height and basal area models were effective to include treatment effects, two growth and yield systems were proposed and compared, one with no treatment effects (system 1) and another with the treatment effects in both models (system 2). These systems are summarized in table 1. The system with better fit statistics was chosen to model the three variables of interest.

Parameter Estimation

Parameters for the two systems proposed were estimated using maximum likelihood in the Julia programing language (Bezanson and others 2017). In addition to the parameters for each one of the models from table 1 (i.e., global parameters), the initial values that define the trajectories (in any of the three variables) for each one of the plots, were defined as additional parameters to be estimated as part of the optimization procedure (i.e., local parameters per plot).

Each of the models from table 1 was first fitted individually assuming a normal distribution of the errors [i.e., H: ε_i~$N(0, \sigma_H)$, N: ε_i~$N(0,\sigma_N)$, B: ε_i~$N(0,\sigma_B)$]. Then, the system was simultaneously estimated by fixing the local parameters previously estimated per plot. That is, when

Table 1—Models for growth and yield systems 1 (without treatment effects) and 2 (includes treatment effects in dominant height and basal area)

Variable	System 1		System 2	
Dominant height	$\frac{dH}{dt} = \mu_0 H e^{-Kt}$	Eq. 1	$\frac{dH}{dt} = \mu_0 b_1^{Z_1} H e^{-K b_2^{Z_2} t}$	Eq. 2
Mortality	$\frac{dN}{dt} = (\alpha_0 + \alpha_1 * FR)\, N t^{\delta}$	Eq. 3	$\frac{dN}{dt} = (\alpha_0 + \alpha_1 * FR)\, N t^{\delta}$	Eq. 3
Basal area	$\frac{dB}{dt} = [\beta_1 + \beta_2 H + \beta_3 N] \frac{B}{t^{\beta_4}}$	Eq. 4	$\frac{dB}{dt} = [\beta_1 + \beta_2 H + \beta_3 N] \frac{B}{t^{\beta_4}} \delta_1^{Z_1} \delta_2^{Z_2}$	Eq. 5

H = dominant height (m); N = trees per ha; B = basal area (m^{2}ha^{-1}); t = time in years; Z_1 and Z_2 = dummy variables equal to 1 if bedding or vegetation control was applied, respectively, and zero otherwise; FR = the proportion of trees affected by fusiform rust on a given plot at age 5; and μ_0, K, b_1, b_2, α_0, α_1, δ, β_1, β_2, β_3, β_4, δ_1 and $\delta 2$ = parameters to be estimated.

simultaneous estimation was done, only the global parameters were estimated, this was necessary to simplify the estimation procedure. For the simultaneous estimation, a multinormal distribution (*MN*) was assumed in which the errors are described by the following variance-covariance matrix:

$$\vec{\epsilon} \sim MN(\vec{0}, \Sigma),\ \Sigma = \begin{bmatrix} \sigma_H^2 & \sigma_{HxN} & \sigma_{HxB} \\ .. & \sigma_N^2 & \sigma_{NxB} \\ .. & .. & \sigma_B^2 \end{bmatrix} = \begin{bmatrix} \sigma_H^2 & \sigma_H\sigma_N\rho_{HxN} & \sigma_H\sigma_B\rho_{HxB} \\ .. & \sigma_N^2 & \sigma_N\sigma_B\rho_{NxB} \\ .. & .. & \sigma_B^2 \end{bmatrix}$$

where

$\vec{\epsilon}$ is the vector of errors (observed–predicted)

Σ is the variance-covariance matrix (symmetrical)

σ_x^2 is the variance of the X variable (H, N, or B)

$\sigma_{X\chi Y}$ is the covariance between variables X and Y

$\rho_{X\chi Y}$ is the correlation between variables X and Y

The following statistics were calculated to evaluate model fit:

Root mean square error (RMSE):

$$RMSE = \sqrt{\frac{\sum_{i=1}^{n}(Y_i - \hat{Y}_i)^2}{n-p}} \tag{6}$$

Mean difference (MD) or bias:

$$MD = \frac{\sum_{i=1}^{n}(Y_i - \hat{Y}_i)}{n} \tag{7}$$

Mean absolute difference (MAD):

$$MAD = \frac{\sum_{i=1}^{n}|Y_i - \hat{Y}_i|}{n} \tag{8}$$

and AIC was used for model comparison:

$$AIC = -2\ loglik + 2p \tag{9}$$

where

n is the total number of observations

p is the number of parameters in each model

Y_i is the observed value

$\hat{Y}_i$ is the estimated value.

RESULTS

Results comparing the two growth and yield systems tested are presented in table 2. The AIC value for system 1 (no treatments) was 1,536.86, while for system 2 it was 778.36, indicating that the system with treatment factors performed better than the system without treatment effects (lower AIC values indicate better fit). From table 2 it can be seen how there was significant gain in precision (reduction of error and bias) when using treatment modifiers. After adding these modifiers, the average error (RMSE) for the dominant height model was reduced from 0.71 to 0.57 m (20 percent reduction), while the error for the basal area model was reduced from 1.88 to 1.25 $m^2\ ha^{-1}$ (34 percent reduction). Bias (MD) was reduced 67 percent for dominant height and 78 percent for basal area. The RMSE for mortality did not differ between the systems [46.04 trees per hectare (TPH)] and the average bias was 0.83 TPH. Ramirez and others (2023) showed that mortality was not affected by bedding and vegetation control, but that the inclusion of fusiform rust was crucial to describe the survival trajectories. An additional comparison was then made for the mortality component by fitting the same model but excluding the fusiform rust information [i.e., model from equation (3) with $\alpha_1 = 0$]. When fusiform rust was not included into the model, the average error (RMSE) increased from 46.04 to 77.53 TPH and the bias changed from 0.83 to -0.43 TPH. Given these results, system 2 was selected as the best growth and yield system and therefore, the results presented in this section refer to this system.

Parameter estimates and fit statistics for each of the components of system 2 are presented in tables 3 and 4, respectively. The estimated values in table 3 correspond to the values obtained with the simultaneous estimation of the global parameters using the multivariate normal in which the correlation between the variables was estimated and the local values per plot

Table 2—Fit statistics for dominant height and basal area models with the two systems proposed

Variable	Growth and yield system	RMSE	MD	MAD
Dominant height (m)	1	0.71	0.03	0.55
	2	0.57	0.01	0.45
Basal area ($m^2 ha^{-1}$)	1	1.88	0.18	1.48
	2	1.25	0.04	0.94

System 1 is without treatment effects, system 2 is with treatment effects in dominant height and basal area

RMSE = root mean square error; MD = mean difference; MAD = mean absolute difference.

were taken from the independent estimation. To test for the effect of modeling the correlation between the variables, the same model was fitted assuming zero correlation between the errors of the variables. With this model, which simulated independent estimation of each variable in the model, parameter estimates were not different for the dominant height model but differed for the mortality and basal area models. When comparing the estimated values of the standard error of the parameters, no differences were found for the dominant height model and opposite trends were found for the other two variables, with an increase in the standard error for the mortality parameters, but a decrease in the standard error for the basal area parameters when including correlation. Despite these

Table 3—Parameter estimates for the best growth and yield system for slash pine

Variable	Parameter	Estimated value	Standard error
Dominant height (m)	μ	0.3737	0.0042
	K	0.1128	0.0010
	b_1	0.9178	0.0020
	b^2	1.1057	0.0019
Mortality (trees per ha)	α_0	-0.0151	0.0026
	α_1	-0.3596	0.0571
	δ	-0.6292	0.0674
Basal area (m^2ha^{-1})	β_1	10.4090	0.3921
	β_2	-0.2776	0.0097
	β_3	-1.4977	0.0649
	β_4	1.5512	0.0183
	δ_1	0.8747	0.0024
	δ_2	0.7449	0.0021
Variance-covariance matrix (Σ)	$\ln(\sigma_H)$	-0.5556	0.0290
	$\ln(\sigma_N)$	-3.0782	0.0293
	$\ln(\sigma_B)$	0.2253	0.0294
	$\rho_{H\chi N}$	-0.0054	0.0418
	$\rho_{H\chi B}$	0.4408	0.0340
	$\rho_{N\chi B}$	0.4172	0.0354

H = dominant height (m); N = trees per ha; B = basal area (m^2ha^{-1}); t = time in years; Z_1 and Z_2 = dummy variables equal to 1 if bedding or vegetation control was applied, respectively, and zero otherwise; FR = the proportion of trees affected by fusiform rust on a given plot at age 5; and μ_0, K, b_1, b_2, α_0, α_1, δ, β_1, β_2, β_3, β_4, δ_1, δ_2, σ_H, σ_N, σ_B, $\rho_{H\chi N}$, $\rho_{H\chi B}$, and $\rho_{N\chi B}$ = the parameters estimated.

Table 4—Fit statistics for the three variables of the best growth and yield system for slash pine

Variable	Fit statistic	Value with correlation	Value without correlation
Dominant height (m)	RMSE	0.57	0.57
	MD	0.01	0.00
	MAD	0.45	0.45
Mortality (trees per ha)	RMSE	46.04	45.67
	MD	0.83	-0.14
	MAD	32.85	32.64
Basal area (m^2ha^{-1})	RMSE	1.25	1.24
	MD	0.04	-0.01
	MAD	0.94	0.94

RMSE = root mean square error; MD = mean difference; MAD = mean absolute difference.

differences, the fit statistics were not significantly different when comparing the systems with and without correlation (table 4).

Although no improvement was obtained in terms of model fit when accounting for correlation, accounting for this value during the estimation procedure is statistically sound and therefore, the estimated parameter values from table 3 were used to plot the predicted trajectories and calculated residuals for the three variables of interest in figure 1. Overall, a good fit was obtained, and the residuals did not show any trend. The small errors and bias observed from the proposed growth and yield system might be the result of using local parameters per plot, which are responsible for the individual curves observed in figure 1. Therefore, the robustness of the proposed system was evaluated by testing how accurate the predictions were when local parameters were not used. This consisted of using only the estimated global parameters from table 3 and utilizing the observed values as starting points for solving the differential equations to predict the trajectories forward. This simulates how the system can be used with a new dataset. Different starting points were tested. For example, the first observation (at age 5) was first used as the starting point to predict the whole series until year 31, then, the second observation (at age 8) was used to predict the values from this age forward (until age 31), and this was repeated until the second to last observation was used to predict

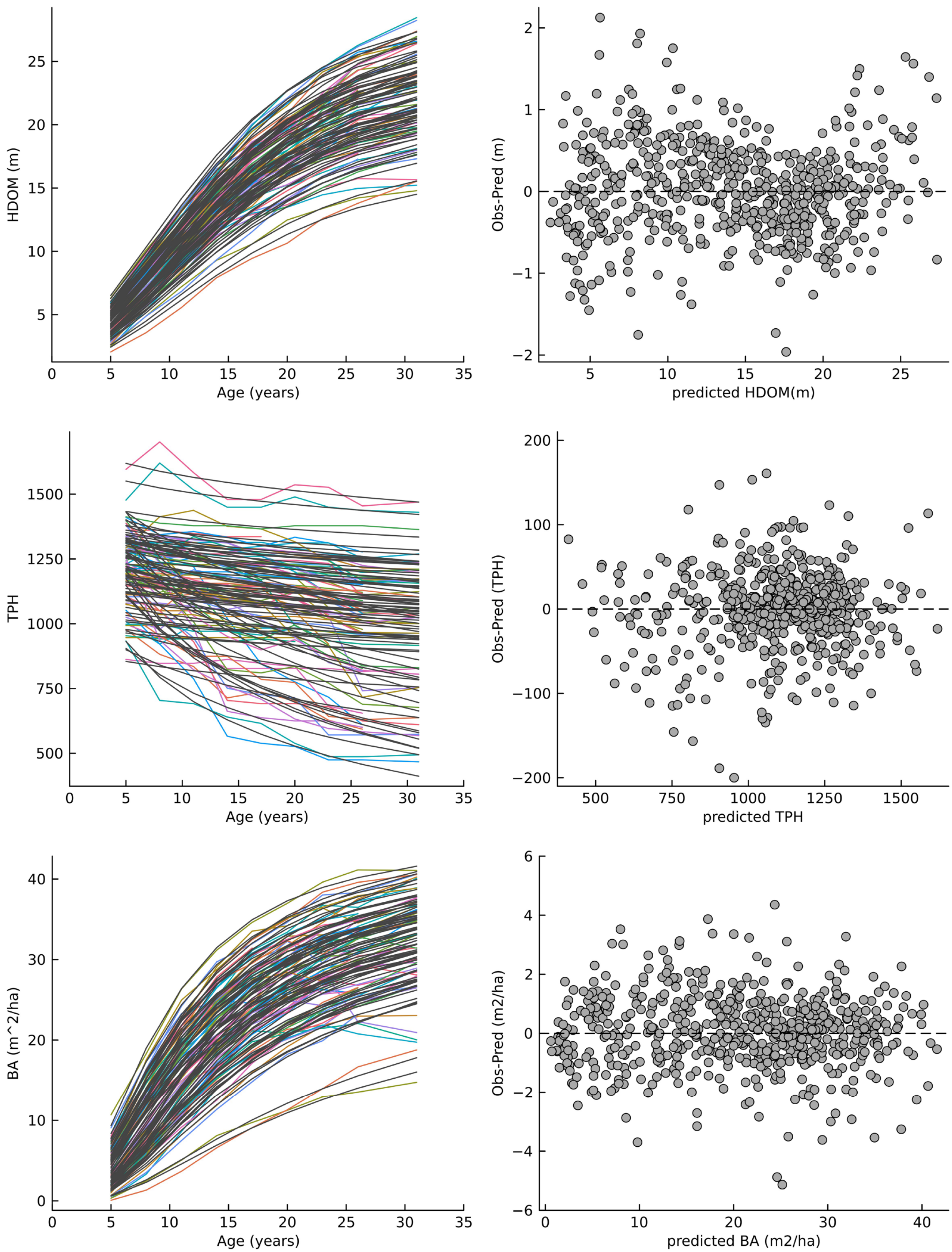

Figure 1—Dominant height (HDOM), mortality (TPH), and basal area (BA) predicted curves and residuals using the best growth and yield system for slash pine.

the last observation. An additional prediction was made when using only the closest point to predict the following observation (e.g., observation at age 5 used to predict observation at age 8, observation at age 8 used to predict observation at age 11, and so on). For these different scenarios, the average error (RMSE) and bias were calculated and the results were summarized in figure 2.

In forestry applications, accuracy and precision decrease when the projection interval increases (Wang and others 2020). This fact was particularly important for the growth and yield system described here given that the differential equations proposed are highly influenced by the starting point of the state variables. This was checked and it is shown in figure 2. In this graph, the average length of the projection interval was plotted against the RMSE and the average bias (MD). Higher errors were obtained when the first observation (at year 5) was used to predict all the points forward (until year 31). This error was reduced when the projection interval was reduced. In figure 2, the red diamond indicates the error obtained when the projection was made using the closest previous observation to predict the current observation; this meant a projection length of 3 years for most of the observations. Although not all possible combinations of projection lengths were used for evaluating the model, it is clear that this system has better performance with short predictions. The RMSE was consistently reduced when the projection length was reduced. No clear trend was observed for bias. Overall, when evaluating the magnitude of the errors, basal area was the most sensitive variable, while mortality was the least affected variable. Results from this analysis are relevant to model users who would want to apply this model for a given projection length.

From the growth and yield system presented, the dominant height and mortality model can be integrated analytically. These two models are presented in equation (10) and equation (11). Nevertheless, the basal area model cannot be integrated analytically and therefore, the differential equation form needs to be used when

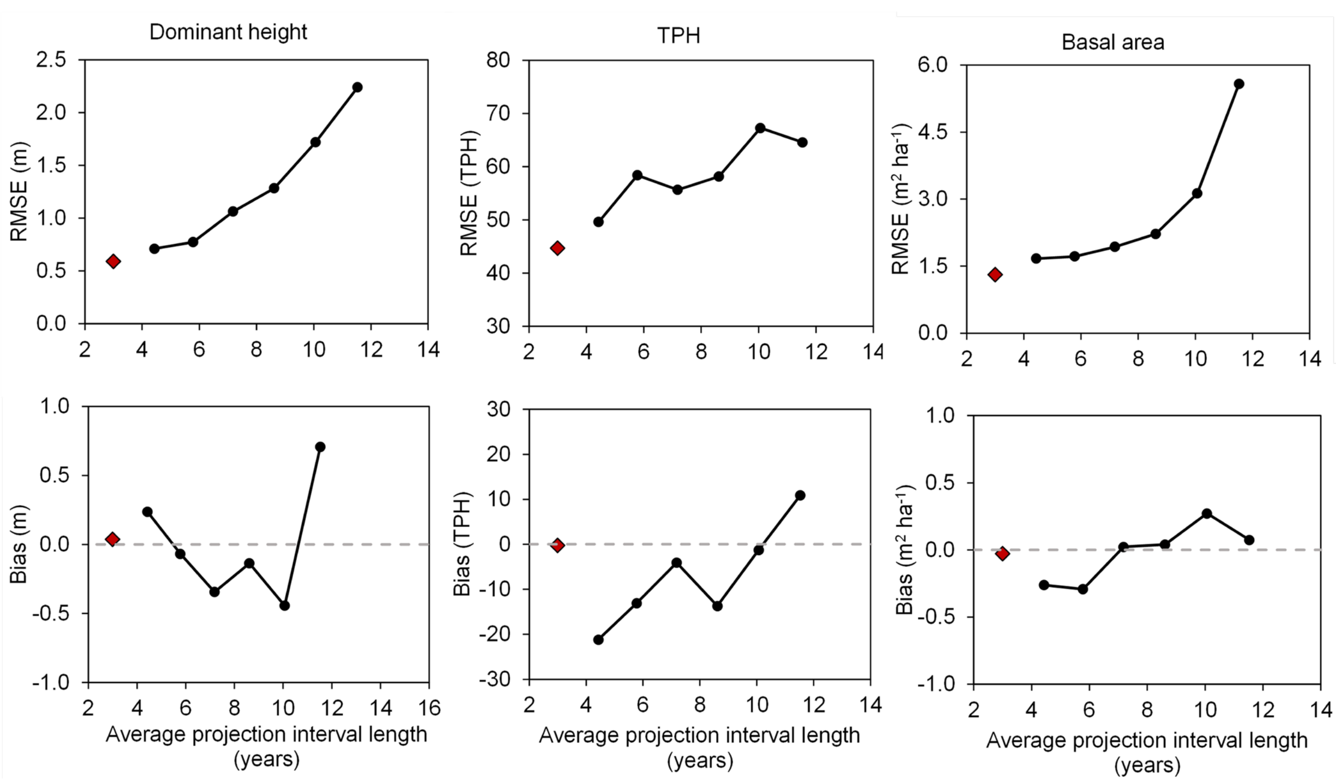

Figure 2—Root mean square error (RMSE) and bias for dominant height (m), mortality (TPH), and basal area (m^2ha^{-1}) when projecting starting from a different age. The red diamond indicates prediction using the immediate previous point to project.

using the model. Therefore, a routine in R (R Core Team 2018) to use the proposed growth and yield system was included as an appendix to this manuscript.

$$H_2 = H_1\ exp\left[\frac{\mu_0 b_1^{Z_1}}{K b_2^{Z_2}}\left(e^{-Kb_2^{Z_2}t_1} - e^{-Kb_2^{Z_2}t_2}\right)\right] \quad (10)$$

$$N_2 = N_1\ exp\left[\frac{\alpha_0 + \alpha_1\ FR}{\delta + 1}\ \left(t_2^{\delta+1} - t_1^{\delta+1}\right)\right] \quad (11)$$

DISCUSSION

In this research, the effect of bedding and vegetation control was successfully incorporated into a growth and yield system for slash pine using parameter modifiers. This technique has been commonly used in forestry models (e.g., Hynynen and others 1998) and has the advantage of incorporating treatment interactions and using both control and treatment plots during the fitting procedure, which avoids assigning all of the variability of the data to the treatment effect, which is the case when treatment effects are incorporated as an additive function to a base model (Gyawali and Burkhart 2015, Logan and Shiver 2006, Mason and Milne 1999, Pienaar and Rheney 1995). Both average error and bias were reduced when treatment modifiers were added to the base growth and yield system, accounting for the treatment effects. These treatments, nevertheless, did not affect mortality as shown in other research by Ramirez and others (2023), and therefore, the system proposed did not include parameter modifiers for this component of the system, although it did include fusiform rust infection rates which showed to improve model fit, reducing both error and bias significantly.

When constructing growth and yield systems for forest stands, it is common to find variables that appear in both the left and right side of the equations, generating an interdependent system of equations that requires simultaneous estimation to get unbiased estimates of the parameters of the system (Borders and Bailey 1986, Goelz and Burk 1996). In addition, the correlation between the errors of the variables should be addressed. Although unbiased estimates of the parameters can be obtained when correlation is present, the standard error of the parameters is not accurate when correlations exist and are not taken into account. The parameters of the system proposed were estimated simultaneously using maximum likelihood and the variance-covariance matrix was estimated for the system, addressing these issues.

Several authors have modelled before the response to silvicultural treatments in growth and yield systems, although without making use of simultaneous estimation (Bailey and others 1989, McTague 2008, Pienaar and Rheney 1995). When including simultaneous estimation, most of the authors have focused on the baseline system, in which silvicultural treatments are not considered (Borders and Bailey 1986, Gallagher and others 2019, Murphy and Sternitzke 1979, Pienaar and Harrison 1989, Sullivan and Clutter 1972). Fewer authors have included both response to silvicultural treatments and simultaneous estimation (Fang and others 2001, Martin and others 1999). To the knowledge of the authors this is the first growth and yield system for slash pine plantations where silvicultural treatments were included using a system of differential equations and simultaneous estimation was used. Nevertheless, accounting for the correlation between the errors of the different components of the system did not improve model fit and although the estimated value for the standard error changed for the mortality and basal area models, this change was not unidirectional.

The use of differential equations generally helps to construct the models when they need to be modified to incorporate treatment effects or the influence of pathogens like fusiform rust infection. This is because it is relatively easy to determine what parameters should be modified according to the treatment being considered. An additional factor that must be considered when using differential equations is how the equation behaves upon different starting values. For the models proposed, a big influence of these values was found because the trajectories of the variable being modeled will highly differ with small variations on the initial value. For these models, the initial starting point defines the asymptote for each one of the curves. For this reason, when using the observed values instead of the predicted values as initial points to solve the differential equation, the errors increased considerably.

Nevertheless, when points closer to the asymptote (later ages) and shorter projection intervals were used, the errors decreased.

CONCLUSIONS

A growth and yield system including dominant height, mortality, and basal area was fitted for slash pine plantations. The effect of bedding and vegetation control was successfully incorporated into dominant height and basal area components by using dummy variables. The average error and bias were reduced when these modifiers were added, compared to base models without these factors. Fusiform rust infection rates were crucial to describe mortality rates. These rates were modeled as a function of the initial infection rate per plot. Dominant height and mortality were used as predictor variables for the basal area model proposed, adding correlation within the system which was addressed by estimating the variance-covariance matrix of the system. The growth and yield system proposed was shown to have lower errors for short projection intervals, and therefore its use is recommended for these intervals.

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APPENDIX: R CODE FOR GROWTH AND YIELD SYSTEM FOR A SINGLE PREDICTION

```
# Loading the packages
library(deSolve)

#---------Estimated parameters----------------
#DH parms
u0 <- 0.3737; K <- 0.1128; b1 <- 0.9178; b2 <- 1.1057
#N parms
a0 <- -0.0151; a1 <- -0.3596; d <- -0.6292;
#BA parms
B1 <- 10.4090; B2 <- -0.2776; B3 <- -1.4977 ; B4 <- 1.5512; d1 <- 0.8747;

d2 <- 0.7449

parms_sys <- c(u0, K, b1, b2, a0, a1, d, B1, B2, B3, B4, d1, d2)

#--------Initial conditions-------------------
hini  <- 3
Nini  <- 1100/1000 #Needs to be divided by 1000
BAini <- 1.5
t1    <- 5
t2    <- 8
FR    <- 0.1
Z1    <- 0.0
Z2    <- 0.0

#--------Define system (differential equations)------
System <- function(t, u, p) {
  h0  <- u[1]
  N0  <- u[2]
  BA0 <- u[3]

  dH <- (h0 * p[1] * p[3]^Z1) * exp(-p[2] * p[4]^Z2 * t)
  dN <- N0 * (p[5] + p[6] * FR) * t^p[7]
  dB <- (p[8] + p[9] * h0 + p[10] * N0)*BA0 / t^p[11]) * p[12]^Z1 * p[13]^Z2

  return(list(c(dH, dN, dB)))
}

#-----Solve the system numerically--------------------
y0    <- c(hini, Nini, BAini)
times <- c(t1,t2)
sol   <- ode(y = y0, times = times, func = System, parms = parms_sys)

#---- extract the values of interest-----------------
HDOM_pred <- sol[2,2]
N_pred    <- sol[2,3] * 1000 #Needs to back transform the variable
BA_pred   <- sol[2,4]
```