Using disaggregation to link individual-tree and whole-stand growth models

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Abstract: Data from 200 plots randomly selected from the Southwide Pine Seed Source Study of loblolly pine (*Pinus taeda* L.) were used to fit whole-stand and individual-tree equations. Another 100 plots, also randomly selected, were used for validation. Outputs from the individual-tree model were then adjusted to match observed stand attributes (number of trees, basal area, and volume per hectare) by four disaggregation methods: proportional yield, proportional growth, constrained least squares, and coefficient adjustment. The first three are existing methods, and the fourth is new. The four methods produced similar results, and the coefficient adjustment was then selected as the method to disaggregate predicted stand growth among trees in the tree list. Results showed that, compared to the unadjusted individual tree model, the adjusted tree model performed much better in predicting stand attributes, while providing comparable predictions of tree diameter, height, and survival probability. The proposed approach showed promise in the ongoing effort to link growth models having different resolutions.

Résumé : Les données de 200 parcelles-échantillons choisies au hasard dans le projet Southwide Seed Source Study sur le pin à encens (*Pinus taeda* L.) ont été utilisées pour dériver des équations aux échelles du peuplement et de l'arbre. Un autre groupe de 100 parcelles, aussi choisies au hasard, ont été utilisées pour la validation. Les extrants du modèle à l'échelle de l'arbre ont ensuite été ajustés pour correspondre aux attributs du peuplement (nombre de tiges, surface terrière et volume à l'hectare) par quatre méthodes de désagrégation : rendement proportionnel, croissance proportionnelle, moindres carrés contraints, et coefficient d'ajustement. Les trois premières méthodes existent et la quatrième est nouvelle. Les quatre méthodes ont produit des résultats similaires et le coefficient d'ajustement a alors été sélectionné comme méthode pour désagréger la croissance prédite à l'échelle du peuplement parmi les arbres dans la liste. Les résultats montrent que, comparativement à un modèle à l'échelle de l'arbre non ajusté, le modèle à l'échelle de l'arbre ajusté est beaucoup plus performant pour la prédiction des attributs du peuplement, tout en fournissant des prédictions comparables du diamètre, de la hauteur et de la probabilité de survie des arbres. L'approche proposée est très prometteuse dans le cadre d'un effort continu pour relier les modèles de croissance ayant différentes résolutions.

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Introduction

Growth and yield models provide information on which forest management decisions are based. These models range from relatively simple, whole-stand models (low resolution) to models that give detailed volume for each tree size class (medium resolution), to complicated individual-tree simulation models (very high resolution). There are advantages and disadvantages to each type of model. Stand-level outputs from individual-tree models and size-class models typically suffer from accumulation of errors and subsequently poor accuracy and precision. On the other hand, outputs from whole-stand models are often better behaved but lack detailed information on forest stand structures.

The parameter-recovery method (e.g., Matney and Sullivan 1982; Baldwin and Feduccia 1987) was an attempt

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to link a whole-stand model to a diameter-distribution model. Clutter and Jones (1980), Pienaar and Harrison (1988), and Nepal and Somers (1992) developed methods to link a stand table projection model to a whole-stand model. Daniels and Burkhart (1988) advocated an integrated system approach, which started with a highly detailed individual-tree model that was collapsed dimensionally to a size-class model, and finally to a whole-stand model.

A method commonly used involved adjusting diameter predictions from individual-tree models such that the resulting stand basal area equaled that predicted by a whole-stand model (Harrison and Daniels 1988; Dhote 1994; Moore et al. 1994; McTague and Stansfield 1994, 1995; Ritchie and Hann 1997a). Another approach dealt with constraining volume growth of individual trees (Dahms 1983; Zhang et al. 1993). Ritchie and Hann (1997b) wrote an excellent review of the disaggregative approach, in which information obtained from an individual-tree model is used to disaggregate stand growth (which is predicted by a whole-stand model) among trees in the tree list. The result is a bridge between whole-stand and individual-tree simulators.

The objective of this study was to develop a new method to link a whole-stand model to an individual-tree model by adjusting coefficients of the tree growth model such that the resulting stand outputs match those predicted from the whole-stand model.

Data

Data used in this study were from the Southwide Pine Seed Source Study, which included 15 seed sources of loblolly pine (*Pinus taeda* L.) planted at 13 locations across 10 southern states (Wells and Wakeley 1966). Seedlings were planted at 1.8 m × 1.8 m spacing. Each plot of 0.0164 ha consisted of 49 trees. Tree diameter and height were measured at ages 10, 15 or 16, 20 or 22, and 25 or 27 years.

A subset, consisting of 200 plots, was randomly selected from the original data as the fit data set, to be used for fitting the models. Furthermore, only one growth period was randomly chosen from each plot. The fit data set therefore consisted mostly of 5-year growing periods (160 plots), with some intervals of 4 years (23 plots), 6 years (4 plots), and 7 years (13 plots).

The validation data sets were formed by randomly selecting 100 plots from the remaining data. All possible growth periods (e.g., 10–15, 10–20, 10–25, 15–20, 15–25, and 20–25 years) from these plots were used to evaluate the models, resulting in a total of 600 plot observations. Summary statistics for the fit and validation data sets are presented in Table 1.

Since both the fit and validation data were randomly selected from the original data, variations due to seed source planting location interactions were assumed to be negligible in view of the performance of the growth models.

Methods

Height–age relationship

Site quality, as defined by either site index or current stand height (average height of dominant and codominant trees), has played an important role in predicting forest growth and yield. The following height–age equation form (Bailey and Clutter 1974) was used for predicting growth of stand height:

$$[1] \qquad H_{t+q} = \exp\{\lambda_1 + [\ln(H_t) - \lambda_1](A_{t+q}/A_t)^{\lambda_2}\} + \varepsilon$$

where

H_t and H_{t+q} are stand height at ages A_t and A_{t+q}, respectively;

t is a subscript denoting age at the beginning of the growth period;

q is length of the growing period;

A_t and A_{t+q} are age at the beginning and at the end of the growth period, respectively;

λ_h are regression parameters; and

ε is random error.

Whole-stand model

Models that rely on annual predictions of stand attributes were found to outperform compatible growth and yield models (Ochi and Cao 2003). In this study, the whole-stand growth model was based on annual projections of stand survival, basal area, and volume in a recursive manner as follows:

Year ($t + 1$)

$$[2a.1] \quad N_{t+1} = \frac{N_t}{\{\eta_1 + \exp(\eta_2 + \eta_3 RS_t + \eta_4 H_t + \eta_5 N_t/A_t + \eta_6/A_t)\}}$$

$$[2b.1] \quad B_{t+1} = \exp\{\ln B_t[1 + \exp(\theta_1 + \theta_2 RS_t + \theta_3 A_t \ln N_t)]\}$$

$$[2c.1] \quad V_{t+1} = \exp\{\ln V_t[1 + \exp(\kappa_1 + \kappa_2 RS_t + \kappa_3 \ln B_t + \kappa_4 A_t)]\}$$

Year ($t + q$)

$$[2a.q] \quad N_{t+q} = \frac{N_{t+q-1}}{\{\eta_1 + \exp(\eta_2 + \eta_3 RS_{t+q-1} + \eta_4 H_{t+q-1} + \eta_5 N_{t+q-1}/A_{t+q-1} + \eta_6/A_{t+q-1})\}} + \varepsilon$$

$$[2b.q] \quad B_{t+q} = \exp\{\ln(B_{t+q-1})[1 + \exp(\theta_1 + \theta_2 RS_{t+q-1} + \theta_3 A_{t+q-1} \ln(N_{t+q-1}))]\} + \varepsilon$$

$$[2c.q] \quad V_{t+q} = \exp\{\ln(V_{t+q-1})[1 + \exp(\kappa_1 + \kappa_2 RS_{t+q-1} + \kappa_3 \ln(B_{t+q-1}) + \kappa_4 A_{t+q-1})]\} + \varepsilon$$

where

N_j is number of trees per hectare at age A_j; $j = t, t+1, \ldots, t+q$;

B_j is stand basal area (in m²/ha) at age A_j;

V_j is stand volume (in m³/ha) at age A_j;

$RS_j = \dfrac{\sqrt{10000/N_j}}{H_j}$ is relative spacing at age A_j; and

η_h, θ_h, and κ_h are regression parameters.

The seemingly unrelated regression (SUR) method suggested by Borders (1989) was used to simultaneously estimate the parameters of the system of equations at the end of the growth period (eqs. 2*a*.*q*, 2*b*.*q*, and 2*c*.*q*). Variation of the period length (between 4 and 7 years) might affect the variances of the error terms, but this problem was assumed to be negligible in this study.

Table 1. Means (standard deviations in parentheses) of stand- and tree-level attributes, by data type and age.

Age (years)	No. of sample plots	No. of trees/ha	Basal area (m²/ha)	No. of sample trees	Tree diameter (cm)	Tree total height (m)
Fit data set[a]						
10	67	2258 (488)	21.13 (6.95)	2480	11.1 (2.9)	8.0 (1.7)
15	44	1765 (506)	30.52 (5.75)	1273	14.3 (3.9)	11.6 (2.2)
16	23	1270 (159)	29.81 (3.65)	479	16.9 (3.8)	14.8 (2.0)
20	54	1114 (425)	28.68 (8.01)	986	17.6 (4.2)	15.1 (2.5)
22	12	890 (173)	19.58 (4.78)	175	16.4 (3.5)	14.1 (1.9)
25	43	1023 (415)	31.77 (10.06)	721	19.3 (4.6)	17.4 (2.9)
27	23	793 (175)	28.58 (6.45)	299	20.9 (4.8)	17.1 (3.2)
Validation data set[b]						
10	100	2071 (437)	22.13 (6.12)	10182	11.2 (3.3)	8.1 (1.9)
15	86	1735 (463)	30.66 (6.20)	4892	14.5 (3.9)	11.8 (2.4)
16	14	1273 (194)	29.89 (3.25)	584	16.8 (4.0)	14.7 (2.2)
20	95	1301 (323)	35.23 (7.70)	2025	18.1 (4.3)	15.8 (2.6)
22	5	952 (119)	19.11 (8.23)	78	15.3 (4.6)	12.8 (2.5)
25	72	1208 (328)	40.35 (9.31)	4275	20.1 (4.8)	18.1 (3.0)
27	28	795 (201)	32.35 (6.82)	1095	22.1 (5.6)	18.9 (3.6)

[a]The fit data set consisted of 200 plots. Growth periods (one randomly selected per plot) spanned from 10 to 15 or 16 years (67 plots), 15 to 20 or 22 years (44 plots), 16–20 years (23 plots), 20 to 25 or 27 years (54 plots), and 22–27 years (12 plots).

[b]The validation data set consisted of 100 plots. All possible growth periods from each plot resulted in a total of 600 observations: 4–7 years (300), 10–12 years (200), and 15–17 years (100).

Individual-tree model

The individual-tree model employed the same approach used by Cao's (2002) model, which consisted of a system of inter-relating equations to predict annual tree survival, diameter growth, and height growth in a recursive manner.

Year $(t + 1)$

$$[3a.1] \quad P_{i,t+1} = \frac{1}{\{1 + \exp[\alpha_1 + \alpha_2 H_t + \alpha_3(d_{i,t}/\mathrm{Dq}_t)]\}}$$

$$[3b.1] \quad d_{i,t+1} = d_{i,t}\{1 + \exp[\beta_1 + \beta_2 \ln B_t + \beta_3 A_t + \beta_4 \ln H_t + \beta_5(d_{i,t}/\mathrm{Dq}_t) + \beta_6 \ln h_t]\}$$

$$[3c.1] \quad h_{i,t+1} = h_{i,t}\{1 + \exp[\gamma_1 + \gamma_2 \ln B_t + \gamma_3 A_t + \gamma_4 \ln H_t + \gamma_5(d_{i,t}/\mathrm{Dq}_t) + \gamma_6(h_{i,t}/H_t) + \gamma_7 \ln d_t]\}$$

Year $(t + q)$

$$[3a.q] \quad P_{i,t+q} = \frac{P_{i,t+q-1}}{\{1 + \exp[\alpha_1 + \alpha_2 H_{t+q-1} + \alpha_3(d_{i,t+q-1}/\mathrm{Dq}_{t+q-1})]\}}$$

$$[3b.q] \quad d_{i,t+q} = d_{i,t+q-1}\{1 + \exp[\beta_1 + \beta_2 \ln(B_{t+q-1}) + \beta_3 A_{t+q-1} + \beta_4 \ln(H_{t+q-1}) + \beta_5(d_{i,t+q-1}/\mathrm{Dq}_{t+q-1}) + \beta_6 \ln(h_{t+q-1})]\} + \varepsilon$$

$$[3c.q] \quad h_{i,t+q} = h_{i,t+q-1}\{1 + \exp[\gamma_1 + \gamma_2 \ln(B_{t+q-1}) + \gamma_3 A_{t+q-1} + \gamma_4 \ln(H_{t+q-1}) + \gamma_5(d_{i,t+q-1}/\mathrm{Dq}_{t+q-1}) + \gamma_6 \ln(h_{t+q-1}/H_t) + \gamma_7 \ln(d_{t+q-1})]\} + \varepsilon$$

where

$p_{i,j}$ is the probability that tree i is alive at age A_j; $j = t, t+1, …, t+q$;

$d_{i,j}$ is diameter (in cm) of tree i at age A_j;

$h_{i,j}$ is total height (in m) of tree i at age A_j;

Dq_j is quadratic mean diameter (in cm) at age A_j;

α_h, β_h, and γ_h are regression parameters; and

ε is random error.

Parameters of the tree diameter and height growth equations were simultaneously estimated using SUR as in the whole-stand model. Maximum likelihood estimation of parameters of the tree survival equation was obtained by use of weighted nonlinear regression, as shown by Walker and Duncan (1967).

Linking models using disaggregation

This study considered four methods to link an individual-tree model and a whole-stand model such that the stand outputs from the individual-tree model match those predicted from the whole-stand model.

Proportional yield method

In this method, the adjusted survival probability, diameter, and total height of tree i at the end of the growing period ($\tilde{P}_{i,t+q}$, $\tilde{d}_{i,t+q}$, and $\tilde{h}_{i,t+q}$, respectively) were proportional to the respective survival probability, diameter, and total height predicted from eqs. 3a.q to 3c.q ($\hat{P}_{i,t+q}$, $\hat{d}_{i,t+q}$, and $\hat{h}_{i,t+q}$, respectively):

$$[4a] \quad \tilde{P}_{i,t+q} = \hat{P}_{i,t+q} \left(\frac{sN_{t+q}}{\sum_j \hat{P}_{i,t+q}} \right)$$

$$[4b] \quad \tilde{d}_{i,t+q}^2 = \hat{d}_{i,t+q}^2 \left[\frac{sB_{t+q}/K}{\sum_j (\hat{P}_{j,t+q}\ \hat{d}_{j,t+q}^2)} \right]$$

$$[4c] \quad \tilde{h}_{i,t+q}^2 = \hat{h}_{i,t+q} \left[\frac{s(V_{t+q} - aN_{t+q})}{b\sum_j (\hat{P}_{j,t+q}\ \hat{d}_{j,t+q}^2\ \hat{h}_{j,t+q})} \right]$$

where

s is plot size in hectares; K is $\pi/40\,000$ (to convert diameter in centimetres to basal area in metres squared); and a and b are coefficients in the tree volume equation $v = a + bd^2h$, and the sum includes all trees in the plot (these trees are identified by subscript j).

McTague and Stansfield (1994, 1995) used an equation similar to eq. 4b to constrain tree basal area. Even though the formulas are different, the proportional yield concept has been frequently applied in the past to adjust tree basal area (Clutter and Allison 1974; Clutter and Jones 1980; Pienaar and Harrison 1988; Somers and Nepal 1994).

Proportional growth method

Research has been carried out to disaggregate stand-level growth to individual trees for diameter (Leary et al. 1979), basal area (Campbell et al. 1979; Moore et al. 1994), and volume (Dahms 1983; Zhang et al. 1993).

In this study, tree survival probability was adjusted based on the ratio of dead and alive probabilities as follows:

$$[5a] \quad \frac{1 - \tilde{P}_{i+t+q}}{\tilde{P}_{i+t+q}} = m_p \left(\frac{1 - \hat{P}_{i+t+q}}{\hat{P}_{i+t+q}} \right) \text{ or}$$

$$\tilde{P}_{i,t+q} = \frac{\hat{P}_{i,t+q}}{\hat{P}_{i,t+q} + m_p(1 - \hat{P}_{i,t+q})}$$

where m_p was iteratively solved such that $\sum_j \tilde{P}_{j,t+q} = sN_{t+q}$.

The adjusted squared diameter growth of each tree was proportional to the predicted squared diameter growth:

$$[5b] \quad \tilde{d}_{i,t+q}^2 = d_{i,t}^2 + m_d(\hat{d}_{i,t+q}^2 - d_{i,t}^2)$$

where

$$m_d = \frac{(sB_{t+q}/K) - \sum_j (\tilde{P}_{j,t+q}\ d_{j,t}^2)}{\sum_j (\tilde{P}_{j,t+q}\ [\hat{d}_{j,t+q}^2 - d_{j,t}^2])}$$

The height growth of each tree was adjusted in the same manner:

$$[5c] \quad \tilde{h}_{i,t+q} = h_{i,t}$$
$$+ \left[\frac{s(V_{t+q} - aN_{t+q}) - b\sum_j (\tilde{P}_{j,t+q}\ \tilde{d}_{j,t+q}^2\ h_{j,t})}{b\sum_j (\tilde{P}_{j,t+q}\ \tilde{d}_{j,t+q}^2\ [\hat{h}_{j,t+q} - h_{j,t}])} \right]$$
$$\times (\hat{h}_{i,t+q} - h_{i,t})$$

Constrained least squares method

The constrained least squares (LS) procedure (Matney et al. 1990; Cao and Baldwin 1999) was applied to adjust tree survival probability by minimizing $\sum_j (\tilde{P}_{j,t+q} - \hat{P}_{j,t+q})^2$, subject to $\sum_j \tilde{P}_{i,t+q} = sN_{t+q}$. Using Lagrange multiplier method to solve this problem yields

$$[6a] \quad \tilde{P}_{i,t+q} = \frac{\hat{P}_{i,t+q} - (\sum_j \hat{P}_{j,t+q} - sN_{t+q})}{n}$$

where n is number of trees in the plot.

Future tree diameter was adjusted by minimizing $\sum_j (\tilde{d}_{j,t+q}^2 - \hat{d}_{j,t+q}^2)^2$, subject to $K\sum_j \tilde{P}_{j,t+q}\ d_{j,t+q}^2 = sB_{t+q}$. This results in

$$[6b] \quad \tilde{d}_{i,t+q}^2 = \hat{d}_{i,t+q}^2 - P_i \left[\frac{\sum_j (\tilde{P}_{j,t+q}\ \hat{d}_{j,t+q}^2) - sB_{t+q}/K}{\sum_j \tilde{P}_{j,t+q}^2} \right]$$

Similarly, by minimizing $\sum_j (\tilde{h}_{j,t+q} - \hat{h}_{j,t+q})^2$ subject to $\sum_j \tilde{P}_{j,t+q}(a + b\tilde{d}_{j,t+q}^2\ \tilde{h}_{j,t+q}) = sV_{t+q}$, future tree height was adjusted as follows:

$$[6c] \quad \tilde{h}_{i,t+q} = \hat{h}_{i,t+q} - \tilde{P}_{i,t+q}\ \tilde{d}_{i,t+q}^2$$
$$\times \left[\frac{\sum_j (\tilde{P}_{j,t+q}\ \tilde{d}_{j,t+q}^2\ \hat{h}_{j,t+q}) + s(aN_{t+q} - V_{t+q})/b}{\sum_j (P_{j,t+q}^2\ \tilde{d}_{j,t+q}^4)} \right]$$

Coefficient adjustment method

An adjusting coefficient (m_p) was added to modify coefficient α_3 of the tree survival model:

$$[7a] \quad P_{i,t+1} = \frac{P_{i,t}}{\{1 + \exp[\alpha_1 + \alpha_2 H_t + \alpha_3 m_p(d_{i,t}/\mathrm{Dq}_t)]\}}$$

The goal was for eq. 7a to produce the same total number of trees per hectare as predicted by the stand survival model. Similarly, other adjusting coefficients (m_d and m_h) were added to the tree diameter and height growth equations, respectively, to ensure that the resulting stand basal area and volume predictions were identical to those produced by the whole-stand model:

$$[7b] \quad d_{i,t+1} = d_{i,t}\{1 + \exp[\beta_1 + \beta_2 \ln B_t + \beta_3 A_t + \beta_4 \ln H_t + \beta_5 m_d(d_{i,t}/\mathrm{Dq}_t) + \beta_6 \ln h_t]\} + \varepsilon$$

$$[7c] \quad h_{i,t+1} = h_{i,t}\{1 + \exp[\gamma_1 + \gamma_2 \ln B_t + \gamma_3 A_t + \gamma_4 \ln H_t + \gamma_5 m_h(d_{i,t}/\mathrm{Dq}_t) + \gamma_6(h_{i,t}/H_t) + \gamma_7 \ln d_t]\} + \varepsilon$$

The three adjusting coefficients were then simultaneously solved for each plot–age combination using the SAS procedure MODEL (SAS Institute Inc. 2000). Other methods involving adjusting various combinations of coefficients in eqs. 7a–7c were explored and they all yielded similar results. The set of coefficients that were finally selected for adjustment (α_3, β_5, and γ_5) involved variable ($d_{i,t}/\mathrm{Dq}_t$), because we think it makes intuitive sense that the adjustment amount should depend on the tree size.

Results

The parameter estimates and their standard errors for the equations that form the whole-stand and individual-tree models are presented in Table 2. Outputs from the individual-tree model were then adjusted by each of the four disaggregation methods to match observed number of trees, basal area, and volume per hectare. Observed rather than predicted stand attributes were used in this step so that the resulting statistics (Table 3) enabled a fair evaluation that did not depend on how well the whole-stand model performed.

It is apparent that the four disaggregation methods produced similar results, but the proportional growth and coefficient adjustment methods were slightly better than the rest of the methods. These two methods consistently ranked either first or second in predicting tree diameter, height, and survival probability in terms of the mean difference between observed and predicted values, mean absolute difference, fit index (analogous to R^2 in a regression), and log-likelihood values. For the rest of the study, the coefficient adjustment approach was selected as the method to disaggregate predicted stand growth among trees in the tree list.

The individual-tree model was then evaluated against the whole-stand model based on predictions of stand attributes in terms of number of trees, basal area, and volume per hectare (Table 4). Without exception, the whole-stand model produced better evaluation statistics, higher fit index, and smaller values of mean difference and mean absolute difference than did the individual-tree model.

Because stand attributes were more reliably predicted by whole-stand models, it is logical to adjust or constrain individual-tree models to match these predicted stand attributes. Table 5 shows how the unadjusted individual-tree model compares against the adjusted model in tree-level evaluations. For short-term projections, the adjusted tree model predicted tree diameter and survival probability better than did the unadjusted model, whereas the reverse was true for

Table 2. Estimates and standard errors (SE) of parameters in whole-stand and individual-tree equations.

Equation	Parameter	Estimate	SE
1	λ_1	4.1962	0.1731
	λ_2	–0.5246	0.0586
2a	η_1	1.0241	0.0031
	η_2	72.6433	25.5892
	η_3	–211.7320	74.7250
	η_4	–2.7617	0.9250
	η_5	–0.1447	0.0541
	η_6	243.3647	97.9521
2b	θ_1	–3.8339	0.2771
	θ_2	7.5228	0.6093
	θ_3	–0.0189	0.0019
2c	κ_1	–4.9844	0.2863
	κ_2	7.5291	0.4973
	κ_3	0.2571	0.0553
	κ_4	–0.0892	0.0044
3a	α_1	0.6971	0.2063
	α_2	–5.0433	0.1846
	α_3	0.0357	0.0112
3b	β_1	1.0073	0.1234
	β_2	–0.4235	0.0260
	β_3	–0.0526	0.0033
	β_4	–2.2287	0.1257
	β_5	–0.2236	0.0480
	β_6	1.5496	0.1066
3c	γ_1	1.9712	0.1204
	γ_2	–0.1384	0.0261
	γ_3	–0.0447	0.0029
	γ_4	–1.7456	0.0690
	γ_5	–0.2578	0.0757
	γ_6	–1.7763	0.1172
	γ_7	0.9610	0.0697

tree height, based on all evaluation statistics. For medium and long projection lengths, the adjusted tree model produced better evaluation statistics in predicting tree diameter (six of six) and tree survival probability (four of six), but did not fare as well in predicting tree height (two of six). The adjustment did not improve tree height projection, perhaps because it was made to match stand volume instead of aiming directly for tree height. It should be noted that in most cases, the evaluation statistics from the two models were very close in value; the maximum difference in the mean absolute difference was 0.1 cm for tree diameter, 0.11 m for tree height, and 0.004 for tree survival probability.

Values of the adjusting coefficients, m_p, m_d, and m_h, varied for each plot–age combination; their summary statistics are shown in Table 6. We also tried to carry out the adjustment at the end of each year instead of at the end of a growth period, but we found that annual adjustments did not improve the performance of the adjusted tree model.

Table 3. Evaluation statistics for the validation data set from four methods that adjusted outputs from the individual-tree model to match observed number of trees, basal area, and volume per hectare.

Evaluation statistic	Method			
	Proportional yield	Proportional growth	Constrained least squares	Coefficient adjustment
Tree diameter (cm)				
Short projection				
MD	–0.27	**–0.13**	–0.21	–0.18
MAD	0.92	**0.87**	0.93	**0.87**
FI	**0.94**	**0.94**	**0.94**	**0.94**
Medium projection				
MD	–0.43	**–0.13**	–0.28	–0.22
MAD	1.58	**1.49**	1.56	**1.49**
FI	0.82	**0.84**	0.82	**0.84**
Long projection				
MD	–0.41	**–0.08**	–0.21	–0.14
MAD	2.23	2.13	2.22	**2.12**
FI	0.67	**0.71**	0.68	**0.71**
Tree height (m)				
Short projection				
MD	–0.15	**–0.11**	–0.12	**–0.11**
MAD	0.71	**0.70**	0.73	**0.70**
FI	0.93	**0.94**	0.93	**0.94**
Medium projection				
MD	–0.22	**–0.15**	–0.16	**–0.15**
MAD	0.94	**0.92**	0.97	**0.92**
FI	0.84	**0.85**	0.83	**0.85**
Long projection				
MD	–0.22	**–0.13**	–0.15	–0.14
MAD	1.16	**1.15**	1.24	**1.15**
FI	0.76	**0.77**	0.73	**0.77**
Tree survival probability				
Short projection				
MD	**0.000**	**0.000**	**0.000**	**0.000**
MAD	0.215	0.213	0.212	**0.204**
$-2\ln(L)$	5355	**4967**	5191	5038
Medium projection				
MD	**0.000**	**0.000**	**0.000**	**0.000**
MAD	0.310	0.299	0.300	**0.292**
$-2\ln(L)$	5716	**5206**	5462	5346
Long projection				
MD	**0.000**	**0.000**	**0.000**	**0.000**
MAD	0.327	0.314	0.318	**0.309**
$-2\ln(L)$	3459	**3167**	3244	3176

Note: For each evaluation statistic and projection length, a number in bold denotes the best of the four methods. MD, mean difference between observed and predicted values; MAD, mean absolute difference; L, likelihood function; FI, fit index: $\mathrm{FI} = 1 - \Sigma(y_j - \hat{y}_j)^2 / \Sigma(y_j - \bar{y})^2$, where y_j and $\hat{y}_j$ are observed and predicted values of the jth observation, respectively, and $\bar{y}$ is the mean of y. Short projection: 4–7 years; medium projection: 10–12 years; long projection: 15–17 years.

Discussion

Effects of projection length

The models were developed from growth measurements obtained at short intervals (4–7 years) and were applied to validation data, not only from short intervals, but also from medium (10–12 years) and long (15–17 years) intervals that required extrapolation in growth projection. Results from Table 4 show that the whole-stand model fared much better when extrapolation was necessary. With increasing projection lengths, predictions from the individual-tree model deteriorated more quickly in terms of accuracy and precision as compared to predictions from the whole-stand model. The gap between the two types of models widened as the individual-tree model produced very poor stand-level predictions for projection periods of 15 years or more, as evi-

Table 4. Evaluation statistics computed from the validation data set for the individual-tree and whole-stand models based on stand attributes.

Evaluation statistic	Projection length[a]					
	Short		Medium		Long	
	Individual-tree model	Whole-stand model	Individual-tree model	Whole-stand model	Individual-tree model	Whole-stand model
Stand density (trees/ha)						
MD	−41	**−40**	−116	**−67**	−153	**−92**
MAD	193	**179**	260	**230**	311	**305**
FI	0.70	**0.76**	0.15	**0.33**	−0.14	**0.03**
Stand basal area (m²/ha)						
MD	−1.42	**−0.18**	−4.11	**−0.59**	−7.46	**−0.50**
MAD	4.08	**3.22**	7.81	**4.95**	11.81	**6.76**
FI	0.65	**0.77**	−0.16	**0.52**	−1.49	**0.17**
Stand volume (m³/ha)						
MD	−3.21	**−0.70**	−16.03	**−3.59**	−37.50	**−3.91**
MAD	23.23	**18.67**	45.82	**30.60**	74.84	**50.26**
FI	0.86	**0.90**	0.45	**0.72**	−0.42	**0.29**

Note: For each evaluation statistic and projection length, a number in bold denotes the better of the two methods. MD, mean difference between observed and predicted values; MAD, mean absolute difference; and FI, fit index.
[a]Projection lengths include short (4–7 years), medium (10–12 years), and long (15–17 years).

Table 5. Evaluation statistics at the tree level for the adjusted and unadjusted individual-tree models computed from the validation data set.

Evaluation statistic	Projection length[a]					
	Short		Medium		Long	
	Unadjusted	Adjusted	Unadjusted	Adjusted	Unadjusted	Adjusted
Tree diameter (cm)						
MD	−0.44	**−0.03**	−0.73	**−0.08**	−0.99	**0.31**
MAD	1.04	**1.03**	1.77	**1.75**	2.60	**2.50**
FI	0.92	**0.93**	0.76	**0.78**	0.55	**0.58**
Tree height (m)						
MD	**0.05**	−0.10	0.20	**−0.19**	0.32	**−0.13**
MAD	**0.92**	0.93	**1.29**	1.31	**1.67**	1.78
FI	**0.90**	0.89	**0.72**	0.70	**0.52**	0.42
Tree survival probability						
MD	−0.021	**−0.024**	−0.062	**−0.036**	−0.074	**−0.044**
MAD	0.233	**0.229**	0.322	0.326	**0.349**	0.353
−2ln(L)	6483	**6409**	6556	**6400**	3953	**3815**

Note: For each evaluation statistic and projection length, a number in bold denotes the better of the two methods. MD, mean difference between observed and predicted values; MAD, mean absolute difference; FI, fit index (analogous to R^2); L, likelihood function. Unadjusted, unadjusted individual-tree model; adjusted, individual-tree model modified using the coefficient adjustment method.
[a]Projection lengths include short (4–7 years), medium (10–12 years), and long (15–17 years).

Table 6. Summary statistics for the three adjusting coefficients.

Statistic	m_p	m_d	m_h
Mean	1.05	1.69	0.74
Standard deviation	0.16	0.90	0.56
Min.	0.72	−0.59	−4.36
Max.	2.91	9.18	2.03

denced by the negative fit indices for all stand attributes. A negative fit index value from the individual-tree model indicates that its stand-level predictions were worse than the mean of the stand attribute. Even though individual-tree growth predictions were still reasonable (fit index greater than 0.5) for long projection periods, stand-level measures obtained by summing up these values suffered greatly from cumulative errors. Linking the individual-tree model and the whole-stand model via a disaggregation method in this case makes considerable sense.

Effects of disaggregation on tree-level predictions

The adjusted tree model had its coefficients modified for each plot, and therefore it had the potential to be more flexible than did the unadjusted model, whose coefficients were determined from all plot observations. Since predictions of tree attributes (diameter, height, and survival) were constrained to match predicted stand attributes from the whole-stand model, the performance of the adjusted tree model depended on how close these stand predictions were to the observed values. This point was verified when observed rather than predicted stand attributes were used to constrain the individual-tree model (Table 3).

Table 5 shows that adjusting the tree model to match observed stand values in short projection cases resulted in a decrease in mean absolute difference (MAD) of 16% for tree diameter, 24% for tree height, and 12% for survival probability. For long projection periods, the decreases in MAD were 18%, 31%, and 11%, respectively.

When predicted stand attributes were used to adjust the individual-tree model, the improvements on tree-level predictions were much smaller; MAD values decreased by 1%–4% for tree diameter, 1%–7% for tree height, and 2% to –1% for survival probability.

Conclusions

This study aimed to link two different types of growth models, stand level and tree level, by disaggregating stand survival, basal area, and volume growth to individual trees. The four methods evaluated in this study produced similar results, and the coefficient adjustment was then selected as the method to disaggregate predicted stand growth among trees in the tree list. Results showed that the adjusted tree model combined the best features of whole-stand and individual-tree models. Compared to the unadjusted tree model, the adjusted model performed better in predicting stand attributes in terms of stand density, basal area, and volume, especially for long projection periods. The adjusted model also provided comparable predictions of tree diameter, height, and survival probability. This approach shows promise in the ongoing effort to link growth models having different resolutions.

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