Evaluation of individual-tree and disaggregative prediction methods for Douglas-fir stands in western Oregon[1]

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Abstract: The efficiency of six disaggregative methods and two individual-tree methods was evaluated in terms of their ability to predict 5-year basal area increment for Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco) stands in western Oregon. Models were developed for predicting gross stand basal-area increment and individual-tree diameter increment. In addition, models were developed to disaggregate the active increment prediction methods to the tree level. Passive and active prediction schemes were evaluated for both the tree and stand levels. Generally, the individual-tree approach was superior to the disaggregative approach for prediction of both stand and tree growth. This was less evident, however, when crown ratio was eliminated from the individual-tree models. This suggests that at least some of the disparity between the two is due to the presence of crown ratio in an individual-tree passive aggregation approach. The additive disaggregation approach appeared to be best suited to young stands (less than 50 years of age). The linearity assumption required for this particular model appeared to be violated for older stands with larger trees. Generally, the two whole-stand, gross-growth models used in this study were inferior to the individual-tree method for predicting gross basal area growth for one period.

Résumé : Six modèles qui décomposent la croissance du peuplement et deux modèles de croissance d'arbre sont évalués pour leur capacité à prédire l'accroissement quinquennal en surface terrière des peuplements de Douglas taxifolié (*Pseudotsuga menziesii* (Mirb.) Franco) dans l'Ouest de l'Orégon. Les modèles d'arbre prédisent directement l'accroissement de l'arbre en diamètre alors que les modèles de croissance du peuplement prédisent directement l'accroissement brut du peuplement en surface terriè et len accriamètrarbre llemen de prsive et active sont évalués pour le double niveau de l'arbre et du peuplement. En général, l'approche par arbre est supérieure à celle du peuplement pour prédire la croissance de l'arbre et du peuplement. Néanmoins, cette supériorité s'atténue lorsque la longueur relative du houppier est éliminée des modèles d'arbre. Ce résultat suggère que certaines disparités entre les deux approches sont dues à la présence de la longueur relative du houppier dans les modèles d'arbre à recomposition passive. L'approche de décomposition additive semble la plus adéquate pour les peuplements juvéniles (âgés de moins de 50 ans). L'hypothèse de linéarité requise par cette approche de décomposition ne semble pas aussi valable dans les peuplements plus âgés avec des arbres plus gros. Les deux modèles de peuplement analysés qui font appel à la croissance brute sont inférieurs au modèle d'arbre pour prédire la croissance brute en surface terrière sur une période de temps.

[Traduit par la Rédaction]

Introduction

Stand dynamics can be modeled with a variety of methods, which may be distinguished from one another by their associated levels of resolution (Munro 1973). The differences in levels of resolution associated with contrasting modeling philosophies, however, are often not readily apparent. Whole-stand – disaggregative and individual-tree – distance-independent simulators, although functionally different, are similiar in their ability to produce output of the same resolution. Thus, the functional disparity between these two may be obscured by the unity of apparent resolution. Examples of the whole-stand –

disaggregative models have been described by Dahms (1983), Harrison and Daniels (1988), and Zhang et al. (1993). Individual-tree – distance-independent models include Prognosis (Stage 1973), CACTOS (Wensel et al. 1986), and ORGANON (Hann et al. 1993).

The individual-tree modeling approach is based on growth projections for each individual in a sample of trees that represents the stand, or aggregate. The functional components of the individual-tree approach predict such traits as height growth, diameter growth, probability of mortality, and crown dynamics. These predictions are used to update the sample tree list; stand-level attributes are derived from the aggregate of these predictions. This can be described as a *passive aggregation* scheme (Ijiri 1971). Individual-tree models are capable of simulating stands that are diverse in structure and species composition. Furthermore, because more information is required to run individual-tree models, they have the potential for better predictions because they are based on a more detailed representation of the stand than that employed in whole-stand models.

In contrast, the whole-stand – disaggregative approach makes predictions about the dynamics of the aggregate through *active aggregation*. This is accomplished by modeling

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whole-stand parameters such as gross basal area growth (e.g., Harrison and Daniels 1988) or gross volume growth (e.g., Dahms 1983). Thus, this represents a whole-stand implementation with the added ability to distribute a growth projection among trees in a sample tree list. For some simulators, the step of disaggregating growth is an option based on the resolution of the input data. Up to the point where the disaggregation takes place, the simulator is no different from a traditional whole-stand growth model.

Disaggregative models may be structured so that forecasts can be driven by stand-level attributes alone or with the more complete stand description afforded by a tree list. This is a very attractive feature, as users are not obligated to provide a tree list, but may do so if one is available. If a tree list is maintained, then the disaggregation function is the means by which the stand-growth predictions are linked to tree-level descriptions of the stand.

A disaggregation function may be structured in such a way as to maintain invariance between stand growth and the aggregation of tree growth. That is, if disaggregated growth is summed, the resulting stand growth is equal to the stand-level prediction. Therefore, aggregation of tree values does not affect stand-level prediction of growth. A model built in this manner can be said to maintain a *constrained consistency*, or *invariance* (Ijiri 1971).

Disaggregation functions vary in complexity and in methods for allocating growth. In this paper we attempt to empirically address two questions pertaining to these different methods: (1) Does the disaggregative approach adequately predict growth of individual trees? (2) Which approach best reflects aggregate (stand-level) dynamics? To evaluate these questions, we focus on gross basal area increment for a single, 5-year growth period. The use of multiple growth periods would unnecessarily complicate the analysis by incorporating additional components and design features that vary greatly from one simulator to another and are often an expression of the modeler's unique approach to the problem at hand. Because separate components of simulators do not function independently, we do not want to confound results with other aspects of simulator design.

Data

The data in this study are from 105 Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco) stands in the mid-Willamette Valley of western Oregon. The stands are located on McDonald Forest, which is a research forest of the College of Forestry at Oregon State University. The stands are mainly composed of even-aged, second-growth Douglas-fir, although some stands have a minor component of other conifers, primarily grand fir (*Abies grandis* (Dougl. ex D. Don) Lindl.). Among these stands, King's (1966) site index ranged from 27.4 to 41.5 m (90 to 136 ft) with breast-height base age of 50 years. Stand ages (at breast height) ranged from 26 to 142 years, with breast-height basal area of 2.75 to 62.0 m^2/ha (12 to 270 ft^2/acre).

The sampling methods were described in detail by Hann and Larsen (1991). A grid of points was installed in each stand, at densities ranging from one per acre to one per 5 acres (1 acre = 0.40 ha). At each point on the grid, a nested plot design consisting of a variable-radius plot (basal area factor of 4.59 m^2/ha, or 20 ft^2/acre) for trees > 20.3 cm (8.0 in.), a

0.0071-ha (0.017-acre) plot for trees 10.4–20.3 cm (4.1–8.0 in.), and a 0.0018-ha (0.0044-acre) plot for trees <10.4 cm (4.1 in.) in diameter was installed. All conifers >10.16 cm (4.0 in.) in diameter at breast height (DBH) (1.37 m, 4.5 ft) were bored to obtain past 5-year radial increment. In addition, tree heights, diameters, and crown ratios were measured. These measurements were used to establish stand and tree growth.

Because the measurement of past diameter growth of trees <10.16 cm (4.0 in.) DBH was not consistently obtained across the entire data set, this analysis only considers those trees in the stand with DBH >10.16 cm (4.0 in.). That is, we define stand growth as the growth of trees >10.16 cm (4.0 in.) DBH. While this is not the optimal method for the development of a working simulator, we feel it will not dramatically affect the results of this analysis. For most of these stands, the understory trees <10.16 cm (4.0 in.) are suppressed, many of which are not contributing substantially to stand growth, and are prime candidates for mortality in the near future. For the full implementation of some of the disaggregative approaches discussed in this paper, a more complete range of diameters may be desirable.

Model construction

Gross basal area growth rate function

Two equation forms were chosen for predicting the aggregate of gross basal area growth rate. The first is based on age, King's site index (1966), and stand density index (Reineke 1933). Application of this basal area growth equation does not require any tree-level information beyond DBH to estimate stand basal area and trees per acre. The second equation replaces stand density index with an estimate of crown surface area for the stand. A number of different crown surface area estimation methods were initially applied; the best were those of Biging and Wensel (1990). Since the crown surface area equations are dependent on more individual-tree information, such as height and crown ratio, this equation is limited in application to stands for which such information is available.

We used linear regression and a log transformation of the dependent variable to fit the equations. This transformation was found to provide residuals that appeared to be approximately normally distributed, implying an approximate lognormal distribution for conditional basal area growth. The first gross basal area growth equation is expressed as

$$[1] \quad E(\Delta \mathrm{BA}) = \exp\left[\theta_{01} + \theta_{11}\ln(A) + \theta_{21}\frac{S}{A} + \theta_{31}\ln(\mathrm{SDI})\right]$$

where

$\Delta \mathrm{BA}$ is 5-year aggregate gross basal area growth (m^2/ha)

A is breast-height stand age

S is site index (m)

SDI is stand density index (trees/ha), Reineke (1933)

θ_{ij} are parameters to be estimated

The second aggregate gross basal area growth equation is expressed as

$$[2] \quad E(\Delta \mathrm{BA}) = \exp\left[\theta_{02} + \theta_{12}\ln(A) + \theta_{22}\frac{S}{A} + \theta_{32}\ln(\mathrm{CSA}) + \theta_{42}\,\mathrm{CSA}^2\right]$$

Table 1. Parameter estimates (and standard errors) and residual mean-squared error from the log transformation, linear regression of models [1] and [2].

Model	$\hat{\theta}_0$	$\hat{\theta}_1$	$\hat{\theta}_2$	$\hat{\theta}_3$	$\hat{\theta}_4$	MSE
1	−1.256 001	−0.654 745	0.563 248	0.805 055	—	0.0617
	(0.953)	(0.204)	(0.296)	(0.0646)	—	
2	0.887 219	−0.435 310	0.576 562	0.879 799	−0.000 595 242	0.0434
	(0.810)	(0.166)	(0.249)	(0.0631)	(0.000 220)	

Note: Intercept terms are corrected for log bias with MSE/2 (Flewelling and Pienaar 1981).

where CSA is crown surface area, proportion of unit area, e.g., vertical projection of crowns expressed as a proportion of 1 ha, where crown area is estimated using equations of Biging and Wensel (1990).

A number of variations of [1] and [2] were also investigated, but those presented here provided the lowest mean squared error (MSE). The ordinary least squares (OLS) parameter estimates for [1] and [2] are shown in Table 1. The adjusted R^2 values ($\overline{R}^2$) for these two log–linear fits were 0.74 and 0.82, respectively. In general, we have a predictive equation, $\Psi(Z, \hat{\theta}_j)$, within which expected gross stand basal area increment is expressed as a function of some vector of stand attributes, Z, and a vector of parameter estimates, $\hat{\theta}_j$, $j = 1$ and 2 for models [1] and [2] (Table 1), respectively.

Additive disaggregation function

While a number of approaches have been used in developing a disaggregation function, these generally allocate growth either additively or proportionately. Harrison and Daniels (1988) presented a methodology for the development of a disaggregative simulator that can be used to illustrate an additive disaggregation function

$$[3] \quad \left[\Delta ba_i - \frac{\Psi}{TPH} \right] = \kappa [ba_i - \overline{BA}]$$

where

Δba_i is individual-tree basal area increment of tree i in the aggregate

Ψ is estimated gross basal area growth for trees in the given aggregate

TPH is trees per unit area

ba_i is basal area of tree i in the aggregate

$\overline{BA} = \Sigma_i (ba_i n_i) / TPH$

n_i is number of trees per unit area represented by the subject tree

κ is a parameter to be estimated

This disaggregation function is based on the assumption that tree growth is linearly related to tree size in any given stand. Parameter $\hat{\kappa}$ varies from stand to stand and is expressed as a function of site index and dominant height (H) with the following assumed relationship:

$$[4] \quad E(\hat{\kappa}) = \gamma_1 S^{\gamma_2} \exp(\gamma_3 H)$$

The simplicity of this model is an attractive feature. The allocation function is dynamic. That is, the disaggregation coefficient $\hat{\kappa}$ changes over time with changes in dominant height.

Model [3] is formulated to provide constrained consistency (Ijiri 1971) because the sum of $ba_i - \overline{BA} = 0$. This ensures

Fig. 1. Three selected plots illustrating the relationship between basal area and basal area increment for sampled trees.
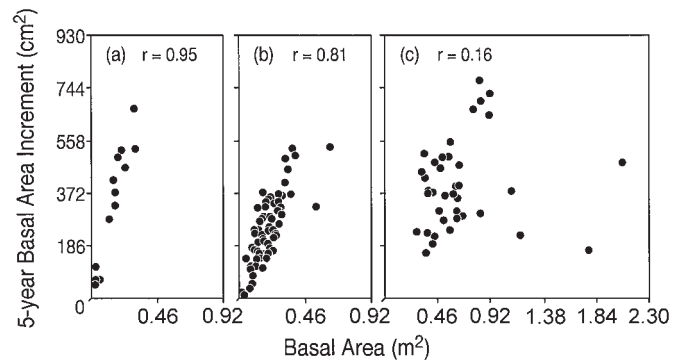
invariance to aggregation of stand-level forecasts. That is, data from a tree list may be aggregated to stand-level statistics prior to initiation of the simulator without affecting predictions of stand growth. In theory, a more generalized model may be developed by adding terms to the disaggregation function, as long as any additional terms also maintain a linear relationship with basal area increment.
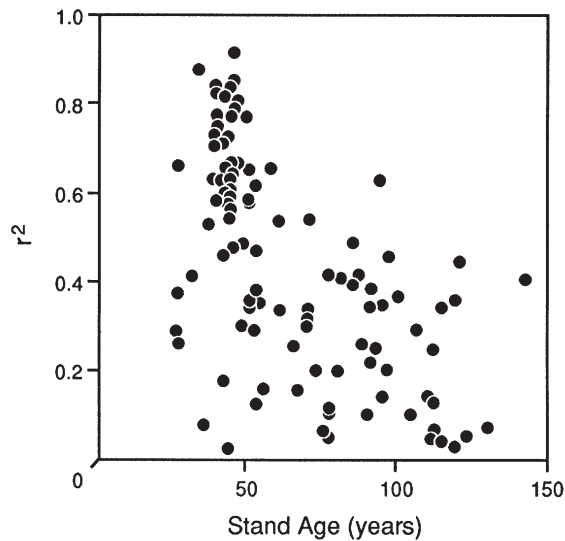
For each of 105 stands, κ_1 was estimated with OLS as the slope of a model that related basal area growth and basal area:

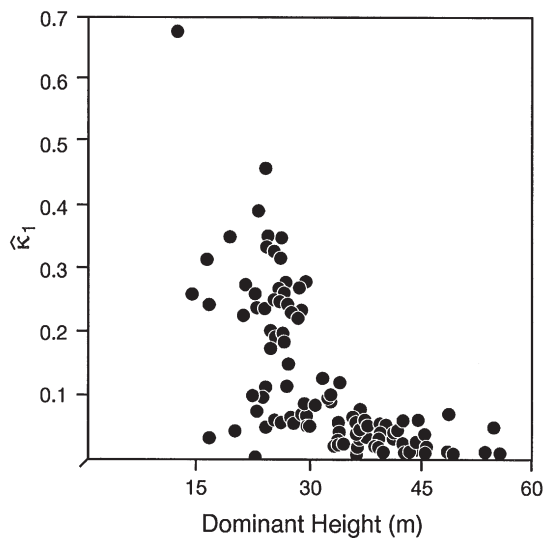$$[5] \quad \Delta ba_{ip} = \kappa_{0p} + \hat{\kappa}_{1p} \, ba_{ip} + \varepsilon_{ip}$$

for tree i in stand p. With OLS, the estimate of the slope term is unaffected by applying a mean correction to the dependent and independent variables. κ_0 is a nuisance parameter. The values obtained for $\hat{\kappa}_{1p}$ ranged from 0.003 89 to 0.678, with a mean of 0.1245. All of these were significantly different from zero; the largest p-value associated with t-tests of the significance of $\hat{\kappa}_{1p}$ (H$_0$: $\kappa_{1p} = 0$) was 0.017, and most were well below 0.001. In terms of linear association between basal area and basal area increment, there is a tremendous range (Fig. 1). The plots in Fig. 1 were selected to cover the range of linear associations between tree growth and tree basal area. In general, the best linear relationships were associated with the youngest stands. Considering the correlation coefficient as an index of the linear association between basal area and basal area increment for each stand, we found some values were as high as 0.95, yet others were less than 0.10. These fits tended to be worse for older stands (Fig. 2), which possibly indicates a shortcoming in predicting tree growth for older stands. This finding was further evaluated by adding a quadratic term to [5].

On all but three of the stands, a quadratic term was significant (p-values less than 0.05), with most p-values for the quadratic

Fig. 2. Indices of fit (r^2) plotted over stand age for the ordinary least squares fit of $\Delta ba_i = \kappa_0 + \kappa_1 ba_i + \varepsilon_i$ for 105 Douglas-fir stands in western Oregon.

Fig. 3. Plot of $\hat{\kappa}_1$ over dominant height for 105 Douglas-fir stands in western Oregon.

Fig. 4. Plot of $\hat{\kappa}_1$ over King's (1966) site index for 105 Douglas-fir stands in western Oregon.

considered a similar model, which employed age instead of dominant height in eq. 4; the dominant height equation, however, provided superior fit statistics. The disaggregation coefficient, $\hat{\kappa}_1$, was negatively correlated with H (Fig. 3). This result met with our expectation that the coefficient may be interpreted as an estimator of the ratio of standard deviations of basal area growth and basal area, that is, $\kappa_1 \cong \sigma_{bag}/\sigma_{ba}$. Since tree basal area is the sum of basal area increment, and the variance of the sum of increments should exceed the variance for any one increment period, we anticipated that κ_1 would be <1.0 and would decrease as stand age (or dominant height) increased. The values of $\hat{\kappa}_1$ did vary from 0.003 89 to 0.678; the largest value was somewhat of an outlier, as all but three estimates were below 0.40.

There was a weak relationship between site index and $\hat{\kappa}_1$ (Fig. 4). This relationship was not as well defined as that between $\hat{\kappa}_1$ and H. Three-dimensional graphical analysis of this data did not reveal any other trends, which may have been hidden when dominant height and site index were viewed independently.

A function may be developed by obtaining estimates for the parameters [γ_1, γ_2, and γ_3] in [4]. This procedure results in a predictive system that is sensitive to stand age and site productivity. Because dominant height in the disaggregation function and stand age in the gross-growth function are both even aged stand concepts, the application of this system to stands that are not even aged is inappropriate. The values of $\hat{\kappa}_{1p}$ for each of the stands ($p = 1, 2, ..., 105$) were used as the dependent variables in model [4] above. We reparametrized [4] in the following manner:

$$[6] \qquad E(\hat{\kappa}_1) = \exp[\hat{\gamma}_1 + \hat{\gamma}_2 \ln(S) + \hat{\gamma}_3 H]$$

The parameter estimates for model [6] were obtained using weighted nonlinear least squares with a weight of $1/V(\hat{\kappa}_1)$, where $V(\hat{\kappa}_1)$ is the estimated variance of κ_1 from the OLS fit. The results of this regression are shown in Table 2. The unweighted $\bar{R}^2$ is 0.6081. The application of [6] in eq. 3 is then
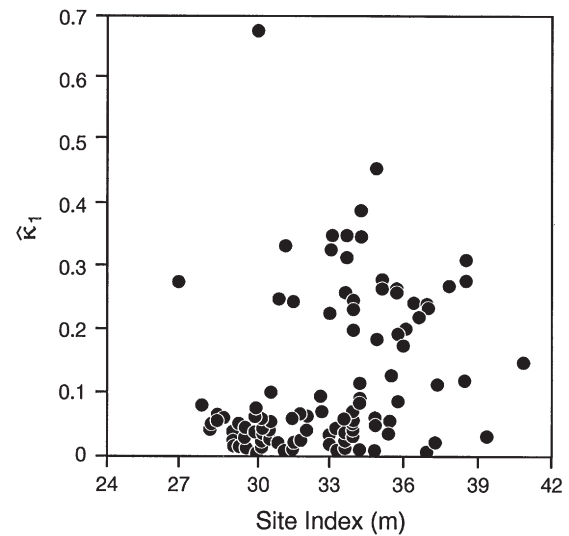
term less than 0.01. This problem was most evident in stands with large trees. Homogeneous young stands did indeed seem to maintain a nearly linear relationship; however, the presence of any large trees formed a positively skewed diameter distribution, which seemed to accentuate the problem of nonlinearity in eq. 5.

The linearity assumption apparently is not as reliable among older stands, where increasing variability in stand structure with stand age results in a more complex relationship between increment and basal area. This within-stand heterogeneity may also reflect changes in management strategies over time. It is not known whether the young stands of today will, in time, develop into the older stands reflected in this data set.

The disaggregation coefficient is predicted for individual stands as a function of dominant height and site index. We also

Table 2. Results of nonlinear regression on disaggregation coefficient, $\hat{\kappa}_1$ in eq. 6.

Parameter	Estimate	Asymptotic standard error
γ_1	−4.300 50	3.214
γ_2	0.977 218	0.866 1
γ_3	−0.018 287	0.009 311

$$[7] \quad \Delta\hat{ba} = \frac{\Psi(Z, \hat{\theta}_1)}{TPH} + \hat{\kappa}_i \{ba - \overline{BA}\}$$

The technique suggested by Harrison and Daniels (1988) for disaggregation is not limited to the simple linear equation expressed above. The model can be generalized by adding additional terms. One possible generalization is the addition of crown ratio to the model

$$[8] \quad \Delta ba_{ip} = \kappa_{0p} + \kappa_{1p}\, ba_{ip} + \kappa_{2p}\, cr_{ip} + \varepsilon_{ip}$$

where cr_{ip} is live crown ratio.

In this formulation the parameter κ_1 can be fit with the same eq. 6 used in the restricted model. We applied the above techniques to obtain parameter estimates with OLS regression, which we used in a nonlinear fit of [6] (Table 3). It should be noted that in the regression analysis of [8], the κ_2 term was often of marginal value. The improvements in fit statistics were not dramatic, $\overline{R}^2$ values rarely increased more than 0.10.

This generalization has the advantage that information contained in crown ratio is brought to bear on predictions of individual-tree growth. Crown ratio as a variable has been used extensively in individual-tree growth equations (Stage 1973; Wensel et al. 1987; Hann and Larsen 1991). The obvious disadvantage is that a simple list of diameters alone is not sufficient to power the disaggregation component of the model; that is, crown ratio will be required. In addition, this system would require equations for crown change when projecting over multiple growth periods.

We could find no trends for relating $\hat{\kappa}_2$ to any stand parameters. Accordingly, we employed a weighted mean for all stands as a predictor. The weighted mean was 0.4104 with a standard error of 0.019.

The application of this particular model in allocating tree growth is then

$$[9] \quad \Delta\hat{ba}_i = \frac{\Psi(Z, \hat{\theta}_2)}{TPH} + \hat{\kappa}_1\{ba_i - \overline{BA}\} + \hat{\kappa}_2\{cr_i - \overline{CR}\}$$

where

$$\overline{CR} = \frac{\sum_i (cr_i n_i)}{TPH}$$

n_i is the number of trees per unit area represented by the subject tree

Note that as with the simpler version of this model, invariance is maintained: $\Sigma_i(\Delta\hat{ba}_i n_i) = \Psi(Z, \hat{\theta}_2)$. The remaining terms all sum to zero.

Proportional allocation disaggregation function
Another means of disaggregating growth or yield is a proportional allocation approach, such as that used by Clutter and

Table 3. Results of nonlinear regression on disaggregation coefficient, $\hat{\kappa}_1$ in eq. 8, a generalization of the Harrison and Daniels (1988) disaggregation model.

Parameter	Estimate	Asymptotic standard error
γ_1	−2.952 29	3.224 8
γ_2	0.588 352	0.872 1
γ_3	−0.064 330 8	0.009 688

Jones (1980) and Dahms (1983). The general form of this type of model is

$$[10] \quad \frac{w_i}{W} = \frac{g(u_i)}{\sum_i (g(u_i) n_i)}$$

where

w_i is some trait of subject tree (e.g., tree volume growth or tree basal area)

W is the predicted aggregate of w

$g(u_i)$ is a function of some measured tree dimension (e.g., diameter, height)

An example of [10] for basal area growth is

$$[11] \quad \frac{\Delta ba_i}{\Delta BA} = \frac{ba_i}{\sum_i (ba_i n_i)}$$

where ΔBA is estimated from some stand-level function. By multiplying both sides of [11] by trees per unit area, the left side could be viewed as an index of relative tree growth and the right side as an index of relative tree dimension as was done by Zhang et al. (1993). In the Zhang et al. (1993) generalization, the left side of [11] is specified as relative tree growth (rtg), and the right side is a polynomial of relative tree size (rts). Zhang et al. (1993) explicitly defined rts as predicted tree volume divided by stand volume. That is, $g(u_i)$ is a tree volume function. The Zhang et al. (1993) generalization is

$$[12] \quad rtg_i = \phi_0 + \phi_1\, rts_i + \phi_2\, rts_i^2$$

The parameters in [12] are estimated as a function of stand attributes. Equation 10 is then (approximately) a special case of [12], with $\phi_0 = 0$, $\phi_2 = 0$, and $\phi_1 = 1$. One problem with this generalization is that unlike the more simplified model of Dahms (1983), invariance is not maintained.

A constraint can be established that will produce the desired invariance in application of the system. This constraint may be expressed as

$$[13] \quad \hat{\phi}_0 = \frac{1}{\sum_i n_i}\left\{1 - \hat{\phi}_1 - \hat{\phi}_2\, \frac{\sum_i g(u_i)^2 n_i}{(\sum_i g(u_i) n_i)^2}\right\}$$

We used both the restricted and generalized proportional allocation models to develop predictors for basal area increment. For this application, we defined the following variables

$$rtg_i = \frac{\Delta ba_i}{\Psi(Z, \hat{\theta}_1)}$$

$$rts_i = \frac{ba_i}{BA}$$

The estimates of ϕ for these stands did not reveal any trends useful for predicting either ϕ_1 or ϕ_2. Although the two are highly correlated, as was found by Zhang et al. (1993), neither parameter showed any significant relationship with other stand variables. Therefore, we calculated weighted means for both parameters: $\hat{\phi}_1 = 0.807\,35$ (SE = 0.0252), $\hat{\phi}_2 = 3.5167$ (SE = 0.250). The function for the intercept term, $\hat{\phi}_0$ is then

$$\hat{\phi}_0 = \frac{1}{\text{TPA}}\left\{0.192\,65 + 3.5167\left(\frac{\sum_i \text{ba}_i^2 n_i}{\text{BA}^2}\right)\right\}$$

Predicted growth with this model is then

$$[14] \quad \Delta\hat{\text{ba}}_i = \Psi(Z, \hat{\theta}_1)\{\hat{\phi}_0 + \hat{\phi}_1\,\text{rts}_i + \hat{\phi}_2\,\text{rts}_i^2\}$$

Individual-tree growth rate equation as a disaggregation function

An individual-tree growth equation can also be used as a disaggregation function. Generally, this does not maintain symmetry with any particular whole-stand growth function other than that implied by the passive aggregation of such a function. Within the context of the particular application, however, some individual-tree functions may actually act as symmetric allocators of growth. An example of this is the use of individual-tree mortality functions in ORGANON (Hann and Wang 1990). In this application, situations may arise wherein the individual-tree mortality functions are scaled according to an aggregate-level prediction, provided by the size–density trajectory of Smith and Hann (1984). Invariance is maintained and the simulator operates from a disaggregative approach for mortality.

Similarly, the basal area growth equation may be scaled by a whole-stand basal area growth prediction, thereby maintaining symmetry with the active aggregation scheme. Given an aggregate gross basal area growth equation, $\Psi(Z, \hat{\theta})$, and an established individual-tree equation

$$[15] \quad \Delta\hat{\text{ba}}_i = \psi(x_i, \hat{\beta})$$

where x_i is a vector of predictors for individual-tree diameter growth for tree i, the proper allocation of growth can then be established by the ratio

$$[16] \quad \hat{R} = \frac{\Psi(Z, \hat{\theta})}{\sum_i(\psi(x_i, \hat{\beta})n_i)}$$

A disaggregation function, ψ', then can be developed to allocate gross basal area growth to tree i by combining [15] and [16]

$$[17] \quad \psi' = \Delta\hat{\text{ba}}_i\hat{R}$$

This is actually another proportional allocation scheme, not unlike that used by Dahms (1983). Instead of tree dimension, however, this method [17] uses estimated basal area growth divided by the aggregate of estimated basal area growth. Therefore, another perspective of proportional allocation is that predicted tree growth is scaled by the ratio of the two estimates of stand gross basal area growth. For this predictive model, an individual-tree model is required. For our analysis, we fit individual-tree diameter growth regressions for Douglas-fir and grand fir.

The regression for individual-tree diameter growth functions was based on the findings of Hann and Larsen (1991) for conifer species in southwestern Oregon. Hann and Larsen

(1991) found that the basal area growth prediction function was unreliable for very small trees, and instead used diameter increment as a response variable. Employing the fully specified model for predicting individual-tree diameter increment, parameter estimates were obtained for the model

$$[18] \quad E(\Delta d) = \exp\Big[\beta_0 + \beta_1 f_1(d) + \beta_2 f_2(d) + \beta_3 f_3(S) + \beta_4 f_4(\text{bal}, d) + \beta_5 f_5(\text{BA}) + \beta_6 f_6(\text{cr})\Big]$$

where

$$f_1(d) = \ln(d + 2.54) \times 0.1$$
$$f_2(d) = d^2 \times 0.0001$$
$$f_3(S) = \ln(S - 1.37)$$
$$f_4(\text{bal}, d) = \frac{\text{bal}^2 \times 0.000\,01}{\ln(d + 12.7) - 0.932\,16}$$
$$f_5(\text{BA}) = \sqrt{\text{BA}} \times 0.01$$
$$f_6(\text{cr}) = \ln\left\{\frac{\text{cr} + 0.2}{1.2}\right\}$$
$$\text{cr} = \frac{\text{live crown length}}{\text{total tree height}}$$

d is diameter at breast height (cm)
bal is aggregate basal area in trees larger than the subject tree (m²/ha)
BA is aggregate basal area (m²/ha)

The parameters β_i were estimated (Table 4) with the nonlinear least-squares technique of Marquardt (1963). This fit was iteratively reweighted with the assumption that the variance of the error term was proportional to the predicted growth. This weight was found to be optimal by Hann and Larsen (1991). There are 9526 Douglas-fir and 595 grand fir sample trees in the data sets. Examples of disaggregative models have, by convention, avoided inclusion of crown ratio. In a disaggregative setting, where crown information is generally absent, a growth function without crown ratio is more appropriate. Accordingly, we fit a reduced form of model [18], as model [19]

$$[19] \quad E(\Delta d) = \exp\Big[\beta_0 + \beta_1 f_1(d) + \beta_2 f_2(d) + \beta_3 f_3(S) + \beta_4 f_4(\text{bal}, d) + \beta_5 f_5(\text{BA})\Big]$$

Results of this regression are shown in Table 5.

Application of models

Individual-tree prediction

Eight models for individual-tree basal area growth (P_1–P_8) were established:

P₁: reduced individual-tree diameter growth rate model [19]
P₂: full individual-tree model [18]
P₃: disaggregative model [17], with reduced individual-tree model [19] scaled by predicted stand basal area growth model [1]
P₄: disaggregative model [17], with full individual-tree model [18] scaled by predicted stand basal area growth model [2]
P₅: Harrison and Daniels (1988) disaggregative model [7] with predicted stand basal area growth model [1]

Table 4. Results of nonlinear regression on the full individual-tree diameter growth rate equation [18].

	Full model			
	Douglas-fir		Grand fir	
Parameter	$\hat{\beta}$	SE($\hat{\beta}$)	$\hat{\beta}$	SE($\hat{\beta}$)
0	2.707 11	0.223 7	−1.308 56	1.0294
1	3.395 17	0.175 2	5.946 42	0.8051
2	−0.663 786	0.019 39	−1.512 960	0.2271
3	1.156 15	0.060 69	0.555 335	0.2769
4	−84.690 5	4.878 6	−55.156 7	16.364
5	−4.947 03	0.830 41	−9.827 21	3.6274
6	1.199 51	0.023 74	1.127 12	0.1058

Table 5. Results of nonlinear regression for individual-tree diameter growth rate equation excluding crown ratio [19].

	Reduced model			
	Douglas-fir		Grand fir	
Parameter	$\hat{\beta}$	SE($\hat{\beta}$)	$\hat{\beta}$	SE($\hat{\beta}$)
0	−3.320 87	0.250 4	−0.945 285	1.132
1	3.006 11	0.197 6	6.276 48	0.8772
2	−0.568 888	0.213 7	−1.565 84	0.2514
3	1.328 08	0.067 92	0.446 850	0.3061
4	−117.103	5.565 54	−54.160 1	17.6662
5	−14.848 4	0.901 424	−22.371 5	3.6149

P_6: simple proportional allocation disaggregative (eq. 11) method with predicted stand basal area growth model [1]

P_7: Harrison and Daniels (1988) generalization model [9] with predicted basal area growth model [2]

P_8: constrained generalized proportional allocation model [14] with predicted basal area growth model [1]

Two of these are standard individual tree – distance independent predictive models (P_1 and P_2); the remaining models are disaggregative with a constrained invariance.

For P_1 and P_2, diameter increment for an individual tree was estimated as dictated and then transformed into basal area increment. Those models requiring crown ratio were paired with the whole-stand equation [2] because that whole-stand growth model is dependent on an aggregation of individual-tree crown measurements.

The residuals (observed – predicted) from these eight models were used to calculate MSE and $\overline{R}^2$ for the complete data set (Table 6).

Aggregate (stand-level) prediction

Four aggregate predictive methods may be implied by the preceding tree-level models:

AP_1: predictions based on the aggregate of the reduced individual-tree model [19]

AP_2: predictions based on the aggregate of the full individual-tree model [18]

AP_3: predictions based on whole-stand predictive model [1] (with SDI)

Table 6. Individual-tree summary statistics for the residuals of predictive methods P_1–P_8 on the entire data set, where residual = observed – predicted (units are m² of basal area per tree).

Method	$\overline{R}^2$	Bias ($\hat{b}_i$)	Variance ($\hat{\sigma}_i^2$)	MSE
P_1	0.3903	−0.002 438	0.000 280 4	0.000 286 4
P_2	0.4701	−0.000 368 7	0.000 248 7	0.000 248 8
P_3	0.2781	0.002 214	0.000 334 2	0.000 339 1
P_4	0.4001	−0.001 592	0.000 279 3	0.000 281 8
P_5	0.1260	0.003 205	0.000 400 3	0.000 410 6
P_6	−2.9963	−0.011 60	0.001 742	0.001 877
P_7	0.2288	0.003 965	0.000 346 5	0.000 362 2
P_8	0.1735	0.001 055	0.000 388 3	0.000 389 4

Table 7. Summary statistics for the residuals of aggregate predictive methods AP_1–AP_4 for 105 Douglas-fir stands in western Oregon.

Method	$\overline{R}^2$	Bias ($\hat{b}_i$)	Variance ($\hat{\sigma}_i^2$)	MSE
AP_1	0.6914	−0.080 559	0.027 325 6	0.033 815 4
AP_2	0.8193	−0.008 238 7	0.019 740 4	0.019 808 3
AP_3	0.6517	−0.004 955 25	0.381 466	0.381 491
AP_4	0.7797	−0.000 124 50	0.025 171	0.025 171

AP_4: predictions based on whole-stand predictive model [2] (with CSA)

The first two stand-level predictions (AP_1 and AP_2) are based on an aggregate of the predictions from the individual-tree predictive models. These predictions are made by summing the product of predicted tree growth and the per-acre expansion factor. The other two models predict the stand-level gross growth directly. Since gross growth is used here, there is no reduction in expansion factors for mortality. The summaries of residuals for these four models are shown in Table 7.

Results

The summaries in Table 6 indicate the superiority of the full individual-tree model over the other methods. The reduced individual-tree (P_1) and disaggregated full individual-tree (P_4) models appear to work equally well. For these data, therefore, the loss in predictive power is approximately equal for dropping crown ratio and imposing a stand-level growth constraint. The reduced individual-tree model with a whole-stand basal area growth constraint (P_3) shows a substantial reduction in predictive ability. Both of the more traditional disaggregative approaches (P_5 and P_6) are much worse than the individual-tree-based approaches (P_1–P_4), even those that use a tree function in a disaggregative approach. The addition of crown ratio to the Harrison and Daniels (1988) method resulted in a modest reduction in MSE, from 0.000 41 to 0.000 36. However, P_4 had a substantially lower MSE (0.000 28), so if crown ratio is to be used, the individual-tree function is superior. The generalization (P_8) of the proportional allocation model (P_6) resulted in a substantial reduction in MSE, but even with that improvement, the MSE was substantially worse than any of the individual-tree-based methods.

It should be noted that the presence of a negative $\overline{R}^2$ indicates that the prediction generated was worse (had a larger

Table 8. Individual-tree summary statistics for the residuals of predictive methods P_1–P_8 for stands less than 50 years of age, where residual = observed – predicted (units are m^2 of basal area increment).

Method	$\bar{R}^2$	Bias ($\hat{b}_i$)	Variance (σ_i^2)	MSE
P_1	0.5579	−0.002 937	0.000 139 8	0.000 148 4
P_2	0.6525	0.000 127 6	0.000 117 1	0.000 117 1
P_3	0.1812	0.000 841 8	0.000 275 3	0.000 276 0
P_4	0.5362	0.000 105 8	0.000 156 3	0.000 156 4
P_5	−0.1373	0.003 491	0.000 371 1	0.000 383 3
P_6	−8.4282	−0.006 010	0.003 142	0.003 178
P_7	0.2079	0.002 945	0.000 258 3	0.000 267 0
P_8	−0.2503	0.002 076	0.000 417 1	0.000 421 4

Table 9. Results of analysis of residuals for linear trends.

Method	Intercept	Slope	$\bar{r}^2$
P_1	0.005 939	−0.094 930	0.0279
P_2	0.020 862	−0.078 417	0.0069
P_3	0.071 061	−0.282 00	0.0872
P_4	0.051 342	−0.207 63	0.0586
P_5	0.131 64	−0.349 18	0.0933
P_6	0.224 01	−0.797 34	0.7966
P_7	0.098 231	−0.205 71	0.0254
P_8	0.122 34	−0.389 22	0.1433

MSE) than the sample mean. In typical regression applications, residual sum of squares is constrained to be less than the total sum of squares; thus, in most instances, $\bar{R}^2$ is positive. Since these predictions are not the direct result of OLS regression, the residual sum of squares is not so constrained.

Crown ratio, or the absence thereof, appeared to be an important determinant of model performance. This was also found to be the case in prediction of height growth for individual trees in the organon simulator (Hann and Ritchie 1988; Hann et al. 1993). The addition of crown ratio in the generalization of the Harrison and Daniels (1988) model P_7 did result in an improvement. Among disaggregative approaches, however, the use of an individual-tree growth model (either P_3 or P_4) as an allocator of growth was still superior.

The generalization of the proportional disaggregation method (P_8), while superior to P_6, still does not approach any of the individual-tree approaches.

As we observed, the assumptions required for the additive disaggregation method seemed to be affected by stand age. If so, then perhaps the benefit of using an individual-tree method would be less evident among younger stands. We calculated summary statistics for the predictive methods for stands less than 50 years old (Table 8). While MSE for the Harrison and Daniels (1988) model did improve, so did all of the individual-tree-based methods. Therefore the Harrison and Daniels (1988) model is no better suited to younger stands than are the individual-tree models. However, MSE increased for both the proportional allocation model (P_6) and its generalization (P_8) in the younger stands.

An ideal prediction scheme would be one for which there was nearly a one to one linear correspondence between observed Δba_i and prediction, P_{im}. This was evaluated by fitting a linear regression for residual as a function of predicted for each of the m predictive methods ($m = 1, 2, ..., 8$). The results of this analysis are shown in Table 9. The ideal predictor has a slope and intercept of zero, or nearly so. A high $\bar{r}^2$ is indicative of poor fit, a linear trend in the residuals with respect to predicted growth, P_m. The individual-tree methods were superior to the disaggregative methods, although the Harrison and Daniels (1988) method was not much worse than a reduced individual-tree growth function; inclusion of crown ratio appeared to result in a better fit (Table 9). It should be noted that all parameter estimates were statistically significant at the 5% level, except the intercept for P_1.

The cumulative distribution of the absolute value of the residuals expressed as a percent (ε') is displayed for P_3, P_5, and P_6 in Fig. 5. The ideal predictor would have zero values for all residuals and, therefore, would display a horizontal line at the 100% level over ε'. Among the disaggregative approaches without crown ratio, the proportional allocation method was the least effective. However, either of the models with crown ratio (whole-stand disaggregative or traditional individual-tree) were superior to any without crown ratio (Fig. 6).

Among stand-level predictions, the full specification of the individual-tree predictive method (AP_2) had the lowest MSE; however, the bias was smallest with AP_4, a whole-stand predictive method. For long projections, therefore, the whole-stand approach may provide better predictions. For short-term projections, the individual-tree approach appeared to be superior. It should also be noted that the observed bias may be offset by an underestimate of stand density over time and resulting overestimates of growth.
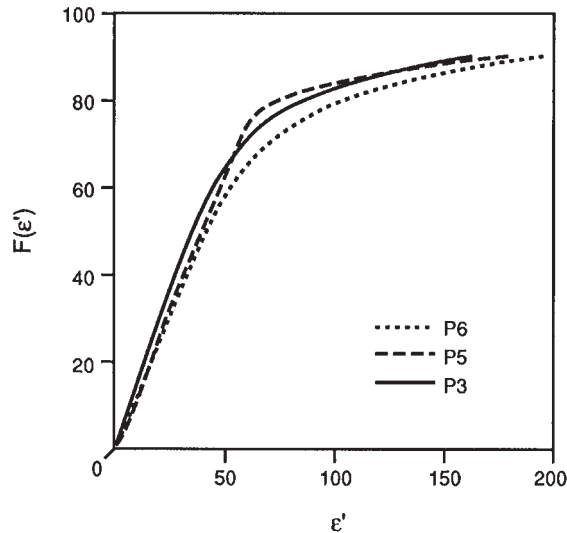
The individual-tree method without crown ratio (AP_1), although not as good as the whole-stand model with crown surface area (AP_4), had a lower MSE than the model based on stand density index (AP_3). Note, however, that AP_4 is dependent on the information needed for an individual-tree-based model. To calculate the crown surface area with the Biging and Wensel (1990) equations, a list of trees with crown ratio is required. In general, whole-stand models, even disaggregative systems, do not maintain this information. A more standard approach, such as AP_3, which does not require crown information, is only marginally better in terms of bias, and is much worse in terms of variance than the individual-tree prediction with crown ratio (AP_2).

The cumulative distribution of the absolute value of relative residuals expressed as a percentage showed that the distributions were very similar, and that nearly all of the predictions of AP_2 were within 40% of the actual growth (Fig. 7). This is a great improvement over the predictions made at the tree level.
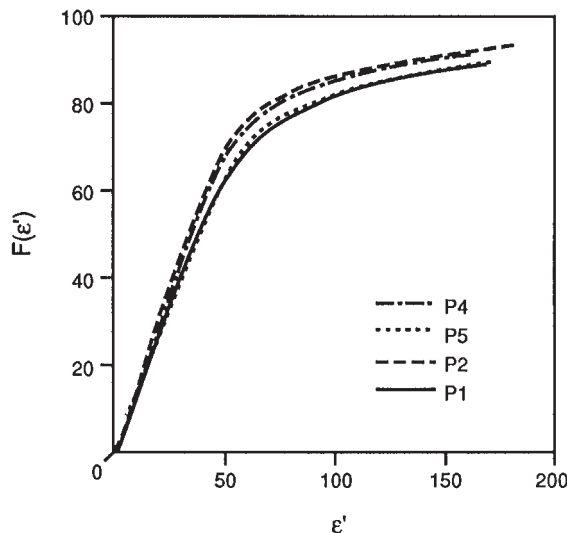
Despite the established knowledge of stand growth and yield, and the fact that stand growth is generally well defined for even-aged stands, the individual-tree approach including crown ratio was a superior predictive technique for this one observed growth period (Fig. 7). Figure 7 also illustrates the general improvement in estimating stand growth versus tree growth among the individual-tree prediction methods when compared with Fig. 6. This does not necessarily mean that this trend will hold over a long projection. Much of the difficulty in obtaining reasonable long-term projections with an individual-tree approach may be due to mortality functions. Existing functions

Fig. 5. Cumulative distribution of the percent absolute deviation of residuals (ε') for all trees in the data set, for three of the active aggregation methods: reduced individual-tree scaled by predicted stand basal area growth (P_3), Harrison and Daniels (1988) type model (P_5), and simple proportional allocation model (P_6).

Fig. 7. Cumulative distribution of the absolute value of residuals (ε'), expressed as a percent, for stand-level predictions on 105 Douglas-fir stands: aggregate of reduced individual-tree model (AP_1), aggregate of the full individual-tree model (AP_2), whole-stand predictive model [1] (AP_3), and whole-stand predictive model [2] (AP_4).

Fig. 6. Cumulative distribution of the percent absolute deviation (ε') of residuals for all trees in the data set, for three predictive methods: reduced individual-tree model (P_1), full individual-tree model (P_2), reduced individual-tree model scaled by predicted basal area growth (P_5), and full individual-tree model scaled by predicted basal area growth (P_4).

Crown ratio appears to be an important component in prediction of both tree and stand gross growth; the full individual-tree model consistently outperformed both additive- and proportional-allocation disaggregative models. In predicting stand or tree growth, the use of individual-tree functions in a disaggregative approach did not result in any improvement over the more traditional application of unconstrained individual-tree growth models.

Of the two disaggregative approaches, we found that the additive allocation system patterned after Harrison and Daniels (1988) was far superior to the simple proportional allocation for predicting basal area increment. Adding a constraint to the proportional allocation [13] greatly improved the model. While it appears that the linearity assumption of the Harrison and Daniels (1988) model does not hold as well for older stands in this data set, the effect of stand age on predictions is also evident for individual-tree methods.

Since these stands are mostly even aged and are dominated by a single species, we cannot say what the results would be for more complex stand structures. In general, one would expect that whole-stand models would suffer in their ability to predict growth for such stands. If disaggregative models were to work well anywhere, it should be in even-aged, single-species stands, such as those in this study. In general it should be noted that results for a single 5-year period do not necessarily hold for long-term projections. The superiority of an individual-tree approach for gross-growth estimation may not hold for predicting net growth; this is partially dependent on mortality estimation, which may be an area where disaggregative methods would be beneficial.
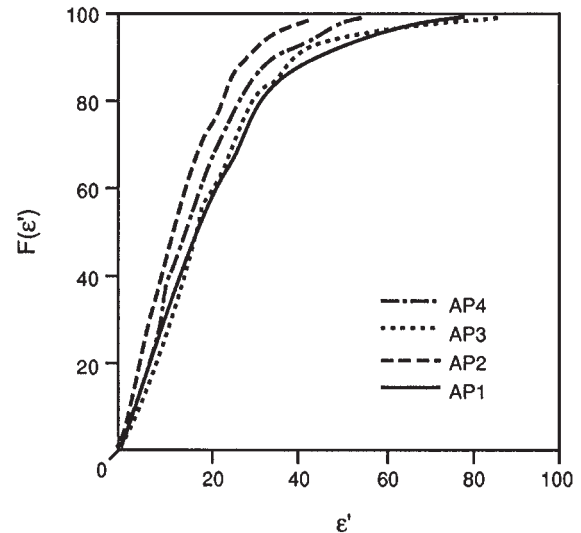
for estimating individual-tree probability of mortality may not aggregate reliably. The effects of mortality prediction are beyond the scope of this study, and unconstrained mortality estimation techniques are certainly not necessary for individual-tree architecture.

Conclusions

We found no evidence to suggest that the disaggregative approach is able to predict tree or stand gross basal area growth as well as an individual-tree approach for a single 5-year period.

References

Biging G.S., and Wensel, L.C. 1990. Estimation of crown form for six conifer species of northern California. Can. J. For. Res. **20**: 1137–1142.

Clutter, J.L., and Jones, E.P. 1980. Prediction of growth after thinning in old field slash pine plantations. USDA For. Serv. Res. Pap. SE-217.

Dahms, W.G. 1983. Growth simulation model for lodgepole pine in central Oregon. USDA For. Serv. Res. Pap. PNW-302.

Flewelling, J.W., and Pienaar, L.V. 1981. Multiplicative regression with lognormal errors. For. Sci. **27**: 282–289.

Hann, D.W., and Larsen, D.R. 1991. Diameter growth equations for fourteen tree species in southwest Oregon. Oreg. State Univ. For. Res. Lab. Res. Bull. 69.

Hann, D.W, and Ritchie, M.W. 1988. Height growth rate of Douglas-fir: a comparison of model forms. For. Sci. **34**: 165–175.

Hann, D.W., and Wang, C.-H. 1990. Mortality equations for individual trees in the mixed-conifer zone of southwest Oregon.Oreg. State Univ. For. Res. Lab. Res. Bull. 67.

Hann, D.W., Olsen, C.L., and Hester, A.S. 1993. ORGANON user's manual. Department of Forest Resources, Oregon State University, Corvallis.

Harrison, W.C., and Daniels, R.F. 1988. A new biomathematical model for growth and yield of loblolly pine plantations. *In* Forest Growth Modeling and Prediction. Vol. 1. Proceedings, IUFRO Conference, 23–27 Aug. 1987, Minneapolis, Minn. *Edited by* A.R. Ek, S.R. Shifley, and T.E. Burk. USDA For. Serv. Gen. Tech. Rep. NC-120. pp. 293–304.

Ijiri, Y. 1971. Fundamental queries in aggregation theory. J. Am. Stat. Assoc. **66**: 766–782.

King, J.E. 1966. Site index curves for Douglas-fir in the Pacific Northwest. Weyerhaeuser Co., Centralia, Wash. For. Pap. 8.

Marquardt, D.W. 1963. An algorithm for least squares estimation of non-linear parameters. J. Soc. Ind. Appl. Math. **11**: 431–441.

Munro, D.D. 1973. Forest growth models—a prognosis. *In* Growth models for tree and stand simulation. *Edited by* J. Fries. Royal College of Forestry, Stockholm Res. Note 30. pp. 7–21.

Reineke, L.H. 1933. Perfecting a stand-density index for even-aged forests. J. Agric. Res. **46**: 627–638.

Smith, N.J., and Hann, D.W. 1984. A new analytical model based on the 3/2 power rule of self-thinning. Can. J. For. Res. **14**: 605–609.

Stage, A.R. 1973. Prognosis model for stand development. USDA For. Serv. Res. Pap. INT-137.

Wensel, L.C., Meerschaert, W.J., and Biging, G.S. 1986. Tree height and diameter growth models for northern California conifers. Hilgardia, **55**(8).

Wensel, L.C., Daugherty, P.J., and Meerschaert, W.J. 1987. CACTOS user's guide: the California conifer timber output simulator. Agricultural Experiment Station, University of California Division of Agriculture and Natural Resources, Berkeley. Bull. 1920.

Zhang, L., Moore, J.A., and Newberry, J.D. 1993. Disaggregating stand volume growth to individual trees. For. Sci. **39**: 295–308.