Modeling Forest Dynamics Based on Stand Level Resource Allocation

Geoffrey Candler Poole
*Utah State University*

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MODELING FOREST DYNAMICS BASED ON STAND LEVEL RESOURCE ALLOCATION

by

Geoffrey Candler Poole

A thesis submitted in partial fulfillment of the requirements for the degree of
MASTER OF SCIENCE
in
Forest Ecology

Approved:

UTAH STATE UNIVERSITY
Logan, Utah

1989
For Marti and "Chief"...
ACKNOWLEDGEMENTS

I would first like to thank Dr. Dave Roberts who, armed with endless patience, imperishable humor, "abundant free time," and a mere VAX-Station 2000, has guided me with near impunity through my master's studies. How we both made it through is T.D.F.M. I am also indebted to my other committee members, Dr. Jim Haefner and Dr. Dick Fisher, who both shared freely of their time and resources. I thank, too, Dr. Charles Romesburg, who expanded my thinking.

To Stefan Zeglen, I owe my sanity. I thank him for helping me keep things in perspective with his sarcasm and wit. The assistance of my "co-idiot," Doug Wight, was invaluable during the first field season and throughout my days in Logan. My field assistants, Sam Bourn, Chris Bourn, and Ken Culmone, were an immense help in my second summer in the field. I thank John and Ann Mull, Steve Jack, Scott Roberts, Deb Bumpus, Gardner Bent, Dave Verbyla, Cathy Jean, Linda Abbott, Steve Compton, and other graduate students for their assistance and their comradery at "the big game," "dollar-night," and elsewhere.

A very special thanks to my parents and grandparents for their unselfish support and encouragement. They have made excellent role models. Finally, and most sincerely, I thank my wife, Susan, for her love, support, and especially her patience. Words cannot describe the importance of her contribution to this effort.

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Geoffrey C. Poole
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ABSTRACT

Modeling Forest Dynamics Based on Stand Level Resource Allocation

by

Geoffrey Candler Poole, Master of Science

Utah State University, 1989

Major Professor: Dr. David W. Roberts
Department: Forest Resources

An ecologically based model of forest succession is presented. In the model, trees compete for a share of limited growth resources available from their environment. Competition is reflected by each tree's effect on the resource pool and is not explicitly modeled. Model parameters were fit to field data from subalpine forests of the Rocky Mountains. A technique for estimating model parameters from understory-tolerance rankings and silvical characteristics of each species is also presented. The model's output was consistent with our current understanding of forest dynamics. Emergent properties of the model also mimicked natural processes such as self-thinning, release, and maximum stand basal area as a function of species present and site quality. (46 pages)
INTRODUCTION

Applicability of forest models to new areas and species, or generality, is desirable but difficult to achieve. Forest models, whether theoretically or empirically based, are often data intensive and may not be applicable to conditions dissimilar to those where the data were gathered (Roberts and Morgan 1989, Sievänen et al. 1988). Often a model's structure limits its generality.

To be truly general, a model should be theoretically based to facilitate extrapolation. Its parameters should be easily obtainable from site and species characteristics. At present, few forest models meet these requirements. Vital attributes models (Nobel and Slatyer 1980, Cattelino et al. 1979, Kessell and Potter 1980) are quite general but produce only qualitative or semi-quantitative predictions of species abundance and, therefore, lack the detail necessary for many management purposes. The simplicity of these models, however, is appealing. Simple models not only have parameters that are easier to estimate, they are also easier to understand and evaluate critically (Walters 1986). Lorimer (1983) and Haight and Getz (1987) show that predictions from simpler forest models can be as good as predictions from more complex forest models.

Huston and Smith (1987) argue that modeling forest stands at the level of the individual has the potential to explain the variety of successional dynamics that occur in nature. Though the process of succession is observed at the community level, it is driven by the replacement of individual trees. They also point out that life history and physiological traits of each species determine whether it will be successful in its environment and that the traits that confer superior competitive ability differ depending on the plant's
environment. Further, a plant's environment is to some extent dependent on the stage of succession of the surrounding community. Bazzaz (1979) reviews the life history and physiological characteristics that often separate early successional (or understory-intolerant) species from late successional (or understory-tolerant) species. For the model presented here, the most notable are (1) early successional species tend to be more efficient at converting resources to growth, and (2) late successional species tend to have lower respiration rates.

Empirically derived models often require large amounts of data to formulate relationships within the model and are unreliable when extrapolating beyond the scope of the original data set. PROGNOSIS (Wykoff et al. 1982) uses an empirically derived equation to predict diameter growth based on habitat type, geographic location, aspect, slope, elevation, crown competition, crown ratio, and total basal area of trees larger than the subject tree. The equation also uses 12 species-specific regression coefficients. While different variants of this model have been developed for specific regions of the western U.S., the task has been laborious, requiring much time, manpower, and money for data collection in each new area.

Models based in ecological theory are considered more general but still may have high data requirements for calibration. Many calculate tree growth by assuming a maximum growth curve for individual trees and decrementing that growth based on competition and site characteristics (Lorimer 1983). JABOWA (Botkin et al. 1972) and CACTOS (Wensel et al. 1987) are both models that employ this technique. CACTOS uses the equation:

\[ \text{Growth} = \text{Potential Growth} \cdot (1 - \text{Competition}) \]
Site characteristics are considered when calculating the competition coefficient. JABOWA uses the equation:

\[ \text{Growth} = \text{Potential Growth} \cdot \text{Moisture} \cdot \text{Light} \cdot \text{Temperature} \]

The light, moisture, and temperature factors are fractional values based on deviation of site conditions from theoretically optimal levels. Competition is included when calculating light availability.

Sievänen et al. (1988) present a growth-and-yield model that has physiologically interpretable parameters. However, they fail to define a method by which these parameters can be estimated given different stand and species characteristics.

Roberts and Morgan (1989) suggest several guidelines for designing models of forest dynamics. To be useful to forest managers, a forest succession model should provide sufficient detail to determine appropriate management opportunities but needs not provide a wealth of detail unnecessary for forest management. The model should operate at a geographic scale suitable for modeling individual stands yet be capable of modeling large areas of land composed of numerous individual stands. It should utilize information obtainable by forest managers and be compatible with the other forest management tools currently in use. The model should be simple in concept, incorporating our current understanding of successional processes; have low computational overhead such that hardware requirements can be easily met; and require minimal vegetation sampling and analysis for recalibration.

The model presented here is a successional model of Rocky Mountain subalpine forests (specifically the ABLA/BERE habitat type (Mauk and Henderson 1984, Steele et al. 1983, Youngblood and Mauk 1985)).
designed according to the criteria of Roberts and Morgan (1989). The model predicts community composition and structure as well as population-level characteristics. The model's predictions are based on individual trees' ability to capture and convert resources to growth and the amount of energy each tree needs for metabolism.

OBJECTIVES

The specific model objective is to predict, at a level of detail appropriate for land managers, plant community composition and stand structure at specified points in time. In a broader sense, the model is intended as a suitable succession model to be used in conjunction with forest habitat type classifications (e.g., Steele et al. 1981, Steele et al. 1983, Mauk and Henderson 1984) and seral community classification following the guidelines of Steele (1984). The ultimate objective is the ability to model large areas of land composed of multiple habitat types at different stages of succession in a single model.

STUDY AREA

The ABLA/BERE habitat type is the most ubiquitous habitat type in northern Utah and southern Idaho (Mauk and Henderson 1984) and occurs commonly in southern and central Utah (Youngblood and Mauk 1985). It also extends into western Wyoming almost to the Montana border (Steele et al. 1983). Our model is thus presently applicable to a broad area of forest land in the central Rocky Mountains and was designed to be easily calibrated for other habitat types. The dominant overstory species in the ABLA/BERE type are quaking aspen (Populus tremuloides Michx.), lodgepole pine (Pinus contorta Dougl. ex Loudon), Douglas fir (Pseudotsuga menziesii (Mirbel) Franco), and subalpine fir (Abies
IG. 1. Common successional pathways in the ABLA/BERE habitat type. IFL and PIEN never achieve dominance, but the ranges in which they usually occur are shown.

*Populus tremuloides* = Pseudotsuga menziesii
*Pinus contorta* = Picea engelmannii
*Pinus flexilis* = Abies lasiocarpa

Trees often grow asymmetrically (i.e., growth-ring width on one
side of the tree may be consistently larger than on the other). This affects the calculation of basal area increment when converting radial growth recorded on a single increment core to basal area growth. To correct for bias from asymmetric growth, I assumed the 10-year diameter increment to be proportional to the measured 10-year radial increment (measured to nearest 0.02 inch (0.05 cm)) divided by the distance from cambium to pith on the increment core:

\[ \text{DInc} / \text{DBH} = \frac{\text{Rinc}}{\text{Rad}} \]

Diameter increments were then converted to basal area increments.

THE MODEL

The model presented here is based on a conceptual model called "stand level resource allocation," which eliminates the need for a true competition index. Rather than assume each tree has a maximum potential for growth that is decremented by environment and competition, I assume each stand's environment has a maximum potential to support tree growth. Light, water, and nutrients are grouped into a "growth resource pool" and are not modeled explicitly. Growth resources are measured in terms of site potential growth and are divided among the individuals. To do this, a "resource demand" is calculated for each tree based on the tree's size and species. These demands are summed, and each tree is allocated resources based on the fraction its demand comprises of the total demand.

Model design

The plot size modeled is one-tenth acre (0.04 ha), and the time step is 10 years. Species are defined by four general characteristics: understory tolerance, maximum basal area, maximum
growth rate (growth rings per inch), and minimum growth rate (growth rings per inch). The site is defined by potential annual growth resource on the plot determined from habitat type and phase. It predicts, at 10-year intervals, total basal area of tree species and a 2-inch (5.08 cm) diameter class stand table by species.

Input variables

In an effort to make this model simple to calibrate, I chose input variables that can be estimated from knowledge of the silvics of the species:

Maximum Size (basal area) -- An estimate of approximately how large the tree commonly grows in the habitat type modeled, not the maximum size of the largest tree on record for that species.

Maximum Growth Rate (growth rings per inch) -- Estimate of how quickly, at best, the tree grows in the habitat type modeled.

Minimum Growth Rate (growth rings per inch) -- The model uses this value to determine whether a tree runs the risk of death. It is useful to think of this as the minimum growth rate of a healthy individual.

Understory Tolerance Ranking -- A rank based on understory tolerance; 0 is extremely intolerant, 10 is extremely tolerant. The rankings are not relative only to the species in the habitat type modeled but to species of the temperate zone in general.

Resources Available (potential growth in basal area) -- A measure of potential growth resources on the site. Generally, 50% more than the plot's average 10-year basal area growth is a good first estimate.

To aid in the discussion of the model, definitions of all model constants, input values, and variables are provided in Table 1.
Table 1. Definitions of model constants, input values, and variables

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Definition</th>
<th>Units</th>
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<tr>
<td><strong>Constants</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>j</td>
<td>Converts user's area-units to feet$^2$</td>
<td></td>
</tr>
<tr>
<td>k</td>
<td>Converts user's area-units to inches$^2$</td>
<td></td>
</tr>
<tr>
<td>n</td>
<td>Converts user's liner-units to inches</td>
<td></td>
</tr>
<tr>
<td><strong>Input values</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MaxBA&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Species-specific maximum basal area</td>
<td>m$^2$</td>
</tr>
<tr>
<td>MaxG&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Species-specific maximum growth rate</td>
<td>rings/cm</td>
</tr>
<tr>
<td>MinG&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Species-specific minimum growth rate</td>
<td>rings/cm</td>
</tr>
<tr>
<td>UT&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Understory tolerance ranking</td>
<td></td>
</tr>
<tr>
<td>RA</td>
<td>Resources available on the site</td>
<td>m$^2$</td>
</tr>
<tr>
<td><strong>Variables</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DBH</td>
<td>Measured diameter at breast height</td>
<td>cm</td>
</tr>
<tr>
<td>DInc</td>
<td>Estimated 10-year diameter increment</td>
<td>cm</td>
</tr>
<tr>
<td>Rad</td>
<td>Radius (pith to cambium) from increment core</td>
<td>cm</td>
</tr>
<tr>
<td>RInc</td>
<td>10-year radial increment from increment core</td>
<td>cm</td>
</tr>
<tr>
<td>ΔBA&lt;sub&gt;i&lt;/sub&gt;</td>
<td>Individual growth</td>
<td>m$^2$</td>
</tr>
<tr>
<td>ΔBA&lt;sub&gt;min&lt;/sub&gt;</td>
<td>Minimum growth needed to be unstressed (from MinG&lt;sub&gt;s&lt;/sub&gt;)</td>
<td>m$^2$</td>
</tr>
<tr>
<td>BA&lt;sub&gt;i&lt;/sub&gt;</td>
<td>Individual basal area</td>
<td>m$^2$</td>
</tr>
<tr>
<td>FR&lt;sub&gt;i&lt;/sub&gt;</td>
<td>Fraction of resources allocated to respiration</td>
<td></td>
</tr>
<tr>
<td>FR&lt;sub&gt;0.5&lt;/sub&gt;</td>
<td>Fraction of resources allocated to respn @ BA&lt;sub&gt;i&lt;/sub&gt;=0.5 ft$^2$</td>
<td></td>
</tr>
<tr>
<td>RC&lt;sub&gt;i&lt;/sub&gt;</td>
<td>Individual resource capture</td>
<td>m$^2$</td>
</tr>
<tr>
<td>RD&lt;sub&gt;i&lt;/sub&gt;</td>
<td>Individual resource demand</td>
<td>inches$^2$</td>
</tr>
<tr>
<td>Str&lt;sub&gt;i&lt;/sub&gt;</td>
<td>Stress rating</td>
<td></td>
</tr>
<tr>
<td><strong>Species-level</strong></td>
<td></td>
<td></td>
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<tr>
<td>#Reg&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Number of trees for species s</td>
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<td>Basal area regenerated for species s</td>
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<tr>
<td>RCC&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Resource capture and conversion coeff. for species s</td>
<td></td>
</tr>
<tr>
<td>Rmnd&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Remaining regeneration after integer division</td>
<td>m$^2$</td>
</tr>
<tr>
<td>RspA&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Respiration coefficient #1 for species s</td>
<td></td>
</tr>
<tr>
<td>RspB&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Respiration coefficient #2 for species s</td>
<td></td>
</tr>
<tr>
<td>UA&lt;sub&gt;s&lt;/sub&gt;</td>
<td>Understory abundance of species s</td>
<td>% cover</td>
</tr>
<tr>
<td><strong>Stand-level</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RA</td>
<td>Resources available to the stand</td>
<td>m$^2$</td>
</tr>
<tr>
<td>RBA</td>
<td>Basal area regenerated on plot</td>
<td>m$^2$</td>
</tr>
</tbody>
</table>
Stand initialization

The user defines the initial stand conditions by providing either a stand table by species or the fraction of the total basal area composed of each species. When a stand table is provided, trees of the same species and diameter class are spread evenly throughout the diameter class. When the fraction of basal area by species is provided, a probable diameter distribution is estimated for each species based on its basal area, understory tolerance, and the understory tolerance and basal area of the other species present. The assumptions used to estimate stand structure for each species are as follows: If a species comprises a small fraction of the biomass in a stand and is not as understory tolerant as most of the rest of the stand, chances are that the individuals of this species are large and the more tolerant species have invaded beneath them. If a species comprises little of the biomass in a stand and is more understory tolerant than the rest of the stand, chances are the trees are small and invading beneath a previously established canopy. When a species comprises the majority of a stand's biomass, the structure of the species tends towards that of a monoculture regardless of its understory tolerance.

The field data generally support these assumptions (Figure 2). The data also show that intermediate stand structures can often be estimated using a weighted mean of the stand structures described above, which I term standard structures (Figure 2). While there are some obvious discrepancies, I think the resulting estimates of stand structures are highly satisfactory given the precision of the stand description (fraction of total basal area by species). If more accurate initial conditions are required, the stand table input option should be used.
FIG. 2. Predicting basal area distribution from fraction of basal area and relative understory tolerance with respect to the remainder of the stand. "Predictions" are weighted means of the four "standard" distributions. Field data are shown for comparison.
Growth

Growth of individual trees is a function of the growth resources available on the site and the individual's species and size. Given unlimited resources, each tree would use only a fraction. I term this measure individual resource demand. Individual resource demand should increase with basal area. I therefore hypothesized that this relationship could be expressed by:

\[ RD_i = (BA_i \cdot k)^{RCG} \]  

Total resource demand is the sum of individual resource demands. This is our measure of competition on the site. I hypothesized that each tree should capture a fraction of the available resources equal to the fraction its demand comprises of the total:

\[ RC_i = RA \cdot \left( \frac{RD_i}{\sum(RD_i)} \right) \]

Each tree allocates its growth resources to either growth or respiration. As the tree size increases, the fraction of resources allocated to respiration should also increase. Therefore, I chose a flexible but constantly increasing curve shape for the respiration curve:

\[ FR_i = RspA_s \cdot (BA_i \cdot j)^{RspB_s} \]

Growth is equal to that fraction of the captured resources not used for respiration:
\[\Delta B_i = RC_i \cdot (1 - FR_i)\]

This algorithm may allocate excessive growth to individuals when the stand being modeled is poorly stocked. The model allocates all of the site's potential growth to trees no matter what the stand density. To correct for this, if predicted growth exceeds a species-specific maximum, growth is set to that maximum.

**Stress and mortality**

Trees are considered stressed and may be subject to mortality if their growth is less than a species-specific minimum. Minimum growth is determined by converting the minimum radial increment to minimum basal area increment, and stress is calculated as:

\[St_i = \frac{(BA_i + \Delta BA_i)}{(BA_i + \Delta BA_{min})}\]

The minimum growth requirement represents a larger fraction of the denominator for small trees than for large trees. As a result, small trees with half their required minimum growth will be assigned a more severe stress rating than large trees with half their required minimum growth. However, since large trees allocate a relatively larger fraction of their resources to respiration than do small trees, minimum growth is harder for large trees to achieve. Accordingly, small trees and trees approaching maximum size are most easily stressed.

The number of trees removed from the simulation is determined from a ranked list of the stressed trees. Trees are removed from the simulation one at a time, in order of stress, until either all of the stressed trees are removed or 5% of the total basal area has been removed. This limit of 5% of the total basal area is necessary
because growth in the model occurs in 10-year increments, and
competition (resource demand) on the plot may reach unreasonably high
levels before stress is calculated. When this occurs, an excessive
fraction of the stand is classified as stressed.

Regeneration

Regeneration occurs by inserting trees into the 2-inch (5.08 cm)
diameter class. The amount of regeneration occurring, calculated in
basal area, is determined by comparing the total resource demand to
the resource available:

\[ RBA = RA \cdot (1 - \frac{\sum (RD_i)}{2 \cdot k \cdot RA})^{0.1} \]

Maximum regeneration occurs at a total resource demand of zero and
decreases rapidly as total demand begins to increase. As total demand
continues to increase, regeneration decreases less rapidly, finally
reaching zero when resource demand is twice the available resources.
At this point, competition for resources is intense, and established
trees suppress the ingrowth of any new trees. The regeneration basal
area is divided among the species according to their understory
abundance:

\[ RBA_s = RBA \cdot \frac{UA_s}{\sum (UA_s)} \]

Understory abundance is modeled empirically based on data
collected over two field seasons. Abundance is correlated to
overstory composition using fuzzy set theory (Roberts 1989) and the
successional pyramid (Steele 1984) in Figure 3.

Any plot can be classified using this pyramid. The upper species
within each cell of the pyramid represents the least understory-
FIG. 3. Successional pyramid for the ABLA/BERE habitat type.

Tolerant species on the plot. This determines which row the plot is on. The plot is then assigned membership values in each of the cells on that row according to the basal area of each species. For instance, if the basal area of a plot were comprised of 20% P. contorta, 30% P. menziesii, and 50% A. lasiocarpa, the plot would be assigned membership values of 0.2, 0.3, and 0.5 in PICO/PICO, PICO/PSME, and PICO/ABLA, respectively.

Field data were used to calculate regeneration values (the number of trees, on average, entering the 2-inch (5.08 cm) diameter class during a 10-year period) for each cell of the pyramid. Some community types of the pyramid are rare and were never observed in the field. Regeneration for these community types was interpolated from the neighboring cells of the pyramid.

Regeneration values for each cell of the pyramid are used by the model to estimate understory abundance. Fractional membership in each
cell of the pyramid is calculated for predicted stands. Understory abundance is estimated by taking a mean of the regeneration values for each cell, weighted by the predicted stand's fractional membership in that cell.

The number of trees regenerated is determined by dividing the regeneration basal area for each species by the basal area of a 2-inch (5.08 cm) DBH tree. Any remainder is retained and added to the next iteration's regeneration basal area for that species:

\[
\text{#Regs} = \text{INT} \left[ \frac{(RBAs + Rmnds)}{(n^2 \cdot \pi)} \right]
\]

GROWTH PARAMETER ESTIMATION

Reasonable estimates of maximum tree basal area, maximum growth rate, minimum growth rate, and understory-tolerance ranking can be easily obtained from knowledge of the silvics of the species. However, the growth parameters, RCC, RspA, and RspB, are less intuitive, and estimating them is not as straightforward.

**Fitting growth parameters to field data**

Two methods, the descent method and the constrained-fit method, were used to fit growth parameters to the field data. The descent method is a descent algorithm similar to a simplex (Caceci and Cacheris 1984). It differs in that parameters are varied in a predetermined order, and the step remains constant. The constrained-fit method uses ecological theory to estimate RCC and then fits RspA and RspB by examining all combinations of the two within a reasonable range. Both of these methods are fitting techniques in which measures of error, calculated by comparing predictions to field data, are minimized iteratively.
The measure of error that is minimized by the descent method is calculated by finding the average absolute difference between predicted and measured sample tree basal area growth for each species on each plot. These values are then summed over all species and all plots. The measure is sensitive not only to how much growth is predicted but also to which species and which diameter classes within each species the growth is allocated.

The advantage of the descent method is that all 18 growth parameters (3 for each of 6 species) can be fit simultaneously. The disadvantage is a problem with local minima.

Local minima, when present, are problematic for any descent algorithm. To check for local minima, the descent method was repeated using several different starting points. When the parameters were varied at least ±0.2 in each iteration, all starting points converged to the same minimum. However, when precision was increased by decreasing the step, local minima became apparent. It was impossible to determine which set of parameters was actually "best" because parameters in the best several parameter sets tended to vary as much as 30% of their value while the difference in the error term was less than 1%. I attribute this to the interdependency of the parameters for each species.

The results of this technique using a step of ±0.2 are presented because it was the only technique that fit the resource capture and conversion exponents (RCC) to the data. However, the precision is poor, so an alternative fitting method was used.

The constrained-fit method uses a combination of ecological theory and error minimization to estimate the growth parameters. An algebraic manipulation of Stand Density Index (Long and Smith 1984) predicts values for RCC should be about 0.8. Estimates from the
Table 2: Estimated understory tolerance and maximum size for species of the ABLA/BERE habitat type.

<table>
<thead>
<tr>
<th>Acronym</th>
<th>Species</th>
<th>Maximum Basal Area (ft² / m²)</th>
<th>Understory Tolerance</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABLA</td>
<td><em>Abies lasiocarpa</em></td>
<td>4.28 / 0.398</td>
<td>10</td>
</tr>
<tr>
<td>PIEN</td>
<td><em>Picea engelmannii</em></td>
<td>6.68 / 0.621</td>
<td>9</td>
</tr>
<tr>
<td>PSME</td>
<td><em>Pseudotsuga menziesii</em></td>
<td>6.68 / 0.621</td>
<td>5</td>
</tr>
<tr>
<td>PIFL</td>
<td><em>Pinus flexilis</em></td>
<td>4.91 / 0.456</td>
<td>3</td>
</tr>
<tr>
<td>PICO</td>
<td><em>Pinus contorta</em></td>
<td>2.64 / 0.245</td>
<td>2</td>
</tr>
<tr>
<td>POTR</td>
<td><em>Populus tremuloides</em></td>
<td>1.07 / 0.099</td>
<td>0</td>
</tr>
</tbody>
</table>

Descent method suggests similar values. Ecological theory suggests understory-intolerant species are more efficient at capturing resources and converting those resources to growth (Bazzaz 1979), as is evidenced by higher photosynthetic rates at high resource availability. Therefore, I theorize that RCC should vary with understory tolerance. The following equation sets RCC to 0.9 for the least tolerant species and to 0.7 for the most tolerant species, with other species spaced evenly between:

\[ RCC_s = 0.9 - (UT_s \cdot 0.02) \]

Understory-tolerance rankings for the 6 species (Table 2) were used to calculate RCC for each species, and those values were subsequently fixed. By fixing the values of RCC, values of RspA and RspB could be estimated independently for each species to a precision of 0.01 by calculating error for all reasonable combinations of the two coefficients. The measure of error was the per-plot average absolute difference between predicted and actual sample tree growth summed over...
all plots for each species. Even though it was included in all the analyses, I lacked the data to accurately fit parameters for Engelmann spruce because its role in the ABLA/BERE habitat type is so minor. To reflect this, the results for spruce included in the tables and figures are enclosed in parentheses or shaded.

*Estimating growth parameters from species characteristics*

A third technique, the silvics-based method, was developed to estimate the growth parameters based on ecological theory and understory-tolerance rankings for each species.

RCC can be estimated using equation [12], which spreads RCC evenly between 0.7 and 0.9. RspA and RspB are estimated by forcing equation [6] through two points. The first point is calculated from the understory-tolerance ranking of the species. Ecological theory suggests that understory-tolerant trees have lower respiration costs than intolerant trees (Bazzaz 1979). The values of RspA and RspB estimated using the descent method suggest that a tree whose basal area is 0.5 ft$^2$ (464.5 cm$^2$) allocates between 20% and 70% of its resources to respiration, depending on the species. I therefore hypothesize that a species whose understory-tolerance ranking is 0 should have a respiration fraction of 0.7 at 0.5 ft$^2$, and a species whose understory-tolerance ranking is 10 should have a respiration fraction of 0.2 at a basal area of 0.5 ft$^2$. Other species should have values spread between 0.2 and 0.7 depending on their understory-tolerance rankings:

\[
FR_{0.5} = 0.7 - (UT_s \cdot 0.05)
\]
The second point is defined by the maximum size of the species. By definition, the fraction of resources allocated to respiration at maximum size is 1. By substituting these values into equation [6] we find:

\[ FR_{0.5} = Rsp_A \cdot (0.5)^{Rsp_B} \]

and:

\[ 1.0 = Rsp_A \cdot (MaxBA_A)^{Rsp_B} \]

Equations 15 and 16 can then be solved simultaneously to find RspA and RspB:

\[ Rsp_A = \frac{[MaxBA_A (\log(FR_{0.5}))]}{1/\log(2 \cdot MaxBA_A)} \]

and:

\[ Rsp_B = \frac{[\log(FR_{0.5}) - \log(Rsp_A)]}{\log(0.5)} \]

Measuring accuracy of growth equations

Predicted stand growth was compared to stand growth estimated from field data to measure the accuracy of the growth equations. To estimate overall stand growth, the stand structure of sample plots was reconstructed from stand tables by spreading trees of the same species and diameter class evenly throughout the diameter class. Each tree's basal area was then backdated using the 10-year diameter increment from the sample tree of the same species and diameter class. The
backdated stands were subsequently modeled and the results compared to the original stands.

Our measures of accuracy were the mean percent error of predicted overall stand growth and bias of overall stand growth. To estimate these for both the descent method and the constrained-fit method, a tenfold cross validation (Verbyla 1986) was performed on the field data. Parameters were estimated on 90% of the data and those parameters were applied to the remaining 10% of the data to measure model accuracy. This technique was repeated nine more times with a different 10% of the data excluded from the parameter estimation and used to measure model accuracy. In this way, the accuracy of the model is measured on every stand, yet the same data were not used to fit parameters and measure accuracy in any given replicate. Since the silvics-based method does not fit the parameters to the field data, a tenfold cross validation was not necessary.

Accuracy of the growth equations was also tested using 2 parameter sets drawn at random from a uniform distribution between 0.0 and 1.0. This was compared to the fit parameters to test the sensitivity of the model to the choice of growth parameters.

RESULTS AND DISCUSSION

A comparison of the final parameter estimates from each of the three techniques is found in Table 3. Estimates of RspA and RspB from understory tolerance and maximum size were close to the values fit to the field data. All of the sample output presented in this paper was calculated using the parameters from the silvics-based method.

Measures of the accuracy of the growth equations using parameters from each of the three estimation techniques are shown in Figure 4. Accuracy of the growth equations using the random parameters are also shown. The similarity in accuracy of the three estimated parameter
# Table 3: Comparison of growth parameters and coefficients of variation

<table>
<thead>
<tr>
<th>Method</th>
<th>ABLA</th>
<th>(PIEN)</th>
<th>PSME</th>
<th>PIFL</th>
<th>PICO</th>
<th>POTR</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>RCC C.V.</td>
<td>RCC C.V.</td>
<td>RCC C.V.</td>
<td>RCC C.V.</td>
<td>RCC C.V.</td>
<td>RCC C.V.</td>
</tr>
<tr>
<td>Descent</td>
<td>0.8 0.00</td>
<td>(1.0) (0.03)</td>
<td>0.9 0.01</td>
<td>0.8 0.02</td>
<td>0.8 0.00</td>
<td>0.6 0.00</td>
</tr>
<tr>
<td>Eco-fit</td>
<td>0.70 --</td>
<td>(0.72) --</td>
<td>0.80 --</td>
<td>0.84 --</td>
<td>0.86 --</td>
<td>0.90 --</td>
</tr>
<tr>
<td>Theory</td>
<td>0.70 --</td>
<td>(0.72) --</td>
<td>0.80 --</td>
<td>0.84 --</td>
<td>0.86 --</td>
<td>0.86 --</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Method</th>
<th>RspA C.V.</th>
<th>RspA C.V.</th>
<th>RspA C.V.</th>
<th>RspA C.V.</th>
<th>RspA C.V.</th>
<th>RspA C.V.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.4 0.00</td>
<td>(0.4) (0.05)</td>
<td>0.6 0.00</td>
<td>0.6 0.06</td>
<td>0.6 0.00</td>
<td>1.0 --</td>
</tr>
<tr>
<td>Eco-fit</td>
<td>0.30 0.01</td>
<td>(0.13) (0.12)</td>
<td>0.55 0.01</td>
<td>0.71 0.04</td>
<td>0.71 0.00</td>
<td>0.99 --</td>
</tr>
<tr>
<td>Theory</td>
<td>0.34 --</td>
<td>(0.36) --</td>
<td>0.56 --</td>
<td>0.66 --</td>
<td>0.74 --</td>
<td>0.96 --</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Method</th>
<th>RspB C.V.</th>
<th>RspB C.V.</th>
<th>RspB C.V.</th>
<th>RspB C.V.</th>
<th>RspB C.V.</th>
<th>RspB C.V.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0.4 0.07</td>
<td>(0.7) (0.07)</td>
<td>0.2 0.00</td>
<td>2.2 0.20</td>
<td>0.1 0.09</td>
<td>0.6 0.00</td>
</tr>
<tr>
<td>Eco-fit</td>
<td>0.45 0.05</td>
<td>(0.26) (0.22)</td>
<td>0.25 0.03</td>
<td>0.28 0.16</td>
<td>0.20 0.01</td>
<td>0.19 0.04</td>
</tr>
<tr>
<td>Theory</td>
<td>0.75 --</td>
<td>(0.53) --</td>
<td>0.31 --</td>
<td>0.26 --</td>
<td>0.31 --</td>
<td>0.45 --</td>
</tr>
</tbody>
</table>

**NOTE:** Coefficients of variation were calculated from 10-fold cross validations of parameters fit to the field data.

Sets is surprising, and, therefore, I suspected that the model was insensitive to the choice of parameters. However, considering the mean errors for the random parameter sets were 50% to 95% higher, the variances of the mean errors were nearly as great or greater than the means themselves, and the biases were between 3 and 72 times higher, I am confident the choice of parameters is important.
It is useful to consider the mean percent error in growth in terms of basal area. The mean error of less than 1.0 ft² per tenth acre (2.3 m²/ha) over 10 years converts to less than 1.0 ft² per acre (0.23 m²/ha) on an annual basis. Since fully stocked stands in the ABLA/BERE type carry roughly 200 ft² per acre (46 m²/ha), the annual error amounts to less than 1/2 of 1% of the basal area of a fully
FIG. 5. Modeled stand dynamics from three different starting mixes: (A) pure POTR, (B) pure PICO, (C) mix of POTR, PICO, PIFL, PSME, and ABLA.

stocked stand. Further, since the bias is nearly zero, the errors would have a tendency to cancel out if several stands were modeled.

Figure 5 represents modeled succession from three different starting species mixes. The model predicts different successional pathways depending on the starting point. Obviously, the starting species mix affects stand composition during the first generation of trees. However, the starting species mix also affects subsequent
generations in this model because overstory composition determines the abundance of regeneration for each species in the understory. In this manner, alternate pathways of succession are modeled.

The model exhibits several emergent properties that mimic known stand dynamics. For instance, maximum stand basal area is not explicitly limited. Rather, the maximum basal area is controlled by minimum growth rates, maximum sizes and understory tolerance of species, and the resources available on the plot. The model predicts a maximum basal area of roughly 240 ft\(^2\)/acre (55 m\(^2\)/ha) for the ABLA/BERE habitat type. Mauk and Henderson (1984) report values between 210 and 230 ft\(^2\)/acre (48 to 53 m\(^2\)/ha). The model also predicts that intolerant species will generally have lower maximum stand basal areas than do tolerant species, which agrees with our field data.

Figure 6 shows the self-thinning dynamics produced by the model for a single-species, even-aged stand. The model predicts that during thinning, a plot of ln(number of trees) vs. ln(mean tree basal area) follows a slope of roughly -1.25, which is consistent with the concept of Stand Density Index (Long and Smith 1984). The -3/2 thinning rule of Yoda et al. (1963) compares volume, not basal area, to tree density.

Figure 7 shows a typical individual growth curve resulting from the interaction between resources captured and respiration. While it is not modeled explicitly, it mimics known size-growth relationships very closely.

The model also demonstrates the process of release -- sudden bursts of growth by invading species as the overstory breaks up. In Figure 5, this is best illustrated by A. lasiocarpa. In each case, its basal area increases rapidly as the dominant species declines.
The method for predicting RCC, RspA, and RspB from understory tolerance looks very promising. Figure 8 compares respiration curves from the constrained-fit method and the silvics-based method (RCC exponents being equal). The parameters predicted by the silvics-based method are partially dependent on the field data since the appropriate ranges for the predicted parameters were established using fit parameters. However, since the ranges only establish the extremes (A. lasiocarpa and P. tremuloides), the excellent agreement of the
FIG. 7. Growth curve -- interaction of resource capture and respiration.

intermediate species (P. menziesii, P. flexilis, and P. contorta) is especially significant. Further, the error and bias measured using the predicted parameters were nearly the same as those resulting from the fit parameters (Figure 4). In order to fully validate this estimation technique, however, it must be used to estimate growth parameters for species in other habitat types and the model's predictions compared to field data.

The regeneration portion of the model is fairly data intensive. This is the factor most limiting the generality of the model. Further research is planned to develop an alternative regeneration scheme so the model will be completely free of high data requirements. However, when considering the data requirements of most of other the options available to a land manager at the present time, this model is a great improvement.
Fig. 8. Comparison of respiration curves fit to data (constrained-fit method) and estimated from species' characteristics (silvics-based method). Data needed to fit the curve for PIEN were lacking.

The structure of this model encourages the addition of other subroutines to model additional forest processes and management schemes. Pathogens could be easily considered. When present, they would claim a portion of each tree's captured resources in a manner similar to the existing respiration routine. Estimates of tree volume could be obtained from known basal area / volume relationships.
inning and other management activities could be easily simulated by moving individual trees or classes of trees from the simulation.

The model was successful in fulfilling both short- and long-term objectives, as well as the guidelines set down by Roberts and Morgan (1989). It predicts plant community composition and stand structure at specified points in time with minimal input requirements. Because of the form of its input requirements, it is well suited for use with forest habitat type classification and seral community classification. Its relative simplicity and speed, as well as its design, will allow it to be easily incorporated into a landscape-level forest succession model and ensures efficient execution on personal computers. The model requires input similar to that of existing conceptual models, yet produces quantitative output useful to the forest manager as well as for model validation. It has the potential to be calibrated for new areas in hours rather than days or even years. At the present time, the model has been calibrated for and tested only on the BLA/BERE habitat type. However, plans are underway to collect the data necessary to test the model on other habitat types.

The model is based on many simplifying assumptions with respect to site quality, tree growth and respiration, and competition. However, the accuracy of the growth equations, the agreement of the emergent properties with natural processes, and the similarity of theoretical and fit parameters all suggest that the processes modeled, as simplified as they are, may be some of the predominant factors that control forest dynamics.
LITERATURE CITED


APPENDIX
PROGRAM MASS10

IMPLICIT NONE

INTEGER*2 MAXSPC
INTEGER*2 MAXCLA
INTEGER*2 MAXTRE
INTEGER*2 SUCPYR

PARAMETER (MAXSPC=6)
PARAMETER (SUCPYR=(MAXSPC**2+MAXSPC)/2)
PARAMETER (MAXCLA=16)
PARAMETER (MAXTRE=1000)

INTEGER*2 I,J,K,L
INTEGER*2 CHS
INTEGER*2 NUMSPC
INTEGER*2 STDTBL(MAXSPC,MAXCLA)
INTEGER*2 NUMTRE
INTEGER*2 SPE(MAXTRE)
INTEGER*2 YEARS
INTEGER*2 AGE
INTEGER*2 NUMPERSPC(MAXSPC)
INTEGER*2 DTBL(MAXSPC,MAXCLA)
INTEGER*2 NEWTREES(MAXSPC)
INTEGER*2 UTRNK(MAXSPC)
INTEGER*2 SZCL

REAL*4 RES
REAL*4 DEADBA(MAXSPC)
REAL*4 RCEXP(MAXSPC)
REAL*4 RSPA(MAXSPC)
REAL*4 RSPB(MAXSPC)
REAL*4 MING(MAXSPC)
REAL*4 MAXG(MAXSPC)
REAL*4 MAXT(MAXSPC)
REAL*4 SPREAD
REAL*4 DBH
REAL*4 TREEBA(MAXTRE)
REAL*4 BAPERSPC(MAXSPC)
REAL*4 TOTBA
REAL*4 NEWBA(MAXSPC)
REAL*4 UDRSTR(MAXSPC,SUCPYR)
REAL*4 LOREG(MAXSPC)

CHARACTER*20 SPNAME(MAXSPC)
CHARACTER*30 OUTFL

DATA NUMPERSPC / MAXSPC*0 /
DATA BAPERSPC / MAXSPC*0 /
DATA LOREG / MAXSPC*0 /

COMMON / STAND / STDTBL,NUMPERSPC,BAPERSPC,TOTBA,
+     DEADBA,DTBL,NEWTREES,NEWBA
COMMON / FIXPAR / SPNAME,UTRNK,MING,MAG,MAXT,RES,NUMSPC
COMMON / EXP / RCEXP,RSPA,RSPB
C* MASS10 ************************** ONE *******************************
C  Determine method of initialization and call proper subrtn.
C* MASS10 ************************** ONE *******************************

WRITE(*,'(''******** Welcome to MASS-10 ********'',//)')

CALL SETUP(YEARS,UDRSTR)

10 WRITE(*,'(**** Initializing the stand can be done in one'',//,
+ '' of two ways:'',//,
+ '' 1. Enter the basal area of each species'',//,
+ '' in the stand'',//,
+ '' 2. Read a stand table of 2 inch diameter'',//,
+ '' classes from a file'',//,
+ '' Enter the number of your choice: '';$)')

READ(*,'(I1)')CHS

IF(CHS.EQ.1)THEN
  CALL BAREA(SPNAME,NUMSPC,NUMTRE,TREEBA,SPE,MAXT,UTRNK)
ELSE IF(CHS.EQ.2) THEN
  CALL GETINP(STDTBL,NUMSPC,NUMTRE,TREEBA,SPE)
ELSE
  WRITE(*,'(**** Invalid choice. Enter 1, 2 or 3''',//)')
  WRITE(*,'(**** Invalid choice. Enter 1, 2 or 3''',//)')
  GOTO 10
ENDIF

C* MASS10 *************************** TWO ******************************
C  Main simulation loop
C* MASS10 *************************** TWO ******************************

20 DO 20 I=1,NUMTRE
  TOTBA = TOTBA + TREEBA(I)
  DBH = SQRT(TREEBA(I)/0.005454)
  SZCL = INT(DBH/2.0)
  IF(CHS.EQ.1)STDTBL(SPE(I),SZCL)=STDTBL(SPE(I),SZCL)+1
  NUMPERSPC(SPE(I))=NUMPERSPC(SPE(I))+1
  BAPERSPC(SPE(I))=BAPERSPC(SPE(I))+TREEBA(I)
  CONTINUE

21 CONTINUE

22 CALL REPORT(AGE,NUMTRE,NUMSPC,SPNAME)

WRITE(*,'('+Calculating year: ''',I7)')AGE

AGE=AGE+10
IF(AGE.GT.YEARS)GOTO 23

CALL GROWTH (NUMTRE,TREEBA,SPE,UDRSTR,LOREG)  ! grow for 10 yrs

GOTO 22

23 CLOSE(3)
SUBROUTINE SETUP(YEARS, UDRSTR)

IMPLICIT NONE

INTEGER*2 MAXSPC
INTEGER*2 SUCPYR

PARAMETER (MAXSPC=6)
PARAMETER (SUCPYR=21)

INTEGER*2 NUMSPC
INTEGER*2 UTRNK(MAXSPC)
INTEGER*2 YEARS
INTEGER*2 PSIZE

INTEGER*2 I, J

REAL*4 MING(MAXSPC)
REAL*4 MAXG(MAXSPC)
REAL*4 MAXT(MAXSPC)
REAL*4 RES
REAL*4 UDRSTR(MAXSPC, SUCPYR)
REAL*4 UNDTOL(MAXSPC)
REAL*4 RCEXP(MAXSPC)
REAL*4 RSPA(MAXSPC)
REAL*4 RSPB(MAXSPC)
REAL*4 RSPS
REAL*4 HIGHUT
REAL*4 CURUT
REAL*4 MAXBA

CHARACTER*30 FLNM
CHARACTER*20 VFMT1
CHARACTER*20 VFMT2
CHARACTER*20 SPNAME(MAXSPC)

COMMON / FIXPAR / SPNAME, UTRNK, MING, MAXG, MAXT, RES, NUMSPC
COMMON / EXP / RCEXP, RSPA, RSPB

WRITE(*,'('' Enter the parameter file name (MASS10.PRM): '',$) ')
READ(*,''(A30)')FLNM
IF(FLNM.EQ.' ')FLNM='MASS10.PRM'
OPEN (UNIT=1, FILE=FLNM, STATUS='OLD')

WRITE(*,'('' Enter the output file name (MASS10.OUT): '',$) ')
READ(*,''(A30)')FLNM
IF(FLNM.EQ.' ')FLNM='MASS10.OUT'
OPEN (UNIT=3, FILE=FLNM, STATUS='NEW')

READ(1,120) NUMSPC
DO 10 I=1, NUMSPC
   READ(1,110) SPNAME(I)
10 CONTINUE
READ(1,100) (UNDTOL(I),I=1,NUMSPC)
READ(1,100) (MING(I),I=1,NUMSPC)
READ(1,100) (MAXG(I),I=1,NUMSPC)
READ(1,100) (MAXT(I),I=1,NUMSPC)
READ(1,100) RES
READ(1,120) YEARS

DO 11 I=1,NUMSPC
   READ(1,130) (UDRSTR(I,J),J=1,21)
11 CONTINUE
CLOSE (1)

100 FORMAT (12F10.4)
110 FORMAT (A20)
120 FORMAT (I6)
130 FORMAT (21F4.2)

C * MASS10 SETUP ************* TWO ***********************
C
** MASS10 SETUP ************* THREE ***********************

WRITE(3,*)' MASS10: Multiple Age-class Stand Simulator'
WRITE(3,300) RES
WRITE(3,*)' SITE SPECIFIC PARAMETERS:
WRITE(3,300) RES
WRITE(3,*)' SPECIES SPECIFIC PARAMETERS:
WRITE(3,300) RES
WRITE(3,*)' CALCULATED PARAMETERS:

C
DO 30 I=1,NUMSPC
   MING(I)=20/MING(I)
   MAXG(I)=20/MAXG(I)
30 CONTINUE
C
C 300 FORMAT(' Potential Growth Resources:', F8.2)
C
C* MASS10/SETUP ************** FOUR ****************************
C****************************************************************
C****************************************************************
C
HIGHUT=11
CURUT=-1
DO 40 I=1,NUMSPC
   DO 41 J=1,NUMSPC
      IF(UNDTOL(J) .LT.HIGHUT.AND.UNDTOL(J) .GT.CURUT)THEN
         UTRNK(J)=I
         CURUT=UNDTOL(J)
      ENDIF
41 CONTINUE
   HIGHUT=CURUT
   CURUT=-1
40 CONTINUE
C
RETURN
C
END
C
C* MASS10/INPUT ****************** SUBROUTINE GETINP ******************

SUBROUTINE GETINP(STDTBL,NUMSPC,NUMTRE,TREEBA,SPE)

IMPLICIT NONE

INTEGER*2 MAXSPC
INTEGER*2 MAXCLA
INTEGER*2 MAXTRE
PARAMETER (MAXSPC=6)
PARAMETER (MAXCLA=16)
PARAMETER (MAXTRE=1000)

INTEGER*2 I,J,L
INTEGER*2 NUMSPC
INTEGER*2 STDTBL(MAXSPC,MAXCLA)
INTEGER*2 SPE(MAXTRE)
INTEGER*2 NUMTRE
REAL*4 SPREAD
REAL*4 DBH
REAL*4 TREEBA(MAXTRE)
CHARACTER*30 FLNM

WRITE(*,100)
100 FORMAT(/,' Enter the stand table file name (STAND.TBL): ',$)
READ(*,'(A20)')FLNM
WRITE(*,*)
IF(FLNM.EQ."")FLNM='STAND.TBL'
OPEN (UNIT=2,FILE=FLNM,STATUS='OLD')
DO 10 I=1,NUMSPC
   READ(2,110) (STDTBL(I,J),J=1,MAXCLA)
10 CONTINUE
110 FORMAT (20I4)
CLOSE (2)

C* MASS10 ***********************TWO*****************************
C Convert stand table into 1D array of individual trees
C* MASS10 ***********************TWO*****************************
DO 21 I=1,NUMSPC
   DO 22 J=1,MAXCLA
      IF (STDTBL(I,J) .GT. 0) THEN
         SPREAD = 2.0 / STDTBL(I,J)
         DO 23 L=1,STDTBL(I,J)
            NUMTRE = NUMTRE + 1
            DBH = (J*2) + (L*SPREAD) - (SPREAD/2)
         ENDIF
      ENDIF
   CONTINUE
21 CONTINUE
RETURN
END

* MASS10/BAREA ****************** SUBROUTINE BAREA ********* *
SUBROUTINE BAREA(SPNAME,NUMSPC,NUMTRE,TREEBA,SPE,MAXT,UTRNK)
IMPLICIT NONE
INTEGER*2 MAXSPC
INTEGER*2 MAXTRE
PARAMETER (MAXSPC=6)
PARAMETER (MAXTRE=1000)
INTEGER*2 NBA
INTEGER*2 NUMSPC
INTEGER*2 UTRNK(MAXSPC)
INTEGER*2 NUMTRE
INTEGER*2 NUM2ADD
INTEGER*2 SPE(MAXTRE)
INTEGER*2 I,J,K
REAL*4 TOTBA
REAL*4 TOTAL
REAL*4 LTOVR
REAL*4 CLSIZE
REAL*4 CLMAX
REAL*4 CLMIN
REAL*4 CLMEAN
REAL*4 MAXT(MAXSPC)
REAL*4 ST(10)
REAL*4 DT(10)
REAL*4 SI(10)
REAL*4 DI(10)
REAL*4 DIST(10)
REAL*4 FRACBA(MAXSPC)
REAL*4 FRACMT
REAL*4 SPREAD
REAL*4 TREEBA(MAXTRE)
CHARACTER*20 SPNAME(MAXSPC)

DATA
+ ST/0.144,0.211,0.242,0.186,0.122,0.057,0.024,0.014,0.000,0.000/
+ DT/0.036,0.124,0.189,0.211,0.183,0.122,0.073,0.033,0.019,0.010/
+ SI/0.005,0.038,0.093,0.143,0.196,0.192,0.167,0.110,0.057,0.000/
+ DI/0.017,0.136,0.215,0.226,0.176,0.112,0.064,0.037,0.017,0.000/

WRITE(*,'(/,'' Enter the PER ACRE stand basal area '',
+ '' to the NEAREST square foot (200): '',S)')
READ(*,'(I5)')NBA
IF(NBA.EQ.0)THEN
   TOTBA=20.0
ELSE
   TOTBA=NBA/10.0
ENDIF

WRITE(*,*)'
10 TOTAL=0
DO 11 I=1,NUMSPC
12 WRITE(*,'('' Enter the FRACTION basal area for '',
   + A20,''':''),S)')SPNAME(I)
   READ(*,'(F8.4)')FRACBA(I)
   IF(FRACBA(I).GT.1.0.OR.FRACBA(I).LT.0.0)THEN
      WRITE(*,*)' ***ERROR: FRACTION must be between 0 and 1. '
      WRITE(*,*)' ***ERROR: FRACTION must be between 0 and 1. '
      GOTO 12
   ENDIF
   TOTAL=TOTAL+FRACBA(I)
11 CONTINUE

IF(ABS(TOTAL-1.0).GT.0.01)THEN
   WRITE(*,*)'
   WRITE(*,*)'*** ERROR: FRACTIONS must sum to 1.0. Reenter...'
   WRITE(*,*)'
   GOTO 10
ENDIF
WRITE(*,*)''}
NUMTRE=0
DO 20 I=1,NUMSPC
   FRACMT=0
   DO 21 J=1,6
      IF (UTRNK(J).LT.UTRNK(I)) FRACMT=FRACMT+FRACBA(J)
   CONTINUE
   IF (1.0-FRACBA(I).GT.0) THEN
      FRACMT=FRACMT/(1.0-FRACBA(I))
   ELSE
      FRACMT=0
   ENDIF
   DO 22 J=1,10
      DIST(J)=(ST(J)*(1-FRACBA(I))*(1-FRACMT) +
               DT(J)*FRACBA(I)*(1-FRACMT) +
               SI(J)*(1-FRACBA(I))*FRACMT +
               DI(J)*FRACBA(I)*FRACMT)
      DIST(J)=DIST(J)*FRACBA(I)*TOTBA
   CONTINUE
   LFTOVR=0
   CLSIZE=(MAXT(I)-2)/10.0
   DO 23 J=10,1,-1
      CLMAX=((J*CLSIZE)+2)**2*0.005454
      CLMIN=((J-1)*CLSIZE)+2)**2*0.005454
      CLMEAN=(CLMAX+CLMIN)/2.0
      DIST(J)=DIST(J)+LFTOVR
      NUM2ADD=INT(DIST(J)/CLMEAN)
      LFTOVR=DIST(J)-(NUM2ADD*CLMEAN)
      DO 24 K=1,NUM2ADD
         NUMTRE=NUMTRE+1
         SPREAD=2*(CLMAX-CLMEAN)/NUM2ADD
         TREEBA(NUMTRE)=CLMAX-(SPREAD/2.0)-(K-1)*SPREAD
         SPE(NUMTRE)=I
      CONTINUE
   CONTINUE
20 CONTINUE
21 CONTINUE
22 CONTINUE
23 CONTINUE
24 CONTINUE
RETURN
END

C* MASS10/GROWTH ****************** SUBROUTINE GROWTH ************
C
SUBROUTINE GROWTH(NUMTRE,TREEBA,SPE,UDRSTR,LOREG)

IMPLICIT NONE

INTEGER*2 MAXSPC
INTEGER*2 MAXCLA
INTEGER*2 MAXTRE
INTEGER*2 SUCPYR

PARAMETER (MAXSPC=6)
PARAMETER (SUCPYR=21)
PARAMETER (MAXCLA=16)
PARAMETER (MAXTRE=1000)
INTEGER*2 I,J,K,L

INTEGER*2 NUMSPC
INTEGER*2 STDTBL (MAXSPC, MAXCLA)
INTEGER*2 STRTRE (MAXTRE)
INTEGER*2 SPE (MAXTRE)
INTEGER*2 NUMSTR
INTEGER*2 NUMTRE
INTEGER*2 NUMERSPC (MAXSPC)
INTEGER*2 KILL
INTEGER*2 DTBL (MAXSPC, MAXCLA)
INTEGER*2 INDEX
INTEGER*2 PASTNT
INTEGER*2 NREG
INTEGER*2 NEWTREES (MAXSPC)
INTEGER*2 REGSPC (MAXSPC)
INTEGER*2 IND
INTEGER*2 UTRNK (MAXSPC)
INTEGER*2 SZCL

REAL*4 RES
REAL*4 DEADBA (MAXSPC)
REAL*4 MAXT (MAXSPC)
REAL*4 MING (MAXSPC)
REAL*4 MAXG (MAXSPC)
REAL*4 DEMAND
REAL*4 RD (MAXTRE)
REAL*4 TREEBA (MAXTRE)
REAL*4 RCEXP (MAXSPC)
REAL*4 RSPA (MAXSPC)
REAL*4 RSPB (MAXSPC)
REAL*4 RSP
REAL*4 GROW
REAL*4 SHAR
REAL*4 MAXSIZE
REAL*4 MINSIZE
REAL*4 CDBH
REAL*4 NEXTBA
REAL*4 STRESS (MAXTRE)
REAL*4 TOTBA
REAL*4 BAPERSPC (MAXSPC)
REAL*4 DBH
REAL*4 STRBA
REAL*4 REGRES
REAL*4 TOTWT
REAL*4 REGWT (MAXSPC)
REAL*4 SPREAD
REAL*4 NEWBA (MAXSPC)
REAL*4 TOTRW
REAL*4 UDRSTR (MAXSPC, SUCPYR)
REAL*4 ABUNDA (21)
REAL*4 SPETOT (MAXSPC)
REAL*4 SUM
REAL*4 LOREG (MAXSPC)
REAL*4 REGBA

CHARACTER*20 SPNAME (MAXSPC)
**C MASS10/GROWTH ************************* ONE **************************

**C Initialize stand variables**

DEMAND = 0.0

DO 10 I=1,NUMSPC
    DEADBA(I) = 0
    DO 11 J=1,MAXCLA
        DTBL(I,J) = 0
    11 CONTINUE
10 CONTINUE

**C MASS10/GROWTH **************************** TWO **************************

**************TWO*****************************
Calculate individual growth and find stressed trees
**************TWO*****************************

DO 20 I=1,NUMTRE ! for all trees in stand
    RD(I) = (TREEBA(I)*144)**RCEXP(SPE(I)) ! calc res demand
    DEMAND=DEMAND+RD(I) ! sum stand res demand
20 CONTINUE

NUMSTR = 0 ! init num stressed trees
STRBA = 0.0

DO 21 I=1,NUMTRE ! for all trees
    RSP = RSPA(SPE(I))*TREEBA(I)**RSPB(SPE(I)) ! calc respiration
    SHAR = (RD(I)/DEMAND)*RES ! calc resource gain
    GROW = SHAR*(1-RSP) ! calc growth
    CDBH = SQRT(TREEBA(I)/0.005454154)
    NEXTBA = TREEBA(I) + GROW
    TOTBA=TOTBA+GROW
    MINSIZE = (CDBH + MING(SPE(I)))**2 * 0.005454154
    MAXSIZE = (CDBH + MAXG(SPE(I)))**2 * 0.005454154

    IF (NEXTBA .LT. MINSIZE) THEN
        NUMSTR = NUMSTR + 1 ! increment stress count
        STRTRE(NUMSTR) = I ! memorize stressed tree
        STRESS(NUMSTR) = GROW ! calc stress level
        STRBA = STRBA + TREEBA(I)
        TREEBA(I) = -1 * (TREEBA(I)+GROW) ! flag stressed tree
    ELSE
        IF (NEXTBA.GT.MAXSIZE) THEN
            TREEBA(I) = MAXSIZE
        ELSE
            TREEBA(I)=TREEBA(I)+GROW
        ENDIF
    ENDIF
21 CONTINUE

**C MASS10/GROWTH **************************** THREE **************************

**C Kill off trees with most stress and fill holes in array by**
**C taking live trees from end and moving them up into array**
elements left open by dead trees.

C* MASS10/GROWTH ************************** THREE ******************

IF (STRBA .GT. TOTBA*0.05) THEN ! test vs. number stressed
   CALL SORTSTR(NUMSTR,STRESS,STRTRE,TREEBA,KILL,TOTBA) ! sort
ELSE
   KILL=NUMSTR
ENDIF

PASTNT = NUMTRE
NUMTRE = NUMTRE - KILL
DO 30 I=1,KILL ! for all trees to be killed
   DEADBA(SPE(STRTRE(I))) = DEADBA(SPE(STRTRE(I))) +
   + TREEBA(STRTRE(I))
   INDEX = INT(SQRT(TREEBA(STRTRE(I))/-0.005454) / 2)
   DTBL(SPE(STRTRE(I)),INDEX) =
   + DTBL(SPE(STRTRE(I)),INDEX) - 1
   IF (STRTRE(I) .GT. NUMTRE) GO TO 30 ! check for overflow
32 IF (TREEBA(PASTNT).LT.0.0) THEN
   PASTNT = PASTNT - 1
   GOTO 32
ENDIF
TREEB(A(STRTRE(I)) = TREEBA(PASTNT) ! swap dead tree with last
SPE(STRTRE(I)) = SPE(PASTNT) ! tree in list
PASTNT = PASTNT - 1 ! decrement # of trees
30 CONTINUE

C* MASS10/GROWTH ****************************** FOUR ******************
C Calculate which species regenerate
C* MASS10/GROWTH ****************************** FOUR ******************

REGRES=0
REGRES=MAX(0.0,RES*(1-(DEMAND/(288*RES))**.01))

TOTWT = 0.0
NREG = 0
DO 40 I=1,NUMSPC
   NEWTREES(I)=0
   BAPERSPC(I)=0
   NEWBA(I)=0
40 CONTINUE

DO 41 I=1,NUMTRE
   BAPERSPC(SPE(I))=BAPERSPC(SPE(I))+TREEBA(I)
41 CONTINUE

IND=1
SUM=0
DO 42 I=1,NUMSPC
   REGWT(I)=0
   IF(BAPERSPC(I).NE.0) IND=MAX(IND,UTRNK(I))
   SUM=SUM+I
42 CONTINUE

DO 43 I=1,SUM
   ABUNDA(I)=0
43 CONTINUE

SUM=0
DO 44 I=1,IND
    SUM=SUM+I
 44 CONTINUE
C
TOTRW=0
DO 45 I=1,NUMSPC
    IF(BAPERSPC(I).GT.0) THEN
        INDEX=SUM-(UTRNK(I)-1)
        ABUNDA(INDEX)=BAPERSPC(I)/TOTBA
        DO 46 J=1,NUMSPC
            REGWT(J)=REGWT(J)+(UDRSTR(J,INDEX)*ABUNDA(INDEX))
            TOTRW=TOTRW+(UDRSTR(J,INDEX)*ABUNDA(INDEX))
        46 CONTINUE
    ENDIF
 45 CONTINUE

NREG=0
DO 47 I=1,NUMSPC
    REGWT(I)=REGWT(I)/TOTRW
    IF(REGWT(I).GT.0) THEN
        NREG=NREG+1
        REGSPC(NREG)=I
    ENDIF
 47 CONTINUE

DO 48 I=1,NREG
    REGBA=REGWT(REGSPC(I))*REGRES + LOREG(REGSPC(I))
    NEWTREES(REGSPC(I)) = INT(REGBA/.0218)
    LOREG(REGSPC(I))=REGBA - NEWTREES(REGSPC(I))*0.0218
    DO 49 J=1,NEWTREES(REGSPC(I))
        SPREAD = 2.0 / NEWTREES(REGSPC(I)) ! calculate spread
        DBH = 2 + ((J-1)*SPREAD) ! calculate DBH
        TREEBA(I,J) = DBH**2 * 0.005454 ! calculate BA
        SPE(I,J) = REGSPC(I) ! store species ID
        NEWBA(REGSPC(I))=NEWBA(REGSPC(I)) + TREEBA(I,J)
        BAPERSPC(REGSPC(I))=BAPERSPC(REGSPC(I)) + TREEBA(I,J)
    49 CONTINUE

C* MASS10/GROWTH ********************************************* FIVE **********
C
50 TOTBA = 0.0
   DO 51 I=1,NUMSPC
      NUMPERSPC(I) = 0
   DO 52 J=1,MAXCLA
      STDTBL(I,J) = 0
 52 CONTINUE
 51 CONTINUE

   DO 53 I=1,NUMTRE
      TOTBA = TOTBA + TREEBA(I) ! sum up basal area
      DBH = SQRT(TREEBA(I)/0.005454) ! calc new stand table
      SZCL = INT(DBH/2.0)
      SZCL = MIN(SZCL,MAXCLA)
      STDTBL(SPE(I),SZCL)=STDTBL(SPE(I),SZCL)+1
      NUMPERSPC(SPE(I))=NUMPERSPC(SPE(I))+1
 53 CONTINUE
SUBROUTINE SORTSTR (NUMSTR, STRESS, STRTRE, TREEBA, KILL, TOTBA)

IMPLICIT NONE

PARAMETER (MAXTRE = 1000)

INTEGER*2 KILL
INTEGER*2 NUMSTR
INTEGER*2 STRTRE (MAXTRE)

INTEGER*2 I, J

REAL*4 STRESS (MAXTRE)
REAL*4 TREEBA (MAXTRE)
REAL*4 TEMSTR
REAL*4 TETMRE
REAL*4 TOTBA
REAL*4 BALOST

BALOST = 0.0
KILL = 0

DO 10 I = 1, NUMSTR - 1
   DO 11 J = I + 1, NUMSTR
      IF (STRESS (J) .LT. STRESS (I)) THEN
         TEMSTR = STRESS (I)
         TEMTRE = STRTRE (I)
         STRESS (I) = STRESS (J)
         STRTRE (I) = STRTRE (J)
         STRESS (J) = TEMSTR
         STRTRE (J) = TEMTRE
      ENDIF
   11 CONTINUE
  10 CONTINUE

BALOST = BALOST + (-1 * TREEBA (STRTRE (I)) )
IF ((BALOST .GT. TOTBA * 0.15) .AND. (KILL .EQ. 0)) THEN
   KILL = I
   GOTO 14
ENDIF

13 CONTINUE

14 DO 12 I = KILL + 1, NUMSTR
   TREEBA (STRTRE (I)) = -1 * TREEBA (STRTRE (I))
 12 CONTINUE

RETURN

END
SUBROUTINE REPORT (AGE, NTREES, NUMSPC, SPNAME)

IMPLICIT NONE

INTEGER*2 MAXCLA
INTEGER*2 MAXSPC

PARAMETER (MAXCLA=16)
PARAMETER (MAXSPC=6)

INTEGER*2 NUMSPC
INTEGER*2 NTREES
INTEGER*2 STDTLB(MAXSPC, MAXCLA)
INTEGER*2 NUMPERSPC(MAXSPC)
INTEGER*2 TABS
INTEGER*2 AGE
INTEGER*2 DEAD(MAXSPC)
INTEGER*2 DTBL(MAXSPC, MAXCLA)
INTEGER*2 NEWTREES(MAXSPC)
INTEGER*2 LENLINE
INTEGER*2 I, J

REAL*4 DEADBA(MAXSPC)
REAL*4 BAPERSPC(MAXSPC)
REAL*4 TOTBA
REAL*4 NEWBA(MAXSPC)

CHARACTER*20 SPNAME(MAXSPC)
CHARACTER*30 VFMT1, VFMT2, VFMT3, VFMT4, LFMT
CHARACTER*130 OLINE

COMMON/STAND/STDTLB, NUMPERSPC, BAPERSPC, TOTBA,
  DEADBA, DTBL, NEWTREES, NEWBA

TABS=(MAXCLA*4)+25
WRITE(VFMT1,100)TABS
WRITE(VFMT2,110)MAXCLA
WRITE(VFMT3,120)MAXCLA
WRITE(VFMT4,130)(MAXCLA-1)*4
WRITE(3,*)''
WRITE(3,'(3,VFMT1)'' YEAR = ',AGE,' NUMBER BA''

DO 10 I=1,NUMSPC
  DEAD(I)=0
  LENLINE=24
DO 11 J=1,MACL
  DEAD(I)=DEAD(I)+DTBL(I,J)
  IF (DTBL(I,J).EQ.0) THEN
    WRITE(LFMT,140)LENLINE
    WRITE(DLINE,LFMT)DLINE,
  ELSE
    WRITE(LFMT,150)LENLINE
    WRITE(DLINE,LFMT)DTBL(I,J)
ENDIF

LENLINE = LENLINE + 4
11 CONTINUE
C
WRITE (LFMT, 160) LENLINE
WRITE (DLINE, LFMT) DLINE, DEAD(I), DEADBA(I)
C
IF ((NUMPERSPC(I) .GT. 0) .OR. (DEADBA(I) .NE. 0)) THEN
  IF (NEWTREES(I) .NE. 0) WRITE (3, VFMT4) NEWTREES(I),
     NEWTREES(I), NEWTREES(I),
  WRITE (3, VFMT2) SPNAME(I), (STOTBL(I, J), J=1, MAXCLA),
     NUMPERSPC(I), NUMPERSPC(I)
  IF (DEADBA(I) .NE. 0) WRITE (3, '(A130)') DLINE
ENDIF
10 CONTINUE
WRITE (3, VFMT3) (I*2, I=1, MAXCLA), '+', NTREES, TOTBA
C
100 FORMAT ('(A8, I4, T, I3, A13)')
110 FORMAT ('(4X, A20, I2, I4, I7, F8.2)')
120 FORMAT ('(24X, I2, I4, I1, I6, F8.2)')
130 FORMAT ('(24X, I4, I3, X, I7, F8.2)')
140 FORMAT ('(A, I3, A4)')
150 FORMAT ('(A, I3, I4)')
160 FORMAT ('(A, I3, I7, F8.2)')
C
RETURN
C
END