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Key Algorithms Used in GR02: A Computer Simulation Model for Predicting Tree and Stand Growth

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Abstract

The Vermont Woodland Resource Analysis Program (VWRAP) is an interactive computer program designed to help forest-land owners make decisions. GR02 is a simulation model written as a subprogram in VWRAP for predicting individual tree and stand growth over time. The model can be characterized as an individual tree, distance-independent model. It performs five major functions during each run: (1) updates diameter at breast height, (2) updates total height, (3) estimates mortality, (4) determines regeneration, and (5) updates crown class. The key algorithms used in GR02 are presented.

Introduction

An inventory of standing timber is one of the main requirements in the preparation of a forest management plan. However, an inventory is static, and it is only valid for the time when the data were collected. One method of making the inventory dynamic is through simulation. By simulating changes that take place in the growing forest, an inventory taken at one time can be projected to some future time.

In Vermont, 90 percent of the commercial forest land is privately owned (Kingsley 1977). Excluding forest industry, corporate ownership, and forest land owned by private organizations, there are 74,000 individual owners of 3 million acres of commercial forest land in Vermont. A system that integrates a static concept of forest inventory with the dynamics of growth simulation can improve decisions made by forest-land owners and managers of this land.

The Vermont Woodland Resource Analysis Program (VWRAP) is designed to help forest-land owners make decisions; VWRAP consists of three computer programs: DATA2, YIELD, and GR02. Data from a forest inventory collected in a prescribed format are entered into a computerized data base via DATA2, an interactive program. The user can then produce a summary inventory of the woodlot on a stand-by-stand basis with the interactive program YIELD.

Long-term projections of growth for trees in the data base can be obtained with GR02, a computer simulation model for predicting individual tree and stand growth over time. The model is an individual tree, distance-independent model with both continuous and discrete variables (Ek and Dudek 1980). It can project the growth of stands composed of mixtures of species in all-aged or even-aged stands. The model, written in FORTRAN-20, version 5, is designed to run on a DEC-System 20 computer using the TOPS-20 operating system.

In this paper we present the key algorithms used to model the growth of individual sample trees and sample plots from which stand growth is inferred. The "Vermont Woodland Resource Analysis Program (VWRAP) User's Manual" describes how to use the model.¹

¹ A copy of the manual can be obtained by writing: Extension Forester, School of Natural Resources, University of Vermont, Burlington, Vermont 05405.

Model Philosophy

Trimble (1969) reported that crown class is the most important predictor of the diameter growth of trees. We tested and confirmed Trimble's conclusion using radial increment measurements from core samples in Vermont. Given a number of diameter-growth predictor variables to choose from—d.b.h., crown length, crown width, basal area, crown class, and vigor class—for a given species on the same site, crown class was the best overall predictor of current diameter growth at breast height (Trimble 1969). Trimble's result suggested a method that was both simple and reliable.

The model relies heavily on crown class, dominant, codominant, intermediate, and overtopped (Trimble 1969), because of the statistical correlation between crown class and diameter growth. The detailed model description that follows shows that the computational algorithms that use crown class for growth prediction are relatively simple and quick to execute.

Diameter growth is projected on the basis of a tree's crown class. The total height of each sample tree is updated during a simulation run; new relative heights are computed, and Monte-Carlo techniques are used to determine a tree's crown class based on its current relative height.

For simplicity in introducing the model, the preceding discussion has ignored several other important factors in tree growth. Among these are species, site index, stocking density expressed by basal area per acre, species-specific response to release, and damage as a result of injury or disease. These factors are treated in the sections that follow.

A Dynamic Hypothesis

To use crown class as a growth predictor, it is necessary to know the crown class of a tree at any stage in its development. The growth simulator must be able to determine a tree's crown class at any point in time. This problem was solved empirically, using measurements taken from sample plots scattered throughout northern and central Vermont. Figure 1 illustrates the solution and represents the dynamic hypothesis which is the key concept in the simulation model.

Figure 1 shows the proportion of trees in a particular crown class as a function of relative height.

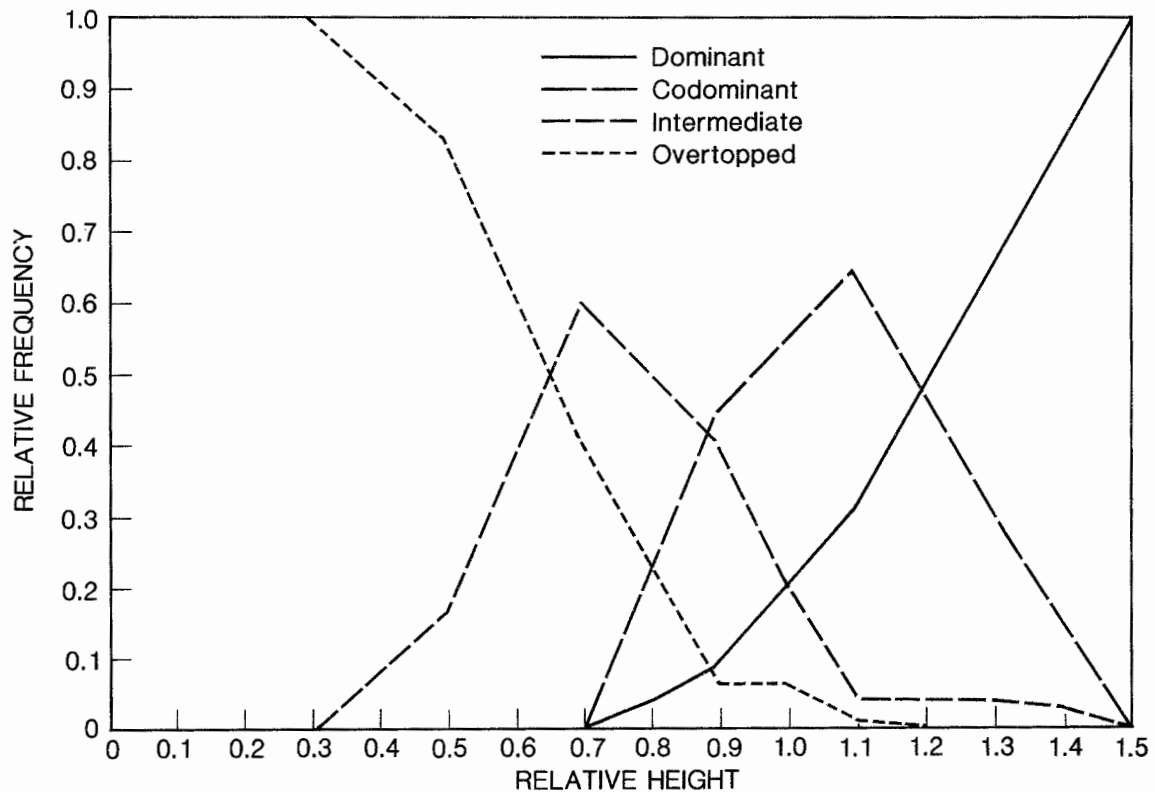


Figure 1.—Relative frequency of crown class as a function of relative tree height or height of tree expressed as a proportion of canopy height.

The proportions sum vertically to 1 at each relative height. As a tree's relative height increases, it is more likely to be in one of the higher crown classes, thus increasing its annual radial-growth rate. As a tree's relative height decreases, because it is overtopped by surrounding trees, it is more likely to be in a lower crown class, thus decreasing its annual radial-growth rate.

An individual tree's relative height depends on the height of surrounding trees on the plot. Relative height of the i^{th} tree on a sample plot is defined by the expression:

$$RH_i = H_i / \bar{H} \quad (1)$$

where

RH_i = relative height of the i^{th} tree,

H_i = total height of the i^{th} tree,

and

\bar{H} = canopy height.

The canopy height, \bar{H} , is the weighted average height of the trees on the plot, where each tree's total height has been weighted by the tree's basal area. For variable-radius plots, it follows that the canopy height is the simple average height of the sampled trees.

The largest diameter trees on a plot make up the canopy, whereas the smaller diameter trees shape the understory. This agrees with the observation that one can remove a large number of smaller diameter (understory) trees from an area with little effect on the height of the canopy. The relative heights of the remaining trees are changed little by removing the smaller trees. With this model, growth rates of the remaining trees also change little. However, removing the larger trees from the same area reduces the canopy height, changes the entire relative height distribution, and thrusts the remaining trees into higher crown classes with a resulting increase in their overall growth rate.

Key Algorithms in the Growth Model

Initializing GR02

Tree data are entered into GR02 by plot. In GR02, each sample plot is expanded to 1 acre, regardless of whether the information was obtained from variable-radius or fixed-area plots, before the simulation begins. Each of these 1-acre plots is treated independently as if there were n independent forests all growing at the same time within the model.

This process associates a frequency per acre with each sample tree on a plot. This frequency or expansion factor is used to compute the per-acre contribution of each sample tree to a given variable. For example, multiplying a tree's total biomass by its frequency per acre gives its contribution to the total biomass per acre for that plot.

Stand information tables, on the other hand, are the result of averaging all of the information contributed by the independent sample plots. Growth characteristics depend only on information associated with a single plot; stand table information depends on data supplied from all the plots entered into the simulation.

By not aggregating plot information during the growth simulation, the heterogeneity of the forest is maintained. Different parts of the forest will grow at different rates depending on site characteristics and tree species composition.

Basal Area

Tree basal area is the basal area (in square feet) associated with a sampled tree. Tree basal area per acre is defined as the product of tree basal area of a sample tree and its corresponding frequency per acre. For example, when a 10-factor prism is used to sample trees in the inventory process, a single 10-inch-diameter tree on an expanded sample plot represents 18.3 simulator trees per acre. During the model initialization process, a frequency of 18.3 trees per acre is associated with this sample tree. The tree basal area per acre of this sample tree equals the product of the tree basal area (0.5454 ft²) and the sample tree frequency (18.3 trees per acre), or 10 ft² per acre. Total basal area per acre is defined as the sum of all the tree basal areas per acre on the same sample plot.

The GR02 model performs five major functions during each run: (1) updates diameter at breast height, (2) updates total height, (3) estimates mortality, (4) determines regeneration, and (5) updates crown class. Each function is treated in detail in the following sections. Together, they provide the mechanisms for modeling the dynamics of growth of a forest.

Updating Diameter at Breast Height

The diameter at breast height outside bark is updated once each growing season during a simulation. First, radial increment inside the bark is determined for each sample tree; radial increment is converted to diameter increment outside the bark; and diameter increment is added to the current diameter outside bark to give updated breast height diameter.

Estimating the annual radial increment. On the basis of an analysis of 432 core samples taken throughout the State of Vermont, the annual radial increment (inside bark), RINC, was determined to be primarily a function of species, crown class, site index, and stand density.

Within a given crown class (dominant, codominant, intermediate, and overtopped), the minimum radial increment for trees in stands with a total basal area per acre of 100 ft² and greater is determined from the expression:

$$\text{MNRINC} = X_0 + X_1 (\text{SITE}) \quad (2)$$

where

$$\text{MNRINC} = \text{minimum radial increment (mm)} \\ (100 \text{ ft}^2 \text{ BA/A and greater),}$$

$$\text{SITE} = \text{site index at breast height age 50,}$$

and

$$X_0, X_1 = \text{species dependent coefficients.}$$

Similarly, the maximum radial increment for 40 ft² and lower basal area is determined from the expression:

$$\text{MXRINC} = X_0 + X_1 (\text{SITE}) \quad (3)$$

where

$$\text{MXRINC} = \text{maximum radial increment (mm)} \\ (40 \text{ ft}^2 \text{ BA/A and lower).}$$

Within a given crown class and between 40 and 100 ft² of basal area, linear interpolation gives:

$$RINC = MNRINC + \frac{MXRINC - MNRINC}{100 - 40} (100 - LBAPA) \quad (4)$$

where

RINC = radial increment (40 ft² < BA/A < 100 ft²)

and

LBAPA = total basal area per acre.

Coefficients for expressions (2) and (3) were estimated for annual radial increment (in millimeters) for the following species: red spruce, white pine, hemlock, red maple, sugar maple, yellow birch, white birch, American beech, white ash, and northern red oak (Appendix, Table 6). Two additional sets of coefficients were developed for all hardwood species and for all softwood species. These are used to determine radial increment for species not included here.

If more appropriate coefficients are available from another source for a species we did not include, users can add them to the program or can substitute one of the available sets. The simulation program, and VWRAP in general, were designed to easily accommodate user modifications.

Trees are classified during the field inventory by condition and damage class. Trees with live, intact tops showing no signs of damage are assigned a radial increment as calculated previously. All other trees suffer an arbitrary degradation in radial increment by a factor between 0 and 1 selected at random from a rectangular distribution by the program. In other words, because no data were collected to correlate growth with damage, the expected value for the growth rate of damaged trees is assumed to be half the rate of undamaged trees.

To obtain the diameter increment outside bark, radial increment is first doubled, then converted to diameter increment outside bark by dividing by the species-specific ratio of diameter inside bark to diameter outside bark. The species-specific ratios were estimated by regression analysis of the trees in the growth-rate data base (Table 1). The values for an additional 12 species were obtained from Martin (1981). Other species are assigned a value of 0.926 for this ratio.

When trees change crown class, the model gradually changes diameter increment (Forrester 1961). Diameter increments are weighted by species-specific response times which have been developed from the shade-tolerance ratings assigned to various species

(Spurr and Barnes 1980). Using these weighting factors causes shade-tolerant trees to take three growing seasons to respond fully to a change in crown class, whereas shade-intolerant species may take as long as 15 years.

Table 1.—Average DIB/DOB ratios, by species, for growth-rate trees

Species	DIB/DOB ratio	n
American beech	.930	48
Northern red oak	.917	53
Red maple	.937	47
Sugar maple	.913	59
White ash	.915	47
White birch	.948	35
Yellow birch	.915	38
Eastern hemlock	.916	37
Eastern white pine	.929	42
Red spruce	.936	26

Updating Total Height

The total height of each sample tree is updated once each growing season during a simulation run; GRO2 uses information obtained from site-index curves to update height. Site-index curves used in GRO2 were obtained from Hampf (1965) for red spruce, eastern hemlock, and eastern white pine; from Carmean (1978) for red maple, American beech, and northern red oak; and from Curtis and Post (1962) for sugar maple, yellow birch, white birch, and white ash.

Information in site-index curves. Site-index curves are the family of curves showing the total height for a given species plotted as a function of age at breast height for different site-index values. Within a foot or two, most of the published curves can be expressed as:

$$HGHT = TMXH + (4.5 - TMXH)e^{-T/THTC} \quad (5)$$

where

HGHT = total height (feet),

TMXH = tree maximum height (feet),

T = breast height age (years),

and

THTC = tree height time constant (years).

Breast height age is the independent variable; the maximum height (TMXH) and height time constant (THTC) are parameters of the particular curve chosen. When T equals zero in expression (5), the height is 4.5 feet; when T is very large, the total height is approximately equal to the maximum height.

Height increment (HINC) can be written as:

$$\text{HINC} = \left[\frac{1}{\text{THTC}} \right] (\text{TMXH} - \text{HGHT}) \quad (6)$$

Equation (6) is the approximate solution to equation (5), which fits the site-index curves. It is a powerful tool for simulation because it gives the rate of height growth as a function of the height and not the age of the tree.

The two constants, TMXH and THTC, are obtained for any site-index curve by fitting equation (5) exactly to two points on the curve. The values of TMXH and THTC were obtained by using an iterative approximation technique. The reader is cautioned against a strictly biological interpretation of the two constants because the shape of some of the curves implies values that we would not expect to observe in the field.

In GRO2, site-index values are grouped into 10-foot classes (Table 2). Values of TMXH and THTC for 10 species and seven site-index classes within species are contained in GRO2 (Appendix, Table 7). Currently, other hardwoods use the values for yellow birch, and other softwoods use the values for white pine. Values for other species can be added, or existing values changed.

Annual height-increment modifier. Understory trees grow taller more slowly than overstory trees. The height-growth modifier quantifies this observed change in rate of height growth. If the sample tree belongs to the intermediate or overtopped crown classes, the computed height increment is multiplied by the tree height-growth modifier, THGM.

We assumed that the maximum height constant, TMXH, is not affected for understory trees, but that the height time constant, THTC, becomes larger. If THTC1 is the time constant for dominant and codominant trees of the species and site under consideration, and THTC2 is the time constant for an understory tree, the height-growth modifier is defined as the ratio:

$$\text{THGM} = \text{THTC1}/\text{THTC2}; \text{THTC2} > \text{THTC1} \quad (7)$$

Table 2. Site-index classes used in GRO2

Number	Site-index values	Site-index class
1	00-44	40
2	45-54	50
3	55-64	60
4	65-74	70
5	75-84	80
6	85-94	90
7	95+	100

Height-growth modifiers were calculated from the calibration data for each of 10 species, other hardwoods, other softwoods, and for the intermediate and overtopped crown classes. Substituting for THTC1 and THTC2 in equation (7) and simplifying yields:

$$\text{THGM} = \frac{\ln [(HGHT2 - \text{TMXH})/(4.5 - \text{TMXH})]}{\ln [(HGHT1 - \text{TMXH})/(4.5 - \text{TMXH})]} \quad (8)$$

Potential height, HGHT1, was read from the site-index curve; actual height, HGHT2, was observed from the calibration data; and TMXH was estimated from the same site-index curve. Averages for each species and understory crown class were calculated and are stored in GRO2.

Mortality

The mortality segment of GRO2 was adapted from Buchman (1979). The estimated annual probability of a tree dying is given by the expression:

$$\text{MR} = [1.0 + \exp(A + B \text{DINC}^C)]^{-1} + D \quad (9)$$

where

MR = mortality rate,

DINC = exponentially weighted diameter increment outside bark (inches/year),

and

A, B, C, D = species specific parameters (Appendix, Table 8).

The mortality rate depends on the rate of diameter growth. At a high rate of diameter growth, the mortality is approximately equal to the constant, D. Mortality rate approaches its maximum value as diameter growth drops to zero. Between zero diameter growth and a high rate of diameter growth, mortality rate decreases exponentially.

In GRO2, trees in the understory will be growing more slowly than those in the overstory, and have higher mortality rates. Fast-growing dominant trees will have the highest survival rate. Undamaged trees generally will have a higher diameter increment than damaged trees; thus, the damaged trees will die at a higher rate.

Coefficients provided with Buchman's expressions (1979) were adjusted so that the more shade-tolerant species had a lower mortality rate at lower levels of diameter increment. Shade-intolerant species had a higher mortality rate at the lower levels of diameter increment. Species intermediate in shade tolerance were not adjusted.

Once the mortality rate is determined for a given tree, a new frequency is computed for that tree by multiplying the current frequency by 1 minus the mortality rate. A new basal area per acre also is computed by multiplying the tree basal area by the newly computed frequency.

We assumed that the higher the site index for a given plot, the higher the maximum basal area that can be supported on that plot. It also is assumed that softwood plots can support higher basal areas than hardwood plots; GRO2 keeps the total basal area per acre from exceeding some maximum value for each sample plot.

Given these conditions, the maximum total basal area per acre that can be supported on a 1-acre sample plot is assumed to follow the relation:

$$LMBA = MBAH + RSBA(MBAS - MBAH) \quad (10)$$

where

LMBA = maximum total basal area (ft² per acre),

MBAH = maximum basal area for hardwoods (ft² per acre),

MBAS = maximum basal area for softwoods (ft² per acre),

and

RSBA = ratio of softwood total basal area to hardwood total basal area per acre.

For hardwoods, the maximum basal area per acre is given by the expression:

$$MBAH = 2.5 \text{ WASI} \quad (11)$$

where

WASI = weight-averaged site index (ft at breast height age (Bha) = 50).

For softwoods, the maximum basal area per acre is given by the expression:

$$MBAS = 3.375 \text{ WASI} \quad (12)$$

The weight-averaged site index for each sample plot is determined from the expression:

$$\text{WASI} = \frac{\sum_{i=1}^N \text{Site}_i \text{BA}_i}{\sum_{i=1}^N \text{BA}_i} \quad (13)$$

where

WASI = weight-averaged site index (ft at Bha = 50),

SITE_i = species site index for the ith sample tree (ft at Bha = 50),

BA_i = basal area per acre contributed by the ith sample tree (tree basal area x frequency),

and

N = number of sample trees (not the frequency) on the sample plot.

Substituting for MBAH and MBAS in expression (10) yields:

$$LMBA = 2.5 \frac{\text{WASI}}{\text{WASI}} (1 - RSBA) + 3.375 RSBA \quad (14)$$

Expression (14) is used in GRO2 to determine the maximum allowable total local basal area per acre for a given sample plot.

After the number of simulator trees is reduced through mortality, the total basal area per acre is computed and compared with the maximum allowable for each plot. If the total exceeds the maximum, the plot reenters the mortality subprogram; otherwise, no more mortality occurs on the plot for the current growing season.

Determining Regeneration

New trees are brought into the model in proportion to the basal area of existing species. This simple model of regeneration ignores the many complexities observed in natural regeneration; however, it does provide for ingrowth on the sample plots. For the length of simulation that we envisioned, the species composition and timing of regeneration are of little consequence. To focus on the simulation of regeneration, a more complex model would be needed.

Determining the number of new trees to enter. Only species currently existing on a sample plot are regenerated on that plot. Trees are entered into the 1-inch d.b.h. class at a fixed diameter of 0.5 inch at breast height outside bark, a height of 8.5 feet, and an overtopped crown class.

To determine how many trees to enter on a sample plot, GRO2 examines the total basal area per acre in the 1-inch diameter class (0.50 to 1.49 inches) at the end of each growing season. GRO2 maintains between 1.84 and 5.0 ft² basal area per acre in the 1-inch diameter class.

When regeneration occurs, a tree is created for each species existing on the plot. The basal area per acre associated with each new tree is computed from the expression:

$$BA_i = PROBA_j (MXBA1 - TOTBA1) \quad (15)$$

where

BA_i = basal area per acre associated with the i^{th} new tree (ft² per acre),

$PROBA_j$ = proportion of total basal area per acre contributed by the j^{th} species on this plot,

$MXBA1$ = maximum basal area assigned to 1-inch d.b.h. class (ft² per acre),

and

$TOTBA1$ = total basal area per acre in 1-inch class (ft² per acre).

The frequency associated with each new tree is given by the expression:

$$FREQ_i = BA_i / TBA_i \quad (16)$$

where

$FREQ_i$ = frequency associated with i^{th} new tree (trees per acre),

and

TBA_i = tree basal area of i^{th} new tree (ft² per acre).

The GRO2 model allows regeneration only when the basal area of the sapling crop in the 1-inch diameter class falls below some arbitrary value (1.84 ft²). If GRO2 allowed regeneration to occur annually, the number of trees would increase rapidly with little observable impact on the growth characteristics of the larger trees, but with a marked impact on the model's run-time performance.

In practice, the number of new trees entering a simulation usually is small (though the associated frequency may seem large). The reason for this is that mortality of trees in the 1-inch d.b.h. class is balanced by basal-area growth of survivors, which keeps the basal area above the level for entering new trees. Also, trees in this diameter class generally are slow to grow out of it.

Updating Crown Class

At the end of each simulated growing season, a new crown class is selected for each sample tree on each plot. The selected crown class may be the same or different from the prior one. The probability of a sample tree being assigned a given crown class depends on its relative height (Fig. 1).

At the end of each growing season, GRO2 computes a new canopy height for each sample plot. Once the canopy height is known for a plot, the relative height of each tree is determined from the ratio of sample tree height to canopy height.

Sample trees are assigned to one of 16 relative height classes ranging from 0 to 1.5 in steps of 0.1. A discrete probability distribution based on Figure 1 is included in GRO2 for each of the relative height classes. The distribution gives the probability that a tree will be assigned to a given crown class.

A random number between 0 and 1 is selected by GRO2. This number is matched to the cumulative

Calibration Data

distribution function for the relative height class, and an appropriate crown class is selected for the sample tree under consideration. The process of selecting crown classes continues until all sample trees on all sample plots have been assigned a crown class.

The possibility of changing crown classes each year is not as unrealistic as it may sound at first. Trees that are at the extremes of relative height, either high or low, have a high probability in GRO2 of remaining in the same crown class from year to year. When changes do occur, it is most often to an adjacent crown class. Rarely does a tree shift two classes in one year. However, because of the relative height probability distribution, this outcome is possible. Five trees on one plot from the 1983 Vermont forest inventory were monitored for changes in crown class for a simulation period of 51 years (Table 3).

The stochastic treatment of crown class serves two functions. First, it models the random variation in radial increment. If radial growth of a particular tree is defined as the sum of a constant and a random term, we have said in GRO2 that radial increment changes "as if" the crown class were changing.

The second function deals with changes in canopy height and relative heights of sample trees. These changes may be the result of height growth, thinning, or harvesting. But they alert the model that a tree's competitive position and, therefore, its radial growth may change.

The algorithms in GRO2 illustrate how the model simulates change in a forest stand. Although presented independently of DATA2 and YIELD, the three computer programs complement each other in VWRAP by allowing input of plot data, processing of that data, and output of stand summary tables. However, GRO2 can be used separately as a subprogram if desired.

In addition to generating the logic and FORTRAN code, the development of GRO2 also required the specification of the functional relationships that described the dynamics of forest stands, and the empirical estimation of the parameters of those functions. The calibration of the model was accomplished with a set of data from 530 trees. There were 432 growth-rate trees (Table 4) and 309 site-index trees, with 211 trees used in both capacities. These data were collected by the Service Foresters in the Vermont Department of Forests, Parks, and Recreation. Because of the relatively small sample size, a probability sample was not attempted. Instead, a matrix of species (10) by crown class (4) was constructed and sample trees were selected from around Vermont to fill each cell. The trees were selected arbitrarily from forest stands with a basal area of 100 ft² per acre or more. Only live, nondiseased trees were selected. The key data collected for each tree included: species; crown class; increment core at breast height through the pith; total height; d.b.h.; and site index.

Table 3.—Results of changes in crown class for five trees for a 51-year simulation using GRO2

Tree number	Species	Initial crown class	Final crown class	Total number of crown class changes in 51 years	Total number of crown class changes exceeding 1 class ^a
1	Yellow birch	4	2	22	4
2	Eastern hemlock	2	2	27	7
3	Sugar maple	2	1	7	0
4	Sugar maple	3	1	24	2
5	Sugar maple	2	1	5	0

^a No change in excess of two classes occurred.

Table 4.—Number of growth-rate trees, by crown class

Species	Crown class				Total
	Dominant	Codominant	Intermediate	Overtopped	
American beech	13	12	12	11	48
Northern red oak	14	16	11	12	53
Red maple	13	12	12	10	47
Sugar maple	16	15	13	15	59
White ash	15	13	10	9	47
White birch	10	9	9	7	35
Yellow birch	8	13	8	9	38
Eastern hemlock	9	10	8	10	37
Eastern white pine	14	10	9	9	42
Red spruce	6	7	6	7	26
Total	118	117	98	99	432

The increment cores for growth-rate and site-index trees were analyzed in the laboratory. Radial increment was measured to the nearest 0.1 mm for the most recent 12 growth rings. The age at breast height, from a ring count, and the distance from the cambium to pith also were recorded. Each core was analyzed twice to reduce measurement errors.

The data were analyzed statistically to obtain the annual radial-increment coefficients in the Appendix

(Table 6). The growth-rate trees were used to obtain the coefficients on sites exceeding 100 ft² basal area per acre. The site-index trees were used to obtain the radial-growth coefficients on sites with less than 40 ft² basal area per acre. These trees were either in the dominant or codominant crown class, free from disease, damage, and suppression, and between 30 and 100 years at breast height. In other words, they represented the best expression of growth potential on the site for the species.

Sample Output From GRO2

The GRO2 model has been tested for soundness of its results; that is, for the stands in which it has been used to simulate change, the results seem reasonable. A systematic program of testing using actual stand growth data is planned.

The data summaries available from GRO2 include a Stand Table, Basal Area Table, Biomass Table (dry tons per acre), Biomass Value Table, Net Biomass Table (net of sawlogs), Net Biomass Value Table, Sawtimber Volume Table, Sawtimber Value Table, Sawtimber Stand Table, Sawtimber Basal Area Table, and

D.b.h./Stems per acre Histogram. All or any combination of tables can be printed. Biomass weight is estimated by equations developed by Monteith (1979).

As an example, 11 plots were taken in a typical mixed stand in the Sugar Maple-Beech-Yellow Birch forest type in northern Vermont. Table 5 is the stand table from GRO2 at the time of data collection, November, 1982. The stand is pole- to small sawtimber-sized, with 97.3 ft² basal area per acre. It has not been managed actively, though merchantable timber has been cut in the past.

Table 5.—Beginning stand table produced by GRO2 for a northern hardwood stand in Vermont

D.b.h. class	Sugar maple	Yellow birch	Black cherry	American beech	Red maple	Red spruce	Total
<i>Inches</i>	<i>No. stems/acre</i>						
3	49.5	24.7	0.0	0.0	0.0	0.0	74.2
4	12.2	12.2	0.0	0.0	0.0	0.0	24.4
5	21.6	5.9	0.0	11.4	5.9	6.2	51.1
6	22.4	5.5	0.0	4.8	0.0	5.3	38.0
7	3.0	7.1	3.8	0.0	13.6	0.0	27.5
8	0.0	5.1	0.0	0.0	2.5	0.0	7.6
9	21.5	3.9	4.1	4.1	2.2	0.0	35.7
10	6.6	1.8	0.0	4.7	3.1	0.0	16.3
11	4.3	1.3	1.4	5.5	2.9	2.7	18.0
12	5.7	2.4	1.2	0.0	2.3	0.0	11.7
13	1.0	0.0	1.0	0.0	2.0	0.0	4.1
14	0.0	0.9	0.9	1.7	0.9	0.0	4.3
15	0.0	0.7	0.0	0.0	0.7	0.0	1.4
16	0.7	0.0	0.0	0.7	0.6	0.0	2.0
17	0.6	0.6	0.0	1.8	0.0	0.0	3.0
18	1.0	0.0	0.0	0.0	0.5	0.0	1.6
19	0.0	0.0	0.0	0.5	0.0	0.0	0.5
30	0.2	0.0	0.0	0.0	0.0	0.0	0.2
Total	150.3	72.1	12.4	35.1	37.2	14.2	321.3

Using GRO2, the stand growth was simulated for a 25-year period assuming no silvicultural practices or harvesting. Figures 2 through 4 show some of the data summaries that can be made from GRO2 output. Figure 2 shows how species composition changed over the 25-year period. Figure 3 shows the trend in

sawtimber volume by species; Figure 4 shows the change in the diameter distribution of the stand from 1982 to 2007. In addition, total biomass of the stand increased from 63.1 dry tons per acre in 1982 to 89.1 tons in 2007.

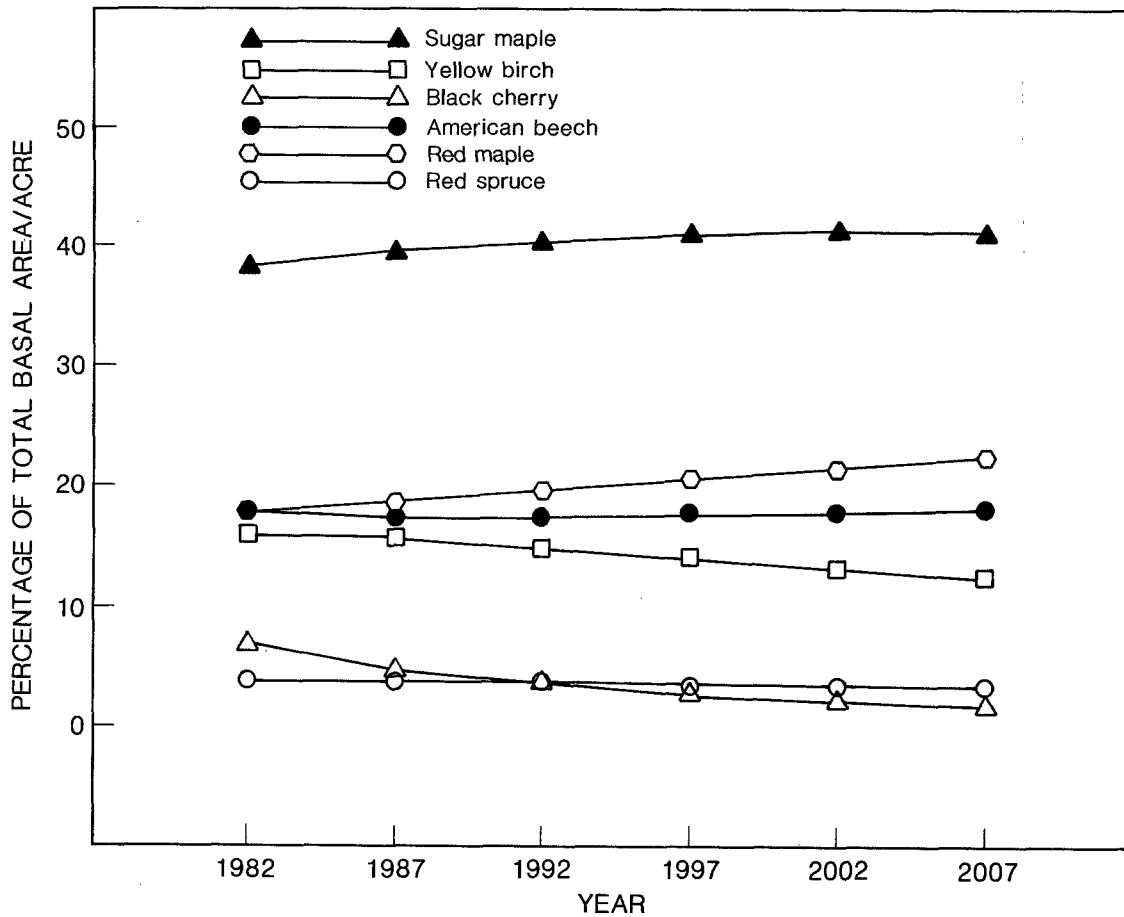


Figure 2.—Simulated changes in basal area in a northern hardwood stand in Vermont for a 25-year period.

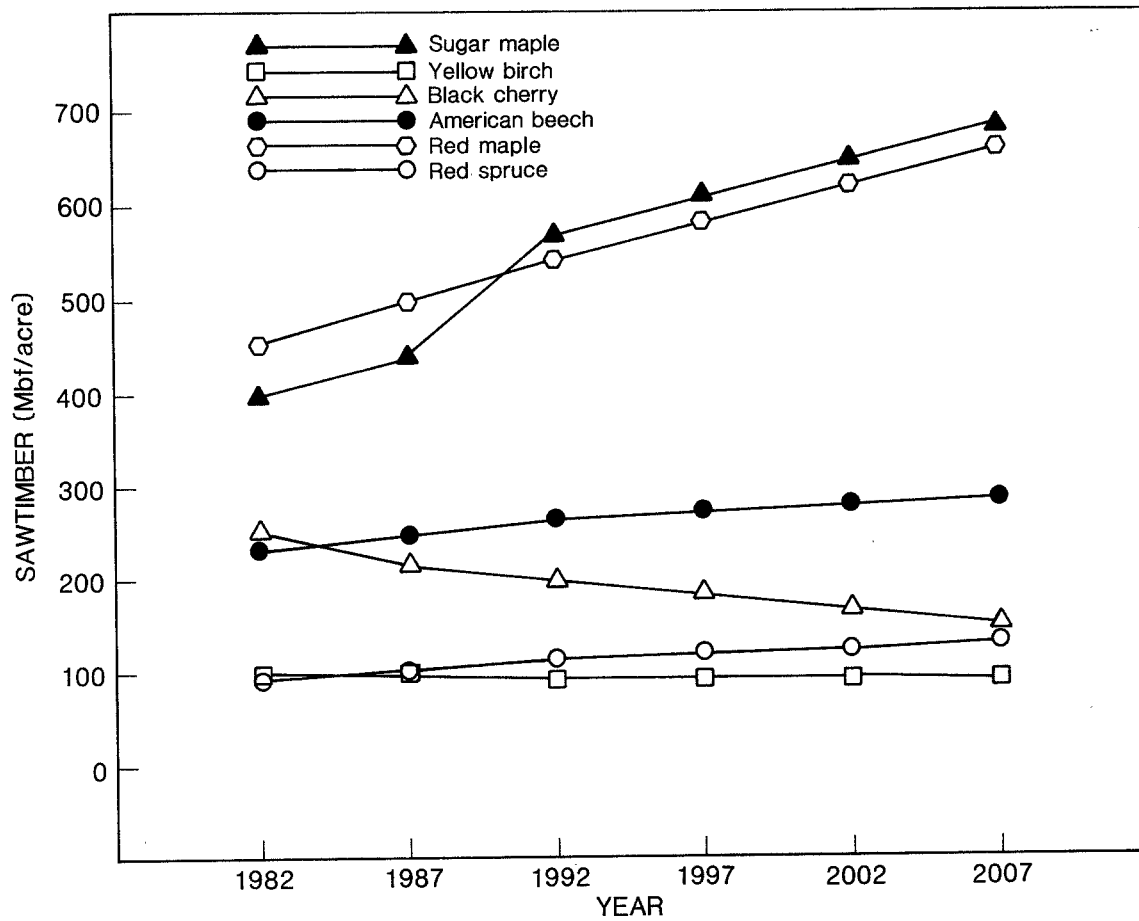


Figure 3.—Simulated changes in sawtimber volume in a northern hardwood stand in Vermont for a 25-year period.

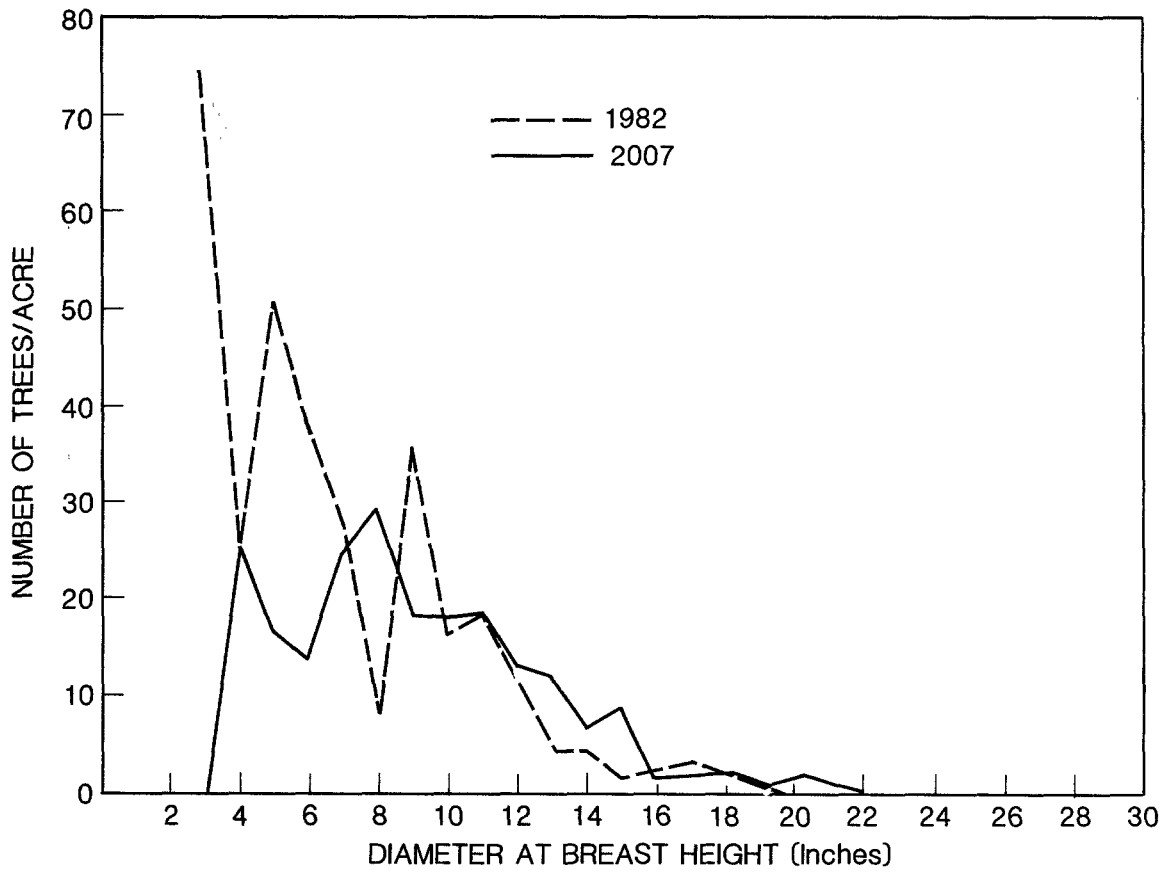


Figure 4.—Diameter (d.b.h.) distribution for a northern hardwood stand in Vermont for 1982 and 2007.

Conclusion

We believe that in its intended application, as a growth simulator in VWRAP, GRO2 is useful for the kinds of forest management decisions made by land-owners and managers in Vermont. It can give land-owners and managers a reasonable view of the future consequences of their potential management decisions. Together with an economic analysis, GRO2 should improve the decision-making process and could lead to more acreage of forest land under management.

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Appendix

Table 6.—Annual radial-increment coefficients (mm) used in GRO2, by total basal area per acre and crown class

Species	Total basal area/acre									
	> 100 ft ² /acre								< 40 ft ² /acre	
	Crown class									
	Dominant		Codominant		Intermediate		Overtopped		X ₀	X ₁
X ₀	X ₁	X ₀	X ₁	X ₀	X ₁	X ₀	X ₁			
American beech	1.5977	0.0	1.2967	0.0	0.7367	0.0	0.5345	0.0	0.8776	0.018170
Northern red oak	1.9500	0.0	1.6550	0.0	1.0055	0.0	0.5383	0.0	1.1841	0.021559
Red maple	1.4492	0.0	1.3733	0.0	0.6425	0.0	0.5140	0.0	0.1642	0.033667
Sugar maple	-0.1525	0.02115	1.2167	0.0	0.6338	0.0	0.3420	0.0	0.1117	0.030261
White ash	-0.3110	0.03311	-0.3730	0.02716	0.9100	0.0	0.5378	0.0	1.5380	0.015797
White birch	1.1150	0.0	0.7833	0.0	0.5333	0.0	0.2186	0.0	0.8734	0.022506
Yellow birch	1.5012	0.0	1.0215	0.0	0.4812	0.0	0.3289	0.0	2.1992	0.0
Eastern hemlock	1.3611	0.0	0.7856	0.0	0.7856	0.0	0.1620	0.0	0.1364	0.034360
Eastern white pine	2.9271	0.0	1.7990	0.0	1.1211	0.0	0.1533	0.0	1.0984	0.033930
Red spruce	1.3983	0.0	1.1886	0.0	0.2933	0.0	0.2500	0.0	2.1871	0.0
Other hardwoods	0.3545	0.01997	1.2822	0.0	0.7147	0.0	0.4375	0.0	0.6948	0.025041
Other softwoods	2.1248	0.0	1.2478	0.0	0.8091	0.0	0.1827	0.0	-0.1300	0.046049

Table 7.—Values of time height constant (THTC) and maximum height (TMXH), by species and site index

Species	Site-index class													
	40		50		60		70		80		90		100	
	<i>THTC</i>	<i>TMXH</i>	<i>THTC</i>	<i>TMXH</i>	<i>THTC</i>	<i>TMXH</i>	<i>THTC</i>	<i>TMXH</i>	<i>THTC</i>	<i>TMXH</i>	<i>THTC</i>	<i>TMXH</i>	<i>THTC</i>	<i>TMXH</i>
American beech	796.88	588.16	161.13	175.07	88.38	132.96	63.09	124.17	47.61	120.64	39.75	123.96	60.35	174.04
Northern red oak	205.08	168.58	78.71	101.27	57.32	99.87	43.12	99.92	33.59	102.01	19.73	97.36	43.36	144.05
Red maple	115.86	105.63	91.60	112.66	86.13	130.54	71.97	135.29	64.55	144.56	57.23	151.27	52.25	159.53
Sugar maple	53.71	63.11	53.76	79.65	53.71	96.12	53.76	112.68	53.76	129.20	53.76	145.72	56.40	166.93
White ash	38.09	53.06	38.04	66.71	38.04	80.38	38.04	94.06	38.04	107.73	38.04	121.40	39.65	137.77
White birch	32.50	50.94	33.11	64.19	33.57	77.47	33.84	90.71	34.08	103.98	34.25	117.24	37.99	136.63
Yellow birch	45.12	57.50	45.17	72.46	45.12	87.36	45.12	102.28	45.12	117.22	45.12	132.14	48.95	153.73
Eastern hemlock	33.11	50.07	50.24	76.69	47.75	90.01	49.31	107.30	53.61	129.00	60.45	156.45	52.25	159.53
Eastern white pine	141.60	123.82	98.83	119.10	80.08	124.01	70.61	133.57	73.63	157.69	60.45	156.45	47.56	151.30
Red spruce	33.11	50.07	50.24	76.69	47.75	90.01	46.09	103.44	56.98	133.75	60.45	156.45	47.59	151.30

Table 8.—Tree mortality coefficients used in GRO2

Species	Coefficient			
	A	B	C	D
American basswood	3.18	25.3602	0.8900	0.00317
American elm	1.9889	44.5414	1.0965	0.00899
Bigtooth aspen	0.8805	56.5925	1.2154	0.01288
Black ash	1.70	13.3384	0.7500	0.00018
Hickory	2.75	63.4946	1.0498	0.00134
Paper birch	1.52	21.50	0.8000	0.00029
Quaking aspen	1.2199	693.5903	2.0753	0.02384
Red maple	2.68	53.5938	1.0500	0.00494
Red oak	2.3092	6,999.820	2.6615	0.00468
Sugar maple	3.1831	82.5642	1.3605	0.00405
White ash	1.7821	232.3075	1.7267	0.00222
White oak	2.89	95.6369	1.4517	0.00188
Yellow birch	2.6705	63.1477	1.3819	0.00382
Balsam fir	2.92	29.5772	0.9500	0.00265
Black spruce	2.8774	432.9522	1.8576	0.00235
Eastern hemlock	2.8233	89.5603	1.0966	0.00320
Eastern white pine	2.3507	33.6094	1.0088	0.00201
Jack pine	1.2178	149.3669	1.3699	0.00856
Northern white cedar	13.0	1.0	1.0	0.00402
Red pine	1.65	17.3086	0.7500	0.00042
Tamarack	1.35	30.0	1.0	0.01334
White spruce	2.8806	30.7737	1.2309	0.00396
Other softwoods	2.3507	33.6094	1.0088	0.00201
Other hardwoods	2.2339	29.6290	1.3427	0.00748

Hughes, Garrett A.; Sendak, Paul E. **Key algorithms used in GRO2: A computer simulation model for predicting tree and stand growth.** Res. Pap. NE-570. Broomall, PA: U.S. Department of Agriculture, Forest Service, Northeastern Forest Experiment Station, 1985. 17 p.

GRO2 is an individual tree, distance-independent simulation model for predicting tree and stand growth over time. It performs five major functions during each run: (1) updates diameter at breast height, (2) updates total height, (3) estimates mortality, (4) determines regeneration, and (5) updates crown class.

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