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A Stand Model for Upland Forests of Southern Arkansas

D. L. Mielke
H. H. Shugart
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ENVIRONMENTAL SCIENCES DIVISION
Publication No. 1134

OAK RIDGE NATIONAL LABORATORY
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A STAND MODEL FOR UPLAND FORESTS OF SOUTHERN ARKANSAS

D. L. Mielke, H. H. Shugart, and D. C. West

ENVIRONMENTAL SCIENCES DIVISION
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Submitted as a thesis by D. L. Mielke to the Graduate Council of the University of Tennessee in partial fulfillment of the requirements for the degree of Master of Science.

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ABSTRACT

MIELKE, D. L., H. H. SHUGART, and D. C. WEST. 1978. A stand model for upland forests of Southern Arkansas. ORNL/TM-6225. Oak Ridge National Laboratory, Oak Ridge, Tennessee. 104 pp.

A forest stand growth and composition simulator (FORAR) was developed by modifying a stand growth model by Shugart and West (1977). FORAR is a functional stand model (Botkin et al. 1972a) which used ecological parameters to relate individual tree growth to environment rather than using Markov probability matrices or differential equations to determine single tree or species replacement rates. FORAR simulated tree growth and species composition of upland forests of Union County, Ark., by considering 33 tree species on a 1/12 ha circular plot.

Once a year trees were stochastically chosen to be killed or grown and new trees were stochastically planted on the plot. Individual trees were killed by a probability function scaled according to the maximum age of the appropriate species. Stocking of new individuals depended on the computed leaf area index of the plot and the existing conditions for soil, temperature, wildlife populations, and epidemics. Trees grew according to a species-specific optimum growth function modified by factors for soil moisture, competition, available light, and climate degree-days. The optimum growth function for each species was a function of the maximum age, diameter at breast height and height recorded for the species. The driving variable for the model was growing degree-days, which was randomly chosen at the beginning of each year from a normal distribution with appropriate mean and variance.

FORAR was validated using historical accounts, density-diameter distribution curves, and USDA Forest Service Continuous Forest Inventory (CFI) species composition data. Historical accounts agreed generally with FORAR output on the species of primary importance in upland forests of southern Arkansas. FORAR density-diameter curves corresponded to those of West et al. (1976) for southeastern forests, except that the simulated plots were not harvested. There was a statistically significant ($p < 0.1$) correlation in species composition between model output and USDA-Forest Service CFI data.

FORAR was used to examine the effects of two timber management schemes upon Red-cockaded Woodpecker (Dendrocopus borealis) nesting habitat. Leaving twelve trees per hectare on all or part of the management unit resulted in significantly more large, dying pines than removing all trees and a significantly greater number of years in which large pines, healthy or dying, were present. Further work is necessary to determine the relationship between Red-cockaded Woodpecker nesting habitat and woodpecker population numbers.

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I. INTRODUCTION AND LITERATURE REVIEW

The purpose of this study was to build and validate a forest stand model for upland forests of Union County, Arkansas, which could be used for many different types of ecological research. The type of use demonstrated in this study was the examination of the effects of two timber management schemes upon the presence of nesting habitat for the Red-cockaded Woodpecker (Dendrocopus borealis Vieillot). Stand models can be useful in studying changes in stand structure and species composition due to succession or longterm perturbations. Consequences of different timber and wildlife habitat management techniques can be predicted. Changes in species abundance (e.g., to dominance or extinction) can be determined. Better understanding of the importance of the structure and function of ecosystems results from the modeling. The usefulness of different measures of such things as diversity, productivity, or stability, or the usefulness of such parameters, can be studied. Also, sensitivity analysis can show where and how research efforts should be directed for greater efficiency.

The first step in this study was to determine which of the various types of stand models most suited the purpose of this study. Forest stand models have generally been built to study either timber management or vegetation succession. Those models simulating succession are probably more useful in ecological studies because they contain more ecological information. Because the objective of this study was to develop a multi-purpose stand model, only those models which simulate succession were examined. Several stand models have been built to simulate single species (Bosch 1971) or managed stands (Amidon and Akin 1968, Peden et al. 1973, Lembersky and Johnson 1975, see Monserud 1975 for a more detailed review). Since these models do not keep track of species composition, none were considered appropriate to simulate natural secondary forest succession at the stand level.

Early attempts at modeling forest stand succession made use of birth and death rates, Markov matrices, or differential equations and focussed primarily on stand by stand replacement. Leak (1970) used birth and death rates to model species composition changes in a north-eastern hardwood forest. Data from past years must be used to determine the birth and death rates for each species, and initial conditions must be supplied. The birth/death rates can be constant, density-dependent, or serial; and up to 25-50 years of forest dynamics can be extrapolated.

According to Whittaker (1953), the "few universal properties of succession...are statistical results of any plant-by-plant replacement process." These statistical properties can be useful if any recognizable patterns or generalities emerge, even if the associated biology or ecology is not fully understood (Pielou 1975). One generality that emerges from the plant replacement process is that species composition changes through succession appear to be similar to a Markov process (MacArthur 1958). A Markov matrix is a matrix of transition probabilities of the states of a system and is used to calculate the condition of the system at time t+1 from the condition of the system at time t:

$$\vec{X}_{t+1} = \overline{M}\vec{X}_t$$

where;

$\vec{X}$ = the vector of system states (defining the condition of the system) and

$\overline{M}$ = the matrix of transition probabilities.

The condition of the system at time t+1 depends only on the condition of the system at time t and the transition probabilities of the Markov matrix. If the state vector is known at time t_0, $\vec{X}_0$, a chain of multiplications $\vec{X}_1 = \overline{M}\vec{X}_0$, $\vec{X}_2 = \overline{M}\vec{X}_1$, etc., can be used to determine the condition of the system at any time t. One useful property of Markovian processes is that regular Markov chains converge to the same stationary distribution, with each stage having the possibility of being reached from every other stage (Bharucha-Reid 1960). Secondary forest succession, similarly, tends to converge to the same stationary species distribution, although every seral stage may not have the possibility of being reached from every other stage (Horn 1975b). To use a Markov transition matrix to model forest succession, one must have separate, identifiable succession stages (cover-states); data to determine the transition rates between them, and data showing initial conditions. The assumptions necessary are that the number of cover-states is finite, that the transitions must take place at (arbitrarily small) discrete instants, and that the transition rates are independent of time (Slatyer 1976).

Waggoner and Stephens (1970) used a Markov transition matrix to model species composition in a Connecticut forest after noting that their forest appeared to have the necessary Markov properties. Since they were concerned mainly with climax (steady-state) conditions, they did not need to input particular initial conditions. Any set of initial conditions would result in the same steady-state distribution.

A slightly different approach to modeling forest succession makes use of differential equations. These differ from Markov matrices in that the transitions are considered rate processes rather than probabilities. Assumptions that must be made are (1) that there are a finite number of cover-states; (2) that the effects of spatial heterogeneity are relatively constant; and (3) that the cover-states have definable, determinate input-output behavior. A fourth condition, that the input-output relations are superposable (Shugart et al. 1973, DiStephano et al. 1967) is necessary to assume linearity. One advantage of the differential equation approach is that it usually takes less computer time. Analyses of Markov matrices, on the other hand, can give information on variances, stability, convergence, mean passage time, and time to absorption of the various cover-states (Shugart et al. 1973).

Some new ideas on succession consider the changes in species composition to be a function of environmental gradients and of the dispersal and survival characterisitics of individuals (Drury and Nisbet 1973, Slatyer 1976), rather than as a "superorganism" moving from one seral stage to another with Markovian probabilities (Clements 1916, MacArthur and Connell 1966, MacArthur 1968). Markov matrices and functional stand models have accordingly been used to model succession on a tree-by-tree, instead of a stand-by-stand, basis. Instead of having a number of cover-states, Horn's (1975a) transition matrix for a New Jersey forest gave the probabilities of a tree of one species being replaced by a tree of another species. In setting up his transition matrix, Horn

(1975b) assumed (1) there was a constant, proportional rain of seeds on the plot; (2) abundance in the understory implies a competition advantage in the canopy; (3) the probability that a given species will be replaced by another given species is proportional to the number of saplings of the latter in the understory of the former; and (4) the transition probabilities do not change with species composition, successional stage, or edaphic condition.

One of the major drawbacks of the Markov approach is that it does not explicitly take into account dynamic ecological factors and stresses on individuals. Functional stand models, based on concepts rather than specific field data, have been built in an attempt to do this. Functional stand models deal stochastically with the birth, growth, and death of individual trees in a forest stand, using a list of parameters that characterize the physical environment and the traits of each tree species. If the recent concepts of succession are correct, i.e., that replacement should be looked at on the individual level and distinguishable cover-states do not always exist, then this functional approach should result in a more accurate simulation of succession. To parameterize a functional stand model, one must have relatively general information on the climate and several species-specific characteristics such as maximum age and shade tolerance. One advantage of this type of model is that this information can usually be found in textbooks of dendrology or silvics such as Fowells (1965) or Harlow and Harrar (1969) (Shugart and West 1977). In addition to the parameters, one must choose equations to describe growth and relations between tree dimensions (height to diameter, for instance).

The first functional stand model was developed by Botkin et al. (1972b) for a northeastern hardwood forest. Parameters were added only when the existing model did not exhibit satisfactory behavior. JABOWA, the resulting model (Botkin et al. 1972a,b), contained 10 parameters to characterize each tree species and seven to characterize the environment. The three main processes in JABOWA were the birth, death, and growth of individual trees on a 1/100 hectare (ha) plot. New trees were added to the plot on the basis of the relative shade, growing degree-day, and soil moisture tolerances of each species and the annual condition of the environment. A seed source was assumed to be available for each species. Death of an individual tree was considered a random process, with only 2% of the saplings of a species reaching the maximum age of that species. A tree that grew less than 0.01 cm in diameter at breast height (dbh) per year was subjected to another death process that gave it a 1% chance of surviving 10 years. While birth and death were modeled as stochastic functions, growth was deterministic. The potential growth increment for each tree was a function of the species and tree size. The potential growth increment was modified by factors relating to light competition, climate, and soil quality (competition for nutrients, etc.). This increment was added to the individual tree's dbh, from which the height was calculated using a quadratic function. Two other assumptions of the model were that the climate was constant and that the tree species were nonhydrophytic. The model commonly simulated 250-300 years of forest dynamics, which was long enough for the "climax" to develop.

Shugart and West (1977) modified the Botkin model to simulate a lower-slope forest of East Tennessee. The plot size was changed from 1/100 ha to 1/12 ha to lessen the abnormal effects from shading and root competition and climate was changed from a constant to a stochastic variable with a normal distribution. Because tree growth was affected by climate, birth, death, and growth were all stochastic processes. This model, FORET, simulated 100 stands for 600, and often 1000, years.

The FOREST stand model of Ek and Monserud (1974) was different from JABOWA and FORET in that the plot size was not fixed and in that tree location was explicitly considered. Growth was deterministic, while birth and death were stochastic. Height and diameter growth were treated separately as nonlinear functions of species, tree size, and a competition index. The competition index was a function of crowding, shade tolerance, and the height and crown width of both the individual tree and its competitors. Since this model was oriented toward sivicultural practices, shorter runs of up to 50 years were usual. This type of model shows great detail for one stand, but it is prohibitively expensive to replicate hundreds of stands in the manner of JABOWA and FORET.

Compared to the birth/death rates, Markov matrix, and differential equation stand models described earlier, functional stand models are more flexible, have more detail, explicitly consider ecological dynamics, and can be used for more general purposes (Monserud 1975, Ek and Monserud 1974, Botkin et al. 1972b). Three of the most important applications of functional stand models are in testing different forest management strategies (Ek and Monserud 1974), in looking for generalities in succession, and in statistically testing hypotheses (Botkin et al., 1972a). Another potential use of this kind of model is in management of wildlife habitat. Where Markov matrix or differential equation stand models could identify a desired habitat down to general species composition and general tree size, the functional stand model can identify a desired habitat down to specific species composition and abundance and individual tree sizes.

Botkin et al. (1972b) originally constructed their model to include the minimum number of parameters necessary to adequately simulate the Hubbard Brook forest of New Hampshire. Because this type of model tends to use much computer time, it is important to know in what regions and under what conditions a model containing the minimum number of parameters does an adequate job of simulating forest stands. Shugart and West (1977) were able to simulate a forest of East Tennessee without any major additions other than a sprouting subroutine and more detail in the birth subroutine. In this study, FORAR, a modified version of FORET, was used to simulate an upland forest of south central Arkansas. A moisture factor modifying tree growth was added because FORAR simulated an upland forest farther west than the two previous functional stand model simulations. The model was validated using historical accounts, density-diameter curves, and USDA Forest Service species composition data. The validated model was then used to determine the presence through time of Red-cockaded Woodpecker nesting habitat under two timber management schemes.

II. MODEL DEVELOPMENT

The model described here (FORAR) simulated an upland forest typical of the type found in south central Arkansas. The model was developed from a modified version (Shugart and West 1977) of the JABOWA model used by Botkin et al. (1970, 1972a, 1972b) for the Hubbard Brook forest. FORAR simulates growth and succession by keeping account of the dbh, age, and species of all trees greater than 1.27 cm dbh on a 1/2 ha circular plot (radius = 5.1 m). The model also computes number of stems and biomass of each species. Once a year each tree was stochastically killed or grown and new trees were stochastically planted. Individual trees were killed by a probability function that was scaled according to the maximum age recorded for the appropriate species. The probability that a specific tree would die during a given simulated year was increased if its growth rate fell below an acceptable minimum (0.1 cm yr^{-1}). Stocking of new individuals in a given simulated year depended on the computed leaf area index of the plot and the condition of five environmental variables: mineral soil, litter layer, temperature, wildlife populations, and epidemics. The tree species to be stocked were randomly chosen from those species which could germinate under the existing environmental conditions. Trees grew according to a species-specific optimum growth function that was modified by soil moisture, competition, climate, and available light. The optimum growth function for each species was a function of the maximum known age, the maximum dbh, and the maximum height recorded for the species. The driving variable for the model was physiological growing degree-days based on average daily temperature, which was approximated by assuming the yearly temperature cycle was a sine curve. A value for degree-days was randomly chosen each year from a normal distribution with appropriate mean and variance.

FORAR was written in FORTRAN IV and has been implemented on IBM 360 series and PDP-10 computers. The present version of the model considered up to 35 tree species and up to 700 individual trees and ran for any number of years. A detailed documentation of the FORTRAN program is given in the Appendix. Only a general description of the model input is given here.

FORAR read 19 parameter values to characterize each of 33 tree species used (see page 45 in Appendix). Most of the parameters, such as shade tolerance or maximum age, can be derived from information contained in standard dendrology or silvics textbooks (see Harlow and Harrar 1969 and Fowells 1965). Species used in the model were important timber species growing on upland sites in southern Arkansas (Little 1971; Moore 1960; Carl Amason, personal communication 1975).

For shade tolerance, all species described as intermediate in tolerance were classified as tolerant. The C values (see Appendix) of 1. for hardwoods and 2. for conifers were kept the same as those in FORET (Shugart and West 1977). The growth constant G was derived from equation (8) in Appendix, page 55, and the assumption that 2/3 of the maximum dbh of a tree is reached at 1/2 the maximum age. The value of G for each species can be solved for directly from equation (8) (Botkin <u>et al</u>. 1972b) or determined with a simple computer program of tree growth (Appendix A-2).

The S array was used to determine which of the tree species' seeds could germinate under the simulated annual conditions for mineral soil, litter, temperature, wildlife populations, and epidemics. Mineral soil was considered to be present if the biomass on the simulated plot was less than 0.2 metric tons ha^{-1} and if trees had been present on the plot less than 15 years. A litter layer was considered to be present any time the biomass on the plot was greater than 0.1 metric tons ha^{-1}. A "drought" year was approximated by a year that was hotter than normal, i.e., DEGD had a value greater than its mean, because the model did not contain a separate driving variable for moisture. The star rating system from Martin _et_ _al_. (1951) was used to determine if a tree species is a highly-preferred wildlife food in the Southeast. The use percentages for all animals of the Southeast were added, using the mean for each percentage class. If the total was 75 or more, it was considered possible for a larger than average wildlife population to consume the entire seed source of that species during a given year. Ozark chinkapin (_Castanea_ _ozarkensis_ Ashe) (Latin and common names of trees are from Little 1954) and short leaf pine (_Pinus_ _echinata_ Mill.) are being attacked by chestnut blight and southern pine beetle, respectively, in southern Arkansas, but the American elm (_Ulmus_ _americana_ L.) has yet to be attacked by Dutch elm disease (Carl Amason, personal communication 1975). Thus, Ozark chinkapin and shortleaf pine were the only species in the model that could be affected by epidemics. The chances of having higher than normal wildlife populations and epidemics were left at 0.5 as in FORET (Shugart and West 1977) from lack of information to the contrary. The variable KTIME was used to limit the germination of pioneer species to the early years of succession. Values were taken mainly from Shugart and West (1977). It was assumed that unless a parent tree of a pioneer species was present on the plot, that species could not germinate on the plot after KTIME years for lack of a seed source.

A soil moisture variable affecting tree growth, SOIM, was added to the model. An alternative would have been to add soil moisture as another model driving variable. However, the realism gained would not outweigh the increased complexity resulting from adding an additional level of resolution to the model. SOIM is a measure of how well a species grows on an upland site compared to its typical growth. To get a quantitative estimate, species presence and growth were examined along a transect from El Dorado, Arkansas, to San Antonio, Texas (Figure 1). Soil type (United States Soil Conservation Service 1967), solar radiation (Environmental Data Service 1962), mean monthly average, minimum, and maximum temperature (U.S. Geological Survey 1965a,b,c), degree-days (Environmental Data Service 1960a), and potential vegetation (Küchler 1966) are all relatively constant along this transect. Annual precipitation and annual pan evaporation, however, change relatively linearly along this transect from approximately 50 inches of rain and 60 inches of evaporation in El Dorado to approximately 30 inches of rain and 80 inches of evaporation in San Antonio (Environmental Data Service 1960b,c) (Figure 2). Therefore, it was assumed that water stress would be the most important factor in determining the western limit of the range of each species along the transect. Foresters along the transect (Dick Pike, Dan Cates,

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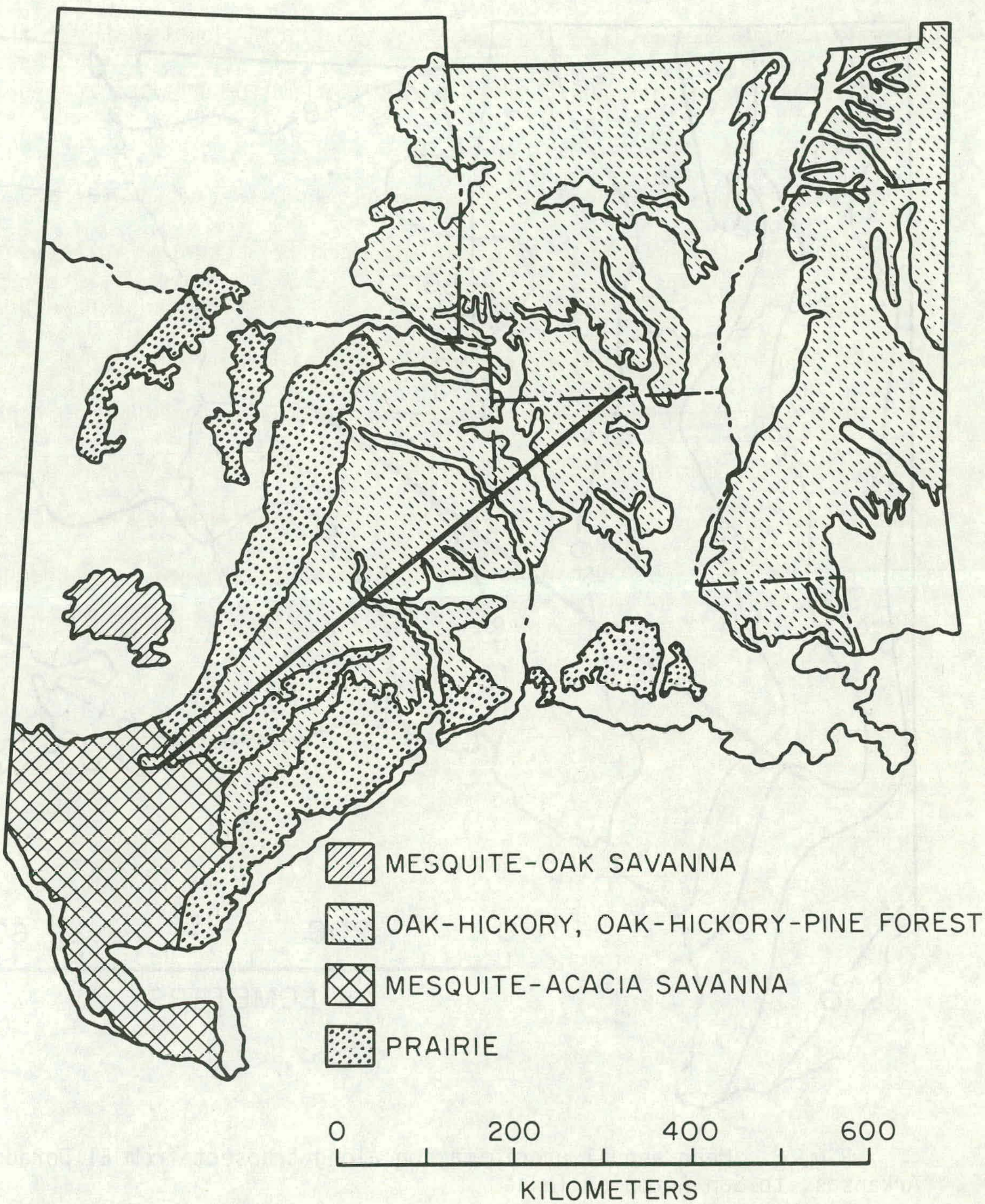

Fig. 1. Potential natural vegetation of transect from El Dorado, Arkansas, to San Antonio, Texas (redrawn from Küchler 1966).

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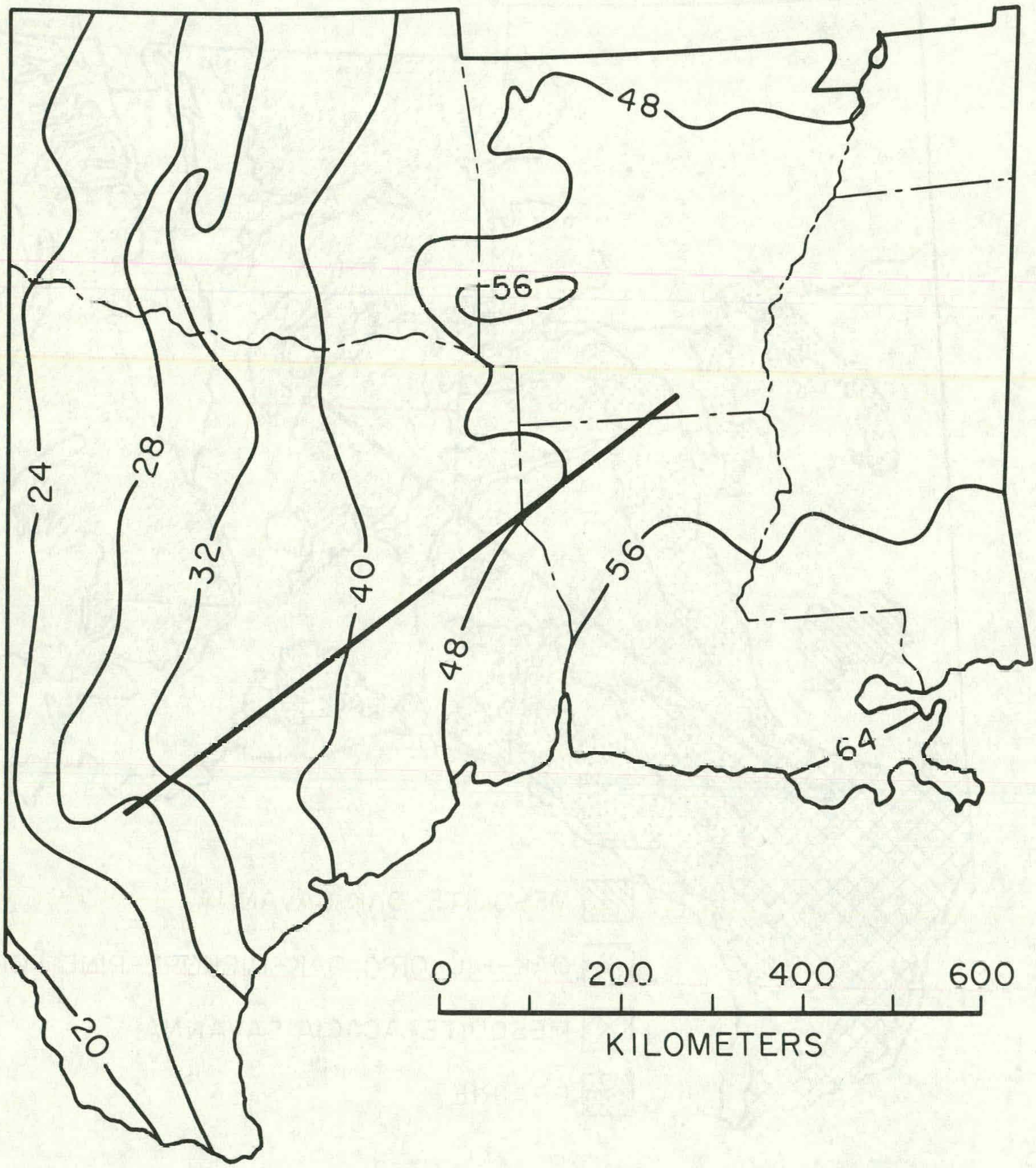

Fig. 2. Mean annual precipitation along transect from El Dorado, Arkansas, to San Antonio, Texas.

David M. Moehring, personal communications 1975) were contacted to determine where along the transect each species dropped out on upland sites and how well it grew there compared to its maximum size. These two factors were multiplied and normalized against the value for loblolly pine (Pinus taeda L.) to determine SOIM for each species. Loblolly pine was used as the normalizing species because it is the species of importance that makes the best growth on upland sites in southern Arkansas.

Degree-days (DEGD) was the driving variable of the model. The mean of DEGD was calculated by assuming the January and July mean temperatures for El Dorado, Arkansas, were the minimum and maximum values of a yearly sine curve of average daily temperature (see Appendix). The coefficient of variation of DEGD was assumed to be 0.08 (Shugart and West 1977).

III. MODEL OUTPUT AND VALIDATION

To simulate natural secondary succession, 100 stands were simulated for 1000 years each. Mean biomass and percent biomass values for each species were calculated from the 100 simulation values for each of the 1000 years. Total biomass (Figure 3) increased steadily from year zero with the increasing size of the dominant species, loblolly pine. Around year 275 the total biomass value dropped about 30% as the pine died out and sweetgum (Liquidambar styraciflua L.) and southern red oak (Quercus falcata Michx.) captured the site. After year 600 mature southern red oaks dominated and total biomass remained relatively steady at an intermediate value. Leaf area generally followed the same trends as total biomass (Figure 3). Number of trees (Figure 3) decreased steadily from year one, when all species were free to germinate on the plot, to a minimum when loblolly pine dominated. Number of individuals increased briefly after the last pines died and the canopy opened up, then decreased to a relatively steady value when southern red oak became dominant.

Percent biomass for each species each of the 1000 years was calculated in the same manner as total biomass and is shown in Figure 4. Distance between lines is the percent biomass of that species for that year. The larger the distance between the lines, the more important that species is to the total biomass. Loblolly pin quickly outgrew all other species and dominated for 250-300 years. Sweetgum and southern red oak increased in relative importance as the pines disappeared, with southern red oak eventually becoming dominant.

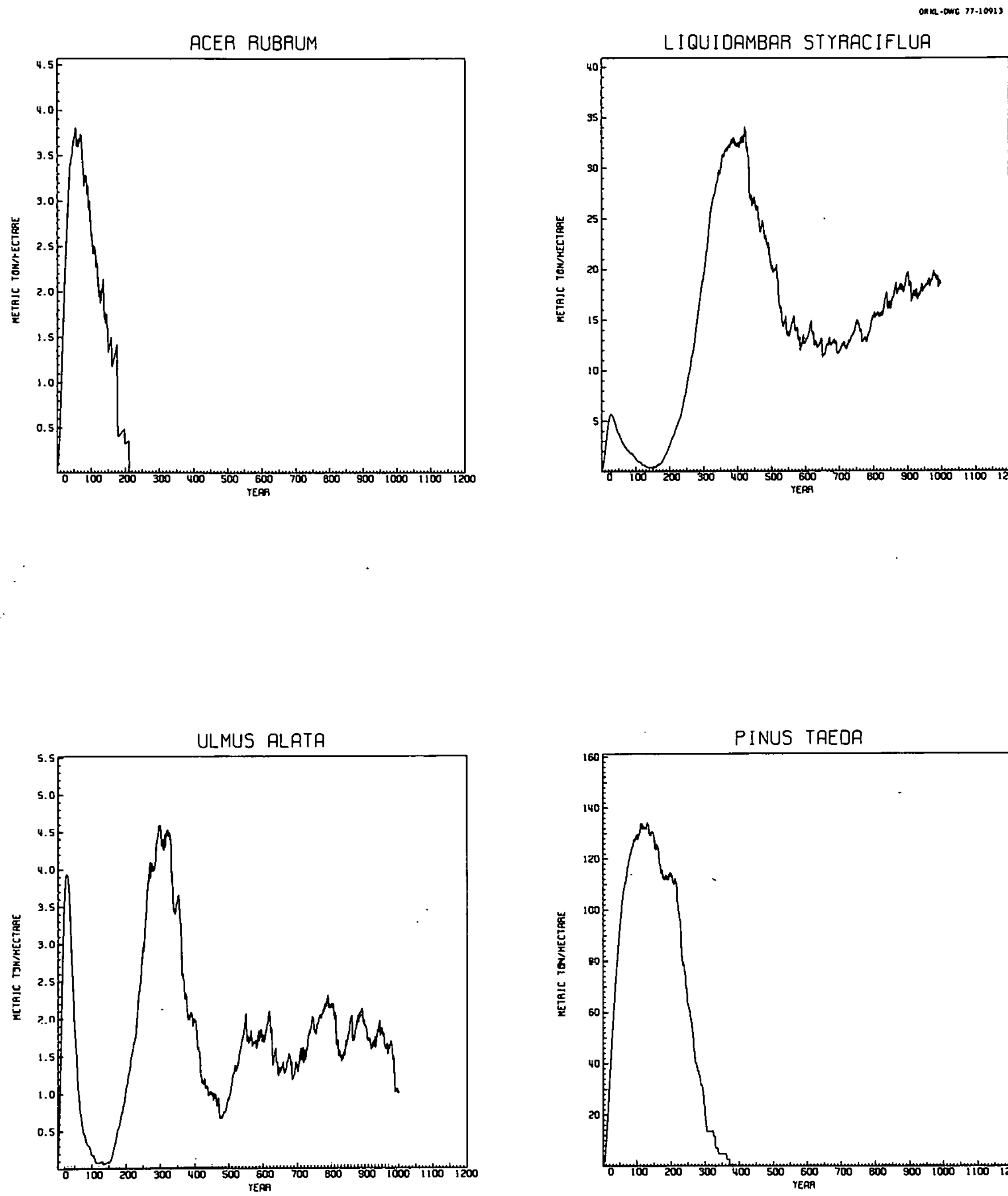

Fig. 3. Model output showing biomass values through time for the major species.

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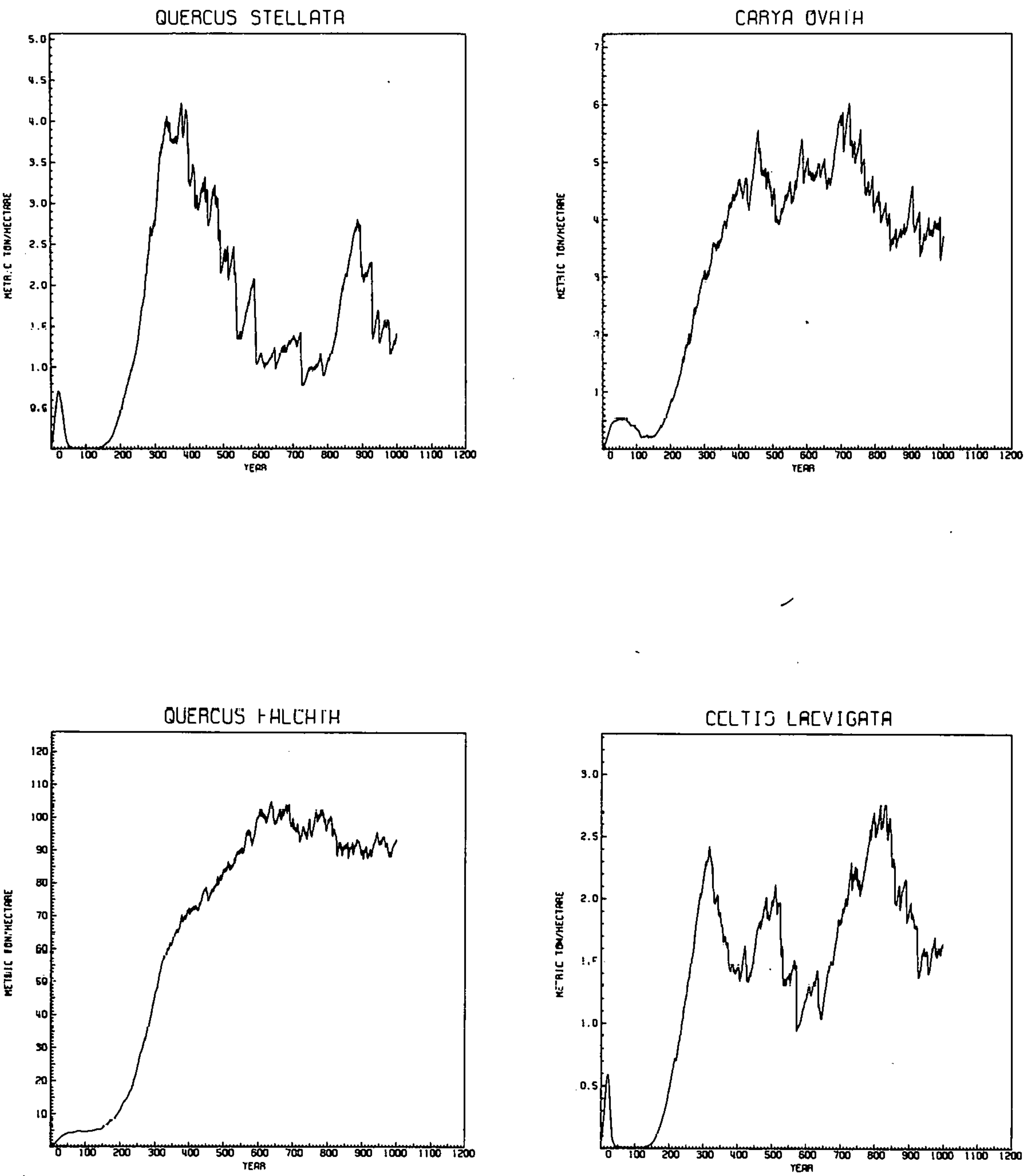

Fig. 3. (continued).

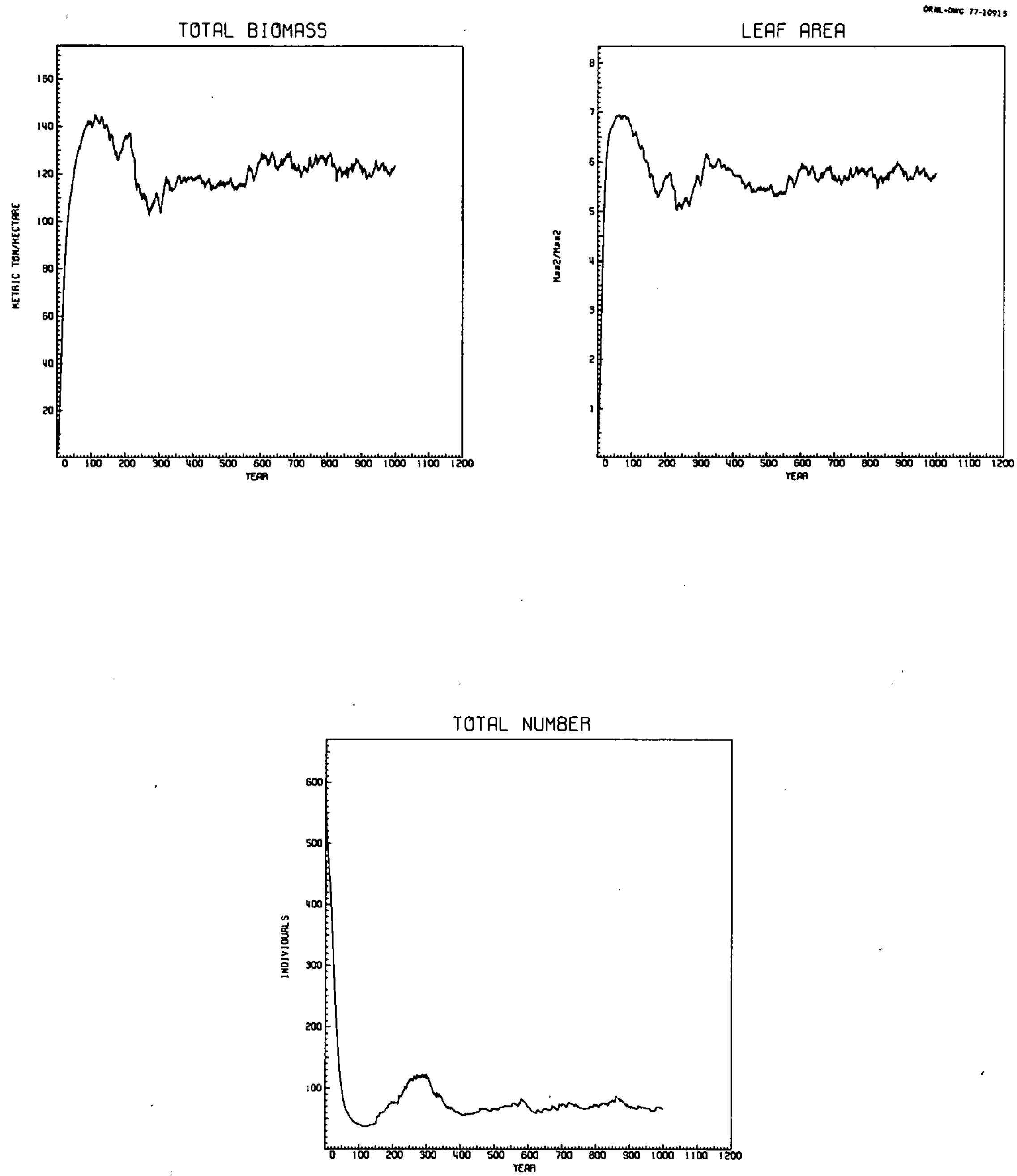

Fig. 3. (continued).

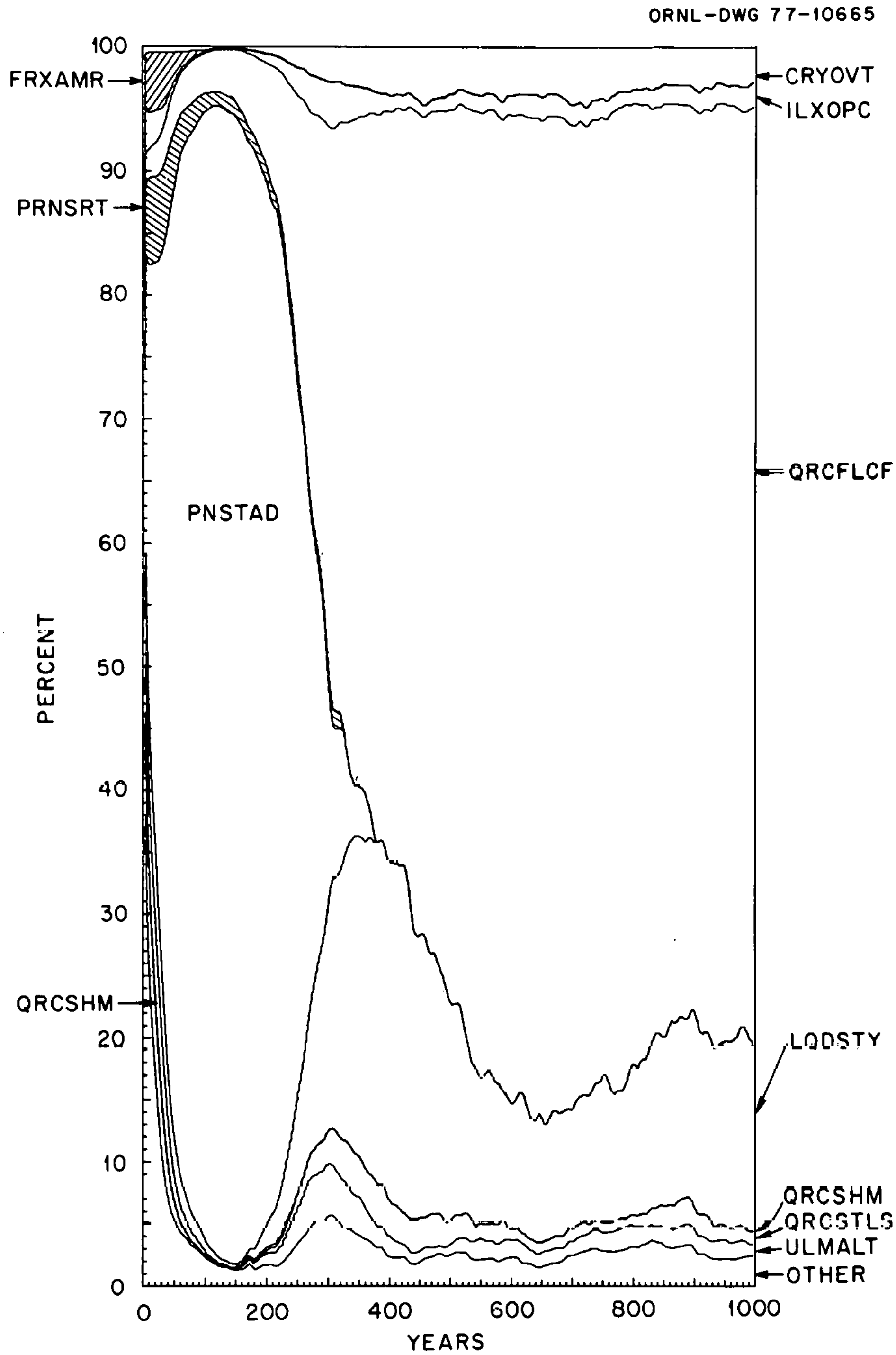

Fig. 4. Percent biomass through time for the major species, from FORAR output. Mnemonics for tree species are from Goff et al. (1974). Distance between lines the species name is between is the percent biomass of that species for that year.

Two of the major problems associated with modeling forest stand growth and composition are determination of input parameters and model validation. Both of these problems are caused by the time necessary for forest growth and change in species composition. To obtain species birth and death rates or cover-state transition rates directly, tens of years must be spent collecting data. Functional stand models such as FORAR circumvent this problem by using general information that can be drawn largely from standard forestry textbooks. All types of forest stand models, however, must use an independent set of data against which to test the predictions of the model.

Botkin et al. (1972b) validated JABOWA by reviewing the reactions of experienced field observers to model predictions and by testing the ability of JABOWA to predict change in species composition with changes in elevation. Data from Hubbard Brook plots were used in the validation.

Shugart and West (1977) validated FORET by running the model with two sets of input parameters. One set, representing present forest conditions on lower slopes in East Tennessee, was used to develop and tune the model. The second set of parameters was identical to the first except that it included American chestnut (Castanea dentata [Marsh.] Borkh) and represented the historical forest of East Tennessee before the chestnut blight. The results of the model simulation of pre- and post-blight forests using the second set of parameters was then tested against historical data to validate the model.

There are no good historical data which show the effects of man's activities or catastrophic events (such as the chestnut blight) upon the growth and composition of an upland forest in Union County, Arkansas. Neither are there any growth or composition differences resulting from gross spatial differences such as elevation. As a result, separate studies were made to test the ability of FORAR to simulate the growth and composition of upland forest stands in south-central Arkansas.

In a geological reconnaissance of the middle and southern counties of Arkansas in 1859 and 1860, M. Leo Lesquereux recorded some descriptions of the natural vegetation encountered: "The yellow sandy uplands, mostly derived from tertiary or cretaceous sandstone, are characterized by the Loblolly Pine...With these trees are seen upon all the dry uplands and recent formations the White, the Black, the Spanish [southern red] Oaks in abundance and of beautiful growth, more rarely the Shellbark [shagbark] Hickory, the Blackjack and the Post Oak, with the Holly" (Owen 1860). Although the records from the expedition are not from Union County, FORAR generally agrees with the importance accorded the different groups by Lesquereux. Pines, red and white oaks (Quercus spp.), hickories (Carya spp.), and holly (Ilex opaca Ait.) are all among the top ten groups in biomass in the model output. FORAR agrees with Lesquereux upon the importance of holly, although the species is only a minor component of the upland forests of Union County today. Harlow and Harrar (1969) suggest that the extermination of the species in some places may be caused by the taking of leaf sprays by people for use as Christmas decorations.

To get a better estimate of the model's ability to accurately simulate species composition, the biomass on each of the USDA Forest

Service Continuous Forest Inventory (CFI) plots in Union County was calculated. Biomass was determined using equations from Shugart and West (1977) and West *et al*. (1976). Stems greater than 5 inches were calculated by the equation:

$$\frac{\text{Biomass}}{\text{Ha}} = \frac{\text{Biomass}}{\text{Stem}} \cdot \frac{\text{Stems}}{\text{Hectare}}$$

$$= 0.1193 \times (2.54 \times D)^{2.393} \times \frac{687.55}{D^2} \times 2.47$$

$$= \frac{(2.54 \times D)^{2.393}}{D^2} \times 202.6,\ D = \text{diameter in inches} \quad .$$

Stems less than 5 inches were calculated by the equation:

$$\frac{\text{Biomass}}{\text{Hectare}} = \frac{\text{Biomass}}{\text{acre}} \times 100 \times 2.47,\ D = \text{diameter in inches} \quad .$$

The resulting biomass figures, which varied from 10 to 200 metric tons ha^{-1}, were separated into 10-ton categories (5-15 metric tons, 15-25 metric tons, etc.) to group stands of similar biomass values. Only the 95-105 metric tons ha^{-1} group had a sufficient number of plots (10) to calculate a meaningful average. The relative biomass of each species on the "average" plot was used to numerically rank the species. A similar ranking was made from the FORAR output from those years in which the total plot biomass was between 95 and 105 metric tons ha^{-1}. The rankings of model output and the CFI data were compared using Spearman's rank correlation coefficient, r_s (Snedecor and Cochran 1972):

$$r_s = 1 - \frac{6\Sigma d_i^2}{n^3-n} \quad ,$$

where d_i = difference in ranked positions and n = number of species. The calculated value, $r_s = 0.458$, indicates that there is a significant correlation ($p < 0.1$) (Beyer 1966) between the predicted species biomasses of the model and the actual species biomasses of the CFI "average" plot. If one leaves out black cherry (Prunus serotina Ehrh.), which contributes an unusually high biomass in the early years of this model as it did in FORET (Shugart and West 1977), the significance of the correlation improves ($p < 0.05$).

The CFI "average" plot biomass percentages were used to calculate an expected biomass value for each species on a 100 metric tons ha^{-1} plot. Table 1 compares the expected values with the values generated by FORAR. The species which lie outside the 95% confidence level are "hickory," American beech (Fagus grandifolia Ehrh.), shortleaf pine, blackgum (Nyssa sylvatica Marsh.), "white oaks," and "others." A larger sample of CFI plots might correct the errors for "hickory," blackgum, and "others;" however, an adequate sample would probably still show the model to be "low" in American beech, shortleaf pine, and "white oaks." The error for shortleaf pine is unexplained, but a more accurate soil moisture factor would probably increase the beech and white oak biomass. Shugart and West (1977) have shown that a functional stand model can adequately simulate the red and white oak groups for a lower slope forest of East Tennessee. It would appear that the soil moisture variable of the model is not accurate enough to account for the red oak and white oak biomasses on the sandy upland soils of south central Arkansas.

Table 1. Species biomass values from CFI plots and from FORAR output

Species[1]	FORAR 95% confidence interval (metric tons ha^{-1})	Expected value from CFI plots (metric tons ha^{-1})
Acer Rubrum	3.01 ± 3.78	0.06
Carya[2]	0.49 ± 0.63	2.39
Celtis laevigata	0.10 ± 0.17	0
Cornus florida	0.45 ± 0.65	0.07
Diospyros virginiana	1.25 ± 1.57	0.62
Fagus grandifolia[2]	.002 ± .004	0.56
Fraxinus americana	4.48 ± 5.78	0
Ilex opaca	1.71 ± 1.33	0.41
Juglans nigra	.0006 ± .003	0
Juniperus virginiana	0.37 ± 0.87	0.03
Liquidambar styraciflua	5.45 ± 3.91	11.32
Morus rubra	0.62 ± 1.07	tr
Nyssa sylvatica[2]	0.04 ± 0.10	1.56
Pinus echinata[2]	2.08 ± 2.77	13.92
Pinus taeda	60.82 ± 22.40	52.65
Prunus serotina	6.49 ± 6.57	0.20
White Oaks[2]	0.78 ± 0.83	6.27
Red Oaks	7.67 ± 2.71	6.94
Sassafras albidum	0.89 ± 0.77	0
Ulmus alata	3.69 ± 2.12	0.47
Ulmus americana	0.20 ± 0.36	0.55
Other[2]	0.10 ± 0.13	2.87

[1] Some spp. were grouped according to genus or subgenus to conform more easily with CFI data.
[2] A significant difference between model and expected values.

The ability of FORAR to predict stand growth was tested using density-diameter curves. Figure 5 shows the distribution curve resulting from 540 simulated plots generated by the model. The gray area includes all the density-diameter curves calculated by West et al. (1976) from USDA Forest Service CFI data for the regional forests of eastern Oklahoma, northern Arkansas, Tennessee, and North Carolina. The differences between the curves can probably be ascribed to the cultural practices affecting the real forests.

Theoretically, the distribution plotted logarithmically should be a straight line if the per cent mortality for each diameter class is equal and diameter is a linear function of age (Meyer 1952). Deviations from linearity result from species and individual tree physiology, interactions among species (such as competition or soil enrichment) and historical cultural practices (West et al. 1976). The actual distribution curves of West et al. (1976) tend to show two areas of nonlinearity, a plateau around 38 cm and a nonlinearity in the larger diameter classes. Goff and West (1974) showed that a plateau region in the density-diameter curve is a natural condition in forest stands. It occurs when understory trees reach canopy level and their mortality rates are reduced. The diameter at which the plateau occurs is a function of stand age. A younger stand has a lower canopy and a plateau farther to the left, etc. The nonlinearity of the larger diameter classes is affected by cultural practices, especially logging. Logging would make the curve more convex, whereas leaving behind economically useless trees would make the curve more concave.

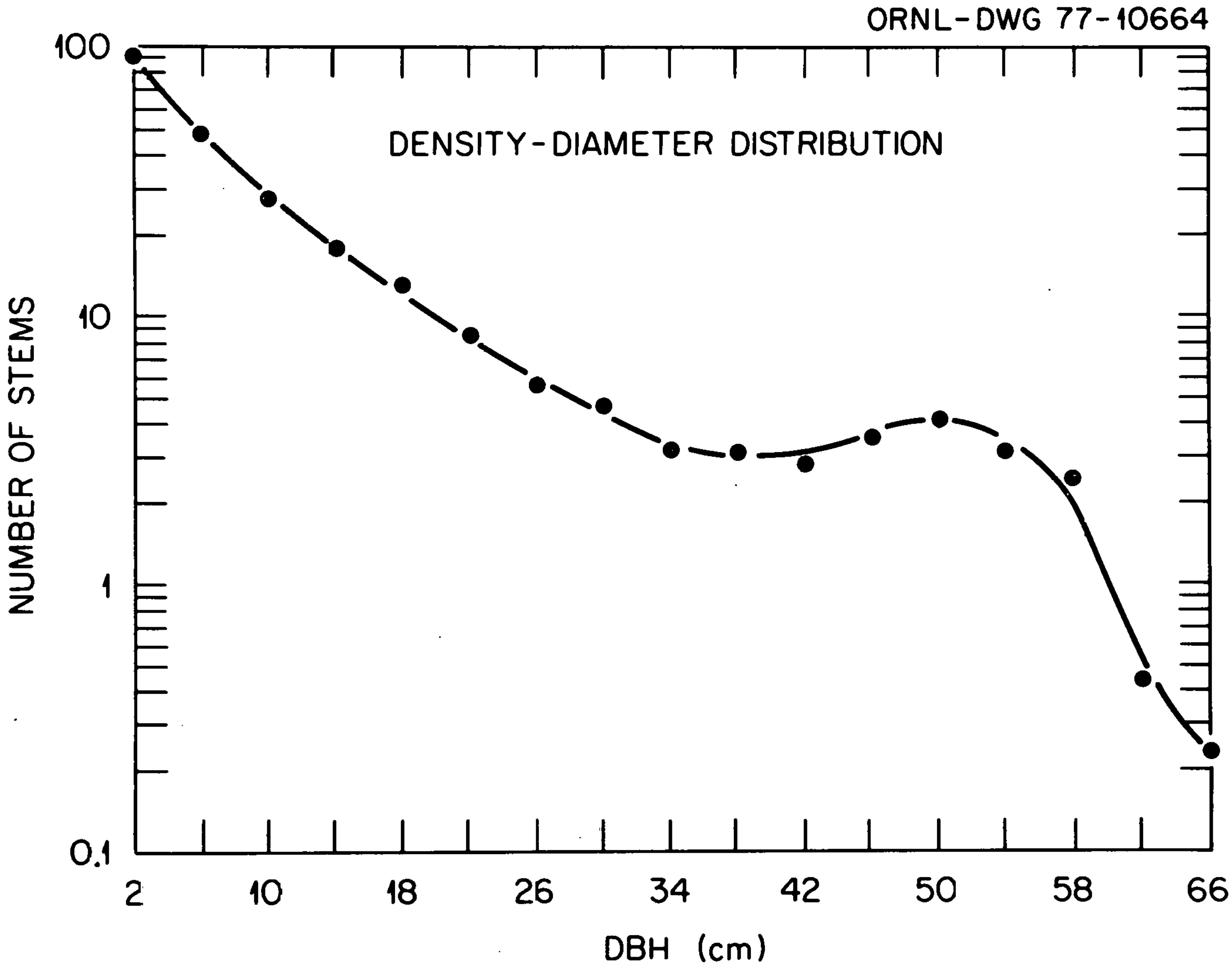

Fig. 5. Density-diameter distribution of FORAR output.
the distribution curves of West et al. (1976).

The plateau of the density-diameter distribution curves of the FORAR-generated plots was pushed far to the right. This was due to the average age of the simulated plots being 250 years, far greater than the average of the CFI stands used by West et al. (1976). The curve was convex in the larger diameter classes because trees died quickly in the model and because the two tree species of upland forests in southern Arkansas that attain a relatively large size can be thought of as pioneer species. Pioneer species tend to have convex density-diameter curves because they start growing in full sunlight, competing only for space. As the trees grow larger competition for sunlight and nutrients increases and the mortality rate increases, causing the density to decrease more rapidly (West et al. 1976). Loblolly pine, the species that makes up almost half the timber biomass in Union County, is a true pioneer species. The first 100 to 300 years of secondary succession in Union County are typified by even-aged stands of loblolly pine. When the pine overstory dies, the southern red oaks then present in the understory form the new canopy and start to grow in relatively full sunlight. In this respect, some southern red oaks acted as "pioneers" in the model and contributed to the convexity of the distribution curve in the larger diameter classes.

The density-diameter curves generated from FORAR output generally had a flatter slope than the actual curves of West et al. (1976), although the densities were comparable at the smaller diameters. West et al. (1976) state that the slope of the distribution curve is probably related to timber harvesting, the heaviest timber harvesting causing the steepest slope. It would appear that the KILL subroutine assumption that 1% of the seedlings of a species reach maximum age is reasonable for undisturbed forest stands but too high for stands that are affected by cultural practices. The sensitivity of the model predictions to this factor could be tested, but it was not done in this study.

Taken together, these several factors support the validity of the FORAR model. The validity of the functional stand model approach has been demonstrated using JABOWA (Botkin et al. 1972a,b) and FORET (Shugart and West 1977). The composition of the model forest agreed generally with the forest composition reported in the 19th century (Owen 1860). There was fair agreement in species rank between the model output and USFS CFI data, even though the CFI data were limited and were collected at various places. The density-diameter curves of the simulated plots agreed generally with the curves of West et al. (1976), the differences being due to the simulated forest being undisturbed for hundreds of years. These factors, along with agreement between model output and descriptions of the upland forest of Union County, Arkansas, by local naturalists, lend credulence to the validity of FORAR. To gather data to better validate or improve the model would require many man-years of effort involving remeasurement of fixed plots.

IV. MODEL APPLICATION

The Red-cockaded Woodpecker (Dendrocopus borealis Vieillot) is an endangered species native to the pine forests of the southeastern United States. The range of the species extends from Florida and Georgia to eastern Texas on the west and to southern Missouri and eastern Maryland on the north. Audubon described the species as abundant in the 1800's, but a census in 1973 estimated the population between 3000 and 10,000 birds (Chamberlain 1974). The species was added to the endangered species list in 1968 (Lay and Swepston 1975).

Red-cockaded Woodpeckers are birds of open, overmature pine forests. They live in family groups called clans, which may consist of a breeding pair, other adults, yearlings, and young of the year. In this respect they are more gregarious than most woodpecker species (Bent 1964, Ligon 1971). The nonbreeding adults, ranging from zero to seven in number, assist in feeding the young (Lay and Swepston 1975).

The clan lives in a stand of overmature pines, most of which have redheart (Fomes pinii), a fungous parasite which rots the heartwood of an infected tree. The stand usually contains two to nine overmature pines and occupies an area up to 0.4 km distance across (Lay et al. 1971, Hopkins and Lynn 1971). The stand containing the overmature pines ranges from 2 to 18 ha (Chamberlain 1974, Crosby 1971). The birds chip out roost and nest cavities in the relatively brittle wood of the rotten hearts of the pines. Around each cavity the birds drill many openings into the sapwood, which causes pine resin to flow down on the bark and form a whitish glaze around the cavity. The functions this behavior serves are not known, although it may be to protect against predators, to remove the cambium layer to protect the cavity from being grown over, to establish territories, or to aid in identification of cavity trees (Beckett 1971, Dennis 1971). When sap will no longer flow from the diseased tree red-cockadeds cease using the cavity for nesting, although it may still be used for roosting. The birds will also abandon the nest if the understory vegetation grows up to the nest cavity.

The Red-cockaded Woodpecker has become an endangered species primarily because timber harvesting has removed most of the suitable habitat - old-age, open pine stands. Czuhai (1971) predicted that by 1980 most of the remaining overmature timber of the South will have been harvested. If the species is to survive, it will be found in those areas of the Southeast that are 75-100% forested, have frequent fires, and are primarily pine (Jackson 1971). Union County, Arkansas, rates high in all three categories. FORAR can be a valuable tool in investigating the effects of present logging practices in Union County on the availability of Red-cockaded Woodpecker nesting habitat through time.

To use FORAR, Red-cockaded Woodpecker habitat had to be defined in terms of model information. The major factor of old-growth stands which defines the habitat appears to be the nest tree (Ligon 1970). Unlike the most recently extirpated Picidae, the Ivory-billed Woodpecker (Campephilus principalis) (Tanner 1942), the Red-cockaded Woodpecker does not depend on the mature forest for all its food. It will feed in cornfields (Bent 1964, Baker 1971) and second-growth stands of young pines (Beckett 1971). Neither is the species overly disturbed by moderate logging in the area of the nest (Ligon 1970). Thus, the critical factor appears to be large, dying pines in open areas.

FORAR was modified slightly to keep track of every pine on the 1/12 ha simulated plots that had a dbh greater than or equal to 25 cm, the approximate minimum loblolly pine cavity tree diameter reported (Baker 1971, Thompson and Baker 1971, Lay and Russell 1970). Any large pine growing less than 0.1 cm dbh per year was considered a diseased and dying tree. This was a conservative estimate, based on Lay and Russell's (1970) 0.15 cm yr^{-1} mean dbh growth of cavity trees in eastern Texas. The basal area (openness) of the simulated plot was not explicitly considered because the presence of even one large pine on a simulated plot suppressed the understory enough to leave much of the pine bole above the understory and thus useable by the bird. When management for timber was simulated, the plots were burned every five years to keep the stands open (Williams, personal communication 1975).

FORAR was run under 2 different management schemes to determine the effects on the presence of Red-cockaded Woodpecker habitat, i.e., pines greater than or equal to 25 cm dbh. The first management scheme represented the current forest management practices of private industry in south central Arkansas. The simulated loblolly pine stands were clearcut after 40 years and replanted in pine. The young plots were burned once every five years after the pines reached sapling size. Herbicide treatments were considered equivalent to burning by the simulator. The simulated plots were stocked with enough pines to produce approximately 160 pines ha^{-1} at rotation age to avoid modeling precommercial thinning (rather than stocking several hundred pines and thinning them), since pre-commercial-sized trees were unimportant in this application of the model. The second management scheme, which was a theoretical plan rather than a suggested management practice, was similar to the first except that one large pine was left uncut when the simulated plot was logged. This would be equivalent to leaving 12 large pines per hectare on part or all of the management unit. After five years the remaining trees were taken and the plot was replanted with pines. If the remaining trees did not last five years the plot was replanted earlier. It was assumed that management units of different ages would be interspersed so that the large pines left in an average management unit would be within 0.4 km (the maximum reported distance between cavity trees) of other utilizable large pines. Thus, a Red-cockaded Woodpecker clan on the plot(s) could find enough large pines around the management unit to continue to use the habitat, or a clan in the surrounding management units could come in and utilize the remaining pines.

Total trees present through the simulation and total number of years with at least one large tree present on the plot were monitored (1) for large pines, and (2) for large, dying pines (Table 2). The second management scheme, that of leaving 12 trees per hectare, was significantly higher in all categories except total number of large pines. The number of large pines present was not significantly different between the two schemes. This shows the importance of knowing what acceptable Red-cockaded Woodpecker habitat is and of studying the integrated effects of managing for the species. For

Table 2. Comparison of Red-cockaded Woodpecker nesting habitat availability between two timber management schemes. Scheme 1 removes all trees; scheme 2 leaves 12 trees per hectare

	Management scheme 1	Management scheme 2	Level of significance
Total large pines present through simulation	3170	3255	N.S.
Total large, dying pines present through simulation	172	213	**
Number of years with at least one large pine present on plot	388	405	*
Number of years with at least one large, dying pine present on plot	40	52	**

*$p < 0.05$.
**$p < 0.01$.

instance, leaving 12 large pines per hectare five extra years would not significantly increase habitat availability through time if the critical habitat factor were number of large pines; but habitat availability would increase if the critical factor were total number of years with large, dying pines present. Habitat studies could better define what is acceptable habitat and how Red-cockaded Woodpecker population numbers relate to habitat availability.

V. SUMMARY AND CONCLUSIONS

Forest stand models can be useful in studying changes in species abundance and composition due to succession or longterm perturbations. Current ideas consider succession to be based on dynamic ecological factors and stresses on individuals. If those ideas are correct, functional stand models using ecological concepts rather than specific field data on tree or stand replacement rates should simulate succession more accurately than Markov matrices or differential equations. The functional stand model FORAR simulated an upland forest of Union County, Arkansas, using 18 parameters for each tree species and six parameters for the environment. Because the study location was farther west than the previous application in East Tennessee, a general soil moisture factor modifying the growth of each tree species was added.

The validity of the functional stand approach to modeling forest stand succession has been demonstrated using JABOWA (Botkin et al. 1972b) and FORET (Shugart and West 1977). The composition of the stands simulated using the FORAR model generally agreed with 19th century reports (Owen 1860). Compared to USDA Forest Service Continuous Forest Inventory data, FORAR was "low" in American beech, shortleaf pine, and white oaks. The generated density-diameter distribution curves generally agreed with the curves of West et al. (1976), the discrepancies probably being due to the forests of the model not being harvested for hundreds of years. All these factors support the validity of the FORAR model. To gather data to better validate or improve the model would require many man-years of effort involving remeasurements of fixed plots.

FORAR was used to simulate through time the presence of Red-cockaded Woodpecker nesting habitat in two timber management schemes. In the theoretical example examined in this study, leaving 12 trees ha^{-1} after logging resulted in significantly more large, dying pines than taking all trees and a significantly greater number of years in which large pines, healthy or dying, were present. A better definition of acceptable habitat might show whether these or other factors are actually important in determining use by the species. This, in turn, needs to be related to Red-cockaded Woodpecker population numbers to aid in determining optimal management policies.

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APPENDIX

INTRODUCTION

Because of the relative ease of estimating the necessary input parameters and because the model retains information on both individuals and species, FORAR (FORest in ARkansas stand simulation model) is versatile enough to be used in several different types of ecological studies. Changes in species composition through succession or because of long-term perturbations can be examined and consequences of different timber and wildlife habitat management techniques can be predicted. Changes in tree species abundance (e.g. to dominance or extinction) can be determined. The model provides dynamic simulations of what is classically referred to as the structure and function of ecosystems. The usefulness of different measures of such indices as diversity, productivity, or stability can be studied.

This user's manual describes the FORAR model, which simulates an upland forest of Union County in southcentral Arkansas. The model was developed from FORET (Shugart and West 1977), a modified version of the JABOWA model used by Botkin et al. (1972a, 1972b). The logging subroutine has been expanded in FORAR. A subroutine to burn the plot and probabilities of trees dying from fire damage has been added. Soil competition is computed using basal area instead of biomass. A fifth environmental variable, species-specific epidemics, has been added to subroutine BIRTH to affect seedling establishment. In addition, variables have been added, deleted, renamed, or shifted to other subroutines to make the program more efficient.

FORAR simulates composition and growth of a forest stand on the basis of each tree greater than 1.27 cm in diameter at breast height (dbh) on a 1/12 ha circular plot. The model computes (1) the numbers and biomass of each species and (2) the dbh, age, and species of each individual tree. Once a year, trees are stochastically killed or deterministically grown and new trees are stochastically planted. Individual trees are killed by a probability function that is scaled according to the maximum age recorded for the appropriate species. The probability that a specific tree will die during a given simulated year is increased if its growth rate (expressed as diameter increment) falls below an acceptable minimum (0.1 cm/yr). Stocking of new seedlings and sprouts in a given simulated year depends on the computed leaf area index of the plot and the condition of five environmental variables discussed below. The tree species to be stocked are chosen randomly from those species which can germinate under the existing conditions for soil, temperature, wildlife populations, and epidemics. Trees grow according to a species-specific optimum growth function that is modified by soil moisture, competition, available light, and climate. The optimum growth function for each species is a function of the maximum known age, the maximum dbh and the maximum height recorded for the species. The driving variable for the model is degree-days, which is randomly chosen at the beginning of each year from a normal distribution with appropriate mean and variance. FORAR is written in FORTRAN IV and has been implemented on IBM 360 series and PDP-10 computers. The present version of the model considers up to 35 tree species and up to 700 individual trees and can simulate the forest for any prespecified number of years.

PROGRAM DESCRIPTION

The deck setup of FORAR is shown in Figure 6. The control cards shown are those necessary to run the program on the ORNL IBM 360/91 computer. The program is listed in Appendix A-3. In a typical run the maximum computer core used is 270K. Computer time needed will depend on the size of the run, i.e., how many different plots are wanted, how many species are used and how many years each plot is run. A run of three plots, each potentially having 33 species and running for 600 years, takes approximately two minutes of CPU time.

INPUT

The program currently reads in parameter values for each tree species using the format:

6A4,F6.0,F5.0,F4.3,F5.2,I1,F4.0,F2.0,F5.1,F2.0,F4.1,F4.0,5L1,I4,F3.1 .

This format can easily be changed in subroutine DATA to suit the user. Table 3 lists and describes the input variable names in the order in which they are entered in the above format. Most of the parameters, such as shade tolerance or maximum age, are relatively straightforward and can be derived from standard textbooks of dendrology or silvics. Harlow and Harrar (1969) and Fowells (1965) were used in the present case for such parameter estimations.

DMAX and DMIN are the maximum and minimum degree-day values associated with the geographic range of each species. They are calculated (using a sine wave, see Appendix A-1) from the January and July mean temperatures at the northern and southern ends of the range of each species (e.g., Figure 7). B2 and B3 are the coefficients of the following equation (Ker and Smith 1955) relating height to diameter (in cm):

$$H = 137 + B2D - B3D^2 . \qquad (1)$$

Solving for B2 and B3, using $H=H_{max}$ and $\frac{dH}{dD} = 0$ when $D=D_{max}$ Botkin *et al.* 1972a) results in:

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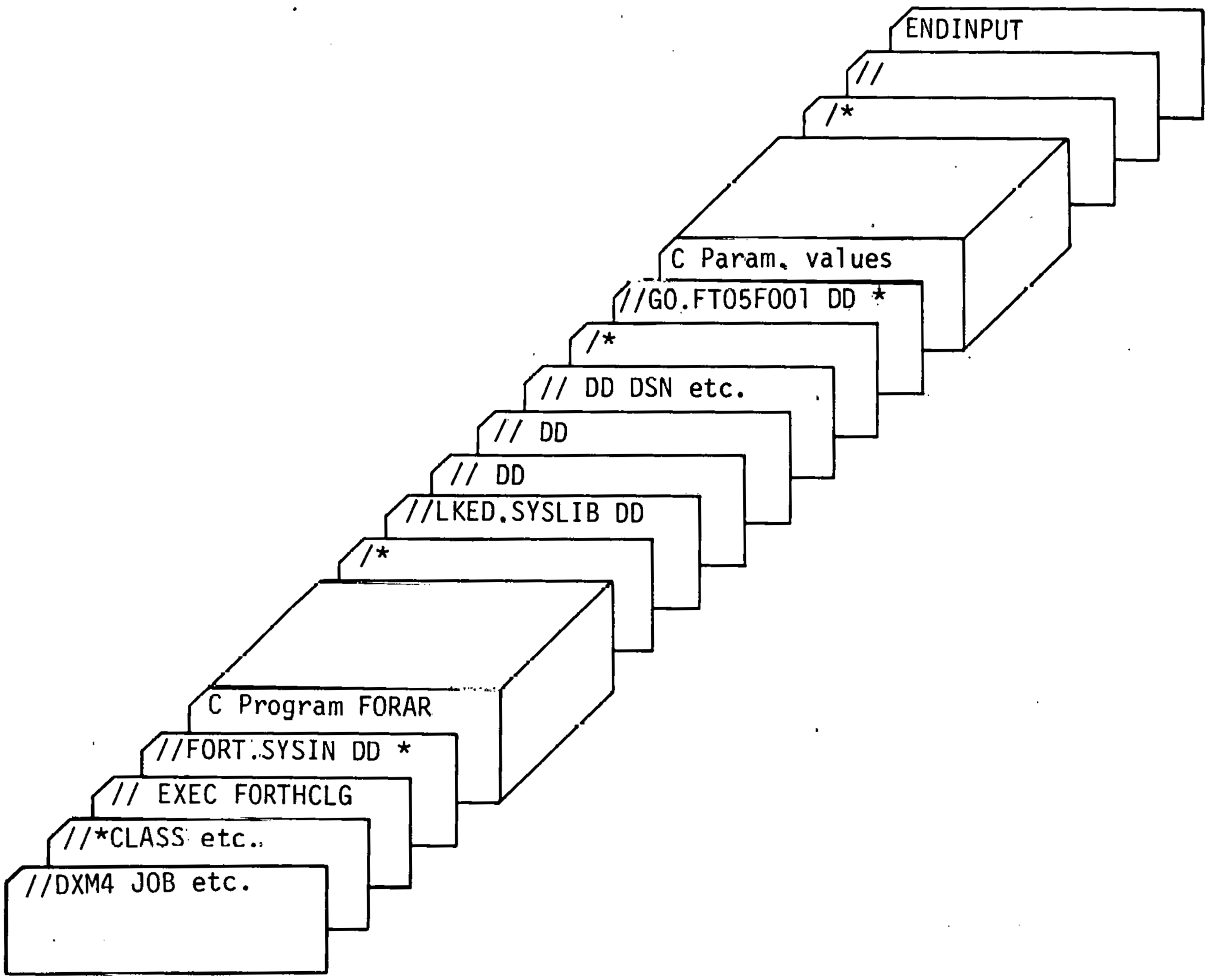

Fig. 6. Deck structure and job setup for program FORAR.

Table 3. Parameters used in the FORAR model. Table 4 lists the values used for each tree species. See text for explanation of variables.

Parameter Name	Meaning	Field
AAA	Scientific name (up to 24 letters)	xxxxxxxxxxxxxxxxxxxxxxxx
DMAX	Maximum degree-days for species range (see text)	xxxxx.
DMIN	Minimum degree-days for species range (see text)	xxxx.
B3	Derived growth parameter (see text)	.xxx
B2	Derived growth parameter (see text)	xx.xx
ITYPE	Shade tolerance 1 = tolerant 3 = intolerant	x
AGEMX	Maximum age recorded for the species	xxx.
C	Leaf area constant 1 = deciduous 2 = coniferous	x.
G	Derived Growth constant (see text)	xxx.x
STEND	Tendency to sprout Value of 0.,1.,2.,or 3.	x.
SPTMIN	The minimum dbh of a tree that will sprout	xx.x
SPTMAX	The maximum dbh of a tree that will sprout	xxx.
S(1)	Must the seed have a litter layer to germinate? value of T of F	x
S(2)	Must the seed have mineral soil to germinate? value of T or F	x
S(3)	Is the seedling susceptible to hot years? value of T or F	x
S(4)	Is the seedling a highly-preferred food for wildlife? value of T or F	x
S(5)	Is an epidemic seriously damaging the species? value of T or F	x
KTIME	Number of years after a bare plot that a species is liable to be present	xxx
SOIM	The fraction of maximum recorded dbh the species will attain on an upland site	x.x

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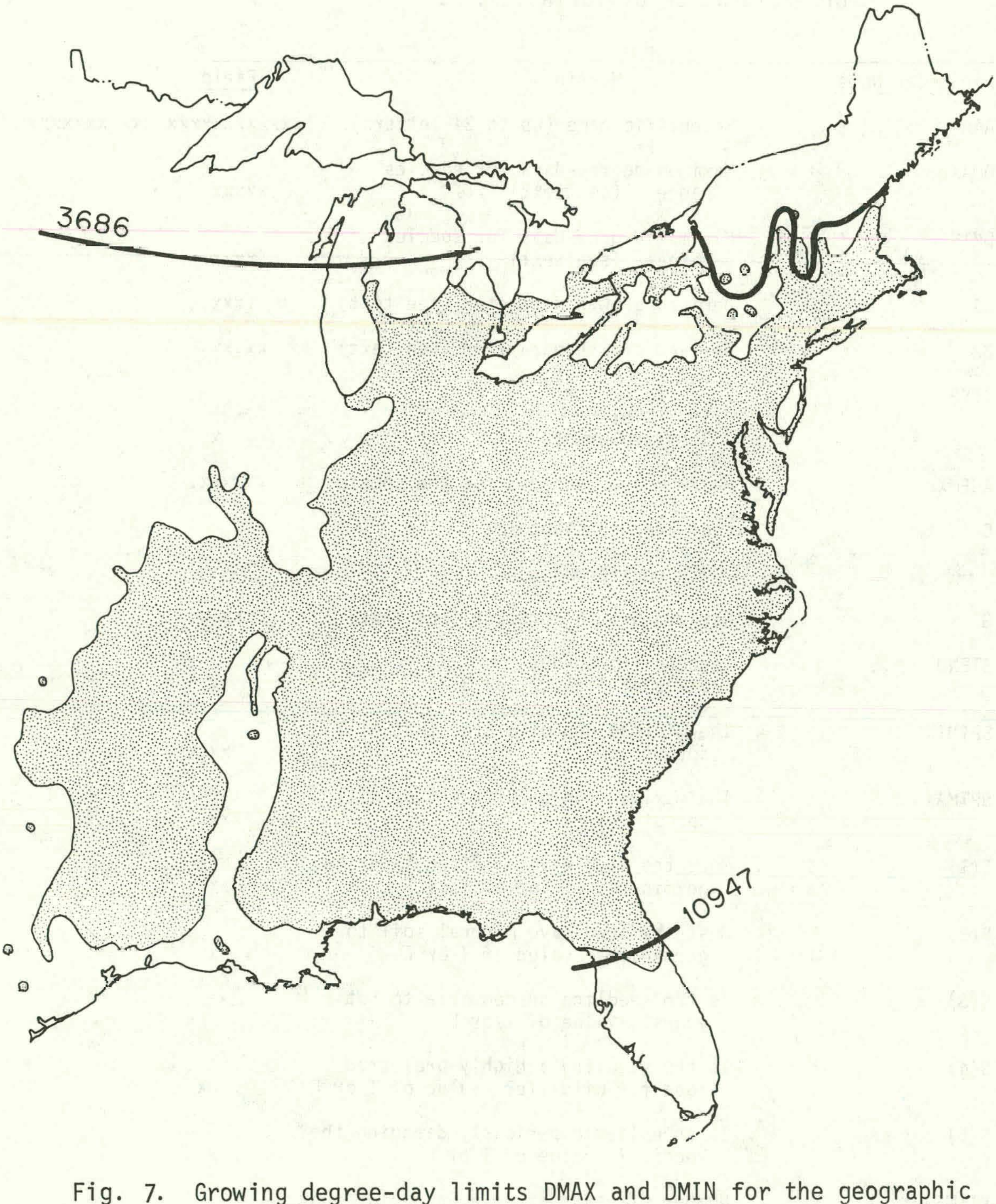

Fig. 7. Growing degree-day limits DMAX and DMIN for the geographic range of flowering dogwood (Cornus florida). Isopleths for growing degree days are calculated from U.S. Geological Survey (1965) and from program DATGEN (Appendix A-1).

$$B2 = \frac{2(H_{max} - 137)}{D_{max}} \quad , \quad B3 = \frac{(H_{max} - 137)}{(D_{max})^2} \quad . \qquad (2)$$

The growth constant G is derived from Equation (4) below and the assumption that 2/3 of the maximum dbh of the tree is reached at 1/2 the maximum age. G can be solved for directly (see Botkin et al. 1972b) or found by using a simple program of tree growth on an interactive computer (see Appendix A-2). The variable KTIME is an attempt to handle variation in seed source availability. If there is no parent tree on the plot and if the variable IMYR (the number of years that have passed since the plot had no trees and mineral soil) is greater than KTIME, then it is assumed there is no seed source for the species and that it can not be established by seeding. The input values used in the present version of FORAR are listed in Table 4.

The model usually starts a plot with no trees; however, subroutine LOAD can be used to input any desired initial conditions. If a litter layer is wanted at the beginning of a plot, IMYR should be given an initial value greater than 15.

Subroutines

The flowchart for FORAR is shown in Figure 8. There are 14 subroutines in addition to the main program; however, KILL, BIRTH, and GROW are the main elements in terms of actual computation.

Whenever a random number is needed for any model computation, a call to subroutine RANDOM returns a random number drawn from a flat distribution between 0 and 1. In subroutine DATA the user declares the number of plots wanted, the number of tree species, the number of years each plot will be run, the interval of time between successive outputs, the annual insolation, the maximum basal area a plot can attain, and the mean for DEGD. Subroutines PLOTIN and INIT initialize variables, and PLOTIN also updates and prints the plot number.

Subroutine GAUSS randomly chooses a value for DEGD — total growing degree-days for a year, based on a growing degree-day temperature of 42°F — from a normal distribution. The mean and standard deviation of DEGD can be calculated from data available from the National Climatic Center, Asheville, North Carolina.

Table 4. Parameter values used in the FORAR model. Scientific binomials follow Little (1971).

Species	DMAX[3]	DMIN[3]	B3	B2	ITYPE	AGEMX	C[8]	G	STEND	SPTMIN	SPTMAX	S					KTIME	SOIM
Acer rubrum	13395	1810	0.173	52.58	1[3]	150[2]	1	240.2	2[1]	12.0[8]	150[11]	F[1]	T[1]	T	F[10]	F[8]	9999	0.5
Carpinus caroliniana	10947	2097	0.228	33.56	1[2]	100	1	129.9	2	6.0	70[11]	F	F	F	F[10]	F	9999	0.4
Carya cordiformis	9461	3686	0.306	69.21	3[1]	300[8]	1	117.2	2[5]	12.0[8]	110[11]	T[8]	F[2]	T[8]	F[1]	F[8]	30	0.8
Carya glabra	12652	3686	0.168	49.65	1[1]	300[8]	1	111.3	2[5]	12.0[8]	145[11]	T[1]	F[2]	T[8]	F[10]	F[8]	30	0.5
Carya laciniosa	8718	5081	0.318	72.46	1[1]	300	1	123.2	2[5]	12.0	90[11]	T	F	T	F[10]	F[5]	9999	0.4
Carya ovata	12652	4105	0.312	69.66	1[1]	300[2]	1	116.5	2[5]	2.0[1]	110[11]	T[8]	F[2]	T[8]	F[10]	F[8]	9999	0.7
Carya texana	9461	5526	0.318	57.56	1	300	1	79.6	2[5]	12.0	110[11]	T	F	T	F[10]	F[5]	9999	0.5
Carya tomentosa	10947	3686	0.190	49.41	3[1]	300[8]	1	98.6	2[5]	12.0[2]	130[11]	T[1]	F[2]	T[8]	F[10]	F[8]	9999	0.8
Castanea ozarkensis	7756	5526	0.085	21.72	1	60	1	250.9	2[12]	12.0	125[11]	T	F	T	F[10]	T[5]	9999	0.8
Celtis laevigata	12652	5526	0.336	71.26	1[1]	350	1	112.7	2[1]	6.0[1]	115[11]	T[1]	F	F	F[10]	F	9999	0.6
Cornus florida	10947	3686	0.536	40.81	1[1]	100[8]	1	88.7	3[1]	12.0	35[11]	F[8]	F[1]	T[1]	F[10]	F[8]	9999	0.9
Diospyros virginiana	13395	5526	0.084	35.84	1[1]	150[8]	1	234.1	2[1]	12.0[8]	210[8]	F[1]	F[2]	T[8]	F[10]	F[8]	30[5]	0.3
Fagus grandifolia	10204	2097	0.151	46.20	1[1]	400[2]	1	80.7	2[1]	6.0[8]	30[8]	F[1]	F[2]	T[8]	F[10]	F[8]	9999	0.5
Fraxinus americana	10947	2414	0.080	34.43	3[1]	300[8]	1	113.3	2[1]	6.0[1]	20	F[1]	T[2]	T[8]	F[10]	F[8]	9999	0.9
Ilex opaca	10947	5526	0.156	42.61	1[2]	200[2]	1	133.5	1[5]	6.0	35[11]	F[8]	F	F	F[10]	F	9999	0.5
Juglans nigra	8499	3686	0.074	36.37	3[1]	250	1	161.5	1[1]	6.0[1]	40	T[8]	F[2]	T[8]	F[10]	F[8]	20[5]	0.7
Juniperus virginiana	10204	2966	0.236	57.75	3[1]	300[1]	2	107.1	0[1]	12.0[1]	120[1]	F[1]	T[1]	F[1]	F[10]	F[8]	20[5]	0.9
Liquidambar styraciflua	10947	5526	0.191	55.20	3[1]	300[2]	1	119.4	2[1]	12.0[1]	80[1]	F[1]	F[1]	F[1]	F[10]	F[8]	9999	0.7
Morus rubra	13395	3686	0.061	22.15	1[4]	75[5]	1	260.6	0[5]	12.0[1]	180[11]	T[5]	F[5]	T	F[10]	F	30[5]	0.3
Nyssa sylvatica	12652	3686	0.202	37.00	1[5]	300[8]	1	54.8	1[1]	60.0[1]	90[1]	F[8]	T[8]	F[8]	F[10]	F[8]	9999	0.7
Ostrya virginiana	10204	1810	0.266	49.50	1[7]	100	1	219.1	1	6.0	90	F	F	F	F[10]	F	9999	0.4
Pinus echinata	9461	5526	0.290	70.75	3[1]	300	2	128.4	2[1]	6.0[1]	20[1]	F[1]	T[1]	F[1]	F[10]	F	9999	1.0
Pinus taeda	10947	6391	0.189	60.81	3[1]	350[2]	2	174.6	0[1]	12.0[1]	160[11]	F[1]	T[1]	F[1]	F[10]	F[8]	9999	1.0
Prunus serotina	10947	3899	0.083	35.57	3[2]	250[1]	1	139.5	2[1]	6.0[1]	210[1]	F[1]	T	F[8]	T[10]	F[8]	9999	0.7
Quercus alba	10204	2966	0.074	36.37	1[1]	400[3]	1	100.7	2[1]	12.0[1]	40[1]	T[1]	F[1]	F[1]	T[10]	F[8]	9999	0.8
Quercus falcata	10947	5526	0.078	33.57	1[6]	400	1	82.9	2[1]	12.0[1]	30[1]	T[8]	F[8]	F[8]	F[10]	F[8]	9999	0.9
Quercus marilandica	10204	5081	0.111	24.86	3[5]	400	1	36.3	2	12.0	40	F[5]	F	F	F[10]	F	9999	1.0
Quercus shumardii	10947	5081	0.199	65.19	3[2]	400	1	115.9	2[1]	12.0[1]	160[1]	F[1]	F[1]	F	F[10]	F	30[5]	0.7
Quercus stellata	10947	5526	0.195	47.75	3[1]	400	1	67.9	2[1]	12.0[1]	40[1]	T[1]	F[1]	F[8]	T[10]	F[8]	9999	1.0
Quercus velutina	9461	3313	0.097	41.57	1[2]	200[9]	1	100.1	2[1]	12.0[1]	40[1]	F[1]	T[1]	F[8]	F[10]	F[8]	9999	0.8
Sassafras albidum	10947	3686	0.619	75.51	3[2]	200[8]	1	108.1	3[1]	6.0[1]	60[1]	T[1]	F[1]	F[8]	F[10]	F[8]	20[5]	0.8
Ulmus alata	10947	5526	0.230	51.81	3[1]	125[5]	1	212.5	1	6.0	110	F	F[5]	F	F[10]	F	9999	0.4
Ulmus americana	12652	1522	0.082	39.35	3	300[1]	1	141.8	1[1]	6.0[1]	240[1]	F[1]	F[1]	T[1]	F[5]	T[10]	9999	0.4

[1]From Fowells (1965)
[2]From Harlow and Harrar (1969)
[3]From Little (1971) and U.S. Geological Survey (1965)
[4]From Wigginton (1964)
[5]From Carl Amason (personal communication, 1975)
[6]From Baker (1949)
[7]From Peattie (1950)
[8]From Shugart and West (1977)
[9]From Northeastern Forest Experiment Station (1971)
[10]From Martin et al. (1971)
[11]From Pardo (1973)
[12]From Moore (1960)
[13]All other values not otherwise referenced were developed during the course of this project.

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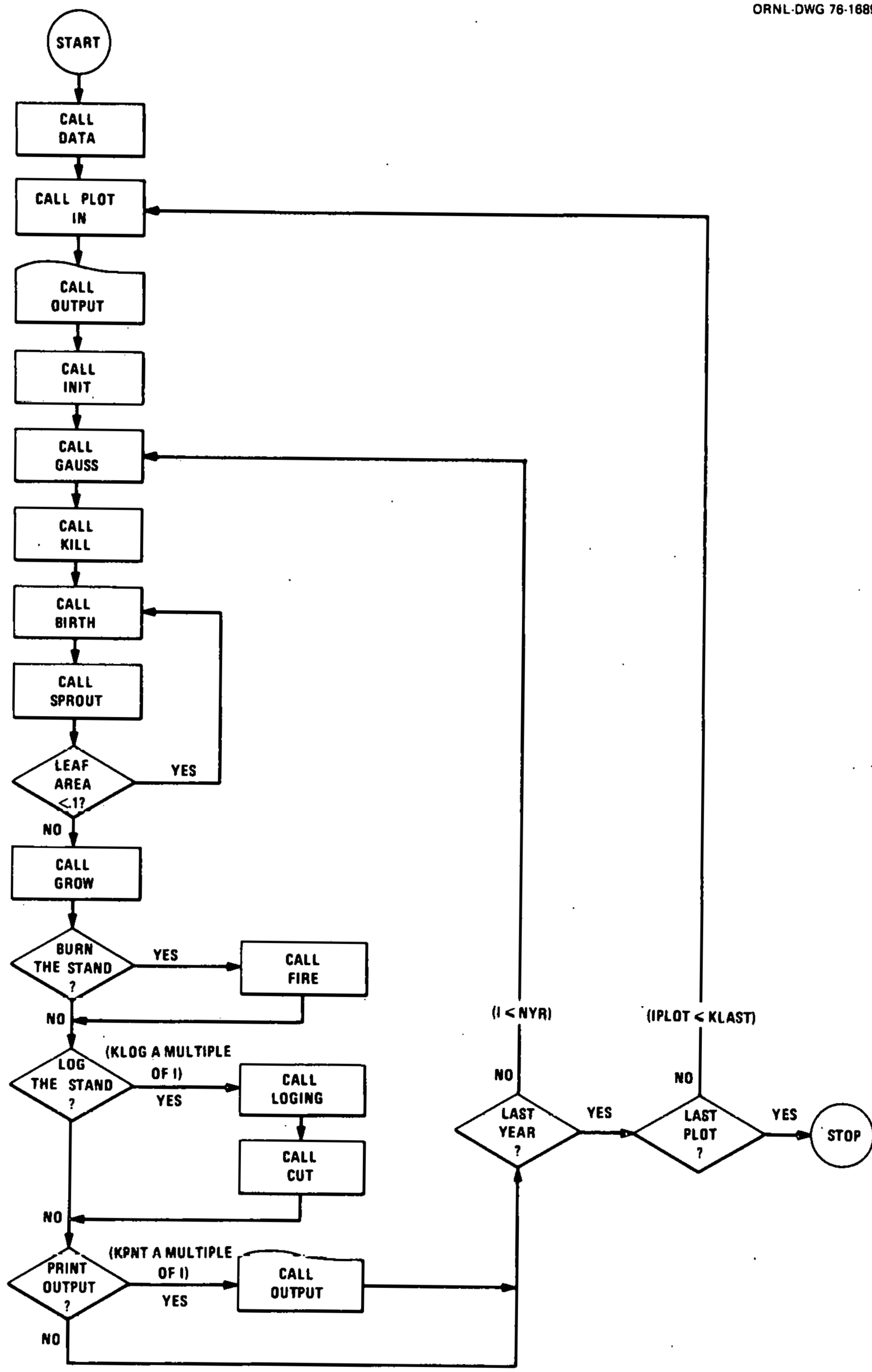

Fig. 8. Flow diagram of the FORAR model.

Subroutine KILL

FORAR, like the Botkin model, assumes that individual tree death can be viewed as a stochastic process, rather than delineating all the different and complex causes of mortality. The probability that a tree will be killed in any one year is $p = 1-(1-\varepsilon)^n$ (Botkin et al. 1972b). The model assumes that 1% of all seedlings of a species will live to reach the maximum age for that species (Figure 9). Setting p equal to 0.99 and n equal to AGEMX (the maximum known age a species can attain) results in:

$$\varepsilon - 4.605/\text{AGEMX} \quad . \tag{3}$$

Once a year KILL generates a random number for every tree, and the tree is killed if the random number generated is less than ε.

In the present version of FORAR, there are two cases in which the kill probabilities of a tree are changed from the above statement. First, the model uses the array NOGRO to keep track of those trees that grow less than 0.1 cm dbh per year. A tree has only one chance in a hundred of surviving 10 years if such a growth rate is maintained (Botkin et al. 1972b). Accordingly, the random number generated has to be less than 0.368 to kill such a tree. Secondly, a moderate fire (described below) will "damage" those species that are susceptible to fire. In the present version of FORAR, a susceptible tree that is present on the plot when a moderate fire occurs is given a 20% chance of living 5 years (J. Warren Ranney, personal communication 1976); thus, the random number generated must be less than 0.275 to kill the tree.

Trees are also killed deterministically if there is logging or a fire. To log the circular plot, the user specifics in subroutine LOGING the upper and lower diameter limits of each species of the trees to be logged. Subroutine CUT then removes all trees on the plot within these diameter limits. In subroutine FIRE the user has a choice of specifying a light, a moderate, or a severe burn. A light fire sets the logging limits of each species to a minimum of 0 cm and a maximum of 12.7 cm and then calls subroutine CUT to remove the trees. A severe fire removes all trees from the plot and resets the bare plot counter IMYR to zero, allowing the pioneer species with small values of KTIME to reenter the plot. A moderate fire uses subroutine CUT in the same way as a light burn to remove all the trees of species that are extremely susceptible to fire damage, all the trees less than 25.4 cm dbh of species that are moderately susceptible to fire damage, and all the trees less than 17.8 cm dbh of resistant species. The susceptibility of each species to fire damage is established in the COMPUTED GO TO statements in subroutine FIRE. The susceptibility values used in FORAR were taken from Davis (1959), Fowells (1965), Harlow and Harrar (1969), Curtis (1959), Grange (1959), or developed in the course of

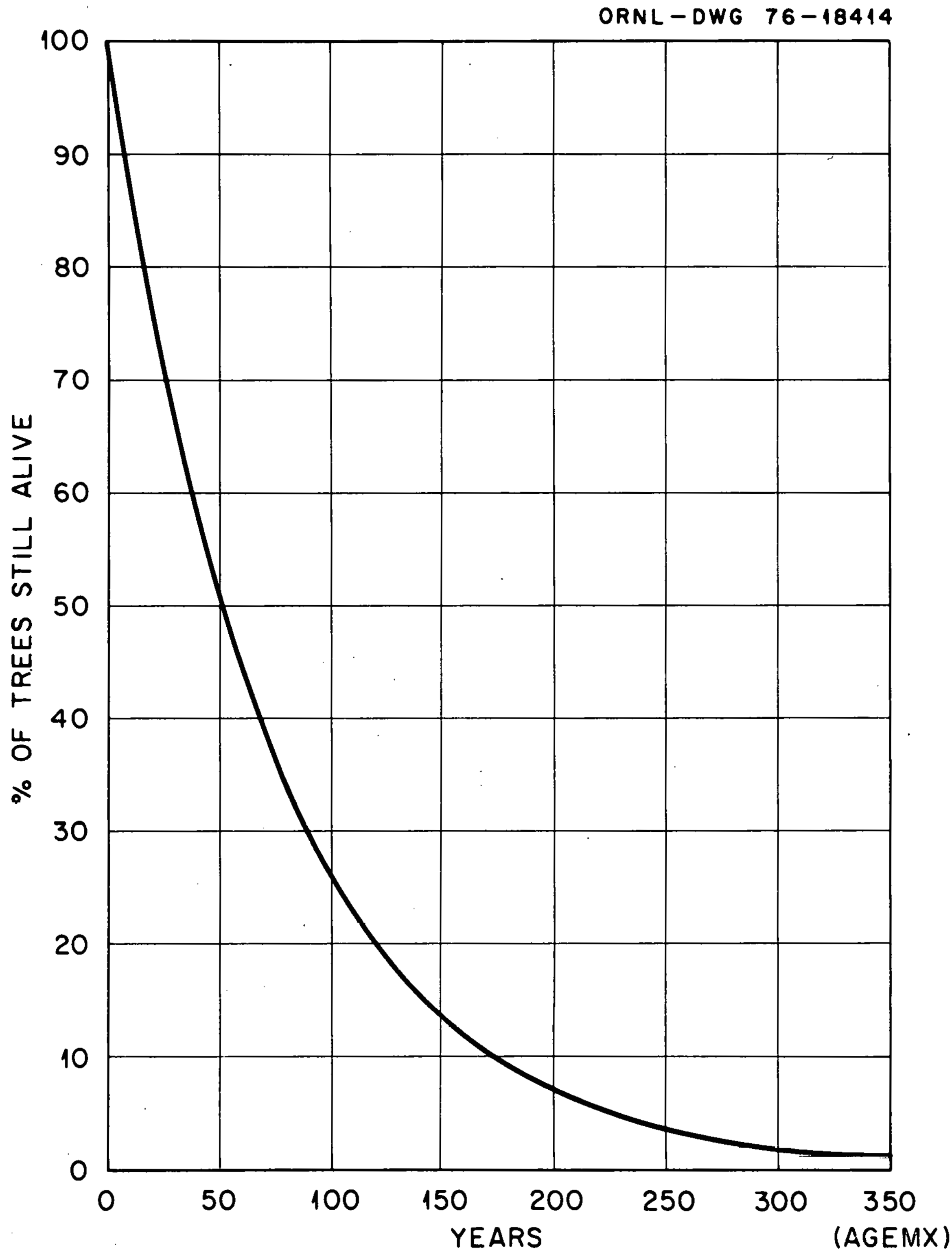

Fig. 9. Functional form for the random death process. The model assumes that 1% of all the seedlings of a species will live to reach the maximum known age. In the example shown, the maximum age of loblolly pine is 350 years.

this project. A moderate fire also resets IMYR to zero and changes the survival probabilities of those damage-susceptible trees that were large enough to survive the fire, as discussed above.

Subroutine BIRTH

BIRTH calculates the biomass already on the plot and sets the correct values for the year for the five environmental variables corresponding to the S array in Table 3. As in the FORET model (Shugart and West 1977), the soil is considered to be mineral soil if the biomass on the plot is less than 0.2 metric ton ha^{-1} and if IMYR (an additional parameter in the FORAR model) is less than 15. The soil is considered to have a litter layer if the plot biomass is greater than 0.1 metric ton ha^{-1}. It is a hot year if DEGD has a value greater than its mean. Wildlife populations are randomly chosen half the time to be large enough to consume the entire seed source of a preferred food species. In the FORAR model, an epidemic is randomly present half the time to destroy the seedlings of certain host species.

BIRTH then separates out those species capable of germinating under existing environmental conditions. For instance, we assume that a species requiring a litter layer to germinate (i.e., S(1) = .TRUE.) cannot be stocked when there is no litter layer on the ground (i.e., when the biomass on the plot is less than 0.1 metric ton ha^{-1}). From the subset of possible species, the program randomly chooses from one to three species to actually stock in a given year. A random number of seedlings between zero and eight are then "born" for each of the one to three species and randomly assigned a dbh around 1.27 cm (Tree seedlings are established 137 cm tall in the model in order to have a nonzero dbh.).

After the new seedlings are established, subroutine BIRTH calls subroutine SPROUT, which checks to see if any trees of a species capable of sprouting have died since the last year. If they have, and if their diameter was within the sprouting range of that species (SPTMIN$\leq$dbh$\leq$SPTMAX), a random number of sprouts between zero and three are randomly given dbh's around 0.1 cm and are added to the plot. Where a maximum of three species of seedlings can enter the plot in one pass through subroutine BIRTH, only one randomly chosen tree can sprout in one pass through subroutine SPROUT.

Subroutine BIRTH then calculates whether the biomass on the plot is less than 0.1 metric ton ha^{-1}. If it is, the program returns to the top of subroutine BIRTH to go through the process again. Before returning to MAIN, BIRTH updates the age of all the trees.

Subroutine GROW

The basic growth function used by FORAR, FORET (Shugart and West 1977), and JABOWA (Botkin *et al*. 1972a, 1972b) is:

$$\delta(D^2H) = R\ LA\ \left(1 - \frac{D\ H}{D_{max}\ H_{max}}\right) , \qquad (4)$$

where

D = dbh,
H = height,
D_{max} = maximum dbh recorded for the species (Pardo 1973),
H_{max} = maximum height recorded for the species,
R = a constant, and
LA = leaf area.

This equation considers the trunk of a tree to be a cylinder and assumes that the change in volume of a tree in one year is proportional to the amount of sunlight the leaves receive times a factor for maintenance of the volume of living tissue already present (Botkin et al. 1972b). The assumptions of the model are as follows (For more details, see Botkin *et al*. 1972b):

$$H = 137 + B2D - B3D^2 , \qquad (5)$$

$$LA\ \alpha\ \text{leaf weight} , \qquad (6)$$

$$\text{leaf weight} = CD^2 ,$$

and $$G = RC , \qquad (7)$$

where C = leaf area constant ,

and G = a growth constant .

Using the above equations in Equation (4) to solve for D, the annual increment of growth, we find:

$$\delta D = GD \frac{\left(1 - \frac{D\ H}{D_{max}\ H_{max}}\right)}{274 + 3B2D - 4B3D^2} . \qquad (8)$$

This is the basic equation for optimum growth on a good site with no competitors. An example of this function for two species is shown in Figure 10.

FORAR modifies the annual growth equation by factors for shading, climate, competition, and soil moisture. In order to modify growth according to the amount of light each tree is receiving, subroutine GROW calculates the amount each tree is shaded, in 0.1 meter increments, by those trees on the plot that are taller. This is done using the equation:

$$AL = PHI\ e^{0.25SLA} , \tag{9}$$

where

AL = available light for a given tree,
PHI = annual insolation (in appropriate units), and
SLA = shading leaf area (Botkin et al. 1972a).

SLA is calculated using Equation (6) as the leaf biomass above a given height (Shugart and West 1977, Sollins et al. 1973). Kramer and Kozlowski (1960) give equations to relate AL to r(AL), the photosynthetic rate:

$$r(AL) = 1 - e^{-4.64(AL-0.05)} \text{ for tolerant species} , \tag{10}$$

$$r(AL) = 2.24(1 - e^{-1.136(AL-0.08)}) \text{ for intolerant species} . \tag{11}$$

The factor r(AL) is then used as the shading factor multiplying the growth equation. Figure 11 shows r(AL) as a function of AL for tolerant and intolerant species.

FORAR assumes a parabolic functional form for the effect of climate upon tree growth, T(DEGD). Figure 12 shows the relationship between the range of the species and T(DEGD). Optimum climatic effect occurs in the middle of the climatic range of the species. DEGD values at the range extremes reduce T(DEGD), and thus the growth of the trees of that species, to near zero.

The crude competition factor in the model is simply:

$$S(BAR) = 1 - BAR/SOILQ , \tag{12}$$

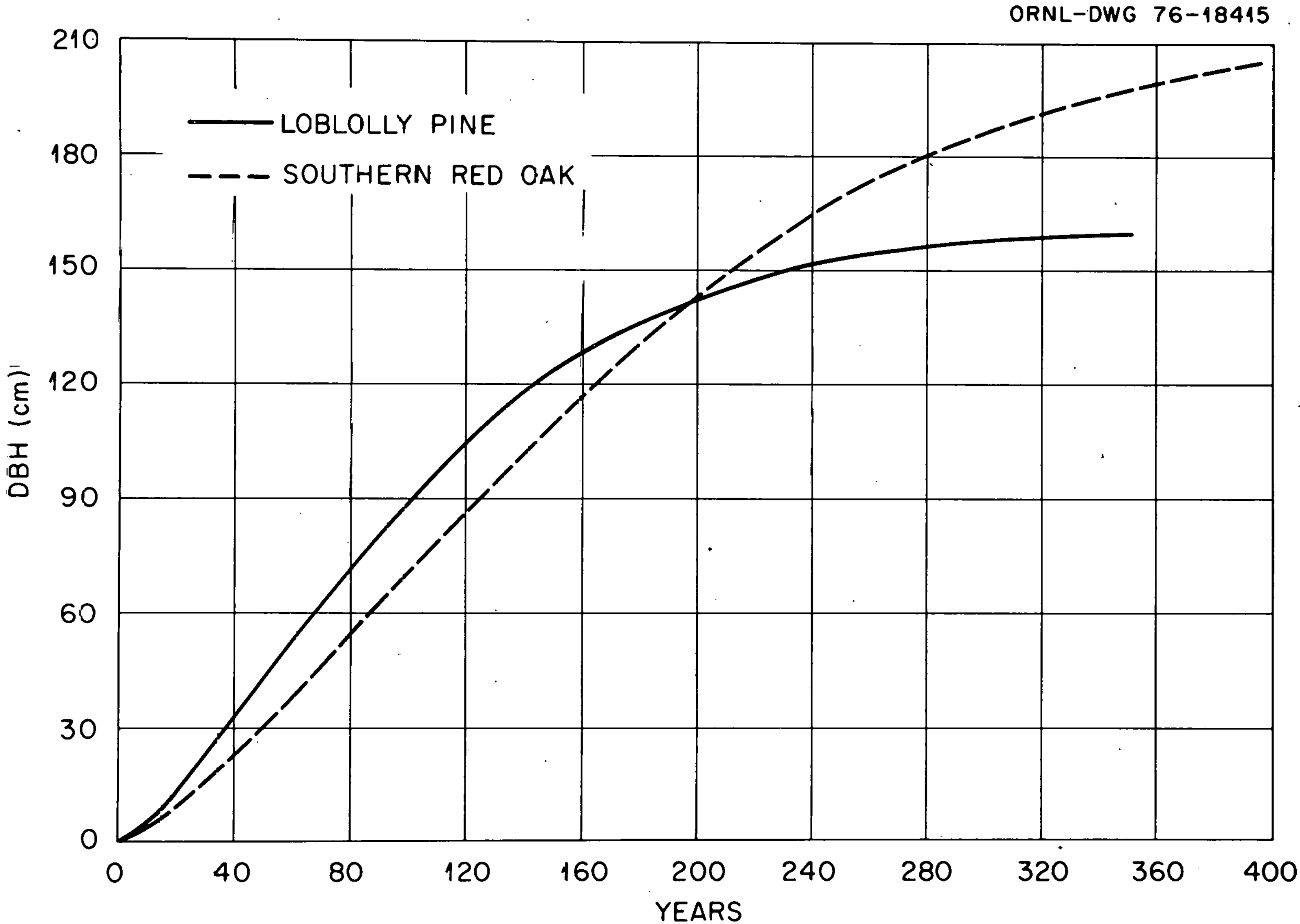

Fig. 10. Functional form for the optimum growth equation. The slope of the curve is a function of AGEMX. The height of the curve is a function of the maximum dbh recorded for the species (Pardo 1973).

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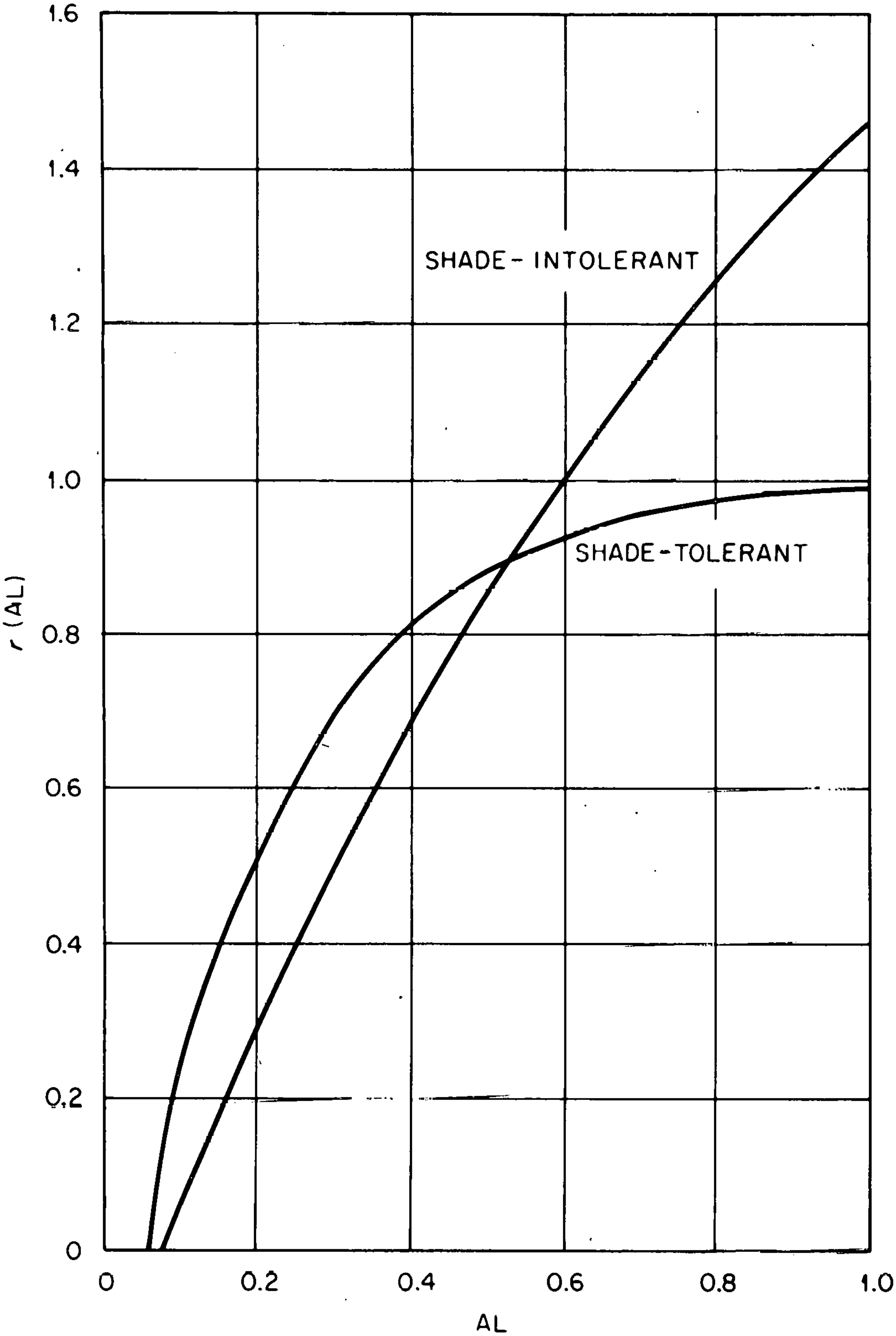

Fig.11. Functional form relating available light AL to photosynthetic rate r(AL). Equations are from Kramer and Kozlowski (1960).

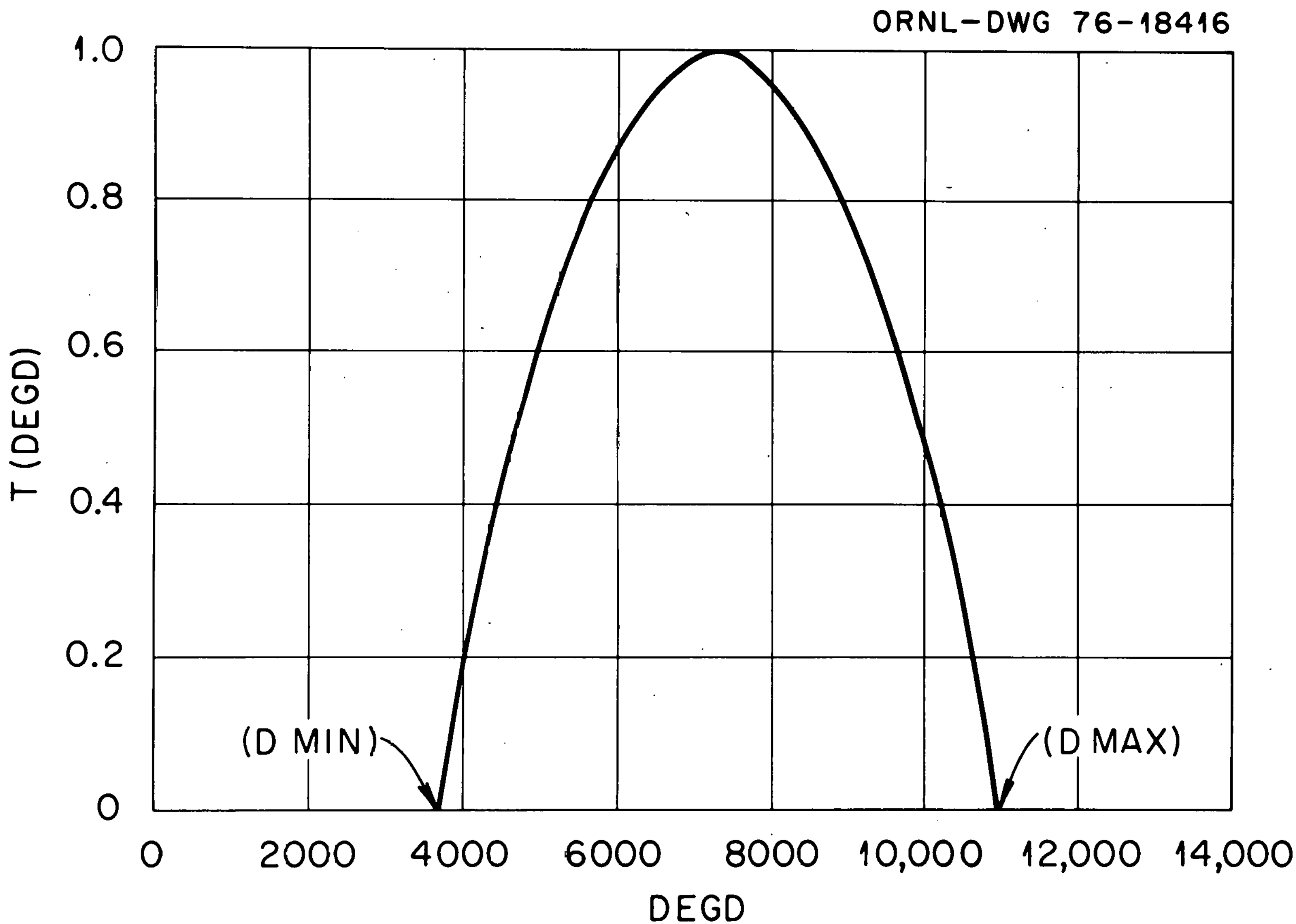

Fig. 12. Functional form relating degree-days DEGD to the effect of climate on the growth of a tree species. In this example, sassafras can not grow if the degree-days are less than 3686 of greater than 10947.

where

S(BAR) = competition factor,
BAR = basal area on the plot, and
SOILQ = maximum basal area the plot can sustain.

A plot of S(BAR) is shown in Figure 13.

The last factor modifying tree growth, soil moisture, was added to FORAR when it was found that primarily-bottomland species were comprising too much biomass on the plot. For simplicity, SOIM was assumed to be a constant factor reducing (usually) the growth of a species on an upland site. A more realistic approach would be to use moisture as another driving variable of the model. This, however, would add another level of resolution to an already complex program. Species that are found primarily on dry, poor soils have values of SOIM near 1.0; whereas species that commonly grow well in bottomlands and grow much more poorly on upland sites may have values of SOIM around 0.5.

The final growth equation for the model is thus:

$$\delta D = G\ D\ \frac{1 - \frac{D\ H}{D_{max}\ H_{max}}}{274 + 3B2D - 4B3D^2}\ r(AL)\ T(DEGD)\ S(BAR)\ SOIM \quad . \qquad (13)$$

OUTPUT

A sample output of FORAR is shown in Appendix A-4. Normal output of FORAR shows, for each species, the number of trees on the plot, their dbh's, and the biomass. Total biomass and leaf area on the plot are also given at the end of the species list. Output frequency (KPNT) is specified by the user in subroutine DATA. The model has an option to list all the trees that have died from random causes since the last printout, all the trees that have been removed by logging and the diameter limits for each species, and all the trees that have been killed by fire.

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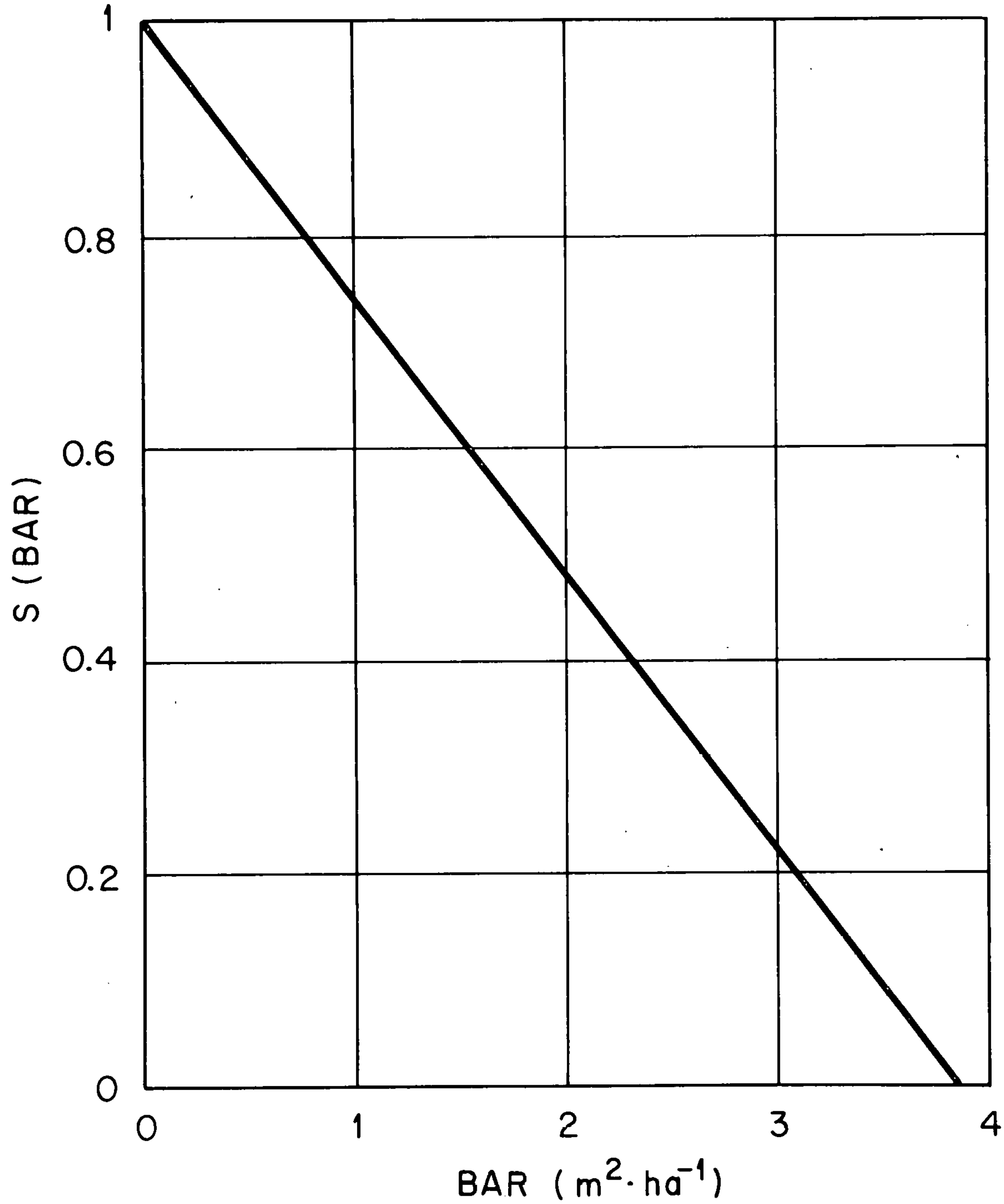

Fig. 13. Linear function relating basal area on the 1/12 ha plot (BAR) to a general competition factor S(BAR). The maximum basal area the plot can maintain is from Dick Williams (personal communication 1975).

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Appendix A-1

Program DATGEN calculates annual degree-days from January and July mean temperatures. A sine function is used to estimate average daily temperature, with the minimum and maximum values equal to the January and July means, respectively. The area under the sine curve and above the 42°F line is then determined by integration and scaled to the proper value for degree-days.

In the listing shown, the degree-days are calculated and printed out for the matrix of January mean temperatures from 0° to 70° and July mean temperatures from 60° to 90°.

```
ISN 0002          DIMENSION DEGD(100,100)
ISN 0003          DO 6 I=1,71,5
ISN 0004         XI=I-1
ISN 0005         DO 4 J=60,90,5
ISN 0006         KK=1
ISN 0007         XJ=J
ISN 0008          AVE=(XJ+XI)/2.
ISN 0009          IF(XI.GE.XJ) GO TO 39
ISN 0011          R=XJ-XI
ISN 0012         R=.5*R
ISN 0013          DO 11 JJ=1,342
ISN 0014            XJJ=JJ
ISN 0015          HEAT=R*SIN(.017214*(XJJ-91.25))+AVE
ISN 0016          IF(KK.EQ.1.AND.HEAT.GE.42.) GO TO 9
ISN 0018          GO TO 10
ISN 0019       9  D1=XJJ
ISN 0020          KK=2
ISN 0021      10  IF (KK.EQ.2.AND.HEAT.LT.42.) GO TO 12
ISN 0023         GO TO 11
ISN 0024      12  D2=XJJ
ISN 0025          KK=1
ISN 0026      11  CONTINUE
ISN 0027         DEGD(I,J)=COS(.017214*(D1-91.25))-COS(.017214*(D2-91.25))
ISN 0028          DEGD(I,J)=.31831*DEGD(I,J)*(D2-D1)*R-(D2-D1)*(42.-AVE)
ISN 0029          GO TO 4
ISN 0030     39   DEGD(I,J)=10000000.
ISN 0031       4  CONTINUE
ISN 0032       6  TYPE 7,(DEGD(I,J),J=60,90,5)
ISN 0033       7  FORMAT(/,7('  ',F8.0))
ISN 0034          STOP
ISN 0035          END
```

Appendix A-2

Program GFIX iteratively determines the value of G, the growth constant, for each tree species. G is calculated using the optimum growth function developed by Botkin et al. (1972a, 1972b) and the assumption that a tree will attain 2/3 of its maximum dbh at 1/2 its maximum age:

$$\delta D = G\ D\ \frac{\dfrac{D\ H}{1 - D_{max}\ H_{max}}}{274 + 3B2D - 4B3D^2}$$

and

$$D = 2/3\ D_{max} \text{ when } t = AGEMX/2 \quad .$$

Any interactive computer system can be used to run this program. The values for DMAX, HMAX, B2, B3, and AGEMX for the species and the initial guess for G are entered in. The value of DBH typed out can then be compared to 2/3 D_{max}, and a better guess for G can be entered for the next iteration. This is repeated until DBH becomes sufficiently close to 2/3 D_{max}.

```
ISN 0002          INTEGER AGEMAX
ISN 0003          TYPE 1
ISN 0004        1 FORMAT (2X,'TYPE IN DMAX,HMAX,B2,B3,AGEMAX,4F10.3,I5')
ISN 0005          ACCEPT 2,DMAX,HMAX,B2,B3,AGEMAX
ISN 0006        2 FORMAT (4F10.3,I5)
ISN 0007        3 TYPE 4
ISN 0008        4 FORMAT (2X,'TYPE IN G, F10.3')
ISN 0009          ACCEPT 5,G
ISN 0010        5 FORMAT (F10.3)
ISN 0011          D=.5
ISN 0012          J=IFIX(AGEMAX/2.)
ISN 0013          DO 10 I=1,J
ISN 0014          H=137.+B2*D-B3*D**2
ISN 0015          DELD=(G*D*(1.-(D-H)/(DMAX*HMAX)))/(274.+3.*B2*D-4.*B3*D**2)
ISN 0016          D=D+DELD
ISN 0017       10 CONTINUE
ISN 0018          TYPE 11,DMAX,HMAX,B2,B3,AGEMAX,G
ISN 0019       11 FORMAT (5X,'DMAX',5X,'HMAX',7X,'B2',9X,'B3',4X,
                 A'AGEMAX',4X,'G',/,4F10.3,I5,F10.3)
ISN 0020          TYPE 12,D
ISN 0021       12 FORMAT (6X,'DBH=',F10.4)
ISN 0022          GO TO 3
ISN 0023          STOP
ISN 0024          END
```

Appendix A-3

Listing of Program FORAR

```
                  C       STAND SIMULATOR MODIFIED FROM:
                  C
                  C           BOTKIN,D.B.,J.F.JANAK,J.R.WALLIS. 1970. A SIMULATOR FOR
                  C       NORTHEASTERN FOREST GROWTH: A CONTRIBUTION OF THE HUBBARD BROOK
                  C       ECOSYSTEM STUDY AND IBM RESEARCH. RC 3140. IBM THOMAS J. WATSON
                  C       RESEARCH CENTER, YORKTOWN HEIGHTS, NEW YORK. 21P.
ISN 0002                 DIMENSION DBH(700),NTREES(35)
ISN 0003                 DIMENSION DBHK(250),NTREEK(35)
ISN 0004                 COMMON /FDATA/ FARDAM(500),ALIMIT(35),BLIMIT(35),IMYR
ISN 0005                 LOGICAL SWITCH(5),S(35,5),LOGS
ISN 0006                 DIMENSION KTIME(35)
ISN 0007                 COMMON /LOGBLK/ SWITCH,KTIME,S
ISN 0008                 COMMON /RUNNR/ NYR,INYR,KPNT,KAGE,KTIMES,KLAST
ISN 0009                 COMMON /HDATA/ B2(35),B3(35),PHI,SOILQ,DEGD
ISN 0010                  CALL DATA
ISN 0011                 IPLOT=0
ISN 0012              11 CONTINUE
ISN 0013                 CALL PLOTIN(IPLOT,DBH,NTREES)
ISN 0014                 IMYR=0
ISN 0015                 INYR=0
ISN 0016                 CALL OUTPUT(DBH,NTREES)
ISN 0017                 DO 9 J=1,KTIMES
ISN 0018                 JJ=J
ISN 0019                 IF (JJ .GT. 1) PRINT 13,IX
ISN 0021              13 FORMAT (/,'   PLOT NUMBER   ',I4)
ISN 0022                 CALL INIT(DBH,NTREES,DBHK,NTREEK,JJ)
ISN 0023                 DO 1 I=1,NYR
ISN 0024                 IMYR=IMYR+1
ISN 0025                 INYR=I
ISN 0026                 CALL GAUSS(IX,700.0,8700.0,DEGD)
ISN 0027                  CALL KILL(DBH,NTREES,IX)
ISN 0028                  CALL BIRTH(IX,NTREES,DBH)
ISN 0029                 CALL GROW(DBH,NTREES)
                  C      IF (R.LT..048) CALL FIRE (DBH,NTREES)
ISN 0030                 IF (I.NE.35) GO TO 5
ISN 0032                 CALL LOGING (LOGS)
                  C      CALL CUT (DBH,NTREES,LOGS)
ISN 0033               5 IF(I-KPNT*(I/KPNT).EQ.0) CALL OUTPUT(DBH,NTREES)
ISN 0035               1 CONTINUE
ISN 0036               9 CONTINUE
ISN 0037                 IF(IPLOT .EQ. KLAST) GO TO 99
ISN 0039                 GO TO 11
ISN 0040              99 CONTINUE
ISN 0041                 STOP
ISN 0042                 END
```

```
ISN 0002                 SUBROUTINE LOAD(DBH,NTREES)
ISN 0003                 DIMENSION DBH(700),NTREES(25)
ISN 0004                 COMMON /IRUN/ INDEX
ISN 0005                 DO 1 I=1,INDEX
ISN 0006               1 NTREES(I)=0.
ISN 0007                  RETURN
ISN 0008                  END
```

```
ISN 0002                 SUBROUTINE LOGING (LOGS)
ISN 0003                 COMMON /IRUN/ INDEX
ISN 0004                 LOGICAL LOGS
ISN 0005                 COMMON /FDATA/ FARDAM(500),ALIMIT(35),BLIMIT(35),IMYR
ISN 0006                 DO 10 J=1,INDEX
ISN 0007                 ALIMIT(J)=25.4
ISN 0008                 BLIMIT(J)=200.
ISN 0009              10 CONTINUE
ISN 0010                 LOGS=.TRUE.
ISN 0011                 RETURN
ISN 0012                 END
```

```
ISN 0002          SUBROUTINE SPROUT(IX,NTREES,DBH)
ISN 0003          COMMON /SDATA/ KSPRT(35),STEND(35),SPTMIN(35),SPTMAX(35)
ISN 0004          COMMON /IRUN/ INDEX
ISN 0005          DIMENSION NTREES(35),ANEW(700),DBH(700),NAGE(700)
ISN 0006          DIMENSION NEW(35)
ISN 0007          COMMON /TRAGE/ IGES(700),IDGE(500)
            C     SMALLEST STUMP SPROUT IS .1 CM ON THE AVERAGE.
ISN 0008          SIZE=.1
ISN 0009          NU=1
ISN 0010          DO 230 LL=1,INDEX
ISN 0011          L=LL
ISN 0012          IF(NTREES(L).EQ.0) GO TO 230
ISN 0014          NNU=NU+NTREES(L)-1
ISN 0015      230 NU=NU+NTREES(L)
ISN 0016          KEND=NU-1
ISN 0017          NIX=0
ISN 0018          DO 205 LL=1,INDEX
ISN 0019          L=LL
ISN 0020          IF(STEND(L).LE.0.) GO TO 205
ISN 0022          IF(KSPRT(L).GE.0) GO TO 205
ISN 0024          NIX=NIX+1
ISN 0025          NEW(NIX)=L
ISN 0026      205 CONTINUE
ISN 0027          IF (NIX .EQ.0) GO TO 74
ISN 0029          DO 2 J=1,KEND
ISN 0030          NAGE(J)=IGES(J)
ISN 0031          ANEW(J)=DBH(J)
ISN 0032        2 CONTINUE
ISN 0033          CALL RANDOM(IX,R)
ISN 0034          NIX=NIX*R+1.0
ISN 0035          N=NEW(NIX)
ISN 0036          KSUM=0
ISN 0037          DO 51 I=1,N
ISN 0038       51 KSUM=KSUM+NTREES(I)
            C     STEND(I) IS THE TENDENCY FOR THE ITH SPECIES TO STUMP
            C OR ROOT SPROUT. THE VALUE OF STEND(I) IS THE AVERAGE
            C NUMBER OF SPROUTS (VIABLE) THAT MIGHT OCCUR WITH A GIVEN TREE DEATH.
ISN 0039          CALL RANDOM(IX,R)
ISN 0040          M=R*STEND(N)+1
ISN 0041           IF(M.EQ.0) GO TO 74
ISN 0043          DO 70 J=1,M
ISN 0044          KSUM=KSUM+1
ISN 0045          NTREES(N)=NTREES(N)+1
ISN 0046          NAGE(KSUM)=0
ISN 0047          CALL RANDOM(IX,R)
ISN 0048          ANEW(KSUM)=SIZE+0.1*(1.0-R)**3
ISN 0049          KEND=KEND+1
ISN 0050          K1=KSUM+1
ISN 0051          DO 60 II=K1,KEND
ISN 0052          I=II
ISN 0053          ANEW(I)=DBH(I-1)
ISN 0054          NAGE(I)=IGES(I-1)
ISN 0055       60 CONTINUE
ISN 0056          IF(KEND .LT.701) GO TO 61
ISN 0058          PRINT 98
ISN 0059          STOP
ISN 0060       61 CONTINUE
ISN 0061       98 FORMAT (' <<<<<<<<<<<<LOOK OUT THE NTREES VECTOR GOT TOO BIG>>>
                 *>>>',13I4/' <<<<<<<<<<<<TRY COMPATIBLE SPECIES AND CLIMATE>>>>>>')
ISN 0062          DO 65 I=1,KEND
ISN 0063          IGES(I)=NAGE(I)
ISN 0064       65 DBH(I)=ANEW(I)
ISN 0065       70 CONTINUE
ISN 0066          N=0
ISN 0067       74 CONTINUE
ISN 0068          DO 9998 I=1,INDEX
ISN 0069     9998 KSPRT(I)=1
ISN 0070          RETURN
ISN 0071          END
```

```
ISN 0002            SUBROUTINE CUT(DBH,NTREES,LOGS)
ISN 0003            DIMENSION DBH(700),NTREES(35),ANEW(100)
ISN 0004            COMMON /FDATA/ FARDAM(500),ALIMIT(35),BLIMIT(35),IMYR
ISN 0005            DIMENSION KAGES(100),NCUT(35),DBHCUT(100),KKAGE(100)
ISN 0006            COMMON /SDATA/ KSPRT(35),STEND(35),SPTMIN(35),SPTMAX(35)
ISN 0007            COMMON /TRAGE/ IGES(700),IDGE(500)
ISN 0008            COMMON /IRUN/ INDEX
ISN 0009            COMMON /TITLE/ AAA(35,6)
ISN 0010            LOGICAL CUTT,CUTSP,LOGS
ISN 0011            NTOT=0
ISN 0012            DO 1 I=1,INDEX
ISN 0013            NTOT=NTOT+NTREES(I)
ISN 0014          1 CONTINUE
ISN 0015            IF (NTOT.EQ.0) RETURN
ISN 0017            CUTT=.FALSE.
ISN 0018            NEW=0
ISN 0019            NFW=0
ISN 0020            KBEG=1
ISN 0021            KEND=0
ISN 0022            IF (.NOT.LOGS) GO TO 18
ISN 0024            PRINT 15
ISN 0025         15 FORMAT (12X,'DIAMETER LIMITS FOR LOGGING, BY SPECIES'/)
ISN 0026            PRINT 14,(J,ALIMIT(J),BLIMIT(J),J=1,INDEX)
ISN 0027         14 FORMAT (12X,I5,2(2X,F5.1))
ISN 0028         18 DO 2 I=1,INDEX
ISN 0029            IF (NTREES(I).EQ.0) GO TO 2
ISN 0031            CUTSP=.FALSE.
ISN 0032            KEND=KEND+NTREES(I)
ISN 0033            DO 5 JJ=KBEG,KEND
ISN 0034            J=JJ
ISN 0035            IF (DBH(J).LT.ALIMIT(I).OR.DBH(J).GT.BLIMIT(I)) GO TO 6
ISN 0037            NTREES(I)=NTREES(I)-1
ISN 0038            NCUT(I)=NCUT(I)+1
ISN 0039            NFW=NFW+1
ISN 0040            DBHCUT(NFW)=DBH(J)
ISN 0041            KKAGE(NFW)=IGES(J)
ISN 0042            IF (DBH(J).GT.SPTMIN(I).AND.DBH(J).LT.SPTMAX(I)) KSPRT(I)=-1
ISN 0044            CUTT=.TRUE.
ISN 0045            CUTSP=.TRUE.
ISN 0046            GO TO 5
ISN 0047          6 NEW=NEW+1
ISN 0048            ANEW(NEW)=DBH(J)
ISN 0049            KAGES(NEW)=IGES(J)
ISN 0050          5 CONTINUE
ISN 0051            IF (CUTSP.EQ.(.FALSE.)) GO TO 72
ISN 0053            II=I
ISN 0054            IF (.NOT.LOGS) GO TO 65
ISN 0056            PRINT 70,II,NFW,(AAA(I,L),L=1,6)
ISN 0057         70 FORMAT (10X,/,2X,'SPECIES',I2,2X,I3,2X,6A4/,X,'DBH LOGS CUT'/)
ISN 0058            GO TO 74
ISN 0059         65 PRINT 71,II,NFW,(AAA(I,L),L=1,6)
ISN 0060         71 FORMAT (/,12X,'SPECIES ',I2,2X,I3,2X,6A4/,X,'   DBH TREES BURNED'/)
ISN 0061         74 PRINT 29,(DBHCUT(K),K=1,NFW)
ISN 0062         29 FORMAT (20X,4F8.2)
ISN 0063            DO 80 K=1,NFW
ISN 0064            DBHCUT(K)=0.
ISN 0065         80 CONTINUE
ISN 0066            NFW=0
ISN 0067         72 KBEG=KEND+1
ISN 0068          2 CONTINUE
ISN 0069            IF (CUTT.EQ.(.FALSE.)) GO TO 13
ISN 0071            IF (NEW.EQ.0) GO TO 10
ISN 0073            GO TO 8
ISN 0074         13 PRINT 20
ISN 0075         20 FORMAT (5X,'NO TREES CUT'/)
ISN 0076          8 DO 7 I=1,NEW
ISN 0077            DBH(I)=ANEW(I)
ISN 0078            IGES(I)=KAGES(I)
ISN 0079          7 CONTINUE
ISN 0080            RETURN
ISN 0081         10 CONTINUE
ISN 0082            PRINT 11
ISN 0083         11 FORMAT (10X,/10X,'ALL TREES WERE CUT'/)
ISN 0084            DO 12 J=1,700
ISN 0085            DBH(J)=0.0
ISN 0086            IGES(J)=0
ISN 0087         12 CONTINUE
ISN 0088            RETURN
ISN 0089            END
```

```
ISN 0002          SUBROUTINE OUTPUT(DBH,NTREES)
ISN 0003          COMMON /TITLE/ AAA(35,6)
ISN 0004          DIMENSION DBH(700),BDH(500),NTREES(35),IDM(500),BAR(35)
ISN 0005          COMMON /KILD/ NOGRO(100),DDBH(500),KDEAD(35),AREA,KD
ISN 0006          COMMON /TRAGE/ IGES(700),IDGE(500)
ISN 0007          COMMON /RUNNR/ NYR,INYR,KPNT,KAGE,KTIMES,KLAST
ISN 0008          COMMON /HDATA/ B2(35),B3(35),PHI,SOILQ,DEGD
ISN 0009          COMMON /IRUN/ INDEX
ISN 0010           PRINT 11
ISN 0011       11 FORMAT(//' YEAR SPEC.   NUM.            NAME                        BIOMA
               ZSS')
ISN 0012          PRINT 21,INYR
ISN 0013       21 FORMAT(I5)
ISN 0014       96 NDEAD=0
ISN 0015          NTOT=0
ISN 0016          DO 1 I=1,INDEX
ISN 0017          NDEAD=NDEAD+KDEAD(I)
ISN 0018        1 NTOT=NTOT + NTREES(I)
ISN 0019          IF(NTOT.EQ.0) GO TO 100
ISN 0021          N=1
ISN 0022          AREA=0.0
ISN 0023          TBAR=0.0
ISN 0024          DO 20 II=1,INDEX
ISN 0025          I=II
ISN 0026          BAR(I)=0.0
ISN 0027          IF(NTREES(I).EQ.0) GO TO 20
ISN 0029          NN=N+NTREES(I) - 1
ISN 0030          N1=NTREES(I)
ISN 0031          DO 50 JJ=N,NN
ISN 0032          J=JJ
ISN 0033       50 AREA=AREA+1.9283295E-4*DBH(J)**2.129
ISN 0034          DO 97 J=1,N1
ISN 0035          N2=J+N-1
ISN 0036          BDH(J)=DBH(N2)
ISN 0037          BAR(I)=BAR(I)+.1193*DBH(N2)**2.393
ISN 0038       97 CONTINUE
ISN 0039          TBAR=TBAR+BAR(I)
ISN 0040          N2=MIN0(12,N1)
ISN 0041          PRINT 2, I,NTREES(I),(AAA(I,K),K=1,6),BAR(I),(BDH(J),J=1,N2)
ISN 0042          IF(N1.GT.12) PRINT 5,(BDH(J),J=13,N1)
ISN 0044        5 FORMAT(20X, 4F8.3,/,20X,4F8.3,/,20X,4F8.3)
ISN 0045          N=N+NTREES(I)
ISN 0046       20 CONTINUE
ISN 0047           TBAR=TBAR*.012
ISN 0048          PRINT 7, NTOT,TBAR,AREA
ISN 0049        7 FORMAT(10X/10X,I7,E12.3,' METRIC TON/HA. LEAF AREA =',F 9.3)
ISN 0050        2 FORMAT(/,5X,I5,'    ',I3,'    ',6A4,'  ',E9.3,'   ',
                Z(/,/,15X,'DBH  ',4F8.3,/,20X,4F8.3,/,20X,4F8.3))
ISN 0051          GO TO 200
ISN 0052      100 PRINT 3,INYR
ISN 0053        3 FORMAT(10X,'YEAR',I5,' NO TREES LIVING')
ISN 0054          THEEND=1810.
ISN 0055          IF (DEGD .GT. THEEND) GO TO 296
ISN 0057      298 PRINT 297
ISN 0058      297 FORMAT(10X,'NONE OF THE SPECIES YOU ARE USING CAN EXIST WITH TH
                 *IS CLIMATE')
ISN 0059          STOP
ISN 0060      296 THEEND=13395.
ISN 0061          IF (DEGD.GT.THEEND) GO TO 298
ISN 0063      200 KD=1
ISN 0064          IF(NDEAD .EQ.0) RETURN
ISN 0066          PRINT 201
ISN 0067      201 FORMAT(' DEAD TREES SINCE LAST PRINTOUT')
ISN 0068          N=1
ISN 0069          DO 99 II=1,INDEX
ISN 0070          I=II
ISN 0071          IF(KDEAD(I).EQ.0) GO TO 99
ISN 0073          NN=N+KDEAD(I) - 1
ISN 0074          N1=KDEAD(I)
ISN 0075          DO 98 J=1,N1
ISN 0076          N2=J+N-1
ISN 0077          BDH(J)=DDBH(N2)
ISN 0078          IDM(J)=IDGE(N2)
ISN 0079       98 CONTINUE
ISN 0080          N2=MIN0(7,N1)
ISN 0081          PRINT 4, I,KDEAD(I),(BDH(J),IDM(J),J=1,N2)
ISN 0082          IF(N1.GT.7)  PRINT 6,(BDH(J),IDM(J),J=8,N1)
ISN 0084        6 FORMAT(27X,F9.3,I4,F9.3,I4,F9.3,I4,F9.3,I4,F9.3,I4,F9.3,I4,F9.3
                 *,I4)
ISN 0085        4 FORMAT(5X,I5,I7,10X,7(F9.3,I4))
ISN 0086          N=N+KDEAD(I)
ISN 0087       99 CONTINUE
ISN 0088          DO 299 I=1,INDEX
ISN 0089          KDEAD(I)=0
ISN 0090      299 CONTINUE
ISN 0091          RETURN
ISN 0092          END
```

```
      SUBROUTINE GROW(DBH,NTREES)
      DIMENSION DBH(700),NTREES(35),PROF(1000)
      COMMON /IRUN/ INDEX
      COMMON /TDATA/ G(35),C(35),ITYPE(35),AGEMX(35),SOIM(35)
      COMMON /KILD/ NOGRO(100),DDBH(500),KDEAD(35),AREA,KD
      COMMON /HDATA/ B2(35),B3(35),PHI,SOILQ,DEGD
      COMMON /CLIMAT/ DMIN(35),DMAX(35)
      NTOT=0
C     REQUIRES EACH TREE TO ADD A 1.0 MM GROWTH RING EACH YEAR
      AINC=0.1
      DO 1 I=1,INDEX
    1 NTOT=NTOT+NTREES(I)
      IF(NTOT.EQ.0) RETURN
      DO 2 I=1,100
    2 NOGRO(I)=0
      DO 9998 MN=1,1000
 9998 PROF(MN)=0.0
      N2=1
      BAR=0.
      DO 8 LL=1,INDEX
      L=LL
      IF(NTREES(L).EQ.0) GO TO 8
      N3=N2+NTREES(L)-1
      DO 7 KM=N2,N3
      K=KM
      BAR=BAR+.785*(DBH(K)**2)
C
C       THE HEIGHT PROFILE IS CALCULATED IN .1 METER UNITS
C
      IHT=IFIX((B2(L)*DBH(K)-B3(L)*DBH(K)**2)/10.+1.)
C
C     DATA FROM SOLLINS ET AL  PAGE 41.  SCALED TO 1/24 HA.
C
      PROF(IHT)=PROF(IHT)+1.9283295E-4*DBH(K)**2.129
    7 CONTINUE
    8 N2=N2+NTREES(L)
      BAR=BAR/10000.
       DO 9997 MN=1,999
      MN1=1000-MN
      PROF(MN1)=PROF(MN1)+PROF(MN1+1)
 9997 CONTINUE
      N=1
      M=1
      DO 10 I=1,INDEX
      IF(NTREES(I).EQ.0) GO TO 10
      NN=N+NTREES(I)-1
      DO 9 KK=N,NN
      J=KK
      HT=B2(I)*DBH(J)-B3(I)*DBH(J)**2
C       SAME SCALE FACTOR AS ABOVE
      IHT=IFIX(HT/10.+2.)
      SLA=PROF(IHT)
      AL=PHI*EXP(-SLA*.25)
      CC=(137.+0.25*B2(I)**2/B3(I))*(0.5*B2(I)/B3(I))
      DINC=G(I)*DBH(J)*(1.0-(137.0*DBH(J)+B2(I)*DBH(J)**2-B3(I)*DBH(J
     *)**3)/CC)/(274.+3.0*B2(I)*DBH(J)
     * -4.0*B3(I)*DBH(J)**2)*(1.0-BAR/SOILQ)*SOIM(I)*4.0*(DEGD-DMIN(I))*
     *(DMAX(I)-DEGD)/(DMAX(I)-DMIN(I))**2
       IF (ITYPE(I).EQ.3) DINC=2.24*(1.0-EXP(-1.136*(AL-0.08)))*DINC
C       IF(ITYPE(I).EQ.2) DINC=.5*DINC*(2.24*(1.0-EXP(-1.136*(AL-.08)))+
C     *(1.0-EXP(-4.64*(AL-.05))))
      IF(ITYPE(I).EQ.1) DINC=(1.0-EXP(-4.64*(AL-.05)))*DINC
      IF(DINC.LT.AINC) DINC=0.0
      IF(DINC.GT.5.0) PRINT 6,J,I,DBH(J),DINC
    6 FORMAT(' DINC IS .GT. 5.0 FOR TREE',I5,' SPECIES',I3,' DBH',F6.
     *1,' DINC',F8.3)
      IF(DINC.NE.0.0) GO TO 91
      NOGRO(M)=J
      M=M+1
   91 DBH(J)=DBH(J)+DINC
    9 CONTINUE
   10 N=N+NTREES(I)
      RETURN
      END
```

```
ISN 0002          SUBROUTINE BIRTH(IX,NTREES,DBH)
ISN 0003          LOGICAL SWITCH(5),S(35,5)
ISN 0004          DIMENSION KTIME(35)
ISN 0005          COMMON /FDATA/ FARDAM(500),ALIMIT(35),BLIMIT(35),IMYR
ISN 0006          COMMON /RUNNR/ NYR,INYR,KPNT,KAGE,KTIMES,KLAST
ISN 0007          COMMON /LOGBLK/ SWITCH,KTIME,S
ISN 0008          COMMON /IRUN/ INDEX
ISN 0009          DIMENSION NTREES(35),ANEW(700),DBH(700),NAGE(700)
ISN 0010          DIMENSION NEW(35)
ISN 0011          COMMON /TRAGE/ IGES(700),IDGE(500)
ISN 0012          COMMON /HDATA/ B2(35),B3(35),PHI,SOILQ,DEGD
             C   SMALLEST TREE IS 1.27 CM OR .5 INCHES
ISN 0013          SIZE=1.27
ISN 0014          CALL RANDOM(IX,R)
ISN 0015          CALL RANDOM(IX,RAT)
ISN 0016           MMMM=3.*R+1.
ISN 0017          DO 777 MMMMM=1,MMMM
ISN 0018      210 WEIGHT=0.0
ISN 0019          NU=1
ISN 0020          DO 230 LL=1,INDEX
ISN 0021          L=LL
ISN 0022          IF(NTREES(L).EQ.0) GO TO 230
ISN 0024          NNU=NU+NTREES(L)-1
ISN 0025          DO 220 MM=NU,NNU
ISN 0026          M=MM
ISN 0027           BIOM=1.9283295E-4*DBH(M)**2.129
ISN 0028      220 WEIGHT=WEIGHT+BIOM
             C       EQUATIONS FOR LEAF MASS FROM SOLLIN'S
ISN 0029      230 NU=NU+NTREES(L)
ISN 0030          KEND=NU-1
ISN 0031          NIX=0
ISN 0032          DO 44 JKL=1,5
ISN 0033       44 SWITCH(JKL)=.TRUE.
             C    SWITCH 1 SETS LOWER LIMIT FOR PLANTS NEEDING LITTER
ISN 0034          IF(WEIGHT.GE..1) SWITCH(1)=.FALSE.
             C    SWITCH 2 SETS UPPER LIMIT FOR TREES NEEDING MINERAL SOIL
ISN 0036          IF(WEIGHT.LE..2.AND.IMYR.LE.100) SWITCH(2)=.FALSE.
             C    SWITCH 3 ELIMINATES DROUGHT SENSITIVE SPECIES
ISN 0038          IF(DEGD.LE.8700.0) SWITCH(3)=.FALSE.
ISN 0040          CALL RANDOM(IX,R)
             C     SWITCH 5 REDUCES SEEDING RATE OF DESIRABLE MAST
ISN 0041          IF(R.GE..5) SWITCH(5)=.FALSE.
ISN 0043          CALL RANDOM(IX,R)
             C    SWITCH 4 ELIMINATES DEER EATEN SPECIES
ISN 0044          IF(RAT.GT..5) SWITCH(4)=.FALSE.
ISN 0046          DO 205 LL=1,INDEX
ISN 0047          L=LL
ISN 0048          DO 444 JKL=1,5
ISN 0049      444 IF(S(LL,JKL).AND.SWITCH(JKL)) GO TO 205
             C    THIS SECTION RESTRICTS THE PLANTING OF CERTAIN TREE SPECIES
             C     THAT TYPICALLY ARE ASSOCIATED WITH OLD FIELD SUCCESSION.
             C     KTIME(I) IS THE LAST YEAR SINCE A CLEARING THAT THE ITH
             C     SPECIES CAN BE EXPECTED TO SEED IN.  SINCE THE LIMITING FACTOR
             C     IS POSTULATED TO BE A SEED SOURCE PROBLEM, WE ALLOW SEEDING IN
             C     IF THERE IS A PARENT TREE ON THE PLOT.
ISN 0051          IF ((IMYR.GT.KTIME(LL)).AND.(NTREES(LL).LE.0)) GO TO 205
ISN 0053          NIX=NIX+1
ISN 0054          NEW(NIX)=L
ISN 0055      205 CONTINUE
ISN 0056          IF (NIX .EQ.0) GO TO 74
ISN 0058          DO 2 J=1,KEND
ISN 0059          NAGE(J)=IGES(J)
ISN 0060          ANEW(J)=DBH(J)
ISN 0061        2 CONTINUE
ISN 0062          CALL RANDOM(IX,R)
             C   VALUE OF 5.0 ASSUMES AN AVERAGE OF 1284 SEEDLINGS/HA.
ISN 0063          M=8.0*R
ISN 0064          CALL RANDOM(IX,R)
ISN 0065          NIX=NIX*R+1.0
ISN 0066          N=NEW(NIX)
ISN 0067          KSUM=0
ISN 0068          DO 51 I=1,N
ISN 0069       51 KSUM=KSUM+NTREES(I)
ISN 0070          DO 70 J=1,M
ISN 0071          KSUM=KSUM+1
ISN 0072          NTREES(N)=NTREES(N)+1
ISN 0073          NAGE(KSUM)=0
ISN 0074          CALL RANDOM(IX,R)
ISN 0075          ANEW(KSUM)=SIZE+0.3*(1.0-R)**3
ISN 0076          KEND=KEND+1
ISN 0077          K1=KSUM+1
ISN 0078          DO 60 II=K1,KEND
ISN 0079          I=II
ISN 0080          ANEW(I)=DBH(I-1)
ISN 0081          NAGE(I)=IGES(I-1)
ISN 0082       60 CONTINUE
ISN 0083          IF(KEND .LT.701) GO TO 61
ISN 0085          PRINT 98
ISN 0086          STOP
ISN 0087       61 CONTINUE
ISN 0088       98 FORMAT (' <<<<<<<<<<<<LOOK OUT THE NTREES VECTOR GOT TOO BIG>>>
                 *>>>',13I4/' <<<<<<<<<<<<TRY COMPATIBLE SPECIES AND CLIMATE>>>>>>')
```

```
ISN 0089          DO 65 I=1,KEND
ISN 0090          IGES(I)=NAGE(I)
ISN 0091       65 DBH(I)=ANEW(I)
ISN 0092       70 CONTINUE
ISN 0093          N=0
ISN 0094       74 CONTINUE
ISN 0095           CALL SPROUT(IX,NTREES,DBH)
ISN 0096          IF(WEIGHT.LT.0.2) GO TO 210
ISN 0098          DO 100 I=1,KEND
ISN 0099          IGES(I)=IGES(I)+1
ISN 0100      100 CONTINUE
ISN 0101      777 CONTINUE
ISN 0102          RETURN
ISN 0103          END
```

```
ISN 0002          SUBROUTINE DATA
ISN 0003          COMMON /TITLE/ AAA(35,6)
ISN 0004          LOGICAL SWITCH(5),S(35,5)
ISN 0005          DIMENSION KTIME(35)
ISN 0006          COMMON /LOGBLK/ SWITCH,KTIME,S
ISN 0007          COMMON /SDATA/ KSPRT(35),STEND(35),SPTMIN(35),SPTMAX(35)
ISN 0008          COMMON /IRUN/ INDEX
ISN 0009          COMMON /TDATA/ G(35),C(35),ITYPE(35),AGEMX(35),SOIM(35)
ISN 0010          COMMON /RUNNR/ NYR,INYR,KPNT,KAGE,KTIMES,KLAST
ISN 0011          COMMON /HDATA/ B2(35),B3(35),PHI,SOILQ,DEGD
ISN 0012          COMMON /CLIMAT/ DMIN(35),DMAX(35)
ISN 0013          INDEX=33
ISN 0014          IX=76123
ISN 0015          KTIMES=1
ISN 0016          KLAST=3
ISN 0017          NYR=500
ISN 0018          KPNT=50
ISN 0019          KAGE=-1
ISN 0020          PHI=1.0
ISN 0021          SOILQ=3.83
ISN 0022          DEGD=8700.
            C       VALUE FOR SOILQ FROM MAX VALUE CITED BY DICK WILLIAMS, GP FORESTER
ISN 0023          DO 23 J=1,INDEX
ISN 0024       23 READ(5,24)(AAA(J,II),II=1,6),DMAX(J),DMIN(J),B3(J),B2(J),ITYPE(J),
                 AAGEMX(J),C(J),G(J),STEND(J),SPTMIN(J),SPTMAX(J),
                 B(S(J,JI),JI=1,5),KTIME(J),SOIM(J)
ISN 0025       24 FORMAT(6A4,F6.0,F5.0,F4.3,F5.2,I1,F4.0,F2.0,F5.1,F2.0,F4.1,F4.0,
                 A5L1,I4,F3.1)
ISN 0026       30 RETURN
ISN 0027          END
```

```
      SUBROUTINE RANDOM(IX,R)
      R=FLTRN(IX)
      RETURN
      END
```

```
      SUBROUTINE GAUSS(IX,S,AM,DEGD)
      Z=0.0
      DO 5 I=1,12
    5 Z=Z+FLTRN(DUM)
      Z=Z-6.
      DEGD=AM+S*Z
      RETURN
      END
```

```
      SUBROUTINE INIT(DBH,NTREES,DBHK,NTREEK,JJ)
      COMMON /IRUN/ INDEX
      DIMENSION DBH(1),NTREES(1),DBHK(1),NTREEK(1)
      COMMON /SDATA/ KSPRT(35),STEND(35),SPTMIN(35),SPTMAX(35)
      COMMON /KILD/ NOGRO(100),DDBH(500),KDEAD(35),AREA,KD
      COMMON /TRAGE/ IGES(700),IDGE(500)
      DO 10 J=1,500
      DDBH(J)=0.0
      IDGE(J)=0
   10 CONTINUE
      DO 11 J=1,100
   11 NOGRO(J)=0
      DO 13 J=1,INDEX
   13 KSPRT(J)=1
      IF (JJ .GT.1) GO TO 1
      DO 2 J=1,INDEX
    2 NTREEK(J)=NTREES(J)
      DO 3 K=1,100
    3 DBHK(K)=DBH(K)
      RETURN
    1 CONTINUE
      DO 4 J=1,INDEX
    4 NTREES(J)=NTREEK(J)
      DO 5 K=1,100
    5 DBH(K)=DBHK(K)
      RETURN
      END
```

```
      SUBROUTINE PLOTIN(IPLOT,DBH,NTREES)
      COMMON /TRAGE/ IGES(700),IDGE(500)
      COMMON /KILD/ NOGRO(100),DDBH(500),KDEAD(35),AREA,KD
      DIMENSION DBH(700),NTREES(35)
      DO 1 J=1,35
      KDEAD(J)=0
      DBH(J)=0.0
      IGES(J)=0
    1 NTREES(J)=0
      DO 2 J=36,700
      IGES(J)=0
    2 DBH(J)=0.0
      IPLOT=IPLOT+1
      PRINT 13,IPLOT
   13 FORMAT (/,'   PLOT NUMBER   ',I4)
      RETURN
      END
```

```
ISN 0002          SUBROUTINE KILL(DBH,NTREES,IX)
ISN 0003          DIMENSION DBH(700),NTREES(35)
ISN 0004          COMMON /FDATA/ FARDAM(500),ALIMIT(35),BLIMIT(35),IMYR
ISN 0005          COMMON /IRUN/ INDEX
ISN 0006          COMMON /SDATA/ KSPRT(35),STEND(35),SPTMIN(35),SPTMAX(35)
ISN 0007          COMMON /TDATA/ G(35),C(35),ITYPE(35),AGEMX(35),SOIM(35)
ISN 0008          COMMON /KILD/ NOGRO(100),DDBH(500),KDEAD(35),AREA,KD
ISN 0009          COMMON /TRAGE/ IGES(700),IDGE(500)
ISN 0010          COMMON /RUNNR/ NYR,INYR,KPNT,KAGE,KTIMES,KLAST
ISN 0011          ID = 1
ISN 0012          IDF=0
ISN 0013          N = 0
ISN 0014          NB=0
ISN 0015          DO 100 J=1,INDEX
ISN 0016          NB=NB+KDEAD(J)
ISN 0017          IF(NTREES(J).EQ.0) GO TO 100
ISN 0019          NA = N + 1
ISN 0020          NN = NTREES(J) + N
ISN 0021          DO 80 II=NA,NN
ISN 0022          I=II
ISN 0023          CALL RANDOM(IX,R1)
ISN 0024          IF (FARDAM(IDF).EQ.I) GO TO 42
ISN 0026          IF(R1.LE.(4.605/AGEM*X(J))) GO TO 50
ISN 0028          GO TO 44
ISN 0029       42 IDF=IDF+1
ISN 0030          IF (R1.LE..275) GO TO 50
ISN 0032       44 IF(NOGRO(ID).EQ.I) GO TO 40
ISN 0034          GO TO 80
ISN 0035       40 ID=ID + 1
ISN 0036          CALL RANDOM(IX,R2)
ISN 0037          IF(R2.GT.0.368) GO TO 80
ISN 0039       50 IF(KAGE.LT.0) GO TO 70
ISN 0041          KDEAD(J)=KDEAD(J)+1
ISN 0042          NB=NB+1
ISN 0043          NUP=KD-NB
ISN 0044          IF(NUP.EQ.0) GO TO 56
ISN 0046          DO 55 KK=1,NUP
ISN 0047          K=KK
ISN 0048          IJ=KD-K+1
ISN 0049          IF(IJ .GT.500) GO TO 99
ISN 0051          DDBH(IJ)=DDBH(IJ-1)
ISN 0052          IDGE(IJ)=IDGE(IJ-1)
ISN 0053       55 CONTINUE
ISN 0054       56 DDBH(NB)=DBH(I)
ISN 0055          IDGE(NB)=IGES(I)
ISN 0056          KD=KD+1
ISN 0057          GO TO 70
ISN 0058       99 PRINT 98
ISN 0059       98 FORMAT(' DEAD TREES VECTOR FILLED, RERUN WITH SMALLER PERIOD BE
                 *TWEEN PRINTOUTS (KPNT)')
ISN 0060          KAGE=-1
ISN 0061       70 NTREES(J)=NTREES(J)-1
            C      THIS IS THE SWITCH TO STUMP SPROUT TREES.
ISN 0062           IF(DBH(I).GT.SPTMIN(J).AND.DBH(I).LT.SPTMAX(J)) KSPRT(J)=-1
ISN 0064          DBH(I)= -1.0
ISN 0065       80 CONTINUE
ISN 0066          N = NN
ISN 0067      100 CONTINUE
ISN 0068          DO 200 II=1,700
ISN 0069          I=II
ISN 0070          IF(DBH(I).EQ.0.0) RETURN
ISN 0072          IF(DBH(I) .GT. 0.0) GO TO 200
ISN 0074      110 DO 120 KK = I,699
ISN 0075          K=KK
ISN 0076          DBH(K) = DBH(K+1)
ISN 0077          IGES(K)=IGES(K+1)
ISN 0078      120 CONTINUE
ISN 0079          DBH(700) = 0.0
ISN 0080          IF(DBH(I).LT.0.0) GO TO 110
ISN 0082      200 CONTINUE
ISN 0083          RETURN
ISN 0084          END
```

```
          SUBROUTINE FIRE (DBH,NTREES)
          DIMENSION DBH(700),NTREES(35)
          COMMON /FDATA/ FARDAM(500),ALIMIT(35),BLIMIT(35),IMYR
          COMMON /SDATA/ KSPRT(35),STEND(35),SPTMIN(35),SPTMAX(35)
          COMMON /IRUN/ INDEX
          LOGICAL LOGS
C         R=0.
          LOGS=.FALSE.
          IF (R.GE..828) GO TO 20
          PRINT 12
       12 FORMAT (5X,  'LIGHT FIRE'/)
          DO 15 J=1,INDEX
          ALIMIT(J)=0.
          BLIMIT(J)=12.7
       15 CONTINUE
          CALL CUT (DBH,NTREES,LOGS)
          RETURN
       20 IF (R.GE..966) GO TO 30
          PRINT 21
       21 FORMAT (5X,'  MEDIUM FIRE'/)
          DO 25 J=1,INDEX
          ALIMIT(J)=0.
          GO TO (22,22,23,23,22,22,23,22,23,22,22,24,22,23,22,24,22,23,22,23
         A,22,24,24,22,23,23,23,23,24,24,23,23,23),J
       22 BLIMIT(J)=500.
          GO TO 25
       23 BLIMIT(J)=25.4
          GO TO 25
       24 BLIMIT(J)=17.8
       25 CONTINUE
          CALL CUT (DBH,NTREES,LOGS)
          N=0
          IJ=0
          DO 42 J=1,INDEX
          NA=N+1
          NN=N+NTREES(J)
          GO TO (35,35,40,40,35,35,40,35,40,35,35,35,35,40,35,35,35,40,35,40
         A,35,35,35,35,40,40,40,40,35,35,40,40,40),J
       40 DO 35 JJ=NA,NN
          IJ=IJ+1
          FARDAM(IJ)=JJ
       35 CONTINUE
          N=NN
       42 CONTINUE
          IMYR=0
          RETURN
       30 DO 36 J=1,INDEX
          IF (NTREES(J).EQ.0) GO TO 36
          KSPRT(J)=-1
          NTREES(J)=0
       36 CONTINUE
          DO 37 J=1,700
          DBH(J)=0.
       37 CONTINUE
          PRINT 38
       38 FORMAT (5X,'SEVERE FIRE--ALL TREES WERE BURNED'/)
          RETURN
          END
```

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Appendix A-4

Sample Output of Program FORAR

SAMPLE OUTPUT OF PROGRAM FORAR

```
 PLOT NUMBER      1

YEAR SPEC.   NUM.            NAME                    BIOMASS
  0
        YEAR     0 NO TREES LIVING

YEAR SPEC.   NUM.            NAME                    BIOMASS
  50

         5      3     CARYA LACINIOSA             0.674E 00

               DBH      1.270     1.364     1.271

         6      3     CARYA OVATA                 0.251E 02

               DBH      9.260     1.472     1.289

        11      2     CORNUS FLORIDA              0.506E 02

               DBH      9.385     9.378

        12      5     DIOSPYROS VIRGINIANA        0.182E 03

               DBH     10.426    10.307    11.507    11.528
                       10.728

        13      6     FAGUS GRANDIFOLIA           0.144E 01

               DBH      1.383     1.270     1.276     1.288
                        1.362     1.451

        14      7     FRAXINUS AMERICANA          0.497E 03

               DBH     14.376    14.365    16.780    14.526
                       16.222    15.875     0.138

        15      3     ILEX OPACA                  0.303E-02

               DBH      0.118     0.172     0.106

        18     11     LIQUIDAMBAR STYRACIFLUA     0.450E 03

               DBH     12.194    13.847    12.539    13.211
                       12.277    12.960    13.946    13.533
                        1.388     1.270     1.427

        19      1     MORUS RUBRA                 0.963E 01

               DBH      6.265

        23     13     PINUS TAEDA                 0.692E 04

               DBH     30.651    31.511    39.092    29.708
                       35.729    38.035    37.236    34.367
                       31.520    33.687    29.159    29.154
                       32.883

        24      8     PRUNUS SEROTINA             0.752E 03

               DBH     17.908    17.181    17.240    16.655
                       16.766    17.733    16.634     0.168

        25      3     QUERCUS ALBA                0.708E 00

               DBH      1.438     1.270     1.270

        26     17     QUERCUS FALCATA             0.531E 03

               DBH     11.952    11.824    12.001    12.693
                       12.748    12.252    11.821    12.005
                       12.555    12.221    11.820     4.430
                        5.289     1.451     1.277     1.321
                        1.273

        27      1     QUERCUS MARILANDICA         0.226E 01

               DBH      3.418

        28      7     QUERCUS SHUMARDII           0.170E 03

               DBH     10.143    11.432    10.429    10.143
                       10.708     1.371     1.458

        31      8     SASSAFRAS ALBIDUM           0.224E 02

               DBH      8.677     1.503     1.301     0.113
                        0.192     1.437     1.389     1.399
```

```
32      19    ULMUS ALATA                  0.628E 03

        DBH    14.744  13.260  12.779  13.492
               12.770  12.772  15.100  14.663
               14.269  12.770   0.100   1.289
                1.287   1.409   0.126   1.270
                1.528   1.298   1.270

33       8    ULMUS AMERICANA              0.560E 02

        DBH     6.175   6.507   6.619   6.079
                5.771   5.768   0.102   1.570

       125   0.124E 03 METRIC TON/HA. LEAF AREA =    7.171

YEAR SPEC.   NUM.          NAME                   BIOMASS
 100

    10   3    CELTIS LAEVIGATA             0.773E 00

        DBH     1.271   1.368   1.487

    18   2    LIQUIDAMBAR STYRACIFLUA      0.460E 00

        DBH     1.271   1.359

    21   8    OSTRYA VIRGINIANA            0.101E 01

        DBH     1.316   1.272   1.287   1.392
                1.519   1.281   1.299   1.305

    23   6    PINUS TAEDA                  0.117E 05

        DBH    63.029  70.297  57.756  46.638
               53.833  50.296

    26   5    QUERCUS FALCATA              0.575E 03

        DBH    18.933  19.034  20.430  19.059
                1.304

    27   2    QUERCUS MARILANDICA          0.553E 00

        DBH     1.517   1.316

    32   1    ULMUS ALATA                  0.211E 00

        DBH     1.270

        27   0.148E 03 METRIC TON/HA. LEAF AREA =    6.904

YEAR SPEC.   NUM.          NAME                   BIOMASS
 150

     2   1    CARPINUS CAROLINIANA         0.323E 00

        DBH     1.516

     5   1    CARYA LACINIOSA              0.231E 00

        DBH     1.317

    18   1    LIQUIDAMBAR STYRACIFLUA      0.214E 00

        DBH     1.276

    21   3    OSTRYA VIRGINIANA            0.768E 00

        DBH     1.399   1.288   1.435

    23   3    PINUS TAEDA                  0.130E 05

        DBH   102.195  58.679  71.723

    25   6    QUERCUS ALBA                 0.162E 01

        DBH     1.275   1.409   1.308   1.436
                1.492   1.270

    26  11    QUERCUS FALCATA              0.391E 03

        DBH    29.130   3.746   4.503   3.188
                0.116   0.110   1.516   1.323
                1.291   1.281   1.316

    32   5    ULMUS ALATA                  0.142E 01

        DBH     1.284   1.550   1.479   1.541
                1.304

    33   2    ULMUS AMERICANA              0.472E 00

        DBH     1.367   1.292

        33   0.161E 03 METRIC TON/HA. LEAF AREA =    6.774
```

YEAR	SPEC.	NUM.	NAME	BIOMASS
200				
	2	2	CARPINUS CAROLINIANA	0.534E 00
		DBH	1.502 1.286	
	7	2	CARYA TEXANA	0.442E 00
		DBH	1.316 1.270	
	10	7	CELTIS LAEVIGATA	0.168E 01
		DBH	1.270 1.327 1.288 1.465 1.289 1.439 1.270	
	21	1	OSTRYA VIRGINIANA	0.264E 00
		DBH	1.394	
	23	2	PINUS TAEDA	0.157E 05
		DBH	125.903 69.541	
	26	10	QUERCUS FALCATA	0.739E 03
		DBH	38.387 1.508 1.273 1.270 1.270 1.302 1.286 1.272 1.516 1.289	
	27	11	QUERCUS MARILANDICA	0.274E 01
		DBH	1.325 1.270 1.393 1.276 1.542 1.270 1.540 1.285 1.271 1.350 1.389	
	29	7	QUERCUS STELLATA	0.174E 01
		DBH	1.281 1.454 1.271 1.303 1.488 1.314 1.391	
	32	4	ULMUS ALATA	0.902E 00
		DBH	1.331 1.270 1.303 1.313	
		46	0.197E 03 METRIC TON/HA. LEAF AREA = 7.786	

YEAR	SPEC.	NUM.	NAME	BIOMASS
250				
	6	5	CARYA OVATA	0.832E 01
		DBH	3.490 3.159 3.150 3.142 1.600	
	8	7	CARYA TOMENTOSA	0.260E 01
		DBH	1.503 1.562 1.574 1.658 1.598 1.808 1.525	
	10	8	CELTIS LAEVIGATA	0.476E 01
		DBH	2.083 1.856 1.865 1.856 2.026 1.897 2.172 1.865	
	11	4	CORNUS FLORIDA	0.805E 01
		DBH	3.344 3.124 3.418 3.124	
	15	13	ILEX OPACA	0.148E 02
		DBH	3.421 3.399 3.563 3.420 2.586 2.617 2.482 2.454 1.274 1.271 1.283 1.270 1.319	
	18	7	LIQUIDAMBAR STYRACIFLUA	0.355E 01
		DBH	1.822 1.843 1.812 1.810 1.886 1.841 1.805	
	21	6	OSTRYA VIRGINIANA	0.532E 01
		DBH	2.615 2.700 2.030 2.090 2.034 2.273	
	26	2	QUERCUS FALCATA	0.147E 04
		DBH	51.207 4.339	

YEAR	SPEC.	NUM.	NAME				BIOMASS
	27	15	QUERCUS MARILANDICA				0.985E 01
		DBH	2.676	2.363	2.429	2.417	
			2.001	2.299	2.035	2.340	
			1.582	1.534	1.641	1.753	
			1.656	1.534	1.549		
	29	1	QUERCUS STELLATA				0.377E 01
		DBH	4.234				
	32	6	ULMUS ALATA				0.311E 02
		DBH	5.226	4.915	5.346	4.915	
			4.917	3.335			
		74	0.188E 02 METRIC TON/HA. LEAF AREA =				0.954

YEAR	SPEC.	NUM.	NAME				BIOMASS
300							
	2	4	CARPINUS CAROLINIANA				0.103E 01
		DBH	1.569	1.386	1.270	1.270	
	5	3	CARYA LACINIOSA				0.692E 00
		DBH	1.376	1.279	1.293		
	6	16	CARYA OVATA				0.283E 03
		DBH	16.100	13.134	9.369	9.139	
			9.157	6.338	6.737	6.385	
			6.815	6.083	2.824	2.813	
			2.962	3.227	2.873	2.909	
	7	2	CARYA TEXANA				0.493E 00
		DBH	1.431	1.271			
	8	10	CARYA TOMENTOSA				0.229E 03
		DBH	15.015	14.841	8.482	8.763	
			7.965	7.749	1.270	1.345	
			1.270	1.352			
	10	11	CELTIS LAEVIGATA				0.216E 03
		DBH	11.299	10.962	11.454	8.471	
			8.459	8.625	8.345	6.664	
			4.288	3.522	3.508		
	11	14	CORNUS FLORIDA				0.640E 02
		DBH	7.389	7.159	7.297	4.481	
			4.555	1.480	2.127	1.918	
			1.505	1.480	1.902	1.588	
			1.486	1.486			
	13	1	FAGUS GRANDIFOLIA				0.218E 00
		DBH	1.288				
	15	6	ILEX OPACA				0.260E 03
		DBH	15.932	13.160	12.649	12.019	
			7.631	0.102			
	18	11	LIQUIDAMBAR STYRACIFLUA				0.498E 03
		DBH	18.288	18.504	15.747	13.676	
			8.819	8.557	8.461	8.461	
			5.405	5.225	0.101		
	21	2	OSTRYA VIRGINIANA				0.275E 00
		DBH	0.101	1.417			
	25	5	QUERCUS ALBA				0.838E 02
		DBH	11.629	11.258	2.438	2.455	
			1.477				
	26	34	QUERCUS FALCATA				0.482E 04
		DBH	77.409	25.001	15.814	16.623	
			15.784	15.972	15.789	10.441	
			6.992	6.904	6.164	5.724	
			6.056	5.721	5.719	6.029	
			5.413	5.870	3.911	3.587	
			3.723	3.592	2.895	2.862	
			2.862	2.864	2.977	2.862	
			2.874	2.862	3.148	2.896	
			2.921	2.995			

```
         27      3    QUERCUS MARILANDICA        0.659E 02

                DBH     9.811    8.891    7.628

         29     20    QUERCUS STELLATA           0.799E 03

                DBH    20.563   13.642   13.651   13.999
                       13.784   13.587   13.728   13.638
                       13.641   14.575    7.393    5.898
                        6.067    5.897    6.470    5.896
                        1.276    1.272    1.270    0.173

         32     11    ULMUS ALATA                0.446E 03

                DBH    22.916   17.756   16.466    4.480
                        4.242    4.289    3.538    3.548
                        1.294    1.665    0.152

         33      1    ULMUS AMERICANA            0.224E 00

                DBH     1.300

               154   0.931E 02 METRIC TON/HA. LEAF AREA =     5.125

YEAR SPEC.     NUM.            NAME                      BIOMASS
 350

          2      2    CARPINUS CAROLINIANA       0.430E 00

                DBH     1.280    1.278

          5      1    CARYA LACINIOSA            0.223E 00

                DBH     1.299

          6     16    CARYA OVATA                0.792E 03

                DBH    27.565   19.406   15.211   14.672
                       14.207    9.856    9.837   10.460
                        0.136    0.112    1.407    1.329
                        1.303    1.282    1.370    1.270

          7      3    CARYA TEXANA               0.675E 00

                DBH     1.284    1.306    1.320

          8      7    CARYA TOMENTOSA            0.349E 03

                DBH    28.040    1.464    1.452    1.347
                        1.366    1.270    1.493

         10      3    CELTIS LAEVIGATA           0.399E 03

                DBH    19.806   20.004   16.148

         11      3    CORNUS FLORIDA             0.788E 00

                DBH     1.288    1.349    1.521

         15      1    ILEX OPACA                 0.342E 00

                DBH     1.553

         18     11    LIQUIDAMBAR STYRACIFLUA    0.192E 04

                DBH    37.444   38.465   29.044   16.818
                        1.425    0.127    1.271    1.276
                        1.412    1.557    1.488

         21      2    OSTRYA VIRGINIANA          0.515E 00

                DBH     1.475    1.273

         26     18    QUERCUS FALCATA            0.386E 04

                DBH    31.984   33.457   31.863   32.422
                       31.914   24.189   19.686   19.530
                       18.363   18.182   17.503   18.110
                       16.980   14.216   13.026   12.955
                       12.952   12.952

         27      2    QUERCUS MARILANDICA        0.450E 00

                DBH     1.332    1.274

         29      5    QUERCUS STELLATA           0.147E 04

                DBH    36.984   25.371   24.921   24.983
                        0.100

         32      1    ULMUS ALATA                0.565E 03

                DBH    34.347
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```
        33      6     ULMUS AMERICANA             0.144E 01

               DBH      1.276    1.274    1.270    1.309
                        1.310    1.562

                81    0.112E 03 METRIC TON/HA. LEAF AREA =     6.327

YEAR SPEC.     NUM.             NAME                    BIOMASS
 400

         5      3     CARYA LACINIOSA             0.641E 00

               DBH      1.270    1.281    1.276

         6      2     CARYA OVATA                 0.263E 03

               DBH     24.955    1.271

         7      4     CARYA TEXANA                0.113E 01

               DBH      1.408    1.491    1.271    1.553

         8      4     CARYA TOMENTOSA             0.902E 00

               DBH      1.270    1.270    1.326    1.350

        10      5     CELTIS LAEVIGATA            0.239E 03

               DBH     23.952    1.283    1.280    1.285
                        1.532

        13      1     FAGUS GRANDIFOLIA           0.216E 00

               DBH      1.282

        26     12     QUERCUS FALCATA             0.823E 04

               DBH     48.937   47.770   50.093   48.447
                       37.638   30.663   30.143   29.821
                       27.980   24.674   23.138   22.998

        27      5     QUERCUS MARILANDICA         0.132E 01

               DBH      1.271    1.392    1.510    1.473
                        1.296

        29      7     QUERCUS STELLATA            0.732E 03

               DBH     38.240    0.101    1.306    1.386
                        1.314    1.273    1.477

        32      1     ULMUS ALATA                 0.218E 00

               DBH      1.287

                44    0.114E 03 METRIC TON/HA. LEAF AREA =     5.819

YEAR SPEC.     NUM.             NAME                    BIOMASS
 450

         2      3     CARPINUS CAROLINIANA        0.764E 00

               DBH      1.422    1.271    1.418

         6      1     CARYA OVATA                 0.635E 03

               DBH     36.062

         7      1     CARYA TEXANA                0.215E 00

               DBH      1.278

         8      4     CARYA TOMENTOSA             0.911E 00

               DBH      1.275    1.285    1.382    1.294

        10      1     CELTIS LAEVIGATA            0.500E 03

               DBH     32.643

        15      2     ILEX OPACA                  0.466E 00

               DBH      1.325    1.319

        25      6     QUERCUS ALBA                0.156E 01

               DBH      1.461    1.418    1.271    1.564
                        1.280    1.270
```

26	11	QUERCUS FALCATA	0.799E 04
	DBH	64.076 69.005 44.239 41.929 33.531 2.805 1.480 1.321 1.473 1.458 1.273	
27	3	QUERCUS MARILANDICA	0.754E 00
	DBH	1.475 1.270 1.338	
32	3	ULMUS ALATA	0.793E 00
	DBH	1.384 1.305 1.486	
	35	C.110E 03 METRIC TON/HA. LEAF AREA =	5.177

YEAR SPEC.	NUM.	NAME	BIOMASS
500			
2	1	CARPINUS CAROLINIANA	0.227E 00
	DBH	1.309	
6	1	CARYA OVATA	0.121E 04
	DBH	47.232	
7	3	CARYA TEXANA	0.848E 00
	DBH	1.271 1.461 1.551	
10	2	CELTIS LAEVIGATA	C.877E 03
	DBH	41.266 1.278	
13	3	FAGUS GRANDIFOLIA	0.780E 00
	DBH	1.540 1.271 1.323	
15	8	ILEX OPACA	0.189E 01
	DBH	1.272 1.565 1.275 1.360 1.285 1.270 1.306 1.282	
21	4	OSTRYA VIRGINIANA	0.990E 00
	DBH	1.511 1.274 1.349 1.272	
26	3	QUERCUS FALCATA	0.119E 05
	DBH	81.316 88.389 58.141	
32	7	ULMUS ALATA	0.188E C1
	DBH	1.288 1.429 1.335 1.519 1.374 1.559 1.293	
	32	0.167E 03 METRIC TON/HA. LEAF AREA =	7.284

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