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PREDICTING SUCCESSIONAL PLANT COMPOSITION
ON A PSEUDOTSUGA MENZIESII/PHYSOCARPUS MALVACEUS
HABITAT TYPE IN WESTERN MONTANA

By

Robert E. Keane II

B.S., University of Maine, 1978

Presented in partial fulfillment of the requirements
for the degree of

Master of Science in Forestry

UNIVERSITY OF MONTANA

1984

Approved by:

Thomas G. ...
Chairman, Board of Examiners

[Signature]
Dean, Graduate School

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Forestry

Predicting Successional Plant Composition on a Pseudotsuga menziesii /Physocarpus malvaceus Habitat Type in Western Montana (96 pp.)

Director: Dr. Hans Zuuring 77.3

As resource management strategies intensify, forest land managers must be able to predict the probable response of forest vegetation to silvicultural treatments and wildfires so that management alternatives can be evaluated. A quantitative computer model of succession has been developed. This model predicts temporal changes in cover for major species in the Pseudotsuga menziesii/Physocarpus malvaceus habitat type. The model is based on a successional classification system which has recently been developed. In the model, species are established according to regenerative strategies and subsequent growth is modeled empirically via regression equations. Output is offered both in tabular and graphic form. Model validation yielded 63 and 85 percent accuracy in determining correct plant species cover. The computer program consisting of 21 subroutines was written in FORTRAN 77 to facilitate the rapid execution of the succession model.

Acknowledgements

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CHAPTER 1

INTRODUCTION

The majority of the diverse seral communities present on western Montana forest lands were created by timber harvesting practices and wildfires. The vegetal composition of these communities influences timber production, wildlife and livestock forage potential, recreation opportunity, watershed characteristics, and reforestation problems. As resource management strategies continue to intensify, land managers must be able to predict the probable response of forest vegetation to silvicultural treatments and wildfires so that various management alternatives can be evaluated. The need to predict successional compositions is magnified by the fact that early to mid-seral community types have been and will continue to be a major component of western Montana forests. Recently, the computer model has become a useful tool in predicting temporal changes in forest vegetation. Unfortunately, many current succession computer models were built for research purposes and are not oriented to management application. This thesis presents a quantitative computer model of succession designed to be used in resource management and planning.

This computer model is empirical in design and based on the successional community classification system of Arno and others (1985). Major plant species of the Pseudotsuga menziesii/Physocarpus malvaceus habitat type (Pfister and others 1977) are individually modeled using

regression equations derived from an extensive successional data base. Initial establishment is based on each species' physiognomic and morphologic regenerative strategies and subsequent growth in canopy coverage is determined from empirical equations. Moreover, since a given stand-removing disturbance in combination with an appropriate silvicultural treatment can create a unique successional community which progresses towards climax along any one of several pathways, it was necessary to stratify species regression equations by pathway.

CHAPTER 2
LITERATURE REVIEW

Succession Theory

Plant succession has been studied by numerous vegetation researchers. As a result, many theories on successional processes have been formulated (for review see Drury and Nisbet 1973, Kessell 1980, van Hulst 1978) and diverse conceptual models have been developed (Cattelino and others 1979, Clements 1928, Connell and Slatyer 1977, Drury and Nisbet 1973, Egler 1954, Everett and Ward 1984, Gleason 1926, Horn 1976, Noble and Slatyer 1980, Odem 1969, Peet and Christensen 1980). However, since Noble (1981) suggests there is no "unifying successional scheme" but only a multitude of species specific trends (Pickett 1976), it can be assumed that no conceptual model can be applicable to all types of vegetation communities.

The "initial floristics" model of Egler (1954) generally describes early mechanisms of succession in western Montana (Arno 1981, Heinzelman 1982, Lyon and Stickney 1974). This model asserts that post-disturbance species dominance is dependent on the survival of intact plants or regenerating plant parts from the predisturbance community. And, as succession is essentially a species by species process (Drury and Nisbet 1973) characteristic of Gleason's (1926) individualistic community theory, multiple successional pathways can emerge depending on ecological characteristics of the plants (Noble and Slatyer 1980) and

severity of the perturbation (Gardener 1980, Gill 1977, Kessell and Fischer 1981). Application of these concepts in the Rocky Mountains is demonstrated by the multiple pathway model of Cattelino and others (1979) and succession community classification system of Arno and others (1985). Therefore, the direction of succession in western Montana forests is dependent on predisturbance plant composition, disturbance severity, and survival mechanisms of individual plant species (Antos and Shearer 1980, Debyle 1981, Lyon 1971, Lyon and Stickney 1974 Zamora 1982).

Current quantitative succession models (summarized in Shugart and West 1980) deal mainly with the tree layer and rarely simulate changes in the undergrowth (examples in West and others 1981). These models use a variety of dependent variables to measure successional growth. Bartos and others (1983) and Shugart and others (1980) used biomass as a measure to define changes in vegetation over time, while Everett and Ward (1984) used percent cover as the successional measure. Variables such as stocking or species frequency (Bella 1970), basal area, and breast height diameter (Ek and Monserud 1974, Stage 1973, Kercher and Axelrod 1984, Botkin and others 1971a) are easily measurable for trees, but prove difficult to sample for undergrowth species. Shrub and herb compositions are frequently measured in percent canopy coverage because of cost efficiency (Arno and others 1985, Cholewa and Johnson 1983, Lyon and Stickney 1976, Pfister and others 1977, Stickney 1980). Lindsey (1956) considers canopy cover "the most important single parameter of a species in its community relations". The shrub succession model of Steinhorst and others (1984) and the FORPLAN model of Kessell and Potter

(1980) have percent cover as the predictive variable.

Forest succession models can be categorized into two approaches; deterministic or stochastic, based on the nature of the driving variables. Deterministic models can further be stratified into three types: mechanistic, theoretical, and empirical. The mechanistic model uses basic physiologic functions to simulate changes in plant growth during succession (Botkin and others 1972a, Kercher and Axelrod 1984). Theoretical deterministic models use estimated or assumed parameters to drive hypothetical growth equations (Bartos and others 1983), while the data-intensive empirical models use regression equations created from substantial data bases to estimate successional growth (Adcard 1974, Arney 1974, Irwin and Peek 1979, Lin 1974, Stage 1973).

Stochastic approaches simulate successional replacement processes using Markov chain, Monte Carlo, and other types of probability models (Binkley 1980, Horn 1976, Leak 1970, Suzuki and Umemura 1974, Wagonner and Stevens 1970). Frequently, succession models are a combination of both approach and types within an approach. Steinhorst and others (1984) modeled succession as stochastic during plant establishment and deterministic thereafter.

Vegetation Ecology

Succession is directly influenced by the biology of each potential plant species. Physiognomic and morphologic characteristics of the vegetation, together with revegetation adaptations or strategies, dictate perturbation response and subsequent establishment and growth. A quantitative succession model must be fundamentally based on plant

species ecology to accurately depict temporal composition changes. Therefore, it is essential to determine key modes of survival, establishment, and growth of the major species to be modeled. The following is an abbreviated summary of principle revegetation mechanisms for major plants modeled for the PSME/PHMA habitat type (Appendix A).

The two tree species modeled for this habitat type are adapted to disperse seeds over short distances to gain reestablishment. Larix occidentalis (LAOC), a major component in only the PSME/PHMA, moist phase, is a rapidly growing, shade-intolerant species whose seeds usually need a mineral seedbed to germinate and grow into an established seedling (Shearer 1976, Schmidt and others 1976). The seeds of the semi-shade-tolerant Pseudotsuga menziesii (PSME) are capable of germinating in more diverse seedbed conditions but subsequent seedling growth is comparatively slower (USDA 1965). Neither species can reproduce vegetatively and, therefore, rely on off-site and surviving seed sources for reestablishment (USDA 1965). Pinus ponderosa (PIPO) and Pinus contorta (PICO) are minor components of this habitat type but, due to their limited occurrence, were not modeled.

Shrub species show the most diverse response adaptations. The key indicator Physocarpus malvaceus (PHMA) sprouts from adventitious buds on the root crown (basal sprouting) after disturbance damage (Crane and Habeck 1983, Habeck and others 1980, Schmidt 1980). However, recent studies revealed that sprouting from adventitious buds and nodes on deep-rooted rhizomes is also responsible for post-disturbance revegetation (Bradley 1984). These two adaptations allow PHMA to regenerate after the most severe disturbances (Bradley 1984, Habeck and

others 1980). Rhizomes account for the most regeneration in Spiraea betulifolia (SPBE), which revegetates with high fecundity under certain environmental conditions, and Symphoricarpos alba (SYAL), which needs large diameter rhizomes to insure adequate carbohydrate reserves for resprouting (Bradley 1984, Crane and Habeck 1983, Habeck and others 1980). Both plants can reestablish after moderate to severe perturbations. Vaccinium globulare, having its perennating rhizomes nearer to the soil surface, is more susceptible to disturbance damage (Antos and Shearer 1980, Bradley 1984, Crane and Habeck 1983, Miller 1976,1977). The major basal (root crown) sprouters in the PSME/PHMA h.t. are the shade-tolerant Acer glabrum (ACGL), the ubiquitous Amelanchier alnifolia (AMAL), and the somewhat shade-intolerant Salix scouleriana (SASC). SASC can also reproduce from numerous, wind-borne seeds but the dry seedbed conditions associated with this habitat type generally inhibit successful establishment via seed germination.

Two shade-intolerant shrubs have the unique adaptational advantage of reproducing from seeds which remain viable in the soil for long periods of time. The nitrogen-fixing Ceanothus velutinus (CEVE) produces seeds which may remain viable for 400 years or more and need heat treatment to stratify the seedcoat for initiate germination (Cholewa and Johnson 1983, Lyon 1971, Lyon and Stickney 1974, Morgan and Nuenshwander 1984, Mueggler 1965, Quick 1959). Although CEVE also has the capability to resprout basally, it is usually absent in stands with greater than 50 percent canopy closure, thus relying on the soil seedbank for creating the dense CEVE shrubfields evident on western Montana landscapes (Arno and others 1985, Lyon 1971, Stickney per.

comm.). The bird-disseminated seed of Prunus virginiana (PRVI) remains viable in the soil for shorter periods of time but expansion is often a result of basal and rhizomatous sprouting (Habeck and others 1980, Mueggler 1965).

Two disturbance response mechanisms are exhibited by the three subshrubs in this habitat type (Appendix A). Linnaea borealis (LIBO) and Arctostaphylos uva-ursi (ARUV) are repent, mat-forming shrubs expanding vegetatively by creeping stems with little or no regeneration from seed (Bradley 1984, Crane and Habeck 1982, Flinn and Wein 1977). Since the majority of plant parts are very close to the soil surface, these species are extremely sensitive to disturbance (Arno and others 1985, Rowe 1977, Bradley 1984). Conversely, Berberis repens (BERE) has moderately deep-rooted rhizomes (10-15 cm) that regenerate after light to moderate disturbances (Bradley 1984, Crane and Habeck 1983, Miller 1976).

All grasses listed in Appendix A, with the exception of Agropyron spicatum (AGSP), regenerate primarily from deeply buried rhizomes. (Antos and Shearer 1980, Lyon 1971, Mueggler 1965). However, Crane and Habeck (1983) found that the most abundant grass, Calamagrostis rubescens (CARU), expands equally from seeds and rhizomes and can potentially double in cover after a disturbance. AGSP can resprout from rhizomes but the "bunchgrass" or tufted form of this perennial protects meristematic tissue from fire, allowing regrowth from the original plant (Stickney per. comm.). The sedges, Carex geyeri (CAGE), Carex rossii (CARO), and Carex conncinnoides (CACO), are usually not mat-forming like CARU but seem to possess the protective traits of the tufted grasses.

Resprouting from rhizomes, stolens, and caudexes are the morphological adaptations to disturbance for forbs in Appendix A. Arnica cordifolia (ARCO), Aster conspicuus (ASCO), and Thalictrum occidentale (THOC) regenerate mainly from rhizomes and are capable of surviving low to moderately severe perturbations (Crane and Habeck 1983, Habeck and others 1980, Lyon 1971, Lyon 1966, Mueggler 1965). Forbs having shallow-rooted rhizomes that are extremely susceptible to disturbance include the shade-tolerant plants Chimaphila umbellata (CHUM), Goodyera oblongifolia (GOOB), and Mitella stauropetala (MIST) (Antos and Shearer 1980, Arno and others 1985, Rowe 1979). Adventitious buds on stolons account for expansion in Fragaria vesca (FRVE) and Fragaria virginiana (FRVI), but due to the close proximity of the stolons to the soil surface, Fragaria coverage is somewhat reduced by moderate to severe disturbances (Rowe 1977). The colonizer Epilobium angustifolium (EPAN) is capable of resprouting from rhizomes providing the intolerant plant is present on post-disturbance sites. However, the major mode of establishment is through production of copious, light seeds that are dispersed over great distances by wind (Arno and others 1985, Crane and Habeck 1983, Flinn and Wein 1977). This latter adaptation is also present to some degree in Hieracium albiflorum (HIAL) and Achillea millefolium (ACMI), although the seeds are usually only locally distributed. The warm, dry seedbed conditions of this habitat type are apparently the cause of reduced germination success for EPAN, HIAL, and ACMI resulting in low post-disturbance coverages (Arno and others 1985, Miller 1976, Rowe 1977) In addition, HIAL and ACMI can resprout from a fibberrot caudex. The taproot caudex of Balsamoriza

sagittata (BASA) is capable of resprouting after low to moderate treatments while the stout, surficial rhizome system of Xerophyllum tenax (XETE) can resprout if left intact after disturbance (Antos and Shearer 1980, Bradley 1984, Habeck and others 1980).

CHAPTER 3

STUDY OBJECTIVES

At present, forest managers use qualitative procedures to assess silvicultural impacts on succession dynamics. Successional classification systems such as Arno and others (1985) and Steele (1984) relate successional pathways to silvicultural treatments and wildfire but magnitudes of compositional changes are absent. This study was initiated to provide quantitative estimates of successional shifts in species coverage to facilitate evaluation of management actions. Therefore, the objective of this modeling study is:

To develop a management-oriented, quantitative succession computer model that would predict post-disturbance plant species' response in the PSME/PHMA successional community types of Arno and others (1985).

CHAPTER 4

METHODS

Study Area

Data for the succession computer model were collected on the PSME/PHMA h.t.'s of the Lolo and Bitterroot National Forests, the southern half of the Flathead National Forest, and parts of the Flathead Indian Reservation (Figure 1). This area is composed of rugged, heavily forested mountains bordered by grasslands and agricultural valleys at low elevations and slow-growing, "upper subalpine" forests at the high elevations (Pfister and others 1977). The surface geology is mainly from the Precambrian Belt Series consisting primarily of quartzites and argillites. However, the Bitterroot National Forest is largely granitic in origin. Soils are medium to coarse-textured and generally shallow and rocky, but deeper mantles sometimes occur on north and east slopes due to deposits of volcanic ash and loess. Cryochrepts and Cryandepts are the major soil great groups of the area. The climate is described as inland maritime with short, warm-dry summers and cold snowy winters. Mean annual precipitation is approximately 15 to 25 inches for this habitat type.

The PSME/PHMA h.t. consists of two phases. The dry phase is more abundant and occurs predominately on moderate to steep, south and west-facing slopes with presence on north and east aspects restricted to drier portions of the study area. Elevation ranges from 3200 to 5800

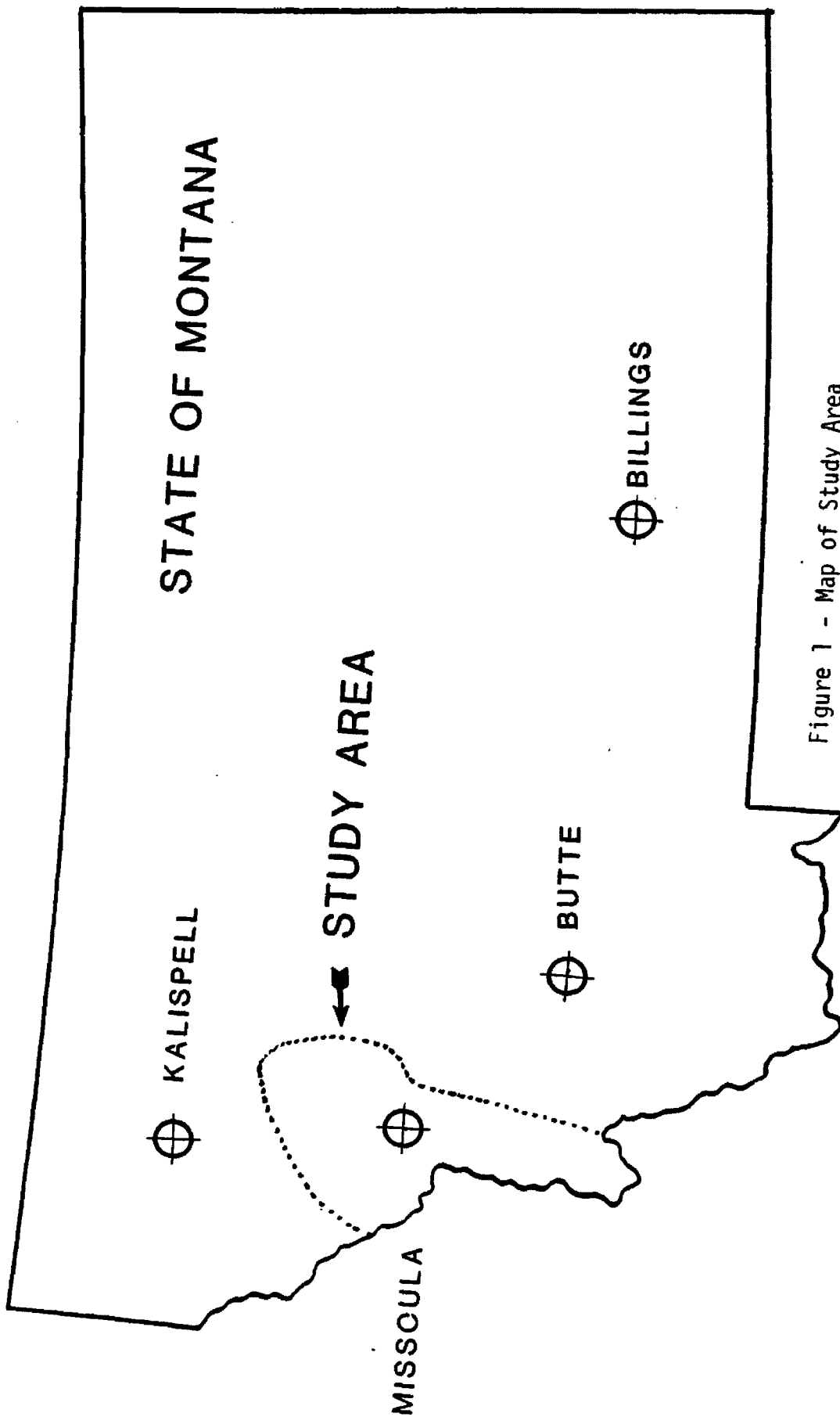


Figure 1 - Map of Study Area

feet. The more productive moist phase of this habitat type occupies moderate to steep, north and east-facing slopes between 3400 and 5300 feet in elevation. The moist phase is not as abundant as the dry phase being absent from the Bitterroot National Forest south of Stevensville and from the Lolo National Forest east of Rock Creek. The moist phase is distinguished from the dry phase by having LA0C as a forest component (Arno and others 1985).

Study Design

The data base used for model construction was created by pooling data collected for the review draft of the Arno and others (1985) classification system with data subsequently collected for an evaluation of the classification system (Keane 1984).

In these studies, potential study sites were selected using the USDA Forest Service Northern Region timber data base and National Forest Ranger District compartment maps. A study site was often composed of several, different-aged stands, and typically a combination of a disturbed stand with an adjacent control or mature stand. This multiple stand sampling was designed to minimize the three main sources of vegetation variation: 1. site variability within a habitat type, 2. geographic variations in the vegetation, and 3. variations in stand histories prior to treatment.

A circular, 375 square meter macroplot was established in a representative portion of each stand in the study site. The representative area was selected as displaying average vegetation compositions and uniform treatment severity across the stand. This

procedure, described by Mueller-Dombois and Ellenberg (1974) as "subjective without preconceived bias", is similar to that employed by Pfister and others (1977) for the Montana forest habitat type classification. Canopy coverage for all woody and herbaceous species on the macroplot was ocularly estimated in cover classes (Table 1) as outlined by Pfister and Arno (1980). In addition, tree species cover was stratified into two diameter classes; coverage of trees less than and greater than four inches diameter at breast height (DBH). Other variables recorded on the macroplot were:

1. Elevation (feet above sea level \pm 100 feet).
2. Slope (percent \pm 5%).
3. Aspect (degrees or azimuth \pm 5 degrees).
4. Plot location (Township, Range, Section).
5. Treatment type (Table 2) from stand records.
6. Treatment intensity type (Table 3) ocular estimation.
7. Percent exposed bare mineral soil (percent) ocular estimation.
8. Total tree cover (nearest five percent) ocular estimation
9. Average stand DBH (inches \pm 1 inch).
10. Stand basal area (square feet per acre \pm 5 sq. ft.) prism.
11. Stand age since treatment (years \pm 1 year) from stand records and field evidence.
12. Successional community type as defined by Arno and others (1985).

The sampling design of the evaluation study differed from that of the original classification study in that only one stand per study site was sampled. This allowed the freedom to sample a wide range of communities within the study area in a limited amount of time. As a consequence, sampling was concentrated on the highly variable early-seral communities. Additional tree data were collected during the classification study but these were not used in the modeling study. A

Table 1

Cover classes used to estimate cover on sample plots.

Cover Class	Cover Range in Percent (%)
T or trace	less than 1
1	1 to 5
2	5 to 25
3	25 to 50
4	50 to 75
5	75 to 95
6	95 to 100

Table 2

Sampled treatment types implemented in the model.

Treatment type	Abbreviation
Wildfire	WF
Clearcutting with broadcast burning	BB
Clearcutting with mechanical scarification	MS
Clearcutting with no site preparation	NP

Table 3

Sampled severity types implemented in the model.

Severity type	Abbreviation
Low or light	L
Moderate or medium	M
High or heavy	H

total of 225 stands were sampled with 146 in PSME/PHMA, dry phase and 79 in PSME/PHMA, moist phase habitat types.

Model Construction

The construction of the computer model of succession was done in a stepwise process. First, field data was inspected to determine appropriate species to model and then analyzed to assess ecological modeling criteria. Regression analyses were then performed on the data to compute equations which would approximately replicate species successional trends. Next, a computer program was written to incorporate equations and ecological modeling criteria into a scheme which simulates succession on a community basis. The model was then tested with additional field data to determine accuracy and precision of predictions and the test results were then used to further refine the model. These steps will now be presented in detail.

The data were entered into computer data files in a format compatible with existing statistical and vegetation analysis programs (Gauch 1977, SPSSX 1984). Synthesis tables (Mueller-Dombois and Ellenberg 1974) were produced to select the most important or frequently occurring species to be modeled. These species (Appendix A) constitute the majority of cover in any succession community type. Also selected from these plants were the most dominant or the species that directed successional progression in any of the community types. (Table 4). These dominant plants are the species used in the succession classification key (Arno and others 1985).

TABLE 4

Major plant species utilized in the regression analysis with their cover as independent variables. These species were the same for both moist and dry phases.

Species name	Common name
1. <i>Pseudotsuga menziesii</i> and <i>Larix occidentalis</i> (PSME + LAOC)	Douglas-fir and western larch
2. <i>Physocarpus malvaceus</i> (PHMA)	Ninebark
3. <i>Calamagrostis rubescens</i> (CARU)	Pinegrass
4. <i>Carex geyeri</i> (CAGE)	Elk sedge
5. <i>Ceanothus velutinus</i> (CEVE)	Evergreen Ceanothus
6. <i>Amelanchier alnifolia</i> (AMAL)	Serviceberry
7. <i>Acer glabrum</i> (ACGL)	Mountain maple
8. <i>Salix scouleriana</i> (SASC)	Scouler's willow

Two types of numerical analyses were employed to create the succession computer model. Ordination techniques were used in the formation of species response groupings and regression analyses were utilized to estimate parameters for the prediction equations associated with the succession computer model.

Ordination is the process of arranging species (or samples) in relation to one or more environmental gradients using vegetation coverage data (Whittaker 1973). Numeric or graphic representation of species similarity along the gradients can be obtained from any of the current ordination programs (Gauch 1977). Using Polar and Reciprocal Averaging Ordination methods (Gauch 1982, 1977) on the data collected for species in Appendix A, similarity between plants along possible succession gradients was indirectly identified and response group clusters were delineated (Huschle and Hironaka 1980, del Moral 1983). Examples of ordination by species for both phases are shown in Figures 2 and 3. Ordination results were used to finalize the response groups defined in the next paragraph.

To simplify model construction, plant species were categorized into response groups using methods of reestablishment, response to disturbance, and tolerance to shade as criteria. Formulation of response groups was facilitated by classifying species according to Raunkiaer's life forms (Chapman and Crow 1980, Mueller-Dombois and Ellenberg 1974) Plant Strategy Types (Grime 1979), and Vital Attributes (Noble and Slatyer 1980, 1977). The results of the species classification and the ordination were used to create 24 response groups (Appendix B). These groups were designed to permit inclusion of

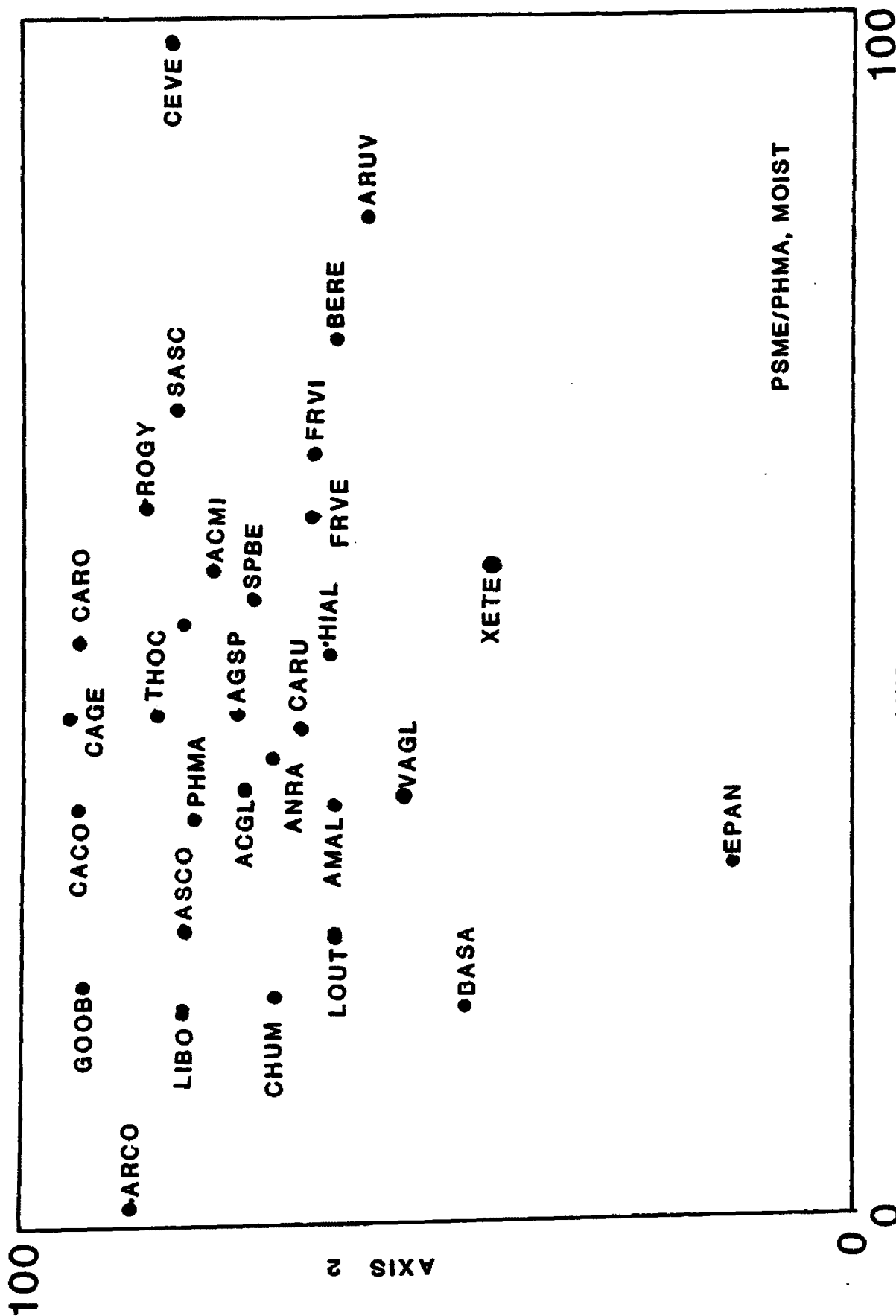


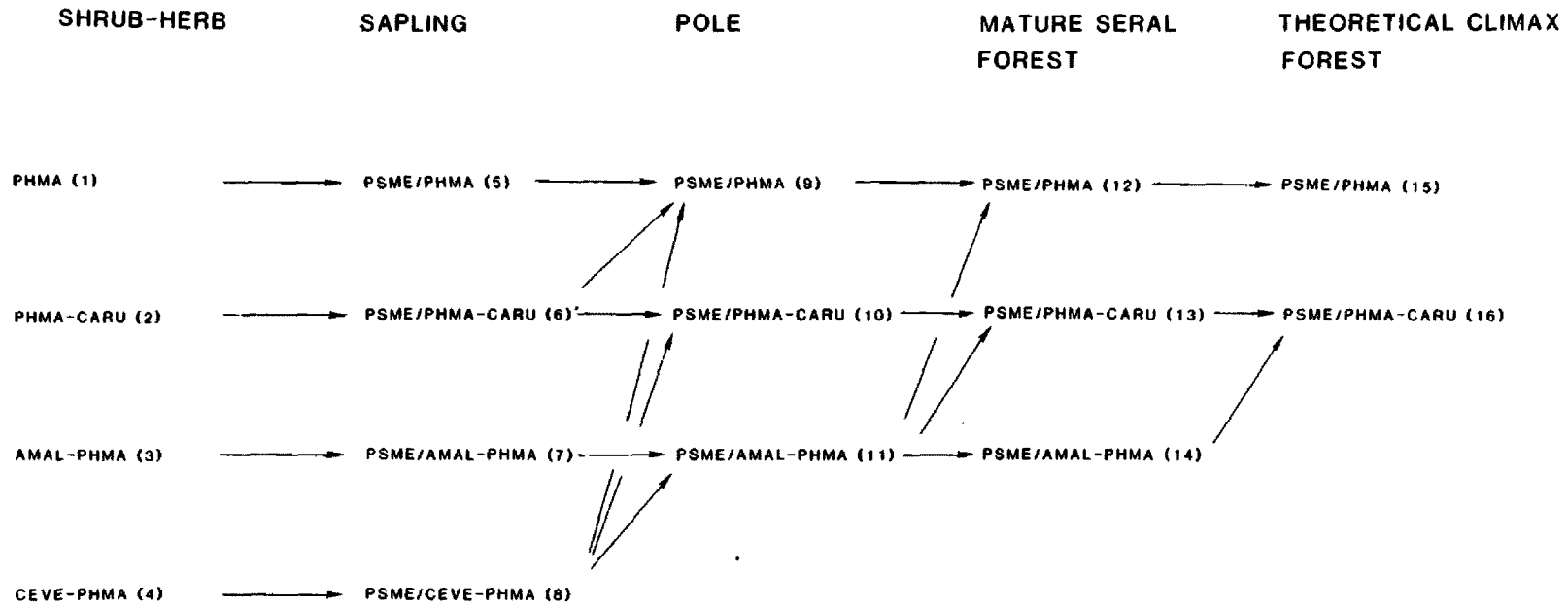
Figure 3 - Sample Ordination by species for the PSME/PHMA, moist phase

additional species as more habitat types are incorporated into the model. With species response groups as guidelines, modeling decisions could be based on ecological attributes of plants.

The model was created empirically using multiple regression analyses. For each phase of the PSME/PHMA h.t., a multiple regression analysis was performed for each species using only data from plots of the community types in each of the successional pathways depicted in Figure 4 and 5. These pathways were identified from the classification system (Arno and others 1985) as explaining the greatest portion of successional variation. The multiple regression analysis was repeated for each successional pathway. The dependent variable for the regression analyses was percent cover for every plant species, and DBH and basal area for the stand. The independent variables included stand age, percent total tree canopy cover, dominant species cover (dominant species are presented in Table 4), elevation, aspect, slope, treatment type, and treatment severity. Predisturbance cover, assumed to be the cover in the control or untreated stand on the same site as the disturbance stand, was often used as an independent variable. However, this eliminated the evaluation data from the data base because the multiple stand sampling technique, which sampled an undisturbed stand adjacent to the disturbed stand, was not employed in that study. All regression equations generated from the regression analyses were developed to be descriptive as well as predictive in the successional sense. Cover class values recorded for all vegetation variables were transformed to percent cover using the percent midpoint for each cover class.

PSME/PHMA, DRY

STRUCTURAL STAGES



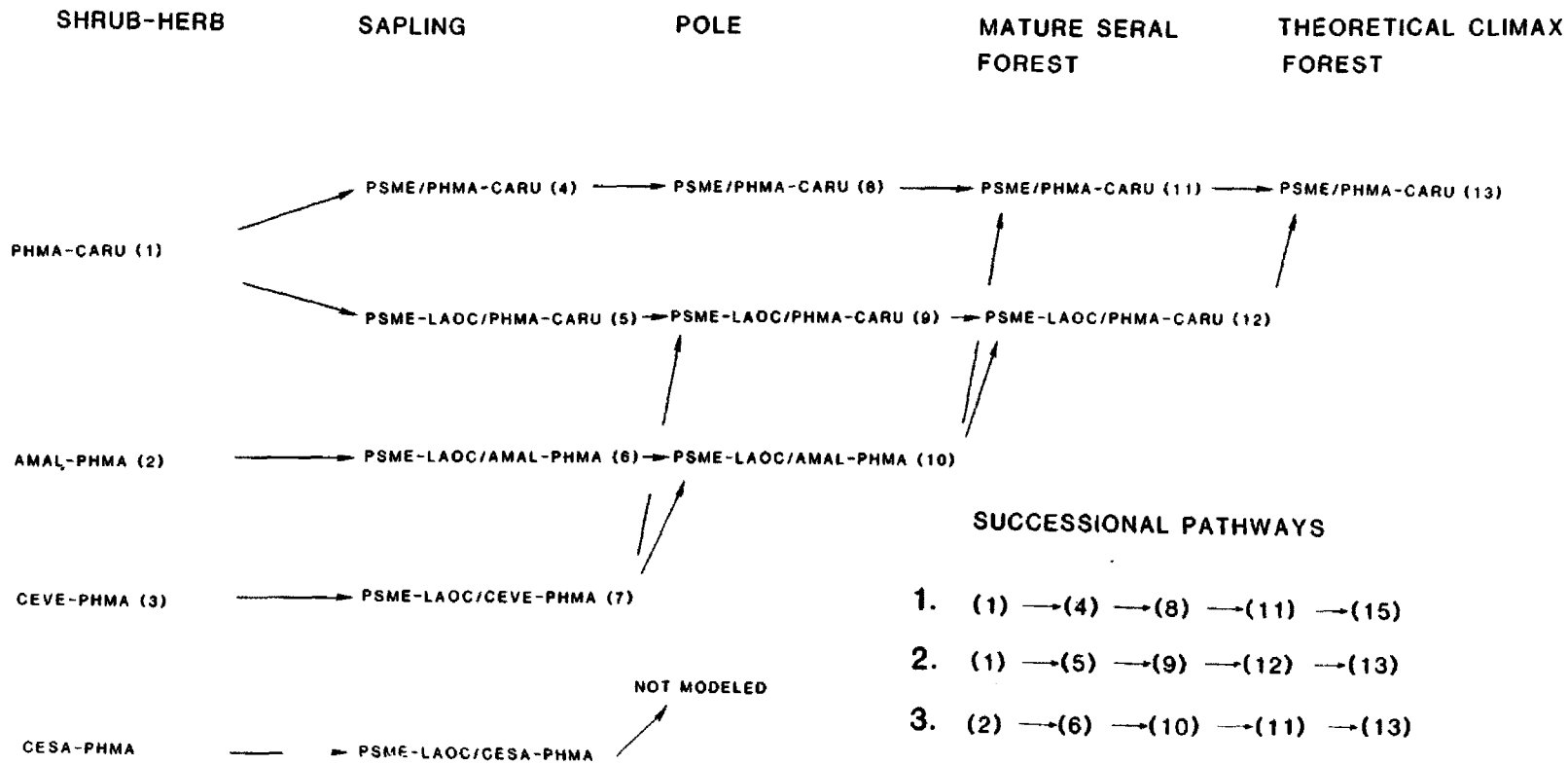
SUCCESSIONAL PATHWAYS

- | | | |
|-----------------------------------|-----------------------------------|-----------------------------------|
| 1. (1) → (5) → (9) → (12) → (15) | 4. (3) → (7) → (11) → (14) → (16) | 7. (4) → (8) → (9) → (12) → (15) |
| 2. (2) → (6) → (10) → (13) → (16) | 5. (3) → (7) → (11) → (13) → (16) | 8. (4) → (8) → (10) → (13) → (16) |
| 3. (2) → (6) → (9) → (12) → (15) | 6. (3) → (7) → (11) → (12) → (15) | 9. (4) → (8) → (11) → (14) → (16) |

Figure 4 - Successional diagram and pathway list for PSME/PHMA, dry phase

PSME/PHMA, MOIST

STRUCTURAL STAGES



SUCCESSIONAL PATHWAYS

1. (1) → (4) → (8) → (11) → (15)
2. (1) → (5) → (9) → (12) → (13)
3. (2) → (6) → (10) → (11) → (13)
4. (2) → (6) → (10) → (12) → (13)
5. (3) → (7) → (9) → (12) → (13)
6. (3) → (7) → (10) → (12) → (13)

Figure 5- Successional diagram and pathway list for the PSME/PHMA, moist phase

Various transformations were performed on the independent variables of stand age, total tree canopy cover, aspect, slope and elevation to compensate for curvilinear trends in the data and variable interactions. Sigmoid and asymptotic transformations were of the form described by Jensen (1979, 1973), Jensen and Homeyer (1970,1971), and Dolby (1963) while interactive transformations were formulated using ecological judgement. A summary of the transformations used in the regression analyses is shown in Appendix C.

Some species cover regression equations may have dominant species cover predictions as an independent variable. To eliminate confounding effects of related predictions for dominant plant species (Table 4), a priority system (Figure 6) was utilized during the regression analyses. In this system, each species was prioritized according to its successional importance or its relative dominance in any successional pathway. Species of a lower priority were not used to predict cover of a species with a higher priority. For instance, CARU coverage is not used to predict PHMA coverage but PHMA coverage is used to predict the coverage of CARU. Since successional importance is based on pathway, CEVE received a priority higher than PHMA, CARU, or CAGE along any of the CEVE pathways.

Regression analyses were performed using the REGRESSION procedure in the SPSSX (1983) statistical software package on the University of Montana DEC 2060 computer. Regression coefficients associated with each pathway prediction equation were estimated by a stepwise process known as "backward elimination". All independent variables were entered into an equation and then each was tested for removal using statistical

FIGURE 6

Priority system for species cover variables used in the regression analysis for model development. Cover for species with higher priorities are not used as independent variables in building regression equations for species of lower priorities. This priority system is for both PSME/PHMA, dry and moist phases.

FIRST PRIORITY -- Total tree canopy coverage

SECOND PRIORITY -- PHMA

THIRD PRIORITY -- CARU and CAGE

FOURTH PRIORITY -- CEVE (except in CEVE
pathways where it is
SECOND PRIORITY)

FIFTH PRIORITY -- AMAL and ACGL and
SASC

SIXTH PRIORITY -- All other plants

significance criteria (F value, tolerance). Once all insignificant variables were removed, each would again be entered to determine if the variable accounted for additional variation. Combinations of seventy variables or variable transformations were used in the stepwise procedure with each combination selected to best represent successional trends for a given species. The estimated coefficients for each equation, along with the standard deviation about regression at mean Y, number of observations, and coefficient of determination were stored in an external data file to be accessed by the computer program.

The programming requirements for the model were that it had to be easily implemented on the new Forest Service FLIPS mini computers produced by the Data General Corporation and it had to be in a programming language compatible with many Forest Service compilers. Since large storage requirements for programs built on mini computers consume valuable computer time, it was decided to store all parameters, output labels, and simulation results in external files to be accessed by the program when appropriate.

Model Assumptions

Since models are simplifications of reality, certain assumptions must be made to compensate for data limitations. The assumptions for this model are:

1. If a vegetatively reproducing plant is not present in the predisturbance community, it will not be present after disturbance.
2. The pathways displayed in Figures 4 and 5 represent succession on the PSME/PHMA habitat type.

3. There is always a seed source for the tree species.
4. The dominant plants in the priority system affect coverage of species with lower priorities.
5. Presence of CEVE or EPAN on a predisturbance site or in an immediate area indicates CEVE seed in soil or EPAN seed source.
6. Basal sprouting is the main method of expansion after disturbance for SASC in the PSME/PHMA h.t.
7. Cover class is an adequate measure of species composition dynamics.
8. Any plant species has only one main method of expansion, all others are considered to be insignificant.

Model Validation

The model was tested with actual field data to assess the accuracy of postdisturbance cover class predictions. During the summer of 1984, 20 new disturbance sites (13 in PSME/PHMA, dry and 7 in PSME/PHMA, moist habitat types) were sampled as previously described using the multiple stand sampling technique. Measurements for the control or untreated community adjacent to the disturbance stand were used as inputs to the model. Cover class predictions for each species from the computer model were then compared with the corresponding values recorded for the sampled disturbance community using regression techniques and frequency tables.

CHAPTER 5

RESULTS

Model Structure

The computer model was structured in modular form, using a main driver to direct control to subroutines that perform unique tasks. A simplified flow chart is presented in Figure 7.

At the start of a simulation run, the defaults and flags initialized in the driver. Subroutine GREET is then called to interactively describe the model and ask for the title of the simulation run and habitat type phase to be modeled. Using habitat type phase as a key, the number of species, major species (in the priority system), and transformation parameters are determined. External device numbers are also set to access proper files. MAJNAME is then called to read the major species names from an external file. These names are stored in an array in order of decreasing successional priority so that the current year's coverage of high priority species can be used to predict coverage for lower priority species. The input data entry routine is then activated by calling IREAD.

The data entry routine is an interactive subroutine with a variety of features for entering input values. Two skill levels are available to the user. The Novice skill level explains in detail the input value to be entered, while the Advanced level expedites data entry by printing a short, one line prompt or query with minimal input value description.

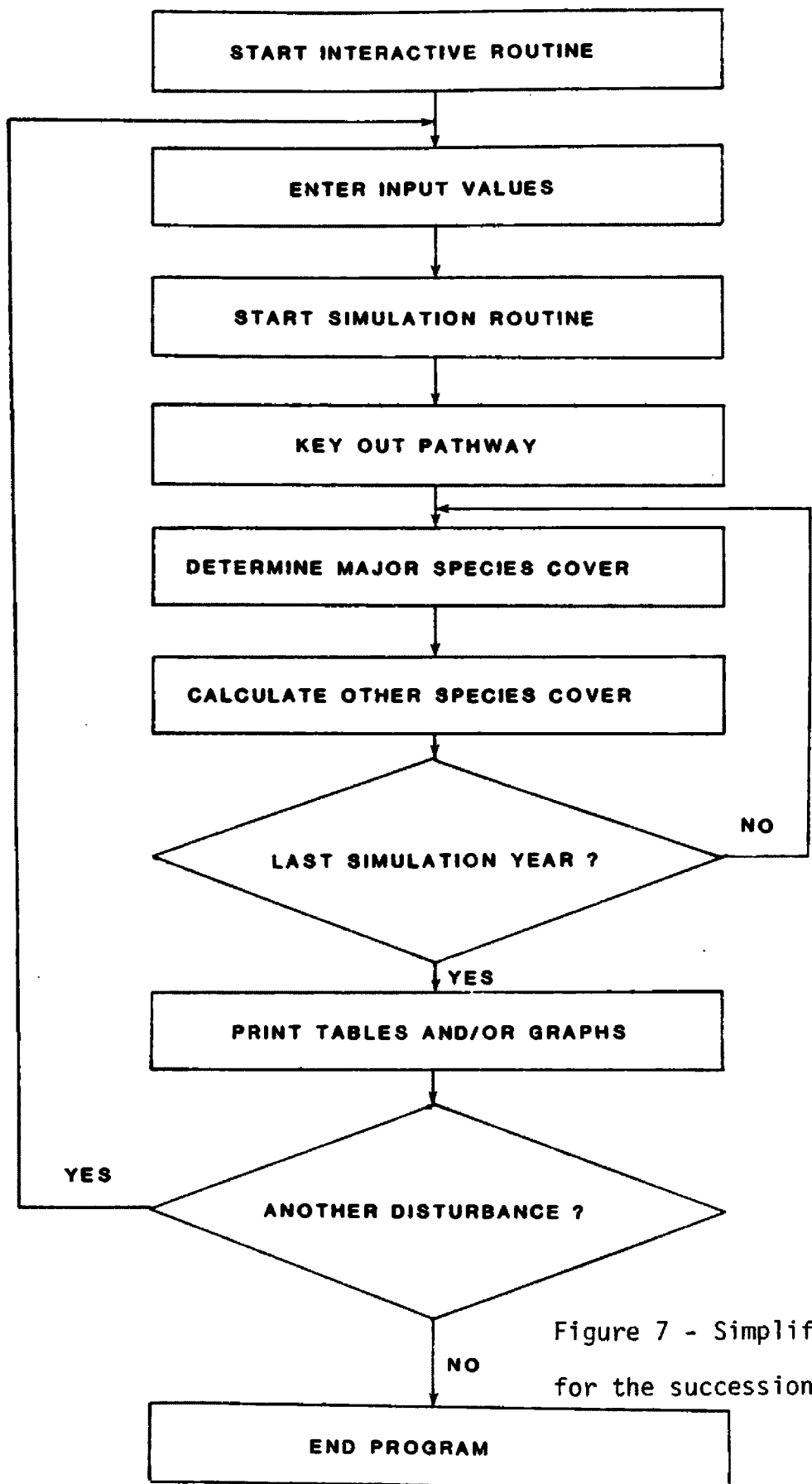


Figure 7 - Simplified flowchart for the successional computer model.

Once the input value has been entered, the subroutine scans for entry or data boundary violations. Data boundary violations occur when the entry is not within the range of data used for model construction. The following is a summary of data boundary errors.

1. Succession cannot be modeled past year 300.
2. Succession can only start on or after year five. Stands younger than five years old were not used in model construction because of the inherent variability within early-seral communities.
3. Elevation boundaries range from 3500 to 5800 feet.
4. Canopy coverage can never exceed 100 percent for any species.
5. The number of individual simulation years cannot exceed fifty. This is a limitation of the program not the data. The number of simulation years can be determined by dividing the maximum year to model by the age increment.
6. Slope cannot exceed 100 percent.
7. Aspect must be between zero and 360 degrees.

If the program detects an error, subroutine ERROR is called and a message describing the type of error is printed. The user has the option of entering cover class or percent cover for predisturbance plant coverages. However, model output is always presented in cover classes. A summary of all entered values is printed at the conclusion of the entry session and the user is then able to change any of the input values. An example of an entry session is presented in Appendix D.

Two unique situations occur during entry of predisturbance plant coverages. If the user enters zero cover for either CEVE or EPAN, a

message is printed asking the user if there is evidence of these plants offsite. If so, the model assumes, based on response groupings, that viable propagules of these species are either on site (CEVE) or can disperse onto the site (EPAN). The predisturbance cover is then altered to reflect this potential.

After data entry, the successional pathway is determined in subroutine PATHWAY. This procedure is the most sensitive component of the model since failure to predict the correct pathway results in calculating cover from wrong regression equations. The successional pathway is assessed from predisturbance composition using a modified Arno and others (1985) classification key for each phase (Figures 8 and 9). These keys attempt to predict pathway before disturbance actually occurs.

Successional simulation commences once the pathway is established. Species cover for each simulation year is calculated in a two staged process. First major species' coverage is calculated in subroutine MAJOR in order of decreasing successional priority. Cover for remaining species is then calculated in subroutine COVER. To calculate coverage, both subroutines pass regression parameters obtained from external data files to REGRESS. This subroutine creates regression equations from seventy variables or variable transformations using the regression parameters as selection criteria. Response groups are used to decide how to model a species that does not occur on the predisturbance site. If the species is from group 1 or 2 (Appendix B), or occurs offsite and is from groups 8 or 17, its coverage is calculated via regression equations. If the species is a member of any other group, the

FIGURE 8

Successional pathway key implemented in the model for the PSME/PHMA, dry habitat type phase. The cover requirements are for predisturbance conditions. Start at the top of key and stop at the first requirement that fits.

1. CEVE greater than 5% canopy cover (cc) and treatment is
 - WF or BB at moderate to high severity 1a
 - 1a. AMAL* greater than 5% cc PATHWAY 9
 - 1b. CARU** greater than 25% cc PATHWAY 8
 - 1c. Not as above PATHWAY 7
2. AMAL greater than 5% cc 2a
 - 2a. AMAL greater than 15% cc PATHWAY 4
 - 2b. CARU greater than 25% cc PATHWAY 5
 - 2c. Not as above PATHWAY 6
3. CARU greater than 25% cc 3a
 - 3a. CARU greater than 37.5% cc PATHWAY 2
 - 3b. PHMA greater than 60.0% cc and low severity
 - treatment PATHWAY 3
 - 3c. Not as above (assumed) PATHWAY 2
4. PHMA greater than 15% cc PATHWAY 1
5. Not as above (assume depauperate) PATHWAY 1

* AMAL = AMAL + ACGL + SASC

** CARU = CARU + CAGE

FIGURE 9

Successional pathway key implemented in the model for the PSME/PHMA, moist habitat type phase. The cover requirements are for predisturbance conditions. Start at the top of key and stop at the first requirement that fits.

- 1. CEVE greater than 5% cc and treatment is WF
 or BB at moderate to high severity 1a
 - 1a. AMAL* greater than 5% cc PATHWAY 5
 - 1b. CARU** greater than 25% cc and LAOC greater
 than 5% cc PATHWAY 6
 - 1c. Not as above (assumed) PATHWAY 6
- 2. AMAL greater than 5% cc 2a
 - 2a. LAOC greater than 5% cc and moderate to high
 severity treatment PATHWAY 3
 - 2c. Not as above PATHWAY 4
- 3. LAOC greater than 5% cc and moderate to high
 severity treatment PATHWAY 2
- 4. Not as above 4a
 - 4a. PHMA greater than 15% cc PATHWAY 1
 - 4b. Not as above (assumed) PATHWAY 1

* AMAL = AMAL + ACGL + SASC

** CARU = CARU + CAGE

successional coverage is assumed to be zero. REGRESS also scans computed coverage for negative values and values over 100 percent and adjusts to zero or 100% respectively.

Subroutine REGRESS also contains equations that were not empirically developed. Data for some plant species were so poorly represented along a successional pathway that a statistically sound regression equation could not be constructed. In these cases, successional coverage estimates were based on a qualitative assessment of the limited data, or, more simply, equations were designed to represent a plant's successional trends in general terms from visual inspection of the data. Three types of variables were used to qualitatively assess cover changes as a result of disturbance, namely treatment severity, tree canopy cover, and age. Species in obligate climax (21), stoloniferous shade intolerant (20), and repent mat-forming climax (12) (Appendix B) response groups were assumed to be eliminated from the site after moderate to severe disturbances, but retained predisturbance coverage after light treatments. Species in response groups 17 and 8 were assumed to be absent from the site after 50 percent canopy closure. These assumptions were incorporated into the model in equation form by using treatment severity or canopy coverage as parameters.

Calculated species coverages for each simulation year are written to an external output file in subroutine OUTFILE. This file is accessed by subroutines which display simulation results.

The user can print results on the terminal or the line printer in two types of formats. Successional coverage can be presented in tabular

format using subroutines TABLE (for line printer) or SCREEN (for terminal). Graphic display is also available for individual species. Subroutines GRAPH (for line printer display) or DISPLAY (for terminal display) are used for this task. These two subroutines create graphs with percent cover on the Y axis and succession years on the X axis. Since succession is modeled using only cover classes, the graphs depict only trends in coverage rather than actual percent and should be interpreted as such.

Statistics associated with each pathway regression equation may be displayed to indicate the reliability of the prediction. These regression equation statistics are read from an external file in subroutine STATS and printed either on the line printer or terminal. The printed statistics are coefficient of determination (R^2), standard deviation about regression at mean Y ($S_{y.x}$), and total number of observations (n).

After the output is displayed for a particular simulation, the user has the option of implementing another disturbance on the same site. There are two ways by which an additional disturbance can be modeled. The user can model a new disturbance after the old disturbance in which case the coverage of species during the last simulation year is used as the new predisturbance plant cover. Or, the user can implement a new disturbance in place of the old disturbance and the original predisturbance coverages are used. If an additional disturbance is not modeled, the program execution ends and all output files are erased.

Model Specifications.

This computer model was programmed in FORTRAN 77 and executed on a Perkin-Elmer 1200 mini computer located at the Northern Forest Fire Laboratory, Missoula, Montana. The code can be easily transferred to the FLIPS system now available at many National Forest district offices. The program has low storage requirements (88 kilobytes) because all parameters, results, and output labels are stored externally. Twenty one subroutines, using 2100 lines of structured code, are accessed by the driver. A copy of the code is presented in the User's manual (Keane 1984). The average entry session requires approximately seven minutes at the Advanced skill level. There are currently seven external files which are accessed by the program including two temporary output files.

Parameter Estimation

A list of all regression equations with respective coefficients is presented in Appendix E. For each equation, the following statistics are also listed: coefficient of determination (R^2), standard deviation about regression ($S_{y.x}$), and the total number of observations (n). Of the possible 603 regression equations (312 regression equations for the dry phase and 213 for the moist phase of the PSME/PHMA habitat type), 78 are qualitative estimates. The R^2 values range from 0.44 to 0.99 with standard deviation about regression from 0.010 to 18.000. This large variation associated with these statistics is a direct consequence of poor data representation in some of the less sampled pathways.

Simulation Runs

Outputs of a simulation run are presented in Appendixes F and G. Information printed for the user includes a description of the site, the keyed successional pathway, and the predicted coverage (in cover classes) for each species by simulation year (Appendix F). Graphic output (Appendix G) displays plots of species percent cover on the Y axis versus stand age on the X axis. Statistics associated with the user-specified species regression equations are also printed to indicated reliability of the predicted coverages. All outputs may be printed on the terminal or line printer.

Model Validation

The validation data for the undisturbed stands were used as model inputs and the simulation predictions were then compared with the actual cover estimated on the adjacent, disturbed stand. The model averaged 63% accuracy in predicting cover class for all species, with dry phase simulations more accurate than moist phase simulation results (Table 5) probably due to the more extensive data base for the dry phase. Tree species proved to be the most difficult to model (55% accurate) when compared with the undergrowth (65% accurate). The PSME-CARU and CEVE pathways had the highest predictive ability (63% and 67% respectively), but this may be due to low validation sampling frequency in the remainder of the pathways (Table 6). Accuracy by treatment type is presented in Table 7. Species cover is best predicted on the mechanically scarified stands (65%), but treatment type accuracy is difficult to compare due to frequent sampling for this disturbance.

TABLE 5
Results of model validation by habitat type phase.

Phase	Percent correct (%)		Number of plots
	Range	Average	
Dry	45-74	65	13
Moist	45-74	59	7
Total	45-74	63	20

TABLE 6
Results of model validation by successional pathway.

Pathway	Percent correct (%)		Number of plots
	Range	Average	
PHMA	45-45	45	1
PHMA-CARU	50-74	63	11
AMAL-PHMA	45-74	64	5
CEVE-PHMA	60-71	67	3

TABLE 7
Results of model validation by treatment type.

Treatment	Percent correct (%)		Number of plots
	Range	Average	
WF	not sampled		0
BB	50-71	62	8
MS	45-74	64	10
NP	54-64	59	2

In addition to comparing species cover, predicted successional pathways were compared with observed pathways to test pathway key reliability. The model determined the correct successional pathway in all 20 cases.

A common procedure for evaluating the accuracy of a model is to regress predicted values as dependent variables with observed values as independent variables and statistically test for a slope of 1.000 and a y-intercept of zero. The slopes for this model were 0.79 for the moist phase and 0.88 for the dry phase of the PSME/PHMA habitat type. However, statistical tests on the slopes (t value) show that they both were not significantly different from 1.0 with alpha or level of significance equals 0.05 (null hypothesis: $\beta = 1.0$, alternative hypothesis: β not equal to 1.0). Y-intercept values for the phases are 1.28 (moist) and 0.78 (dry) with both these values not significantly different from zero. The results of the validation regression analyses show the model is over-estimating cover in the lower cover classes and underestimating cover in the higher cover classes. These results were used to refine the model after validation analysis was completed.

CHAPTER 6

DISCUSSION

Model Structure

The program was designed to easily accept additional habitat types. However, because ecological relationships between habitat types are not identical, new transformations, different major species, and other pathway keys will be required when new habitat types are added in the future. A procedure for implementing habitat types into the model is presented in the User's Manual (Keane 1984).

Parameter Estimation

The regression coefficients were estimated according to species response groups. Equation parameters for species regenerating vegetatively (response groups 4 thru 6, 9 thru 16, and 18 thru 24) were estimated using only plots in which the species was present. This assumes that species which are not present before treatment will never become established after treatment, and conversely, species which are represented in the predisturbance stand will never be eliminated from the site. However, a species could possibly be eliminated from the site as a result of a severe treatment, particularly if the species is in response groups 12, 18, 20, 21, or 23. In these cases, all plots were used in regression equation construction, but only if the pathway was a result of a severe treatment as described by Arno and others (1985).

Regression analyses for species in groups 1, 2, 7, 8, and 17 had every plot added to the regression data base because it was assumed these species could potentially become established on the site regardless of predisturbance cover.

The use of predisturbance cover as an independent variable was also governed by response group. Regression analyses for groups 1, 2, 7, 8, and 17 never integrated predisturbance cover as an independent variable in the equations because these species either did not occur in mature, closed-canopy stands or their method of revegetation was not dictated by surviving members. Equations for species in the remaining response groups employed predisturbance cover as an independent variable whenever it was statistically significant.

Predisturbance cover proved invaluable as an independent variable. This confirms concepts presented in past studies which describe succession in terms of the predisturbance composition (Lyon and Stickney 1974, Stickney 1983, Steele 1984). Moreover, magnitudes of the predisturbance cover coefficients, approximately 1.0 or slightly less (Appendix E), indicate postdisturbance cover will be as much as predisturbance cover or slightly less depending on severity of treatment. Predisturbance coefficients associated with the equations used to predict SASC cover were sometimes greater than 1.0 indicating a gain in coverage as a result of disturbance. This gain could be explained as expansion via seed, but is more likely due to aggressive sprouting from severely suppressed plants. Unfortunately, predisturbance cover was rarely used as a predictor in the moist phase equations because few multiple-stand sites were sampled by Arno and

others (1985). Future modeling efforts should sample mature stands adjacent to disturbed communities so predisturbance cover can be incorporated into regression equations.

In some instances, regression equations only explained data characteristics rather than describe successional tendencies. This was a consequence of inadequate pathway plot representation coupled with high species cover variability between sites. This situation was especially prevalent in the PSME/PHMA, moist phase. Some successional pathways were poorly represented because they were rarely observed in natural situations. For example, the dry phase PHMA pathway (Pathway 1 in Figure 4) had inadequate plot representation because silvicultural and natural disturbances seldom create proper conditions for development of this pathway. Data in these poorly represented pathways were often combined with data from similar pathways to more adequately explain variation in successional communities. For instance, dry phase Pathway 9 (Figure 4) did not have enough observations for some species to adequately build reliable regression equations, so parameters were estimated using additional data from Pathways 7 and 8. These pathways are similar in that all are CEVE dominated during early seral stages.

Certain age groups are absent in the data base for similar reasons. Disturbed stands between the ages of 35 to 64 years are uncommon in western Montana because of fire suppression policies and the fact that early logging activities were usually partial cuttings rather than clearcuts. This limited age distribution in the data base could explain underestimations in species cover predictions.

Even in mature stands, plant species cover can vary greatly between sites of the same habitat type phase. Past disturbance histories such as underburning and thinning, and subsequent seed germination success rates are factors which might explain cover variations. For example, frequent surface fires might enhance seed germination of an otherwise sprouting plant eventually resulting in increases in cover. Another site, similar in physical site climatic characteristics, but experiencing little understory burning might have comparatively less cover for the same species because of the absence of reproduction by seed. The model cannot account for these differences in stand histories because light surface treatments were not incorporated into the regression equations. As a result, there is inherent variability in the coverage data due to these and other unknown factors and this variability strongly affects regression equation form and precision. Initial regression analyses produced equations containing transformations which apparently made no sense ecologically but explained the greatest proportion of variation. In such instances, equations were reformulated so that only transformations which reflected known successional processes were used. Unfortunately, standard deviations about regression usually increased as a result of this reformulation, as would be expected.

The error of the cover estimate is often compounded when predictions are used as independent variables in the regression equations. Since major species cover predictions are commonly used as independent variables in minor species cover equations, additional variation is bound to be introduced. Yet, the compounded error of the

minor species cover estimate is hopefully absorbed in the conversion of cover percent to cover class.

Validation and Refinement

This "brute force" validation procedure (described by Shugart and West 1980) is limited in scope because site and vegetation conditions are not constant between disturbance and untreated stands. A mosaic of species cover between stands on the same site influences the reliability of the model predictions. Differences in microsite and dispersal patterns are factors affecting the spatial distribution of species cover. The model can not handle a vegetatively regenerating species which is present in the disturbance stand but not in the adjacent control or mature stand (Assumption 1 in Methods). This situation was often evident in the validation data. If these cases are eliminated from validation data base, accuracy increases by 3% to 5%.

An important ecological measure of model validity is the magnitude of difference between predicted coverage values and observe values. It makes little difference ecologically if a species occurs at a trace (0.1% to 1% coverage) or cover class one (1% to 5% coverage), unless of course the species is rare or endangered which is not the case in this model. If these two classes are combined and validation data again analyzed, the average accuracy increases to 85% correct.

An important result of the validation process was the inability of the model to predict tree species cover reliability. This was probably due to the establishment of trees from a seed source in or adjacent to the disturbed area. The amount of seed (seed crop) and subsequent

dispersal is dictated by highly variable weather conditions. The stochastic nature of these weather variables makes it extremely difficult to model tree establishment deterministically. Regression equations only predict average species cover regardless of current or past weather influences. Therefore, coverage predictions for individual tree species should be interpreted as averages.

CHAPTER 7

CONCLUSIONS

Empirical models do have their limitations. Regression equations do not indicate cause and effect relationships, therefore, changes in species cover are modeled as "black boxes" which produce desired outputs but give no insights as to why these changes occur. Basic successional processes such as nutrient allocation, microclimate alteration, and competition are not addressed in this empirical model. On the other hand, mechanistic models which simulate these basic processes rarely produce outputs that can be used in resource management because dependent variables are not of the form useful in management planning. Future modeling efforts should bridge the gap between the empirical and mechanistic designs to produce management-oriented succession models which are founded on fundamental ecological interactions.

Model Improvement

The data base for the model could be improved by sampling successional communities along the infrequently observed pathways at the same intensity as the other pathways. Although these communities are less common in west-central Montana, they must be adequately represented so that statistically reliable regression equations can be built. A more evenaged plot distribution is also needed to accurately describe shifts in species coverages.

Additional pathways within a habitat type phase could improve model accuracy. Successional variation in species cover could be more accurately assessed by the inclusion of more successional pathways stratified by new community types. However, a larger data base will be required to properly represent each of the new pathways.

An alternative modeling design is to simulate successional changes by response groups rather than by species. If collective cover of a species within response groups could be used as the dependent variable, perhaps the high variability between plots could be decrease. Of course, this assumes species within response groups occupy approximately the same ecological niche. Another modeling approach involves the use of factor analysis on the dependent variables. Since data is collected in discrete categories (cover classes), is converted to percent for analysis, and then reconverted back to categories, it might prove beneficial to use Factor analysis on the cover classes categories to more accurately predict successional compositions.

Implications

This model can be used for any phase of management planning where the major emphasis is on the vegetation component. Wildlife managers might need to assess the effect of two alternative treatments on the cover of a major browse species. Timber specialists could determine the natural regeneration success of LAOC after two types of cuttings. Recreation planners might wish to evaluate the consequence of clearcutting with respect to visual quality. The outputs of this model could be used as an evaluation tool for each of these concerns.

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APPENDIXES

APPENDIX A

List of the species which were modeled.

APPENDIX A

List of the most frequently occurring or the most dominant plant species on the PSME/PHMA habitat type. Also included is the common name and the four letter abbreviation for that species.

TREES

Larix occidentalis
(western larch)
Diameter classes:
WL<4-less than 4 " dbh
WL>4-greater than 4" dbh
WLAL-total cover all dbh

Pseudotsuga menziesii
(Douglas-fir)
Diameter classes:
DF<4-less than 4" dbh
DF>4-greater than 4" dbh
DFAL-total cover all classes

SHRUBS

Acer glabrum - ACGL
(mountain maple)

Amelanchier alnifolia - AMAL
(serviceberry)

Ceanothus velutinus - CEVE
(snowbush)

Lonicera utahensis - LOUT
(Utah honeysuckle)

Physocarpus malvaceus - PHMA
(ninebark)

Prunus virginiana - PRVI
(chokecherry)

Rosa gymnocarpa - ROGY
(rose)

Salix scouleriana - SASC
(Scouler's willow)

Spiraea betulifolia - SPBE
(spiraea)

Symphoricarpos albus - SYAL
(snowberry)

Vaccinium globulare - VAGL
(blue huckleberry)

GRASSES

Agropyron spicatum - AGSP
(Bluebunch wheatgrass)

Calamagrostis rubescens
(pinegrass) - CARU

Carex concinnoides - CACO
(northwest sedge)

Carex geyeri - CAGE
(elk sedge)

Carex rossii - CARO
(Ross's sedge)

FORBS

Achillea millefolium - ACMI
(yarrow)

Antennaria racemosa - ANRA
(woods pussytoes)

Arnica cordifolia - ARCO
(Heart-leaved arnica)

Aster conspicuus - ASCO
(showy aster)

Balsamorhiza sagittata-BASA
(arrowleaf balsamroot)

Chimaphilla umbellata -CHUM
(prince's pine)

Epilobium angustifolium-EPAN
(fireweed)

Fragaria vesca - FRVE
(strawberry)

Fragaria virginiana - FRVI
(Virginia strawberry)

Goodyera oblongifolia -GOOB
(rattlesnake plantain)

Hieracium albertinum and
albeflorium (hawkweed)-HIAL

APPENDIX A (con't)

List of the most frequently occurring or the most dominant plant species on the PSME/PHMA habitat type.

SUBSHRUBS

Arctostaphylos uva-ursi - ARUV
 (kinnickinnic)
 Berberis repens - BERE
 (creeping Oregon grape)
 Linnaea borealis - LIBO
 (twinflor)

FORBS (con't)

Mitella stauropetala -MIST
 (starry mitrewort)
 Thalictrum occidentale
 (meadowrue) - THOC
 Xerophyllum tenax - XETE
 (beargrass)

APPENDIX B
Species Response Groupings

APPENDIX B

Species Response Groupings for the 33 species in the PSME/PHMA habitat type.

TREES

Group 1 - Shade tolerant (climax)
Pseudotsuga menziesii

Group 2 - Shade intolerant (seral)
Larix occidentalis Pinus ponderosa*

Group 3 - Serotinous seral
Pinus contorta*

SHRUBS

Group 4 - Root-crown sprouting seral
Prunus virginiana Salix scouleriana**

Group 5 - Root-crown sprouting climax
Lonicera utahensis Rosa gymnocarpa

Group 6 - Root-crown sprouting meso-seral
Acer glabrum Amelanchier alnifolia

Group 7 - Light-seed producing seral
Salix scouleriana**

Group 8 - Soil dormant seed producing seral
Ceanothus velutinus

Group 9 - Rhizomatous climax
Vaccinium globulare Symphoricarpos albus
Spiraea betulifolia

Group 10 - Rhizomatous meso-seral
Rubus parvifolia

Group 11 - Root-crown sprouting and rhizomatous climax
Physocarpus malvaceus

APPENDIX B (con't)

Species Response Groupings for the 33 species in the PSME/PHMA habitat type.

SUBSHRUBS

Group 12 - Repent mat-forming climax
Arctostaphylos uva-ursi Linnaea borealis

Group 13 - Rhizomatous climax
Berberis repens

GRASSES

Group 14 - Mat-forming rhizomatous climax
Calamagrostis rubescens

Group 15 - Tufted rhizomatous climax
Carex concinnoides Carex geyeri

Group 16 - Tussocked or bunched climax
Agropyron spicatum Carex rossii

FORBS

Group 17 - Widely-dispersed, light seed producing seral
Epilobium angustifolium

Group 18 - Locally dispersed light seed producing seral
Achillea millefolium** Hieracium albertinum

Group 19 - Rhizomatous climax
Arnica cordifolia Antennaria racemosa

Group 20 - Stoloniferous seral
Fragaria vesca Fragaria virginiana

Group 21 - Obligate climax
Chimaphilla umbellata Goodyera oblongifolia

APPENDIX B (con't)

Species Response Groupings for the 33 species in the PSME/PHMA habitat type.

FORBS (con't)

Group 22 - Rhizomatous seral

Thalictrum occidentale Mitella stauropetala

Group 23 - Caudex perenniating seral

Balsamorhiza sagittata Achillea millefolium

Group 24 - Stout rhizome climax

Xerophyllum tenax

* Species was not modeled but used to create a response group to facilitate addition of new habitat types.

** Species demonstrates dual revegetation mechanisms

APPENDIX C

Transformations and Interactions used in Regression analyses

APPENDIX C

Transformations used in the regression analysis for model construction.

TRANSFORMATIONS

VARIABLES	
Elevation (feet)	PHMA (%)
Aspect (degrees)	CARU (%)
Slope (percent)	CEVE (%)
Severity type (categorical)	AMAL+ACGL+SASC (%)
Treatment type (categorical)	(CAGE+CARU) (%)
Age (years)	DBH (inches)
Tree canopy cover (CC) (percent)	
Predisturbance coverage (percent)	

SINGLE VARIABLE TRANSFORMATIONS

(Agemax - Age)**5.0	CC**2
(Agemax - Age)**3.0	Age**2
(Agemax - Age)**(0.15)	Age**3
Age / (1.0 + Age**2)	1 / Age
1 / CC	

INTERACTIONS

Elevation / Aspect	CC / Age
Slope / Aspect	CC**2 / Age**2

POWER TRANSFORMATIONS

Age**(0.15)	Age**(-0.20)
Age**(0.40)	Age**(-0.30)
Age**(0.35)	Age**(-0.40)
Age**(0.65)	Age**(0.50)
Age**(0.10)	Age**(-1.50)
Age**(0.25)	Age**(-2.00)
CC**(0.40)	CC**(0.30)
CC**(-0.01)	CC**(0.25)
CC**(-0.20)	CC**(-1.50)
CC**(-2.00)	CC**(-0.40)
CC**(-0.60)	CC**(0.15)

APPENDIX C (con't)

Transformations used in the regression analysis for model construction.

TRANSFORMATION

SIGMOID TRANSFORMATIONS

$\text{EXP}((1.0 - \text{Age}/\text{Agemax})/0.7)**5.0)$
 $\text{EXP}((1.0 - \text{Age}/\text{Agemax})/0.6)**6.0)$
 $\text{EXP}((1.0 - \text{Age}/\text{Agemax})/0.9)**8.0)$
 $\text{EXP}((1.0 - \text{Age}/\text{Agemax})/0.7)**8.0)$
 $\text{EXP}((1.0 - \text{Age}/\text{Agemax})/0.8)**8.0)$
 $\text{EXP}((1.0 - \text{Age}/\text{Agemax})/0.8)**9.0)$
 $\text{EXP}((1.0 - \text{Age}/\text{Agemax})/0.8)**10.0)$
 $\text{EXP}((1.0 - \text{Age}/\text{Agemax})/0.6)**4.0)$
 $\text{EXP}((1.0 - \text{Age}/\text{Agemax})/0.9)**10.0)$
 $\text{EXP}((1.0 - \text{CC}/\text{CCmax})/0.8)**5.0)$
 $\text{EXP}((1.0 - \text{CC}/\text{CCmax})/0.6)**6.0)$
 $\text{EXP}((1.0 - \text{CC}/\text{CCmax})/0.8)**10.0)$
 $\text{EXP}((1.0 - \text{CC}/\text{CCmax})/0.7)**8.0)$
 $\text{EXP}((1.0 - \text{CC}/\text{CCmax})/0.9)**8.0)$
 $\text{EXP}((1.0 - \text{CC}/\text{CCmax})/0.7)**5.0)$
 $\text{EXP}((1.0 - \text{CC}/\text{CCmax})/0.7)**8.0)$
 $\text{EXP}((1.0 - \text{CC}/\text{CCmax})/0.8)**9.0)$
 $\text{EXP}((1.0 - \text{CC}/\text{CCmax})/0.6)**4.0)$

APPENDIX D

Sample Interactive Data Entry Session.

FOREST Succession Model

This is a computer model which predicts the coverages of major plant species existing on a habitat type over time.

Do you wish further information on the operation of this model?
Please answer Y (yes) or N (no):
>Y

This computer model reads input information given by the user and utilizes the input information in a number of multiple regression equations. These regression equations predict the coverages of the major species in a habitat type phase over a user-specified time span. The successional simulation starts on the fifth year after the stand renewing disturbance.

The user will be asked a variety of questions pertaining to:
1. The site to be modeled.
2. The time period and interval to model.
3. The post-disturbance coverages of the major plant species.
4. The types of outputs to be generated.

It is important that the user input only one value per prompt (question) and end the entry with a carriage return. If there are any questions concerning the data entry procedures, please consult the USER'S GUIDE before proceeding.

DATA ENTRY PROCEDURE

Please enter a title for your simulation run:

The title cannot exceed 60 characters and should describe the unique aspects of this simulation. (ex: BIG FORK CREEK TIMBER UNIT PSRE/PHMA,DRY)
>DEMO RUN PSRE/PHMA, DRY BOB KEANE

Please enter the number corresponding to the habitat type phase which you wish to model. If you desire more information on which habitat type phase your land area keys to, please consult the publication "FOREST SUCCESSION ON FOUR HABITAT TYPES IN WESTERN MONTANA" to obtain the necessary information.

The phases implemented in this model are:
1 - PSRE/PHMA,DRY
2 - PSRE/PHMA,MOIST
4 - ABLA/XETE,VACL
5 - ABLA/XETE,VASC

Please enter the habitat type phase number:
(ex: An entry of "2" would cause the model to simulate succession on the PSRE/PHMA,MOIST habitat type phase.)
>1

THE INPUT OF SITE VARIABLES

Please enter the elevation of the disturbance site in feet:
(ex:4500)
>4800

Enter the aspect of the site in degrees:
(ex:135 - this would be a northerly aspect)
>160

Please enter the slope in percent: (ex:45)
>45

INPUT OF PRE-DISTURBANCE VEGETATION COVERAGE

You will now be presented with the latin name for each of the major species occurring on this habitat type phase. After the name, please enter the coverage (cover class or percent) for that plant species.
(ex:Acer glabrum)45)

There are two ways to enter pre-disturbance coverages. you can enter coverage classes or the actual percent of canopy coverage.

Do you wish to enter cover classes? (Please enter "Y" (yes) or "N" (no))
>Y

The cover classes implemented in this model are:

- 0 - zero or no canopy coverage
- 1 - trace or 0.1 to 1.0 % can. cov.
- 2 - 1.0 to 5.0 % can. cov.
- 3 - 5.0 to 25.0 % can. cov.
- 4 - 25.0 to 50.0 % can. cov.
- 5 - 50.0 to 75.0 % can. cov.
- 6 - 75.0 to 95.0 % can. cov.
- 7 - 95.0 to 100.0 % can. cov.

Please use only these values for canopy coverage codes.

Enter the coverage for all tree species (CCAL):
>4

Enter the average Diameter at breast height (DBH), in inches, for all trees in the stand:
>13

Enter the average Basal Area of the stand in square feet per acre:
>130

Enter the coverage for Douglas-fir less than 4 inches DBH (DF<4):
>1

Enter the coverage for Douglas-fir greater than 4 inches DBH (DF>4):
>4

Enter the coverage for all Douglas-fir (DFAL):
>4

Enter the coverage for Acer glabrum (ACGL) or mountain maple:
>1

Enter the coverage for Amelanchier alnifolia (AMAL) or serviceberry:
>1

presence of seed creating the potential for a CEVO CUT. With no visible evidence of Ceanothus on the site. However, presence of Ceanothus seed on site can usually be determined by two means. First, are there Ceanothus plants on the most disturbed portions of the stand (road cuts or fills, skid roads, etc). And second, are there many consecutive Ceanothus plants in the stand which do not constitute great coverage? If the answer is yes to either one of these questions please enter "Y", otherwise enter "N" ...

Enter the coverage for Lonicera utahensis (LOUT) or Utah honeysuckle:
>0

Enter the coverage for Physocarpus malvaceus (PHMA) or ninebark:
>1

Enter the coverage for Prunus virginiana (PRVI) or chokecherry:
>0

Enter the coverage for Rosa gymnocarpa (ROGY) or wild rose:
>1

Enter the coverage for Salix scouleriana (SASC) or Scouler's willow:
>1

Enter the coverage for Spiraea betulifolia (SPBE) or white spiraea:
>2

Enter the coverage for Symphoricarpos albus (SYAL) or snowberry:
>1

Enter the coverage for Vaccinium globulare (VAGL) or blue huckleberry:
>0

Enter the coverage for Arctostaphylos uva-ursi (ARUU) or kinnikinnick:
>0

Enter the coverage for Berberis repens (BERE) or creeping Oregon grape:
>1

Enter the coverage for Linnaea borealis (LIBD) or twinflower:
>0

Enter the coverage for Agropyron spicatum (ACSP) or bluebunch wheatgrass:
>1

Enter the coverage for Calamagrostis rubescens (CARU) or pinegrass:
>2

Enter the coverage for Carex concinnaoides (CACD) or northwestern sedge:
>0

Enter the coverage for Carex geyeri (CAGE) or elk sedge:
>2

Enter the coverage for Carex rossii (CARO) or Ross sedge:
>0

Enter the coverage for Achillea millefolium (ACMI) or yarrow:
>1

Enter the coverage for Antennaria racemosa (ANRA) or wood's pussytoes:
>1

Enter the coverage for Arnica cordifolia (ARCO) or heartleafed arnica:
>1

Enter the coverage for Aster conspicuus (ASCO) or showy aster:
>0

Enter the coverage for Balsamorhiza sagittata (BASA) or arrowleaf balsamroot:
>1

Enter the coverage for Chinaphila umbellata (CHUM) or pipsissewa:
>1

Enter the coverage for Epilobium angustifolium (EPAN) or fireweed:
>0

Fireweed (EPAN) has the potential to disperse many light seeds over wide ranges. Is there evidence of Fireweed in areas that are off-site?
Please enter yes (Y) or no (N)...

>1

Enter the coverage for Fragaria vesca (FRUE) or strawberry:
>1

Enter the coverage for Fragaria virginiana (FRVI) or Virginia strawberry:
>0

Enter the coverage for Geodyera oblongifolia (GDDB) or rattlesnake plantain:
>0

Enter the coverage for Hieracium spp. (HIAL) or hawkweed:
>1

Enter the coverage for Mitella stauropetala (MIST) or starry Mitrewort:
>1

Enter the coverage for Thalictrum occidentale (THOC) or western meadowrue:
>1

Enter the coverage for Xerophyllum tenax (XETE) or beargrass:
>0

THIS IS THE END OF THE PRE-DISTURBANCE VEGETATION COMPOSITION ENTRY PROCEDURE

INPUT OF MANAGEMENT VARIABLES

Please enter the number corresponding to the treatment type which will be implemented on the disturbance site. The treatment types and their respective numbers are:

- 1 - WILDFIRE
- 2 - BROADCAST BURN
- 3 - MECHANICAL SCARIFICATION (includes pile and burn)
- 4 - NO SITE PREPARATION

Please enter the treatment type number: (ex: an entry of 2 would result in modeling a broadcast burn treatment disturbance)

>1

Please enter the number corresponding to the intensity or severity type of the treatment. The severity types with their respective numbers are:

- 1 - LIGHT OR LOW SEVERITY
- 2 - MODERATE SEVERITY
- 3 - HIGH OR HGT SEVERITY

Please enter the severity type number: (ex: an entry of 2 results in the modeling of a moderately severe treatment)
>2

INPUT OF THE TIME CONSTRAINTS

You will be asked to enter two time variables to model succession. The first time variable is the total amount of time (in years) you wish to model. The second time factor is the time increment at which you wish to examine the successional coverages. For example, if you wished to model a disturbance site from year 5 to year 200 (after disturbance) and you want to look at the species coverages every 10 years, simply enter 200 after the first prompt and 10 after the second. There is, however, one rule which you must remember: the model can only handle 50 time intervals. This means that the time span (in this example 200) divided by the time interval (10) must not be greater than 50 (in this case 200/10 = 20).

Please enter the time span which you wish to model succession. (ex: an entry of 200 would result in the prediction of the major species coverages up to the 200th year after disturbance)
>200

Please enter the time interval at which you wish to view succession. (ex: an entry of 20 would allow you to examine the coverages of the major plant species every 20 years up to the maximum year you specified above)
>25

Would you like to see the results of your successional simulation in tabular form? (Please enter "Y" (yes) or "N" (no))
>N

**** ERROR ****

A " Y " or a " N " was not entered. Please try again ...

Would you like to see the results of your successional simulation in tabular form? (Please enter "Y" (yes) or "N" (no))
>Y

Would you like response graphs for the major species?
(Please enter "Y" (yes) or "N" (no))
>Y

SUMMARY OF THE DATA INPUT SESSION

- THE FOLLOWING ARE THE VALUES WHICH WERE ENTERED:
- (1) ELEV (FT)= 4800.
 - (2) ASPECT (DEG)= 160.
 - (3) SLOPE (%)= 45.
 - (4) TREATMENT TYPE (1-WF, 2-BB, 3-HS, 4-NP) = 1
 - (5) INTENSITY TYPE (1-LOW, 2-MOD, 3-HIGH) = 2
 - (6) TIME SPAN TO MODEL = 200 YRS
 - (7) TIME INTERVAL = 25 YRS
 - (8) TABLE FORMAT (0-NO, 1-YES) = 1
 - (9) GRAPH GENERATION (0-NO, 1-YES) = 1

If you wish to change any of the input values, please enter the number (in parenthesis) next to the input value which you wish to change. If you are satisfied with the entries, enter zero (0) to continue. (ex: if you wish to change the elevation value, enter the number 1)
>0

PREDISTURBANCE PLANT SPECIES COVERAGES

THESE VALUES ARE PERCENT COVERAGE EXCEPT DBH & BA:

- NOTE: The midpoints of the cover classes will be presented.
- (1) CCAL) 62.5 (2) DBH) 13.0 (3) BA) 130. (4) DF(4) 3.0
 - (5) DF(4) 62.5 (6) DFAL) 62.5 (7) ACGL) 3.0 (8) AMAL) 3.0
 - (9) CEVE) 0.0 (10) LOUI) 0.0 (11) PHMA) 0.5 (12) PRVI) 0.0
 - (13) ROGY) 0.5 (14) SASC) 0.5 (15) SPBE) 15.0 (16) SYAL) 3.0
 - (17) VAGL) 0.0 (18) ARUV) 0.0 (19) BERE) 3.0 (20) LIRO) 0.0
 - (21) AGSP) 0.5 (22) CARU) 15.0 (23) CACO) 0.0 (24) CALF) 15.0
 - (25) CARO) 0.0 (26) ACMI) 0.5 (27) ANRA) 0.5 (28) ARCO) 0.5
 - (29) ASCU) 0.0 (30) BASA) 0.5 (31) CHUM) 0.5 (32) EPAN) 5.0
 - (33) FRVE) 0.5 (34) FRVI) 0.0 (35) GOOD) 0.0 (36) HIAL) 0.5
 - (37) MIST) 0.5 (38) THOC) 0.5 (39) XETE) 0.0 (40)) 0.0

If you wish to change any of the pre-disturbance coverages, please enter the number (in parenthesis) next to the plant name whose coverage you wish to alter. If no corrections are necessary, enter zero (0). (Ex: to change the total coverage of all tree species (CCAL), enter the number 1)
>11

Enter the coverage for Physocarpus malvaceus (PHMA) or ninebark:
>4

PREDISTURBANCE PLANT SPECIES COVERAGES

THESE VALUES ARE PERCENT COVERAGE EXCEPT DBH & BA:

- NOTE: The midpoints of the cover classes will be presented.
- (1) CCAL) 62.5 (2) DBH) 13.0 (3) BA) 130. (4) DF(4) 3.0
 - (5) DF(4) 62.5 (6) DFAL) 62.5 (7) ACGL) 3.0 (8) AMAL) 3.0
 - (9) CEVE) 0.0 (10) LOUI) 0.0 (11) PHMA) 62.5 (12) PRVI) 0.0
 - (13) ROGY) 0.5 (14) SASC) 0.5 (15) SPBE) 15.0 (16) SYAL) 3.0
 - (17) VAGL) 0.0 (18) ARUV) 0.0 (19) BERE) 3.0 (20) LIRO) 0.0
 - (21) AGSP) 0.5 (22) CARU) 15.0 (23) CACO) 0.0 (24) CALF) 15.0
 - (25) CARO) 0.0 (26) ACMI) 0.5 (27) ANRA) 0.5 (28) ARCO) 0.5
 - (29) ASCU) 0.0 (30) BASA) 0.5 (31) CHUM) 0.5 (32) EPAN) 5.0
 - (33) FRVE) 0.5 (34) FRVI) 0.0 (35) GOOD) 0.0 (36) HIAL) 0.5
 - (37) MIST) 0.5 (38) THOC) 0.5 (39) XETE) 0.0 (40)) 0.0

If you wish to change any of the pre-disturbance coverages, please enter the number (in parenthesis) next to the plant name whose coverage you wish to alter. If no corrections are necessary, enter zero (0). (Ex: to change the total coverage of all tree species (CCAL), enter the number 1)
)0

You have the option of either printing the output on this terminal or on the line printer. Do you wish to view the output on this terminal? Please answer yes (Y) or no (N).
)Y

DATA INPUT SESSION NOW CONCLUDED... SIMULATION WILL COMMENCE.

CURRENTLY SIMULATING YEAR 25.
 CURRENTLY SIMULATING YEAR 50.
 CURRENTLY SIMULATING YEAR 75.
 CURRENTLY SIMULATING YEAR 100.
 CURRENTLY SIMULATING YEAR 125.
 CURRENTLY SIMULATING YEAR 150.
 CURRENTLY SIMULATING YEAR 175.
 CURRENTLY SIMULATING YEAR 200.

 TITLE :DEMO RUN PSME/PHMA, DRY ROB KEANE

DESCRIPTION OF THE SIMULATION AREA:
 ELEVATION : 4800. FEET TREATMENT TYPE : WILDFIRE
 ASPECT : 160. DEGREES INTENSITY TYPE : MODERATE
 SLOPE : 45. (DEGREES) HABITAT TYPE PHASE : PSME/PHMA, DRY

SUCCESSIONAL PATHWAY DIAGRAM:
 AMAL-PHMA -----> PSME/AMAL-PHMA ----->
 PSME/AMAL-PHMA -----> PSME/PHMA-CARU ----->
 PSME/PHMA-CARU

Press "C" to continue the display of output
)C

Spp name	SPECIES COVERAGE (CLASSES) AT VARIOUS AGES (YEARS)							
	25	50	75	100	125	150	175	200
CCAL	3	4	4	4	4	4	4	4
DBH	2	5	8	11	13	14	15	16
BA	22	67	105	136	159	177	196	199
DF(4	0	0	0	0	0	0	0	0
DF(4	2	3	3	3	3	4	4	4
DFAL	3	4	4	4	4	4	4	4
ACGL	2	2	2	2	2	2	2	2
AMAL	3	3	3	3	3	3	3	3
CEVE	0	0	0	0	0	0	0	0
LOUT	0	0	0	0	0	0	0	0
PHMA	4	4	3	3	3	3	3	3
PRUI	0	0	0	0	0	0	0	0
ROCY	T	T	T	T	T	T	T	T
SASC	T	T	T	T	T	T	T	T
SPRE	3	3	3	3	3	3	3	3
SYAL	1	1	1	1	1	1	1	1
VAGL	0	0	0	0	0	0	0	0

Press "C" to continue the display of output
)C

Spp name	SPECIES COVERAGE (CLASSES) AT VARIOUS AGES (YEARS)							
	25	50	75	100	125	150	175	200
ARUV	0	0	0	0	0	0	0	0
BERE	T	T	T	T	T	T	T	T
LIBO	0	0	0	0	0	0	0	0
AUSP	0	0	0	0	0	0	0	0
CARU	2	2	2	2	2	2	2	2
CACO	0	0	0	0	0	0	0	0
CAGE	2	2	2	2	-	-	-	-
CARO	0	0	0	0	0	0	0	0
ACMI	T	T	T	T	T	T	T	T
ANRA	0	0	0	0	0	0	0	0
ARCO	0	0	0	0	0	0	0	0
ASCO	0	0	0	0	0	0	0	0
BRSA	T	T	T	T	T	T	T	T
CHUM	T	T	T	T	T	T	T	T
EPAN	T	0	0	0	0	0	0	0
FRUE	1	T	0	0	0	0	0	0
FRUI	0	0	0	0	0	0	0	0

Press "C" to continue the display of output
)C

Spp name	SPECIES COVERAGE (CLASSES) AT VARIOUS AGES (YEARS)							
	25	50	75	100	125	150	175	200
GOOR	0	0	0	0	0	0	0	0
HIAL	T	T	T	T	T	T	T	T
HIST	T	T	T	T	T	T	T	T
THOC	T	T	T	T	T	T	T	T
XETE	0	0	0	0	0	0	0	0

Press "C" to continue the display of output
)C

APPENDIX E

List of the Pathway Regression Equations.

This appendix is composed of many tables containing regression equations stratified by pathway for each species. Each variable in the equations has been assigned a four-letter abbreviation to condense the format. A key to the abbreviations is presented at the beginning of the appendix. The appendix is also stratified by the two phases; PSME/PHMA, dry and PSME/PHMA, moist. Equations that were formed qualitatively (not from regression analyses) have zero values for the coefficient of determination (R^2), number of observations (N), and standard deviation about regression (STD DEV).

ABBREVIATION KEY FOR TRANSFORMATIONS

ABBREVIATION	TRANSFORMATION FORM
ELEV	ELEVATION / 100.0
ASPT	ASPECT
SLOP	SLOPE
SVRT	SEVERITY
TRMT	TREATMENT TYPE
AGE1	AGE
TREE	TREE CANOPY COVER(CC)
CCP1	CC**2.0 / 100.0
AGE2	AGE**2.0 / 100.0
AGE3	AGE**3.0 / 100000.0
PHMA	PHMA
CARU	CARU
CEVE	CEVE
SHRB	(AMAL + ACGL + SASC)
GRSS	(CARU + CAGE)
CCA6	CC / AGE
CCA2	CC**(2.0) / AGE**(2.0)
AGE4	AGE**(0.15)
AGE5	AGE**(-0.01)
AGE6	AGE**(0.40)
EXP1	EXP(((1.0-AGE/AGEMAX)/0.7)**(5.0))
EXP2	EXP(((1.0-AGE/AGEMAX)/0.6)**(6))/10000
EXP3	EXP(((1.0 - AGE/AGEMAX)/0.9)**(8.0))
EXP4	EXP(((1.0-AGE/AGEMAX)/0.7)**(8))/10E06
EXP5	EXP(((1.0 - AGE/AGEMAX)/0.8)**(8.0))
EXP6	EXP(((1.0 - AGE/AGEMAX)/0.8)**(9.0))
EXP7	EXP(((1.0-AGE/AGEMAX)/0.8)**(10))/1000
AGE7	AGE**(0.35)
EXP8	EXP(((1.0 - AGE/AGEMAX)/0.6)**(4.0))
CCP2	CC**(-0.40)
AGE8	(AGEMAX - AGE)**(5.0) / 10E10
AGE9	(AGEMAX - AGE)**(3.0) / 10E6
AG10	AGE**(-0.30)
AG11	AGE**(-0.40)
AG12	AGE**(0.25)
CCP3	CC**(0.40)
CCP4	CC**(-0.01)
CCP5	CC**(-0.2)
CCP6	CC**(-2.00) / 1000.0
CCP7	CC**(-0.60)
EXP9	EXP(((1.0 - CC/CCMAX) / 0.8)**(9.0))
EX10	EXP(((1.0-CC/CCMAX)/0.6)**(6))/10E6
EX11	EXP(((1.0-CC/CCMAX)/0.8)**(10))/10000.0
EX12	EXP(((1.0-CC/CCMAX)/0.7)**(8))/1000000.0
EX13	EXP(((1.0 - CC/CCMAX)/0.9)**(10.0))
1/CC	1.0 / CC
1/AGE	1.0 / AGE
AG13	AGE / (1.0 + AGE**2.0)
CCP8	CC**(0.30)
PRED	PREDISTURBANCE COVERAGE
SLAS	SLOPE / ASPECT
CCP9	CC**(0.25)
DBH	DIAMETER BREAST HEIGHT (DBH)
ELAS	(ELEVATION / ASPECT) / 100000.0
AG14	AGE **(-1.50)
EX14	EXP(((1.0-CC/CCMAX)/0.6)**(4) * 1000.0
AG15	AGE **(-0.40)
EX15	EXP(((1.0 - AGE/AGEMAX)/0.9)**(10.0))
AG16	(AGEMAX - AGE)**(0.15)
AG17	(SQRT(AGE))
CP10	(CC**(-1.50))
EX16	(EXP(((1.0 - CC/CCMAX)/0.9)**(8.0))
AG18	(AGE**(-2.00))
EX17	(EXP(((1.0-CC/CCMAX)/0.7)**(5.0))
AG19	(AGE**(0.60))
AG20	(AGE**(0.10))
EX18	EXP(((1.0 - CC/CCMAX)/0.7)**(8.0)
EX19	(EXP(((1.0-CC/CCMAX)/0.8)**(9))/1000.0
AG21	AGE**(-0.20)
CP11	CC**(0.15)
DUMY	(DUMMY VARIABLE)
TSEV	<<< SEV. TYPE TO ELIMINATE SPECIES
TAGE	<<< AGE WHICH SPECIES DIES FROM STAND

APPENDIX E (con't)

Regression equations for PSME/PHMA, dry phase.
Nine successional pathways.

***** PATHWAY REGRESSION EQUATIONS FOR CCAL OR TOTAL TREE CANOPY COVER (%) *****

PATH	REGRESSION EQUATION FORM	R SQ	F	STD DEV
1	CCAL = 101.744 + (-13.844)*EXP3 + (-11.327)*SVRT	0.74	24	16.559
2	CCAL = 65.690 + (-12.256)*EXP3 + (- 8.938)*TRMT	0.90	36	23.095
3	CCAL = 73.044 + (-11.407)*EXP3	0.50	68	20.792
4	CCAL = -10.664 + (-11.624)*EXP3 + (2.033)*ELEV	0.67	36	18.997
5	CCAL = 68.922 + (-4.917)*EXP3	0.50	63	19.115
6	CCAL = 75.677 + (-11.229)*EXP3	0.53	34	22.496
7	CCAL = 65.194 + (-9.970)*EXP3	0.57	32	20.194
8	CCAL = 125.350 + (-11.593)*EXP3 + (-0.131)*ASPT + (-0.942)*ELEV	0.71	32	16.953
9	CCAL = 69.030 + (-10.579)*EXP3	0.59	57	26.104

***** PATHWAY REGRESSION EQUATIONS FOR DBH OR AVERAGE DBH OF STAND (INCHES) *****

PATH	REGRESSION EQUATION FORM	R SQ	F	STD DEV
1	DBH = 18.067 + (-0.669)*AGE8 + (-0.143)*SLOP	0.53	26	1.495
2	DBH = 12.255 + (-0.676)*AGE8 + (0.899)*SVRT	0.91	36	1.346
3	DBH = 11.938 + (-0.624)*AGE8 + (0.833)*SVRT	0.90	18	1.535
4	DBH = 17.122 + (-6.768)*AGE9	0.99	34	1.835
5	DBH = 17.314 + (-6.886)*AGE9	0.88	52	2.513
6	DBH = 13.284 + (-0.630)*AGE8	0.86	34	1.835
7	DBH = 13.406 + (-9.649)*AGE8	0.86	32	2.663
8	DBH = 17.411 + (-7.011)*AGE9	0.97	50	2.463
9	DBH = 16.968 + (-6.793)*AGE9	0.90	37	1.875

***** PATHWAY REGRESSION EQUATIONS FOR BA OR AVE STAND BASAL AREA (SQ FT) *****

PATH	REGRESSION EQUATION FORM	R SQ	F	STD DEV
1	BA = 234.354 + (-8.278)*AGE8 + (-2.372)*SLOP	0.80	25	35.084
2	BA = 194.076 + (-10.064)*AGE8	0.86	57	35.618
3	BA = 233.889 + (-8.775)*AGE8 + (-2.301)*SLOP	0.83	39	29.060
4	BA = 161.885 + (-8.007)*AGE8	0.82	36	28.963
5	BA = 209.562 + (-85.426)*AGE9	0.83	52	38.239
6	BA = 155.526 + (-7.664)*AGE8	0.73	34	34.739
7	BA = 156.164 + (-7.667)*AGE8	0.70	32	39.761
8	BA = 209.595 + (-84.945)*AGE9	0.81	50	42.226
9	BA = 181.102 + (-72.856)*AGE9	0.79	36	31.464

***** PATHWAY REGRESSION EQUATIONS FOR DF<4 OR PSEUDOTSUGA MENZIESII (< 4 IN.) *****

PATH	REGRESSION EQUATION FORM	R SQ	F	STD DEV
1	DF<4 = 16.544 + (-3.201)*EXP3	0.85	25	12.904
2	DF<4 = 4.503 + (-3.386)*EXP3 + (9.706)*SLAS + (5.851)*SVRT	0.73	20	8.923
3	DF<4 = 13.883 + (-1.932)*EXP3	0.72	38	14.555
4	DF<4 = -25.677 + (-10.018)*EXP3 + (0.708)*ELEV + (2.327)*AGE8 + (6.013)*SVRT	0.70	31	14.238
5	DF<4 = 62.934 + (2.518)*AGE8 + (-1.044)*ELEV + (-6.302)*SVRT + (-9.917)*EXP3	0.70	31	14.238
6	DF<4 = -23.349 + (-8.857)*EXP3 + (1.073)*ELEV + (0.114)*AGE8 + (6.699)*SVRT	0.56	35	19.294
7	DF<4 = 68.127 + (-11.593)*EXP3 + (-0.131)*ASPT + (-0.942)*ELEV + (2.067)*AGE8	0.71	32	16.953
8	DF<4 = 68.127 + (-11.593)*EXP3 + (-0.131)*ASPT + (-0.942)*ELEV + (2.067)*AGE8	0.71	32	16.953
9	DF<4 = 11.651 + (-9.973)*EXP3 + (2.358)*AGE8	0.57	37	17.468

***** PATHWAY REGRESSION EQUATIONS FOR DF>4 OR PSEUDOTSUGA MENZIESII (> 4 IN.) *****

PATH	REGRESSION EQUATION FORM	R SQ	F	STD DEV
1	DF>4 = 75.204 + (-10.526)*EXP3 + (-22.487)*SVRT + (-0.025)*ELAS + (11.404)*TRMT	0.85	25	12.904
2	DF>4 = 43.729 + (-2.216)*AGE8	0.58	57	16.912
3	DF>4 = 60.620 + (-13.506)*EXP3	0.71	38	14.589
4	DF>4 = -18.774 + (-2.327)*AGE8 + (1.116)*ELEV + (6.013)*SVRT	0.71	34	13.892
5	DF>4 = -10.012 + (-2.518)*AGE8 + (1.044)*ELEV + (6.302)*SVRT	0.70	31	14.238
6	DF>4 = 30.812 + (-2.114)*AGE8 + (6.699)*SVRT	0.58	33	16.247
7	DF>4 = 42.423 + (-2.067)*AGE8	0.50	50	18.708
8	DF>4 = 42.423 + (-2.067)*AGE8	0.50	50	18.708
9	DF>4 = 48.563 + (-2.358)*AGE8	0.56	37	16.468

***** PATHWAY REGRESSION EQUATIONS FOR DFAL OR PSEUDOTSUGA HEIZIESII (TOTAL) *****			
PATH	REGRESSION EQUATION FORM	R SQ	STD DEV
1	DFAL= 103.749+(-15.044)*EXP3+(-11.327)*SVRT	0.74	16.538
2	DFAL= 66.421+(-10.302)*EXP3+ 57.891)*SLAS+(-0.311)*PHMA+(-0.236)*ELAS	0.47	21.543
3	DFAL= 69.503+(-11.633)*EXP3	0.47	9.442
4	DFAL= -26.451+(-10.018)*EXP3+(1.908)*ELEV	0.66	17.120
5	DFAL= 68.922+(-9.917)*EXP3	0.50	19.105
6	DFAL= 6.463+(-8.857)*EXP3+(1.073)*ELEV	0.56	19.294
7	DFAL= 110.550+(-11.593)*EXP3+(-0.131)*ASPT+(-0.942)*ELEV	0.71	16.953
8	DFAL= 110.550+(-11.593)*EXP3+(-0.131)*ASPT+(-0.942)*ELEV	0.71	16.953
9	DFAL= 60.216+(-9.973)*EXP3	0.57	19.773
***** PATHWAY REGRESSION EQUATIONS FOR ACGL OR ACER GLABRUM *****			
PATH	REGRESSION EQUATION FORM	R SQ	STD DEV
1	ACGL= -8.134+(0.954)*PRED+(-0.129)*EX12+(2.727)*SVRT	0.97	0.532
2	ACGL= -0.892+(0.810)*PRED+(-1.058)*EXP4+(3.266)*SVRT+(-2.060)*TRMT	0.75	1.043
3	ACGL= 6.262+(0.759)*PRED	0.59	1.376
4	ACGL= 12.001+(10.982)*CEVE+(-0.174)*GRSS	0.54	6.269
5	ACGL= 25.728+(10.738)*CEVE+(-0.219)*GRSS+(-0.131)*ASPT	0.73	6.211
6	ACGL= 4.796+(0.257)*CCP1+(1.040)*CCA2	0.42	8.843
7	ACGL= -2.200+(0.398)*CCP6+(0.084)*PHMA	0.53	3.798
8	ACGL= -7.776+(0.342)*CCP6+(1.319)*PRED+(0.164)*ELEV	0.74	1.935
9	ACGL= -0.819+(8.602)*CCAG+(1.037)*PREU	0.47	8.558
***** PATHWAY REGRESSION EQUATIONS FOR AMAL OR AMFLANCHIER ALMIFOLIA *****			
PATH	REGRESSION EQUATION FORM	R SQ	STD DEV
1	AMAL= 0.000+(1.000)*PRED+(-3.250)*SVRT	0.62	1.615
2	AMAL= 17.538+(-0.232)*ELEV+(-0.079)*GRSS+(1.966)*1/CC	0.74	1.473
3	AMAL= -8.647+(-0.306)*ELEV+(0.213)*ASPT+(24.352)*SLAS+(1.473)*1/CC+(-0.008)*EXP2	0.82	1.274
4	AMAL= 10.049+(0.681)*PRED+(-5.236)*SVRT	0.44	9.250
5	AMAL= 70.737+(-2.161)*DBH +(-5.249)*EXP4+(-0.822)*ELEV	0.63	8.542
6	AMAL= 14.459+(-7.355)*TRMT+(-0.351)*PHMA+(1.218)*PRED+(1.049)*SLOP	0.78	6.905
7	AMAL= 30.977+(0.306)*GRSS+(-0.605)*ELEV	0.52	6.290
8	AMAL= 31.520+(0.650)*PRED+(0.198)*GRSS+(-0.194)*CAPU+(-0.421)*ELEV+(-0.332)*SLOP	0.66	6.634
9	AMAL= 31.520+(0.650)*PRED+(0.198)*GRSS+(-0.194)*CARU+(-0.421)*ELEV+(-0.332)*SLOP	0.66	6.634
***** PATHWAY REGRESSION EQUATIONS FOR CEVE OR CEANOOTHUS VELUTINUS *****			
PATH	REGRESSION EQUATION FORM	R SQ	STD DEV
1	CEVE= 0.500+(2.000)*TSEV+(50.000)*TAGE	0.0	0.000
2	CEVE= 0.500+(2.000)*TSEV+(50.000)*TAGE	0.0	0.000
3	CEVE= 1.000+(2.000)*TSEV+(50.000)*TAGE	0.0	0.000
4	CEVE= 1.136+(-0.009)*ASPT+(70.000)*TAGE	0.65	1.056
5	CEVE= 3.000+(2.000)*TSEV+(50.000)*TAGE	0.0	0.000
6	CEVE= 3.000+(2.000)*TSEV+(50.000)*TAGE	0.0	0.000
7	CEVE= -95.446+(2.328)*ELEV+(-0.504)*PHMA+(11.759)*SVRT+(6.102)*CCAG+(80.000)*TAGE	0.83	10.542
8	CEVE= -53.421+(-11.304)*AGE3+(1.390)*ELEV+(-0.347)*PHMA+(8.152)*TRMT+(6.555)*CCAG+(-0.000)*TAGE	0.83	12.374
9	CEVE= -61.070+(-14.180)*AGE3+(2.200)*ELEV+(-0.312)*PHMA+(6.764)*TRMT+(6.980)*CCAG+(-0.000)*TAGE	0.87	11.318
***** PATHWAY REGRESSION EQUATIONS FOR LOUT OR LONICERA UTAMENSIS *****			
PATH	REGRESSION EQUATION FORM	R SQ	STD DEV
1	LOUT= 0.226+(0.047)*CARU+(-0.002)*CCP1	0.95	0.233
2	LOUT= 0.500+(1.000)*PRED+(3.000)*TSEV	0.0	0.000
3	LOUT= 0.000+(1.000)*PRED	0.0	0.000
4	LOUT= -0.084+(0.865)*PRED+(0.009)*TREE+(-0.023)*DBH	0.43	0.267
5	LOUT= 0.732+(0.038)*CCP1	0.63	1.800
6	LOUT= -3.011+(0.061)*CCP1+(10.347)*AG11	0.57	1.468
7	LOUT= -0.080+(0.001)*AGE1+(0.325)*PRED	0.50	0.326
8	LOUT= -0.097+(0.946)*PHED+(0.005)*SLOP	0.75	0.301
9	LOUT= 0.000+(1.000)*PRED+(3.000)*TSEV	0.0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR PHMA OR PHYSIDAMPUS CALVACEUS *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	PHMA= 14.094+(1.215)*SLOP+(-8.343)*CCA6	0.50	27	17.686
2	PHMA= 14.986+(0.775)*PRED+(-8.198)*CCA6+(-0.049)*EXP2	0.75	17	11.464
3	PHMA= 893.028+(0.875)*PRED+(-1.142)*TRLE+(*****)*CCP4+(11.320)*SVHT	0.58	21	17.540
4	PHMA= 893.028+(0.875)*PRED+(-1.142)*TRLE+(*****)*CCP4+(11.320)*SVHT	0.58	21	17.540
5	PHMA= 893.028+(0.875)*PRED+(-1.142)*TRLE+(*****)*CCP4+(11.320)*SVHT	0.58	21	17.540
6	PHMA= -16.945+(0.589)*PRED+(1.324)*SLOP	0.57	21	19.215
7	PHMA= -210.720+(5.387)*ELEV+(-12.131)*CCA2+(-0.274)*EXP5+(0.376)*PRED	0.76	17	13.118
8	PHMA= -210.720+(5.387)*ELEV+(-12.131)*CCA2+(-1.274)*EXP5+(0.376)*PRED	0.76	17	13.118
9	PHMA= -210.720+(5.387)*ELEV+(-12.131)*CCA2+(-0.274)*EXP5+(0.376)*PRED	0.76	17	13.118

***** PATHWAY REGRESSION EQUATIONS FOR PRVI OR PRUNUS VIRGINIANA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	PRVI= 0.000+(1.000)*PRED	0.00	0	0.000
2	PRVI= 0.000+(1.000)*PRED	0.00	0	0.000
3	PRVI= 0.000+(1.000)*PRED	0.00	0	0.000
4	PRVI= 0.000+(0.200)*CCP6+(4.250)*PRED	0.60	18	1.750
5	PRVI= 0.000+(0.200)*CCP6+(4.250)*PRED	0.60	18	1.750
6	PRVI= 0.450+(0.189)*CCP6	0.47	21	1.794
7	PRVI= 0.500+(0.113)*CCP6	0.99	4	1.000
8	PRVI= 0.500+(0.113)*CCP6	0.99	4	1.000
9	PRVI= 0.500+(0.113)*CCP6	0.99	4	1.000

***** PATHWAY REGRESSION EQUATIONS FOR RGGY OR ROSA GYMNOCARPA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	RGGY= 0.000+(1.000)*PRED	0.00	11	0.000
2	RGGY= -0.056+(1.755)*PRED+(0.411)*CCA2	0.68	24	0.355
3	RGGY= 4.695+(-0.121)*SLOP+(-0.021)*CAHU	0.70	12	0.624
4	RGGY= -10.926+(0.696)*PRED+(5.963)*AGE4	0.71	11	0.500
5	RGGY= 1.345+(0.951)*PRED+(-57.554)*1/CC	0.97	31	1.342
6	RGGY= -0.524+(0.696)*PRED+(5.963)*AGE4	0.71	11	0.500
7	RGGY= 0.049+(0.183)*EXP7+(0.901)*PRED	0.67	17	0.151
8	RGGY= 0.182+(0.994)*PRED	0.99	37	0.465
9	RGGY= 0.419+(0.792)*PRED+(-0.698)*EXP3+(0.104)*CCP6	0.49	25	0.476

***** PATHWAY REGRESSION EQUATIONS FOR SASC OR SALIX SCOULERIANA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	SASC= 1.388+(-0.012)*PHMA+(-0.023)*SLOP	0.74	11	0.179
2	SASC= 0.162+(1.590)*CCA2+(1.200)*PRED+(-1.350)*CCA6+(0.002)*ASPT	0.94	17	0.246
3	SASC= 0.000+(1.500)*PRED	0.00	0	0.000
4	SASC= -0.523+(1.640)*PRED	0.68	49	2.900
5	SASC= -0.523+(1.640)*PRED	0.68	49	2.900
6	SASC= -0.523+(1.640)*PRED	0.68	49	2.900
7	SASC= -0.268+(46.807)*1/CC+(0.055)*GRSS	0.49	7	0.419
8	SASC= -0.268+(46.807)*1/CC+(0.055)*GRSS	0.49	7	0.419
9	SASC= -0.268+(46.807)*1/CC+(0.055)*GRSS	0.49	7	0.419

***** PATHWAY REGRESSION EQUATIONS FOR SPBE OR SPIRAEA BETULIFOLIA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	SPBE= 10.613+(0.618)*PRED+(-25.915)*CCA2	0.61	11	12.078
2	SPBE= -8.316+(0.967)*PRED+(0.134)*EXP5+(-0.054)*ASPT+(3.126)*SVHT	0.82	17	5.698
3	SPBE= 2.751+(0.654)*PRED	0.51	23	10.755
4	SPBE= 6.943+(0.977)*PRED+(-4.253)*TRMT+(0.163)*PHMA+(-5.872)*1/CC+(0.974)*AGE6	0.94	21	4.049
5	SPBE= 23.265+(0.998)*PRED+(-6.167)*TRMT	0.71	22	8.820
6	SPBE= 24.661+(0.984)*PRED+(-7.999)*SVHT	0.69	21	9.080
7	SPBE= 3.112+(17.200)*1/CC+(0.745)*PRED	0.45	28	8.379
8	SPBE= 0.871+(0.949)*PRED+(7.734)*EXP4+(-4.023)*CCP2	0.92	17	11.828
9	SPBE= 17.030+(0.969)*PRED+(8.054)*EXP4+(-4.030)*CCP2+(-5.440)*SVHT	0.93	23	3.524

***** PATHWAY REGRESSION EQUATIONS FOR SYAL OR SYMPHYLLA ALBA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	SYAL= -26.004+(0.993)*EX12+(1.013)*PRE0+(0.451)*SVPT	0.59	11	1.747
2	SYAL= 2.375+(0.617)*PPED	0.61	26	0.647
3	SYAL= 31.336+(-7.453)*TRMT+(-0.114)*EX10+(0.032)*PPED	0.79	21	0.649
4	SYAL= 1.910+(0.658)*PPED+(22.745)*1/CC	0.56	21	0.717
5	SYAL= 35.111+(32.297)*1/CC+(0.799)*PRE0+(-0.736)*ELEV	0.64	18	0.448
6	SYAL= 21.502+(29.186)*1/CC+(0.748)*PRLU+(-0.417)*ELEV	0.63	22	0.099
7	SYAL= 55.256+(-17.760)*SVMT+(0.550)*CCP6+(0.311)*PRE0	0.77	17	0.501
8	SYAL= 14.006+(11.871)*1/CC+(-7.326)*CCAG	0.50	18	0.440
9	SYAL= 14.006+(11.871)*1/CC+(-7.326)*CCAG	0.50	18	0.440

***** PATHWAY REGRESSION EQUATIONS FOR VAGL OR VACCINIUM GLOBULARE *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	VAGL= 0.000+(1.000)*PRE0	0.00	0	0.000
2	VAGL= 0.000+(0.000)*PRE0+(2.000)*TSEV	0.00	0	0.000
3	VAGL= 0.000+(0.000)*PRE0+(2.000)*TSLV	0.00	0	0.000
4	VAGL= -0.004+(0.000)*AGE2+(0.032)*SLAS+(0.340)*PRE0	0.66	21	0.114
5	VAGL= -0.034+(0.000)*AGE2+(0.032)*SLAS+(0.340)*PRE0	0.66	21	0.114
6	VAGL= -0.034+(0.000)*AGE2+(0.032)*SLAS+(0.340)*PRE0	0.66	21	0.114
7	VAGL= 0.475+(1.010)*AGE3	0.99	7	0.026
8	VAGL= 0.475+(1.010)*AGE3	0.99	7	0.026
9	VAGL= 0.447+(0.025)*CCP1+(-0.003)*AGE3	0.55	10	0.194

***** PATHWAY REGRESSION EQUATIONS FOR ARUV OR ARTOSTAPHYLOS UVA-URSI *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	ARUV= 15.316+(1.407)*CCA2+(-0.526)*SLOP	0.83	35	0.944
2	ARUV= 0.151+(5.418)*PRE0+(0.002)*EXP2+(-0.060)*1/CC+(0.006)*SLOP	0.99	24	0.076
3	ARUV= 0.151+(5.418)*PRE0+(0.002)*EXP2+(-0.060)*1/CC+(0.006)*SLOP	0.99	24	0.076
4	ARUV= 0.598+(0.174)*SLAS+(-0.027)*SLOP	0.47	21	0.511
5	ARUV= 0.668+(0.034)*TREE	0.57	11	0.514
6	ARUV= 0.668+(0.034)*TREE	0.57	11	0.514
7	ARUV= -8.333+(5.185)*TRMT	0.52	7	0.166
8	ARUV= -8.333+(5.185)*TRMT	0.52	7	0.166
9	ARUV= -10.015+(0.134)*CEVE+(3.064)*TRMT	0.59	10	0.012

***** PATHWAY REGRESSION EQUATIONS FOR BERE OR DEPREZIS REPENS *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	BERE= -1.141+(15.963)*CCAG	0.58	12	0.520
2	BERE= 4.322+(0.045)*AGE1+(0.018)*ASPT+(0.173)*ELFV+(-0.150)*SLOP	0.82	26	1.648
3	BERE= 0.647+(17.300)*CCA2+(-6.736)*PRE0	0.72	17	2.398
4	BERE= 5.042+(-0.134)*ELEV+(0.009)*1/CC+(0.079)*SLOP	0.55	34	1.461
5	BERE= -2.053+(0.054)*AGE3+(0.054)*ELEV	1.97	16	0.623
6	BERE= 4.872+(-0.137)*ELEV+(0.008)*1/CC+(0.095)*SLOP	0.56	22	1.494
7	BERE= -0.426+(1.496)*CANU+(-3.839)*EXP7	0.47	13	0.341
8	BERE= 6.723+(0.043)*AGE1+(-18.950)*SLAS	0.52	21	0.154
9	BERE= 2.054+(0.685)*PPED	0.56	30	0.148

***** PATHWAY REGRESSION EQUATIONS FOR LIBO OR LINNAEA BOREALIS *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	LIBO= 0.000+(1.000)*PRE0+(2.000)*TSEV	0.00	0	0.000
2	LIBO= 5.576+(-3.441)*TRMT+(0.402)*SLOP	0.99	5	0.624
3	LIBO= 5.576+(-3.441)*TRMT+(0.402)*SLOP	0.99	5	0.624
4	LIBO= 0.266+(0.196)*SLAS+(-0.009)*PHMA	0.52	21	0.488
5	LIBO= 0.266+(0.196)*SLAS+(-0.009)*PHMA	0.52	21	0.488
6	LIBO= 0.266+(0.196)*SLAS+(-0.009)*PHMA	0.52	21	0.488
7	LIBO= -0.343+(0.438)*PRE0+(0.125)*AG12	0.62	23	0.111
8	LIBO= -0.343+(0.438)*PRE0+(0.125)*AG12	0.62	23	0.111
9	LIBO= -0.343+(0.438)*PRE0+(0.125)*AG12	0.62	23	0.111

***** PATHWAY REGRESSION EQUATIONS FOR AGSP OR AGROPYRUM SPICATUM *****

PATH	REGRESSION EQUATION FORM	R SQ	F	STD DEV
1	AGSP= -0.060+(0.543)*1/CC+(0.002)*AGL1+(0.020)*CCA2	0.59	25	0.1306
2	AGSP= 34.018+(5.426)*1/CC+(-0.203)*CARU+(-0.565)*ELEV	0.59	10	2.777
3	AGSP= 34.018+(5.426)*1/CC+(-0.203)*CARU+(-0.565)*ELEV	0.59	10	2.777
4	AGSP= 0.183+(0.305)*CCP7+(0.199)*PRED+(-0.059)*TRMT	0.99	21	0.146
5	AGSP= 0.415+(0.328)*CCP7+(-0.007)*CARU+(-0.007)*SHRB	0.99	21	0.146
6	AGSP= 0.415+(0.328)*CCP7+(-0.007)*CARU+(-0.007)*SHRB	0.99	21	0.146
7	AGSP= 4.899+(0.653)*PRED+(-0.015)*CCP1+(-0.087)*ELEV	0.70	17	0.477
8	AGSP= 4.899+(0.653)*PRED+(-0.015)*CCP1+(-0.087)*ELEV	0.70	17	0.477
9	AGSP= 4.899+(0.653)*PRED+(-0.015)*CCP1+(-0.087)*ELEV	0.70	17	0.477

***** PATHWAY REGRESSION EQUATIONS FOR CARU OR CALAMAGROSTIS PURESCHENS *****

PATH	REGRESSION EQUATION FORM	R SQ	F	STD DEV
1	CARU= -11.053+(1.250)*PRED+(0.283)*PHMA+(-0.030)*AGE1	0.50	12	1.750
2	CARU= 10.165+(0.673)*PRED+(0.256)*TREE	0.67	24	1.390
3	CARU= 338.921+(-2.639)*ASPT+(*****)*SLAS+(*****)*CEVE+(12.501)*SVPT+(-0.559)*TREE	0.57	17	4.449
4	CARU= 14.342+(0.871)*PRED+(-6.401)*1/CC+(-0.307)*CCP1	0.87	44	10.312
5	CARU= 14.342+(0.871)*PRED+(-6.401)*1/CC+(-0.307)*CCP1	0.87	44	10.312
6	CARU= 14.342+(0.871)*PRED+(-6.401)*1/CC+(-0.307)*CCP1	0.87	44	10.312
7	CARU= 1.793+(0.784)*PRED+(0.155)*CCP6	0.70	17	3.239
8	CARU= 60.912+(0.675)*PRED+(-27.759)*1/CC+(-0.468)*PHMA+(-0.192)*ASPT+(-0.533)*CEVE+(-0.455)*TREE	0.90	57	6.400
9	CARU= 14.693+(0.783)*PRED+(-5.618)*EXP3+(0.897)*CCP6	0.65	23	11.969

***** PATHWAY REGRESSION EQUATIONS FOR CACO OR CAREX CONCINNOIDES *****

PATH	REGRESSION EQUATION FORM	R SQ	F	STD DEV
1	CACO= 0.000+(1.000)*PRED	0.00	0	0.000
2	CACO= 3.177+(-0.276)*EX11+(-0.103)*CCA2+(-0.536)*SVPT	0.50	20	0.904
3	CACO= 0.000+(1.000)*PRED	0.00	0	0.000
4	CACO= -0.228+(1.615)*PRED	0.70	16	1.153
5	CACO= 6.857+(-0.160)*SLOP+(-0.054)*CARU	0.50	14	1.615
6	CACO= 0.000+(0.900)*PRED	0.00	0	0.000
7	CACO= 0.466+(0.395)*CCA2	0.99	3	0.030
8	CACO= -1.903+(1.430)*CCAG+(0.084)*SLOP	0.88	9	0.447
9	CACO= 2.578+(0.814)*CCAG+(-0.770)*SVPT	0.58	10	0.828

***** PATHWAY REGRESSION EQUATIONS FOR CAGE OR CAREX GEYERI *****

PATH	REGRESSION EQUATION FORM	R SQ	F	STD DEV
1	CAGE= 46.256+(1.524)*PRED+(-0.761)*ELEV+(-0.093)*TREE	0.87	11	2.447
2	CAGE= 3.249+(0.492)*PRED+(12.353)*CEVE	0.56	24	11.945
3	CAGE= 3.249+(0.492)*PRED+(12.353)*CEVE	0.56	24	11.945
4	CAGE= 10.124+(0.805)*PRED	0.68	21	15.059
5	CAGE= -2.772+(0.652)*PRED+(39.649)*1/CC	0.47	18	19.954
6	CAGE= 10.124+(0.805)*PRED+(-13.000)*EXP4+(-0.405)*CCP1	0.69	21	15.059
7	CAGE= 70.623+(-2.672)*SLOP+(0.539)*PHMA+(-0.317)*TREE	0.56	17	15.748
8	CAGE= 5.500+(0.887)*PRED+(-9.438)*CCA2+(-1.298)*CCP7+(-2.523)*SLAS	0.82	23	11.120
9	CAGE= 5.500+(0.887)*PRED+(-9.438)*CCA2+(-1.298)*CCP7+(-2.523)*SLAS	0.82	23	11.120

***** PATHWAY REGRESSION EQUATIONS FOR CARO OR CAREX ROSSII *****

PATH	REGRESSION EQUATION FORM	R SQ	F	STD DEV
1	CARO= 0.000+(1.000)*PRED	0.00	0	0.000
2	CARO= 0.424+(1628.000)*CCP6	0.97	8	0.163
3	CARO= 0.000+(1.000)*PRED	0.00	0	0.000
4	CARO= 10.210+(0.600)*PRED	0.50	21	15.040
5	CARO= 0.000+(1.000)*PRED	0.00	0	0.000
6	CARO= 0.000+(1.000)*PRED	0.00	0	0.000
7	CARO= 0.000+(1.000)*PRED	0.00	0	0.000
8	CARG= 0.000+(1.000)*PRED	0.00	0	0.000
9	CARO= 0.000+(1.000)*PRED	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR ACMI OR ACHILLEA MILLEFOLIUM *****

PATH	REGRESSION EQUATION FORM	RSG	N	STD DEV
1	ACMI= 0.309+(0.026)*CARU	0.65	11	1.520
2	ACMI= 1.000+(70.000)*TAGE	0.0	0	0.000
3	ACMI= 1.644+(-0.020)*PHMA	0.63	22	1.983
4	ACMI= -1.498+(1.666)*1/CC+(0.043)*ELEV	0.95	14	0.230
5	ACMI= -1.498+(1.666)*1/CC+(0.043)*ELLV	0.95	14	0.230
6	ACMI= -1.375+(1.672)*1/CC+(0.040)*ELLV	0.94	14	0.242
7	ACMI= 5.642+(-0.093)*ELEV+(0.127)*CCA2+(0.013)*GRSS	0.84	16	0.456
8	ACMI= -14.040+(-0.098)*ELEV+(20.548)*AGE5+(0.451)*CCA2+(-0.950)*CCAG	0.86	20	0.383
9	ACMI= 6.522+(-0.105)*ELEV+(-0.009)*GRSS+(0.594)*CCA2+(-1.235)*CCAG	0.93	16	0.219

***** PATHWAY REGRESSION EQUATIONS FOR ANRA OR ANTEMARIA RACEMOSA *****

PATH	REGRESSION EQUATION FORM	RSG	N	STD DEV
1	ANRA= 1.962+(1.126)*CCA2	0.77	13	3.468
2	ANRA= 0.784+(0.389)*PRED+(-1.337)*CCA2	0.58	24	1.556
3	ANRA= 18.696+(-0.155)*ASPT+(0.712)*PRED+(-13.465)*SLAS	0.20	16	1.307
4	ANRA= -2.652+(1.123)*PRED+(0.077)*CARU	0.70	11	1.868
5	ANRA= -2.652+(1.123)*PRED+(0.077)*CARU	0.70	11	1.865
6	ANRA= 1.388+(1.012)*PRED+(1.739)*SLAS+(*****)*ELAS+(0.000)*SLOP	0.86	22	0.967
7	ANRA= 0.000+(0.900)*PRED+(2.000)*TSEV	0.0	0	0.000
8	ANRA= -2.102+(0.079)*PHMA+(0.033)*CCP1	0.77	8	1.371
9	ANRA= -0.643+(4.800)*ELAS+(-0.052)*SLOP+(0.018)*ASPT	0.90	23	0.555

***** PATHWAY REGRESSION EQUATIONS FOR ARCO OR ARNICA CORDIFOLIA *****

PATH	REGRESSION EQUATION FORM	RSG	N	STD DEV
1	ARCO= 0.264+(0.520)*PRED+(-0.193)*AGE9	0.85	23	0.445
2	ARCO= 0.207+(0.636)*CCAG+(0.002)*AGE3	0.42	24	0.843
3	ARCO= 0.274+(1.013)*PRED+(-0.113)*SVKT	0.95	17	0.200
4	ARCO= 0.274+(1.013)*PRED+(-0.113)*SVKT	0.95	17	0.200
5	ARCO= -0.936+(0.942)*PRED+(-0.204)*SVKT+(-0.009)*CCP6+(-0.005)*PHMA	0.97	17	0.156
6	ARCO= -0.936+(0.942)*PRED+(-0.204)*SVKT+(-0.009)*CCP6+(-0.005)*PHMA	0.97	17	0.156
7	ARCO= -0.212+(0.945)*PRED+(-0.228)*CCA2+(1.923)*CCAG	0.94	19	0.151
8	ARCO= -0.212+(0.945)*PRED+(-0.228)*CCA2+(1.923)*CCAG	0.98	19	0.151
9	ARCO= -0.212+(0.945)*PRED+(-0.228)*CCA2+(1.923)*CCAG	0.94	19	0.151

***** PATHWAY REGRESSION EQUATIONS FOR ASCO OR ASTER CONSPICUUS *****

PATH	REGRESSION EQUATION FORM	RSG	N	STD DEV
1	ASCO= 1.386+(0.335)*CCP6+(0.052)*CARU	0.86	13	1.707
2	ASCO= -0.300+(1.032)*PRED+(2.400)*EXP7+(0.074)*GRSS	0.57	24	0.737
3	ASCO= -44.364+(1.230)*ELEV+(1.769)*CCA2+(-4.924)*CCP3	0.43	24	11.180
4	ASCO= 0.257+(0.072)*1/CC+(0.970)*PRED	0.85	59	0.418
5	ASCO= 0.257+(0.072)*1/CC+(0.970)*PRED	0.85	59	0.418
6	ASCO= 0.257+(0.072)*1/CC+(0.970)*PRED	0.85	59	0.418
7	ASCO= 0.000+(1.100)*PRED	0.0	0	0.000
8	ASCO= 0.000+(1.100)*PRED	0.0	0	0.000
9	ASCO= 3.000+(100.000)*TAGE	0.0	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR BASA OR BALSANORMIZA SAGITTATA *****

PATH	REGRESSION EQUATION FORM	RSG	N	STD DEV
1	BASA= 0.000+(1.000)*PRED	0.0	0	0.000
2	BASA= -0.085+(0.747)*PRED+(0.271)*CCP7	0.91	24	1.136
3	BASA= -0.085+(0.747)*PRED+(0.271)*CCP7	0.91	24	1.136
4	BASA= 1.677+(0.042)*CCP6+(-0.023)*PHMA	0.65	11	0.683
5	BASA= 1.678+(0.042)*CCP6+(-0.023)*PHMA	0.64	11	0.683
6	BASA= 1.580+(0.042)*CCP6+(-0.019)*PHMA	0.60	13	0.648
7	BASA= 0.487+(0.003)*AGE3	0.95	10	0.726
8	BASA= 0.594+(0.111)*CCP1+(-0.044)*TREE	0.84	9	0.386
9	BASA= 0.433+(-0.422)*SLAS	0.66	15	0.381

***** PATHWAY REGRESSION EQUATIONS FOR CHUM OR CHIMAPHILLA LAMPELLATA *****

PATH	REGRESSION EQUATION FORM	RSQ	N	STD DEV
1	CHUM= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
2	CHUM= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
3	CHUM= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
4	CHUM= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
5	CHUM= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
6	CHUM= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
7	CHUM= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
8	CHUM= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
9	CHUM= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR EPAN OR EPILOBIUM ANGUSTIFOLIUM *****

PATH	REGRESSION EQUATION FORM	RSQ	N	STD DEV
1	EPAN= 0.500+(50.000)*TAG2	0.00	0	0.000
2	EPAN= -0.201+(0.192)*EXP3+(-0.229)*1/CC+(-0.001)*EXP2	0.68	24	0.130
3	EPAN= -0.201+(0.192)*EXP3+(-0.229)*1/CC+(-0.001)*EXP2	0.68	24	0.130
4	EPAN= -0.201+(0.192)*EXP3+(-0.229)*1/CC+(-0.001)*EXP2	0.68	24	0.130
5	EPAN= -0.201+(0.192)*EXP3+(-0.229)*1/CC+(-0.001)*EXP2	0.68	24	0.130
6	EPAN= -0.201+(0.192)*EXP3+(-0.229)*1/CC+(-0.001)*EXP2	0.68	24	0.130
7	EPAN= -0.201+(0.192)*EXP3+(-0.229)*1/CC+(-0.001)*EXP2	0.68	24	0.130
8	EPAN= -0.201+(0.192)*EXP3+(-0.229)*1/CC+(-0.001)*EXP2	0.68	24	0.130
9	EPAN= -0.201+(0.192)*EXP3+(-0.229)*1/CC+(-0.001)*EXP2	0.68	24	0.130

***** PATHWAY REGRESSION EQUATIONS FOR FRVE OR FRAGARIA VESCA *****

PATH	REGRESSION EQUATION FORM	RSQ	N	STD DEV
1	FRVE= -2.355+(0.282)*CARU+(-3.527)*CCA2+(11.884)*CCAG+(-0.112)*CCP1	0.72	27	4.846
2	FRVE= 0.705+(0.572)*EXP3+(-0.068)*CCF6+(0.546)*SVRT+(-0.052)*ELEV	0.82	27	0.567
3	FRVE= 0.299+(4.563)*EXP4	0.44	24	0.791
4	FRVE= 0.705+(0.572)*EXP3+(-0.068)*CCP6+(0.546)*SVRT+(-0.052)*ELEV	0.82	27	0.567
5	FRVE= 0.942+(0.558)*EXP3+(-0.069)*CCP6+(0.582)*SVRT+(-0.057)*ELEV	0.81	24	0.596
6	FRVE= 0.864+(0.551)*EXP3+(-0.069)*CCP6+(0.590)*SVRT+(-0.054)*ELEV	0.82	28	0.559
7	FRVE= 10.025+(-0.141)*ELEV+(-0.162)*CCP1+(5.642)*CCAG+(-0.023)*CEVE	0.72	20	1.040
8	FRVE= 10.025+(-0.141)*ELEV+(-0.162)*CCP1+(5.642)*CCAG+(-0.023)*CEVE	0.72	20	1.040
9	FRVE= 10.025+(-0.141)*ELEV+(-0.162)*CCP1+(5.642)*CCAG+(-0.023)*CEVE	0.72	20	1.040

***** PATHWAY REGRESSION EQUATIONS FOR FRVI OR FRAGARIA VIRGINIANA *****

PATH	REGRESSION EQUATION FORM	RSQ	N	STD DEV
1	FRVI= 0.959+(0.074)*1/CC+(-0.035)*ELEV	0.99	27	0.239
2	FRVI= -3.424+(2.133)*EXP4	0.80	11	0.500
3	FRVI= 0.000+(1.000)*PRE0+(1.000)*TSELV	0.00	0	0.000
4	FRVI= 0.000+(1.000)*PRE0+(1.000)*TSELV	0.00	0	0.000
5	FRVI= 1.930+(0.072)*1/CC+(-0.033)*SLOP+(-0.168)*TRMT	0.83	59	0.892
6	FRVI= 1.930+(0.072)*1/CC+(-0.033)*SLOP+(-0.168)*TRMT	0.83	59	0.892
7	FRVI= 1.930+(0.072)*1/CC+(-0.033)*SLOP+(-0.168)*TRMT	0.83	59	0.892
8	FRVI= 0.500+(2.000)*TSELV	0.00	0	0.000
9	FRVI= 0.500+(2.000)*TSELV	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR GOOB OR GOODYERA OBLONGIFOLIA *****

PATH	REGRESSION EQUATION FORM	RSQ	N	STD DEV
1	GOOB= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
2	GOOB= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
3	GOOB= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
4	GOOB= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
5	GOOB= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
6	GOOB= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
7	GOOB= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
8	GOOB= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000
9	GOOB= 0.000+(1.000)*PRE0+(2.000)*TSELV	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR HIAL OR HIERACIUM ALBERTINUM X CYMOLO *****

PATH	REGRESSION EQUATION FORM	RSC	N	STD DEV
1	HIAL= 0.500+(100.000)*TAGE	0.0	0	0.000
2	-HIAL= 0.500+(*****)*TAGE	0.0	0	0.000
3	HIAL= 0.500+(-0.002)*AGE3+(0.000)*AGE2	0.99	12	0.001
4	HIAL= 0.500+(-0.001)*AGE3	0.99	5	0.001
5	-HIAL= 0.500+(-0.001)*AGE3	0.99	5	0.001
6	HIAL= 0.300+(-0.001)*AGE2	0.95	5	0.001
7	HIAL= 0.535+(0.002)*PHMA	0.48	9	0.052
8	-HIAL= 0.535+(0.002)*PHMA	0.48	9	0.052

***** PATHWAY REGRESSION EQUATIONS FOR H1ST OR MITELLA STAUROPETALA *****

PATH	REGRESSION EQUATION FORM	RSC	N	STD DEV
1	H1ST= 0.429+(0.002)*EXP9	0.79	11	0.207
2	-H1ST= 0.429+(0.002)*EXP9	0.79	11	0.207
3	H1ST= 0.429+(0.002)*EXP9	0.75	11	0.207
4	-H1ST= 0.429+(0.002)*EXP9	0.79	11	0.207
5	H1ST= 0.429+(0.002)*EXP9	0.75	11	0.207
6	-H1ST= 0.429+(0.002)*EXP9	0.79	11	0.207
7	H1ST= 0.429+(0.002)*EXP9	0.74	11	0.207
8	-H1ST= 0.429+(0.002)*EXP9	0.79	11	0.207
9	H1ST= 0.429+(0.002)*EXP9	0.79	11	0.207

***** PATHWAY REGRESSION EQUATIONS FOR THOC OR THALICTRUM OCCIDENTALE *****

PATH	REGRESSION EQUATION FORM	RSC	N	STD DEV
1	THOC= 1.141+(-0.317)*TRAT+(-0.286)*CCP5+(-0.002)*GRSS+(0.086)*SVRT	0.95	17	0.065
2	-THOC= 1.141+(-0.317)*TRAT+(-0.286)*CCP5+(-0.002)*GRSS+(0.086)*SVRT	0.95	17	0.065
3	THOC= 1.141+(-0.317)*TRAT+(-0.286)*CCP5+(-0.002)*GRSS+(0.086)*SVRT	0.95	17	0.065
4	-THOC= 0.351+(0.451)*PREO	0.46	12	0.569
5	THOC= 0.607+(0.779)*PREO+(-0.482)*SLAS+(-0.006)*TREE	0.99	10	0.002
6	-THOC= 0.607+(0.779)*PREO+(-0.482)*SLAS+(-0.006)*TREE	0.99	10	0.002
7	THOC= 0.000+(1.000)*PREO	0.0	0	0.000
8	-THOC= 0.000+(1.000)*PREO	0.0	0	0.000
9	THOC= 0.000+(1.000)*PREO	0.0	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR XETE OR XEROPHYLLUM TENAX *****

PATH	REGRESSION EQUATION FORM	RSC	N	STD DEV
1	XETE= 0.000+(0.900)*PREO+(2.000)*TSEV	0.0	0	0.000
2	-XETE= 0.000+(0.900)*PREO+(2.000)*TSEV	0.0	0	0.000
3	XETE= 0.000+(0.900)*PREO+(2.000)*TSEV	0.0	0	0.000
4	-XETE= 0.000+(0.900)*PREO+(2.000)*TSEV	0.0	0	0.000
5	XETE= 0.000+(0.900)*PREO+(2.000)*TSEV	0.0	0	0.000
6	-XETE= 0.000+(0.900)*PREO+(2.000)*TSEV	0.0	0	0.000
7	XETE= 0.000+(0.900)*PREO+(2.000)*TSEV	0.0	0	0.000
8	-XETE= 0.000+(0.900)*PREO+(2.000)*TSEV	0.0	0	0.000
9	XETE= 0.000+(0.900)*PREO+(2.000)*TSEV	0.0	0	0.000

APPENDIX E (con't)

Regression equations for PSME/PHMA, moist phase.
Six successional pathways.

***** PATHWAY REGRESSION EQUATIONS FOR CCAL OR TOTAL TREE CANOPY COVER (%) *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	CCAL = 6.688 + (-49.809)*EXP3 + (737.428)*AG11	0.69	26	15.456
2	CCAL = 14.525 + (-44.402)*EXP3 + (655.276)*AG11	0.55	18	20.041
3	CCAL = 14.525 + (-44.402)*EXP3 + (675.276)*AG11	0.55	18	20.041
4	CCAL = 19.525 + (-43.402)*EXP3 + (665.276)*AG11	0.55	18	20.041
5	CCAL = 120.120 + (-10.983)*EXP3 + (-21.382)*SVRT + (-0.136)*ASPT	0.82	17	14.629
6	CCAL = 124.297 + (-4.256)*AGE8	0.75	19	17.400

***** PATHWAY REGRESSION EQUATIONS FOR DBH OR AVERAGE DBH OF STAND (INCHES) *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	LUM = 17.403 + (-0.422)*AGE8 + (-0.065)*ELEV	0.97	18	0.780
2	DBH = 17.177 + (-5.760)*AGE9	0.97	20	0.817
3	DBH = -35.321 + 27.834*AGE20	0.95	20	1.249
4	DBH = -4.908 + 1.929*AGE17	0.89	20	1.305
5	DBH = 23.008 + (-0.421)*AGE8 + (-0.111)*ELEV + (-0.120)*SLOP + (-0.635)*SLAS	0.98	20	0.730
6	DBH = -22.814 + (26.526)*AGE20 + (-0.146)*ELEV + (-0.152)*SLOP	0.92	19	0.973

***** PATHWAY REGRESSION EQUATIONS FOR BA OR AVE STAND BASAL AREA (SQ FT) *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	BA = 147.193 + (-26.369)*EXP3	0.61	18	36.034
2	BA = 229.419 + (-9.518)*AGE8	0.83	17	40.434
3	BA = 131.406 + (-25.673)*EXP3	0.58	20	47.774
4	BA = -347.896 + (240.745)*AGE4	0.60	20	40.983
5	BA = 320.423 + (-4.473)*AGE8 + (-0.961)*ASPT + (-3.490)*SLOP	0.94	20	21.761
6	BA = 145.368 + (-16.674)*EXP3 + (39.556)*SLAS + (-2.514)*SLOP	0.90	19	17.732

***** PATHWAY REGRESSION EQUATIONS FOR DF<4 OR PSEUDOTSUGA MENZIESII (< 4 IN.) *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	DF<4 = 10.670 + (-10.406)*EXP3 + (1.401)*AGE8	0.52	18	19.020
2	DF<4 = 4.507 + (-3.386)*EXP3 + (9.706)*SLAS + (5.851)*SVRT	0.73	20	6.923
3	DF<4 = 3.439 + (1.652)*CCAG + (0.000)*SLAS	0.40	21	13.650
4	DF<4 = 5.639 + (1.652)*CCAG	0.40	21	13.650
5	DF<4 = -2.304 + (0.288)*CARU	0.52	17	6.413
6	DF<4 = 15.715 + (0.524)*ELAS + (-76.512)*SLAS + (-0.866)*ELEV + (3.346)*AGE3	0.93	19	3.514

***** PATHWAY REGRESSION EQUATIONS FOR DF>4 OR PSEUDOTSUGA MENZIESII (> 4 IN.) *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	DF>4 = 6.688 + (-49.809)*EXP3 + (717.428)*AG11	0.69	26	15.456
2	DF>4 = 43.074 + (-0.980)*AGE8 + (-6.336)*SVRT	0.59	20	9.540
3	DF>4 = 95.143 + (-1.151)*AGE8 + (-1.300)*ELEV	0.64	20	10.791
4	DF>4 = 96.679 + (-0.685)*AGE8 + (-1.544)*ELEV	0.51	20	11.853
5	DF>4 = 62.002 + (-1.119)*AGE8 + (-12.649)*SVRT	0.74	20	9.764
6	DF>4 = -45.597 + (0.513)*AGE2 + (-0.625)*ELAS + (106.487)*SLAS + (1.028)*ELEV	0.88	19	6.512

***** PATHWAY REGRESSION EQUATIONS FOR DFAL OR PSEUDOTSUGA MENZIESII (TOTAL) *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	DFAL = 2.688 + (-49.809)*EXP3 + (727.428)*AG11	0.69	26	15.456
2	DFAL = 5.525 + (-44.402)*EXP3 + (625.276)*AG11	0.55	18	20.041
3	DFAL = 140.525 + (-9.019)*EXP3 + (-1.823)*ELEV	0.70	20	14.551
4	DFAL = 86.679 + (-0.685)*AGE8 + (-1.544)*ELEV	0.51	20	11.853
5	DFAL = 59.442 + (-7.203)*EXP3 + (0.072)*SLAS + (-12.925)*SVRT	0.85	20	10.769
6	DFAL = 68.375 + (-0.484)*ASPT + (-0.965)*SLOP + (7.536)*AGE3	0.95	19	5.838

***** PATHWAY REGRESSION EQUATIONS FOR WL<4 OR LARIX OCCIDENTALIS (< 4 INCHES) *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	WL<4 = 6.795 + (-0.028)*PHHA + (-0.099)*ELEV	0.44	18	1.241
2	WL<4 = -31.003 + (0.556)*TREE + (4.346)*EXP3 + (-5.379)*TRMT	0.53	20	11.336
3	WL<4 = -25.003 + (0.556)*TREE + (4.556)*EXP3 + (-5.379)*TRMT	0.58	20	11.336
4	WL<4 = -55.160 + (0.580)*TREE + (1.789)*AGE8	0.62	20	12.453
5	WL<4 = 9.055 + (-0.319)*SLOP	0.42	17	1.216
6	WL<4 = -0.783 + (0.095)*TREE	0.33	21	4.541

***** PATHWAY REGRESSION EQUATIONS FOR LLDN OR LARIX OCCIDENTALIS (X & Y) *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	LLDN= -5.719+(0.031)*TREE+(0.023)*GRSS+(0.049)*ELEV	0.76	18	0.631
2	LLDN= -43.762+(-1.372)*AGE8+(1.696)*FLLV	0.70	20	9.225
3	LLDN= -2.450+(0.156)*TREE	0.35	17	8.057
4	LLDN= -3.456+(0.228)*AGE1	0.51	20	8.562
5	LLDN= 24.466+(-4.696)*EXP3	0.35	20	13.406
6	LLDN= -4.932+(0.207)*TREE+(0.332)*PHMA	0.61	21	7.733

***** PATHWAY REGRESSION EQUATIONS FOR WLAL OR LARIX OCCIDENTALIS (TOTAL) *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	WLAL= 6.795+(-0.028)*PHMA+(-0.099)*ELEV	0.32	19	1.141
2	WLAL= -10.762+(-1.372)*AGE8+(1.696)*ELEV+(1.346)*EXP3+(0.000)*ELEV	0.70	20	9.225
3	WLAL= -21.590+(0.738)*TREE+(7.364)*EXP3+(-0.216)*GRSS+(-4.813)*TRMT	0.59	20	10.004
4	WLAL= 9.588+(0.474)*TREE+(-5.655)*TRMT	0.55	20	13.702
5	WLAL= 26.811+(-4.811)*EXP3	0.45	20	10.222
6	WLAL= 33.342+(-0.988)*AGE8	0.42	19	10.369

***** PATHWAY REGRESSION EQUATIONS FOR ACGL OR ACER GLABRUM *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	ACGL= 0.139+(1.103)*EXP4+(*****)*CCP6	0.55	17	0.317
2	ACGL= 0.442+(1.005)*EXP4+(*****)*CCP6+(-16.139)*EX11+(-0.006)*GRSS	0.94	20	0.246
3	ACGL= 5.111+(0.199)*CCP6	0.31	15	6.491
4	ACGL= 5.111+(0.199)*CCP6	0.31	15	6.491
5	ACGL= 1.135+(7.398)*EXP4	0.56	10	2.132
6	ACGL= 3.135+(7.398)*EXP4	0.56	10	2.132

***** PATHWAY REGRESSION EQUATIONS FOR AMAL OR AMELANCHIER ALNIFOLIA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	AMAL= 1.670+(1.213)*PRED	0.52	19	6.278
2	AMAL= 1.670+(1.213)*PRED	0.52	19	6.208
3	AMAL= 10.649+(0.681)*PRED+(-5.236)*SVMT	0.44	21	9.250
4	AMAL= 12.049+(0.681)*PRED+(-5.236)*SVRT	0.44	21	9.250
5	AMAL= 5.621+(2.484)*CCA2+(-5.967)*CCA6+(-0.062)*CEVE	0.73	17	2.304
6	AMAL= 6.621+(2.484)*CCA2+(-5.967)*CCA6+(-0.062)*CEVE	0.73	17	2.304

***** PATHWAY REGRESSION EQUATIONS FOR CEVE OR CEANOTHUS VELUTINUS *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	CEVE= 2.000+(50.000)*TAGE	0.00	0	0.000
2	CEVE= 2.000+(50.000)*TAGE	0.00	0	0.000
3	CEVE= 0.374+(0.022)*PHMA+(1.079)*EXP7+(-11.889)*ELAS+(80.000)*TAGE	0.52	20	0.478
4	CEVE= 0.374+(0.022)*PHMA+(1.079)*EXP7+(-11.889)*ELAS+(80.000)*TAGE	0.52	20	0.478
5	CEVE= 112.263+(-61.386)*CP11+(-0.054)*EXP5	0.71	20	15.638
6	CEVE= 115.563+(-60.601)*CP11+(-0.055)*EXP5	0.69	19	15.902

***** PATHWAY REGRESSION EQUATIONS FOR LOUT OR LONICERA UTAHENSIS *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	LOUT= -3.378+(0.015)*EXP5+(0.083)*ELEV	0.67	12	7.745
2	LOUT= -0.797+(0.006)*EXP6+(1.355)*CCA2+(0.705)*SVRT+(-0.261)*TRMT	0.59	14	7.088
3	LOUT= 0.377+(0.015)*CARU	0.43	13	0.445
4	LOUT= 0.377+(0.015)*CARU	0.43	13	0.445
5	LOUT= 0.508+(0.023)*CCP1+(-0.019)*TREE+(0.008)*GRSS+(-0.013)*AGE3	0.97	10	0.103
6	LOUT= 0.370+(0.018)*CCP1+(-0.011)*TREE+(0.005)*GRSS	0.81	12	0.219

***** PATHWAY REGRESSION EQUATIONS FOR PHMA OR PHYSOCARPUS MALVACEUS *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	PHMA= 78.568+(0.563)*PRED+(19.033)*EX12+(-0.114)*EXP9+(-1.490)*ELEV	0.77	19	9.891
2	PHMA= 78.568+(0.563)*PRED+(19.033)*EX12+(-0.114)*EXP9+(-1.490)*ELEV	0.77	19	9.891
3	PHMA= 0.000+(1.000)*PRED+(0.220)*EX12	0.99	12	0.010
4	PHMA= 0.000+(1.000)*PRED+(0.220)*EX12	0.99	12	0.010
5	PHMA= 35.668+(-8.590)*CCA6+(-3.391)*SLAS+(*****)*CCP6+(-0.454)*CARU+(-0.612)*AC15	0.94	17	4.634
6	PHMA= 35.668+(-8.590)*CCA6+(-3.391)*SLAS+(*****)*CCP6+(-0.454)*CARU+(-0.612)*AC15	0.94	17	4.634

***** PATHWAY REGRESSION EQUATIONS FOR PRVI OR PRUNUS VIRGINIANA *****

PATH	REGRESSION EQUATION FORM	RSQ	F	STD DEV
1	PRVI= 0.000+(1.000)*CCP9+(1.000)*TSLV	0.00	0	0.000
2	PRVI= 0.000+(1.000)*CCP9+(1.000)*TSLV	0.00	0	0.000
3	PRVI= 0.000+(1.000)*CCP9+(1.000)*TSEV	0.00	0	0.000
4	PRVI= 0.000+(1.000)*CCP9+(1.000)*TSEV	0.00	0	0.000
5	PRVI= 0.000+(1.000)*CCP9+(1.000)*TSEV	0.00	0	0.000
6	PRVI= 0.000+(1.000)*CCP9+(1.000)*TSEV	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR ROGY OR ROSA GYMNOCARPA *****

PATH	REGRESSION EQUATION FORM	RSQ	F	STD DEV
1	ROGY= 8.716+(0.032)*AGE2+(-0.168)*ELEV	0.53	15	0.975
2	ROGY= 8.716+(0.032)*AGE2+(-0.168)*ELEV	0.53	15	0.975
3	ROGY= -0.270+(0.028)*CCP1	0.66	12	0.870
4	ROGY= -0.296+(0.050)*CCF1+(0.090)*GRSS+(-0.022)*TREE+(-0.025)*CARU	0.78	21	0.659
5	ROGY= 0.592+(0.026)*CCP1+(-0.017)*CARU	0.89	11	0.275
6	ROGY= 0.919+(0.044)*CCP1+(-0.288)*CCP3	0.85	15	0.439

***** PATHWAY REGRESSION EQUATIONS FOR SASC OR SALIX SCOULERIANA *****

PATH	REGRESSION EQUATION FORM	RSQ	F	STD DEV
1	SASC= 0.068+(0.006)*EXP6	0.39	20	0.946
2	SASC= 0.068+(0.006)*EXP6	0.39	20	0.946
3	SASC= -0.359+(0.120)*AGE8+(1.077)*PRED	0.91	17	0.505
4	SASC= -0.359+(0.120)*AGE8+(1.077)*PRED	0.91	17	0.505
5	SASC= -1.045+(0.305)*GRSS	0.40	10	5.464
6	SASC= -1.045+(0.305)*GRSS	0.40	10	5.464

***** PATHWAY REGRESSION EQUATIONS FOR SPBE OR SPIRAEA RETULIFOLIA *****

PATH	REGRESSION EQUATION FORM	RSQ	F	STD DEV
1	SPBE= 4.509+(0.142)*AGE3+(-1.883)*CCA2+(-0.125)*CCP1	0.95	17	3.287
2	SPBE= 44.642+(3.837)*CCA2+(-1.063)*ELEV+(0.416)*SLOP	0.68	19	6.523
3	SPBE= -25.453+(0.691)*PRED+(1.002)*SLOP+(6.905)*SVRT	0.83	13	7.905
4	SPBE= 52.550+(0.129)*AGE3+(-0.936)*ELEV	0.75	15	4.028
5	SPBE= -2.955+(0.101)*AGE3+(-0.257)*PHMA+(0.716)*SLOP	0.66	29	7.517
6	SPBE= 42.704+(0.099)*AGE3+(-0.160)*TREE+(-0.649)*ELEV	0.60	35	7.726

***** PATHWAY REGRESSION EQUATIONS FOR SYAL OR SYMPHORICARPOS ALBUS *****

PATH	REGRESSION EQUATION FORM	RSQ	F	STD DEV
1	SYAL= -1.259+(1.131)*PRED+(1.628)*CEVE	0.98	13	3.134
2	SYAL= -14.329+(0.359)*TREE+(5.079)*CEVE+(0.278)*PHMA	0.48	19	13.743
3	SYAL= 1.027+(0.192)*CCP1+(-2.457)*AGE3	0.45	16	5.304
4	SYAL= -0.390+(0.029)*GRSS	0.78	8	0.552
5	SYAL= 3.708+(0.404)*CCP1+(-0.282)*CARU	0.84	13	5.576
6	SYAL= 3.708+(0.404)*CCP1+(-0.282)*CARU	0.84	13	5.576

***** PATHWAY REGRESSION EQUATIONS FOR VAGL OR VACCINIUM GLOBULARE *****

PATH	REGRESSION EQUATION FORM	RSQ	F	STD DEV
1	VAGL= -8.970+(2.458)*CEVE+(0.019)*ELEV	0.96	9	0.644
2	VAGL= -8.970+(2.458)*CEVE+(0.019)*ELEV	0.96	9	0.644
3	VAGL= 0.000+(1.000)*PRED+(2.000)*TSEV	0.00	0	0.000
4	VAGL= 0.000+(1.000)*PRED+(2.000)*TSLV	0.00	0	0.000
5	VAGL= 0.000+(1.000)*PRED+(2.000)*TSEV	0.00	0	0.000
6	VAGL= 0.000+(1.000)*PRED+(2.000)*TSLV	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR ARUV OR ARTOSTAPHYLOS UVA-URSI *****

PATH	REGRESSION EQUATION FORM	RSQ	F	STD DEV
1	ARUV= -2.461+(0.009)*EXP2+(0.066)*ASPT	0.77	20	2.995
2	ARUV= 4.968+(6.071)*EXP4+(-5.323)*SLAS	0.77	11	3.987
3	ARUV= 14.539+(0.074)*AGE3+(-0.276)*ELEV	0.99	8	1.871
4	ARUV= 0.454+(0.076)*AGE3+(235.881)*AG18+(-0.030)*PHMA	0.98	21	3.139
5	ARUV= 87.137+(-1.537)*ELEV+(-0.207)*CEVE+(0.041)*AGE3	0.92	11	4.752
6	ARUV= 96.082+(-1.412)*ELEV+(-0.232)*CEVE+(-5.860)*TRMT	0.94	10	3.947

***** PATHWAY REGRESSION EQUATIONS FOR NERE OR NEREPIS HEPPYS *****

PATH	REGRESSION EQUATION FORM	R ²	N	STD DEV
1	NERE= 4.340*(-0.156)*SLOP+(0.290)*CCA2	0.40	19	1.262
2	NERE= -7.499*(-0.163)*SLOP+(0.264)*FLLV	0.53	20	1.442
3	NERE= 0.551*(0.001)*AGE2	0.44	16	1.710
4	NERE= 0.051*(0.001)*AGE2	0.48	16	1.700
5	NERE= 0.271*(1.444)*CCA2	0.72	19	1.669
6	NERE= 0.271*(1.444)*CCA2	0.72	18	1.449

***** PATHWAY REGRESSION EQUATIONS FOR LIRO OR LINNAEA HOHEALIS *****

PATH	REGRESSION EQUATION FORM	R ²	N	STD DEV
1	LIRO= -1.262*(0.775)*TREE	0.99	4	0.574
2	LIRO= -15.042*(4.283)*AGE3+(0.367)*GRSS+(3.499)*CCAG	0.98	9	4.205
3	LIRO= 16.729*(0.506)*CARU+(0.217)*TRLE	0.66	11	5.640
4	LIRO= -11.746*(0.566)*CARU+(4.208)*SVRT	0.55	21	6.259
5	LIRO= 0.000*(0.000)*PHED+(1.000)*TSEV	0.00	0	0.000
6	LIRO= 101.517*(0.637)*CARU+(*****)*EXP9+(0.000)*SLOP	0.99	0	62.436

***** PATHWAY REGRESSION EQUATIONS FOR AGSP OR AGROPYRON SPICATUM *****

PATH	REGRESSION EQUATION FORM	R ²	N	STD DEV
1	AGSP= 0.000*(0.750)*PRED+(2.000)*EXP9	0.00	0	0.000
2	AGSP= 0.000*(0.750)*PRED+(2.000)*EXP9	0.00	0	0.000
3	AGSP= 0.000*(0.750)*PRED+(2.000)*EXP9	0.00	0	0.000
4	AGSP= 0.000*(0.750)*PRED+(2.000)*EXP9	0.00	0	0.000
5	AGSP= 0.000*(0.750)*PRED+(2.000)*EXP9	0.00	0	0.000
6	AGSP= 0.000*(0.750)*PRED+(2.000)*EXP9	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR CARU OR CALAMAGROSTIS RUBESCENS *****

PATH	REGRESSION EQUATION FORM	R ²	N	STD DEV
1	CARU= -11.053*(1.250)*PRED+(0.283)*PHMA+(-0.030)*AGE1	0.95	12	1.750
2	CARU= -11.053*(1.250)*PRED+(0.283)*PHMA+(-0.030)*AGE1	0.95	12	1.750
3	CARU= 14.342*(0.871)*PRED+(-6.007)*1/CC+(-0.307)*CCP1	0.87	44	10.212
4	CARU= 14.342*(0.871)*PRED+(-6.007)*1/CC+(-0.307)*CCP1	0.87	44	10.212
5	CARU= -18.928*(0.776)*TREE+(10.835)*TRMT	0.63	17	15.244
6	CARU= -18.928*(0.776)*TREE+(10.835)*TRMT	0.63	17	15.244

***** PATHWAY REGRESSION EQUATIONS FOR CACO OR CAREX CONCINNUOIDES *****

PATH	REGRESSION EQUATION FORM	R ²	N	STD DEV
1	CACO= 2.975*(-0.101)*SLOP+(0.869)*1/CC	0.75	10	0.445
2	CACO= 3.568*(-0.109)*SLOP	0.72	10	0.442
3	CACO= -3.350*(8.752)*EXP7+(0.164)*SLOP	0.55	7	4.656
4	CACO= -20.073*(0.229)*SLOP+(0.253)*ELEV+(1.273)*TRMT+(0.020)*C1P6	0.85	21	1.168
5	CACO= 0.500*(0.142)*EX10	0.00	9	0.000
6	CACO= 0.500*(0.142)*EX10	0.99	9	0.000

***** PATHWAY REGRESSION EQUATIONS FOR CAGE OR CAREX GYNERI *****

PATH	REGRESSION EQUATION FORM	R ²	N	STD DEV
1	CAGE= -2.080*(0.993)*PRED+(-0.036)*AGE2	0.60	13	10.071
2	CAGE= -2.080*(0.993)*PRED+(-0.036)*AGE2	0.60	13	10.071
3	CAGE= 10.124*(0.805)*PRED+(-13.000)*EXP4+(-0.105)*CCP1	0.53	21	12.059
4	CAGE= 10.124*(0.805)*PRED+(-13.000)*EXP4+(-0.105)*CCP1	0.53	21	12.059
5	CAGE= 13.394*(7.508)*EXP4+(-0.277)*FLLV	0.40	20	4.347
6	CAGE= 16.912*(8.417)*EXP7+(0.262)*PHMA+(-0.455)*ELEV	0.78	14	3.277

***** PATHWAY REGRESSION EQUATIONS FOR CARD OR CAREX ROSSII *****

PATH	REGRESSION EQUATION FORM	R ²	N	STD DEV
1	CARD= 0.000*(0.900)*PRED	0.00	0	0.000
2	CARD= 0.000*(0.900)*PRED	0.00	0	0.000
3	CARD= 0.030*(0.001)*AGE3	0.44	15	0.134
4	CARD= 0.030*(0.001)*AGE3	0.44	15	0.134
5	CARD= 0.000*(0.900)*PRED	0.00	0	0.000
6	CARD= 0.000*(0.900)*PRED	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR FCHI OR ACHILLEA MELLEIFOLIA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	ACFI= 0.163*(0.310)*EX11	0.51	26	0.169
2	ACFI= 0.163*(0.310)*EX11	0.51	26	0.169
3	ACFI= 1.024*(-0.013)*TREE	0.48	20	0.795
4	ACFI= 1.024*(-0.013)*TREE	0.48	20	0.795
5	ACFI= 2.485*(-0.070)*PHFA	0.54	9	0.954
6	ACFI= 2.485*(-0.070)*PHFA	0.54	9	0.954

***** PATHWAY REGRESSION EQUATIONS FOR ANRA OR ANTENNARIA RACEMOSA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	ANRA= -15.153*(2.520)*CEVE*(-3.433)*EXP4*(0.361)*ELEV	0.75	13	2.313
2	ANRA= 0.733*(0.752)*PRED	0.74	13	2.572
3	ANRA= -3.124*(9.692)*EXP4*(0.145)*SLOP*(-1.750)*CP10	0.70	20	1.079
4	ANRA= -2.778*(7.289)*EXP4*(-0.004)*EXP9*(0.136)*SLOP	0.68	21	1.087
5	ANRA= 0.025*(0.036)*CARU	0.59	8	0.804
6	ANRA= 0.025*(0.036)*CARU	0.59	8	0.804

***** PATHWAY REGRESSION EQUATIONS FOR ARCO OR ARNICA CORDIFOLIA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	ARCO= 0.440*(0.032)*TREE	0.99	8	0.002
2	ARCO= -0.929*(0.211)*CCP1	0.91	9	2.174
3	ARCO= -0.557*(0.149)*CCP1*(0.148)*TREE	0.92	8	0.482
4	ARCO= -0.594*(0.081)*SLAS*(*****)*CCP6*(0.002)*ASPT*(-0.100)*TRMT	0.96	13	0.056
5	ARCO= -0.926*(0.123)*CCP1	0.48	29	3.021
6	ARCO= -0.926*(0.123)*CCP1	0.48	29	3.021

***** PATHWAY REGRESSION EQUATIONS FOR ASCO OR ASTER CONSPICUUS *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	ASCO= 3.716*(0.125)*CARU*(-2.908)*SVRT	0.36	21	5.198
2	ASCO= -2.025*(*****)*CCP6*(0.048)*GRSS	0.78	28	2.389
3	ASCO= -10.277*(0.187)*SLOP*(0.150)*ELEV*(0.038)*SHRB*(-0.011)*GRSS	0.84	15	0.549
4	ASCO= -0.871*(0.091)*SLOP	0.33	20	1.090
5	ASCO= 35.619*(-1.193)*SLOP*(5.302)*SLAS	0.76	11	3.915
6	ASCO= 36.747*(-3.349)*TRMT*(-0.920)*SLOP*(4.888)*SLAS	0.68	15	3.643

***** PATHWAY REGRESSION EQUATIONS FOR BASA OR BALSAMORHIZA SAGITTATA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	BASA= 0.000*(0.900)*PRED*(2.000)*TSEV	0.00	0	0.000
2	BASA= 0.000*(0.900)*PRED*(2.000)*TSEV	0.00	0	0.000
3	BASA= 0.000*(0.900)*PRED*(2.000)*TSEV	0.00	0	0.000
4	BASA= 0.000*(0.900)*PRED*(2.000)*TSEV	0.00	0	0.000
5	BASA= 0.000*(0.900)*PRED*(2.000)*TSEV	0.00	0	0.000
6	BASA= 0.000*(0.900)*PRED*(2.000)*TSEV	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR CHUM OR CHIMAPHILLA UMBELLATA *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	CHUM= 0.000*(0.750)*PRED*(2.000)*TSEV	0.00	0	0.000
2	CHUM= 0.000*(0.750)*PRED*(2.000)*TSEV	0.00	0	0.000
3	CHUM= -4.343*(0.022)*CARU*(0.026)*TREE*(-0.024)*CCP1*(0.071)*ELEV*(0.231)*TRMT	0.74	20	0.398
4	CHUM= -4.343*(0.022)*CARU*(0.026)*TREE*(-0.024)*CCP1*(0.071)*ELEV*(0.231)*TRMT	0.74	20	0.398
5	CHUM= 6.000*(-2.500)*SVRT	0.97	7	0.000
6	CHUM= 6.000*(-2.500)*SVRT	0.97	7	0.000

***** PATHWAY REGRESSION EQUATIONS FOR EPAN OR EPILOBIUM ANGUSTIFOLIUM *****

PATH	REGRESSION EQUATION FORM	R SQ	N	STD DEV
1	EPAN= 0.010*(3.030)*1/CC	0.90	8	0.243
2	EPAN= 0.010*(3.030)*1/CC	0.90	8	0.243
3	EPAN= 0.350*(8.883)*EXP4*(-1.567)*CEVE*(70.000)*TAGE	0.72	10	1.341
4	EPAN= -2.875*(2.076)*SVRT*(4.297)*EXP4*(70.000)*TAGE	0.72	9	1.249
5	EPAN= 0.401*(-0.005)*TREE	0.36	21	0.208
6	EPAN= -3.634*(3.776)*CCP4	0.40	19	0.255

***** PATHWAY REGRESSION EQUATIONS FOR FRVE OR FRAGARIA VESCA *****

PATH	REGRESSION EQUATION FORM	RSD	N	STD DEV
1	FRVE= -13.367+(6.366)*SVPT+(0.958)*CCA2+(0.101)*CARU	0.53	14	2.778
2	FRVE= -10.722+(0.204)*ASPT+(0.023)*ELAS	0.40	17	4.522
3	FRVE= 0.101+(0.825)*PRED	0.73	8	0.188
4	FRVE= 0.101+(0.825)*PRED	0.73	8	0.168
5	FRVE= -0.333+(1.667)*PRED	0.99	8	0.001
6	FRVE= -0.333+(1.667)*PRED	0.99	8	0.001

***** PATHWAY REGRESSION EQUATIONS FOR FRVI OR FRAGARIA VIRGINIANA *****

PATH	REGRESSION EQUATION FORM	RSD	N	STD DEV
1	FRVI= 0.000+(0.900)*PRED+(1.000)*TSEV	0.00	0	0.000
2	FRVI= 0.000+(0.900)*PRED+(1.000)*TSEV	0.00	0	0.000
3	FRVI= 0.101+(0.825)*PRED	0.73	8	0.108
4	FRVI= 0.113+(4.542)*EXP4	0.42	19	1.292
5	FRVI= 0.571+(0.040)*CCP1+(-0.016)*GRSS	0.85	10	0.350
6	FRVI= 0.500+(-0.001)*AGE3+(0.000)*AGE2+(0.000)*SHRB	0.99	13	0.000

***** PATHWAY REGRESSION EQUATIONS FOR GOOB OR GOODYERA C/PLONGIFOLIA *****

PATH	REGRESSION EQUATION FORM	RSD	N	STD DEV
1	GOOB= 0.000+(0.900)*PRED+(1.000)*TSEV	0.00	0	0.000
2	GOOB= 0.000+(0.900)*PRED+(1.000)*TSEV	0.00	0	0.000
3	GOOB= 0.000+(0.900)*PRED+(1.000)*TSEV	0.00	0	0.000
4	GOOB= 0.000+(0.900)*PRED+(1.000)*TSEV	0.00	0	0.000
5	GOOB= 0.000+(0.900)*PRED+(1.000)*TSEV	0.00	0	0.000
6	GOOB= 0.000+(0.900)*PRED+(1.000)*TSEV	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR HIAL OR HIERACIUM ALBERTINUM & CYNOGLO *****

PATH	REGRESSION EQUATION FORM	RSD	N	STD DEV
1	HIAL= 0.500+(0.000)*DUMY	0.00	0	0.000
2	HIAL= 0.500+(0.000)*DUMY	0.00	0	0.000
3	HIAL= -1.209+(0.034)*ELEV+(-0.012)*PHMA+(0.012)*SHRB+(-0.092)*CCAG	0.68	20	0.162
4	HIAL= -1.209+(0.034)*ELEV+(-0.012)*PHMA+(0.012)*SHRB+(-0.092)*CCAG	0.68	20	0.162
5	HIAL= 0.500+(0.000)*DUMY	0.00	0	0.000
6	HIAL= 0.500+(0.000)*DUMY	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR MIST OR MITELLA STAUIPETALA *****

PATH	REGRESSION EQUATION FORM	RSD	N	STD DEV
1	MIST= 0.473+(0.213)*EX12	0.98	12	0.092
2	MIST= 0.473+(0.213)*EX12	0.98	12	0.092
3	MIST= 0.473+(0.213)*EX12	0.98	12	0.092
4	MIST= 0.473+(0.213)*EX12	0.98	12	0.092
5	MIST= 0.473+(0.213)*EX12	0.98	12	0.092
6	MIST= 0.473+(0.213)*EX12	0.98	12	0.092

***** PATHWAY REGRESSION EQUATIONS FOR THOC OR THALICTRUM OCCIDENTALE *****

PATH	REGRESSION EQUATION FORM	RSD	N	STD DEV
1	THOC= 0.298+(0.570)*CCA2	0.94	9	1.337
2	THOC= -6.053+(0.166)*ELEV+(-0.021)*PHMA	0.81	9	0.592
3	THOC= 0.000+(1.000)*PRED	0.99	8	0.000
4	THOC= 0.000+(1.000)*PRED	0.99	8	0.000
5	THOC= 0.500+(0.900)*PRED+(1.000)*TSEV	0.00	0	0.000
6	THOC= 0.500+(0.900)*PRED+(1.000)*TSEV	0.00	0	0.000

***** PATHWAY REGRESSION EQUATIONS FOR XETE OR XEROPHYLLUM TENAX *****

PATH	REGRESSION EQUATION FORM	RSD	N	STD DEV
1	XETE= -2.131+(3.588)*EXP4+(0.074)*ASPT	0.46	28	3.811
2	XETE= -2.131+(3.588)*EXP4+(0.074)*ASPT	0.46	28	3.811
3	XETE= 6.067+(-1.293)*TRMT+(0.603)*CCA2	0.63	10	2.143
4	XETE= 5.495+(0.052)*ASPT+(-1.183)*TRMT+(-0.136)*SLOP	0.59	20	1.969
5	XETE= -1.865+(0.099)*CARU+(0.160)*SHRB	0.93	8	1.011
6	XETE= 9.228+(-0.303)*SLOP+(-0.050)*PHMA	0.45	19	1.674

APPENDIX F

Sample of Tabular Output Generated by the Model.

.....
 TITLE OF THE SIMULATION RUN: SUCCESSIONAL SIMULATION RUN

DESCRIPTION OF THE SIMULATION AREA:
 ELEVATION : 3500 FEET
 ASPECT : 190 DEGREES
 SLOPE : 45.4 (PERCENT)
 TREATMENT TYPE : WILDFIRE
 INTENSITY TYPE : MODERATE
 HABITAT TYPE PHASE : PSME/PHMA, DRY

A DIAGRAM OF THE MODELED SUCCESSIONAL PATHWAY

SHRUB-HERB SAPLING POLE MATURE SEPAL CLIMAX
 PHMA ----> PSME/PHMA ----> PSME/PHMA ----> PSME/PHMA ----> PSME/PHMA

.....
 PERCENT COVERAGE BY SPECIES FOR SPECIFIED AGES

SPECIES NAME	5	30	55	80	105	130	155	200
TOTAL TREE CANOPY COVER (%)	0	26 - 50	51 - 75	51 - 75	51 - 75	51 - 75	51 - 75	51 - 75
AVERAGE DBH OF STAND (INCHES)	0	4	8	10	12	13	14	14
AVERAGE STAND BASAL AREA (SQ FT)	0	46	96	129	150	163	170	174
PSEUDOTSUGA MENZIESII (< 4 IN.)	0	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25
PSEUDOTSUGA MENZIESII (> 4 IN.)	0	6 - 25	6 - 25	26 - 50	26 - 50	26 - 50	26 - 50	26 - 50
PSEUDOTSUGA MENZIESII (TOTAL)	0	26 - 50	51 - 75	51 - 75	51 - 75	51 - 75	51 - 75	51 - 75
ACER GLABRUM	0	0	0	0	0	0	0	0
AMELANCHIER ALNIFOLIA	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25
CEANOTHUS VELUTINUS	T	T	0	0	0	0	0	0
LONICERA UTAMENSIS	T	T	T	T	T	T	T	T
PHYSOCARPUS MALVACEUS	26 - 50	26 - 50	26 - 50	26 - 50	26 - 50	26 - 50	26 - 50	26 - 50
PRUNUS VIRGINIANA	T	T	T	T	T	T	T	T
ROSA GYMNOCARPA	T	T	T	T	T	T	T	T
SALIX SCOULEMANA	T	T	T	T	T	T	T	T
SPIRAEA BETULIFOLIA	6 - 25	0	0	0	T - 5	T - 5	6 - 25	6 - 25
SYMPHORICARPOS ALBUS	6 - 25	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5
VACCINIUM GLAUCULAPE	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5
ARTOSTAPHYLOS UVA-URSI	T - 5	6 - 25	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5
REPERIS REPENS	T - 5	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	T - 5
LINNAEA BOREALIS	T	T	T	T	T	T	T	T
AGROPYRON SPICATUM	T	0	0	0	0	T	T	T
CALAMAGROSTIS RURESCENS	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25
CAREX CONCINNOIDES	0	0	0	0	0	0	0	0
CAREX GUYERI	26 - 50	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25
CAREX ROSSII	26 - 50	26 - 50	26 - 50	26 - 50	26 - 50	26 - 50	26 - 50	26 - 50
ACHILLEA MILLEFOLIUM	T	T	T	T	T	T	T	T
AMITERNARIA RACEMOSA	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5
ARNICA COPPOLIFOLIA	0	0	0	0	0	0	0	0
ASTER CONSPICUUS	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5	T - 5
BALSAMORHIZA SAGITTATA	T	T	T	T	T	T	T	T
CHIMAPHILLA UMBELLATA	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25	6 - 25
EPILOBIUM ANGUSTIFOLIUM	T	T	0	0	0	0	0	0
FRAGARIA VESCA	T - 5	6 - 25	6 - 25	T - 5	T - 5	T	0	0
FRAGARIA VIRGINIANA	T	T	T	T	T	T	T	T
GOODYERHA OBLONGIFOLIA	T	T	T	T	T	T	T	T
HIERACIUM ALBERTINUM & CYCLOGLO	T	T	T	T	0	0	0	0
MITELLA STALUROPETALA	T - 5	T	T	T	T	T	T	T
THALICTRUM OCCIDENTALE	T	T	T	T	T	T	T	T
XEROPHYLLUM TENAX	T	T	T	T	T	T	T	T

THE STATISTICS FOR CCAL ARE:
 STANDARD DEVIATION = 16.538 R SQUARE = 74 DEGREES OF FREEDOM = 24

THE STATISTICS FOR PHMA ARE:
 STANDARD DEVIATION = 17.686 R SQUARE = 50 DEGREES OF FREEDOM = 27

THE STATISTICS FOR AMAL ARE:
 STANDARD DEVIATION = 1.615 R SQUARE = 62 DEGREES OF FREEDOM = 11

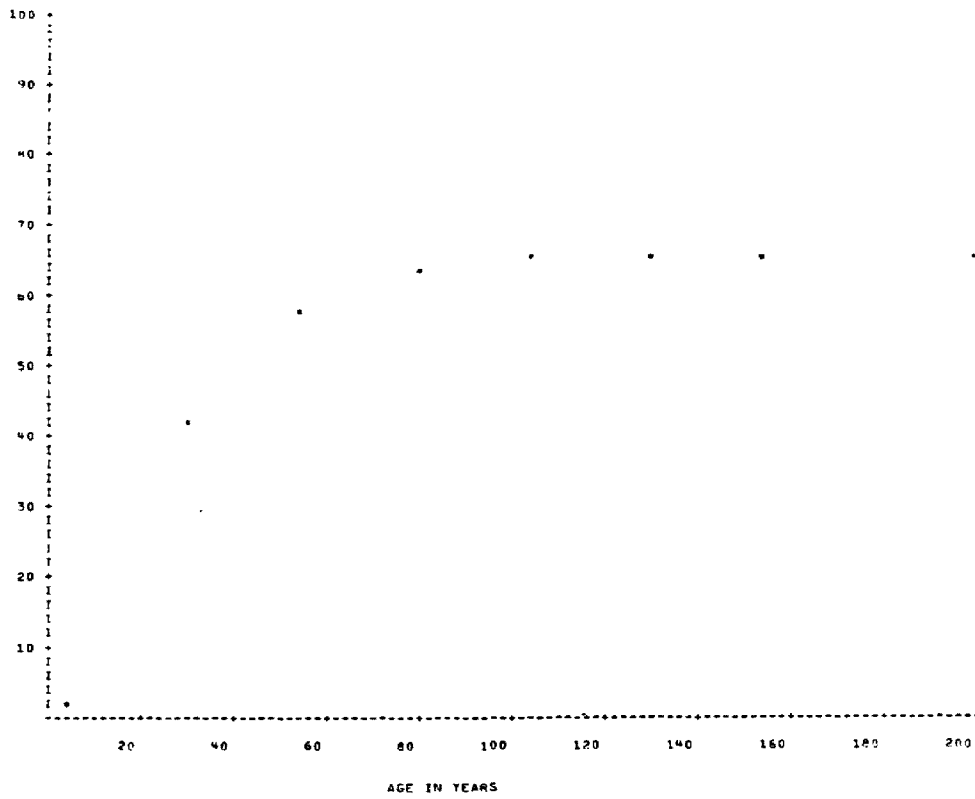
THE STATISTICS FOR ARCO ARE:
 STANDARD DEVIATION = 0.445 R SQUARE = 85 DEGREES OF FREEDOM = 83

APPENDIX G

Sample of Graphic Output Generated by the Model.

TITLE: SUCCESSIONAL SIMULATION RUN

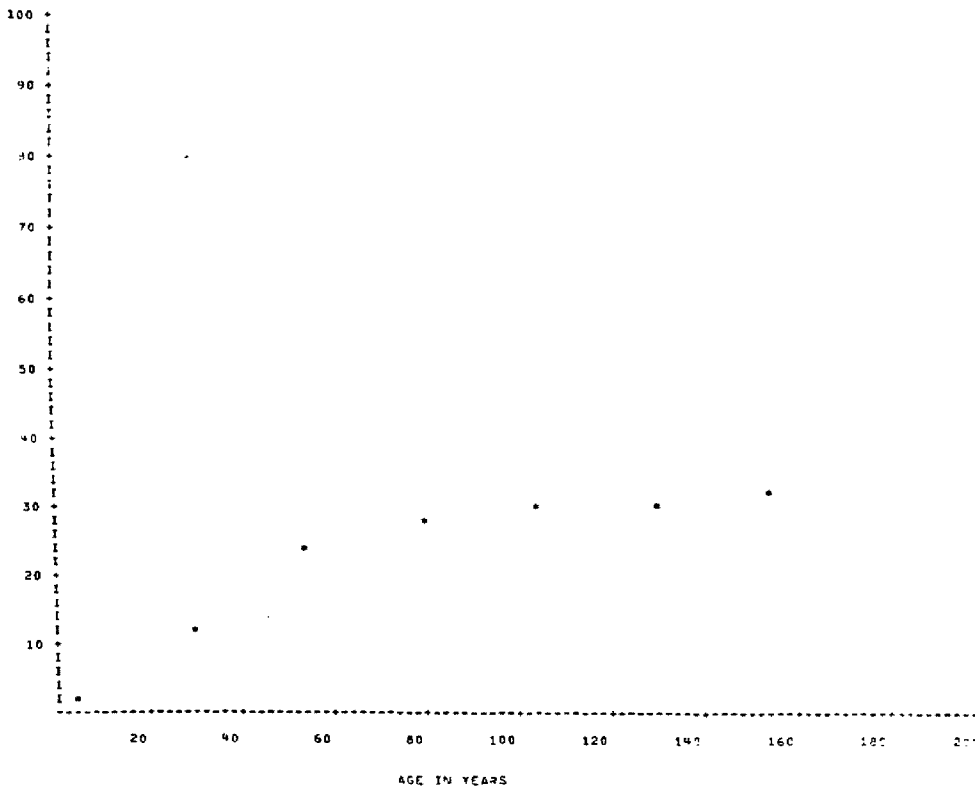
FOR SPECIES: DF>4



THE Y-AXIS IS IN PERCENT COVER (%)

TITLE: SUCCESSIONAL SIMULATION RUN

FOR SPECIES: DF>4



THE Y-AXIS IS IN PERCENT COVER (%)