

TOWARDS TECHNOLOGY TRANSFER
OF A ROOT DISEASE MODEL IN B.C.
MODEL DEMONSTRATION
AND EVALUATION

by

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Foreword

This Pest Control project was funded unilaterally by the Province under the Canada - British Columbia Forest Resources Development Agreement (FRDA), 1985-1990, in the Intensive Forest Management Program, Subprogram Brushing, Weeding and Pest Control.

The project was undertaken to determine if a root disease model developed by the U.S. Forest Service could be useful in southern interior forests of B.C. Opinions and recommendations are those of the contractor, and not necessarily those of the governments or the FRDA management.

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1.0 INTRODUCTION

1.1 Background

Root diseases are pervasive throughout most of the forested lands of western North America. Smith (1984) estimated that root diseases cause an annual average timber loss in the western United States of almost 240 million board feet. In British Columbia alone, estimates of losses of Douglas fir to one root disease species - Phellinus weirii - exceed 1 million cubic meters annually (Wallis, 1976). Problems with root diseases occur throughout the province, with coastal stands being primarily attacked by Phellinus; while interior stands may be subject to Phellinus, Armillaria, blackstain, or tomentosus root diseases.

In response to the effects of root diseases, the U.S. Forest Service and ESSA Ltd. recently completed development of a simulation model of root disease impacts to be used in silvicultural planning. This model simulates the spread of Armillaria and Phellinus root diseases, and calculates their impacts on stand growth, yield and mortality. The model was developed through cooperation between root disease and stand growth research scientists, silviculturalists, and forest pest managers. Members of the development team included staff from the B.C. Ministry of Forests and Lands, and the Canadian Forest Service. The model development effort also included model sensitivity analysis, development of model user guides, improved root disease inventory procedures, and a model communication package. The resulting model represents the best current understanding of root disease dynamics in western North America. It is now being used by silvicultural planners in the USFS on a pilot project basis.

1.2 Project Objectives

Discussions between BCMFL staff members and ESSA Ltd. indicated substantial interest in using this model for exploring alternative management regimes in B.C. stands.

Interest was expressed in using the model initially as a technology transfer tool, to help make forest and pest managers more aware of the effects of different management activities on root disease. Through a preliminary exploratory application of the model, the BCMFL wanted to assess how useful the model was to managers, and to develop a strategy for model implementation in the BCMFL, based on the need for such a modeling tool.

Therefore, the objectives of this project were to:

1. develop and simulate a number of root disease control and management scenarios for some example B.C. stands;
2. present the results of these scenarios, along with a description of the root disease model to groups of forest and pest managers in workshop sessions; and
3. assess the utility of the root disease model for B.C. based on the results of these workshops, and develop recommendations for implementation of a root disease model in the BCMFL.

1.3 Description of this Report

The remainder of this report consists of three main sections. Section 2 gives a detailed description of the structure and operation of the root disease model. Section 3 presents the scenario results and discusses the implications of the results for root disease management in the B.C. Interior. Section 4 summarizes the discussions held during the workshops on the utility of the model for forest managers in B.C., and outlines a process for an implementation of the root disease model into the BCMFL system.

2.0 DESCRIPTION OF THE ROOT DISEASE MODEL

2.1 Overview of the Model

The root disease model (McNamee et al. 1986) simulates the dynamics of infection and spread of Armillaria spp. and Phellinus weirii root disease from tree to tree inside centers or patches of infection. The model uses the spatial relationships between location of inoculum patches, and the distribution, species, and sizes of trees in the stand (as well as other factors) to predict the spread of infection. Persistence of infection between stand rotations is also simulated.

The major relationships captured in the model are: the relative susceptibilities of trees to infection and death resulting from root disease attack, disease related growth reductions, decay of infected root systems, and lifespan of root disease pathogens. Physical or biological events that weaken or kill trees (including windthrow, and attack by pine beetles or bark beetles) can optionally be included in the simulation.

Major Model Components

The system of models that collectively comprise the root disease model are shown in Figure 2.1. The stand growth model to which the root disease submodels are attached is responsible for simulating stand growth and mortality dynamics, and for implementing stand management actions (such as harvesting, thinning, regeneration, etc.). A brief description of the PROGNOSIS stand model (to which the root disease model is currently attached) is provided in section 2.2 below.

The root disease model itself is divided into the following three major submodels:

1. **Stand Interface.** This model computes the sum effects of root disease and other agent impacts on the stand growth and yield indicators;

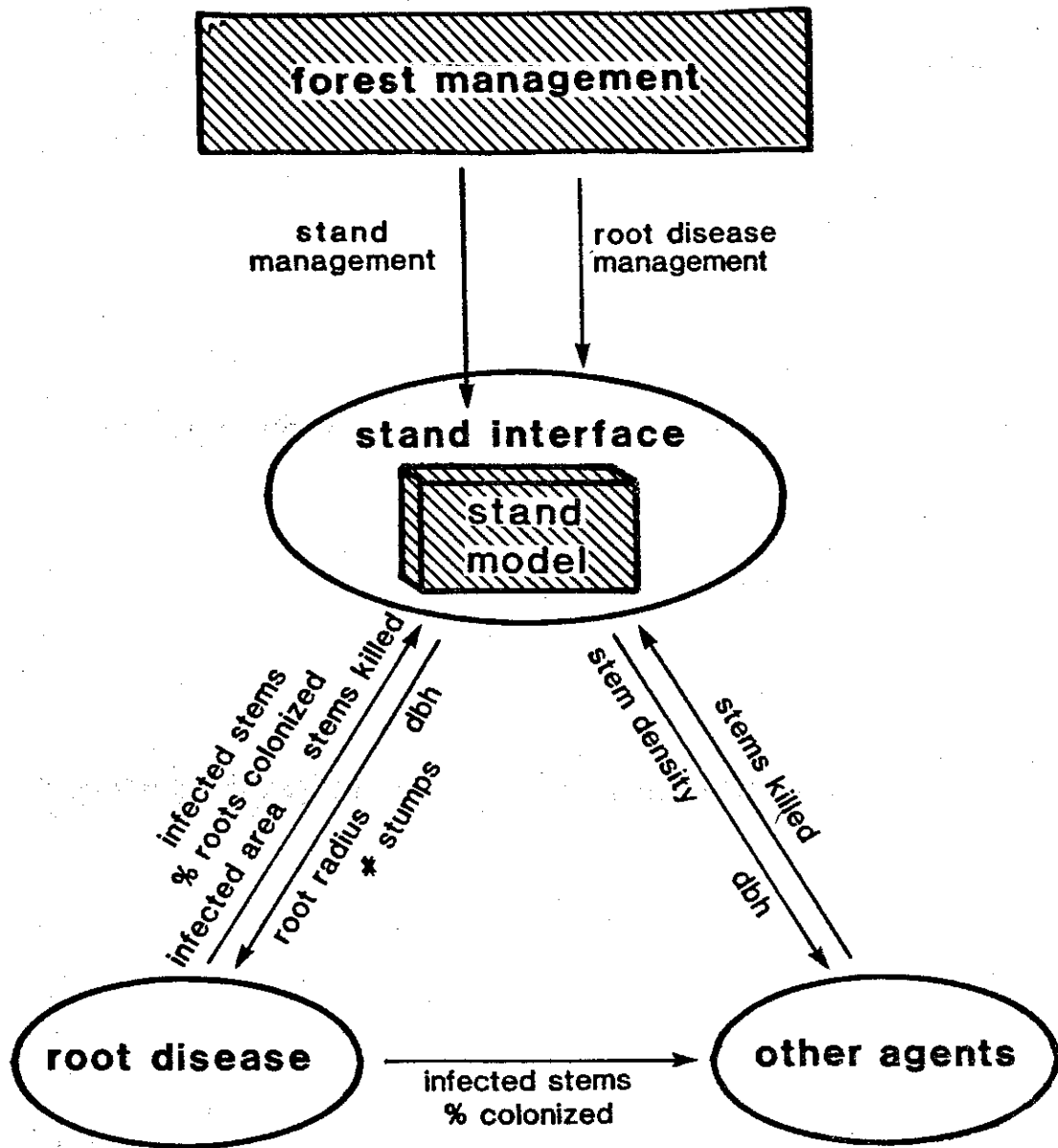


Figure 2.1. Primary components of the root disease model. The major root disease components are enclosed by ellipses; the major stand growth components are shaded. Also shown are the types of information that pass between model components.

2. **Root Disease.** This submodel computes the spread of root disease and its impact on the stand, given the nature of the host stand and management actions taken in the stand. It can simulate the dynamics of either Armillaria spp. or Phellinus weirii; and
3. **Other Agents.** This submodel computes the impact of other major sources of timber mortality in the stand which may influence root disease dynamics.

Figure 2.2 shows the order of calculations in the combined root disease/stand growth model. It delineates those major calculations which already exist in stand growth simulators (such as PROGNOISIS), and those which were developed as part of the root disease modeling project.

The major root disease submodels are described in more detail in sections 2.3 - 2.5 below.

Management Actions and Indicators

There are two major classes of management actions in the model (Table 2.1): actions that influence the nature of the forest and actions that directly influence the spread and impact of root diseases. Most of these management actions are under the control of the stand growth model itself. The root disease model implements only one management action specifically used for control of root disease - that of "pushing" or removal of infected stumps and their root systems. This option can be requested in specific years and with a factor specifying the efficiency with which roots are removed.

Management indicators are those variables which are used to evaluate the consequences of management actions on the stand and on root disease. There are two classes of indicators in the model (Table 2.2): indicators of the biological status of the timber resource, and indicators pertaining to the progression and impact of the root disease itself.

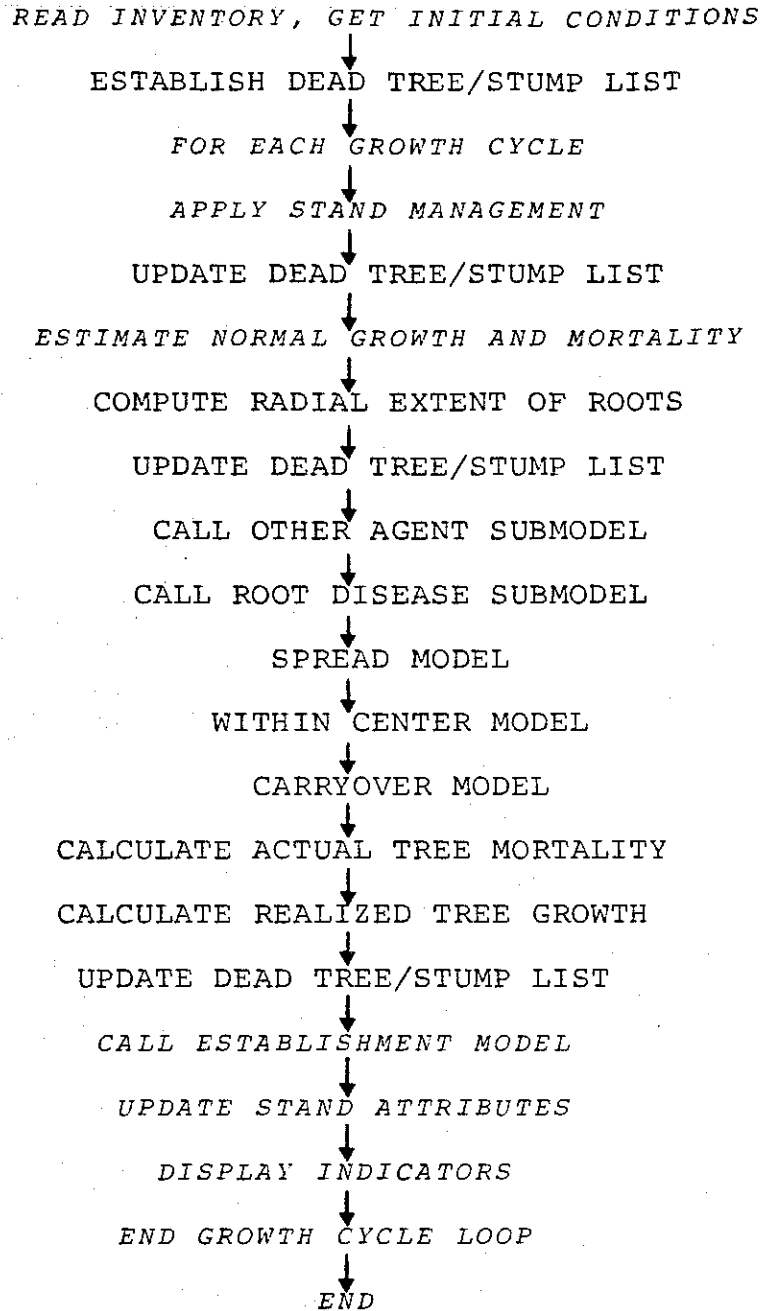


Figure 2.2. Order of calculations in the root disease/stand model. Italicized steps are contained in Prognosis.

Table 2.1. Management actions for the stand and for root disease.

A. Species Manipulations

- shelterwood
- clearcut, plant species
- clearcut without planting
- selective thinning
- understory fire
- seed source selection
- fire management
- sanitation cutting
 - diseased trees
- Site Preparation
 - burning
 - fertilization
 - scarification

B. Direct Root Disease Treatment

- stump removal

Table 2.2. Management indicators for the modeled stand as a whole and for root diseased areas.

A. Stand

- sample tree attributes
 - growth rate
 - mortality rate
 - height
 - diameter
 - volume
- stand attributes
 - periodic annual increment
 - volume
 - species composition
 - diameter distribution
 - basal area
 - tree height
 - stand density

B. Root Disease

- area infected
- # infected stumps/unit area, by diameter class and species
- spread rate
- number of trees killed
- volume of wood killed
- number of root disease centers
- basal area inside root diseased area
- wood volume inside root diseased area
- density of infected and uninfected trees inside root diseased areas

Spatial Resolution of the Model

The model provides a detailed representation of timber and root disease dynamics within a single stand. This is an area ranging in size from 5 to hundreds of acres, and can be considered homogeneous in terms of physical characteristics such as slope. This level of spatial resolution is most useful for silvicultural planning, and at the same time preserves the essential spatial dynamics of root diseases.

Within the modeled stand, the model maintains essentially two separate areas: those areas not currently infected with root disease (areas "outside" root disease centers), and those areas "inside" root disease infection centers. The infected portion is further disaggregated into separate circular infection centers, each characterized by the location of their centers and their radii. This spatial resolution allows expanding infection centers to be modeled as unique entities with expansion rates which can be calculated according to certain rules (see section 2.4.3 below). In addition, the residual distribution of inoculum in the stand (e.g. after a clearcut) can be considered, and the probability of new infection centers being initiated at various locations can be estimated.

This structure can be used to represent a wide continuum of root disease situations:

1. a stand with a series of discrete infection centers which may or may not overlap;
2. a stand with scattered mortality throughout and no discrete centers. This can be considered as one large infection zone with a certain level of infected and uninfected trees, and infected dead trees and stumps; and
3. a young stand with a large amount of inoculum from disease centers in the previous stand which will give rise to a number of new infection centers in the region of previous infection.

Time Scale of the Model

The time horizon of the model is from 80 to 300 years. Within these time frames, users can examine the effects of different management actions over one or several stand rotations.

The root disease model runs on the same time step as the stand model to which it is attached (in the case of PROGNOSIS a typical time step is 10 years). If root disease carryover from one rotation to the next is simulated (see section 2.), the user must run the model in shorter time steps (e.g. 5 year steps) in order to effectively characterize disease in the new, developing stand. Particular root disease processes, such as spread rate, are simulated on an annual basis and extrapolated for the length of the model time step.

2.2 The Stand Growth Model

Underlying the root disease model is a stand growth simulation model that simulates the growth, yield, and regeneration of the stand, and implements the various management actions selected by the user. After the root disease model computes the impacts of root disease in infected areas of the stand for a given growth cycle, it passes measures of tree growth and mortality back to the stand model such that the state of the stand as a whole can be updated.

The root disease model is designed to be linked with any stand model that supports descriptors of trees or tree classes (including species, density, DBH, height, etc.) and which can operate on the spatial and temporal scales required by the root disease model. Currently, the root disease model is linked to the PROGNOSIS (version 5.1) stand growth model (Stage 1973; Wykoff et. al. 1982; Ferguson and Crookston 1984).

The PROGNOSIS model is designed to project the development of mixed species, even and uneven aged stands. The model is initialized with a list of sample trees which collectively represent what the results of an inventory of that stand would be at various points through time. Information about sample trees is used in conjunction with a description of the inventory sampling design to estimate stand statistics such as volume per unit area. Other information about sample trees, (e.g. total height, crown ratio, past growth increment), and about the site of the stand (e.g. slope, aspect, elevation, and habitat type) may optionally be provided by the user. PROGNOSIS produces stand yield estimates that are weighted average effects of the various factors that influence stand growth. One or more "extensions" to PROGNOSIS can be used to explicitly include interactions between the stand and events such as establishment of regenerating stands, pest outbreaks, and understory development. In addition, the results of PROGNOSIS runs can be evaluated by a separate economic analysis program. For further information about PROGNOSIS, see Wykoff et al. 1982 and references cited therein.

2.3 Stand Interface Submodel

The stand interface submodel integrates the effects of root disease impacts, other agent impacts, and root disease management on the growth, and yield of the stand and its root systems. In particular, this submodel:

1. sets up initial stand and root disease conditions inside root disease centers.
2. maintains a dead tree/stump list as sources of inoculum for root disease transmission;
3. predicts radial extent of tree roots;
4. reconciles mortality predicted by the stand model with that predicted by the root disease and other agents submodels; and

5. simulates growth losses due to root disease.

Dead Tree/Stump List

PROGNOSIS describes the stand as a list of tree records representing the current state of a separate tree class tabulated at the time of inventory. Each entry in the list is characterized by a series of attributes such as DBH, height, density, and live crown ratio. Trees from these tree records become dead trees and stumps in the root disease model.

Two assumptions in the root disease submodel dictate the nature of the dead tree/stump list. First, a dead tree or stump becomes an inoculum center only if its root system was colonized by root disease before its death. Second, the dynamics of root disease spread through a dead root system are independent of how the infected tree died. Therefore, the dead tree/stump list is formed strictly from infected trees inside the root disease areas which die from any cause. Trees which die outside the root diseased areas or uninfected trees which die inside the root disease centers cannot become inoculum centers.

The attributes of each element maintained in the dead tree/stump list are the:

1. number of dead trees/stumps in the element;
2. type (e.g. heartwood or non-heartwood);
3. DBH;
4. root radius; and
5. year in which the tree was killed.

Root Extent

Root extent equations in the model are linear functions

of DBH for trees greater than 8.9 cm DBH. Tree height and stand basal area are used as the predictors for trees less than this DBH:

$$R=e^{(.62 \log(Ht) + .04 \log(BA) - .81)}$$

where,

R - root radius;

Ht - height; and

BA - stand basal area.

The equations for root extent in the model predict extent of roots 0.5 cm or more in diameter. This diameter is assumed to be near the lower limit of substrate suitability for root disease spread.

Reconciliation of Mortality

The PROGNOSIS stand model calculates an expected probability of mortality for each tree record in its tree list at the beginning of each growth cycle. These mortality functions were developed from inventory data which accounts for all mortality sources (including root diseases and other pests). Mortality from all these sources may be thought of as the "natural" mortality projected by PROGNOSIS. In order that the total mortality applied at the end of the growth cycle does not exceed the number of trees represented by the tree record, mortality from the three sources: "natural", explicit root disease mortality, or explicit other agent mortality, must be reconciled. Also, the proper mortality sources must be applied to each 'type' of tree in the stand. That is, infected trees within the root disease centers must receive mortality from all three of the above mortality sources, while uninfected trees inside the root disease centers, and trees outside the root disease centers must receive mortality only from causes other than root disease.

Realized Tree Growth

Root disease affects both diameter and height increment of infected trees and these effects are modeled as a function of the proportion of the tree's root system that is colonized (Figure 2.3). These relationships are applied only to infected trees. The actual growth increments for the tree records are calculated as tree density weighted averages of infected trees, uninfected trees inside the root disease centers, and trees outside the root disease centers.

2.4 Root Disease Submodel

The root disease submodel provides a dynamic representation of the spatial epidemiology of Armillaria or Phellinus weirii within the stand. Figure 2.4 shows a diagrammatic example of root disease infection and spread through trees in a disease center, (as well as subsequent tree mortality) as it would be simulated by the model. The model is presently parameterized to reflect the best current understanding of Armillaria and Phellinus weirii epidemiology in the Inland Empire region of the Western United States. These parameters can be easily adjusted to more accurately reflect particular pathogenicities and stand conditions.

The model is based on the concept that the distribution of root disease in a stand can be characterized as a number of spreading root disease centers, each of which contains both infected and uninfected trees and other inoculum sources. The disease patches are defined by their locations in the stand (spatial coordinates) and their size (radii). This structure can be used to represent the different situations and spatial characteristics of root disease:

1. a stand with a series of discrete centers of infection which may or may not overlap;
2. a stand with scattered mortality throughout and no well-defined root disease centers. This can be considered as one large infection zone with a cer-

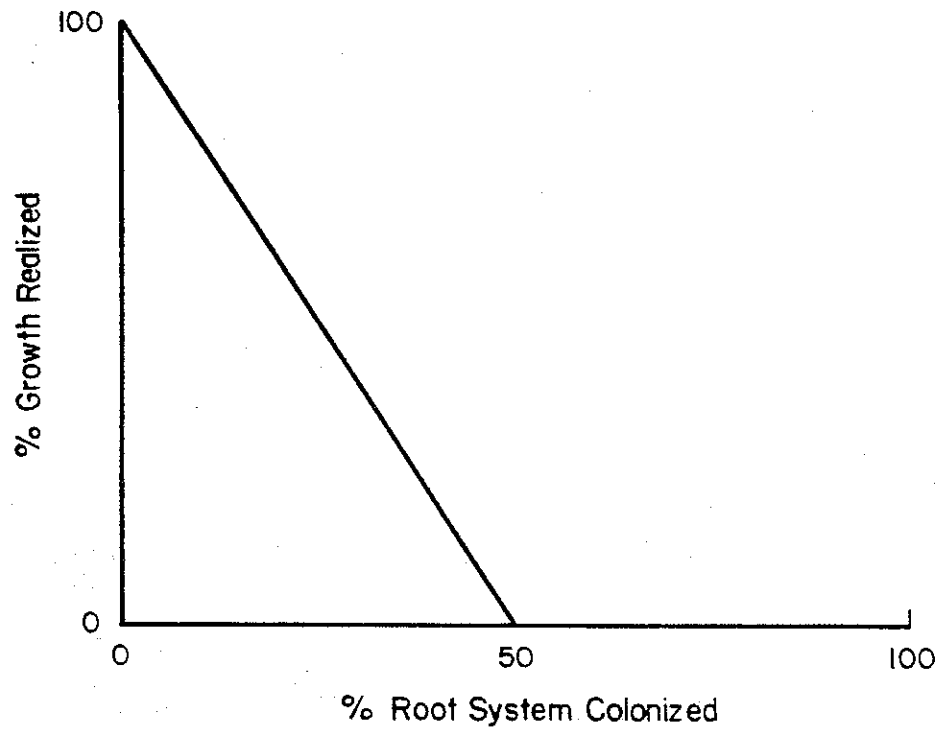


Figure 2.3. The relationship between root disease and tree growth. This relationship is applied to both diameter and height growth.

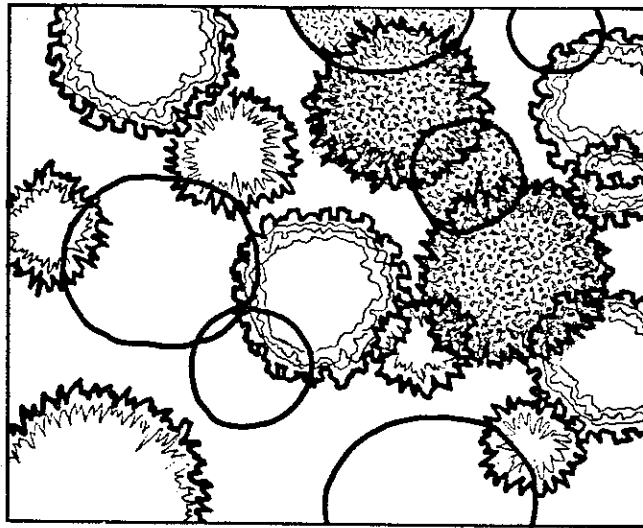
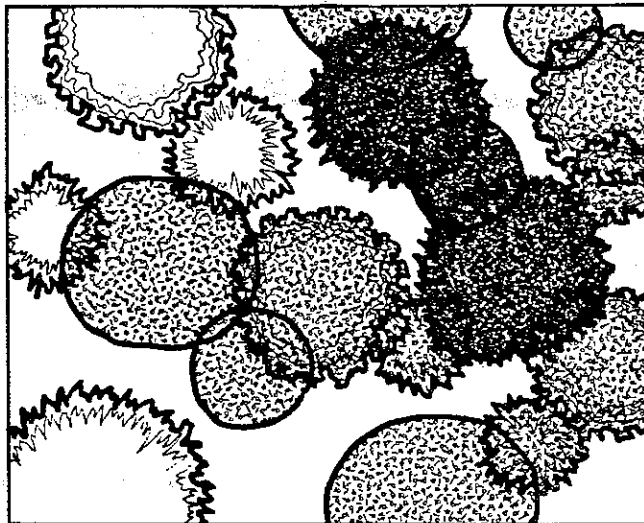


Figure 2.4. Diagrammatic representation of root disease infection and spread through trees in disease centers. Top panel shows 4 trees infected (light shading); bottom panel (several years later) shows 11 infected trees, and 3 trees killed (dark shading). Different tree species are shown with different shapes. Not illustrated here are the growth reductions caused by root disease.

tain level of infected and uninfected trees and dead trees and stumps; and

3. a young stand with a large amount of inoculum from disease centers in the previous stand. This will give rise to a number of new disease centers in the regions of previous infection.

Figure 2.5 shows the order of calculations in the root disease submodel. There are three main sections which arise from the structure described above:

1. calculation of the expansion rate of spreading centers and modeling that spread;
2. simulating the dynamics of infection and inoculum inside root disease centers; and
3. handling the "carry over" from one stand through a clearcut to a new stand with new infection centers.

All three of these components are complex functions of the sizes, distributions, and species of the trees, and the sizes, distributions and species of the inoculum sources, all of which vary through time. In view of this complexity, the approach taken in the model is to simulate small portions of the stand in explicit detail, noting the exact position of a number of trees and the spatial relationships of their roots. The results from these small scale detailed simulations are then expanded to represent their effects on the stand as a whole.

2.4.1 Initial Conditions for Root Disease

In order to initialize the model for root disease, four points must be considered: the number, location, and size of disease centers; the number of live, uninfected trees in infection centers; the number of live, infected trees in infection centers and their degree of infection; and the number of dead infected root systems (and their size and species) inside infection centers.

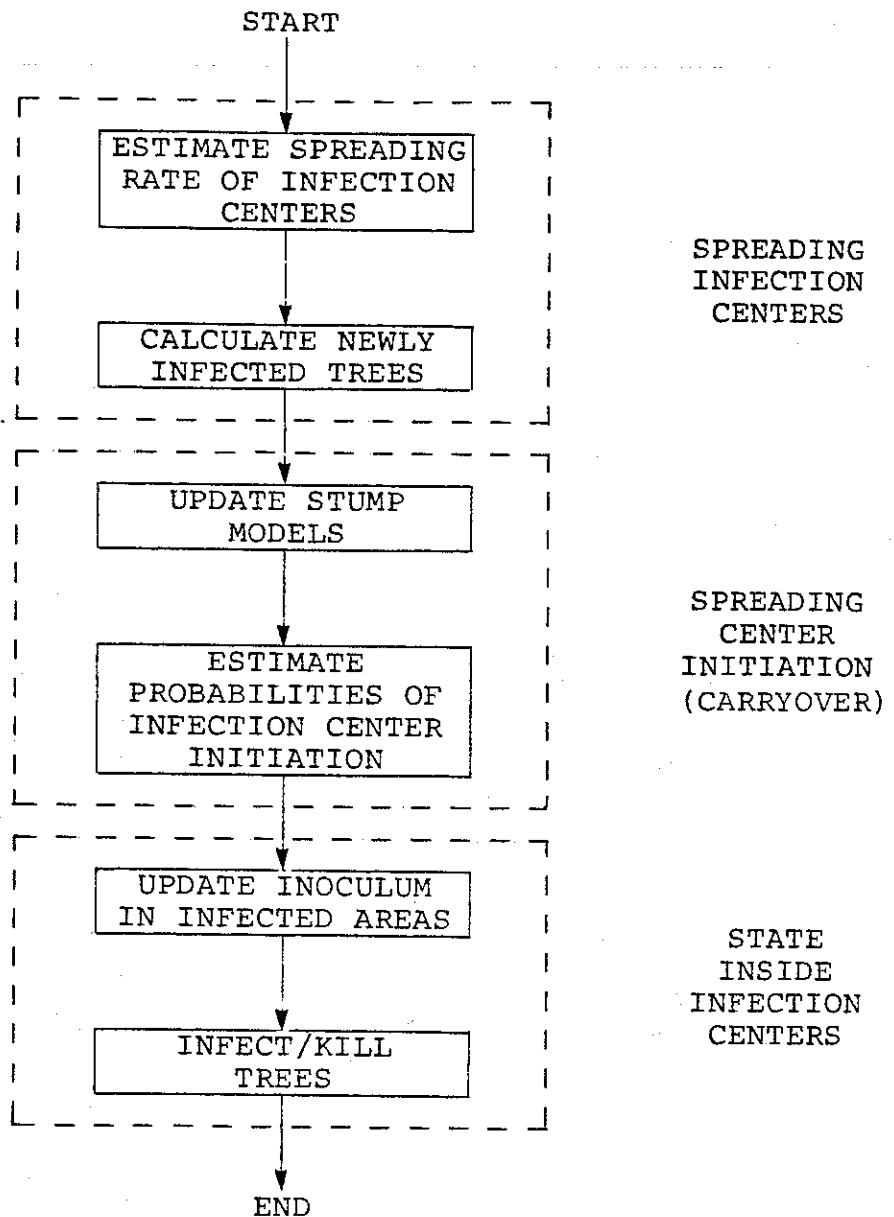


Figure 2.5. Order of calculations in the root disease submodel. These calculations take place once each growth cycle.

Specification of Centers

The root disease centers in the model are each specified by three parameters: the X and Y coordinates of the center, and the radius of the center. The model assumes that the stand is square with the specified area. In practice, the model user may specify either all three parameters for each center, or the total area in root disease centers and the number of centers. In the latter case, the model assumes all centers are the same size and are randomly distributed across the stand.

2.4.2 Progress of Infection Through Root Systems

Figure 2.6 shows the basic relationship which describes the way in which live root systems become infected, trees are killed, and the way the infection spreads in dead, infected roots. In the model the quantity of inoculum is measured in aerial extent since this is assumed to be directly related to the probability of overlap and infection (see below).

A major assumption of the model is that the pathogenic strains of Armillaria and Phellinus which are modeled will not attack and colonize totally uninfected dead root systems. They will only attack live root systems, and in the case of Armillaria, will completely colonize the remaining portions of the infected root system after death. Phellinus is assumed to be a relatively poor saprophyte and is unable to compete and colonize the dead root system.

The relationship shown in Figure 2.7 for the progress of infection and decay after death specifically relates to Armillaria; there are two major differences for Phellinus. First, the maximum proportion of the root system which becomes infected is that which has occurred at the time of death. Second, the minimum length of time for which active inoculum lasts is 20 years. The shape of the various portions of this relationship is a function of the size,

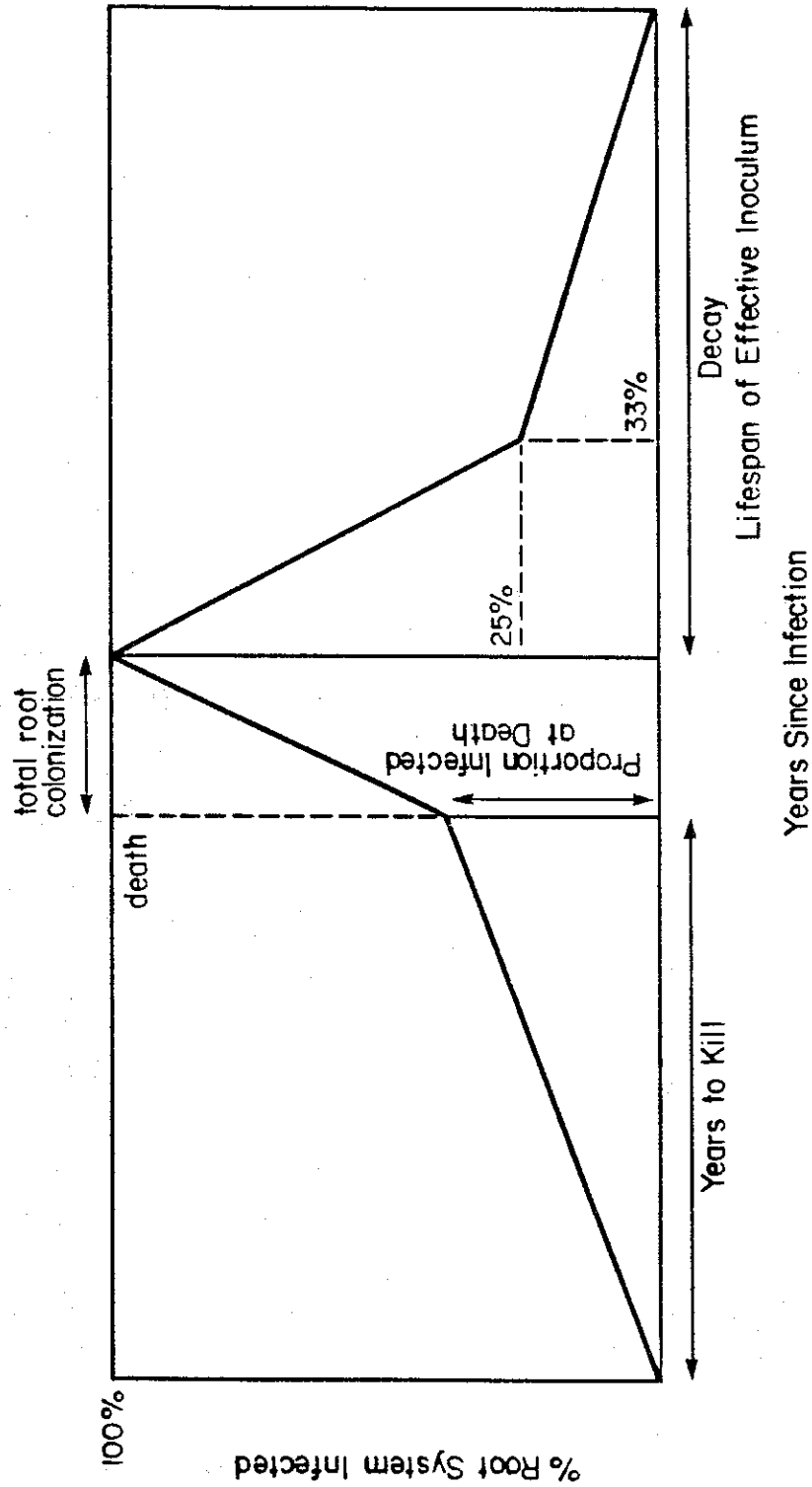


Figure 2.6: Pattern of pathogen spread and inoculum spread through a single root system. This figure is for *Armillaria*; see text for a description of differences in *Phellinus* behavior.

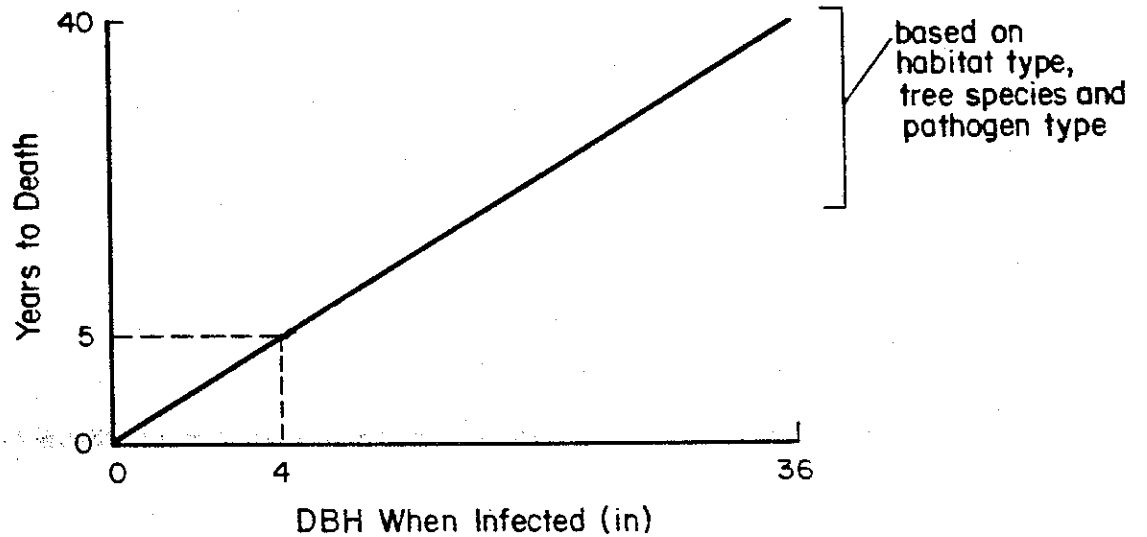


Figure 2.7: Time from infection to death for Douglas-fir on Douglas-fir habitat with Armillaria. This relationship is modified for different habitats, tree species, and root disease pathogen.

species, and origin of the tree in question. These relationships are described in more detail below.

Number of Years to Kill

The number of years it takes for Armillaria to kill a Douglas Fir on Douglas Fir habitat in the interior region of the western United States is defined in the model by the relationship shown in Figure 2.7. This relationship is then modified for other species of trees, root diseases and habitats. The rationale for this is that all trees react to infection in a fundamentally similar way until they are larger than 10 cm. Table 2.3 shows the factors used for various tree species, pathogen species, and habitat types. For Phellinus infecting cedar, it is assumed that trees older than 50 years will not be killed and will reach a maximum level of infection of 10%.

Proportion of Root System Infected at Death

The average proportion of the root system which must be infected at the time of death caused by the pathogen is a function of the pathogen and the tree species as shown in Table 2.3.

Time for Total Root Colonization

Following death, the progress of the disease depends on the species of the pathogen; for Armillaria the fungus rapidly colonizes the complete root system within a period of less than 5 years. For Phellinus the proportion of infected roots at the time of death (for any reason) does not increase, due largely to competition with saprophytic fungi. For both species of pathogen the inoculum then reduces fairly rapidly from its maximum extent.

Lifespan of Effective Inoculum

The maximum lifespan of effective inoculum is a function of the stump size and the species of the tree as shown in Figure 2.8. The tree species are grouped into heartwood

Table 2.3. Parameters defining root disease dynamics.

SPECIES	PROBABILITY OF INFECTION		RELATIVE TIME TO DEATH		% ROOT INFECTION AT DEATH		WOOD TYPE
	ARM.	PHELL.	ARM.	PHELL.	ARM.	PHELL.	
Western white pine	0.1	0.1	1.8	3.0	30	85	Heartwood
Western larch	0.05	0.2	2.0	1.5	100	75	Non-heartwood
Douglas fir	0.5	0.4	1.0	1.0	80	80	Heartwood
Grand fir	0.6	0.4	0.75	1.0	80	60	Non-heartwood
Western hemlock	0.1	0.2	0.9	1.5	80	80	Non-heartwood
Western redcedar	0.1	0.02	1.2	10.0	75	85	Heartwood
Lodgepole pine	0.2	0.1	1.8	3.0	30	85	Heartwood
Engelmann spruce	0.5	0.2	1.1	1.1	75	65	Non-heartwood
Subalpine fir	0.5	0.4	0.75	1.0	80	60	Non-heartwood
Ponderosa pine	0.2	0.1	1.8	3.0	30	85	Heartwood
Mountain hemlock	0.1	0.4	0.9	1.5	80	80	Non-heartwood

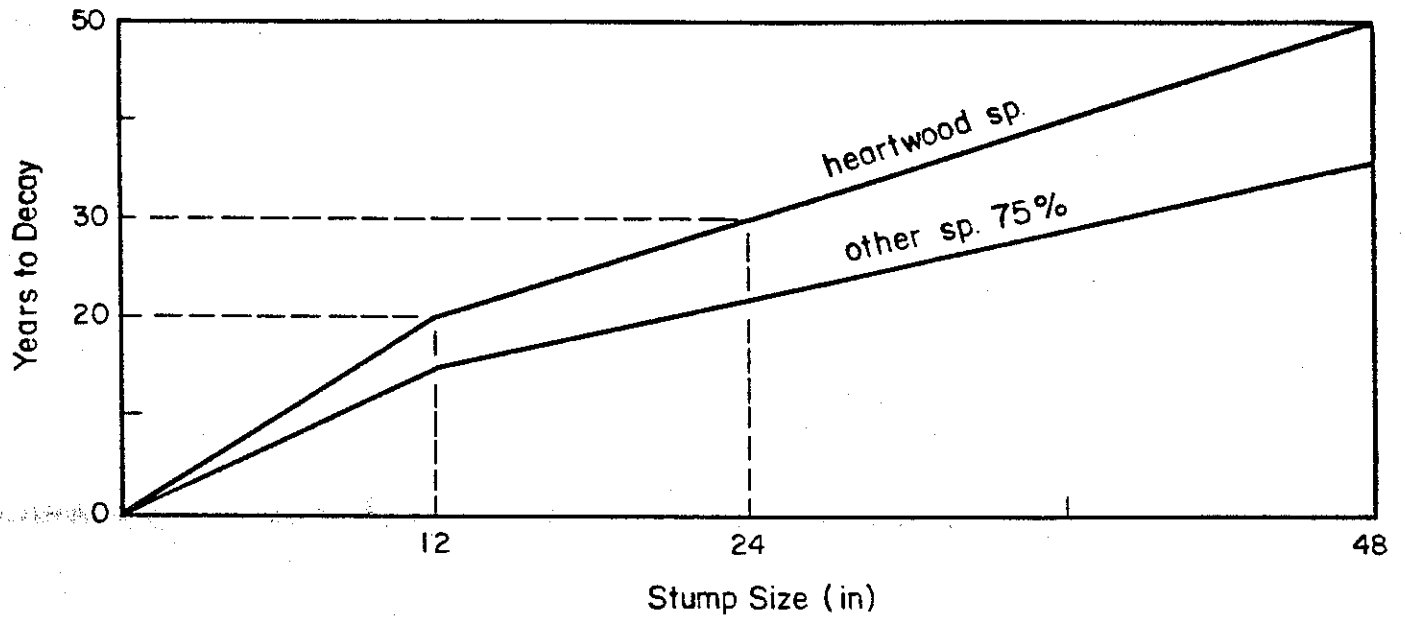


Figure 2.8. Lifespan of inoculum in dead trees and stumps. This relationship is for Armillaria; see text for a description of differences in Phellinus behavior.

types and non-heartwood types. The heartwood species are Douglas Fir, all pines, western red cedar, and western larch. The non-heartwood species are true firs, hemlocks, and spruce.

The inoculum is assumed to decay such that after one third of the total lifespan only 25% are left, with the rest decaying over the remaining time. For Phellinus the minimum lifespan of inoculum is 20 years.

2.4.3 Spread of Infection Centers

The simulation of spread falls into two main components: the estimation of the average rate of spread of the diseased centers; and the translation of that rate into an area of new stand encompassed, and the number of new trees infected.

Estimation of Spread Rate

Spread rate is estimated by simulating a small portion of the stand explicitly for a number of years and determining the length of time it takes for the infection to spread across the simulated portion. In order to control the execution time of the code which implements this algorithm, the number of trees in a simulation remains fixed and the area which is simulated is adjusted to maintain this number; the total number of stems per acre in the tree list is calculated by the stand interface model.

Selection of Trees in the Simulation

The entire tree list is scanned in order to select trees for the simulation. For each tree class where there is more than one tree on the area being simulated, that number of trees is placed in the simulation. In each simulation, if there is a fractional number of trees left after assigning the integral number of trees per class (or in the case where there is less than one tree on average in that area), a random number is drawn to determine whether or not

to include another tree of that class. The probability of a given tree being included in this way is directly related to the number per area; if there are on average 0.25 per simulated area, the chance of inclusion is 25%.

Distribution Pattern of Stems

The model allows one of two different distribution patterns of stems in the stand:

- a) completely random distribution in the simulated area; or
- b) uniform distribution on a grid with a certain level of "fuzz" on each point in the grid.

In general, the random pattern is most useful here as grid patterns of planted trees are never perfect, especially when there is some natural regeneration. However, this flexibility allows users to investigate the effects of different distribution patterns on spread rates of root disease through the stand.

Probability of Infection

The root systems of trees are assumed to be circular for the purposes of estimating the probability of disease transmission. Given the known radius of an inoculum source and the root radius at an uninfected tree from the stand model, it can be determined whether there is root overlap. If there is root overlap then there is a certain probability of transmission in each year. In the current model this probability is set to 75% for all tree and root disease species for a 10 year period; this can, however, be made species specific.

Simulation of Spread

Each tree in the simulation is represented by five characters:

- a) the X coordinate of the tree;
- b) the Y coordinate of the tree;
- c) the radius of the root system;
- d) the radius of the infected portion of the root system; and
- e) the tree species.

The model is initialized with all trees whose roots contact the baseline (the bottom of the simulated area) being infected in 1% of their root systems. The model is then run for twenty, 5 year time steps or until the infection has reached the opposite side of the simulated area. In either case, the rate of movement across the simulated area is used as the estimate of the rate of spread of the root disease in the stand.

Spread is simulated simply by increasing the area of infection of each infected root system appropriately and then checking to see which other uninfected root systems are contacted by this. In this model, the probability of pathogen transmission is assumed to be 100% if the root systems overlap.

In order to make the simulation as rapid as possible, the tree locations are first scanned and the five nearest neighbors to each stem are noted. Then, in searching for contacts between the root systems of trees, it is only necessary to check the five nearest neighbors rather than all other stems.

Spread into Uninfected Areas of the Stand

The spread rate is converted to an increase in the radius of each disease center for the time step of the main model. These increased radii are then converted into an increase in area using the area estimation algorithm

described below, taking account of overlaps between root systems.

Given the increased area inside infection zones, the tree list is processed and the number of new trees of each class now inside the centers is estimated. The model assumes that a certain proportion of all new trees encompassed by the spreading center are infected directly as the center expands, this is the same as the probability of infection described above (75%).

2.4.4 Dynamics of Root Disease Inside Infection Centers

The purpose of this section of the model is to simulate the transmission of the pathogen to uninfected root systems inside infection centers. The transmission process is handled by simulating a small area in explicit detail in a similar fashion to that used in the estimation of spread rates.

The simulated plot is set up with representative inoculum selected from the dead tree/stump list in the same way that live trees are selected in the spread rate simulation described above. Each piece of inoculum is represented by its X and Y coordinates and its radius.

Following the construction of the inoculum test plot, the tree list is processed to estimate the probability that trees of each class will contact the inoculum. A total of 13,500 stems distributed equally among the tree classes are positioned randomly on the test plot. The proportion of those which touch an inoculum source is taken to be the proportion of the uninfected trees inside centers which will become infected in this time step. As before, the probability of pathogen transmission is taken to be 75% if the root systems overlap for a period of 10 years.

2.4.5 Infection Center Expansion on Cutting

At the time of a clearcut it is assumed that there is a

ring of root systems around the outside of each infection center that represent those trees which have just been infected. For Armillaria this means that there is a whole ring of trees through which the root disease will spread very rapidly when they are killed. This will effectively cause the infection center to jump out when the stand is clearcut. This is handled in the model by estimating the mean diameter of all root systems in the uninfected stand at the time of the cut and using this as the distance by which the radii of infection centers increase.

It is possible that the rapid spread of Armillaria through dead and dying root systems after a clearcut may temporarily continue so that more than a single 'ring' (i.e. roots of the trees immediately adjacent to a patch) of root systems is spread through. This is simulated in the model by allowing the user to specify how many rings of root systems will be infected by spread; the current default is one.

2.4.6 Root Disease Carryover Between Rotations

The way in which root disease centers are affected by clearcutting and the regeneration of a new stand is currently not well understood. The model can simulate three different scenarios:

- a) Scenario 1 - the root disease patches from the old stand cease to exist after a clearcut and the disease in the new stand arises in a small number of centers located inside the previously infected area;
- b) Scenario 2 - root disease patches from the old stand retain their integrity, and as the new stand grows up, the patches spread out again starting at the old boundaries; and
- c) Scenario 3 - after a clearcut and regeneration, the root disease patches form around inoculum throughout the old areas of disease and gradually expand until they coalesce.

These three scenarios are in fact part of a continuum which depends upon the density of inoculum and the probability of a piece of inoculum initiating a new spreading center. If the inoculum is very dense and the probability of initiating a center is high, then it is unlikely that the old center will entirely lose its integrity (scenario 1) and one of the other two scenarios is highly likely. If, on the other hand, inoculum (stumps) is actively removed following a clearcut, then it is unlikely that the centers will remain effectively unaltered (scenario 2) and one of the other two scenarios is likely depending on how successful inoculum removal was, and on the density of the regenerating stand and the resistance of the new trees to root disease infection.

The current version of the root disease model addresses this complex problem by simulating the processes of infection from an infected stump at the time of cut in some detail in a separate model (the carryover model). The basic structure is that the root disease model takes a snapshot of the stand at the time of cut and then keeps track of establishment and mortality in the developing stand until the time of root closure and the initiation (in the model) of new infection centers. At this point the entire time since the cut is recapitulated within the carryover model with an emphasis being placed on the events surrounding each type of infected stump.

The underlying question which the carryover model attempts to address is:

What is the probability of each type of inoculum present at the time of cut initiating a new spreading infection center at the time of root closure?

The model attempts to answer this by considering each type of inoculum (classified by stump size and type) and estimating the probability of infection still being present in some

form at the time of root closure and initiation of new centers. Given this probability and the quantity of inoculum present at the time of cut, the number of new spreading centers can be estimated. As in the root disease model, the carryover model assumes that infection may arise from contact between the root systems of regenerating trees and either the infected stumps from the previous stand, or infected trees and stumps from the new stand.

In the model the weighted mean probability of center initiation is used as the measure determining the outcome at root closure. Depending on this mean probability each of the three scenarios described above and all the gradations between can be simulated:

- a) If the mean probability is low then only a small number of new infection centers will be initiated within the area of the old root disease patches and the disease will spread from these new patches.
- b) If the mean probability is somewhat higher then many new root disease centers (up to 100 in the model) may be initiated. These eventually coalesce.
- c) If the mean probability is close to one then a large number of infection centers are initiated, as for (b) above, but the sum of the area of these new centers is close to the sum of the areas of the old centers prior to the clearcut.

The Carryover Model

In many ways the carryover model resembles the entire root disease model in that it must simulate the processes of infection, death and decomposition due to root disease; the relationships used to represent these processes are identical to those used in the main model. There are two critical differences between the carryover model and the main model:

- 1) while the main model considers a stand potentially containing many stumps, the carryover model follows the gradual decomposition and subsequent

infection of other nearby trees for one stump of each class from the time of cut; and

- 2) the carryover model estimates the probabilities of infections occurring and the probability of infection persisting at a particular stump rather than estimating an actual number of infections. That is, the carryover model produces an estimate of the number of new infection centers through probabilistic calculations rather than through the more explicitly spatial simulation used in the main root disease model.

Since the the number of infected stumps in a cut stand may be quite high it is important to estimate the probability of carryover for each type even though this may be quite small; the probability of infection persisting may be only 1 percent but if there are 1000 infected stumps then this would result in approximately 10 new infection centers.

The carryover model loops over finer time steps than the main root disease/stand growth model and simulates the period from the clearcut to root closure. The time step used may be defined by the user; the current default value is 5 years. The basic structure of the carryover model is shown in the form of a flowchart in Figure 2.9. In general, the model loops over each stump type and estimates the probability of infection persisting for the period of the simulation for that type.

The model first reconstructs the pattern of root growth, establishment, and mortality for the period to be simulated, based on information supplied by the stand model. It then simulates forward separately for each stump type.

In each time step of the simulation, for each stump type, the model estimates the probability of infection of each element in the tree list given that it has not been infected in previous time steps. The probability of root overlap between an uninfected tree and an element of inoculum is estimated by assuming that the trees are randomly distributed so that the distribution of the probability of

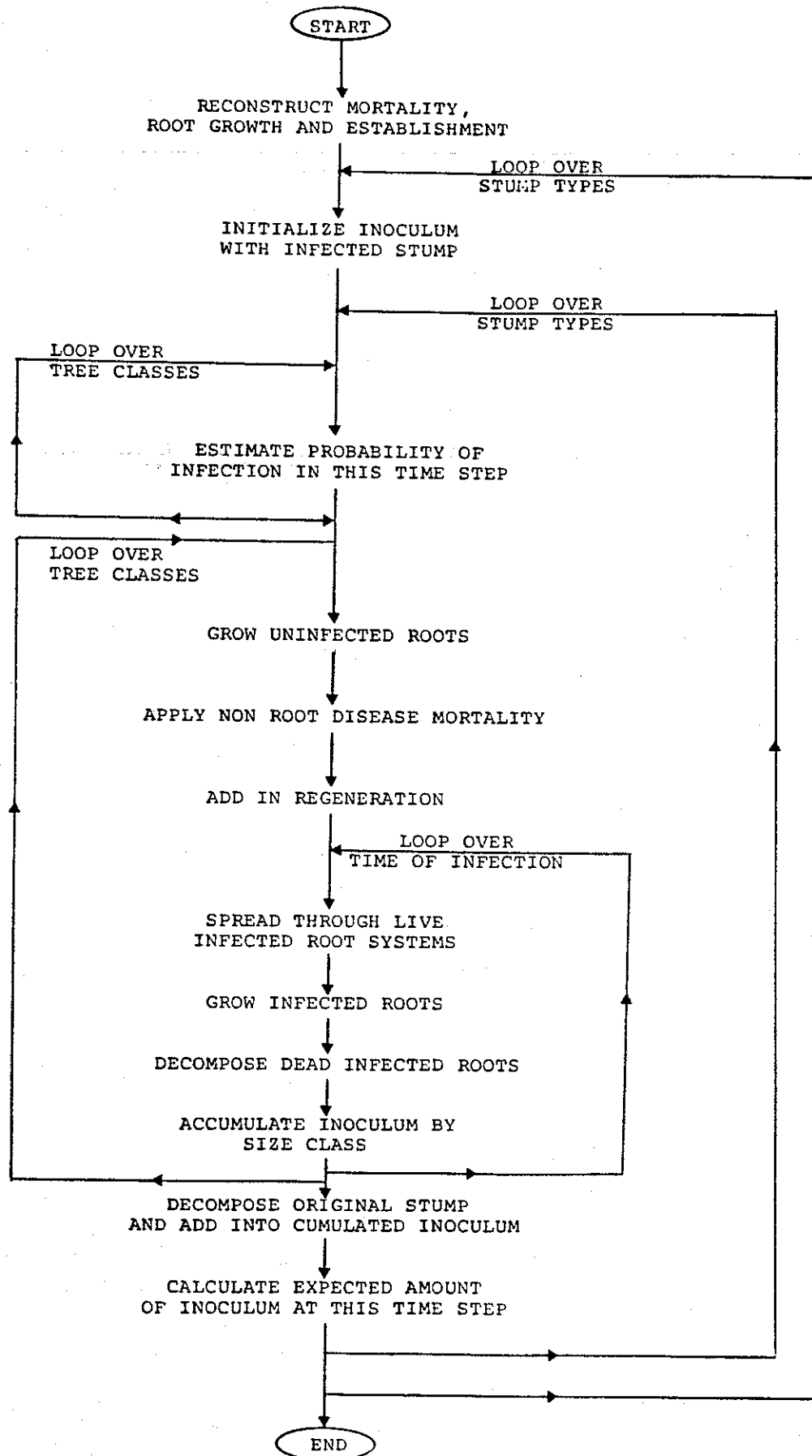


Figure 2.9. Flowchart of carrvover model. This set of calculations occurs once (after a clearcut).

contact at different densities can be derived; this probability distribution was estimated using monte carlo simulations outside of the main model.

The inoculum that is available to infect uninfected elements of the tree list is summarized in the form of a table of the expected number of sources of inoculum of each of eight size classes; the midpoints of the sizes in each of these classes is (in meters): .30, .60, .91, 1.52, 2.44, 4.57, 6.10, 9.14. The probability of infection of an element of the tree list in a given year is thus the sum of the probabilities of infection by each of these classes. Note that sources of inoculum can be the original stumps, infected trees or stumps from infected trees killed in the new stand.

The probability of infection in each time step for each element of the tree list is stored and the subsequent history of that element, infected at that time, is simulated in terms of root growth, the progress of infection, and mortality. (To facilitate the calculations the number actually stored by the model is the probability that the element is NOT infected - one minus the probability that it is infected).

Location of New Centers in the Stand

The assumption made in locating new disease centers within the stand is that they have an equal probability of occurring anywhere there was root disease in the previous stand, and a zero probability of occurring elsewhere.

The stand is divided up into 400 equally sized cells. Each of these cells contains inoculum if its center is within a previously existing spreading center. The probability of any one of these cells containing a new spreading center is estimated from the number of new centers forming in the stand (from one of the methods discussed above) divided by the number of cells containing root disease inoculum. Thus, if there are 20 cells containing inoculum and

approximately 10 new infection centers are expected, then there is a 50% probability of each cell containing a spreading center.

The model allows more than one center per cell up to a maximum number of centers in the stand of 100. The location of centers within each cell is delimited using uniform random numbers.

Invoking the Carryover Model

It is most important to invoke the carryover model when root closure suddenly disappears as a result of cutting and the remaining trees (if any) are unable to exhibit a sufficient growth response to achieve root closure again. Under other conditions, the rest of the root disease model, including the spread and within center dynamics are able to simulate root disease dynamics. Therefore, the carryover model should be invoked after a clearcut, but should not be invoked after a pre-commercial thin. The spread rate (which is closely related to root closure) immediately after the cut is used to determine whether the carryover model should be called. The carryover model is called only if this spread rate is less than 0.3 cm per year.

2.5 Other Agents Submodels

The collection of submodels which make up the other agents component of the root disease model are used to simulate the influence of a variety of physical and biological agents on root disease and stand dynamics. Some agents (such as bark beetles, or windthrow events) may act to promote the spread of root disease by weakening or killing trees and thus providing a food source for the fungi. Conversely, agents such as other root diseases may act to limit disease spread through competition.

The other agents submodels compute mortality to one or more of the following tree lists:

- the infected trees inside disease centers;
- the uninfected trees inside disease centers; and
- the trees outside disease centers.

The mortalities are used by the stand interface submodel to calculate the actual mortality of root disease to infected and uninfected trees.

Although there are many potential agents which could interact with root disease, simulation models of the dynamics of windthrow and three functional types of bark beetle interactions are the only ones that have been developed as part of the current version of the root disease model. These models are outlined below. For a more complete description of these and other possible models, see McNamee et al. 1985.

2.5.1 Windthrow Submodel

The windthrow model simulates major blowdown events in the stand, using three parameters to determine the magnitude of an event:

1. the size criterion for stem dominance;
2. the proportion of dominant/codominant stems to windthrow; and
3. a minimum event criterion (i.e. the minimum number of stems to windthrow).

The user specifies the magnitude of a windthrow event in the model; computations then allocate the effects among the various three classes within the stand. This allocation is first performed between species according to their relative susceptibility to windthrow, and then among the individuals of a species.

The windthrow model operates on all stems which are defined by the user as being dominant or codominant within

the stand. Stems represented by a record in the tree list are defined as dominant or codominant if the basal area percentile for that record equals or exceeds a user-defined criterion for dominance within a stand (usually 80% - 100%). The total number of susceptible stems of a given species and of all species in the stand can be computed by summing the number of trees in the tree list which meet this dominance/codominance criterion. The total number of trees to windthrow is then calculated as a user-defined proportion of the total stems susceptible to windthrow. If this number is less than a user-specified minimum, then no further action is taken. The model will be called once each time step until either the criterion is met or the end of the simulation occurs. If the magnitude of the event exceeds the criterion, windthrow occurs, and the model allocates the effects among the various susceptible tree classes by considering such factors as the relative susceptibility of the species to windthrow, the crown length/height relationship, and the proportion of the root system infected by root disease.

For windthrown trees, the model also determines the number that tip over as opposed to snapping off in order to estimate the number of windthrown trees which become disease centers. Windthrown trees which tip over are assumed to remove the major portion of their root system from the soil and therefore not contribute to the spread of root disease. Infected windthrown stems which snap off become infected stumps which can then act as inoculum sources. In the model, the probability of a stem being uprooted is equal to the proportion of its root system that is infected.

2.5.2 Bark Beetle Submodels

Three functional types of bark beetles are simulated:

1. Type I - dependent only on the density of susceptible stems;

2. Type II - dependent upon windfallen stems as refugia for the beetle population; and
3. Type III - dependent upon stems infected by root disease.

In general, criteria for susceptibility are a function of species and tree size (DBH), and the criterion for permitting an outbreak to occur is simply a user-specified minimum density of susceptible trees. The combinations of beetle-tree interactions simulated, their functional types, susceptibility criteria, and mortality rates are summarized in Table 2.4.

To use the bark beetle models, the user specifies the growth cycle during which the beetles are at epidemic levels. Additional criteria are evaluated to determine whether an outbreak should occur for Type II and III beetles. If the criteria are met, the extent of stem mortality is computed and applied to the stand. No further action is taken if the criterion are not met. In this case, the model is invoked in subsequent growth cycles until the criteria are met or the simulation terminates.

Type I Beetles

Mountain pine beetle targeted on lodgepole pine stands is used as the prototype Type I beetle interaction. Mountain pine beetle and western pine beetle targeted on Ponderosa pine are also modeled as Type I interactions.

The number of trees in the target species which are susceptible to attack is computed as the sum of the trees greater than or equal to a user-specified minimum DBH criterion. Tree mortality is computed only if this sum is greater than a user specified minimum tree density. Tree mortality is applied only to susceptible tree list entries by multiplying the stem density in that class by a mortality rate for the epidemic period (Table 2.4).

Table 2.4. Bark beetle-tree species interactions in the other agents submodel.

BETLE SPECIES	TREE SPECIES	FUNCTIONAL TYPE	MORTALITY RATE	MINIMUM DBH	% ROOT INFECTION
Mountain pine beetle	Lodgepole pine	I	0.85	8	n/a
Mountain pine beetle	Ponderosa pine	I	0.85	8	n/a
Douglas- fir beetle	Douglas-fir	II	0.88	10	n/a
Mountain pine beetle	White pine	III	0.04	8	0.75
<u>Scolytus</u> <u>ventralis</u>	Grand fir	III	0.4	0	0.75
Western pine beetle	Ponderosa pine	I	0.9	20	n/a

Type II Beetles

Douglas-fir beetle targeted on Douglas fir is used as the prototype Type II beetle interaction. Outbreaks of this beetle are precipitated by a windfall event, (implying that the windthrow model must be invoked when this model is invoked). A minimum size (DBH) criterion is applied to both the windthrown trees which provide refugia for the beetle population, and to standing stems subject to subsequent mortality. If the number of windthrown trees of suitable size exceeds the criterion, an outbreak of the beetle is assumed to occur and the number of live trees killed in each of the three succeeding years is calculated depending on the number of windthrown stems and the number of live trees meeting the minimum size criterion.

Type III Beetles

Scolytus ventralis on Grand fir is used as the prototype Type III beetle interaction. For S. ventralis, the model simply kills 40% of the stems which have more than 75% of their root systems colonized by root disease. The same functional relation is used for mountain pine beetle attacking white pine except that this mortality is further restricted to trees with a DBH greater than 20 cm.

Because the pattern of action for Type III beetles is determined by the presence of sufficiently infected trees, the model remains active at all times during a scenario unless otherwise desired by the user.

2.6 Using the Root Disease Model

Model Inputs

To run the current version of the root disease model, users must first describe the stand inventory to the PROG-NOSIS model through the use of a keyword system (fully described in Wykoff et al. 1982). Secondly, users must provide a root disease inventory for the stand such that the

model can build an internal representation of diseased areas in the stand (see below). This inventory is also provided to the model in the form of keywords. Finally, users can control the operation of the root disease model, and modify various parameter values through a number of keywords. The specific details of the keywords needed for operating the root disease model are described in detail in Sutherland and McNamee (1987).

Root Disease Inventory

To make projections for stands with root disease, the root disease model requires 4 types of inventory of root disease infections and extent to characterize a scenario:

1. root disease type (Armillaria or Phellinus);
2. number and location (X and Y coordinates) of root diseased patches (centers), as well as the radius of each center;
3. density of live infected and uninfected trees (trees/ha) inside root disease patches (as well as the extent of infection in infected trees); and
4. characteristics of dead infected trees and stumps in root disease centers:
 - stump type (heartwood-non-heartwood)
 - DBH for the stump class
 - number of stumps represented by the stump class.

In practice, the requirements for item 2 above (number and location of centers) can be considerably relaxed. The user may specify all three parameters for each center (X coordinate, Y coordinate, and radius), or simply the total area in root disease and the number of centers. In the latter case, the model assumes all centers are the same size and are randomly distributed across the stand.

Model Output

Currently, output from the root disease model displays output in tabular form summarizing conditions in the stand during the period covered by the simulation. The outputs specific to the root disease model are: a keyword summary echoing the keywords in effect for the simulation, a summary table displaying the effects of root disease inside disease centers, and a detailed table describing species-specific consequences of root disease infection on growth and mortality.

The summary output from the root disease model is designed to illustrate a number of important indicators of root disease effects in the diseased areas of the stand:

1. measures of the extent of root disease infection, including the number of inoculum centers, the annual spread rate, and the total area of the stand with root disease.
2. the number of infected stumps, and the basal area of those stumps.
3. the density of trees killed by root disease in the current growth cycle and the timber volume loss represented by those trees. Note that the number of trees killed by other agents (if called) are not included here; those losses will be reflected in the stand averages summarized by PROGNOSIS.
4. the density of uninfected trees inside the disease patches.
5. the number of infected trees in the patches and the average percentage of their root systems which are infected.
6. indicators of the volume, and total basal area of live trees in diseased areas.

All the root disease summary outputs are aggregated across the tree species in the root diseased areas. An example summary table from the root disease model is shown in Table 2.5.

Table 2.5. An example summary output table from the root disease model.
Note that the units are in imperial units (not metric). Shown
is the output table for scenario 4 of the Quartz Creek stand
(see section 3). The year number (col 1) has been shifted 10
years from that shown in the output figures.

ROOT DISEASE MODEL																			
VERSION 1.0																			
SUMMARY STATISTICS FOR ROOT DISEASE AREAS																			
LIVE TREE CHARACTERISTICS																			
DEAD TREE CHARACTERISTICS																			
STUMPS																			
DISEASE STATISTICS																			
LOSSES FROM DISEASE																			
UNINF																			
INFECTED																			
OVERALL																			
IDENTIFIERS																			
YEAR	AGE	CENTS	NO OF	DISEASE	SPREAD	TOTAL	BA/	NO OF	VOLUME	NO OF	TREES	NO OF	AVE	MERCH	CU FT	BA/	ACRE	STAND ID	MGMT IO
				AREA	RATE	/ACRE	ACRE	TREES	LOSSES	TREES	/ACRE	TREES	%ROOTS	CU FT					
1968	50	100	40.28		.00	1.	2.	0.	0.	69.	107.	10.0	5032.	151.	SQTZSC04	SC04			
1973	55	100	42.12		.52	4.	6.	24.	11.	63.	78.	36.3	5138.	148.	SQTZSC04	SC04			
1978	100	100	43.56		.57	32.	17.	25.	194.	56.	51.	47.8	5080.	135.	SQTZSC04	SC04			
1983	105	100	73.36		.00	34.	55.	0.	0.	0.	0.	0.	0.	0.	SQTZSC04	SC04			
1988	10	100	73.36		.00	33.	53.	0.	0.	682.	0.	0.	0.	0.	SQTZSC04	SC04			
1993	15	100	73.39		.02	27.	48.	13.	4.	640.	0.	0.	0.	0.	SQTZSC04	SC04			
1998	20	90	10.14		.03	1.	4.	71.	60.	825.	9.	78.9	56.	16.	SQTZSC04	SC04			
2003	25	90	11.21		.19	15.	3.	14.	46.	216.	30.	65.8	163.	38.	SQTZSC04	SC04			
2008	30	90	11.47		.23	31.	6.	31.	124.	184.	27.	57.0	255.	44.	SQTZSC04	SC04			
2013	35	90	11.94		.49	53.	11.	23.	126.	147.	36.	54.6	511.	51.	SQTZSC04	SC04			
2018	40	90	12.48		.43	51.	13.	29.	195.	107.	46.	50.3	742.	53.	SQTZSC04	SC04			
2028	50	90	13.53		.52	71.	23.	71.	747.	67.	15.	69.9	742.	38.	SQTZSC04	SC04			
2038	60	90	15.67		.59	30.	13.	29.	422.	44.	22.	67.4	960.	40.	SQTZSC04	SC04			
2048	70	90	17.32		.56	30.	20.	25.	565.	30.	20.	64.3	965.	36.	SQTZSC04	SC04			
2058	80	90	19.38		.74	27.	22.	20.	578.	22.	18.	60.2	1043.	35.	SQTZSC04	SC04			
2068	90	90	25.68		.78	21.	17.	15.	415.	22.	33.	56.6	2051.	64.	SQTZSC04	SC04			
2078	100	90	29.85		.87	33.	33.	28.	1166.	14.	19.	53.7	1742.	51.	SQTZSC04	SC04			

The detailed output table displays some measures of the effects of root disease for on the attributes of each tree species in diseased areas. At stand inventory, and at the end of each cycle, the numbers of trees killed during that cycle, and the numbers of alive uninfected, and alive infected trees are displayed. In addition, the 5 percentile classes for tree DBH are presented, along with the size of the largest tree in the class, for both the trees killed and live trees. This is intended to illustrate species specific growth effects in the root diseased areas of the stand.

3.0 SCENARIO DESCRIPTIONS AND RESULTS

3.1 Background

In the Nelson Forest Region, Armillaria may be the most important pest in most stands, accounting for up to 40 -50% yield decreases in many sites. For stands infected with root disease many possible silvicultural and harvesting options exist depending on the management phase of the stand (e.g. planting, spacing, commercial thinning, harvesting), the desired goals for root disease control (e.g. spread reduction, tree mortality reduction, site rehabilitation) and the expected cost/benefit relationships for the various options.

Some of the options currently in use in the Region, or under preliminary assessment are:

- **stump removal after harvest.** This is highly effective in reducing inoculum remaining after a cut. However, it may be quite expensive (particularly in sites with diffuse centers) and may cause damage to the site in steeply sloping areas with relatively thin soils, or when done on wet ground.
- **chemical treatment of stumps.** This is also very expensive, is not always effective, and requires extensive monitoring for possible soil, and groundwater contamination.
- **plant a less susceptible species.** Such species as Ponderosa pine, or western larch are among the least susceptible coniferous species to root disease and may result not only in acceptable yields in heavily infected stands, but also act to reduce root disease spread. However, they are not completely resistant to root disease and mortality may still be significant in young stands.
- **reduce stocking density.** Thinly planted stands (e.g. at 1/2 or less of normal stocking density) may reduce the probability of inoculum contact with the young trees, and may allow the inoculum to decline before root closure occurs. This is a relatively cheap option, but its effectiveness is as yet unknown.

- regeneration delay. A delay of several years before allowing regeneration may allow the inoculum sources to decay and disappear. However, it is not clear what the optimum delay period is, and there may be significant costs associated with maintaining a clean site.
- plant an alternative rotation of hardwoods. A short (e.g. 40 year) rotation of a less susceptible species such as birch may also allow inoculum to disappear, and may satisfy other management considerations such as providing suitable habitats for game, recreation, etc. However, not all hardwoods are resistant to root disease, and at the end of the rotation, other operations such as stumping may have to be carried out anyway.
- clearcutting. Clearcutting is an attractive harvesting strategy for infected stands; root systems of clearcut stumps die relatively quickly, and other control measures, such as stump removal and root raking can be done. However, in many stands there may be other management concerns (e.g. needs for visual management, potentials for soil erosion or other impacts), which may reduce the advantages of clearcutting for disease control.
- spacing or selective logging. Spacing in heavily infected stands is usually not recommended (see Morrison 1981): spread of Armillaria may only be temporarily delayed, and many of the remaining trees will eventually die before harvesting age in any case. Similarly, diameter limit cutting may leave many small, infected trees, spreads inoculum through the the root systems of infected harvested trees and leaves quantities of inoculum in the soil.

Other techniques, such as fertilization of regenerating stands and pushover logging in suitable stand types are in experimental phases of assessment.

3.2 Example Scenarios

Because current access to the model is limited (the model is run through submission of keyword lists to researchers at the USFS Computing Center in Fort Collins, Colo.), the possible number of model runs for this project was restricted to 20 or less. Therefore, out of the many

possible scenarios suggested by the above list, the project team chose 6 management scenarios, and 3 "control" scenarios as examples (Table 3.1). Each scenario was run on two example stands (see below) for 110 years (1968 to 2078). These scenarios represent some of the most common management options for the region. If a version of the model becomes implemented in the BCMFL (see section 4.2), many more scenarios, and combinations of scenarios could be run both for exploratory analysis, and for more specific training and stand management planning purposes.

Natural regeneration is simulated with the Regeneration Establishment Extension to the PROGNOSIS model (Ferguson and Crookston 1984). This model stocks new trees in the stand at user-defined intervals based on the current stand description (including habitat type), and silvicultural prescription; such stocking can be scheduled several times. For these model runs, regeneration was called only once: 5 years after the clearcut or other management disturbance. This reduces the confounding effects of different densities resulting from the different treatments. However, it likely underestimates expected tree densities in the new stand. As well, the regeneration model (like PROGNOSIS) is calibrated for the Inland Empire region of the U.S. Thus the species mix of regenerating trees may only approximate the actual mix that would occur in the example stands.

3.3 Example Stands

Two stands, the Quartz Creek and Beaverfoot stands, representative of diseased stands in the Golden B.C. area, were used as examples. Both stands were cut approximately 10 years ago, and currently show signs of active Armillaria infection. Root disease and stand inventory information (Table 3.2a and b) were provided to the ESSA staff by BCMFL personnel. Other parameters required by the PROGNOSIS stand growth model, including site index and the most appropriate habitat type were also estimated and provided to ESSA by

Table 3.1. Scenario descriptions for the example runs of the root disease model. Scenario numbers in this table match the numbers used in the text, and in the output graphs in Appendix A.

Management Scenario	Control Scenario
	1. - simulation of inventory conditions - no management
2. - clearcutting in 1978 - regeneration with planted Douglas fir at 1500 stems/ha in 1979 - natural regeneration - root disease	3. - same management as 2. - no root disease
4. - clearcutting in 1978 - regeneration with planted Douglas fir at 1500 stems/ha in 1979 - natural regeneration - pre-commercial thin from below to 750 stems/ha in 1998 - root disease	5. - same management as 4. - no root disease
6. - clearcutting in 1978 - regeneration with planted Douglas fir at 1500 stems/ha in 1979 - natural regeneration - removal of infected stumps in 1979 - root disease	- compare with scenario 3
7. - clearcutting in 1978 - regeneration with western larch at 1500 stems/ha in 1979 - natural regeneration - root disease	- no non-root disease control - compare with the other management scenarios
8. - clearcutting in 1978 - establish plantation of Douglas fir at 750 stems/ha in 1979 - root disease	- no non-root disease control - compare with scenarios 2, 4
9. - overstory removal in 1978 down to 33 cm DBH - natural regeneration - root disease	- no non-root disease control - compare with the other management scenarios

Table 3.2a. Stand inventory descriptions for the Quartz Creek and Beaverfoot stands.

Attribute	Quartz Creek	Beaverfoot
Inventory Year	1968	1968
Stand Age	100	190
Elevation	1100 m	3500 m
Slope	15%	35%
Aspect	NW	SW
Area	57 ha	12.6 ha
Site Index (100 years)	27 m	33 m
Habitat Type (U.S.)	<u>T. heterophylla/</u> <u>C. uniflora</u>	<u>A. lasiocarpa/</u> <u>L. borealis</u>
Basal Area	34 sq m/ha	50 sq m/ha
Stand Density	435 trees/ha	980 trees/ha

Table 3.2b. Root disease inventory descriptions for the Quartz Creek and Beaverfoot stands. Note that stumps are considered only as trees infected with root disease at the time of death.

Attribute	Quartz Creek	Beaverfoot
Primary Root Disease	<u>Armillaria</u>	<u>Armillaria</u>
Stand Area Infected	17.6 ha (31%)	2.5 ha (20%)
Initial Centers	10 /ha	5 /ha
Average Center Size	.176 ha	.5 ha
% Trees Infected in Centers	43%	33%
Stump Density in Centers	1 /ha	1 /ha
Stump Basal Area	.16 sq m /ha	.1 sq m /ha
Average Root Infection on Infected Trees	10%	10%

BCMFL staff. In the absence of systematic pre-harvest inventory data for these stands, estimates of the stand inventory 10 years prior to harvest were constructed from stand inventories and other data taken from representative and nearby stands. Assumed size and species compositions of the stands at this time are shown in Figure 3.1.

Much of the root disease information was not available in inventory form and had to be estimated using current stand conditions. This likely underestimates disease levels both in the pre-harvest stand, and in the current stand because:

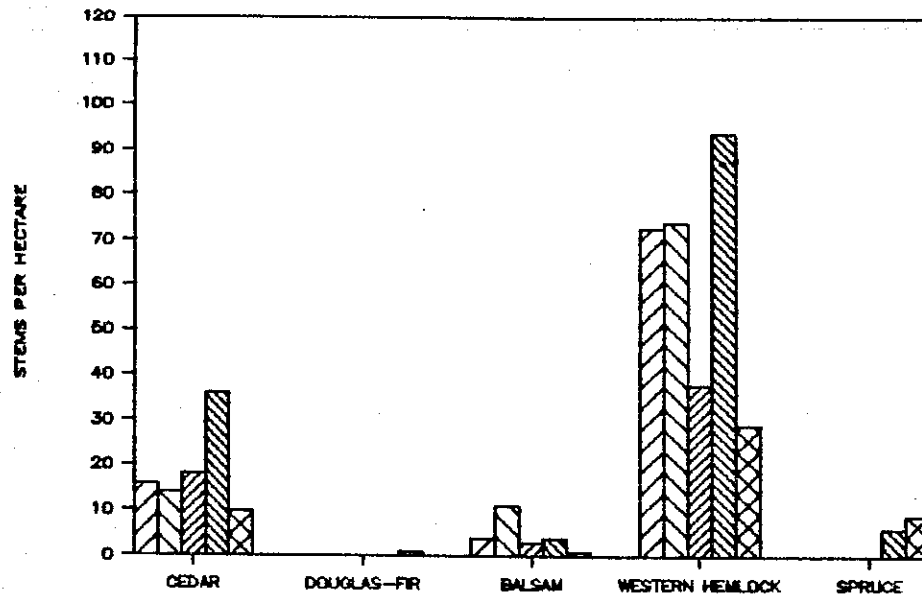
1. without knowledge of the density or sizes of infected stumps in the pre-harvest stand (i.e. those trees killed by root disease before the stand was cut), a possibly very significant source of inoculum in the new stand may be difficult to estimate;
2. the number or sizes of disease centers appearing around stumps of the previous rotation may not become delineated until 15 or 20 years after the cut. Thus estimates made for stands as young as these may be low in relation to the "true" levels of inoculum.
3. the average percentage of roots systems of infected trees containing fungi is very difficult to estimate, especially as trees may not show obvious symptoms of infection until a considerable proportion of their roots are infected.

Thus the disease levels used in these model runs (Table 3.2b) should be considered as conservative estimates of actual conditions.

3.4 Model Results

Output from the model runs were translated from the summary tables (see Table 2.5) into graphs of the most important indicators of stand growth, yield, and root disease infection (refer to Appendix A for the complete set of output graphs). Note that for some indicators (stand

INITIAL DBH DISTRIBUTION, QUARTZ CREEK



INITIAL DBH DISTRIBUTION, BEAVERFOOT

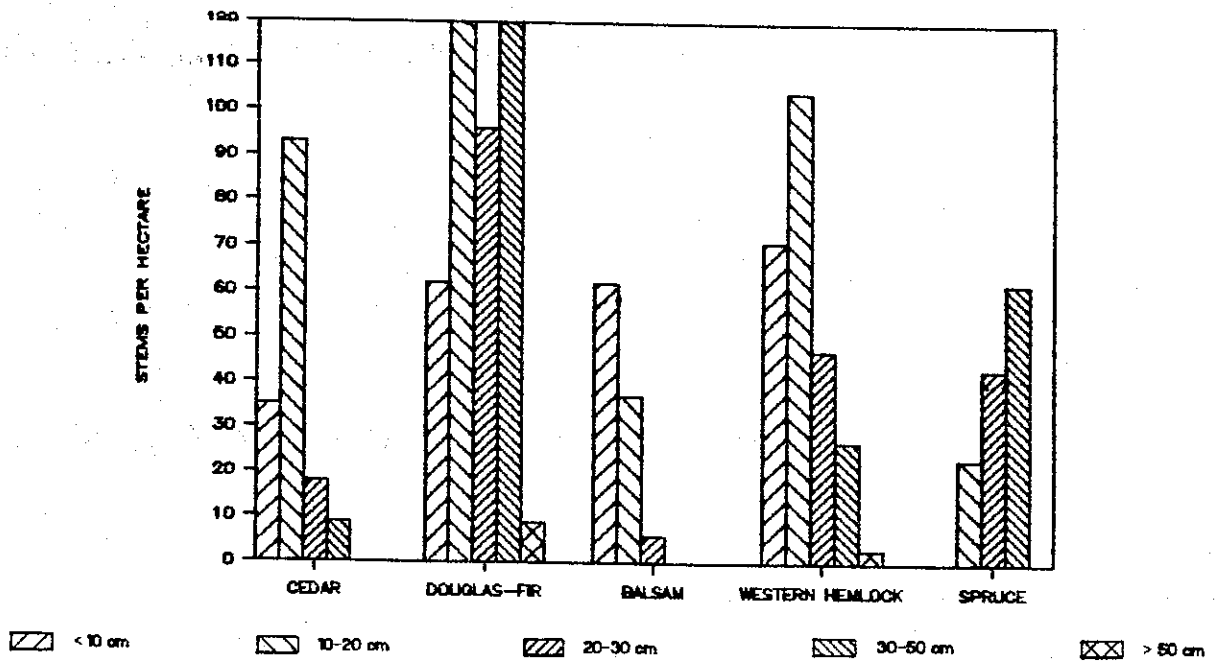


Figure 3.1. Tree size (dbh in cm) distributions for each species at inventory (year 1968) for the Quartz Creek and Beaverfoot stand.

basal area, merchantable volume, mean piece size and stand density), there are 3 results per indicator: "outside" root disease centers, average for the stand (calculated directly by PROGNOSIS), and "inside" root disease centers (calculated directly by the root disease model). The estimates for the stand outside root disease centers is obtained by a weighted difference between these latter two values. Because PROGNOSIS makes no spatial distinctions in the stand, this technique may overestimate conditions outside disease centers. For example, mortality due to root disease causes PROGNOSIS to respond as if the stand as a whole was thinned (rather than only a part of the stand) with a possible overestimate of growth in the remaining trees.

Overall, management options 2, 6, and 9 yielded roughly equivalent stand volumes in Quartz Creek (Figure 3.2); the Beaverfoot stand responded similarly but at lower volumes than expected compared with no management (scenario 1). Scenario 9 (overstory removal) was particularly successful in the Beaverfoot stand - indicating release of the dense population of small inventory trees. In terms of controlling root disease in the stand, scenario 9 was the least, and scenario 6 (stump removal) was the most successful option. With stump removal, root disease completely disappeared within 15 years of the treatment (Figures Q1, Q9 and B1, B9 in Appendix A). For these runs, the default option used in stump removal was that 99% of the infected root systems were removed. In reality, this effectiveness rate should perhaps be somewhat lower (e.g. 75 - 90%).

Trends in stand growth (MAI) and mortality for both stands are similar to those described above for stand volumes (Table 3.3). Note that while growth rates are highest for scenario 9 in both stands, mortality due to root disease is also high; particularly near the end of the scenario when root has spread through more than 50 % of each stand.

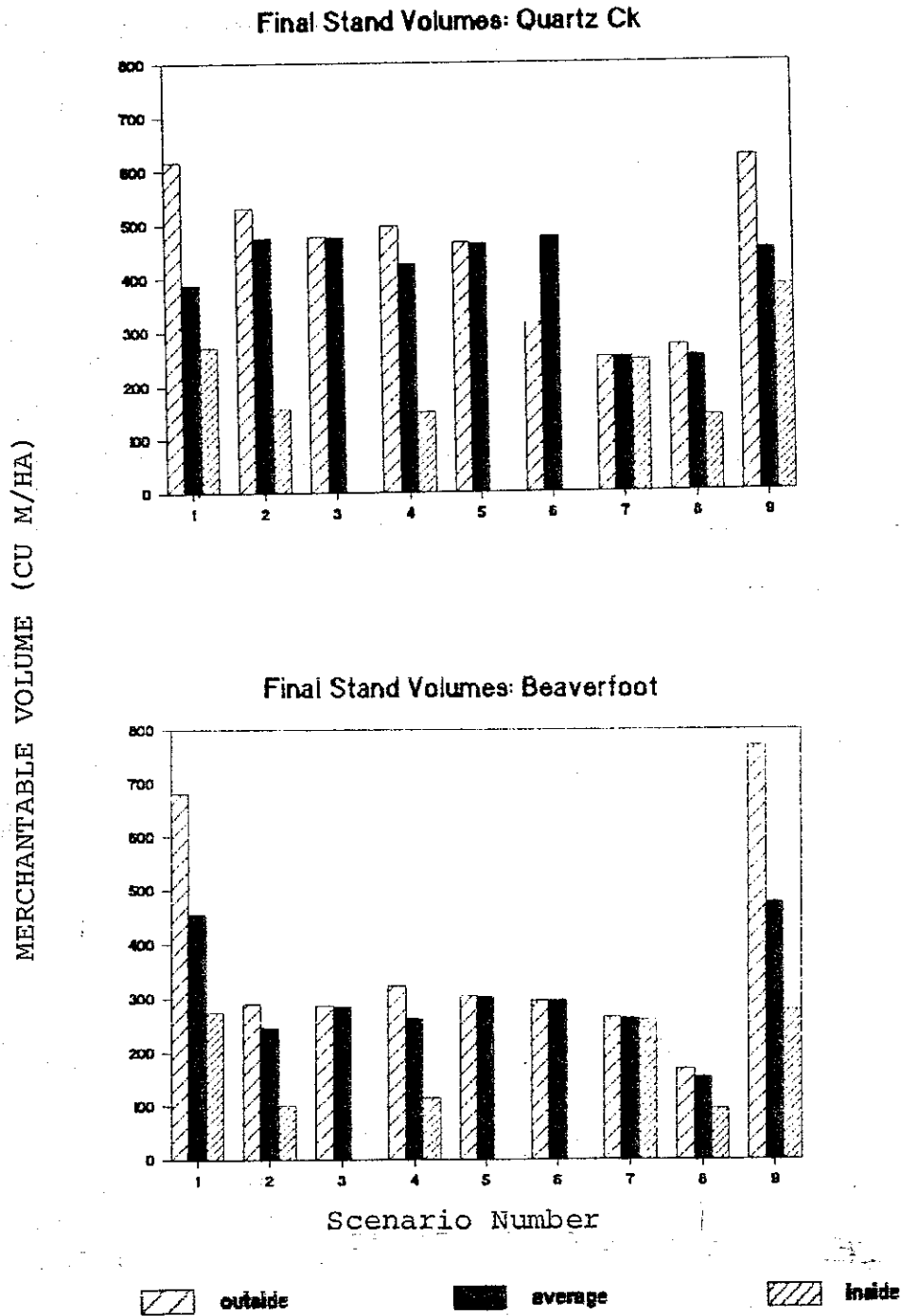


Figure 3.2. Final merchantable timber volumes per ha (volume at the year 2068) remaining in each stand for all 9 scenarios. Volumes are reported for those portions of the stands "outside" root disease centers only, the stand average, and for those portions of the stand "inside" root disease centers.

Table 3.3. Stand growth and mortality in the Quartz Creek and Beaverfoot stands for the 9 model scenarios. Note that total mortality can exceed 100% due to mortality of regenerating trees.

Quartz Creek				Beaverfoot		
Scen	MAI	Total Mortality As % MAI	Root Rot Mortality As % MAI	MAI	Total Mortality As % MAI	Root Rot Mortality As % MAI
1	4.6	115.3	41.9	5.2	106.3	38.2
2	6.5	35.3	15.9	3.4	40.3	30.9
3	6.7	34.7	0	3.7	30.6	0
4	5.6	34.7	22.0	3.4	39.1	35.9
5	5.8	29.9	0	3.5	28.5	0
6	6.6	35.1	4.1	3.6	34.4	11.1
7	3.8	43.6	4.3	3.1	37.8	12.4
8	3.1	35.4	15.7	2.0	44.0	26.3
9	4.9	34.6	29.9	5.9	51.5	38.4

N.B. Mean annual increment is reported in cu m/ha per year. All values are yearly averages over the entire scenario (110 years).

For both stands, planting a less susceptible species (western larch - scenario 7) was quite successful in reducing root disease induced mortality (Table 3.3.) and in controlling root disease in the stand (Figures Q1, Q9 and B1, B9 in Appendix A). However, projected growth of this species was unexpectedly poor in both stands, resulting in relatively low final volumes (Figure 3.2). This slow growth may indicate an underestimate of growth for this species in B.C. sites by the PROGNOSIS model. Planting Douglas fir at a reduced stocking level (scenario 8) resulted in undesirable final volumes (Figure 3.2) and had little effect in controlling root disease spread (Figures Q1 and B1 in Appendix A).

Three indicators of stand yield in Quartz Creek (Figures 3.3, 3.4, and 3.5) are shown for management scenarios 2, 4, and 6 along with their respective "control" or non-root disease scenarios. In each scenario there is a reduction (from 2 - 5%) of average stand volume for scenarios with root disease compared to the same scenario without root disease. MAI resulting from a pre-commercially thin of a stand with root disease (Figure 3.4) is significantly lower than if the stand had no root disease. This suggests that this type of thinning is a poor management strategy; significant mortality will occur to the remaining small trees (Table 3.3) as well as disease-related growth reductions. This is also suggested by comparison with Figure 3.3; there is only a slight reduction in MAI attributable to the disease in that scenario. Interestingly, the effect of root disease-induced mortality early in the stand on both MAI and final yield is suggested by Figure 3.5. While root disease has been wiped out by 1993 in scenario 6, the reduced (5% lower) average stand volume and slightly greater MAI in the maturing stand in scenario 6 is indicative of the thinning effects of root disease in the very young stand.

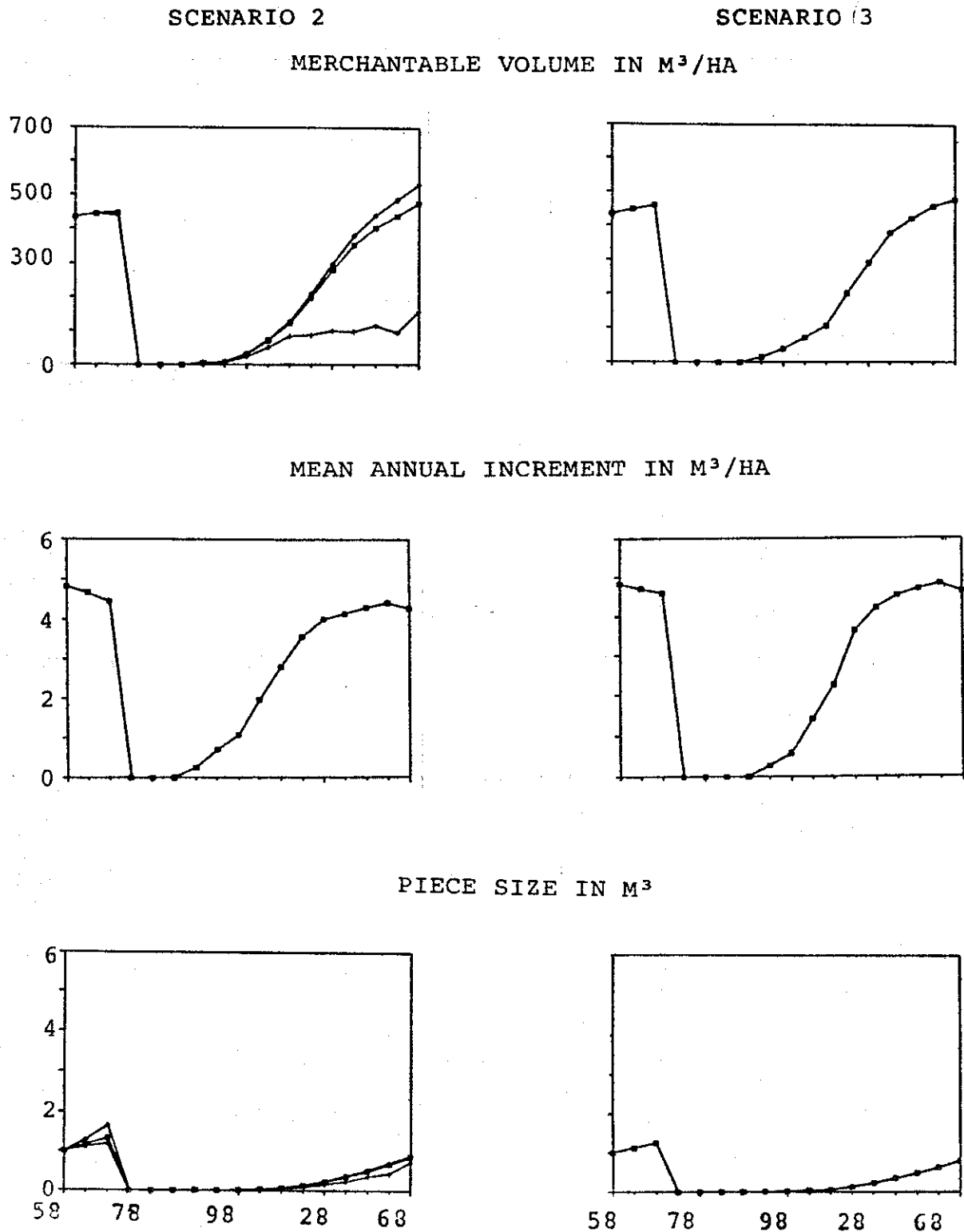


Figure 3.3. Stand yield indicators for scenarios 2 and 3 for the Quartz Creek stand. Merchantable volume and piece size show results for "outside", stand average, and "inside" (see text for details).

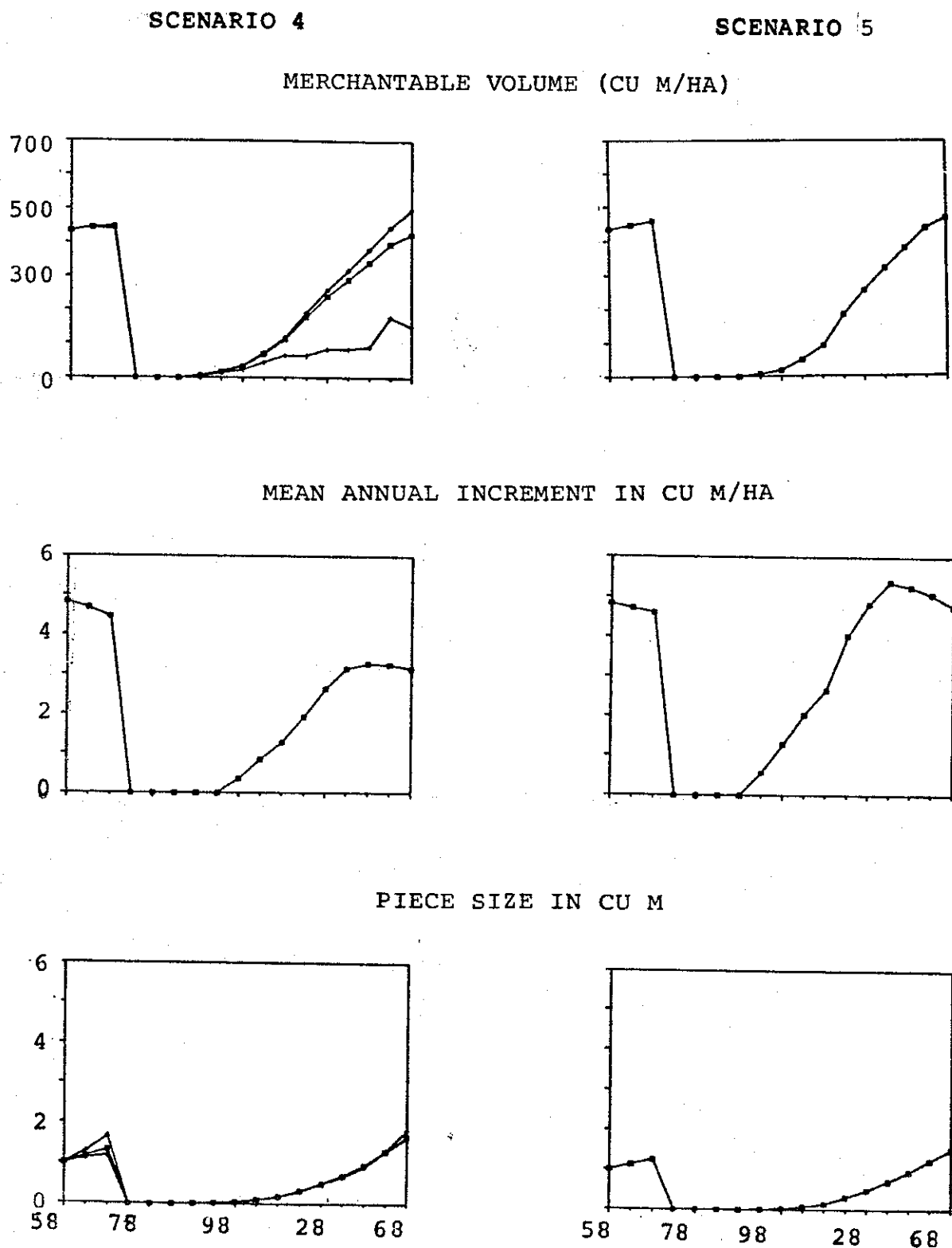


Figure 3.4. Stand yield indicators for scenarios 4 and 5 for the Quartz Creek stand. Merchantable volume and piece size show results for "outside", stand average, and "inside" (see text for details).

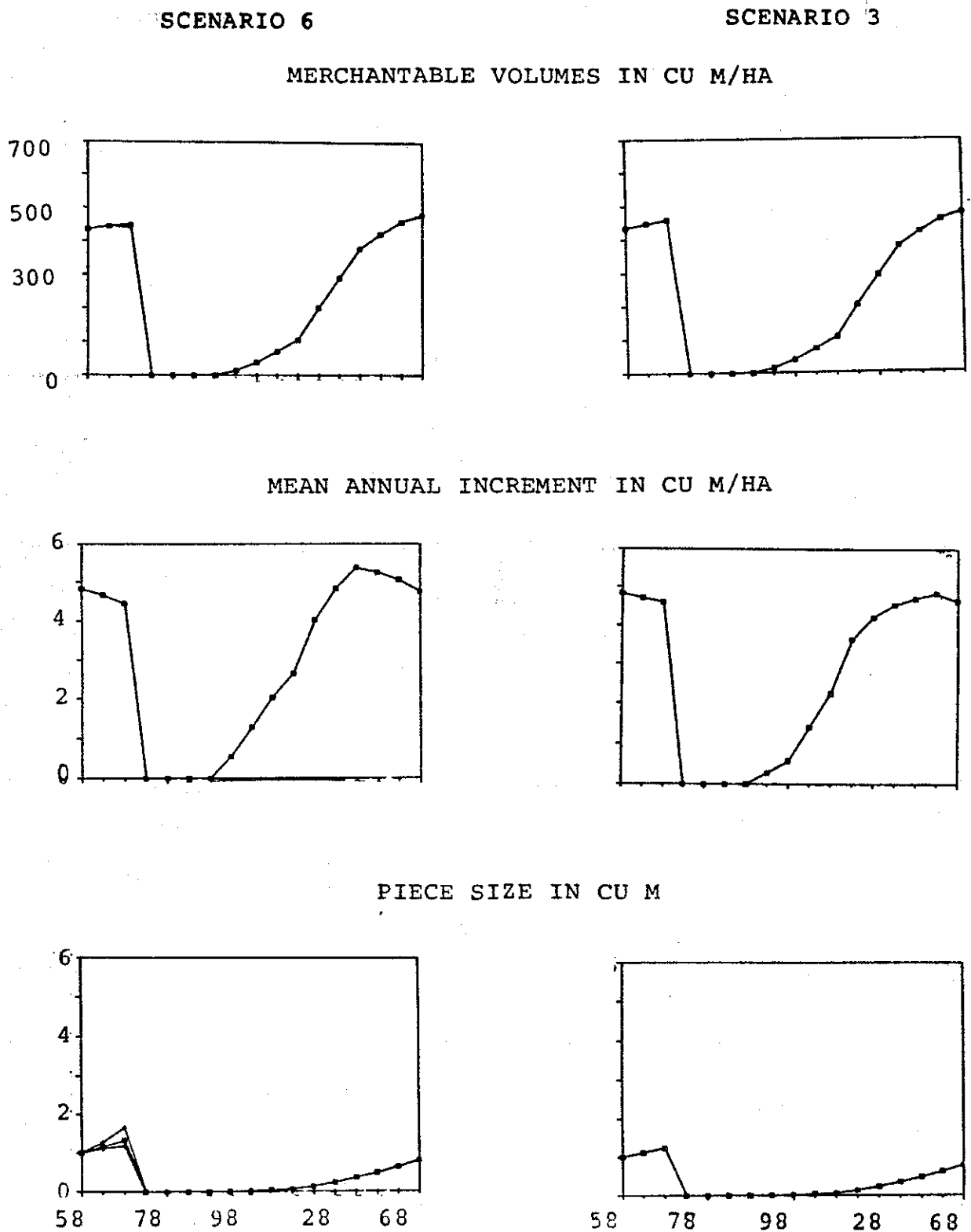


Figure 3.5. Stand yield indicators for scenarios 6 and 3 for the Quartz Creek stand. Merchantable volume and piece size show results for "outside", stand average, and "inside" (see text for details).

As discussed above in section 3.3, the initial inventories of root disease in these stands was conservative, particularly in the initial densities of infected stumps. To examine how the stand yields would respond to higher initial disease levels, we resubmitted scenarios 4 and 9 for the Quartz Creek stand with a 5 X increase in density of initial infected stumps (i.e. at 5 stumps /ha). The results of these runs are shown in Table 3.4. Higher initial stump density results in lower average stand volumes for both management scenarios (and even lower stand volumes inside root disease centers), as well as on MAI. Effects on stand density were not as clear cut, although areas inside root disease centers were significantly thinner at the higher stump density for both scenarios. There was no clear effect of higher initial stump density on the spread of root disease through the stand.

Table 3.4. Comparison of stand yield and root disease infection at 2 densities (low = 1/ha; high = 5/ha) of initial infected stumps. Shown are management scenarios 4 and 9 for the Quartz Creek stand. All indicators are from the final growth cycle of the simulation. "Outside", average, and "inside" are defined in the text.

Scenario	Location	Merch Vol (cu m /ha)	Stand Density (stems /ha)	MAI (cu m/ha)	% Stand Infected
4 - low	Outside	500	400	3.1	21.0
	Average	421	382		
	Inside	180	100		
4 - high	Outside	487	460	2.9	20.0
	Average	413	384		
	Inside	100	64		
9 - low	Outside	660	1000	4.0	72.0
	Average	460	650		
	Inside	401	600		
9 - high	Outside	618	1037	3.6	73.0
	Average	428	614		
	Inside	347	434		

4.0 MODEL EVALUATION AND IMPLEMENTATION

A description of the model, and model results using the stands and scenarios described in section 3 was presented and discussed at two separate 1 day workshops held in Cranbrook (March 16, 1988) and Nelson (March 18, 1988). Participants at these workshops included regional pathologists, silviculturalists, district managers and licencees (see Table 4.1 for a list of workshop participants). Two issues formed the basis of these discussions:

1. What utility does the model have to forest managers and planners in the BCMFL; and
2. If the model is useful, what are the requirements for model implementation in the Ministry?

Results of the discussions are summarized in the following sections.

4.1 Utility of the Model to Forest Managers in B.C.

The root disease model was seen by workshop participants as being able to play a necessary and important role for the MFL in meeting at least three needs: a) as a tool for gaming with alternative stand management options; b) as a tool for educating forest managers, licencees, and contractors on the problems and management of root disease (including techniques for root disease inventory); and c) with further development, as a component in the timber supply planning process. The consensus at both workshops was that the model should be made widely available to Ministry offices at both the regional and district levels, and to industry. Ministry staff members at all levels, as well as licencees should be trained in its use.

Specific suggestions for improving the utility of the model in achieving these goals are outlined in the sections below.

Table 4.1. Project Participants.

Participant	Jan. 15/88 Scoping Workshop Vancouver	Mar. 16/88 Workshop Cranbrook	Mar. 18/88 Workshop Nelson
Rick Baker BCMFL Cranbrook		X	
Jeff Beale BCFML Vancouver	X		
Bill Beard BCMFL Revelstoke			X
Emile Begin BCMFL Invermere		X	
Dave Beseraha Canadian Forest Industries Cranbrook		X	
Steve Byford BCMFL Cranbrook		X	
Reg Davis BCMFL Kootenay Lake			X
Paul Diggle BCMFL Victoria	X		
Ted Evans BCMFL Castlegar			X
Bruce Fraser BCMFL Nelson			X
Bob Gay BCMFL Cranbrook		X	
David Kilshaw BCMFL Grand Forks			X
Mark Mack Western Timber Ltd. Nakusp			X
Wayne Martin BCMFL Smithers		X	

Participant	Jan. 15/88 Scoping Workshop Vancouver	Mar. 16/88 Workshop Cranbrook	Mar. 18/88 Workshop Nelson
Peter McNamee ESSA Ltd. Toronto, Ont.	X		
Hadrian Merler BCMFL Kamloops		X	
Darcy Monchak BCMFL Golden		X	
John Muir BCMFL Victoria	X	X	X
Don Norris BCMFL Nelson	X	X	X
Dave Powers BCMFL Golden		X	
Allen Pollard BCMFL Golden	X		
Larry Price BCMFL Golden		X	
John Przeczek BCMFL Cranbrook		X	
Dan Reiben BCMFL Castlegar			X
Maureen Schulting BCMFL Prince George		X	
Glenn Sutherland ESSA Ltd. Vancouver	X	X	X
Bob Taylor Evans Products Ltd. Golden		X	
John Visslai BCMFL Victoria	X	X	
Ken Weaver BCMFL Grand Forks			X

4.1.1 Enhancements to the Root Disease Model

Revisions to Model Dynamics

The dynamics of root disease as captured by the model are oriented towards representing diseased stands in the Inland Empire region of the western United States. While the basic model relationships governing tree susceptibility, disease transmission, mortality, and growth effects are also applicable in B.C., recent research and experience with root disease in some stands suggests that some modifications and additions to the model should be made:

- Disease pathogens may be spread not only by contact between infected and uninfected root systems, but also by the fungal rhizomorphs themselves and to an unknown extent by spores. Rhizomorph spread may be quite important in Phellinus infected stands, particularly near the coast. For both Armillaria and Phellinus, pieces of active rhizomorphs remaining after such events as selective logging may be disseminated through the infection zones and transmit disease to susceptible trees (particularly in dense stands of lodgepole pine and hemlock).
- In the current model, infected stumps are the sole source of inoculum for a regenerating stand after a clearcut. However, in some B.C. stands, several species of shrubs also appear to act as inoculum sources; the pathogen appears to persist in, and be spread to regenerating trees by these shrubs as well as by contact with stumps from the previous stand.
- Many B.C. stands show mixed infections - Phellinus and Armillaria may in fact coexist in a stand. The current version of the model simulates the impact of only one of these pathogens at a time, not both together. Very often pathologists will detect the presence of Armillaria in Phellinus infected stands after such events as clearcutting. It is not yet clear what the dynamics of this sort of coexistence are.
- Selective logging (for example to remove trees infected with such pests as mistletoe, mountain pine beetle, etc.) may cause "flushing" of Armillaria spread and mortality in the remaining trees. That is, significant numbers of the remaining

trees may be killed by root disease within 3-5 years of the selective cut. Among possible reasons for this rapid mortality are that these trees already have low levels of disease infection, and that they temporarily become much more susceptible to the disease through shock (i.e. soil compaction, microclimate changes) associated with the cut. The current model can simulate some of this behaviour through "jumping out" of the disease into uninfected root systems after a cut, and by modifying the probability of transmission at the time of the cut. However, there is as yet no simple facility to temporarily adjust the susceptibility of tree species for a short 3-5 year period.

- Industry has noted that root disease infection may reduce the market value of harvested timber. While the current model simulates growth reductions and mortality due to root disease infection, it does not deal with this consequence of the disease. This type of factor becomes especially important when considering the economic impacts of disease infection (see below).

In addition to the above, a necessary adjunct to a model revision process would be further sensitivity analysis to identify those root disease parameters currently in the model which will need adjustment to better capture the behaviour of the diseases in B.C. stands.

Modifications to the Model's User Interface

As described in section 2.6, model results are presented in tabular form. While suitable for silvicultural planning and analysis purposes, graphical output provides the most accessible way to communicate model results to people in model gaming and training contexts. In addition, ways to translate some of the model outputs into economic indicators of stand yield and health would be desirable.

Specific suggestions for improvements to the user interface to the model were:

- development of an interactive (non-batch oriented) version of the model, preferably on IBM-compatible

PCs. A PC version allows users unlimited access to the model, allows easy development of graphics (see below), and makes it transportable for training sessions and for public demonstrations. A more central, networked version of the model would also satisfy some of these needs, but may not be as flexible.

- replacement of the current keyword input system with a simpler, screen-editor oriented system. Not only would a screen-based system be easier to demonstrate to inexperienced users, it also facilitates gaming sessions where only one or two inputs are changed between scenarios.
- development of a graphical output system for the model, where one or several model indicators are plotted on the screen as the simulation proceeds (in colour if the hardware permits). This type of output enhances the ability to compare results between runs and can be highly customized to meet the needs of various user groups (pest researchers, managers, licencees, public demonstrations, etc.). The existing tabular output system would remain as a user-selectable option for output, such that further analysis could be done with the data.
- development of a spatial representation of root disease spread (e.g. similar to that shown in Figure 2.4). This system would facilitate discussion about management options and their impact on disease dynamics in training sessions.
- including additional outputs from the model for more precise estimation of disease impact. For example, volume, density and growth measures by individual species (not directly accessible in the current outputs) would be important in stand planning for mixed stands containing disease.
- ability to attach model outputs to an economic analysis program would be important not only for demonstration purposes, but also for timber supply analysis. The current version of the model (with PROGNOSIS) can be run along with an economic analysis package through the CHEAPO option of PROGNOSIS (see Wykoff et al. 1982 for details). Clearly such a system would have to be calibrated for the B.C. situation.

Many of the current user-interface features of the root disease model are consequences of its linkage to

PROGNOSIS (keyword input system, tabular output, inputs and outputs in imperial units rather than metric units). Depending on how the root disease model was implemented in B.C. (see below) the modifications suggested above could be made to the combined root disease/PROGNOSIS system, or to the root disease model and whichever stand model was selected for it in B.C.

4.1.2 Selection of a Stand Model

Choosing an appropriate stand model to use along with the root disease model in B.C. is not a trivial decision. PROGNOSIS offers many advantages as a stand model: it can simulate a wide variety of single and mixed species stands and stand ages, it provides essentially all the management options used in B.C., there is considerable experience in parameterizing it for different forest regions, it has many extensions for simulating common forest pests, stand regeneration and understory dynamics, and it is easily portable among different computers. However, it would require some effort to calibrate the model for B.C., particularly in terms of the growth and mortality parameters for each tree species, and in incorporating the ecosystem classification system into the current habitat type system used by PROGNOSIS.

Because of the perceived utility of the root disease model to the BCMFL, and because it can be linked to other stand models, participants felt that the process of implementing the root disease model should not be made dependent on the choice of stand model to use. For example, the root disease model could be profitably used with even a very simple stand model for the purposes of interactive gaming and training. In these cases, the objective is to examine relative differences in stand performance under alternative management regimes, and not necessarily to compare absolute indices of stand yield.

4.2 A Process For Model Implementation

Based upon the workshop discussions and recommendations, below are outlined a a general set of elements which, if undertaken, would produce a working root disease model adapted for British Columbia conditions. The process for model implementation described below can proceed independently of the stand model which is selected for British Columbia. We envision the implementation process being a two year effort. Naturally, the full details of an implementation process would require careful specification, but there are essentially six major elements in the model implementation process:

1. identification of user needs;
2. model refinement;
3. model sensitivity analysis for British Columbia situations;
4. development of user interface;
5. model and system documentation;
6. training in model use.

Each element will be described in greater detail below.

Of critical importance to the implementation process would be a "core group" of MFL and (perhaps) industry personnel who would bear the responsibility for successful implementation of the model. We suggest that this group be composed of MFL and industry research scientists, inventory specialists, pathologists, silviculturalists, and timber planners.

4.2.1 Identification of User Needs

This project has begun to identify some of the user needs for the root disease model, for example, the type of computing system on which the model should reside and some of the model refinements needed to make the model more accurately reflect the British Columbia situation. These needs will have to be more formally defined in order that the root disease system that is developed will operate in the way that the users of the system would find realistic and informative.

4.2.2 Model Refinements

This element would consist of making the necessary changes to the model structure and dynamics to make it more representative of the disease behaviours in British Columbia stands. Some of the important refinements such as multiple root diseases in a single stand, root disease spread by spores, an economics submodel, and stand-age dependent susceptibility to root disease, have already been identified in the workshops and would be obvious first candidates for model refinements. In addition, all model parameters would have to be reviewed and modified if necessary for British Columbia. At the end of this component of the implementation process, the MFL would have a root disease model which could be called Version 1.0.

4.2.3 Model Sensitivity Analysis

The root disease model is a very complex model and its behavior is not yet well understood. It is likely that the model refinements described above would make the model even more complicated. This element of the implementation process would need to be done so that model users could clearly understand why the model was

giving particular behaviors and how precise various model parameters, such as the root disease inventory, needed to be.

4.2.4 Development Of User Interface

In this element of the implementation process, Version 1.0 of the root disease model would be embedded in a software environment that could make it easily used by all appropriate staff within the MFL and industry. This software would involve giving the model user flexibility and choice in model input and output.

4.2.5 Model and System Documentation

In this element of the implementation process, extensive documentation of the root disease model and the system would be prepared as reference material for model users.

4.2.6 Training In Model Use

The final element of the implementation process would be training in MFL and industry staff in the use of the system. This should involve selection of a number of trainers within the MFL, development of a training package likely centered around workshops and extensive hands on gaming, and conduct of those workshops to interested participants throughout the province. Such demonstration/training workshops would include: model description, the simulation and analysis of alternative scenarios representative of the particular locality, a field trip to the example stand(s) with the results of these runs in hand, discussion of implications, and training in disease identification and appropriate inventory procedures.

5.0 REFERENCES

Ferguson, D.E. and N.L. Crookston, 1984. User's guide to the regeneration establishment model - a Prognosis model extension. U.S. Dept. Agr. For. Ser. Gen. Tech. Rept. INT-161, 23 pp.

McNamee, P.J., T.M. Webb, R.R. Everitt, and L.A. Greig. 1985. Final report of a project to construct a prototype root disease model for silvicultural planning in the western United States. Report submitted to U.S. Forest Service. 104 pp.

McNamee, P.J., T.M. Webb, G.D. Sutherland, and L.P. Rattie. 1986. Report of a two year project to develop a root disease model for silvicultural planning in the western United States. Report submitted to the U.S. Forest Service. 87 pp.

Morrison, D.J. 1981. Armillaria root disease. A guide to disease diagnosis, development and management in British Columbia. Canadian Forestry Service BC-X-203. 15 pp.

Smith, R.S. 1984. Root disease-caused losses in the commercial coniferous forests of the western United States. U.S. Dept. Agr. For. Serv. 21 pp.

Stage, A.R., 1973. Stand Prognosis model for stand development. U.S. Dept. Agr. For. Serv. Res. Pap. INT-137, 32 pp.

Sutherland, G.D. and P.J. McNamee. 1987. User's Guide to the root disease model: a PROGNOSIS model extension. Report submitted to the U.S. Forest Service. 39 pp.

Wallis, G.W. 1976. Phellinus weirii root disease. Detection and management proposals in Douglas-fir stands. Can. for. Serv. for. Tech. Rept. No. 12.

Wykoff, W.R., N.L. Crookston, and A.R. Stage, 1982. User's
guide to the Stand Prognosis model. U.S. Dept. Agr.
For. Serv. Gen Tech. Report INT-133, 112 pp.

APPENDIX A

Detailed Output Figures for the Model Runs

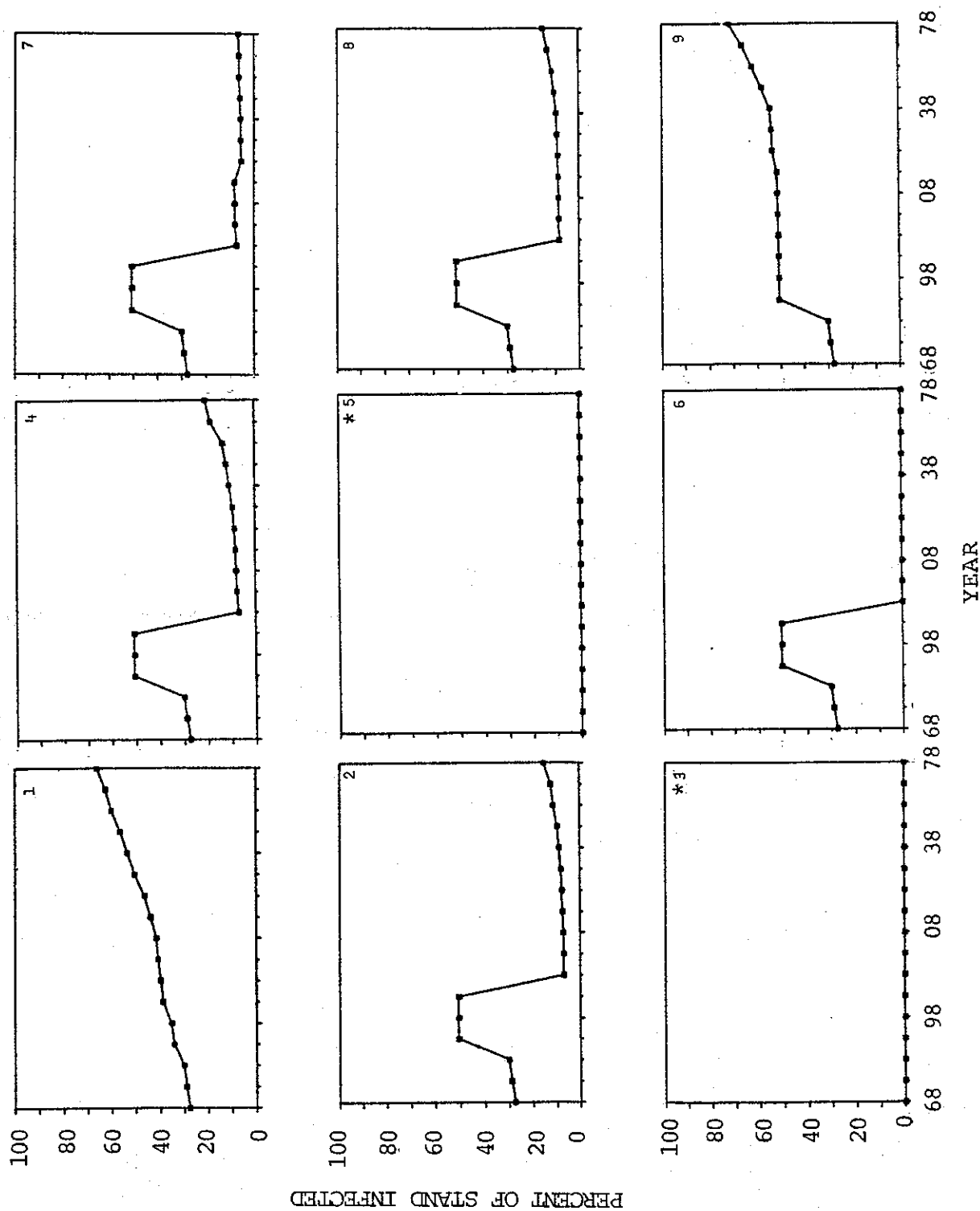


Figure Q.1. Changes in the percentage of the Quartz Creek stand area infected with Armillaria over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. The simulations cover the years between 1968-2078(.5 year time step from 1968-2008; 10 year time step thereafter).

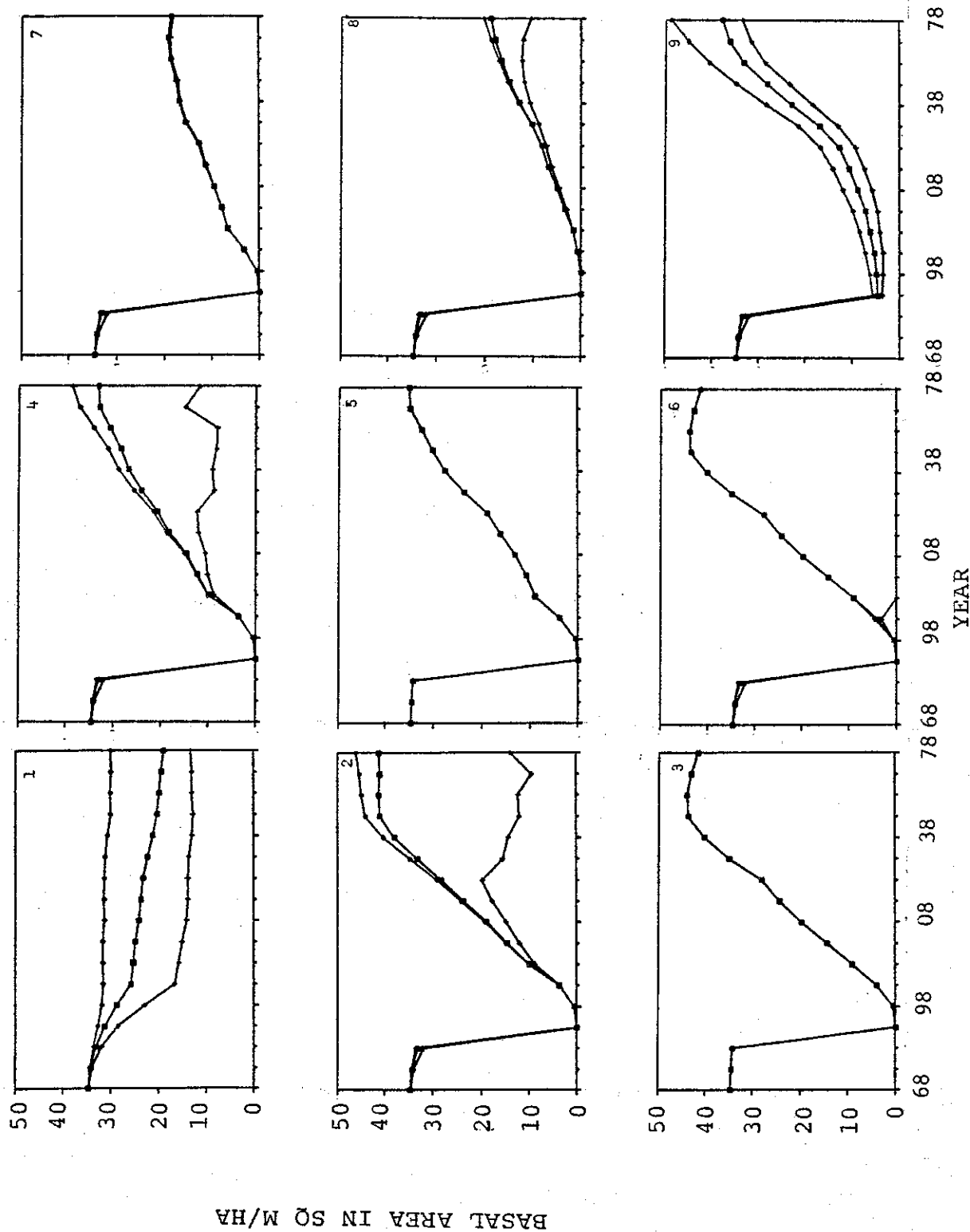


Figure Q.2. Changes in basal area (cu m/ha) in the Quartz Creek stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. Symbols on each graph are: triangles (top line) - areas outside diseased patches only; squares (middle line) - stand average (both diseased and non-diseased areas); plus signs (bottom line) - area inside diseased patches only. The simulations cover the years between 1968 - 2078 (5 year time step from 1968-2008; 10 year time step thereafter).

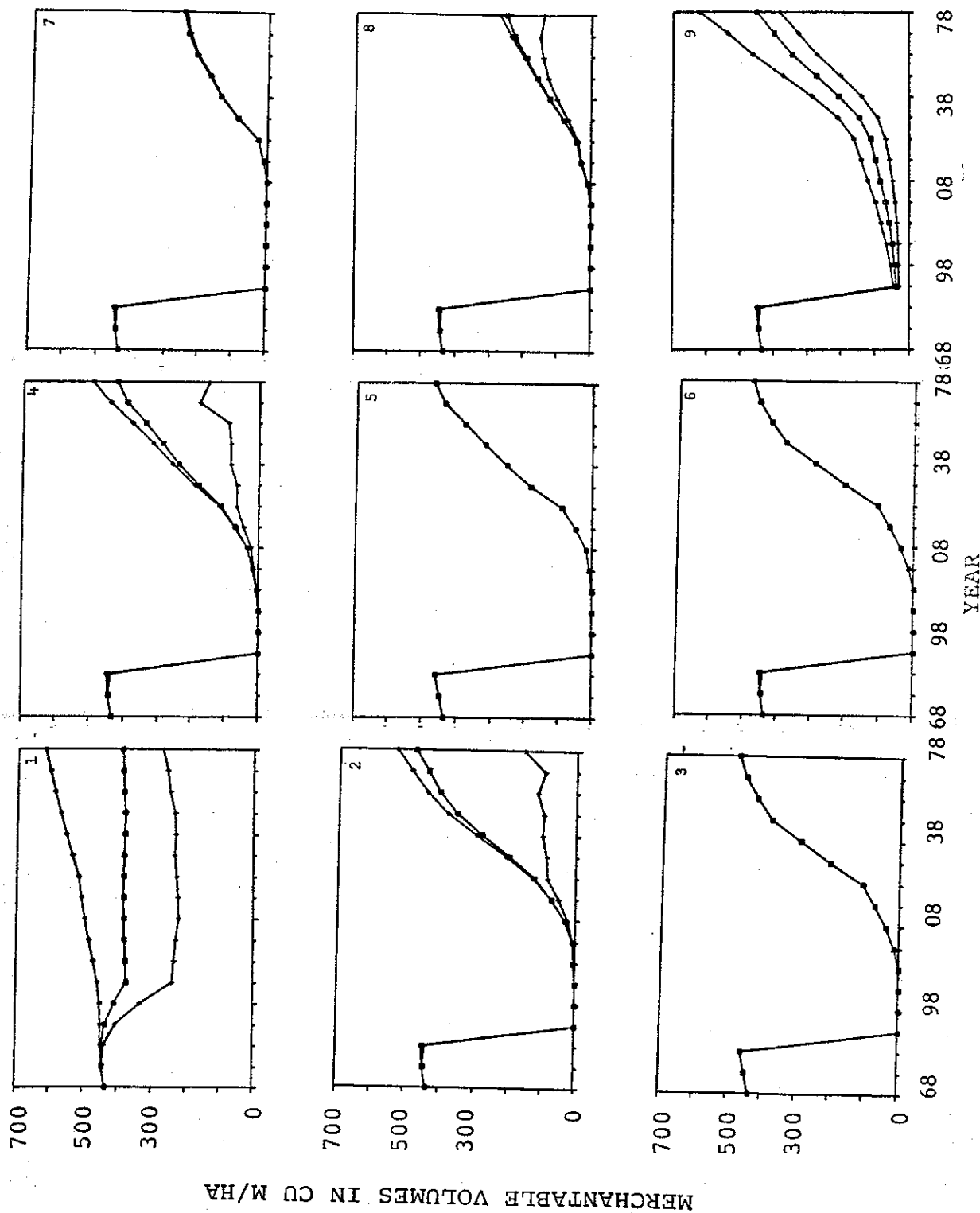


Figure Q.3. Changes in merchantable volume (cu m/ha) in the Quartz Creek stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. Symbols on each graph are: triangles (top line) - areas outside diseased patches only; squares (middle line) - stand average (both diseased and non-diseased areas); plus signs (bottom line) - area inside diseased patches only. The simulations cover the years between 1968 - 2078 (5 year time step from 1968-2008; 10 year time step thereafter).

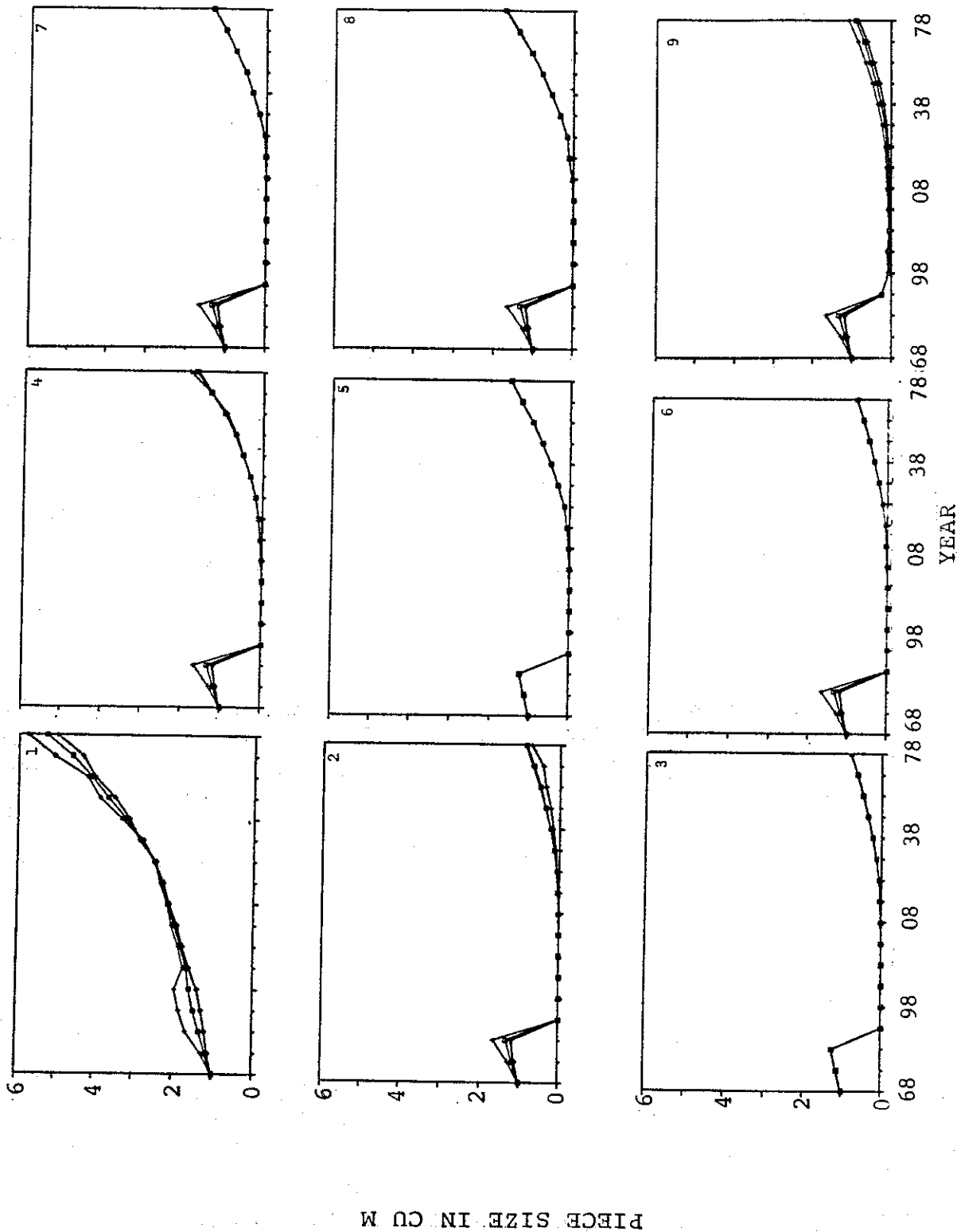


Figure Q.4. Changes in mean piece size (volume in cu m/tree) in the Quartz Creek stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. Symbols on each graph are: triangles (top line) - areas outside diseased patches only; squares (middle line) - stand average (both diseased and non-diseased areas); plus signs (bottom line) - area inside diseased patches only. The simulations cover the years between 1968 - 2078 (5 year time step from 1968-2008; 10 year time step thereafter).

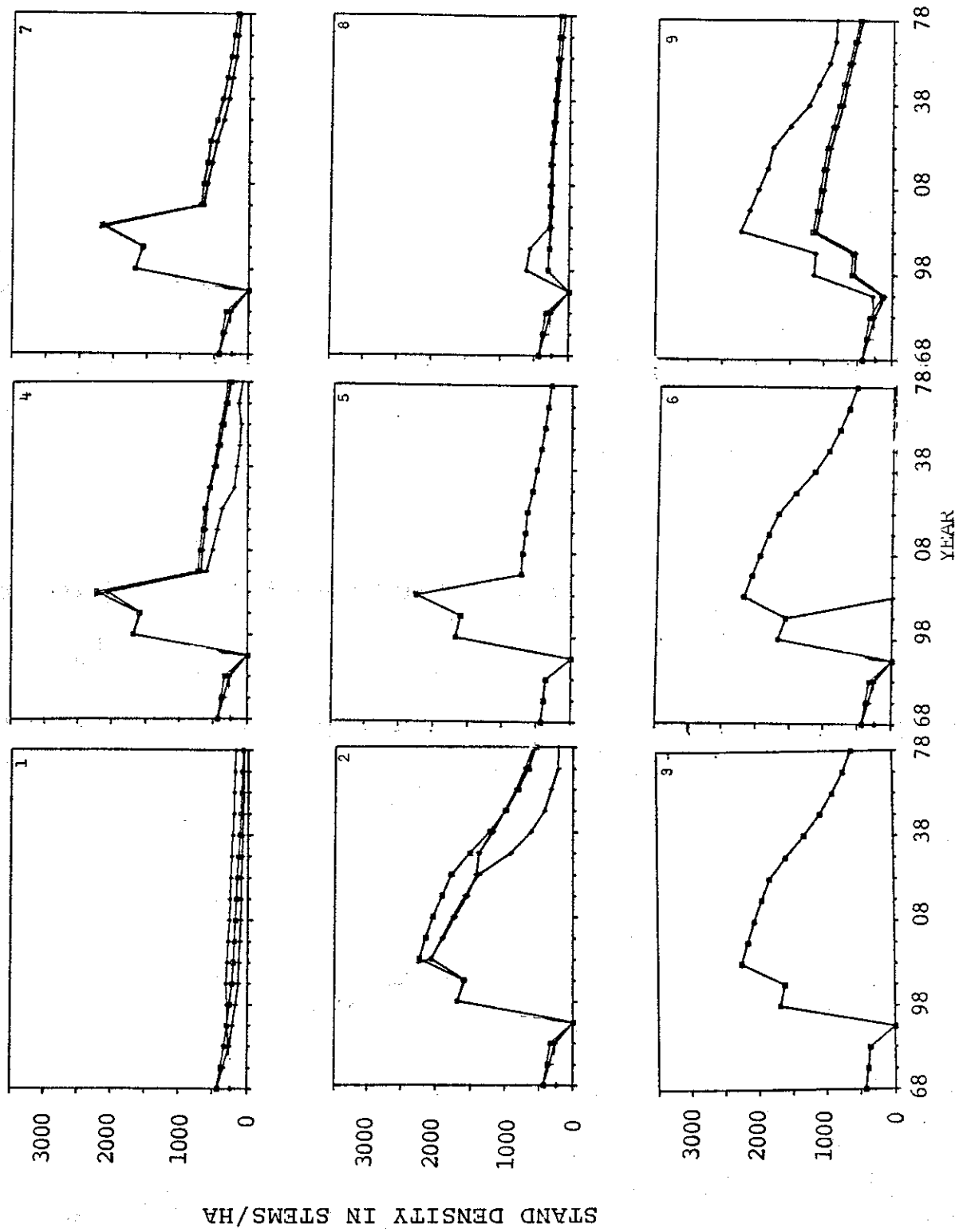


Figure Q.5. Changes in stand density (stems/ha) in the Quartz Creek stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. Symbols on each graph are: triangles (top line) - areas outside diseased patches only; squares (middle line) - stand average (both diseased and non-diseased areas); plus signs (bottom line) - area inside diseased patches only. The simulations cover the years between 1968 - 2078 (5 year time step from 1968-2008; 10 year time step thereafter).

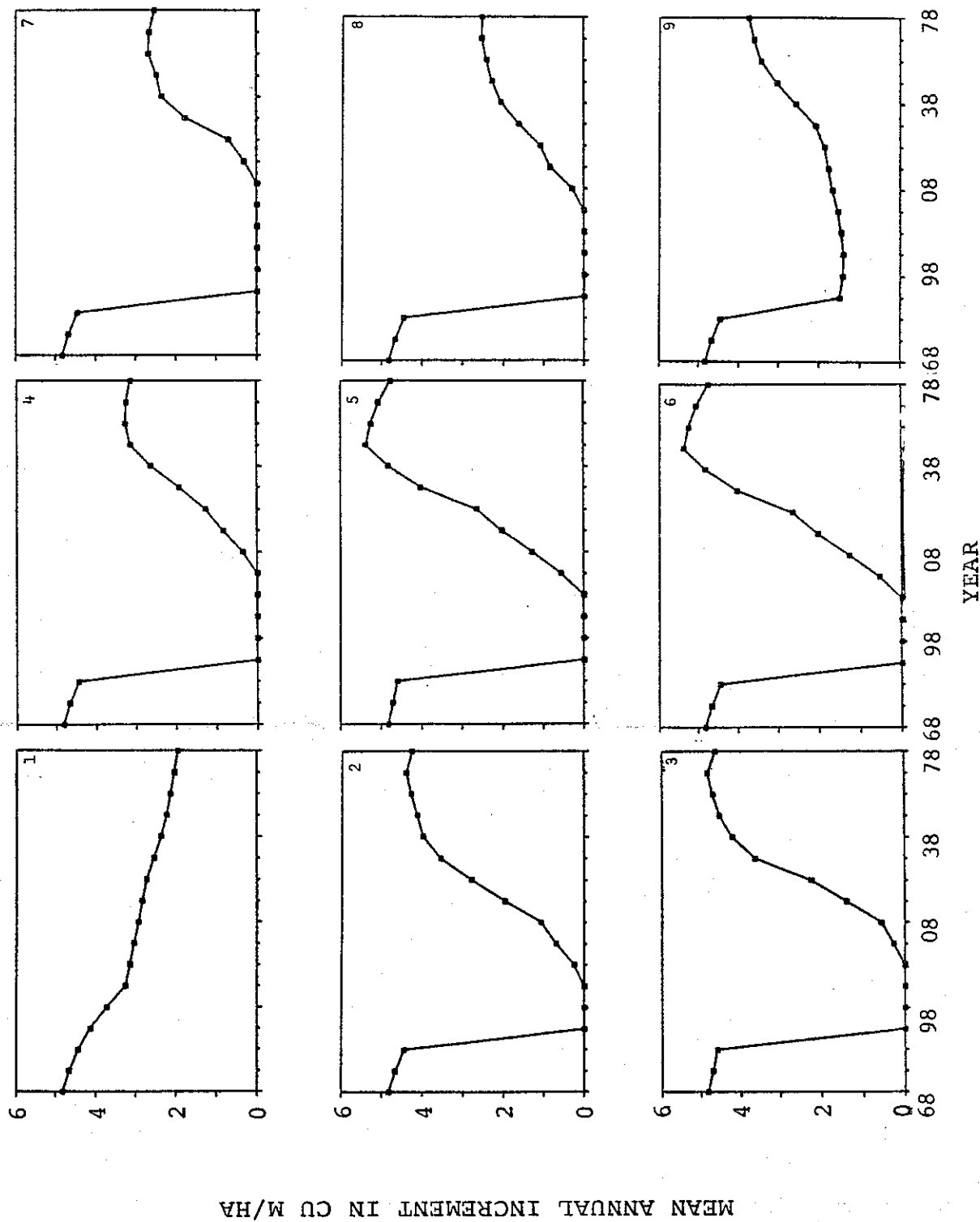


Figure Q.6. Changes in mean annual increment (cu m/ha) in the Quartz Creek stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. The simulations cover the years between 1968 - 2078 (5 year time step from 1968 - 2008; 10 year time step thereafter).

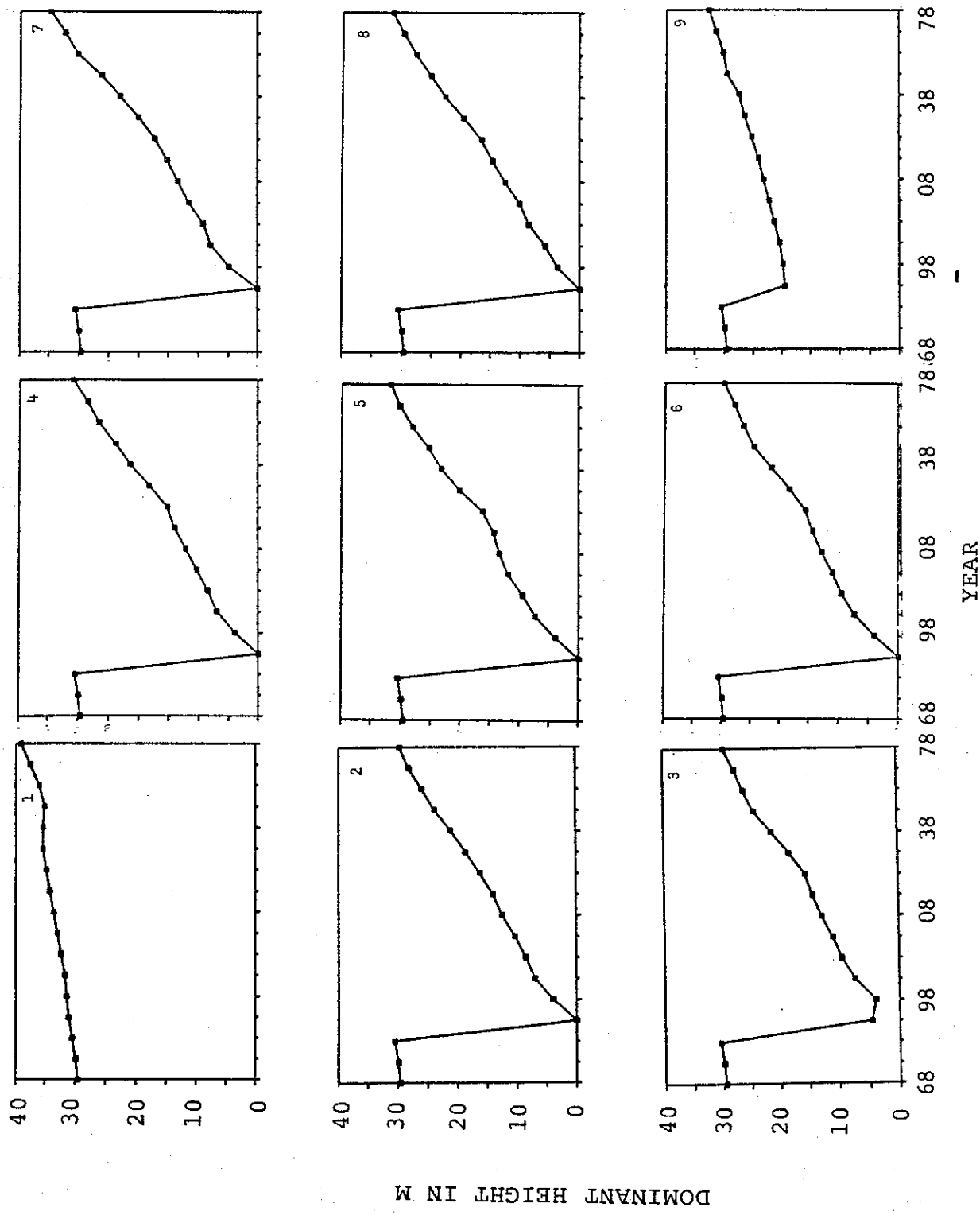


Figure Q.7. Changes in average dominant height (m) in the Quartz Creek stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. The simulations cover the years between 1968 - 2078.(5 year time step from 1968 - 2008; 10 year time step thereafter).

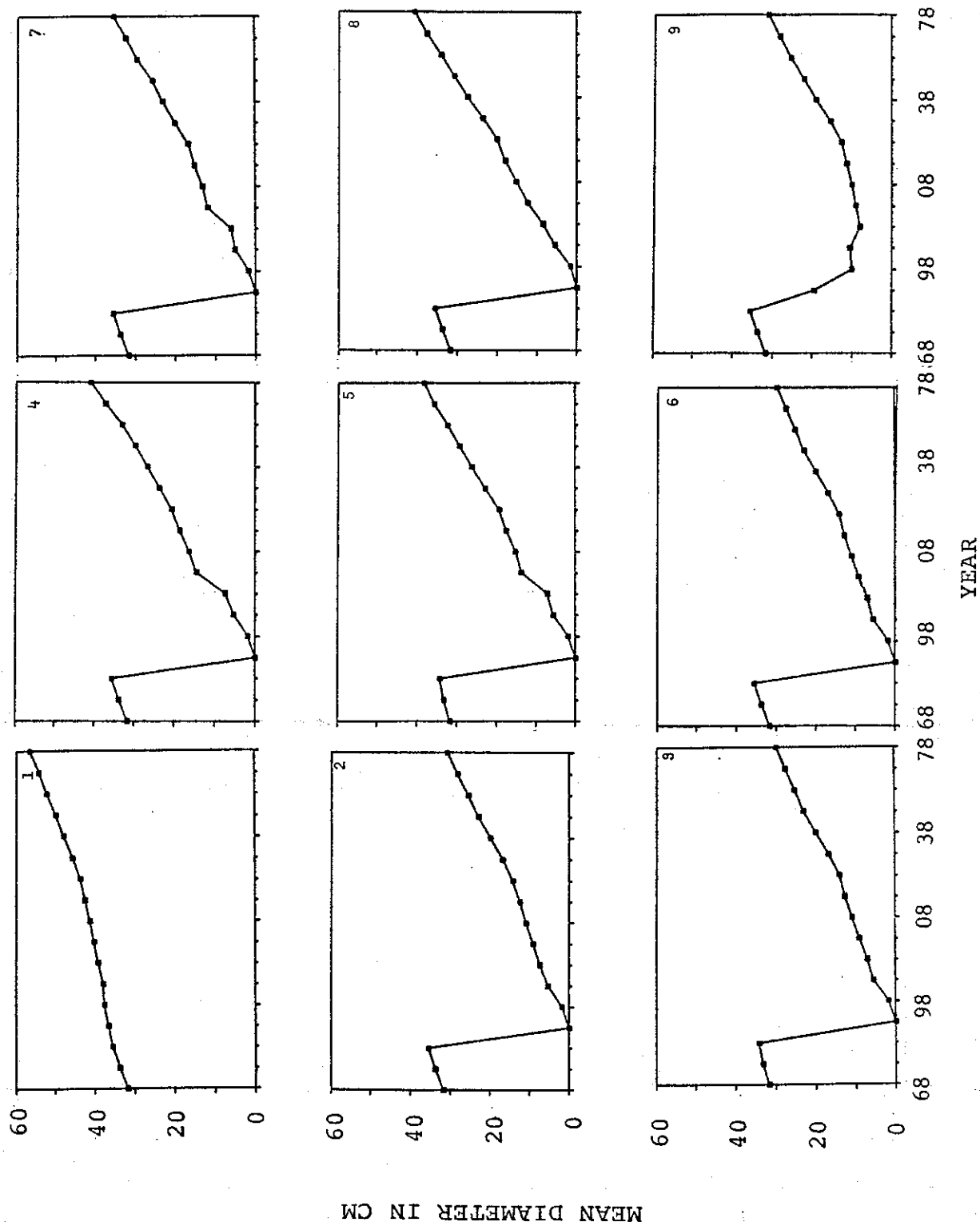


Figure Q.8. Changes in mean tree diameter (cm) in the Quartz Creek stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. The simulations cover the years between 1968 - 2078 (5 year time step from 1968-2008; 10 year time step thereafter).

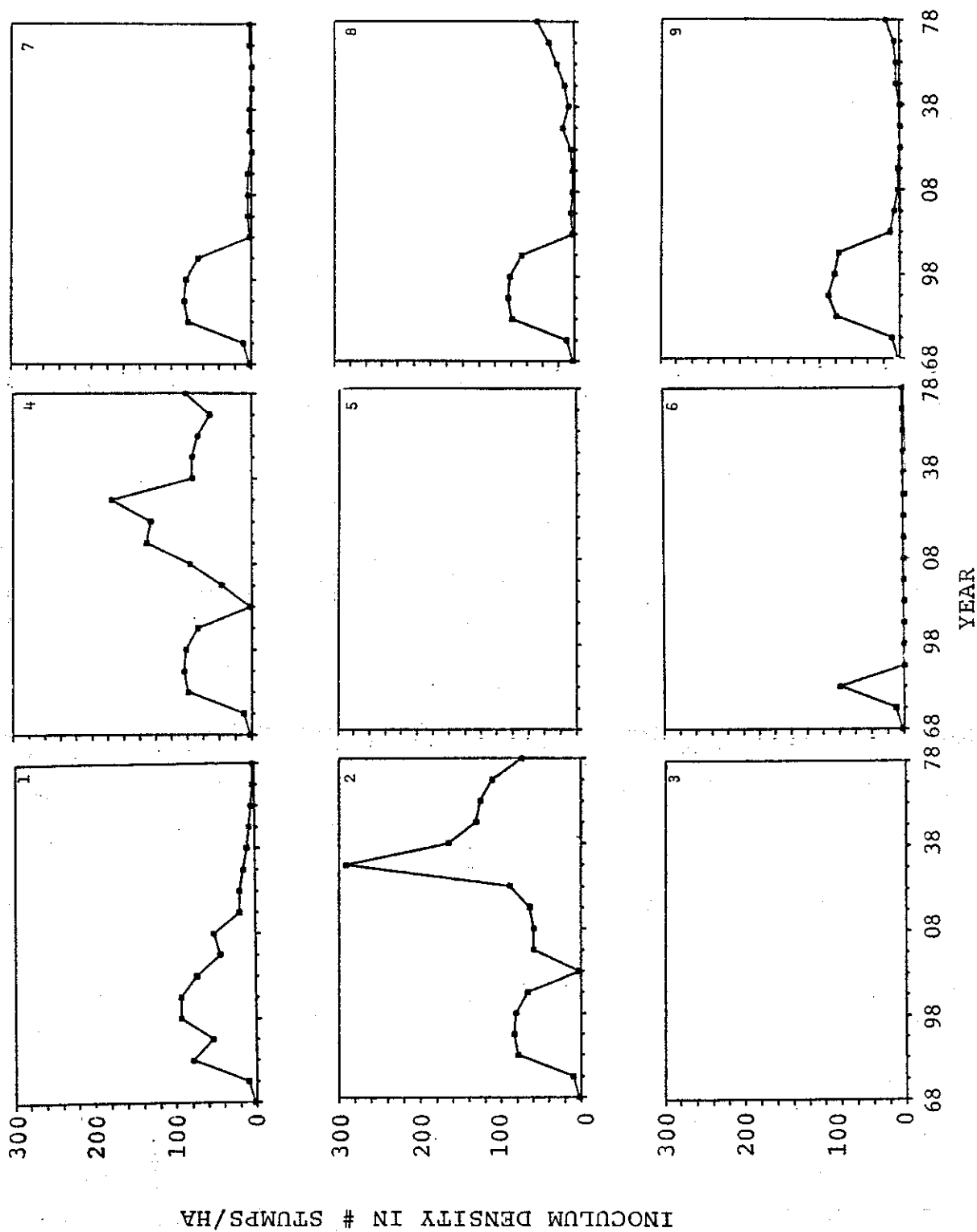


Figure Q.9. Changes in inoculum density (# stumps/ha) in the Quartz Creek stand over time for scenarios 1-9. Stumps in this context refer to remnants of trees that were infected with root disease at the time of death. Numbers in the upper right hand corner of each graph denote the scenario number. The simulations cover the years between 1968 - 2078 (5 year time step from 1968 - 2008; 10 year time step thereafter).

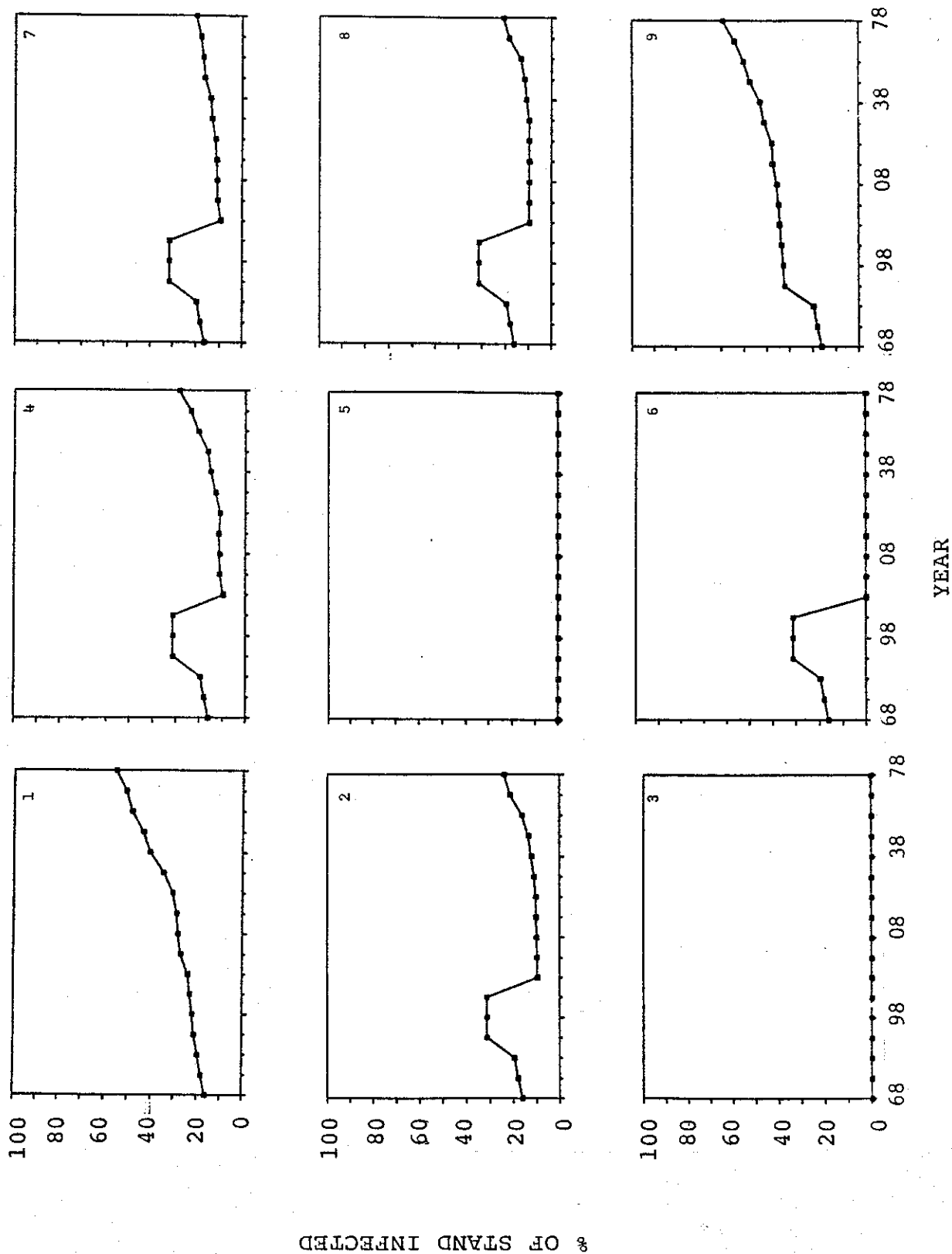


Figure B.1. Changes in the percentage of the Beaverfoot stand area infected with Armillaria over time for scenarios 1 - 9. Numbers in the upper right hand corner of each graph denote the scenario number. The simulations cover the years between 1968 - 2078 (5 year time step from 1968 - 2008; 10 year time step thereafter).

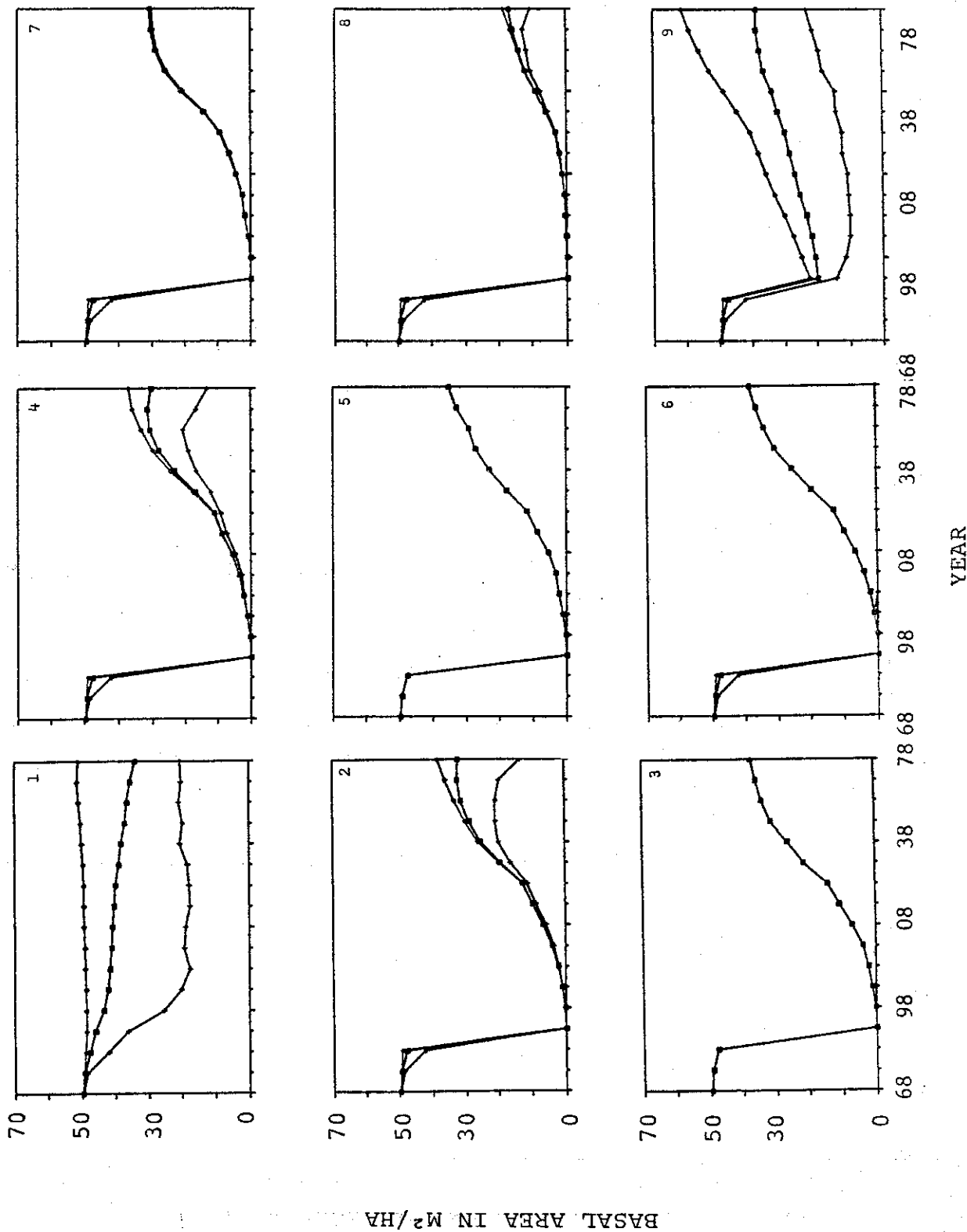


Figure B.2. Changes in basal area ($cu\ m/ha$) in the Beaverfoot stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. Symbols on each graph are: triangles (top line) - areas outside diseased patches only; squares (middle line) - stand average (both diseased and non-diseased areas); plus signs (bottom line) - area inside diseased patches only. The simulations cover the years between 1968 - 2078 (5 year time step from 1968 - 2008; 10 year time step thereafter).

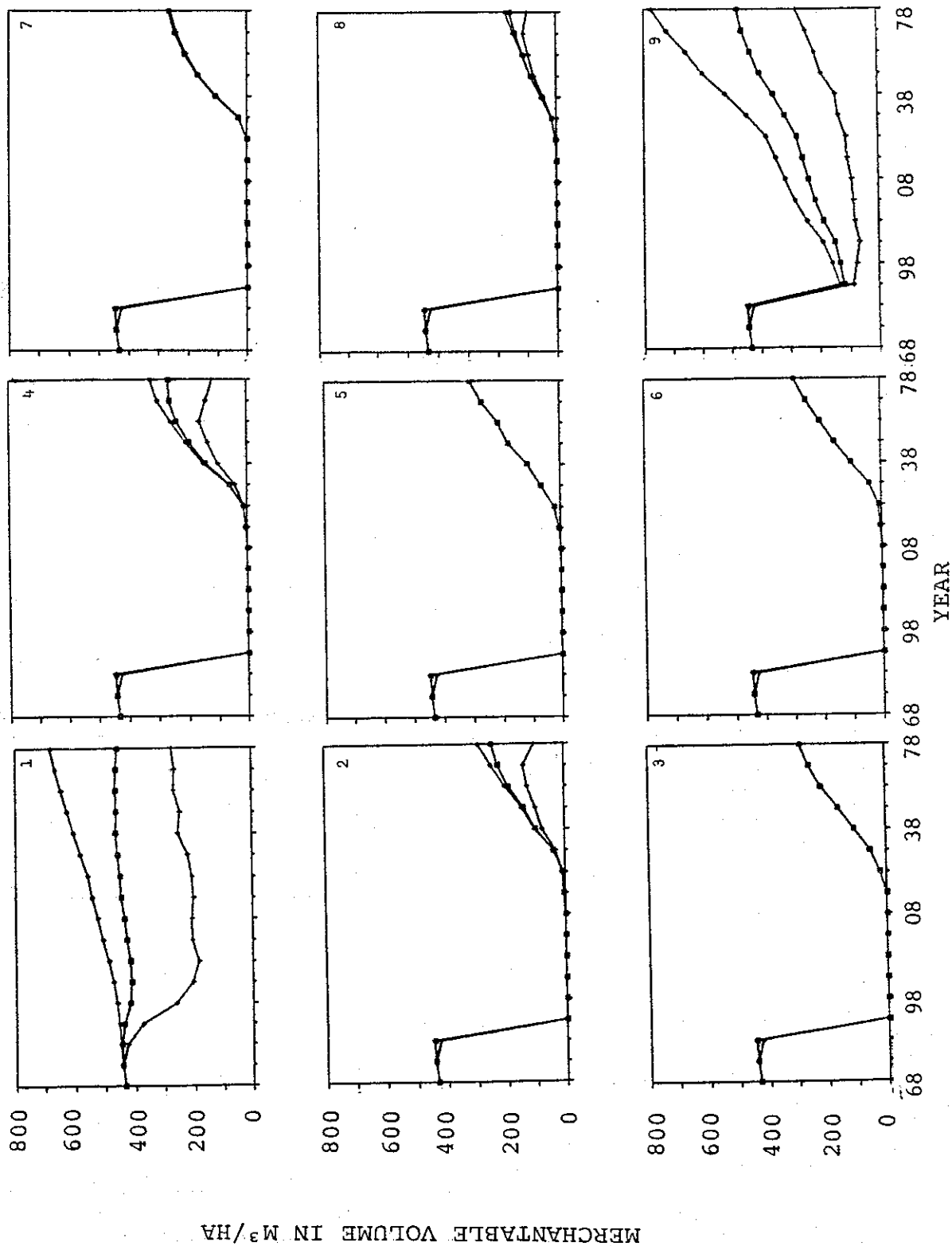
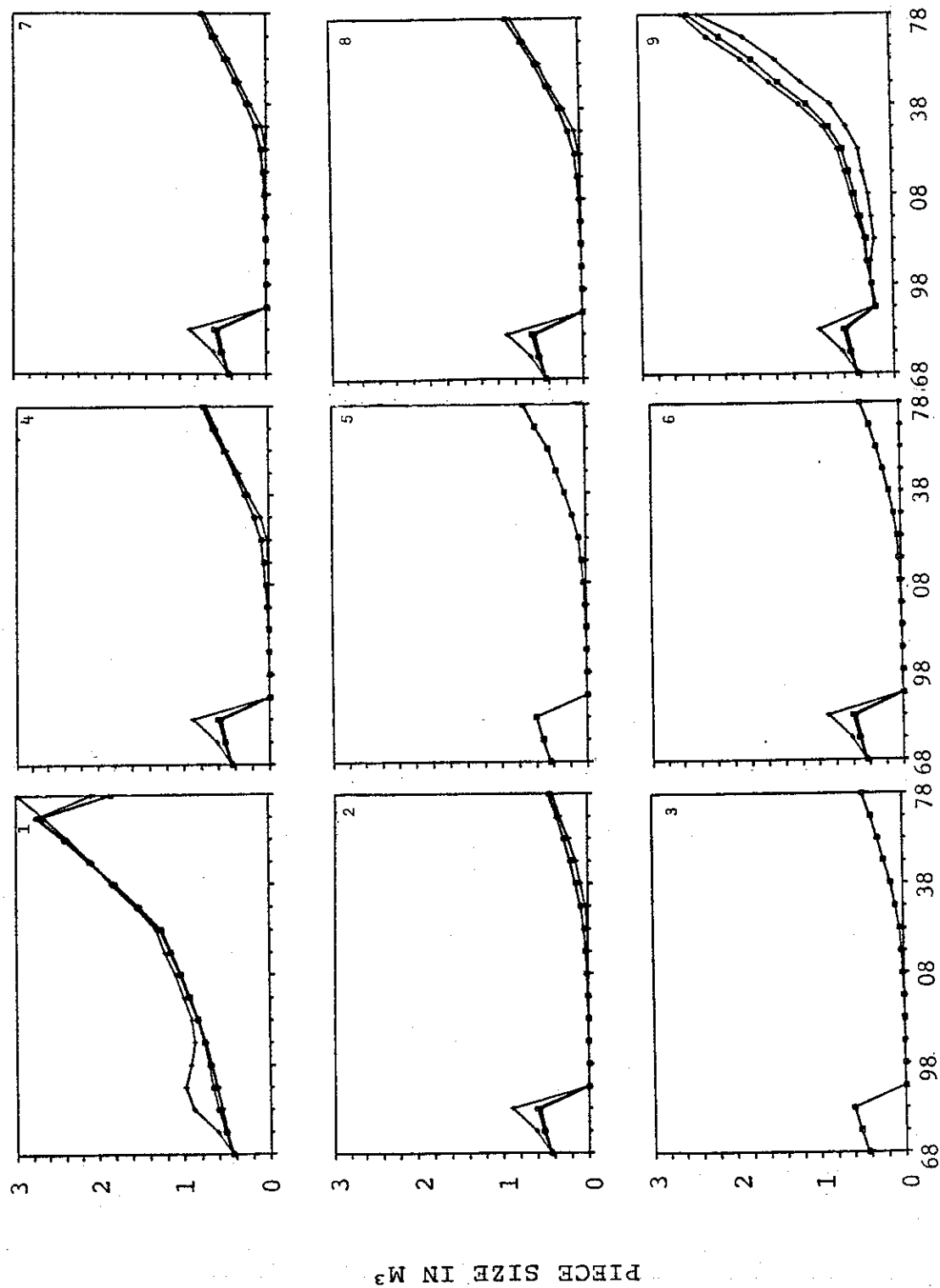


Figure B.3: Changes in merchantable volume (cu m/ha) in the Beaverfoot stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. Symbols on each graph are: triangles (top line) - areas outside diseased patches only; squares (middle line) - stand average (both diseased and non-diseased areas); plus signs (bottom line) - area inside diseased patches only. The simulations cover the years between 1968 - 2078 (5 year time step from 1968 - 2008; 10 year time step thereafter).



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Figure B.4. Changes in mean piece size (volume in cu m/tree) in the Beaverfoot stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. Symbols on each graph are: triangles (top line) - areas outside diseased patches only; squares (middle line) - stand average (both diseased and non-diseased areas); plus signs (bottom line) - area inside diseased patches only. The simulations cover the years between 1968 - 2078 (5 year time step from 1968 - 2008; 10 year time step thereafter).

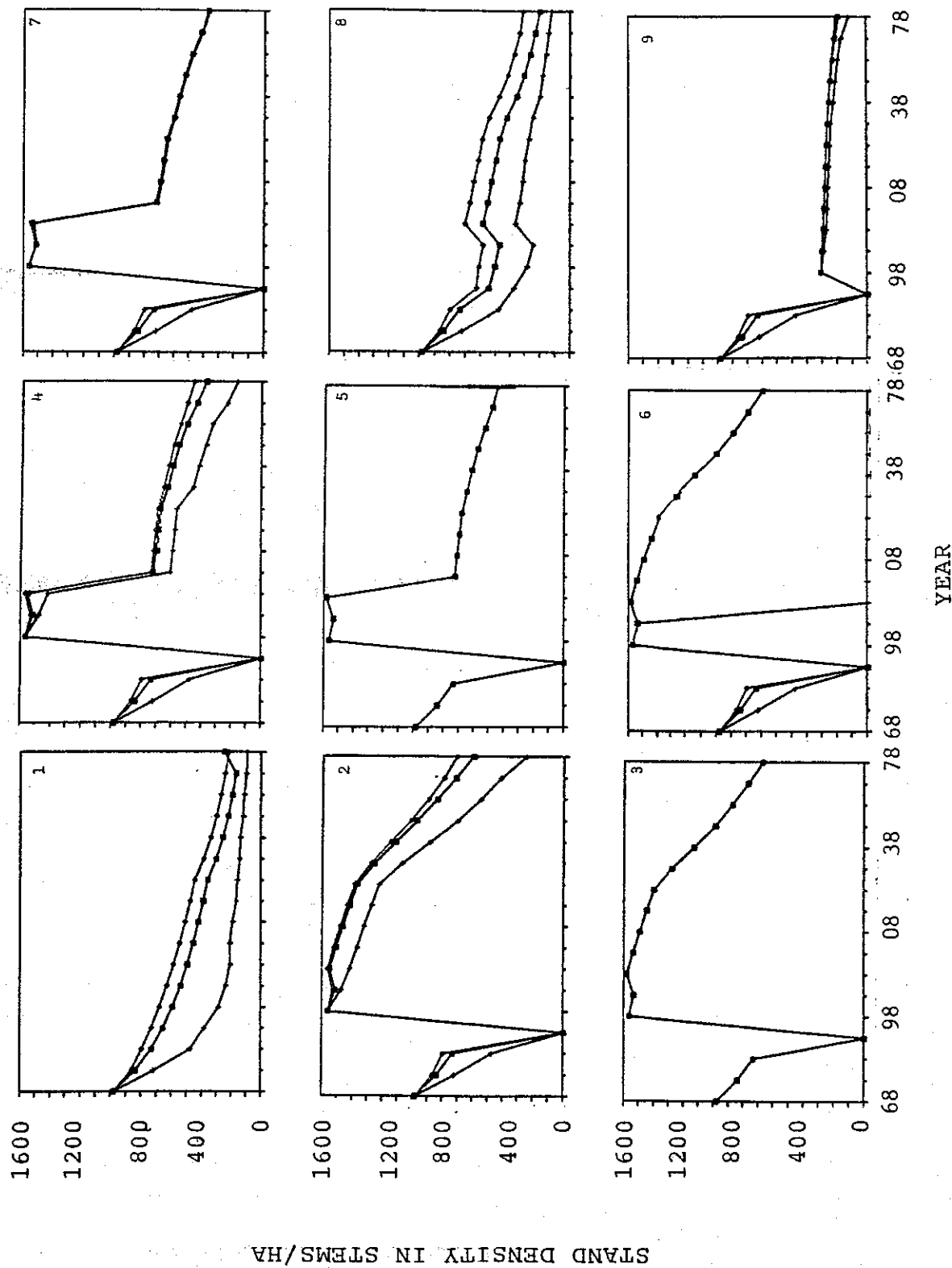


Figure B.5. Changes in stand density (stems/ha) in the Beaverfoot stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. Symbols on each graph are: triangles (top line) - areas outside diseased patches only; squares (middle line) - stand average (both diseased and non-diseased areas); plus signs (bottom line) - area inside diseased patches only. The simulations cover the years between 1968 - 2078 (5 year time step from 1968 - 2008; 10 year time step thereafter).

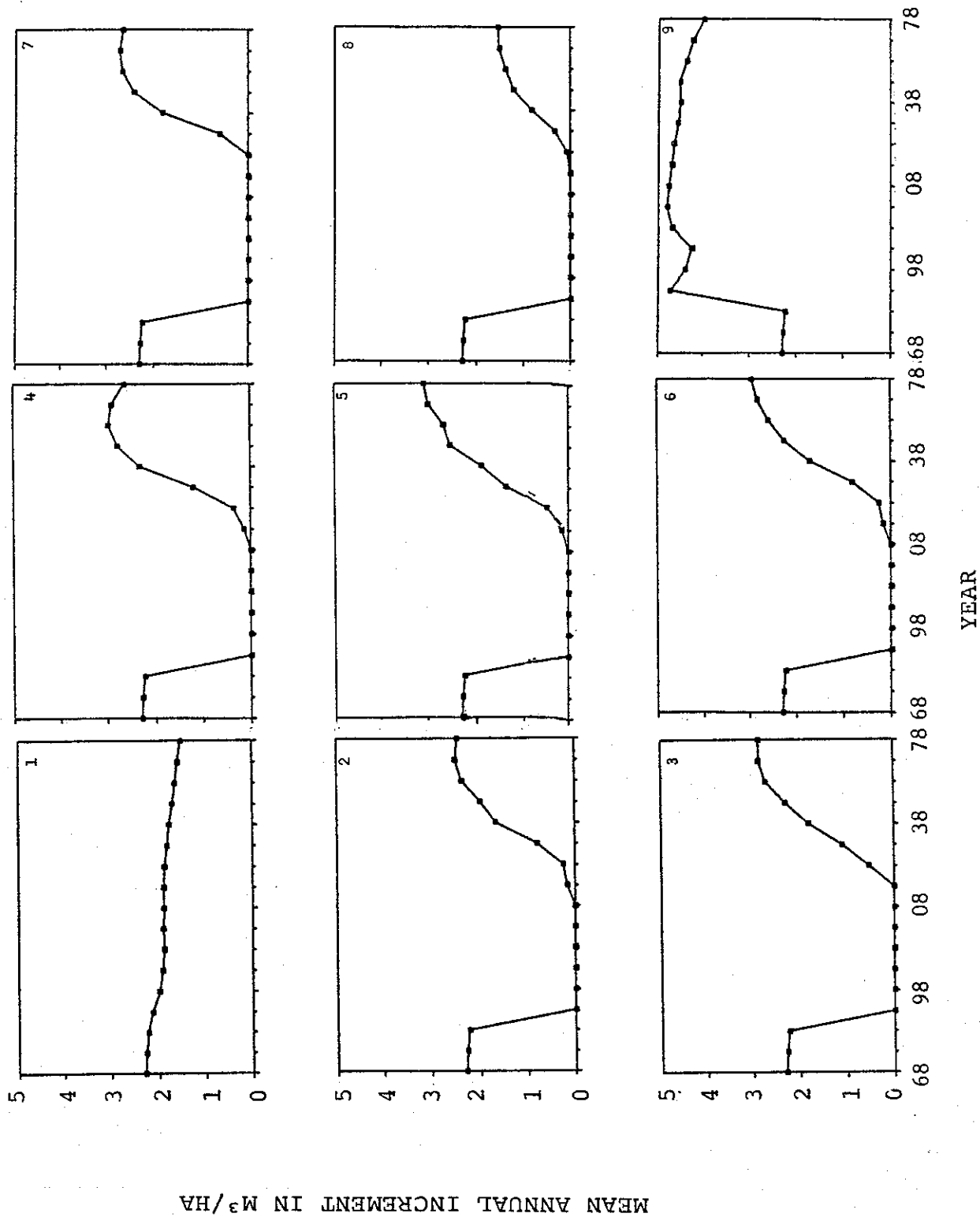


Figure B.6. Changes in mean annual increment (cu m/ha) in the Beaverfoot stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. The simulations cover the years between 1968 - 2078 (5 year time step from 1968 - 2008; 10 year time step thereafter).

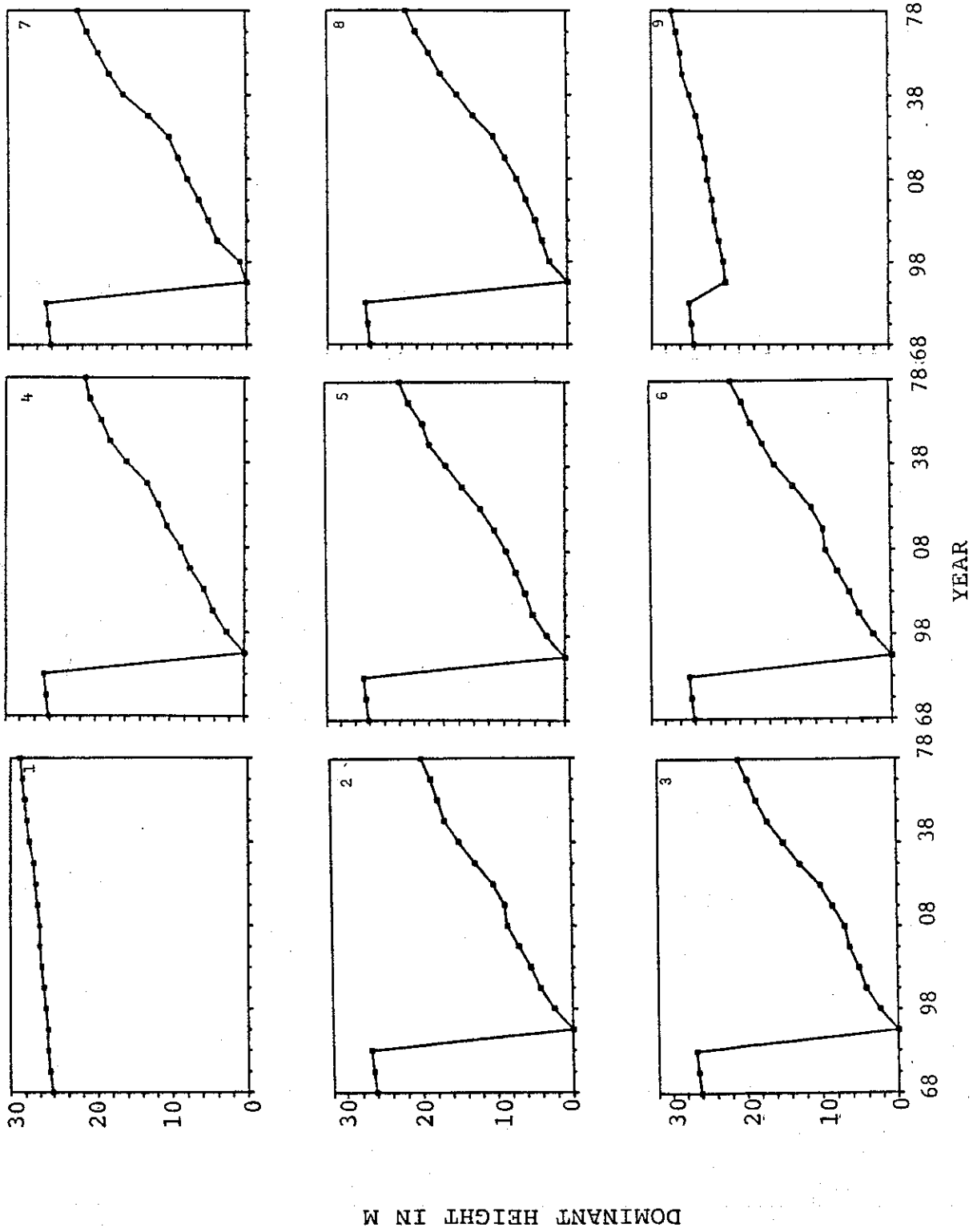


Figure B.7. Changes in average dominant height (m) in the Beaverfoot stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. The simulations cover the years between 1968 - 2078 (5 year time step from 1968 - 2008; 10 year time step thereafter).

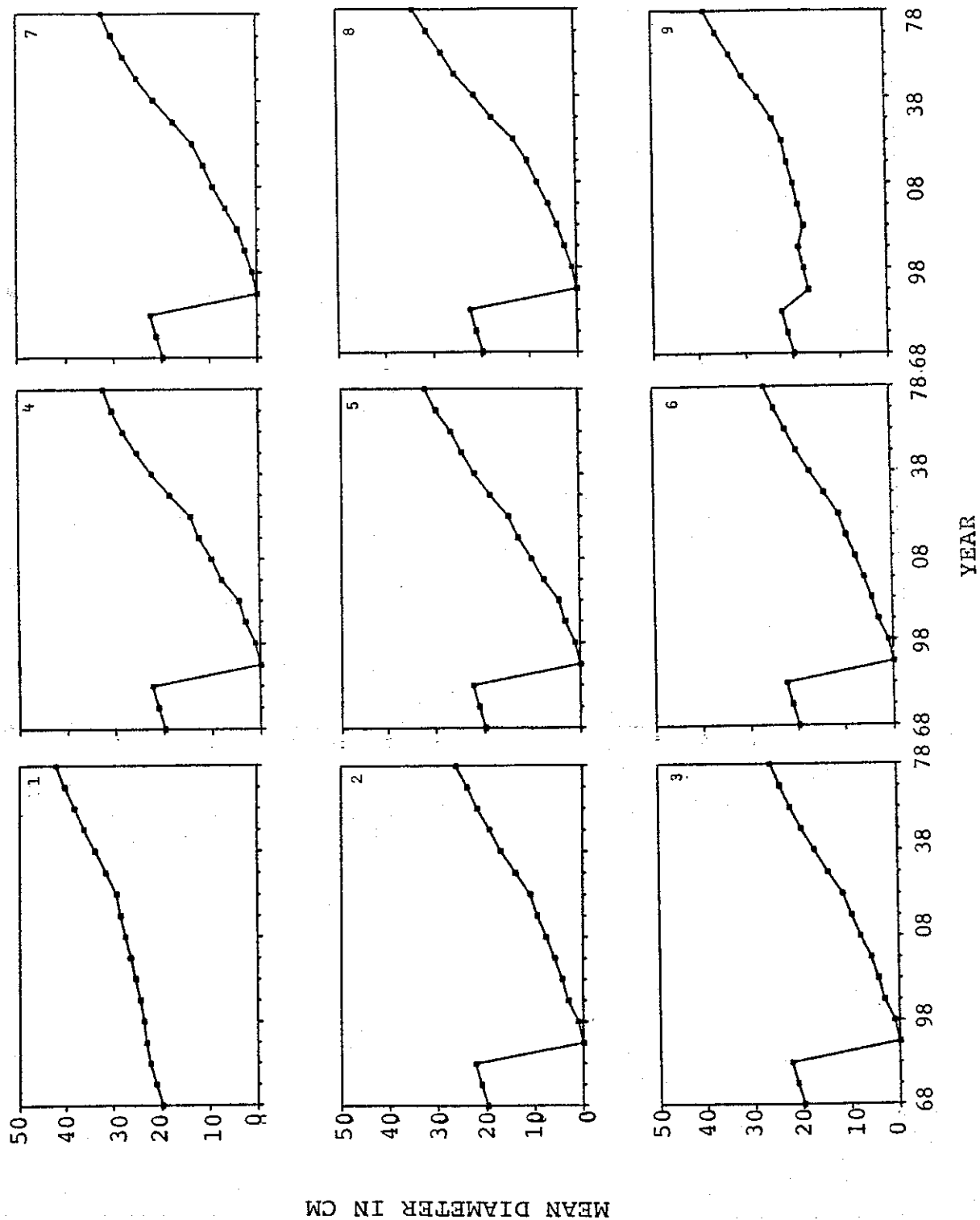


Figure B.8. Changes in mean tree diameter (cm) in the Beaverfoot stand over time for scenarios 1-9. Numbers in the upper right hand corner of each graph denote the scenario number. The simulations cover theyears between 1968 - 2078 (5 year time step from 1968 - 2008; 10 year time step thereafter).

