

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;

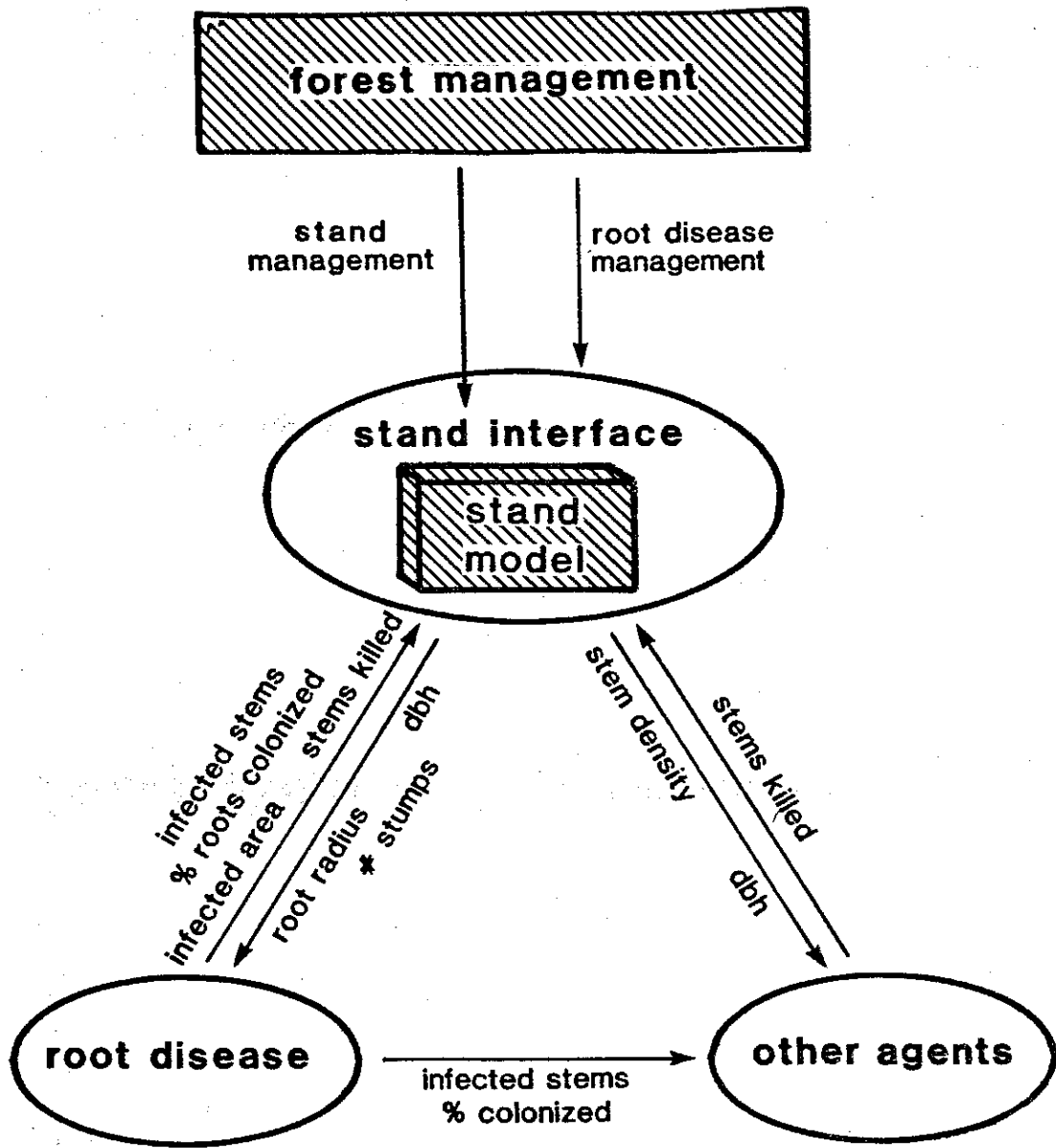


Figure 2.1. Primary components of the root disease model. The major root disease components are enclosed by ellipses; the major stand growth components are shaded. Also shown are the types of information that pass between model components.

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.

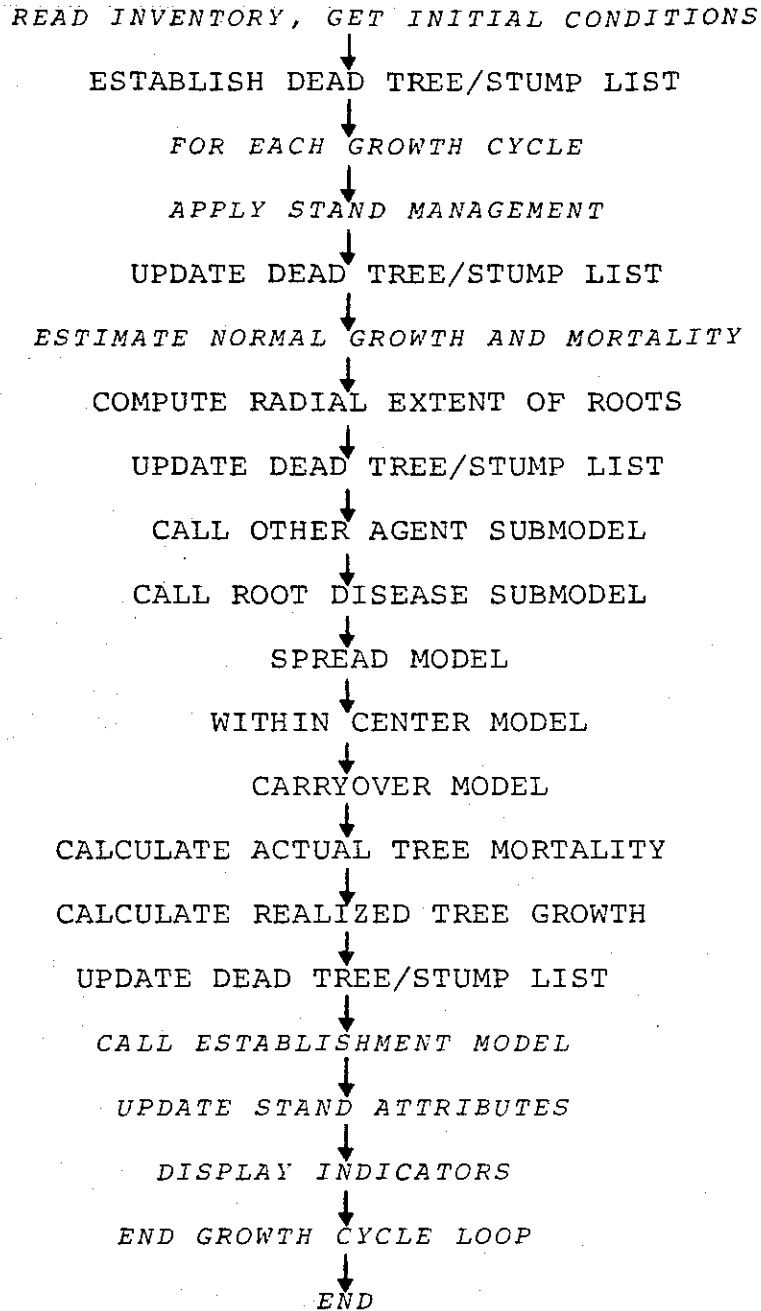


Figure 2.2. Order of calculations in the root disease/stand model. Italicized steps are contained in Prognosis.

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-

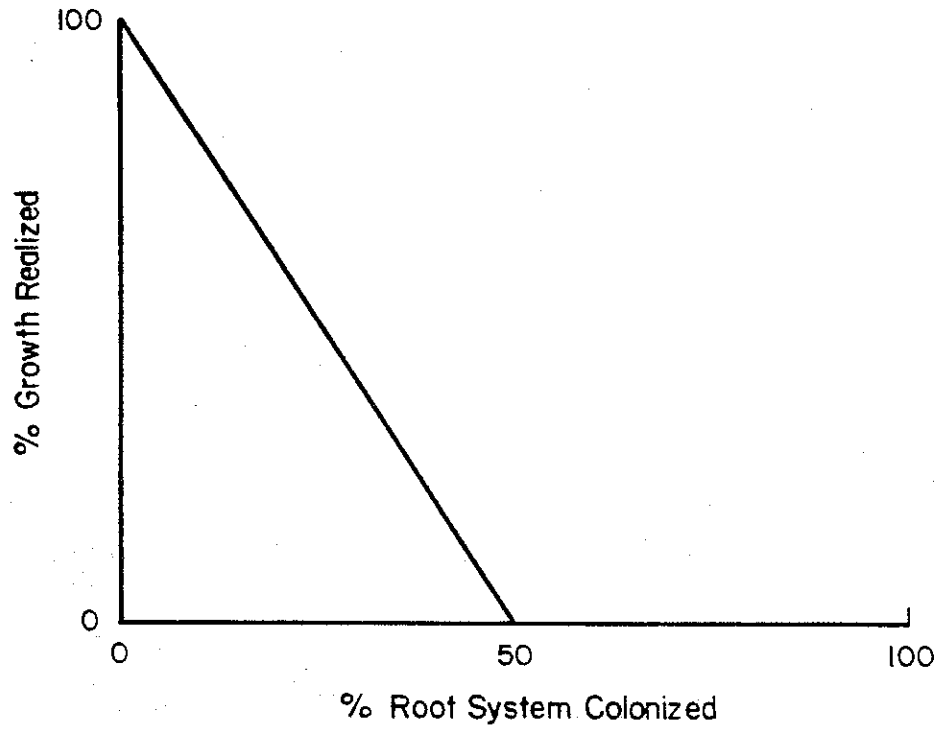


Figure 2.3. The relationship between root disease and tree growth. This relationship is applied to both diameter and height growth.

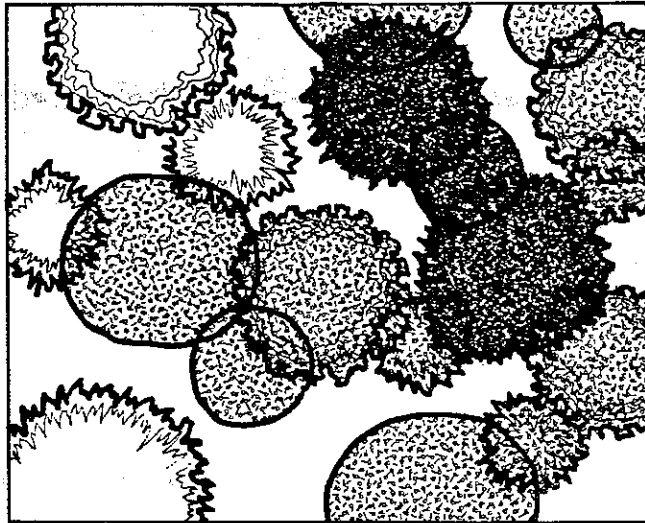
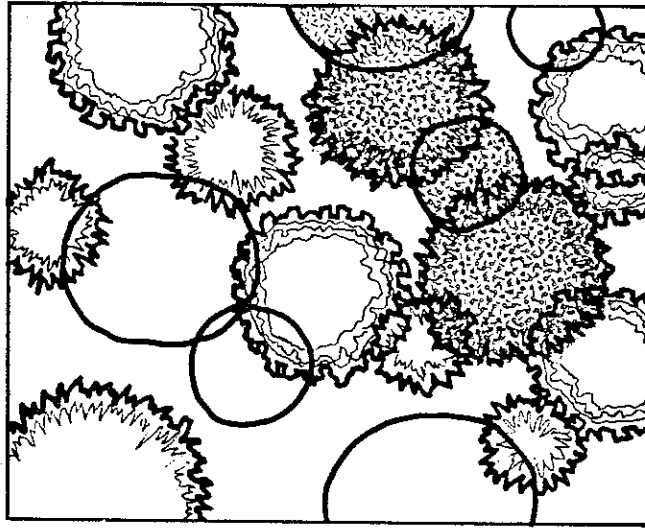


Figure 2.4. Diagrammatic representation of root disease infection and spread through trees in disease centers. Top panel shows 4 trees infected (light shading); bottom panel (several years later) shows 11 infected trees, and 3 trees killed (dark shading). Different tree species are shown with different 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.

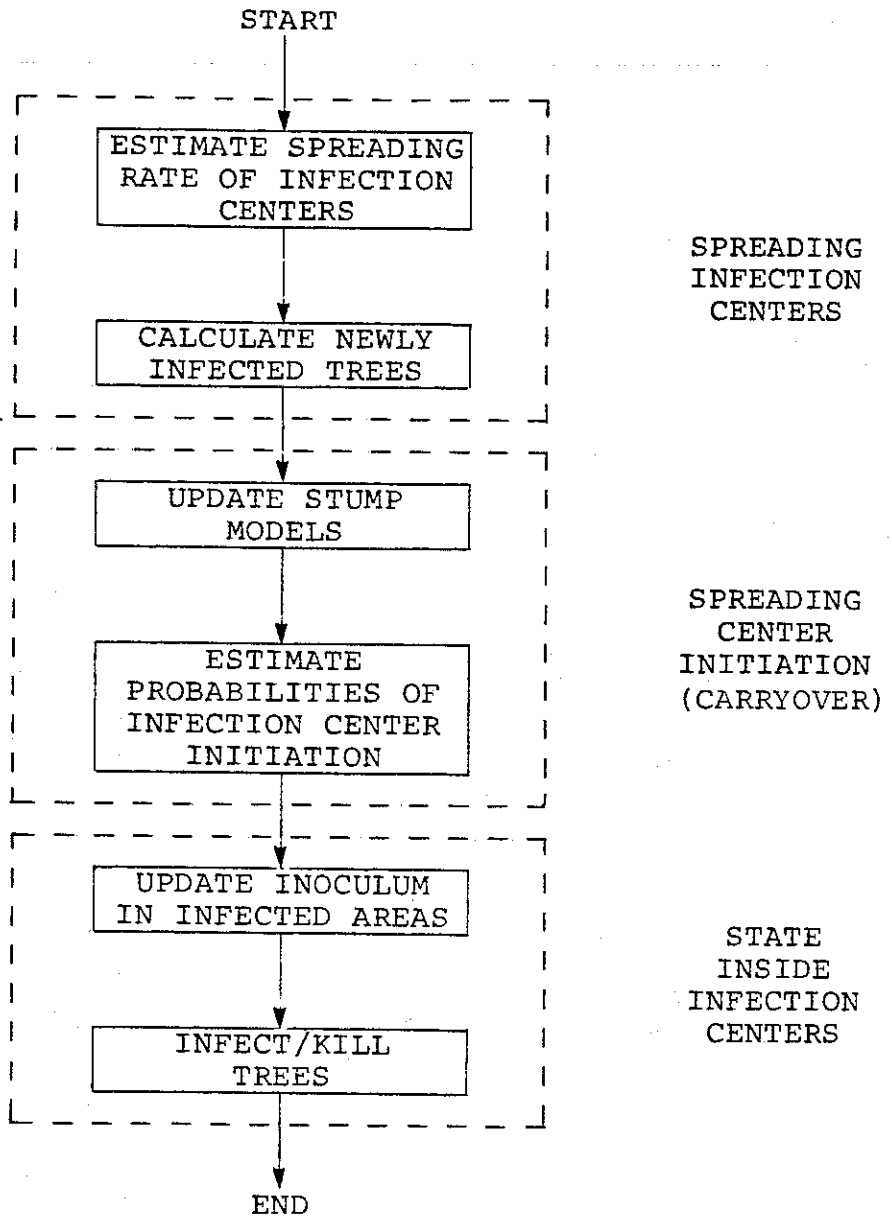


Figure 2.5. Order of calculations in the root disease submodel. These calculations take place once each growth cycle.

### 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,

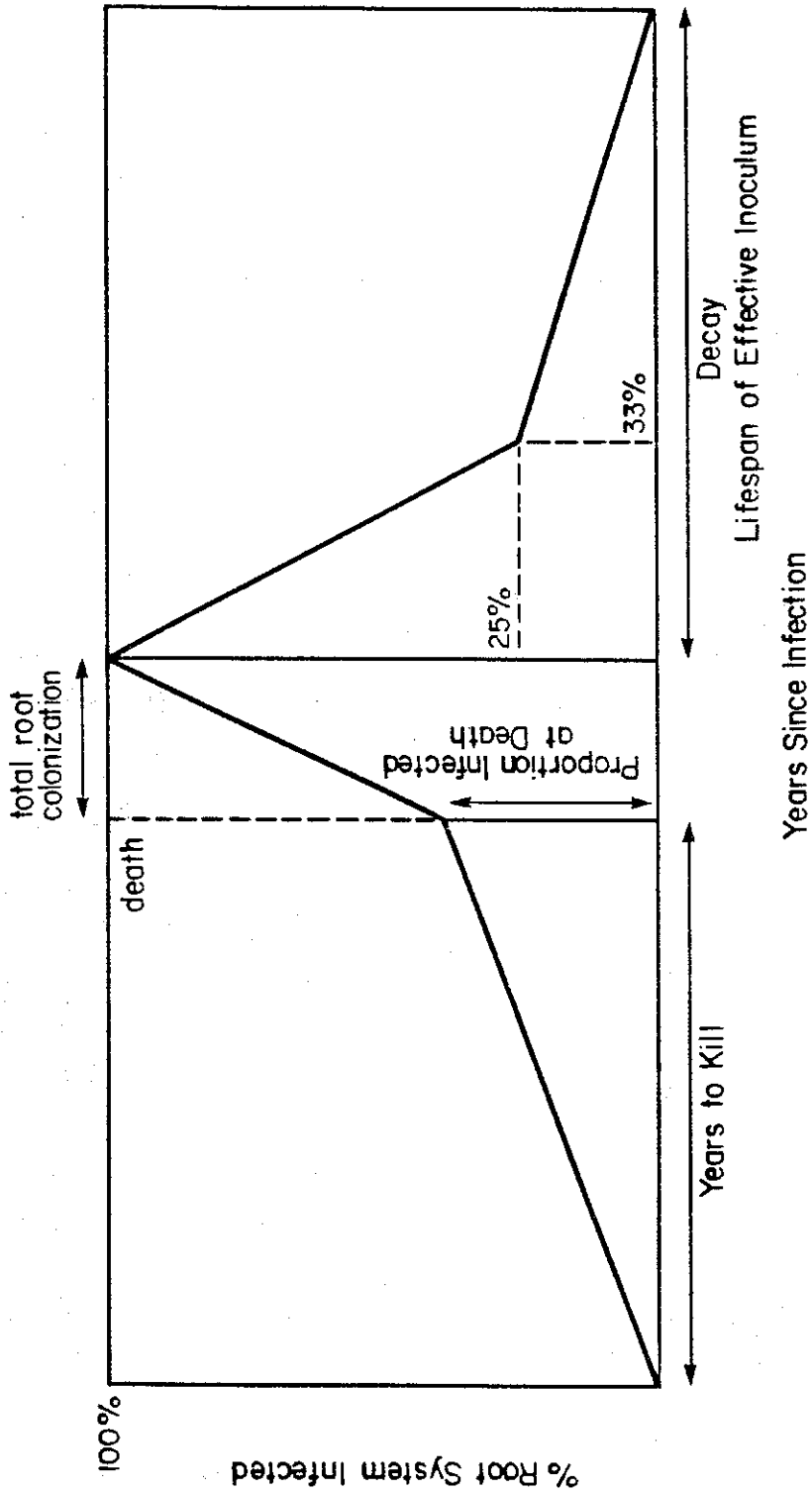


Figure 2.6: Pattern of pathogen spread and inoculum spread through a single root system. This figure is for Armillaria; see text for a description of differences in Phellinus behavior.

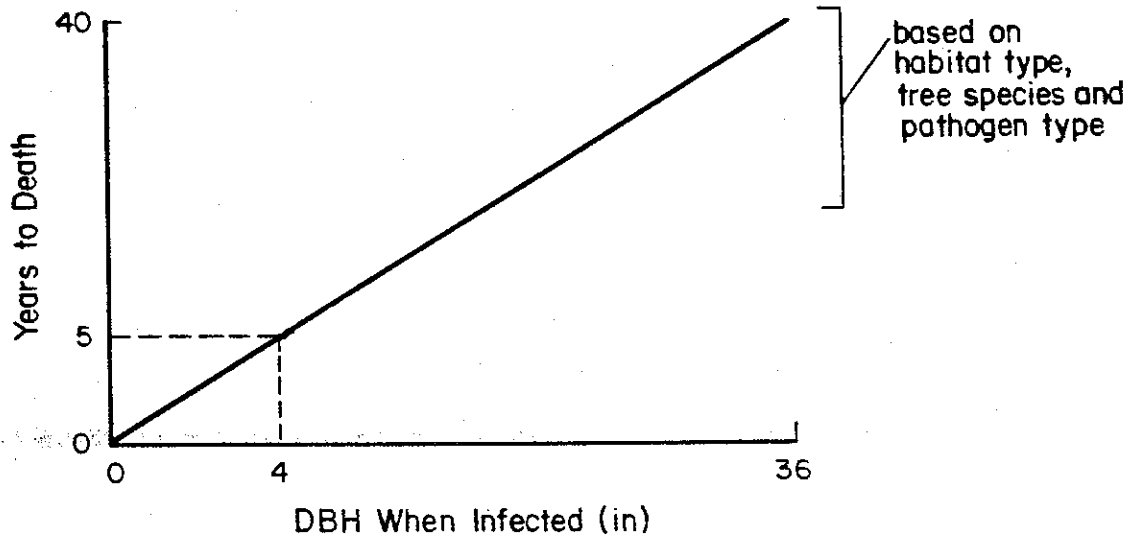


Figure 2.7: Time from infection to death for Douglas-fir on Douglas-fir habitat with Armillaria. This relationship is modified for different habitats, tree species, and root disease pathogen.

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

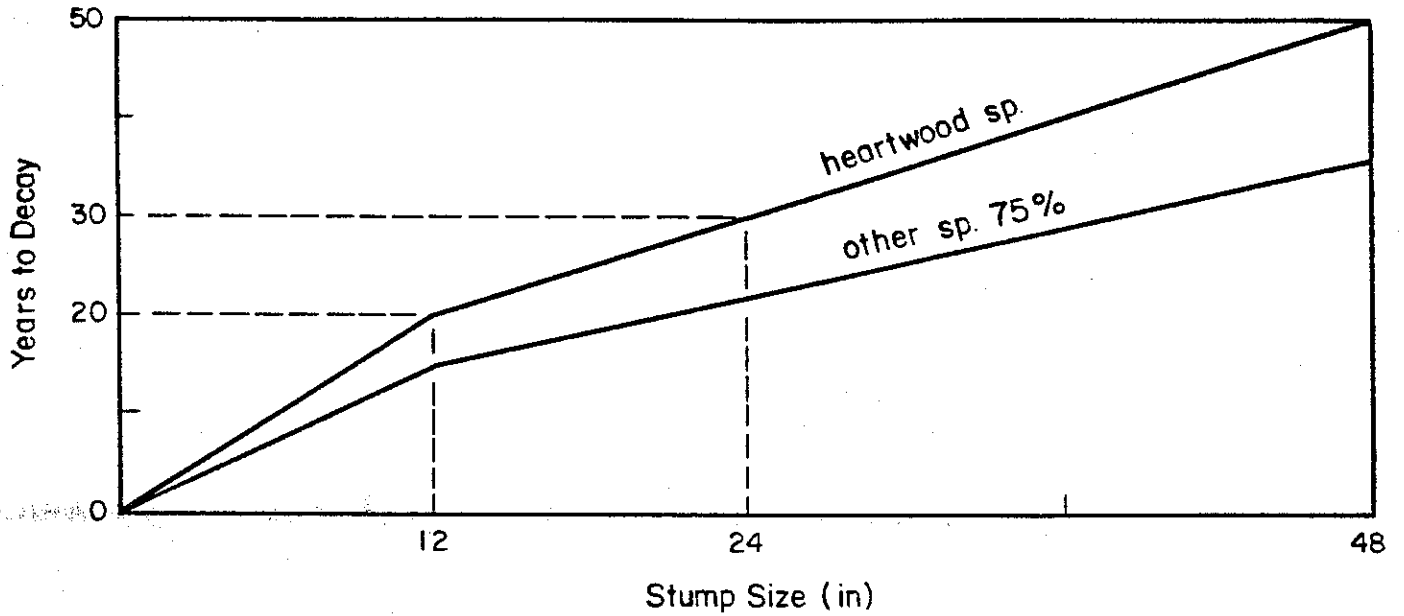


Figure 2.8. Lifespan of inoculum in dead trees and stumps. This relationship is for Armillaria; see text for a description of differences in Phellinus behavior.

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

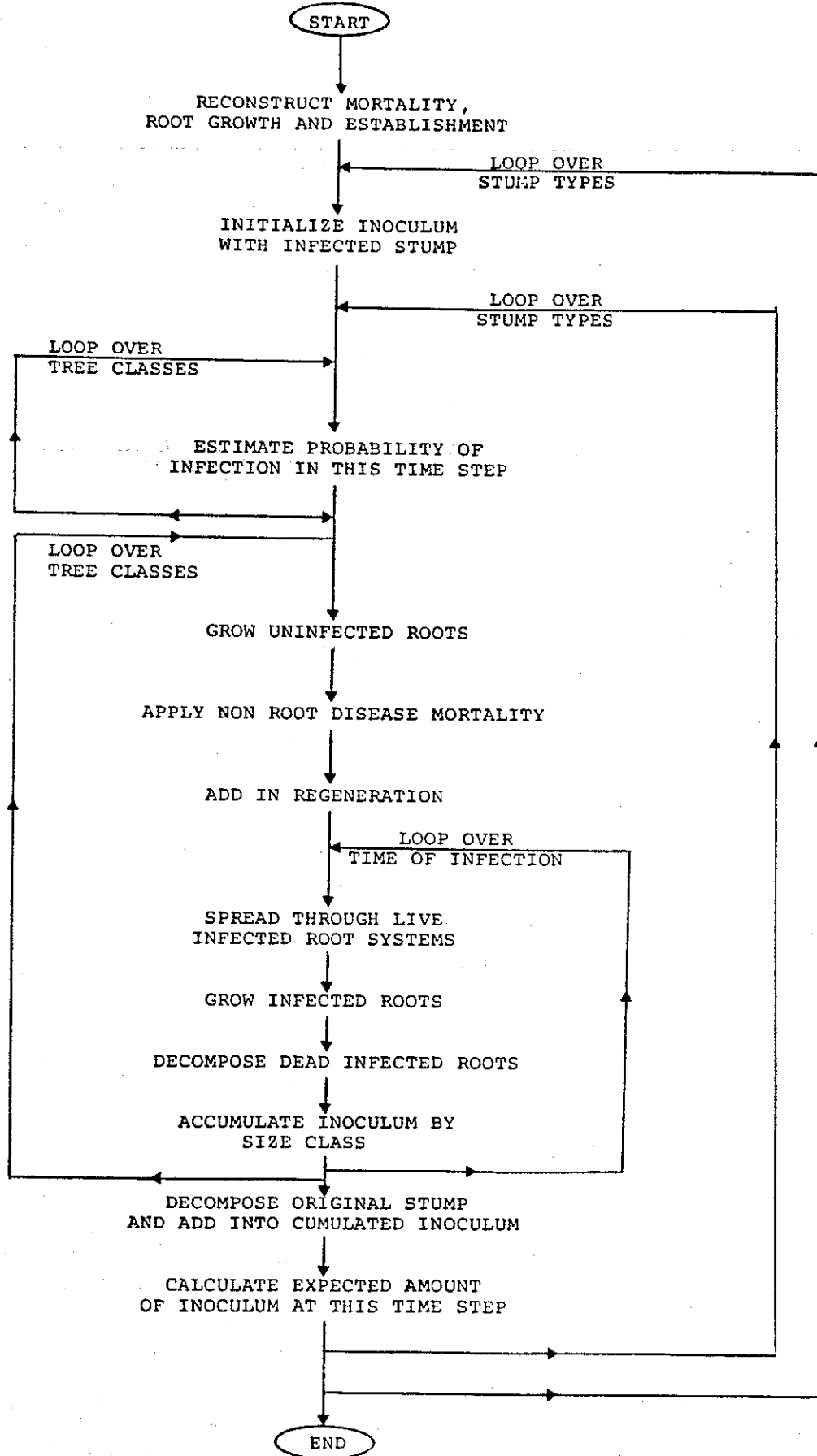


Figure 2.9. Flowchart of carrvoer model. This set of calculations occurs once (after a clearcut).

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 criteria 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.

BEEBLE 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 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														
DISEASE STATISTICS					LIVE TREE CHARACTERISTICS									
YEAR	AGE	NO OF CENTS	DISEASE AREA ACRES	SPREAD RATE FI/YR	TOTAL ACRES	BA/ACRE	NO OF TREES KILLED	VOLUME LOSSES CU FT /ACRE	UNINF TREES /ACRE	INFECTED TREES /ACRE	AVERAGE % OF TREES INFECTED	MERCHANT CU FT /ACRE	BA/ACRE	IDENTIFIERS
1968	50	100	40.49	.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	73.36	.02	27.	48.	13.	4.	640.	0.	0.	0.	0.	SQTZSC04 SC04
1994	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.	44.	SQTZSC04 SC04
2008	30	90	11.47	.23	31.	6.	31.	124.	184.	27.	57.0	255.	46.	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	748.	51.	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.	22.	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
2076	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.