Chapter 1

Characteristics and Consequences of Root Diseases in Forests of Western North America

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Root diseases are somewhat mysterious. Operating as they do within the soil, it is difficult to actually view root pathogens or follow their progress in causing disease. The signs and symptoms that they produce can be quite subtle and variable. Just identifying which pathogen occurs in a specific situation is often challenging. Nevertheless, in the past two decades, forest managers have become increasingly aware of the important roles that root disease organisms play in forests and the significant influences that they exert on our ability to attain desired management objectives.

Root pathogens usually affect groups of neighboring trees in progressively expanding disease pockets or centers. These centers generally contain dead trees that have died at different times over several years and living but infected trees in various stages of decline. They are commonly characterized by much lower stocking levels than surrounding healthy portions of stands, and they also may contain numerous windthrown or broken trees on the ground. Root disease centers vary in size from those involving only a few trees to those covering hundreds of acres. They may be very discrete or they may involve a scattering of affected trees dispersed over a larger area.

On individual trees, crown symptoms associated with most root diseases are similar and include reduced height growth, loss of needles, chlorotic foliage, death of branches, production of distressed cone crops, and, ultimately, host mortality. Accurate identification of which root pathogen or pathogens occur in an area usually requires digging to expose roots, and removing bark from roots and root collars to reveal the inner wood. Often laboratory culturing or more sophisticated techniques such as isozyme and DNA analyses are necessary to identify the biological species or strain of the causal fungi. Although a number of root diseases are found in the West, three are considered to be the most significant. These are laminated root rot, caused by the fungus *Phellinus weirii*; Armillaria root disease, caused by *Armillaria ostoyae*; and Annosus root disease, caused by *Heterobasidion annosum*. The impacts of these fungi on forest stands are modelled in the Western Root Disease Model, Version 3.0. A general understanding of their biology is presented in the next few pages to enhance the reader's ability to input data and interpret outputs.

Laminated Root Rot

Laminated root rot caused by the fungus *Phellinus weirii* (Murrill) R.L. Gilbertson is distributed from the Six Rivers National Forest in California north to northern Vancouver Island, British Columbia and east to western Montana. It is probably the most important tree disease of coastal forests in the Pacific Northwest and also has significant impacts in interior forests (Hadfield 1985, Hadfield and others 1986, Hagle and others 1987, Nelson and others 1981, Scharpf 1993, Thies 1984, Thies and Sturrock 1995, Wallis 1976).

Laminated root rot is distinguished by the characteristic decay that it produces in roots and butts of

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infected hosts. The decayed wood separates easily at the annual rings, is often heavily pitted on both sides of each layer, and has diagnostic reddish-brown to pinkish setal hyphae between the layers. *P. weirii* also forms a grayish-white to buff-colored mycelial sheath, referred to as ectotrophic mycelia, on root surfaces of young trees and within bark crevices on older trees. Fruiting bodies of *P. weirii* are appressed brown, crusty structures with numerous pores that occasionally form on the undersides of downed trees or on exposed roots close to the ground. They are of little diagnostic value because of their rarity and cryptic nature.

On highly susceptible hosts, *Phellinus weirii* causes extensive decay of roots and death of the tree by destroying the roots' ability to take up water and nutrients or predisposing them to windthrow or bark beetle infestation. Less susceptible hosts develop butt rot. All western conifers can be infected by *P. weirii*, but some tolerate the pathogen better than others. Douglas-fir, [*Pseudotsuga menziesii* (Mirb.) Franco], white fir [*Abies concolor* (Gord. & Glend.) Lidl. ex Hildebr.], grand fir [*Abies grandis* (Dougl. ex D. Don) Lindl.], Pacific silver fir [*Abies amabilis* Dougl. ex Forbes], and mountain hemlock [*Tsuga mertensiana* (Bong.) Carr.] are highly susceptible and are readily infected and killed by the fungus. Other true firs, spruces (*Picea* spp.), western hemlock [*Tsuga heterophylla* (Raf.) Sarg.], and western larch [*Larix occidentalis* Nutt.] are considered to be intermediately susceptible; they are often infected but rarely killed by *P. weirii*. Pines and cedars are tolerant or resistant; they are rarely infected and almost never killed by the fungus. All hardwoods are immune to *P. weirii*.

Laminated root rot is a disease of the site. *Phellinus weirii* spreads very little if at all by windborne spores. Virtually all spread involves mycelial growth on or in host roots. The fungus survives a long time (as much as 50 years) in roots and stumps of dead or cut trees that were infected prior to death. The fungus does not colonize dead wood, in part because it is not a good competitor with other fungi. In infected trees that die or are cut, disease-induced resin impregnation of wood surrounding infections and the ability of *P. weirii* to form a protective sheath around itself are responsible for the pathogen's long-term survival. The fungus survives only in the portion of the host's root system that it occupied at the time of host death. The fungus spreads to new hosts when their roots contact colonized roots of infected stumps or snags and the fungus grows onto and colonizes them in turn. Formation of disease centers involves subsequent tree-to-tree spread via root contacts. *P. weirii* does not grow through soil but grows on root surfaces at a rate of about 0.33 to 0.67 meter per year. Detailed information on this disease and its biology, control, and management implications are given by Thies and Sturrock (1995).

Armillaria Root Disease

Armillaria root disease is widely distributed throughout the West and is common in many forest stands (Hadfield and others 1986, Hagle and others 1987, Morrison 1981, Scharpf 1993, Shaw and Kile 1991, Williams and others 1986). However, it acts differently in different areas and on different sites, even some that are quite close to each other. In general, Armillaria root disease is more severe in interior than in coastal forests.

Armillaria root disease is identified on the basis of the occurrence of thick, white mycelial fans under the bark of roots and lower stems of affected trees. On trees that have been dead for some time, mycelial fans fade in color to yellow and eventually disintegrate. However, they leave a fan-shaped impression on the inner bark that can usually be seen for some time after the mycelium itself is gone. Trees infected by *A. ostoyae* almost always exhibit various amounts of basal resin flow or brownish leachate, often in very substantial amounts. Other species of *Armillaria* occur in forests primarily as saprophytes. These *Armillaria* species also may produce mycelial fans under the bark of dying or dead trees, but they are thinner and are not associated with resin flow. The combination of thick mycelial fans and resinosis characterizes infection by *A. ostoyae*. Trees infected by *A. ostoyae* also frequently have black string-like fungal structures called rhizomorphs on their roots or under their bark and exhibit a decay that is yellow, stringy, moist, and malodorous. *A. ostoyae* produces honey-colored mushrooms in autumn on or near dead trees and stumps.

Armillaria ostoyae kills the cambium of susceptible host roots and root collars, girdling the tree. Infected trees are often predisposed to bark beetle attack and usually die standing. Windthrow is rare. All

western conifers and some hardwood trees and shrubs can be infected by *A. ostoyae*. Off-site plantings, wounded trees, and trees growing on compacted soils or in areas with drainage problems are particularly likely to be affected. Tree susceptibility may differ with locale. In coastal forests, *A. ostoyae* is most commonly observed killing Douglas-firs and true firs in plantations under 30 years old. After age 30, trees become increasingly tolerant of the pathogen and are much less frequently killed. In interior forests, *A. ostoyae* commonly causes more mortality than in coastal situations, and host susceptibility may differ from site to site. True firs are usually the most susceptible hosts, Douglas-fir the second, and other species tend to be tolerant or resistant. However, there are areas where pines are very susceptible and some sites where almost all tree species are killed. Because of these differences, it is necessary to analyze host susceptibility on a site-by-site basis. In interior forests, Armillaria root disease often is most evident in partially cut stands where there are numerous wounded residual trees and compacted soils. It is often clearly associated with the occurrence of large conifer stumps and, in some areas, with hardwood shrubs or hardwood tree stumps.

Armillaria ostoyae may be spread on rare occasions by windborne spores that probably infect through wounds or stump surfaces. However, in most cases, Armillaria root disease, like laminated root rot, is a disease of the site. *A. ostoyae* survives for up to 35 years in previously infected stumps and snags. It spreads to nearby susceptible regeneration by growth across root contacts or, less commonly, via rhizomorphs that grow for short distances (about one meter) through soil. Tree-to-tree spread continues by these same avenues at a rate of about 0.33 to 0.67 meter per year. Further details on the biology and management of Armillaria root disease are presented by Shaw and Kile (1991).

Annosus Root Disease

Annosus root disease, caused by *Heterobasidion annosum*, occurs in conifer forests throughout the Northern Hemisphere. It is common and widely distributed in western North America (Hadfield and others 1986, Hagle and others 1987, Morrison and others 1986, Otrosina and Scharpf 1989, Scharpf 1993). However, like Armillaria root disease, it acts differently in different areas.

Annosus root disease can be somewhat difficult to diagnose. The most reliable way to identify the disease in the forest involves finding its fruiting bodies, called "conks." Conks of *Heterobasidion annosum* are formed in or on stumps, on the roots of windthrown trees, and sometimes in or just under the duff layer on roots and root collars of standing hosts. Conks are shelf-shaped with dark concentrically furrowed upper surfaces, creamy white sterile margins, and white lower surfaces with numerous tiny pores. They are perennial and thus may have more than one pore layer. Dead and symptomatic hosts as well as still healthy-appearing individuals associated with stumps, snags, or trees exhibiting *H. annosum* conks will be infected in most cases.

Infection by *Heterobasidion annosum* is often characterized by reddish-brown staining in the roots and lower stems of trees. Resinosis is often associated with infected tissues. Some hosts also exhibit white or buff-colored fungal pustules on their roots. Advanced decay caused by the fungus is variable. It is often laminated with pitting only on one side of the layers and no evidence of setal hyphae. It can also be stringy and moist with white streaks and scattered black flecks. This latter appearance is most common on hosts that develop butt rot. Where necessary, presence of *H. annosum* can be confirmed by culturing wood chips on media and identifying the microscopic fruiting bodies of the asexual state of the fungus, *Spiniger meineckellus* (Olsen) Stalpers.

The fungus is genetically complex. There are several biological species that are not morphologically distinct but are genetically diverse (Otrosina and others 1992). These strains cannot be distinguished on the basis of appearance, but they are intersterile and differ markedly in pathogenicity and host range. In western North America, a "P-strain" that affects mainly pines and an "S-strain" that affects mainly true firs, hemlocks, and Douglas-fir have been identified. On living trees, there is little or no host crossover between the two strains. Unlike living trees, stumps offer no host specificity with respect to biological species and may become infected by either the S or P strains.

These two strains, or biological species, and the variation between tree species and site factors interact to make the host response to Annosus root disease infection highly variable. *Heterobasidion*

annosum kills resinous hosts directly by decaying roots and killing the cambium around the root collar. Trees are often predisposed to bark beetle infestation and usually die standing. Some non-resinous hosts are affected in the same way, but others develop extensive butt decay rather than being killed outright. Older butt-rotted trees (150 years old or greater) often break and fall. White fir, grand fir, and Pacific silver fir are often killed by the pathogen; other true firs and hemlocks usually suffer butt rot. Pines, especially ponderosa pines, are widely infected; however, substantial mortality in these hosts is usually limited to very dry sites. Douglas-fir is severely affected in portions of the Rocky Mountains, but is rarely affected further west.

Heterobasidion annosum is capable of spreading over long distances. Conks release basidiospores that are windborne and can be dispersed over distances of up to 100 miles. Spores that land on freshly cut stump surfaces or fresh wounds germinate, and the fungus colonizes the tree or stump. Subsequently, the pathogen can grow via root contacts into surrounding hosts, creating disease pockets. Rate of radial spread across roots is about 0.5 meter per year, but the fungus does not grow through soil. New disease foci are usually associated with large host stumps (0.5 meter or greater in diameter), and *H. annosum* can survive in large stumps for considerable time periods (up to 60 years). Annosus root disease is especially common in stands that have had partial-cut harvests. It is most severe in stands that have experienced several entries. More detailed information on Annosus root disease may be found in Otrosina and Scharpf (1989).

Root Disease Impacts

It is difficult to find any forested area in the Western United States that has no root diseases. Though West-wide surveys are lacking, numerous smaller surveys done at the stand, watershed, Ranger District, or National Forest level suggest that laminated root rot, Armillaria root disease, and Annosus root disease can be found singly or together over significant proportions of the areas occupied by their hosts. It is estimated that the three major root diseases occur on 7 to 10 percent of the area occupied by coastal forests and 10 to 25 percent of the area occupied by interior forests (Gedney 1981, Goheen and Hansen 1993, Smith 1984). These fungi have co-evolved with their hosts for eons and until a few decades ago were in an equilibrium in forest ecosystems. However, it is apparent that root disease incidence is on the increase. Fire exclusion and management activities such as partial-cut logging and planting of diseased sites with susceptible hosts have favored their spread and intensification. In some areas, stand manipulations have altered ecosystems, and the forest conditions where the trees and root disease fungi were co-existing have been disrupted so they now favor the fungi. The result is similar to the introduction of exotic pests—a rapid increase in pathogen populations and catastrophic effects on host mortality.

Root diseases influence species composition, stand structure, stand density, and direction and rate of forest succession wherever they occur. They are agents of diversity, winnowers of weakened trees, natural thinning agents, and, in some cases, arbitrators of age structures. Basically, root pathogens operate by preferentially killing susceptible hosts. In affected areas, tree species and/or other plants that are tolerant, resistant, or immune to the particular fungi are favored.

From the perspective of a forest manager, the significance of root diseases will differ with management objective. Where timber production is a major concern, root diseases are viewed as being very destructive. Surveys done in rotation age stands show that basal area of live trees in portions of stands where root diseases are present is 10 to 55 percent less than that of adjacent healthy stands, translating into significant volume losses (Bloomberg and Reynolds 1985, Filip and Goheen 1984, Goheen and Hansen 1993, Lawson and others 1983). Root diseases also cause chronic, sub-lethal infections that do not result in dramatic symptom expression but reduce tree growth and vigor. Furthermore, because there are relatively small numbers of trees dying in any one year, salvage opportunities are not as great with root diseases as they may be with other disturbance agents, such as insects or fires, that kill large numbers of trees all at the same time.

Root diseases are also considered very damaging in developed recreation sites because of the high degree of hazard represented by infected trees. Root-diseased trees pose considerable threats to facilities and recreationists because of their increased windthrow potential.

Where wildlife habitat, visual quality, or watershed protection are major management objectives,

root diseases may be viewed as damaging, innocuous, or even beneficial. Effects of the diseases such as small openings in otherwise close-canopied stands, areas of plant species diversity, and groups of dead and down trees can be quite desirable because of associated increases in browse, low cover, small animal prey populations, cavity nesting sites, stand textural differences, and fall colors. However, root diseases can also reduce canopy cover to below desired levels, cause loss of preferred large tree character, and contribute to unacceptable fuel loads. Generally, root diseases are most likely to be considered management concerns when infection centers are large and many trees are being killed over substantial portions of a landscape.

Root Disease Management

There are silvicultural options for managing root diseases. The most common form of management prescription involves species manipulation. In infected areas, tree species that are highly susceptible to the particular root pathogen or pathogens present are discriminated against, and more resistant species that are adapted to the site are favored. Species can be manipulated at the time of final harvest or during intermediate stand entries. An alternative approach involves inoculum reduction. Infected stumps are physically removed from the soil in infection centers, eliminating as much of their colonized root systems as possible. This kind of treatment minimizes likelihood of new regeneration contacting infected material, and, if conscientiously done, may allow sites to be regenerated with susceptible tree species. Some special treatments aimed at certain root disease pathogens are also available. For example, infection of newly created stumps by *H. annosum* can be prevented by treatment with borate compounds.

In making decisions about how to deal with root diseases in their prescriptions, planners need to clearly define their management objectives and carefully consider the likely long-term effects of the diseases in light of the desired future condition for the area under consideration. Clearly, planners will benefit greatly from a predictive tool that enables them to compare future conditions in healthy stands with those infected by root disease, the impacts of various levels of root disease, and the relative effects of different management prescriptions on root diseases. The Western Root Disease Model is such a tool.

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Chapter 2

How to Use the Western Root Disease Model, Version 3.0

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1.0 Model Overview

1.1 Model Background

The Western Root Disease Model, Version 3.0 (WRDM3), provides a dynamic representation of the spatial epidemiology of Armillaria root disease, laminated root rot (caused by *Phellinus weirii)*, or Annosus root disease within a stand (*fig. 1.1*). Only one of the three root disease types may be simulated in a single stand. However, for Annosus root disease, the model distinguishes between types of *H. annosum* that can co-exist within a stand: P-type and S-type. This co-existence in the model is possible because each type infects different tree species (P-type on pine, and juniper, and S-type on true firs and giant sequoia), and there is no interaction between the two disease types.

The WRDM3 is based on the concept that the distribution of root disease in a stand can be characterized as a number of circular root disease centers, each of which contains both infected and uninfected trees and other inoculum sources. Trees can become infected within a center of the disease type to which they are susceptible when the trees' roots contact the infected portion of the roots of live and dead trees. Infection (as measured by the proportion of the tree's root radius that is infected) spreads at a constant rate through the tree's root system until the tree dies. After death, the model tracks and decays the inoculum level of the dead tree. New Annosus root disease centers can be created through the infection of freshly cut stumps by airborne spores, while new centers of *Armillaria* or *Phellinus* cannot. The effects of windthrow and bark beetles can also be simulated in this model.

Details of the parameters, equations, and assumptions in all parts of the model are given in the Detailed Model Description (Chapter 4). New users should note that many of the keywords should be used only by users who are experienced with the model. These keywords are marked as "advanced" in the text box that summarizes the keyword, and at the beginning of the section describing the keyword.

All Forest Vegetation Simulator (FVS) management options can be simulated, using the FVS keywords. The model will respond to the management options in an appropriate manner. In addition, the model contains two options that are specifically aimed at controlling root disease in the stand: (1) borate application to prevent spore infection and the formation of new centers (when Annosus root disease is simulated), and (2) removal of infected stumps.

1.2 Necessary Background Information

Several concepts are important to remember throughout this user's guide, both to use the keywords and to interpret the output. For basic model use, it is not necessary to understand these concepts fully; further information on some of them is given in the Detailed Model Description (Chapter 4). These concepts are:

1. Identification of the root disease type

   Throughout the keywords, the root disease type being simulated is often identified as a number. These numbers are:

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A.

Year 0

B.

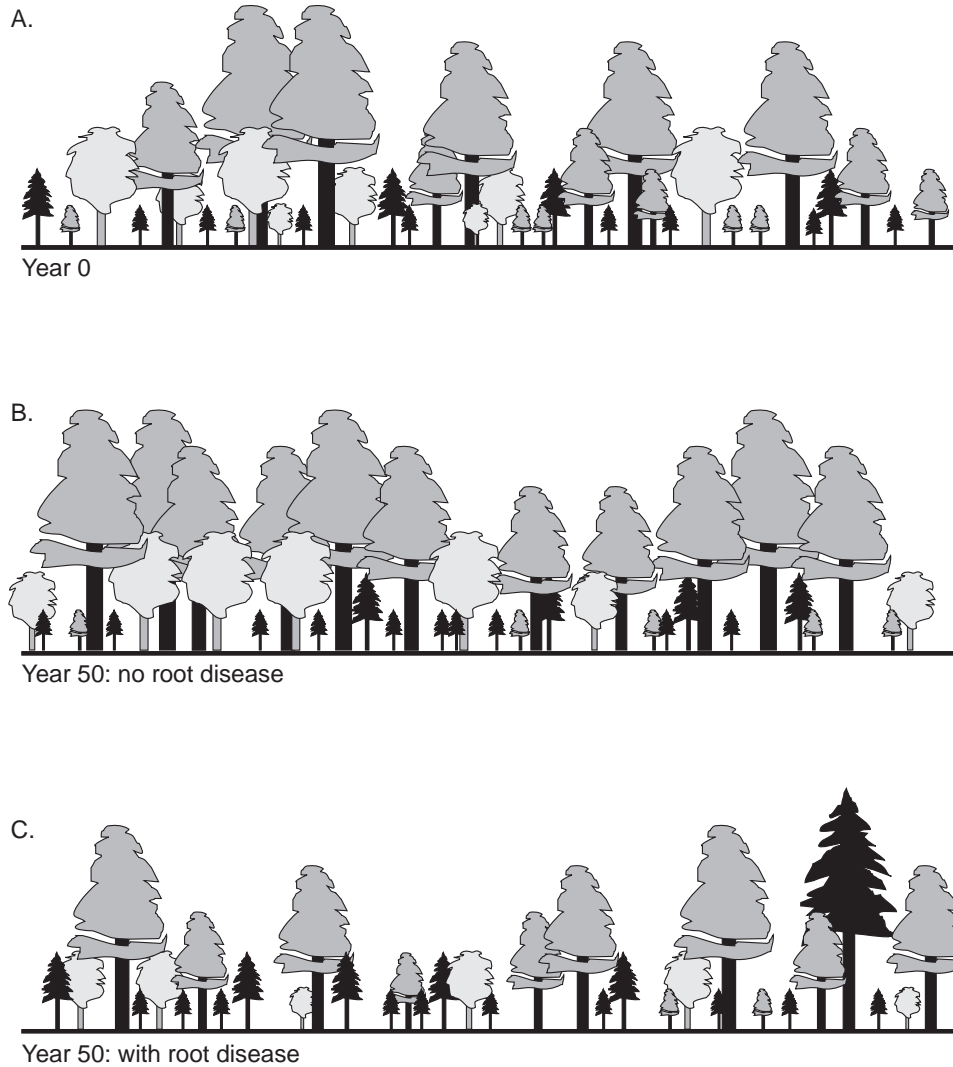Year 50: no root disease

C.

Year 50: with root disease

Figure 1.1 — Predicted changes in a pine stand: (A) Initial conditions; (B) 50 years later, without considering bark beetles and root disease; (C) 50 years later, with root disease and bark beetles accounted for.

1: P-type Annosus root disease
2: S-type Annosus root disease
3: Armillaria root disease
4: *Phellinus weirii* (laminated root rot)

Once the root disease type is selected by the user, it becomes the default for the rest of the keywords, so the identifier is necessary only when simulating P- and S-type Annosus root disease in the same stand. These instances will be clearly marked throughout this user's guide.

2. Root systems are modelled as circles

All root systems are considered to be circles with the tree (or stump) in the middle. The infection level is always given as the percentage of the circle's radius which is infected. Because the root system is a circle, root disease is assumed to expand or contract along the radius in all directions.

3. Size and specification of root disease centers

    A center is described as a circle that contains the total extent of diseased roots (inoculum sources). The statistic of disease area is calculated as the total area inside all centers. Note that the actual area with inoculum may be less than the area containing root disease (*fig. 1.2*). This is especially important to remember when comparing the results of this model against field data.

4. All measures must be entered in imperial or metric units

    The Western Root Disease Model has been developed to be used in the United States or in British Columbia. One major difference, from a user's viewpoint, is that British Columbia uses metric units and the United States uses (generally) imperial units. Either set of units may be used in the keywords in the model. The important point is that the units are consistent: the same units must be used for all keywords in FVS and in the WRDM3. The default is imperial units in the United States and metric units in British Columbia.
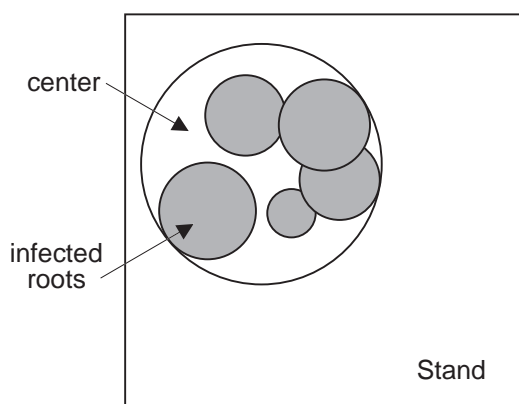

Figure 1.2 – Diagram of root disease in a center in a stand. Root diseased area (areas with inoculum) are shaded, and the extent of the center is defined by the outermost circle. Notice that parts of the center do not contain inoculum.

1.3 Formatting Conventions Used in this Manual

Throughout this manual, different fonts and formats are used for different purposes. Understanding these may assist the reader in using the manual, or in finding items quickly in different sections. Descriptions of these are given below.

1.3.1 Keywords

Keywords are identified in several ways. First, keywords are always in capital letters. In the text, they are further marked by being in bold: **KEYWORD**. A detailed description of the meaning of the keyword, each of its fields, and the default values of the fields is given in a table in the section which is most related to the keyword. These tables have the following format:

KEYWORD		One line keyword description
Field	**Description**	**Default**
1	Short description for the use of field 1	Value that the field has if left blank
2	Short description for the use of field 2	Value that the field has if left blank
...		
7	Short description for the use of field 7	Value that the field has if left blank

Keywords are also used frequently in examples. These will be discussed in the following section.

Finally, an index of keywords is contained at the end of the manual. Each use of the keyword, in text, examples, or tables, is listed in the index. The bold page number in the index identifies the page on which the keyword's fields are defined in a table.

1.3.2 Examples

Numerous examples are given throughout the text. These are designed to give examples of the use of various keywords, and to show some of the flexibility or limitations of different keywords. Examples are contained within a box so that they will be easy to find, should users wish to refer to them at a later date, and to allow others to skip over the examples completely. An example box looks like:

Example: title

Description of the example: what the example is trying to show and what the values mean in each field of the example, if keywords are used.

KEYWORD1
KEYWORD2

Keywords are frequently used in the examples. They are distinguished from regular text by being in a distinctive font. In the examples, if some fields are left blank, these fields will be identified using the symbol "_", since there is no attempt to maintain accurate spacing in the example keywords. Therefore, an example keyword (always given within an example box) would have the general format:

KEYWORD   1   2   3   _   _   6   7

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where the numbers (in this case) show the different fields and the "_" show two examples of fields left blank in the example.

1.3.3 Units

As mentioned in Section 1.2, the model can be run in either metric or imperial units. The only difference in the model is the actual numbers that are entered into each keyword and the values in the output tables. Throughout the text, values are given in imperial units with their metric equivalent in square brackets [ ]. The examples are also in imperial units, but in each example, the metric interpretation of the keyword is also given. Thus for example, if a field in a keyword is a 3, it may mean 3 inches in imperial units or 3 cm in metric units.

2.0 Running the Model

2.1 Quick Start

Only three requirements exist for running the root disease model:

1. The variant of FVS being used must contain the Western Root Disease Model extension. Contact your local FVS specialist if you are unsure whether you have the extension. (In British Columbia, the WRDM3 is part of the Windows interface, and will be part of any run done from within the Windows environment, or using the non-Windows executable version.)

2. Users should have a basic familiarity with FVS and with the use of keywords and management options.

3. Users should have information on root disease either as FVS-ready tree inventories which

contain information about the root disease infection levels in the stand or as the size of root disease centers and the density of live infected and uninfected trees within these centers.

As with FVS, the user communicates with the model through keywords which initialize the model, change assumptions, define scenarios, and choose output files.

A minimum of four keywords is needed to run the model: **RDIN**, **RRTYPE**, **RRINIT** or **RRTREIN**, and **END**. **RDIN** signals that the WRDM3 is being run and indicates the start of the WRDM3 keywords, **RRTYPE** sets the type of root disease that is to be simulated in the stand, **RRTREIN** and **RRINIT** initialize the root disease in the stand, and **END** signifies the end of the WRDM3 keywords. All keywords following the **END** keyword will be interpreted as FVS keywords. Details about each of the keywords, including their full uses and default values, will be given in this chapter. Some examples are given below.

Example: Minimum keywords for running the model

These keywords can be used to run the model for Armillaria root disease (the 3 after **RRTYPE**). With the default conditions, the stand has 20 root disease centers totalling 25 acres [10.12 ha] of infection in a 100-acre [40.47-ha] stand, and all infected trees and stumps are identified in the inventory (so RRTREIN is used to tell the model to process the disease codes in the inventory) .

```
RDIN
RRTYPE          3
RRTREIN
END
```

If the inventory does not contain root disease damage codes, the **RRINIT** keyword must be used instead of **RRTREIN**.

Example: Minimum keywords when there are no damage codes in the inventory

The following keywords can be used to run the model with Armillaria root disease (the 3 in field 1 of RRTYPE) with default root disease assumptions (i.e. the disease is in 20 root disease centers totalling 25 acres [10.12 ha] of infection in a 100-acre [40.47-ha] stand). In this example, there are no disease codes in the inventory so **RRINIT** is used instead of **RRTREIN,** and the model assumes that 50 percent of all trees within centers are infected.

```
RDIN
RRTYPE          3
RRINIT
END
```

The **RRINIT** keyword, especially when used with other keywords, gives users a large amount of control and flexibility over the initial levels of root disease in the stand. For details on the use of this keyword, and on different methods of setting the infection levels in the model, see Section 3 of this chapter.

By default, the WRDM3 prints a summary output table at the end of the FVS main output file. Thus users do not need to use extra keywords to get disease-specific output. Details about all available output files are given in Section 7.

While the model is running using any of the sets of keywords given in the above examples, other parts of the model, such as bark beetles, are also operational. *Table 2.1* lists all the options which in the model are ON by default (i.e., they will occur if the model is used, unless the user requests otherwise). *Table 2.2* lists the

Table 2.1 — Options which are ON by default in the model. The second column gives the keyword that is used to control the option (so that users can turn it off or change the defaults).

Description	Keyword
P-type Annosus root disease in stand	RRTYPE
Dynamic spread model (applying different spread rates to different centers)	SPREAD
Bark beetles types 1, 3, 4	BBTYPE1, BBTYPE3, BBTYPE4
Spore model	SPORE
Summary output table (in main output files)	

Table 2.2 — Options which are OFF by default in the model. The second column gives the keyword that can be used to turn on the relevant option. OFF by default means that these options do not occur unless requested via a keyword.

Description	Keyword
Armillaria or laminated root rot, s-type *Annosus*	RRTYPE
Read disease information from tree list (plots or damage and severity codes)	RRTREIN, PLREAD, PLOTINF
Initial infected stumps	RRTREIN, STREAD
"Jump" in root disease area after a cut	RRJUMP
Bark beetle type 2	BBTYPE2
Windthrow	WINDTHR
Management (borate application, stump pushing)	BORATE, PSTUMP
Effect of Stand Density Index (SDI) on root radius	SDIRMULT
Inside center Monte Carlo simulation (advanced option)	INFSIMS
Output tables (except summary output table in main file)	RRECHO, RRDOUT, BBOUT, SMCOUT, INFSIMS

options which the user must specifically request. Note that if no root disease type is specified, P-type Annosus root disease will be modelled.

By the appropriate use of various keywords, users can change many of the assumptions used throughout the model. Information about the various keywords is given in this document. An index to all keywords is provided at the end of the document.

2.2 Controlling Model Execution

Several keywords are available that control various aspects of the model not directly connected with root disease, management, or other agents. Three of these keywords are important, basic keywords. Discussion of more advanced keywords which control the model is deferred until Section 5.3.

2.2.1 Identifying the WRDM3 in the Keywords

The two most important keywords are **RDIN** and **END**, both of which must be present in order for the model to run. The keyword **RDIN** tells FVS that the keywords following are part of the Western Root Disease Model. The **END** keyword marks the end of the WRDM3 keywords. The **END** keyword can also be used with the **COMMENT** keyword (see below).

RDIN   Beginning of the Western Root Disease Model keywords. This keyword is required.

Field	Description
1-7	Not used. There are no fields associated with this keyword.

END   End of WRDM3 keywords (or end of a comment). This keyword is required.

Field	Description
1-7	Not used. There are no fields associated with this keyword.

> **Example: The use of RDIN and END**
>
> The keyword file to run the WRDM3 would contain:
>
> *various FVS keywords*
> RDIN
> *various root disease model keywords*
> END
> *more FVS keywords*

Examples of the minimum keywords required to run the model are shown in Section 2.1, and examples of complete keyword files are given in Section 8.

2.2.2 Comments

Users may add text or notes to the keyword file which will be printed in the keyword section of the main output file. This is done using the keyword **COMMENT**.

COMMENT   Start of a comment or text in the keyword file.

Field	Description
1-7	Not used. There are no fields associated with this keyword.
Suppl. Record	Comments can be entered in columns 1-80, in as many lines as necessary. Comment terminates with the **END** keyword.

A comment must be at least one line (even if the line is blank), and may be as many lines as needed. Comments terminate with the **END** keyword. All information entered between the **COMMENT** keyword and the **END** keyword will be ignored by the model and will be written to the main output file. Note that keyword sets which include a comment will also have two occurrences of the **END** keyword.

> **Example: The use of END with RDIN and COMMENT**
>
> The keyword file to run the WRDM3 would contain:
>
> RDIN
> *root disease model keywords*
> COMMENT
>   First line of comment
>   Second line of comment
> END
> *root disease model keywords*
> END

3.0 Initializing Root Disease

Many options are available to initialize the root disease in the stand, depending on the amount and type of information available to the user. Various levels of root disease information can be entered in different ways such as:

- Some combination of the area, number, size, and location of centers (Section 3.2);
- The infection status of sample plots (Section 3.3);
- The density of infected and uninfected trees, or the specific trees which are infected (Section 3.4); and
- Infected stumps which may or may not be in the stand inventory (Section 3.5).

Each of these is discussed in more detail in the following sections. In addition, *fig. 3.1* allows users to determine which keywords should be used to initialize the amounts of infected and uninfected trees, given the available information about the infection level in the stand.

One of the most important keywords is **RRTYPE**. This keyword tells the root disease model what type of root disease is being simulated in the stand. If this keyword is entered first, all other keywords can use the appropriate disease type as the default disease type. Thus, in many keywords, there would be one field which could be left blank. Note that the **RRTYPE** keyword allows for the possibility of entering more than one disease type. This is used only for Annosus root disease because S- and P-type *Annosus* can co-exist, without interaction, in the same stand. For Armillaria root disease and *Phellinus weirii*, however, only one disease is allowed in the stand, and neither disease may exist with Annosus root disease also present. If the field is used inappropriately, the model will simply issue a warning message, and simulate only the disease type in field 1.
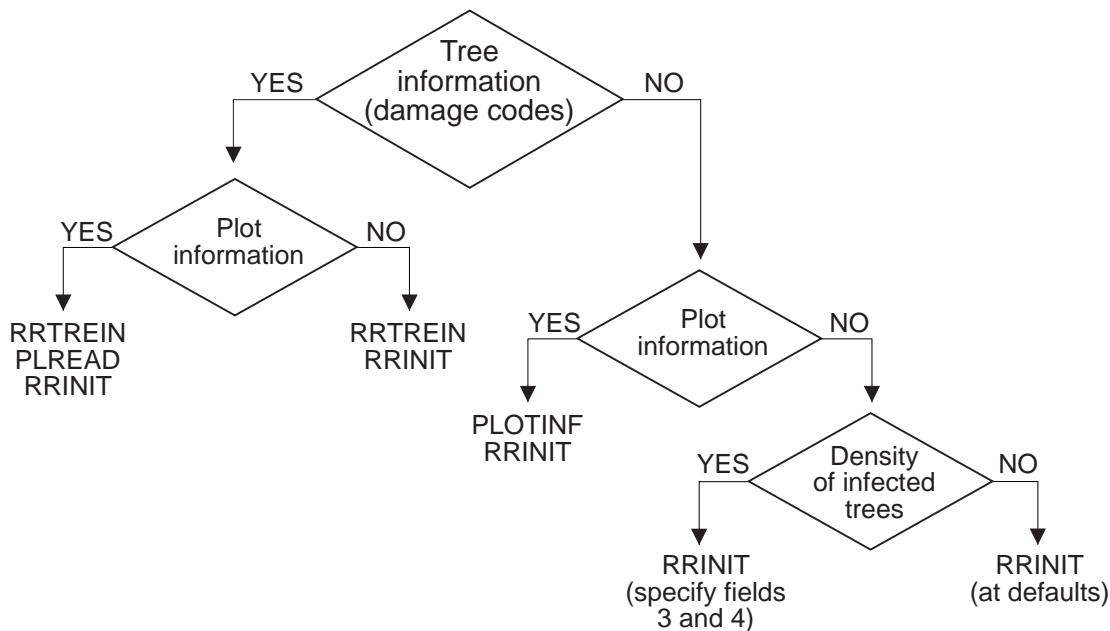

Figure 3.1 — Flowchart to determine which keywords to use to initialize root disease levels. Note that in all cases, the keyword RRINIT should also be used to set the number and size of centers (Section 3.2), and the keyword RRTYPE should be used to set the root disease type being simulated.

RRTYPE	Enter the type of root disease in the stand.	
Field	**Description**	**Default**
1	Type of root disease being simulated. (1,2=P,S-type Annosus root disease, 3=Armillaria root disease, 4=*Phellinus weirii*)	1
2	Second type of root disease being simulated. This field can only be used if Annosus root disease is being simulated (field 1 is a 1 or a 2).	
3-7	Not used	

Valid keywords possibilities are shown in the example below.

Example: Valid uses of the keyword RRTYPE

The first line sets the disease type to be both types of Annosus root disease. The second sets the disease type to be Armillaria root disease, and the third asks the model to simulate *Phellinus weirii*.

```
RRTYPE      2       1
RRTYPE      3
RRTYPE      4
```

Note that if, **RRTYPE** is not entered in the keyword files, the model will assume that P- type Annosus root disease is in the stand.

Users may enter the area of the stand using the keyword **SAREA**. The stand is assumed to be 100 acres [or 40.47 ha], unless otherwise specified. This keyword should be one of the first of the root disease model keywords.

SAREA	Set the area of the stand.	Default Imp.	Met.
Field	**Description**		
1	Area of the stand (acres or hectares)	100	40.47
2-7	Not used		

Imp. = imperial units, Met. = metric units.

3.1 Inventory Tips[3]

The most important step of running the root disease model is initializing it with reasonable infection levels. There are numerous methods for doing this, but most depend on having the initial information about disease levels in the stand of interest.

As with all models, the Western Root Disease Model is more sensitive to some options than to others. The most important component for root disease initialization is the area inside centers (or the proportion of the stand that is inside centers). In general, the more area inside centers, the more impact the disease will have. This is true if the density of infected trees in the *stand* remains constant (*fig. 3.2a*) or if the density of infected trees in the *center* remains constant (*fig. 3.2b*).

---

[3] This section is based, in part, on a similar chapter in the "User-Friendly User's Guide to the Western Root Disease Model" by Goheen and Thompson n.d.
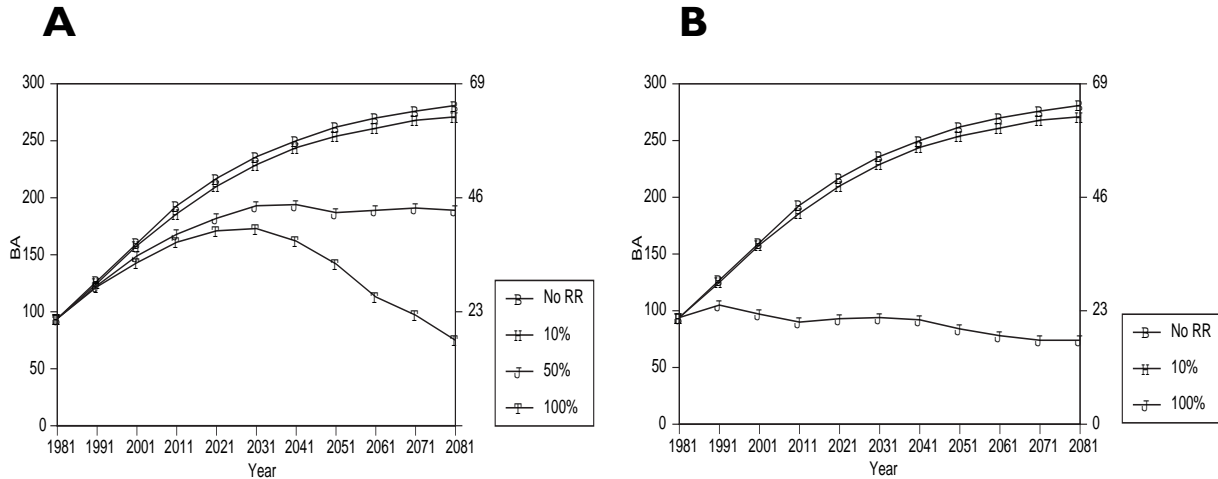
A

B

Figure 3.2 — Effect of center area on basal area. (A) Density of infected trees in the stand is constant between runs at 5 percent of the trees in the stand (i.e., the density of infected trees inside centers varies). (B) Density of infected trees within the center remains constant between runs at 50 percent of the trees in the center (i.e., the density of infected trees in the stand varies). The different symbols used refer to the proportion of the stand that is inside root disease centers at the beginning of the simulation. Note that the left y-axis is in imperial units (sq. ft./acre) and the right y-axis is in metric units (sq. m/ha).

The reason for this effect is that (assuming the centers do not cover the entire stand) more area leads to longer perimeters of centers. The rate of increase in the root disease area in a stand is proportional to the length of the perimeter. Thus as the centers spread, more new area is incorporated into the centers, and more trees become infected (*fig. 3.3*).

In general, the impact of the model on stand dynamics is independent of the number of centers in the stand. Very high numbers of centers, however, may have a greater impact on stand dynamics than low numbers of centers under some stand conditions (*fig. 3.4*).

When the entire stand is modelled as a single center, the density of infected trees becomes the critical factor (*fig. 3.5a*). This density has little impact in mixed species or mixed-age stands in which the centers do not cover the entire stand (*fig. 3.5b*).

The implication of these results on stand initialization is summarized in *table 3.1*. Effort should be made to gather the important information, and not to spend as much time and effort on the items which are of less importance. But, if the only available data does not cover the important points, any information is still better than no information (see *table 3.2*).

Figure 3.1 relates the available information with the appropriate keywords.
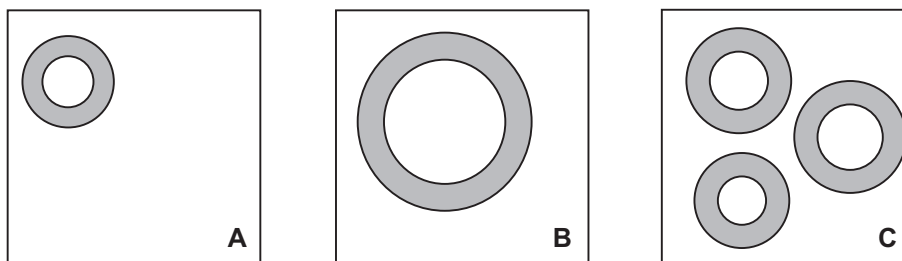
Figure 3.3 — A comparison of the new area generated during center spread. The open circles are the original center and the shaded sections are the area that is newly incorporated into the center after the center has spread. In each example, the radius increase is the same.

A

B
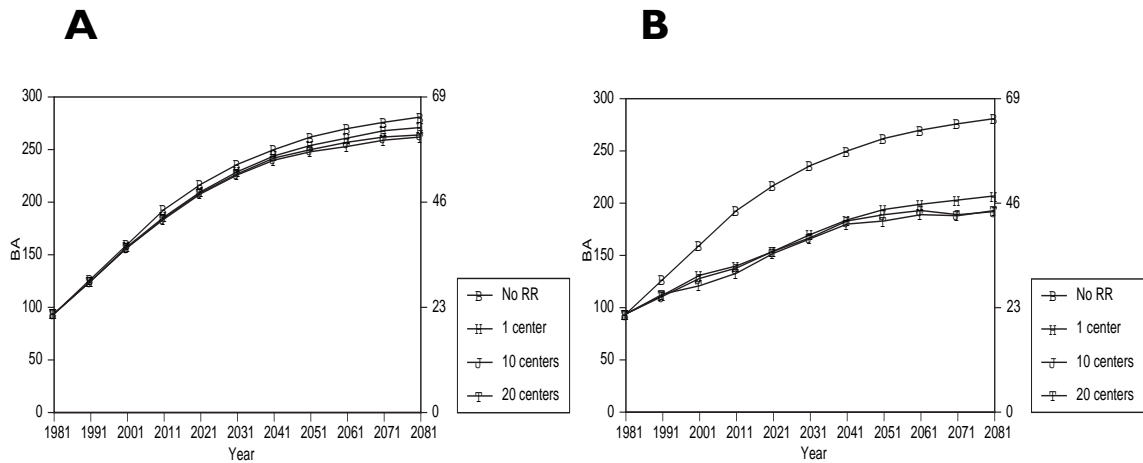
Figure 3.4 — Effect of number of centers on basal area, in a stand with Armillaria root disease. (A) 10 percent of the stand is inside centers. (B) 50 percent of the stand is inside centers. In both cases, the different symbols represent different numbers of centers. Note that the left y-axis is in imperial units (sq. ft./acre) and the right y-axis is in metric units (sq. m/ha).

A

B

Figure 3.5 — Effect of infected tree density on basal area in a stand with Armillaria root disease. (A) Entire stand is a center. (B) 50 percent of the stand is inside a center. In both cases, the different symbols represent the different density of trees infected. Note that the left y-axis is in imperial units (sq. ft./acre) and the right y-axis is in metric units (sq. m/ha).

Table 3.1 — Relative importance of various initialization components.

Component	Root disease in identifiable patches.	Root disease not in clear patches or in numerous tiny patches.
Area in centers	**Important.**	Entire stand should be considered a single center
Number of centers	Little importance.	
Density of infected trees	Defaults should be adequate, if no other values available.	**Important.** Accuracy will improve further if individual tree information (damage and severity codes) is present.

Table 3.2 — Sources of information. In each case, the information is listed in descending order of desirability, i.e., the item at the top would give the best information.
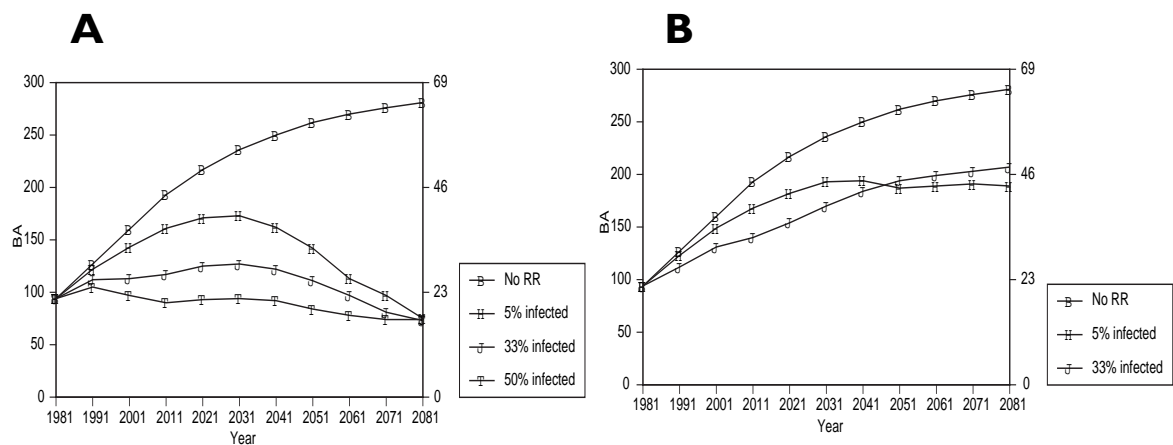
Component	Root disease in identifiable patches.	Root disease not in clear patches or in numerous tiny patches.
Area and number of centers	Stand maps Information on the number of sample plots infected (if random plots only)	Entire stand should be considered a single center
Density of infected trees	Stand exam (including supplemental plots) 'Expert' information Defaults if no other values available.	Stand exam with individual tree damage and severity codes Plot-level proportion of infection 'Expert' or observed information

3.1.1 Gathering Information

Root disease information can be gathered in a variety of ways. Some of these are listed below.

1. Walk the stand. When doing regular stand exams, pay attention to the area between sample points. If possible, try to draw rough maps of the stand showing areas with root disease.

2. Do intensive root disease sampling. In between each of the standard sample points in the stand exam, place two supplemental plots that are just for observing root disease (such as the presence or absence of root disease, the tree size and species infected, and damage and severity codes). Again, try to draw rough maps of the stand showing areas with root disease.

3. Talk to a local pathologist to find out what sort of infection levels may be present in the stand. The pathologist may be able to give some estimates about root disease area, number of centers, or the density of infected trees.

4. See if there are any existing studies or guidelines for doing root disease surveys (such as the *Root Disease Management Guidebook* published by the BC Ministry of Forests and BC Environment [1995]).

When gathering the root disease information it is important that the data correspond to conventions used in the model. Two examples of this are center area and density of trees inside centers. In the first case, a center is measured in the model as a circle which encompasses the perimeter of all infected root systems. Other definitions may be used in the field (*fig. 3.6*). When using the density of trees, the model assumes that stocking density inside and outside centers is the same, unless damage codes are present in the inventory. Thus without damage codes, the relative density of infected and uninfected trees inside centers will be the information that is used inside the model rather than the actual density (see Section 3.2).
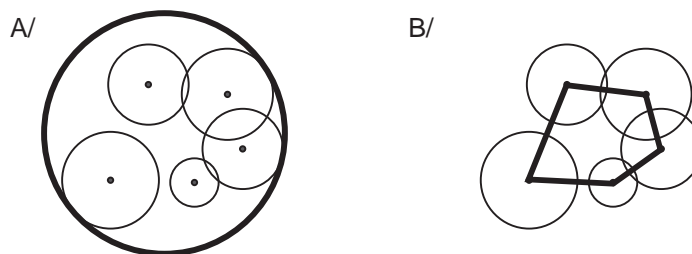
Figure 3.6 — Definition of a center. On the left, the center is defined as a circle which encompasses all the infected root systems (as is done in the model). On the left, the center boundary is drawn from the center of each infected root system (as is occasionally done in the field).

3.2 Entering Root Disease Center Information (area, number, size, location)

The keyword **RRINIT** can be used to initialize the number, size, and location of root disease centers. It can also be used to enter information about infected trees (discussed further in Section 3.4).

RRINIT	Define center information (number, area, location, proportion infected)	
Field	**Description**	**Default**
1	Allow model to choose center locations and sizes (=0) or ask model to read root disease center attributes from supplemental records (=1)	0
2	Number of root disease centers in stand. (If field 1 = 1, then this is also the number of supplemental records.)	20
3	Density or proportion of **infected** trees in root disease centers. Value will be ignored if RRTREIN is used or field 4 is blank. Default is 50 percent of trees inside centers.	
4	Density or proportion of **uninfected** trees in root disease centers. Value will be ignored if RRTREIN is used or field 3 is blank. Default is 50 percent of trees inside centers.	
5	Average proportion of root infection.	0.1
6	Total acres [or hectares] of root disease. Default is 25 percent of stand area. (-1 to calculate area from PLREAD)	
7	Root disease type (1,2=P,S Annosus root disease, 3=Armillaria root disease, 4=*Phellinus weirii*)	1, or type set by RRTYPE

There are two ways to specify the number and size of root disease centers, both cases using the keyword **RRINIT**. The simplest case is if the user has information only about the number of centers and the total area of root disease. In this case, the user can simply use **RRINIT** to enter this information.

Example: Initializing root disease with only the number of centers and diseased area

Suppose the stand has five centers (field 2) which combine to give 3 acres [3 hectares] (field 6) of *Phellinus weirii* (field 7), but the user does not know the sizes or locations of the centers (the 0 in field 1). The keyword **RRINIT** is shown below, and a visual representation of the two stands (actual and modelled) is shown in *figure 3.7*.

RRINIT   0   5   _   _   _   3   4
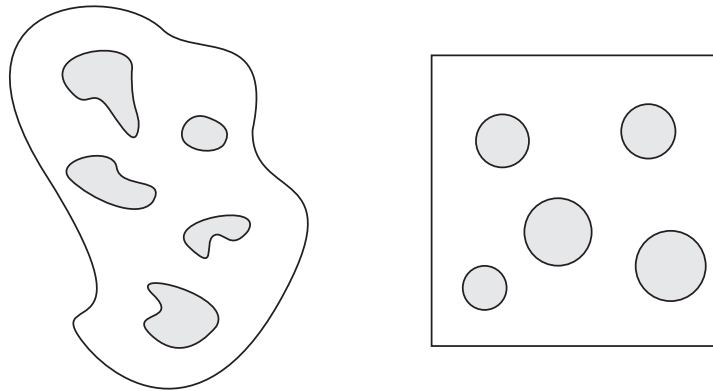
Figure 3.7 — Example of an actual (left) and simulated (right) stand. In both cases, the stand has five centers (the shaded areas). Notice that the model assumes that the stand is square and the centers are circles.

This method has the advantage that the total area inside root disease centers will be preserved, i.e., the area seen in the field is the same as the area simulated in the model. Also, since FVS does not track the location of each tree, little is lost by assigning center locations randomly.

Note that at most 100 centers in each disease type can be simulated. If the user requests more than 100 centers for a particular disease type, an error message will be printed in the main output file and only 100 centers will be used.

If a user does not know the amount of root disease in the stand but does know which plots are inside centers, then the user can ask the model to determine the root diseased area in the stand. For details on this option see the discussion of **PLREAD** (in Section 3.3).

In stands which have been more extensively studied, the location and size of each center may be known. Instead of allowing the model to choose the size and location of the centers, the user can provide X-Y coordinates and the radius of *each* center while still using the **RRINIT** keyword.

Example: Specifying the size and location of centers

The keyword to specify the size and location of 3 centers (field 2) in *Phellinus weirii* (field 7) is given below. In this example, the first center is located at (100, 100) and has a radius of 44.3 feet [13.5 meters]. Note the '1' in field 1 to tell the model that the center size and location are listed after the keyword. A picture of the resulting centers is shown in *figure 3.8*.

RRINIT   1   3   _   _   _   _   4
100   100   44.3
550   430   150.5
400   200   75.1
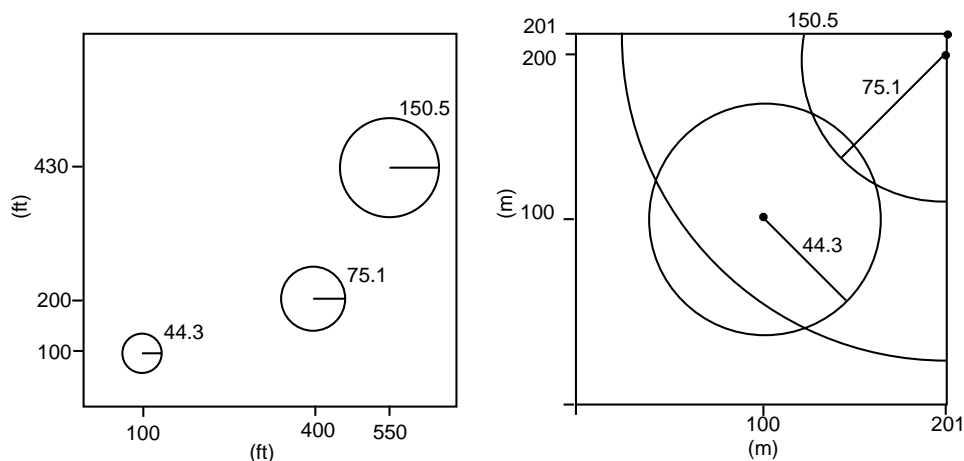
Figure 3.8 — Diagram of the centers entered in the example. The diagram shows the stand and centers as the model sees them. (A) The model is run assuming that the keyword was in imperial units so the stand is a square assumed to be 660 ft per side. (B) The model is assuming that the keyword was in metric units and was 201 m per side. In both cases the centers are circles with the radii measured in feet (A) or meters (B), as appropriate.

In the example above, the "1" in field 1 indicates that the center locations will be entered following the keyword. If this option is used, the user *must* enter one row for each center (the number of centers is given in field 2) which contains, in this order, the X location (feet or meters), the Y location (feet or meters), and the radius of the center (feet or meters). There is no method by which some centers can be entered manually and others of the same root disease can be assigned randomly.

It is important to remember that stands are measured as a square. Most stands in the field are not actually squares, and it is possible that, if the location is not modified, a center could end up being located outside the stand (*fig. 3.9*). The model will print an error message to the main output file, and the coordinate that is outside the stand will be set to the stand's boundary. Also, the area in root disease centers may not be preserved. In one stand, a center may be far from the boundaries, whereas, in the square stand, the center may be on the edge. These considerations are not intended to discourage people from placing the centers in the stand, but rather to ensure that all users have a clear understanding of the consequences of doing so.

Some users will want to run the entire stand as one root disease center. To do this, the keyword **SAREA** *must* be used first to enter the area of the stand. In the keyword **RRINIT**, fields 1, 2, and 6 must be entered.

Example: Simulating the stand as one center

Suppose that a 10 acre [10 hectare] stand (field 6) is to be modelled as one (field 2) Armillaria root disease center (field 7). The keywords to do this are:

```
SAREA        10
RRINIT       0     1     _     _     _     10    3
```

If the entire stand is inside a root disease center, the **PLREAD** keyword (see Section 3.3) is irrelevant and should not be used.

Note: If a center is present and does not include the entire stand, it will spread and infect trees. This is true even if the model had no initial infected live or dead trees because the model always assumes that the entire border of a center is infectious.
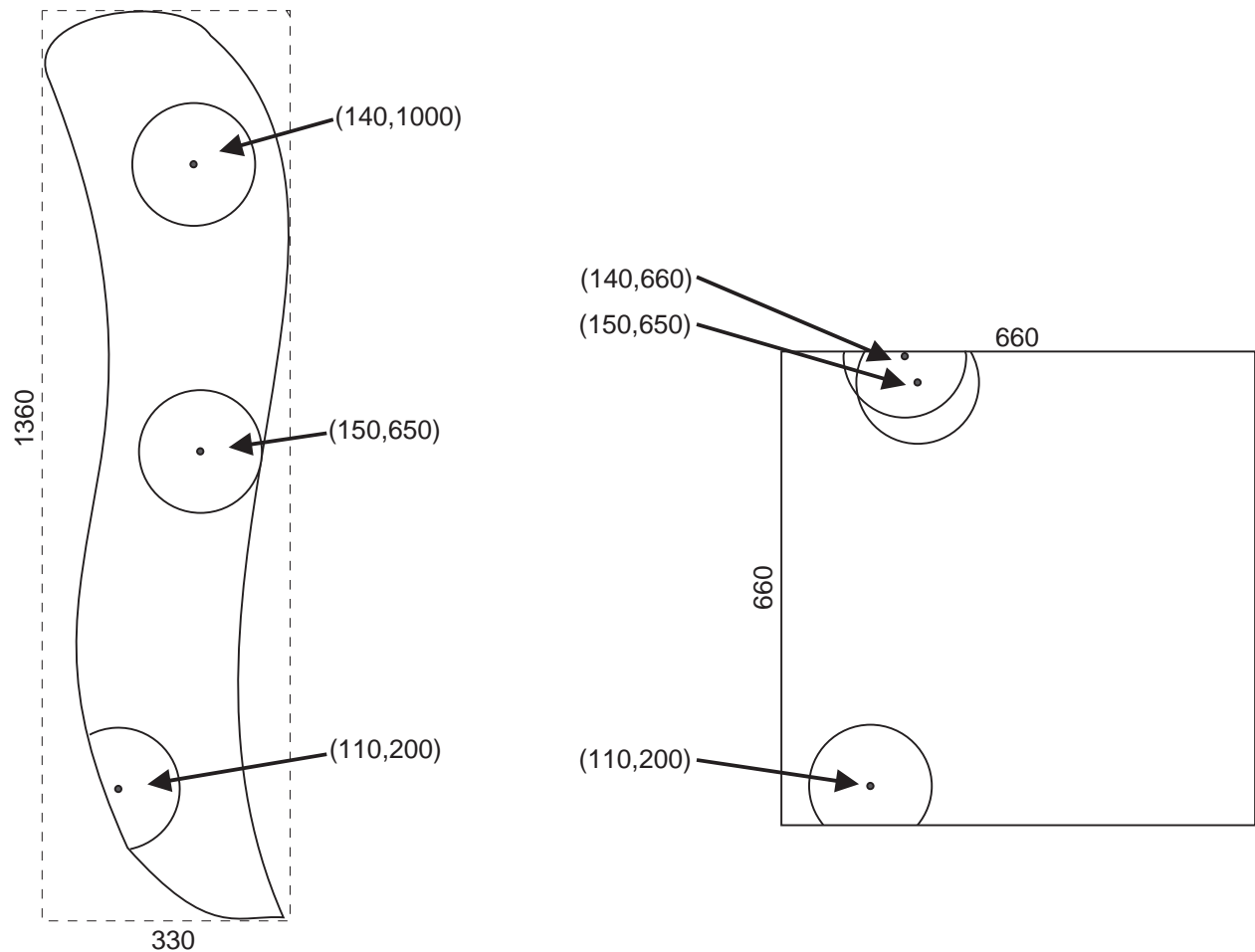
Figure 3.9 — Caveats when placing centers in a stand. On the left, a non-square stand with three centers. On the right, the model's square representation of the same stand. Notice the new location of the uppermost center. Also notice that the stand in the model will have less area in root disease.

Note for Annosus root disease:

Since trees can be hosts of only one of the two types of Annosus root disease (S and P), it is possible to run the stand with large areas in each of the types (*fig. 3.10*). A 10-acre stand can have up to 10 acres inside a P-type root disease center and up to 10 acres inside an S-type center. There is no interaction between the two disease types, except indirectly through the diseases' effects on host trees.

3.3 Entering Plot-Level Information (whether plots are inside centers, outside centers, or both)

In the tree inventory, the records are divided into sampling plots. If the user knows whether the plots were entirely inside or outside root disease centers, the information can be given to the model so that the model can more accurately assess which uninfected trees should be inside centers and which should be outside centers. The keyword **PLREAD** identifies the plots which are inside centers of a specific disease type. This keyword *must* be used with **RRTREIN** so that the model reads the damage codes in the infected plots. All trees in uninfected plots are assumed to be outside centers, and any damage codes (see below) will be ignored.
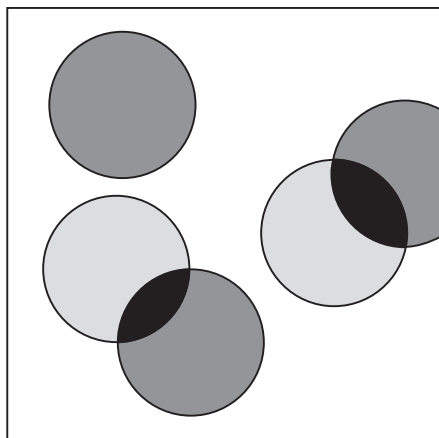
Figure 3.10 — Stand with S- and P-type Annosus root disease centers. The dark circles represent root disease centers of P-type, and the light circles are S-type centers. The black areas contain both types of root disease. If each center were 1 acre, then this stand would contain 3 acres of P-type and 2 acres of S-type _Annosus_.

PLREAD   List the plots inside centers from which to read the damage code information

Field	Description	Default
I	Type of root disease contained in the plots (1=P-type, 2=S-type Annosus root disease, 3=Amillaria root disease, 4= _Phellinus weirii_).	I, or type set by RRTYPE
2-7	Not used	
Suppl. Record	Diseased subplot number as a 4-digit integer, right justified in the first 4 columns of the row. The last row must be '-999'.	

Occasionally the only information the user has about infection levels is that some of the trees (without having specified which ones) in certain plots are infected. In this case the keyword **PLOTINF** can be used to distinguish infected plots and their degree of infection. Note that this keyword should _not_ be used with the keyword **RRTREIN** (which reads tree infection information from the tree list). If there are damage codes in the tree list and the infected plots are known, **PLREAD** provides a more accurate accounting of the disease.

PLOTINF   List the plots inside centers and the proportion of infected trees in each plot.

Field	Description	Default
I	Type of root disease contained in the plots (1=P-type Annosus root disease, 2=S-type Annosus root disease, 3=Armillaria root disease, 4 = _Phellinus weirii_).	I, or type set by RRTYPE
2-7	Not used	
Suppl. Record	Diseased subplot number as a 4-digit integer, right justified in the first four columns of the row. Then, the proportion of the plot which is infected as a real number with 2 decimal places in columns 6-9. The last row must be '-999'.	

Both **PLREAD** and **PLOTINF** provide a list of infected plots. In addition, **PLOTINF** defines the proportion (by number) of the trees in the plot that are infected. In the example below, the keyword set shows the plots specified using **PLREAD**, and the second shows the plots entered using **PLOTINF** and specifying the proportion of the trees in the plot which are infected. Note that only one of these keywords would be used for initializing the root disease in the stand.

Example: Initializing root disease from plot information

In both cases, plots 1004, 1002, and 1007 (listed as supplemental records) contain P-type Annosus root disease (code 1, after the keyword). The '-999' signifies the end of the list of plot numbers. In Example A, both **PLREAD** and **RRTREIN** are used, and the degree of infection in each plot is taken from the disease codes in the tree inventory. In example B, all trees within plot 1004 are infected, plot 1002 is 50 percent infected and plot 1007 is 25 percent infected. Note that only *one* of these keywords (either **PLREAD** or **PLOTINF**) would be present in a keyword set.

Example A:

```
RRTREIN
PLREAD            1
1004
1002
1007
-999
```

Example B:

```
PLOTINF           1
1004              1.00
1002              0.50
1007              0.25
-999
```

When the keyword **PLREAD** is used, the model puts uninfected trees inside and outside centers differently than when **RRTREIN** is used alone. In the first case, different tree densities may occur inside and outside of centers while in the second case (i.e. **RRTREIN** is used alone), the density will be the same inside and outside centers (*fig. 3.11*). In both cases, the correct trees are recognized as being infected. These different densities inside and outside of centers will affect all aspects of the root disease simulation, including spread rate and between-tree transmission.

If a user does not know the area inside root disease centers in the stand but does know which plots are inside centers, the user can use the **PLREAD** keyword in conjunction with the **RRINIT** keyword and ask the model to determine the root diseased area. The model assumes that plots were located systematically in the stand so that all parts of the stand (inside and outside centers) have an equal chance of being sampled (i.e., the plots were not selectively placed in diseased or disease-free areas). Additionally, the model assumes that the proportion of infected plots is representative of the proportion of infected area in the stand.
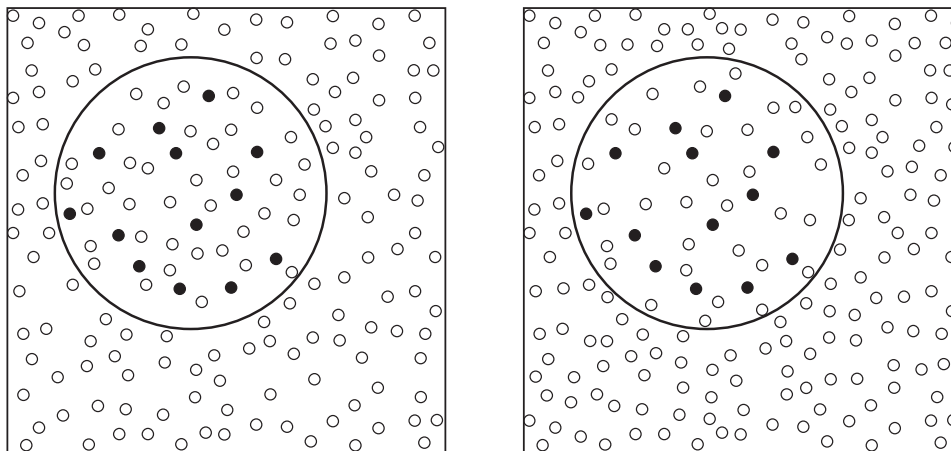
Figure 3.11 — Pictorial representation of the difference in density using different keywords. On the left is the stand when using only RRTREIN, with an even density inside and outside of centers. On the right is the stand when using RRTREIN and PLREAD, showing a lower density inside centers and a higher density outside the center. The overall stand density is the same in both stands.

Example: Initializing the root disease with only the number of centers and the plots with infection

Suppose a series of random plots were placed in the stand and the user knew the number of infected plots but not the area within centers. To ask the model to calculate the area, a "-1" is entered in field 6 of **RRINIT.**

```
RRINIT          0          5          -          -          -1          4
RRTREIN
PLREAD          4
1001
1002
1003
-999
```

Note that if **PLREAD** is used and there is not a "-1" in field 6 of **RRINIT**, the model will use the area given by **RRINIT**. This option should be used if the plots were not selected at random (i.e., they overrepresent the diseased area or if the area in centers is known.

3.4 Entering Tree-Level Information (damage and severity codes, density infected or uninfected)

Some stand inventories include information about which trees are infected with root disease and the degree of infection. In the tree list which is read by the model, infected trees may have been given a damage code, indicating that they are infected with root disease. The model will recognize three different damage codes. These are:

> 61   Armillaria root disease
> 62   *Phellinus weirii*
> 64   Annosus root disease (of either type)

They may also have been given a severity code as follows:

1   The tree was within 30 feet [9.1 m] of a tree with a deteriorating crown or killed by root disease.
2   The tree has diagnostic signs or symptoms of root disease.
3   The tree has crown deterioration and is likely near death due to root disease.

The severity codes are used to assign a degree of infection to the trees. A mean infection level is used for each severity code with some random variation to avoid clumpiness (Marsden and others 1993). Each severity code is associated with a mean infection level: 1 = approximately 10 percent of the value at death, 2 = approximately 65 percent of the amount at death, and 3 = approximately 75 percent of the amount at death. The value at death is a tree-species-specific parameter. (See the Appendix for Chapter 2 infection levels at death, for each tree species. If there are damage codes with no severity codes, the model will assume a severity code of 1.

The keyword **RRTREIN** tells the model to read the damage and severity codes from the inventory to initialize the root disease.

RRTREIN   Assign infection based on damage and severity codes in inventory.

Field	Description
1-7	Not used. There are no fields associated with this keyword.

Each line of the inventory has space for three damage code-severity code pairs (two of which are shown in this example) since trees may be affected by multiple agents.

Example: Section of a tree inventory with root disease damage codes

The following is an example tree inventory entry for a stand containing Annosus root disease (and measures in imperial units). Each line in this example contains a damage code (64 for Annosus root disease) and a severity code (both codes are shaded) to identify infected trees:

```
4   47   13DF   18.9   .0   0   0   .0030   664   1   0   031   0   00   0
4   48   18DF   30.7   .0   0   0   .0064   148   8   0   031   0   00   0
4   49   16DF    4.0   .0   0   0   .0064     3 0   0   0   031   0   00   0
4   50   13DF    2.0   .0   0   0   .0030   364   1   0   031   0   00   0
```

In this example, Douglas-fir trees are infected. Douglas-fir is assumed to be 90 percent infected at death (see the defaults for the **INFKILL** keyword in the appendix, or the Model Description). Therefore, the three records with a severity code of 1 will be assigned an initial infection level of around 9 percent (90 percent times 10 percent). The remaining record, with a severity code of 3, will be given an initial infection level of around 90 percent times 75 percent, or approximately 67.5 percent.

Definitions for the other damage codes can be found in the user's guides for other FVS model extensions. Each extension, including the Western Root Disease Model, retains only information about the relevant code.

The user may have only information about the approximate density of trees within root disease centers, and how many of these trees are infected or uninfected. In this case, the user should use the keyword **RRINIT** (fields 3 and 4, see Section 3.2), to give the density of infected and uninfected trees within centers or the proportion of the trees inside centers which are infected or uninfected. The model will then divide each tree

record into infected and uninfected trees according to the relative densities given in the keyword (see the Detailed Model Description for more information). Initial root disease will be assigned from a distribution about the mean value given in field 5.

Example: Specifying the density of infected and uninfected trees in centers

The keyword to describe a stand which has 3 acres [3 ha] in five S-type Annosus root disease centers (fields 6, 2, and 7) which have about 200 trees/acre [200 trees/ha] uninfected (field 4) and 100 trees/acre [100 trees/ha] infected (field 3), with a mean infection level of 20 percent (field 5) is:

RRINIT   0   5   100   200   0.2   3   2

Note that if the density of trees in the stand (and therefore also in the center) was different from 300 trees/acre, for example 600 trees/acre [600 trees/ha], then the model would use the relative density of infected and uninfected trees. In this example, the model would assign 200 trees/acre infected (600*100/300) and 400 trees/acre uninfected (600 * 200/300).

If the **RRTREIN** keyword is used in combination with **RRINIT** or is inadvertently added at this point, the given values in fields 3 and 4 will be ignored and the model will assign all infection levels from the damage codes in the inventory.

3.5 Entering Stump and Dead Tree Information

Throughout the model, the term "stump" refers to both the remaining part of a harvested tree (in the standard sense of the word "stump") and also any other dead trees. The model retains only information about infected stumps, since they are a source of inoculum.

There are two methods for initializing the infected dead trees and stumps in the stand. A stump can be entered as part of the tree list and given a tree history code which indicates that it has recently died (6, 7, 8, or 9), and a damage code to indicate that the record is infected with root disease.

Example: Infected stumps in the inventory

In the sample inventory below (imperial units),

```
4  47      13DF    18.9    .0  0    0  .0030    664    1    0    031    0    00    0
4  48      18DF    30.7    .0  0    0  .0064    148    8    0    031    0    00    0
4  49      16DF    4.0     .0  0    0  .0064    3 0    0    0    031    0    00    0
4  50      13DF    2.0     .0  0    0  .0030    364    1    0    031    0    00    0
```

the second and third tree records have been coded as recently dead (shown by the 8 and the 6 in bold), and infected with Annosus root disease (bold 64). The severity codes are ignored.

Note also that stumps may be coded in the tree list as trees with a height of 1.5 feet [0.457 m].

Stumps in the inventory are assumed to have been dead for 5 to 15 years, depending on their size (larger stumps are assumed to have been dead longer). In the above example, the model assumes that the 30.7-inch stump has been dead for 15 years and the 4-inch stump for 5 years. The default times since death are calculated by assuming that, in general, it takes about 10 to 20 years before most field crews can recognize stumps as being infected with root disease. Using the default decay rates in the model, however, many stumps smaller than 14 inches [35.6 cm] DBH are no longer present after 15 years. Thus, the smaller stumps in the inventory must have been dead a shorter time. This assumption can be changed using the keyword **TIMEDEAD**.

TIMEDEAD   Time (years) that the average infected tree/stump in the inventory has been dead.

Field	Description	Default
1	Time for size class 0-12 inch [0-30.5 cm] DBH.	5
2	Time for size class >12-24 inch [30.5-61 cm] DBH.	10
3	Time for size class >24-48 inch [61-121.9 cm] DBH.	15
4	Time for size class >48-100 inch [121.9-254 cm] DBH.	15
5	Time for size class >100 inch [>254 cm] DBH.	15
6	All size classes. If there is a value in this field, fields 1-5 are ignored	
7	Not used	

Example: Changing the time since death for stumps in the inventory

Suppose an inventory was done by a root disease specialist who was experienced at identifying early stages of root disease infection. The pathologist knew stumps in the smallest size class (0-12 inches [0-30.5 cm]) could have been dead for only 2 years (field 1) and that stumps in the remaining size classes were dead for only 5 years (fields 2-5). The keyword to tell the model this would be:

TIMEDEAD   2   5   5   5   5   _

The second method for entering infected dead trees and stumps is to use the keyword **STREAD**. The user must specify tree species, diameter class, number represented by this record, disease type, and time since death, in that order.

STREAD   Used for entering infected dead trees/stumps which were not in the inventory.

Field	Description	Default
1	Tree species code.	
2	Diameter class (1=0-12 in., 2=>12-24 in., 4=>48-100 in., 5=>100 in.) [in cm: 1=0-30.5, 2=>30.5-61, 3=>61-121.9, 4=>121.9-254, 5= >254]	
3	Number of stumps with these characteristics	
4	Disease type (1=P-type *Annosus,* 2=S-type *Annosus*, 3= *Armillaria*, 4=*Phellinus*)	
5	Number of years stumps of this species and diameter have been dead.	
6 & 7	Not used	

Any number of stumps may be entered using the keyword multiple times.

Example: Entering initial infected stumps

The example inventory above contained two Douglas-fir stump records (species code 3, field 1 below), one 30.7- inch diameter record and one 4-inch diameter record. Making some assumptions about the number of stumps per acre each record represents, and using the information in the keyword about the size class and age-class, the keywords to enter these stumps manually are:

STREAD	3	3	2	2	15
STREAD	3	1	3	2	5

Note that, in the model, stump diameters are assigned to the mid-point of the size class. For example, a class 1 stump will be given a diameter of 6 inches [15 cm] and a class 2 stump will be given a diameter of 18 inches [45 cm]. These diameters are used for calculating how large the remaining root system is on the stump, and therefore how much inoculum is left. If the stumps that are being entered are close to the boundary of the class, then users should decide whether to put them in the lower class (and lose inoculum more rapidly than expected) or the upper class (and retain inoculum in the stand for longer than would be normally be expected).

4.0 Bark Beetle and Windthrow Models

4.1 Bark Beetles

The model can represent four different types of bark beetles. Each of these is triggered by the density of trees (either all trees, trees with a certain degree of infection, or windthrown trees) above some specified size threshold. Users can also specify the mortality rate which is applied to trees with various characteristics. *Table 4.1* summarizes the differences between the beetle types and *table 4.2* gives examples. Each letter in this table indicates a user-controlled variable for each type of bark beetle, while the blank cells indicate values that are not used for that type of beetle. For example, for beetle type 1 the user may specify the host species for the beetle, the minimum diameter of trees affected by the beetle, a single mortality rate which is applied to trees both inside and outside of root disease areas in the event of an outbreak, and the criterion for triggering the outbreak. Alternatively, the user may choose to rely on default values for some or all of these variables. Some of the differences between the bark beetle types is also shown pictorially in *figure 4.1*. See the Detailed Model Description for more information about each beetle type.

Table 4.1 — A comparison of the four bark beetle types. Each letter indicates a variable under user control, while blank cells indicate values that are not used for that type of bark beetle. Each different letter in a column is a different field in the keyword for that bark beetle type. For Type 2 bark beetles, M* reminds the user that the mortality rate is specified relative to the number of windthrown trees. "D" is minimum DBH and "I" is minimum root disease infection level. SDI is stand density index.

	TYPE 1 BEETLES	TYPE 2 BEETLES	TYPE 3 BEETLES	TYPE 4 BEETLES
Host	H	H	H	H
Min. DBH	D	D	D	D
Min. Infection			I	I
Outside Mortality	M	M*		M1
Fringe Mortality	M	M*		M2
Inside Uninfected Mortality	M	M*		M3
Inside Infected Mortality	M	M*	M	M4 if ≥ I M3 if < I
Outbreak Criteria	Density of host > D *or* SDI (outside / whole stand, whole stand, living / alive in last 2 yrs).	Total density of host >D windthrown in the current growth cycle.	Density in centers of live host > D *and* > I.	Density in centers of host > D *and* > I, including host that died in last 2 years.

Table 4.2 — Example bark beetle types.

Species Type	Type 1	Type 2	Type 3	Type 4
Beetle species	Western pine beetle Mountain pine beetle	Douglas-fir engraver	Fir engraver	Mountain pine beetle
Host tree species	Ponderosa pine Lodgepole pine	Douglas-fir	White fir Grand fir	Ponderosa pine
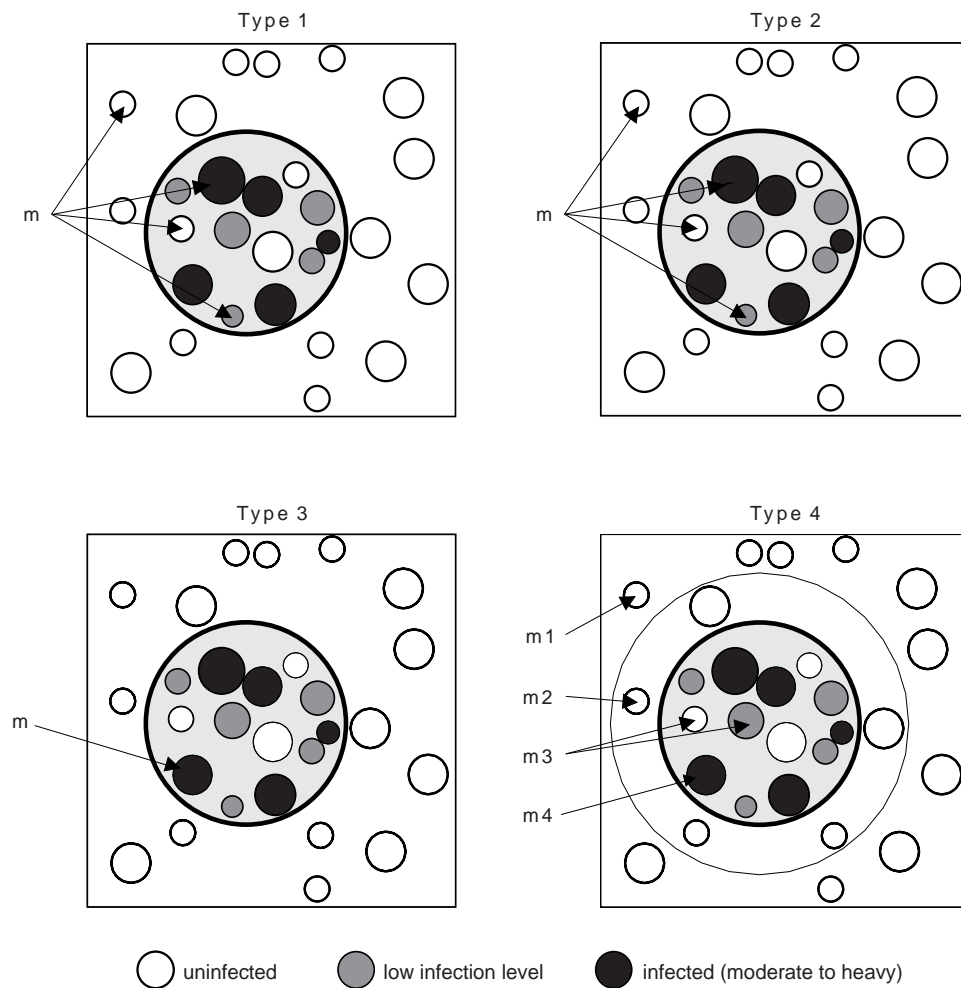
Figure 4.1 — A pictorial representation of some of the differences between bark beetle types. Open circles are uninfected trees, lightly shaded circles represent trees with low root disease infection levels, and darker shaded small circles represent trees with higher levels of infection. The heavily shaded large circle represents a root disease center. "M" means mortality rate due to bark beetle type.

Each of the four bark beetle types is represented by a keyword in which users specify the first year of potential occurrence, the threshold density of trees of a specific size and disease level, and the mortality rates to be applied. By default, bark beetle types 1, 3, and 4 are active in the model at their default values. The keyword **BBCLEAR** (with no fields) allows the user to make the decision to use no bark beetles. If the user wishes to use fewer, more, or different bark beetle types, a keyword (**BBTYPE1**, **BBTYPE2**, **BBTYPE3**, or **BBTYPE4**) must be used for each desired type.

The bark beetle keywords are quite flexible, and with some planning, users should be able to accomplish almost any desired beetle-induced mortality pattern. The same keyword can be repeated for any number of tree species, thresholds, or mortality rates. Up to 33 different varieties of bark beetles (defined as a unique combination of bark beetle type and parameters) may be active in any cycle.

BBTYPE1   Type 1 bark beetle.

Field	Description	Default Imp	Met
1	Earliest date that an outbreak can occur (year or cycle).	1	1
2	Tree species eligible for bark beetle attack (tree species number or character code).	10	10
3	Minimum DBH of trees eligible for attack by the bark beetle (inches or cm).	8	20.3
4	Threshold density of eligible trees/acre [or trees/ha] that must be exceeded for an outbreak to occur.	150	371
5	Mortality rate applied to all eligible trees (fields 2 and 3) if an outbreak occurs.	0.1	0.1
6	Flag for whether the beetle model should remain on once it occurs (0 = yes; 1 = no).	0	0
7	Not used		

Imp. = imperial units, Met. = metric units

BBTYPE2   Type 2 bark beetle (WINDTHR keyword must be present).

Field	Description	Default Imp	Met
1	Earliest date that an outbreak can occur (year or cycle).	1	1
2	Tree species eligible for bark beetle attack (tree species number or character code).	3	3
3	Minimum DBH of trees eligible for attack by the bark beetle (inches or cm).	0.0	0.0
4	Minimum number of *windthrown* trees/acre [trees/ha] necessary for an outbreak to occur. Eligible trees must meet requirements in fields 2 and 3.	10.0	24.7
5	Number of eligible trees (fields 2,3) to die in an outbreak *for each windthrown tree* meeting requirements in fields 2 and 3.	0.88	0.88
6	Flag for whether the beetle model should remain on once it occurs (0 = yes; 1=no).	0	0
7	Not used		

Imp. = imperial units, Met. = metric units

BBTYPE3   **Type 3 bark beetle.**

Field	Description	Default Imp	Met
1	Earliest date that an outbreak can occur (year or cycle).	1	1
2	Tree species eligible for bark beetle attack (tree species number or character code).	4	4
3	Minimum DBH of trees eligible for attack by the bark beetle (inches or cm).	10.0	2.5
4	Threshold density of eligible trees/acre [trees/ha] that must be exceeded for an outbreak to occur.	10	24.7
5	Minimum proportion of root radius infected for attack by bark beetles.	0.30	0.30
6	Flag for whether the beetle model should remain on once it occurs (0 = yes; 1=no).	0	0
7	Mortality rate applied to all eligible trees if an outbreak occurs.	0.88	0.88

Imp. = imperial units, Met. = metric units

BBTYPE4   **Type 4 bark beetle.**

Field	Description	Default Imp	Met
1	Earliest date that an outbreak can occur (year or cycle).	1	1
2	Tree species eligible for bark beetle attack (tree species number or character code).	10	10
3	Minimum DBH of trees eligible for attack by the bark beetle (inches or cm).	4.0	10.2
4	Threshold trees/acre [trees/ha] that must be exceeded for an outbreak to occur.	1.0	2.5
5	Minimum proportion of infected root radius for trees to be eligible for density calculation and to suffer the highest mortality rate (field 7).	0.4	0.4
6	Flag for whether the beetle model should remain on once it occurs (0 = yes; 1=no).	0	0
7	(Highest) mortality rate applied to eligible trees (fields 2,3,5) when outbreak occurs.	0.75	0.75
Required Supplemental Record			
1	Mortality rate applied to eligible trees (fields 2,3) inside centers that are less than field 5 infected ('inside-uninfected' or low infection trees).	0.3	0.3
2	Mortality rate applied to eligible trees (fields 2,3) outside centers which are within an average root diameter of the edge of the center.	0.15	0.15
3	Mortality rate applied to eligible trees (fields 2,3) outside centers which are beyond the average root diameter away from the edge of the center.	0.101	0.01

Imp. = imperial units, Met. = metric units

BBCLEAR Simulate no bark beetles.

Field	Description	Default
1-7	Not used.	

A key part of the bark beetle models is that more than one bark beetle type (or variety) may attack any species or size of tree. It is possible that one bark beetle type can attack the same species of tree with different threshold values and different mortality rates. Thus, the difference between endemic and outbreak levels of bark beetles can be simulated. The example below shows a Type 1 bark beetle attacking ponderosa pine at low levels and sets up outbreak conditions with a much higher threshold.

Example: Bark beetles attacking different size trees at different rates

In both keywords, the first two fields tell the model to start checking for beetle mortality in cycle 1 on ponderosa pine (species 10). The first line gives a low-level bark beetle mortality (such as endemic mountain pine beetle): 1 percent mortality (field 5) will be applied to trees greater than 4 inches [4 cm] DBH (field 3) when there are at least 15 trees/acre [15 trees/ha] (field 4) of that size. The second occurrence of the threshold is much higher (representing outbreak conditions): 100 trees/acre [100 trees/ha] greater than 12 inches [12 cm] DBH, and, at 20 percent, the mortality rate is also greater.

```
BBTYPE1     1      10     4      15     .01
BBTYPE1     1      10     12     100    .20
```

The lower threshold will be met often, and only the low mortality rate will be applied. In the cases in which the higher threshold is reached, the model will apply the higher mortality (20 percent) to all ponderosa pine greater than the larger diameter limit (12 inches [12 cm]) and the lower, background mortality (1 percent) to all trees between 4 inches [4 cm] and 12 inches [12 cm].

Bark beetles remain potentially active in all cycles after they have been switched on. Field 6 of each **BBTYPE*n*** keyword allows the user to stop *all* bark beetles of a certain type (i.e., type 1, 2, 3, or 4). If the user wants any of the varieties of bark beetle to remain on, they must be re-entered following the deactivation. When the bark beetles of one type (type 3 in the example below) are deactivated, any other bark beetle types are unaffected by the deactivation.

Example: Deactivating a bark beetle

Suppose that Type 3 bark beetle (such as fir engraver) was to be active on white fir (species code 4) in all cycles (1-10), and that there was a different Type 3 bark beetle (such as mountain pine beetle) attacking lodgepole pine (code 7) in cycle 5 only. The keywords to do this would be:

```
BBTYPE3     1      4
BBTYPE3     5      7      _      _      _      1      _
BBTYPE3     6      4
```

The '1' in the sixth field of the second bark beetle type turns off all Type 3 bark beetles at the end of the cycle. Since the user wishes the bark beetle that attacks white fir (species code 4) to remain active, the keyword must be re-entered for the next cycle.

Example: Deactivating a bark beetle type (2)

As an example, combine the keywords from the two previous bark beetle examples, but change the last keyword from starting again in cycle 6 to starting again in cycle 7:

BBTYPE1	1	10	4	15	.01		
BBTYPE1	1	10	12	100	.20		
BBTYPE3	1	4					
BBTYPE3	5	7	_	_	_	1	_
BBTYPE3	7	4					

Now look at the bark beetles that are *potentially* active in each cycle from cycle 1 to cycle 8:

Cycle 1:	type1a, type1b, type3a
Cycle 2:	type1a, type1b, type3a
Cycle 3:	type1a, type1b, type3a
Cycle 4:	type1a, type1b, type3a
Cycle 5:	type1a, type1b, type3a, type 3b
Cycle 6:	type1a, type1b
Cycle 7:	type1a, type1b, type3a
Cycle 8:	type1a, type1b, type3a

Notice that turning off the type 3 bark beetle after cycle 5 deactivated *both* type 3 bark beetles but did not affect the type 1 bark beetles.

Type 2 bark beetles are attracted to stands in which windthrow has occurred. Therefore, although bark beetle Type 2 has the same flexibility as the other bark beetle types, it can occur only if windthrow (activated using the keyword **WINDTHR**) has occurred in the same cycle. Its threshold and mortality rates are also totally defined by the number of windthrown trees, so if no windthrow occurs, the bark beetles will not be active. If bark beetle Type 2 (**BBTYPE2**) is in the keyword file and windthrow (**WINDTHR**) is not, a warning message will appear in the main output file, reminding users that bark beetle Type 2 cannot occur.

All thresholds in the model are calculated on the basis of the trees/acre or trees/ha density of eligible trees. The density will change depending on whether it is calculated on the basis of the entire stand, on the area outside root disease centers, or on the area within root disease centers. In general, the area outside of infected centers will have the highest density while the areas inside of centers will have a much lower density because of the increased mortality. The density of the entire stand will be an average of the values. Since the threshold for Type 3 and 4 bark beetles is based on infected trees only, the density is calculated from the area in root disease, while for Type 2 bark beetles, it is based on the total area of the stand. However, for bark beetle Type 1, the threshold may be based on any number of criteria. Users can choose to calculate density by trees/acre or by Reineke's stand density index (SDI). Density can also be calculated on the basis of all trees in the stand (default) or only those that are outside root disease centers, and only living trees (default) or all those alive within the last 2 years. The method of calculating stand density may be changed using the keyword **DNSCALC**.

DNSCALC   Type of density calculation for type 1 bark beetles

Field	Description	Default Imp	Met
1	Method for calculating outbreak density threshold (0=trees/acre [or /ha], 1=SDI)	0	0
2	Areas to include in density calculation (0=entire stand, 1=area outside centers)	0	0
3	Trees to include in density calculation (0=currently living trees, 1=all trees alive in last 2 years).	0	0
4	Slope of the SDI function (used if SDI method is chosen in field 1).	-1.605	-1.561
5-7	Not used.		

Imp. = imperial units, Met. = metric units

Example: Changing the type of density calculation

Suppose a user wanted to have density calculated on the basis of the SDI (field 1) of all living trees (field 3) outside centers (field 2), then the keyword would be:

DNSCALC   1   1   0   _

Note that this keyword affects only the **BBTYPE1** keyword.

4.2 Windthrow

The windthrow submodel simulates a major blowdown event. The model will affect all dominant and codominant trees (trees in the largest 20 percent of the basal area distribution are eligible), whether or not they are infected. Users specify the proportion of these trees that would be windthrown, and the minimum number of eligible trees for the event to occur, using the keyword **WINDTHR**.

WINDTHR   Simulate a blowdown event.

Field	Description	Default
1	Earliest date a windthrow event can occur (calendar year or cycle number).	
2	Proportion of dominant and codominant trees to be windthrown.	0.0
3	Minimum number of eligible tree/acre [trees/ha] necessary for event to occur.	0.0
4-7	Not used.	

If too few trees would be windthrown when the model calculates the proportion of dominant and codominant trees, then the event will not occur, and the submodel will check eligibility again in the following year. Once a windthrow event occurs, the submodel will be turned off.

5.0 Changing Default Conditions

Many of the default parameter values used in the model can be changed by the user. The default values have been chosen, however, by a group of experts to be the best (or most general) representation of what is currently known about each of the root diseases, and should meet the needs of most users. Some of the keywords are considered "advanced" and should be used only by those who are experienced users of the model or who have experience with root disease. The advanced keywords are identified in each section, and are primarily those which define the infection and inoculum parameters. Selected output files (see Section 7) are also only useful for users who want detailed information about particular sections of the model.

It is important to note, before going further, that the processes within the model are highly interconnected. While a single keyword may control one aspect of the model, changing that keyword may have implications in other parts of the model. *Table 5.1* shows some of the key processes in the model and some of the keywords that affect them. The Detailed Model Description has additional details on the direct effects of changing some of the parameters.

5.1 Spread of Infection

Infection can spread through a stand in a variety of ways. It spreads from infected trees and stumps to uninfected trees, both inside and outside of root disease centers. For Annosus root disease, after a harvest the newly formed stumps can be infected by airborne Annosus spores which may create new centers. The keywords governing each of these means of infection are described below.

5.1.1 Infection Within Centers (Advanced)

Within centers, root disease spreads from infected trees (live and dead) and stumps to live healthy trees when the roots of uninfected trees contact infected roots. Details of this process are given in the model description. The calculation of root-to-root infection potentially involves a Monte Carlo simulation in which the infection probability for each tree is calculated multiple times. The keyword **INFSIMS** tells the model the number of times to perform the simulation (field 1), and allows the user to request detailed output about simulation results (field 2; see Section 8 for details on the output). The Monte Carlo simulation can be performed up to 50 times for each root disease type, but each additional simulation noticeably increases the model's simulation time.

Table 5.1 — Summary of the main processes and keywords controlling or affecting them. The 'X' indicates keywords that control the process directly. The 'x' indicates keywords which control the process indirectly, by affecting one of the other processes directly. For example, TTDMULT (the time-to-death multiplier) directly controls the individual tree dynamics. Since the individual tree dynamics affect new infections and center spread rate, the keyword has an indirect effect on these processes.

Keyword	Individual tree dynamics (live)	Mortality	Inoculum dynamics (dead)	New infection	Center spread	New centers
INFMULT				X	x	
TTDMULT (and RRMINK)	X	X		x	x	
INFKILL	X	X		x	x	
INFCOLO	X		X	x	x	
INOCLIFE			X	x	x	
SDIRMULT			X	X	x	
SPREAD (and TDISTN)					X	
RRJUMP					X	
INFSIMS				X		
SPORE						X

This option is for advanced users only, and is useful only at low inoculum densities. At high infection levels the results from the Monte Carlo simulations usually show little variation and thus, the benefit is not worth the increased overall simulation time.

INFSIMS   Specify the number of times to do the inside center Monte Carlo simulation, and request output of the results. *(advanced)*

Field	Description	Default
1	Number of times to perform the inside center Monte Carlo simulation.	1
2	Print an output file? (Any value greater than 0 means yes.)	0
3	Output file number.	25
4-7	Not used	

5.1.2 Spread of Centers

The edge of a center is defined to be the outermost limit of a "patch" of infection. Thus, this edge is capable of infecting uninfected trees outside the center and thereby causing the center to expand. The model assumes that all centers can spread, and that they spread outwards in all directions at an equal rate (i.e., the circle remains a circle). By default, the rate at which centers expand is a dynamic rate which is calculated on the basis of the size, species, and density of trees outside of centers. It can change in each cycle. The model determines the dynamic spread rate using a Monte Carlo simulation approach in which the spread rate is calculated up to 50 times (see the Model Description for details, Chapter 4). Alternatively, users can specify a static spread rate for each disease type which is applied to all centers of the appropriate type in all years or until the user changes the rate.

SPREAD   Specify type and parameters for the center spread rate calculations.

Field	Description	Default Imp	Met
1	First year for the parameters to take effect (cycle number or year).	1	1
2	Type of spread model (0=static spread, 1=dynamic, applying different spread rates to each center, 2=dynamic, applying the average spread rates to each center).	1	1
3	Fixed annual spread rate for the centers (used if field 2 is 0) in feet [meters]. (If both S- and P-type *Annosus* are being simulated, this is for P-type *Annosus*.)	1.0	0.3
4	Fixed annual spread rate for S-type centers (used if field 2 is 0, and both S- and P-type *Annosus* are being simulated) in feet [meters].	1.0	0.3
5	Number of times to simulate the Monte Carlo calculations (used if field 2 is 1 or 2).	10	10
6	Disease type (0 = P- and S-type *Annosus*, 1=P-type *Annosus*, 2= S-type *Annosus*, 3 = *Armillaria*, 4 = *Phellinus*).	1	1
7			

Imp. = imperial units, Met. = metric units

The **SPREAD** keyword allows users to control the type of spread rate and the number of times to do the Monte Carlo simulation. Three types of spread rates exist (numbered according to their value in field 2 of the keyword) and are pictured and described in *figure 5.1*.
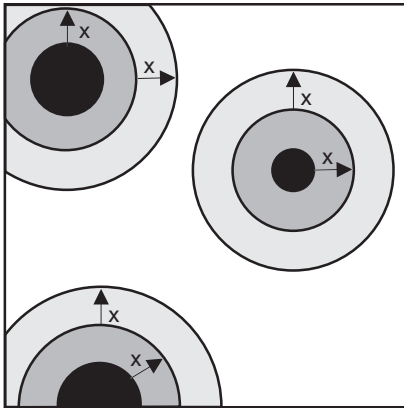
0. **Static spread rate.**

   This enlarges the radius of each center by a constant, user-defined amount (*fig. 5.1a*)
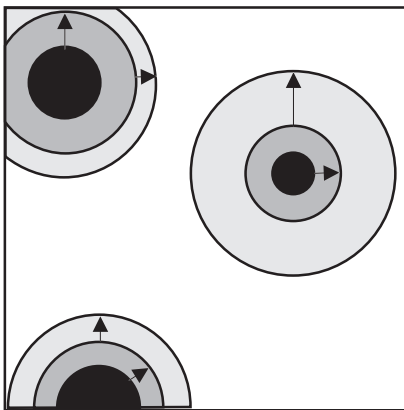
1. **Dynamic spread rate, applying different spread rates to each center.**

   This takes the results from the Monte Carlo simulation and applies different results to different centers. Thus, the radii of different centers may enlarge at different rates from each other, and the rates may change each cycle (*fig. 5.1b*).
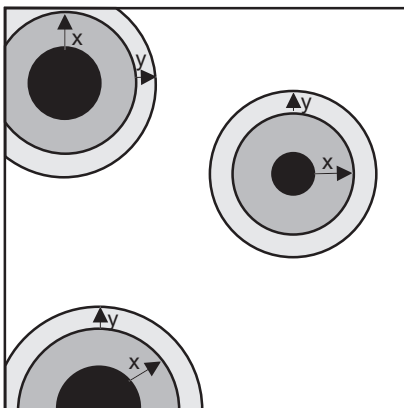
2. **Dynamic spread rate, applying the average spread rate to each center.**

   This takes the average of the results from the Monte Carlo simulation and applies this average to each center. Thus, the radii of each center will enlarge at the same rate, but these rates may still change each cycle (*fig. 5.1c*).

Figure 5.1 — Different types of spread rates. Within each diagram, two cycles of spread rates have been applied. (A) Static spread rate; (B) Dynamic spread rate, applying different spread rates to each center; and (C) Dynamic spread rate, applying the average spread rate to each center.

By default the model will apply the individual spread rates which result from each simulation to different centers. This assumption has the consequence that some centers may stop growing if any of the Monte Carlo simulation results indicate a zero spread rate which can occur if no infection occurs along the center boundary. It also may allow some centers to grow much faster than others, because a range of the possible spread rates are applied. See the model description for details on how these individual spread rates are calculated and applied.

Centers continue to spread and to be counted as individual centers even when they overlap with other centers. The model does, however, account for the area within centers appropriately. See the model description for details.

As mentioned above, the dynamic spread rate of centers is calculated on the basis of simulating the spread of root disease through the uninfected part of the stand. By default, the Monte Carlo simulation is done 10 times, and the results are applied to the various centers, either as the average of the simulations or as individual spread rates (see the model description for more details). The **SPREAD** keyword allows users to change the number of Monte Carlo simulations which are done.

Example: Applying a more representative spread rate

Suppose that the user wanted the spread rate to vary, but wanted the applied spread rate to be a good representation of the stand conditions. The user might then decide to apply only the average spread rate to all centers (a 2 in field 2) in all years (a 1 in field 1 to indicate that this type of spread rate starts in the first year) and, to make the average more representative, to ask the model to do more Monte Carlo simulations (field 5):

```
SPREAD        1        2        _        _        40
```

The spread rate parameters may change in any cycle. Users may enter the keyword as many times as desired, specifying the year that the change will take effect and the new values (see the example below). The type of spread may be changed or the static spread rate may change.

Example: Changing the static spread rate parameters in different cycles

Suppose the centers in a stand grew at a static rate (the 0 in field 2) which was 1 ft/year [1 m/year] (field 3) for the first 30 years (3 cycles, starting in cycle 1, field 1) and thereafter was only 0.25 ft/ year [0.25 m/year] (field 3). The **SPREAD** keyword would be used twice, once to tell the model to start using the new parameters in the first cycle (field 1), and the second time to ask the model to change to the new parameters in cycle 4 (or 30 years later; field 1):

```
SPREAD        1        0        1.0
SPREAD        4        0        0.25
```

Example: Changing the spread rate type in different cycles

Suppose the spread rates for the centers in a stand were known to be constant (at 0.75 ft/year [0.75 m/year]) for the first 20 years of the simulation. Thereafter (cycle 3 and later, field 1), the spread rates are unknown, and the user wishes the model to calculate them, and to apply a range of spread rates to the different centers (indicated by the 1 in field 2).

```
SPREAD        1        0        0.75
SPREAD        3        1
```

Note for Annosus root disease

Note that centers of both *Annosus* disease types (S and P) must spread using the same method. The model cannot have centers of one disease type spreading using a static spread rate and centers of the other disease type using a dynamic spread rate. The model also cannot apply the average spread rate to one type of center but variable spread rates to the other type of center.

Altering the spatial distribution of trees

Spread rates are determined from the density and placement of trees outside centers. The user has some control over the spatial arrangement of trees outside centers using the keyword **TDISTN**. This keyword tells the model whether trees are regularly spaced (as in a plantation) or randomly spaced (default). This keyword can be used multiple times to change the distribution over time to represent the change from a natural forest to regularly spaced conditions, or to represent the ingrowth of trees in a plantation.

TDISTN	Spacing pattern of trees in the stand (used in center spread calculations only).	
Field	**Description**	**Default**
1	Year in which the spatial distribution will change from that specified in field 2 to the other type. Value must be a calendar year (not a cycle number)	
2	**Current** tree spatial distribution (0=random, 1=gridded).	0
3	Standard deviation about the mean distance between trees in a gridded distribution.	1.0
4-7	Not used	

Center spread after a clear-cut

After a stand is thinned or clear-cut, centers may expand and encompass neighboring trees (*fig. 5.2*). Biologically, this occurs because the root systems of the trees immediately surrounding the centers are likely to be in contact with some inoculum inside centers. Once trees have been cut, they can no longer defend themselves and the infection is able to spread rapidly through a relatively healthy root system, leading to an increase in center area. This is not common in all root diseases, and it does *not* occur by default for Annosus root disease or *Phellinus weirii*. It *does* occur by default for Armillaria root disease. Users may request this option using the keyword **RRJUMP**. When the keyword is used, the model assumes that the center will expand after harvest by some multiple (as defined in the keyword) of the average root diameter in the stand.
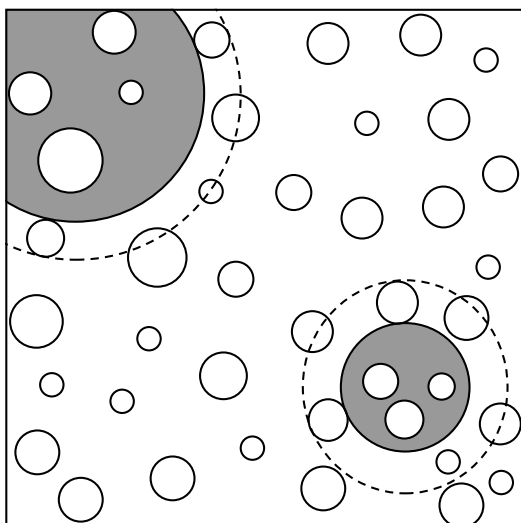
Figure 5.2 — The "jump" in center size after a clear-cut. The original centers are the large shaded areas and root systems of trees are the smaller, open circles. The dotted line shows the new edge of the center, had a cut occurred.

RRJUMP	Set the "jump" in center radius after a harvest.	
Field	**Description**	**Default**
1	Average root diameter multiplier for P-type *Annosus*	0
2	Average root diameter multiplier for the S-type *Annosus*	0
3	Average root diameter multiplier for *Armillaria*	1
4	Average root diameter multiplier for *Phellinus*	0
5-7	Not used.	

Example: Setting the 'jump' in center size after a clear-cut

Suppose after a stand entry, P-type Annosus root disease centers tended to spread out through the ring of trees immediately surrounding the center (i.e., one root system diameter, field 1), while S-type centers only expanded through half of the root system (field 2). The keyword would be:

RRJUMP   1   0.5

5.2 New Centers: Annosus Root Disease Only

New centers can be generated only for Annosus root disease. Stands with Armillaria root disease and *Phellinus weirii* will always have the same number of centers. However, root disease dynamics will continue to reflect the fact that the root disease is not evenly distributed throughout the stand.

New centers can originate only from spore infection on large stumps created during a stand entry in a previous cycle. Stumps from uninfected trees inside and outside of centers may be infected. Newly infected stumps inside of existing centers will not create new centers but if the infected stumps are outside of existing centers, they may create a small new center. Trees in centers created by spore-infected stumps take longer to decay than other stumps, and are less infectious for the first FVS-cycle after creation. Spore infection will *not* occur on stumps created from a windthrow event (**WINDTHR** keyword). Using the keyword **SPORE**, users can control the minimum size stump that can be spore-infected (field 3), the proportion of these stumps that can be infected (field 2), and the change in decay and infection rates (fields 4 and 5). Each of these parameters can be changed for either disease type and in any cycle.

SPORE	Change spore infection parameters (size of stumps, center characteristics).		
Field	**Description**	**Default**	
		Imp	**Met**
1	First year for parameters to take effect (cycle number or calendar year).	1	1
2	Proportion of newly cut stumps to be infected by spores. A '0' in this field will turn off the spore model.	0.1	0.1
3	Minimum stump diameter for forming new root disease centers by spore infection (inches or cm).	14	35.6
4	Multiplier for time-to-death for trees in spore-initiated centers.	3	3
5	Multiplier for the probability of infection transmission, given root overlap, for spore-initiated centers.	0.5	0.5
6	Disease code (1=P-type, 2=S-type Annosus root disease).	1	1
7	Not used.		

Imp. = imperial units, Met. = metric units

Example: Changing the spore-infection parameters for Annosus Root Disease

Suppose that, starting in the first cycle (field1) after a stand entry about 5 percent (field 2) of the S-type trees (field 6) above 12 inches [12 cm] in diameter (field 3) were infected (and could potentially create centers). When new trees are infected in the new centers, their time-to-death is the same as if they had been infected in older centers (field 4). Also, suppose that no P-type spore infection occurred (fields 2 and 6). The keywords would read:

```
SPORE        1        0.05    12      1        _       2
SPORE        1        0.0     _       _        _       1
```

Spore infection occurs by default in the model. It can be turned off by setting the rate of infection to zero for each disease type (as in the second keyword in the above example). Note that "SPORE" will show up as "DONE" in the activity scheduler in the main output file in the cycle when the parameter values are changed, to confirm that the change occurred.

5.3 Infection Parameters (Advanced)

All parameters that determine the course of infection in a live tree can be changed by the user (*fig. 5.3*). The probability of infection given an instance of root overlap can be changed using the keyword **INFMULT** to specify the species and the new probability of infection. Once a tree is infected, the disease spreads through its root system at a rate calculated from the time between root infection and death (changed using the keyword **TTDMULT**), and from the proportion of the root radius that is infected when death occurs (modified using the keyword **INFKILL**). After the tree dies, the root disease immediately spreads through the tree's root system to some final level. The final proportion of the root radius infected is defined by the keyword **INFCOLO**. An example showing the pattern of infection using actual default values is given in *figure 5.4*.
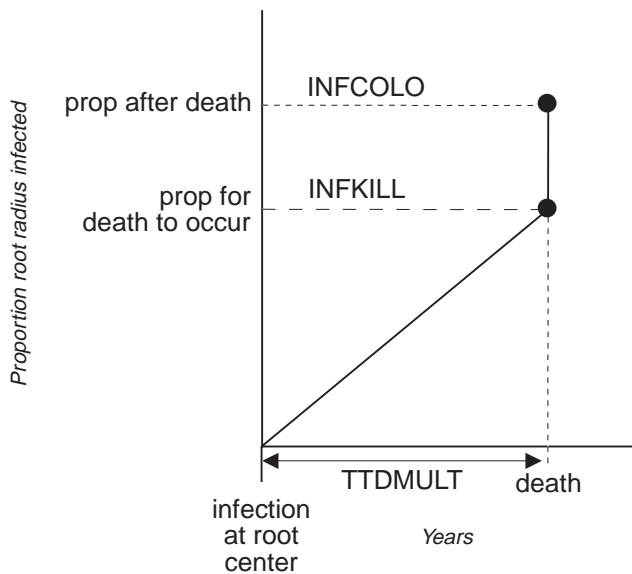
Figure 5.3 — **Pattern of inoculum spread through a healthy root system with parameters under user control labelled with the keyword names.**
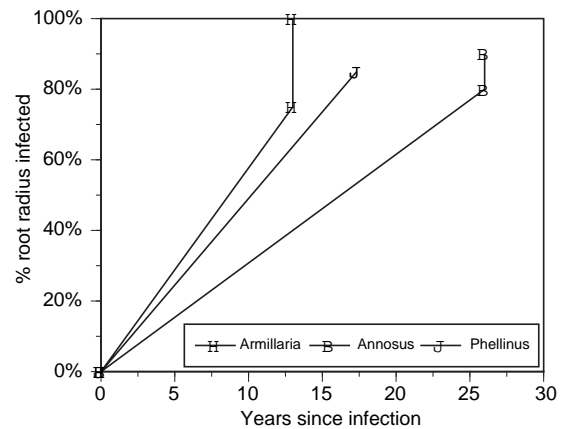
Figure 5.4 — **Default relationships for the progress of infection in each of the root disease types. These curves show the infection in a 15-inch [38 cm] DBH grand fir. On each line the first point is the time of death and the second is the percent of the radius that is infected after death. Differences between the curves represent difference in the default values for time to death, and proportion infected at death and after death.**

INFMULT Probability of infection.

Field	Description
1	Date (calendar year) in which parameters will be modified.
2	Disease type (1=P-type *Annosus*, 2=S-type *Annosus* , 3=*Armillaria*, 4=*Phellinus*). If this field is blank, the model will use the disease type set by the keyword **RRTYPE**.
3	Tree species to be modified (number or character code). A '0' or 'ALL' here indicates all species, and requires a supplemental record.
4	Probability of infection for the species given in field 3. If field 3 indicates all species, this field will be ignored. Defaults are given in Appendix 1.
5-7	Not used
Suppl. Record	11 values starting in column 1, each with a field width of five places (including the decimal). All values must be entered. The supplemental record is only required if field 3 is 0 or 'ALL'.

TTDMULT   Multiplier for the time from infection at the tree's midpoint to death.

Field	Description
1	Date (calendar year) in which parameters will be modified.
2	Disease type (1=P-type *Annosus*, 2=S-type *Annosus*, 3= *Armillaria*, 4= *Phellinus*). If this field is blank, the model will use the disease type set by the keyword **RRTYPE**.
3	Tree species to be modified (number or character code). A '0' or 'ALL' here indicates all species, and requires a supplemental record.
4	Time-to-death multiplier. If field 3 indicates all species, this field will be ignored. Defaults are given in Appendix 1.
5-7	Not used
Suppl. Record	11 values starting in column 1, each with a field width of five places (including the decimal). All values must be entered. The supplemental record is only required if field 3 is 0 or 'ALL'.

INFKILL   Proportion of the root system infected *at* death.

Field	Description
1	Disease type (1=P-type *Annosus*, 2=S-type *Annosus,* 3= *Armillaria*, 4= *Phellinus*). If this field is blank, the model will use the disease type set by the keyword **RRTYPE**.
2	Tree species to be modified (number or character code). A '0' or 'ALL' here indicates all species, and requires a supplemental record.
3	Proportion of the root system infected **at** death for the species given in field 2. If field 2 indicates all species, this field will be ignored. Defaults are given in Appendix 1.
4-7	Not used
Suppl. Record	11 values starting in column 1, each with a field width of five places (including the decimal). All values must be entered. The supplemental record is only required if field 3 is 0 or 'ALL'.

INFCOLO Proportion of the root system infected *after* death.

Field	Description
1	Tree species to be modified (number or character code). A '0' or 'ALL' here indicates all species, and requires a supplemental record.
2	Proportion of the root system infected **after** death for the species given in field 1. If field 1 indicates all species, this field will be ignored. Defaults are given in Appendix 1.
3	Disease type (1=P-type *Annosus*, 2=S-type *Annosus*, 3=*Armillaria*, 4=*Phellinus*). If this field is blank, the model will use the disease type set by the keyword **RRTYPE**.
4-7	Not used
Suppl. Record	11 values starting in column 1, each with a field width of five places (including the decimal). All values must be entered. The supplemental record is only required if field 3 is 0 or 'ALL'.

In the keywords in the following example, notice that **INFMULT** and **TTDMULT** can differ between cycles. The '0' in the first field indicates that these values should be used from the beginning of the simulation. Also notice that the time to death is specified as a multiplier relative to a defined curve (see the model description) which cannot be changed by the user.

Example: Changing root disease parameters

Suppose that a pathologist in Northern Idaho has local information for grand fir (species code 4) that deviates from the default parameter values and wants to explore these alternative parameter values. The pathologist believes that grand fir has only a 40 percent probability of being infected (**INFMULT**, field 4), that it will take twice as long to die as defined by the reference curve (**TTDMULT**, field 4), and that the tree will die when the root radius is 75 percent infected (**INFKILL**, field 3). After death, the root disease will increase to 85 percent of the root radius (**INFCOLO**, field 2). The series of keywords which will perform these changes is:

```
INFMULT     0        _      4      0.4
TTDMULT     0        _      4      2.0
INFKILL     _        4      .75
INFCOLO     4        .85
```

The effect of these changes can be seen in *figure 5.5*.

The relationship between the time from infection to death may not be linear with respect to DBH. The keyword **RRMINK** is a way of allowing users to introduce some non-linearity. Users can specify a limit below which the time-from-infection-to-death multiplier is not effective.
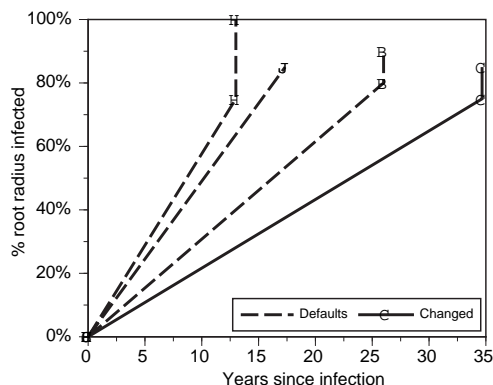
Figure 5.5 — Default and changed values for the increase in infection in a 15-inch [38 cm] DBH grand fir. On both lines the first point is the time of death and the second is the percent of the radius that is infected after death. Notice that since the changed values, based on the keywords, are independent of the root disease species, the new values result in the same curve, no matter which disease is simulated.

RRMINK	Time-to-death below which modifiers in TTDMULT have no effect.	
Field	**Description**	**Default**
I	Time-to-death below which the modifiers specified by the **TTDMULT** keyword do not influence mortality and infection dynamics for trees infected with P-type *Annosus*.	0
2	Time-to-death below which the modifiers specified by the **TTDMULT** keyword do not influence mortality and infection dynamics for trees infected with S-type *Annosus*.	0
3	Time-to-death below which the modifiers specified by the **TTDMULT** keyword do not influence mortality and infection dynamics for trees infected with *Armillaria*.	0
4	Time-to-death below which the modifiers specified by the **TTDMULT** keyword do not influence mortality and infection dynamics for trees infected with *Phellinus*.	0
5-7	Not used.	

Example: Non-linearity in the time to death function

Suppose that an infected ponderosa pine (code 10) will live 25 percent as long as the reference (**TTDMULT**, field 4), but that this multiplier will not apply to the first 20 years of infection (because up to that point the predicted time to death is the same), but after that the multiplier will be added to reduce the remaining time to death. This is done by specifying 20 years in field 1 of the **RRMINK** keyword.

```
TTDMULT      0          _         10        .25
RRMINK       20
```

   To interpret this, for example, suppose that the reference curve states that the tree would live for 40 years after infection. The tree with the above parameters would then live for 20 years (as given in **RRMINK**) plus 20 * 0.25 years (the remaining 20 years of the 40 total, times the 25 percent specified by the **TTDMULT** keyword), to give a total of 25 years from infection to death. Had the **RRMINK** keyword not been present (but the **TTDMULT** keyword was present), the tree would have lived for 40 * 0.25 = 10 years, because the 25 percent multiplier would act on the entire number of years to death.

   The **RRMINK** keyword can cause the tree to live either shorter or longer than it would otherwise, depending on whether the multiplier is greater than or less than 1.0. The effect of **RRMINK** is shown graphically in *figure* 5.6.
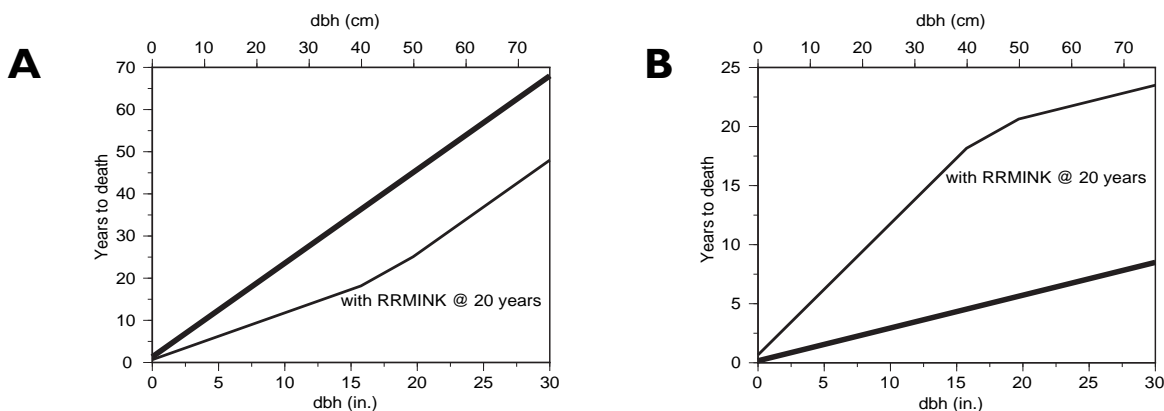
Figure 5.6 — Effect of the RRMINK keyword. These graphs are relative to the base curve for time to death. (A) is using a multiplier of 2, and (B) is using a multiplier of 0.25. In each graph, the dark line is without the keyword, and the light line assumes that RRMINK was set to 20 years. Note that the values on the top of the graph show the DBH in *centimeters* and the values on the bottom of the graph show the DBH in *inches*.

5.4 Inoculum Parameters (Advanced)

The amount of inoculum in the stand is measured by the infected root radii of dead trees and stumps, and inoculum reduction is calculated by decreasing the infected root radii. The model assumes that inoculum decays at a constant rate. When the remaining root radius has decreased such that mainly the stump itself is left, the radius is held constant for a number of years. Although decay continues, the radius of the remaining inoculum is not altered until decay is complete. The keyword **INOCLIFE** allows the user to control various aspects of the reduction in infected root radius (*fig. 5.7*).
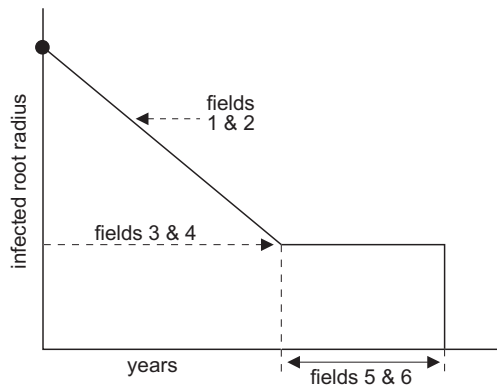
Figure 5.7 — Default decay pattern of infected root radii, showing the aspects that can be controlled by the keyword INOCLIFE.

INOCLIFE   **Set the parameters which describe the decay of inoculum (*advanced*).**

Field	Description	Root Disease	Default Imp	Default Met
1	Slope of the initial decay function as a function of *infected root radius* (feet decay/year/feet root radius [m/year/m]). If the slope is positive, trees with a larger root radius will decay more slowly than trees with a smaller root radius.	*Annosus* *Armillaria* *Phellinus*	0.02212 0.0 0.0	0.02212 0.0 0.0
2	Intercept of the initial decay function (feet/year or meters/year). This is the decay rate at which a tree with almost no infection would decay.	*Annosus* *Armillaria* *Phellinus*	1.2032 1.0 1.0	0.3667 0.3048 0.3048
3	Slope of the function describing the relationship between DBH (inches or cm) and amount of root radius (feet or meters) remaining when the root radius no longer decreases.	*Annosus* *Armillaria* *Phellinus*	0.1667 0.297 0.2377	0.02 0.0356 0.0285
4	Intercept of this relationship (feet or meters)	All	0.0	0.0
5	Slope of the function describing the relationship between DBH and the length of time that the radius will not change in size (years/inch or years/cm).	*Annosus* *Arm*. and *Phel*. ≤12 in. >12 in.	2.0 1.1111 0.5556	0.79 0.4374 0.2187
6	Intercept of this relationship (years).	*Annosus* *Arm*. and *Phel*. ≤12 in. >12 in.	0.0 0.0 6.6667	0.0 0.0 6.6667
7	Disease Type		1 or type set in RRTYPE	1 or type set in RRTYPE

Imp. = imperial units, Met. = metric units.

The number of years that a stump's root radius is decreasing is determined by the size of the infected root radius and by the DBH of the dead tree, so that a large stump will retain some effective inoculum longer than a small stump. Users can control the decay rate of the inoculum, the infected root radius at which inoculum decay seems to stop, and the number of years at which the decline of the radius of infection is negligible (*fig. 5.8*). The overall decay pattern is shown in *figure 5.9* while the length of time needed for the total decay of the inoculum in stumps of different sizes is shown in *figure 5.10*.

A

Decay rate of inoculum

B

Root radius at which to stop decline

C

Number of years to stop decline
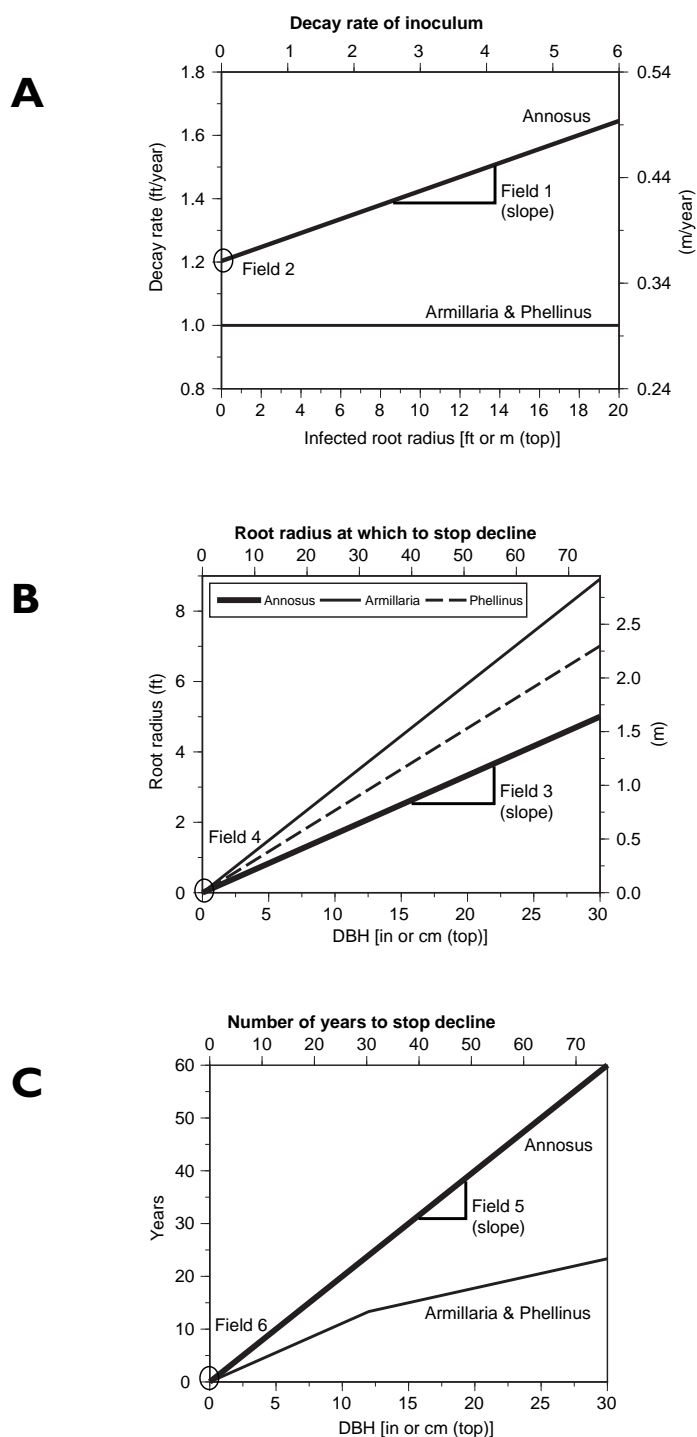
Figure 5.8 — Relationships controlled by the keyword INOCLIFE: (A) decay rate of inoculum; (B) root radius at which to stop decline; (C) number of years to stop decline. The default relationships for each of the root disease types are shown. Notice that the values are given in imperial units on the left y-axis and the bottom x-axis; metric units are shown on the right y-axis and the top x-axis.

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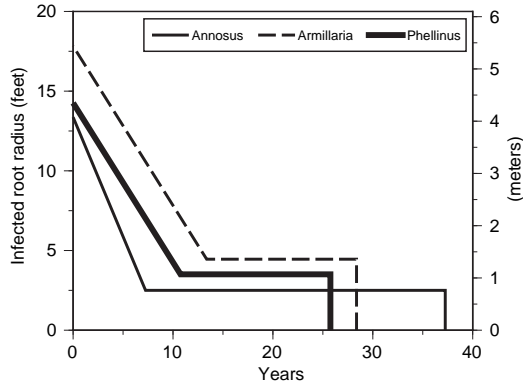
Figure 5.9 — The resulting decay pattern for each disease type. The example is for a 15-inch [38-cm] diameter dead ponderosa pine tree. Notice that each disease type has an initially different infected root radius. This is because each disease type infects a different proportion of the tree's root system after death. Notice that the values are given in imperial units on the left y-axis and metric units on the right y-axis.
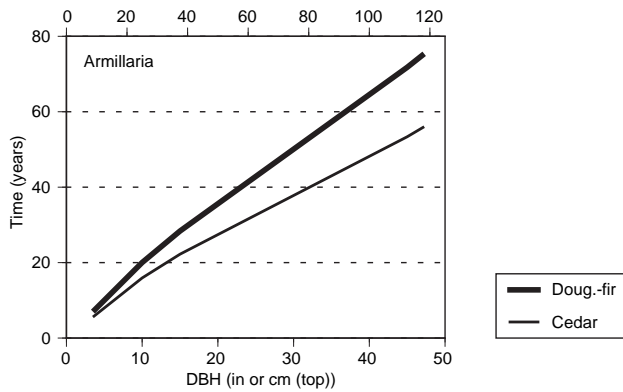
Figure 5.10 — The time required for the inoculum in different sized stumps to decay completely. In each graph, the thick line is Douglas-fir and the thin line is western red cedar. Differences between species occur primarily because of differences in the amount of root infected (based on root radius and the proportion of the radius infected at death). Imperial units are on the bottom x-axis and metric units on the top x-axis.
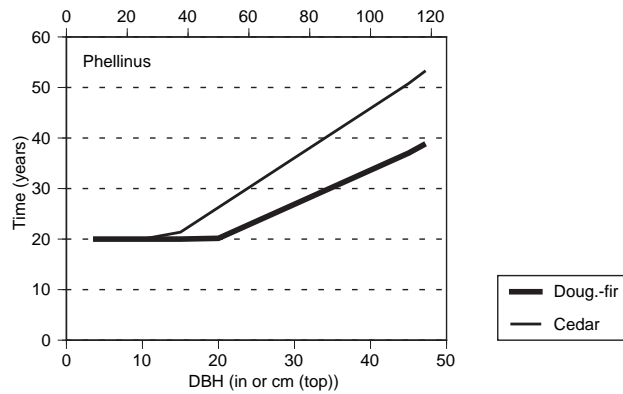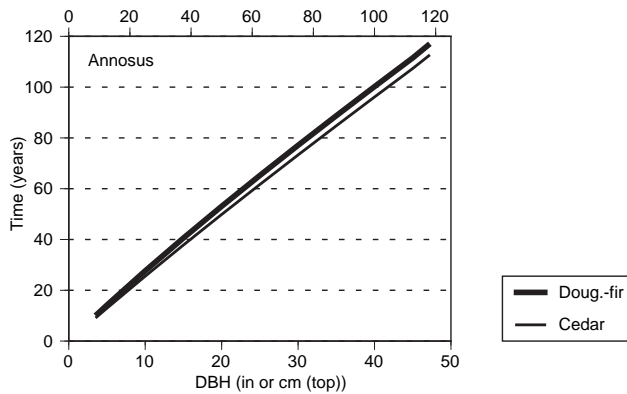
This keyword is very flexible and allows the user to enter a wide variety of decay patterns. The first example below shows how to change inoculum decay relationships without changing the *pattern* of the decay. Alternatively, the user may choose to simulate a linear decay of inoculum without a change in decay rate (see the second example below). Notice that Armillaria root disease and *Phellinus weirii* have default rates that depend on whether the tree is greater than or less than 12 inches [30.5 cm] DBH. When these values are changed in **INOCLIFE**, the same value is applied to both size classes (*fig. 5.11*).

A
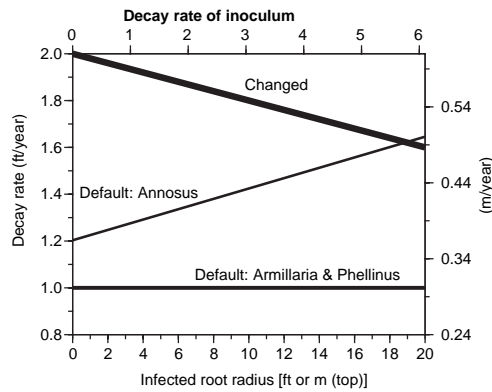
Figure 5.11 — Default and changed relationships in the inoculum decay example. The default relationships are those given in *figure 5.8*, while the changed relationships are those in the example above. Imperial units are used on the left y-axis and the bottom x-axis while metric units are used on the right y-axis (except in the third graph in which the units do not change) and the top x-axis.

B
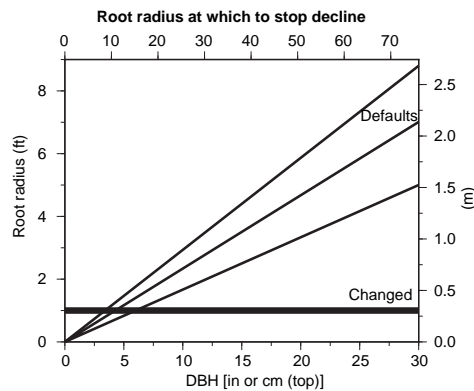
C
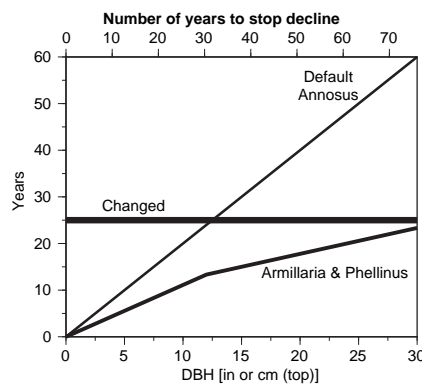
Example:　Changing inoculum decay

Suppose a user decides that the infected portion of a small stump decays faster than that of a large stump (negative slope in field 1) and that all root radii (indicated by a 0 in fields 3 and 5) stop declining for 25 years (field 6) when the radius reaches one foot (field 4). The keyword would be:

INOCLIFE　　　-0.02　　2.0　　　0.0　　　1.0　　　0　　　25

If the same relationship were to be derived in metric units, the keyword would become:

INOCLIFE　　　-0.02　　0.61　　0.0　　　0.3　　　0　　　25

Figure 5.11 shows the new relationships for each component.　*Figure 5.12* shows the resulting pattern of the decay.
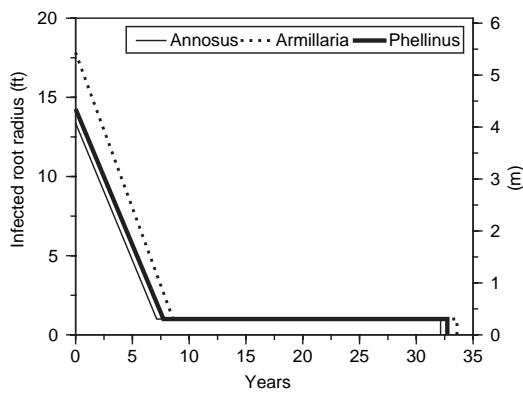
Figure 5.12 — Changed inoculum decay.　This example is for a 15-inch [38-cm] diameter ponderosa pine stump.　The default decay patterns are shown in *figure 5.9.* **The scale on the left is in imperial units and that on the right is in metric units.　The results are slightly different for each disease type because they each start with a different proportion of their root radius infected.**

Example: Setting a single inoculum decay rate

Suppose that a pathologist decided that the decay rate of the inoculum did not change, i.e., the pathologist eliminates the final part of the decay line. This can be done by setting fields 3-6 to zero (i.e., telling the model to stop radius decline at 0 feet for 0 years for all sizes of trees).

INOCLIFE　　　_　　　_　　　0.0　　　0.0　　　0.0　　　0

Shown in *figure 5.13* is the resulting decay curve as it would affect each root disease type.
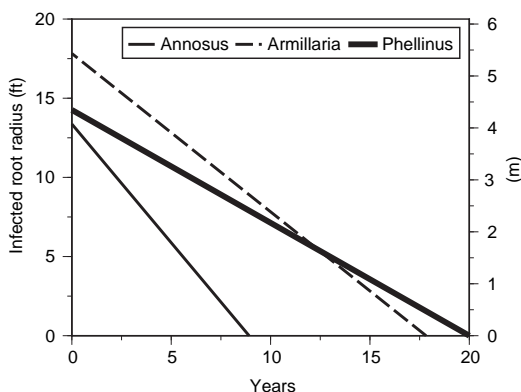
Figure 5.13 — Inoculum decay with a single decay rate, for the changed parameters.　This example is for a 15-inch [38-cm] diameter ponderosa pine stump.　The default pattern is shown in *figure 5.9.* **Note that** *Phellinus* **has a minimum lifespan of 20 years, so the decay rate is lower than specified in the keyword.　Metric units are given on the right y-axis and imperial units are on the left y-axis.**

It is important to realize that all values given in the keyword **INOCLIFE** assume that the tree is a resinous species (see Model Description, Chapter 4, *table 2.1*) and that there is no minimum lifespan of inoculum. If the tree is non-resinous, the decay rate will be increased slightly (*fig. 5.14*), while if there is a minimum lifespan, the decay rate will be decreased.

The user has control over the minimum lifespan of inoculum by using the keyword **INOCSPAN** to specify the desired minimum number of years for inoculum to be present. This minimum number of years will slow the initial rate of decay, but not the number of years at which the size of the root radius remains constant (*fig. 5.15*).
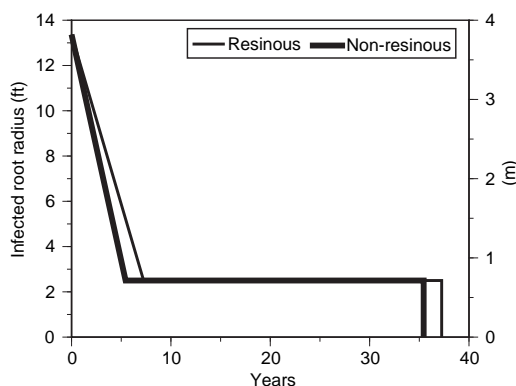
Figure 5.14 — Comparison between the decay rates of a resinous and non-resinous tree. Notice the increased decay rate for the non-resinous tree. This example shows the pattern for Annosus root disease only, but the relationship is similar for the other root disease types. Metric units are given on the right y-axis and imperial units are on the left y-axis.
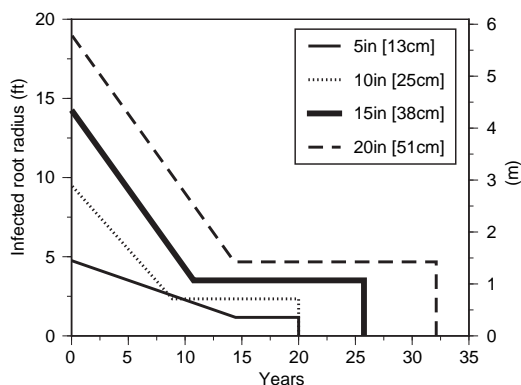
Figure 5.15 — The effect of minimum lifespan on the decay pattern in *Phellinus*-infected stumps. The minimum lifespan is 20 years. Smaller stumps would normally decay in a shorter amount of time, but since they must live at least 20 years, their initial rate of decay is slower. Metric units are given on the right y-axis and imperial units are on the left y-axis.

INOCSPAN　　Set the minimum number of years each type of inoculum is present.

Field	Description	Default
1	Minimum life span (years) for P-type *Annosus.*	0
2	Minimum life span (years) for S-type *Annosus.*	0
3	Minimum life span (years) for *Armillaria.*	0
4	Minimum life span (years) for *Phellinus.*	20
5-7	Not used.	

5.5 Assumptions About Trees

5.5.1 Host Tree Species (Advanced, Annosus Root Disease Only)

When Annosus root disease is simulated, the tree species are assigned as susceptible to P-type or S-type, and each species is susceptible to only one of these types. Some advanced users may wish to use the model to simulate a different root disease, and may therefore need to change the host tree species for a disease type. This can be done using the keyword **RRHOSTS**. With this keyword, users can specify the new Annosus root disease type for each tree species.

RRHOSTS   Specify the host disease type for each tree species *(Advanced, Annosus root disease only)*

Field	Description
1	Tree species to be modified (number or character code). A '0' or 'ALL' here indicates all species, and requires a supplemental record.
2	New disease type for which this tree is considered host (1=P-type *Annosus*, 2=S-type *Annosus*). This field is ignored if field 1 indicates all species. Defaults are given in Appendix 1.
3-7	Not used.
Suppl.	Eleven values starting in column 1, each with a field width of five places Record (including the decimal). All values must be entered. The supplemental record is required only if field 1 is 0 or 'ALL'.

Notice that if more than one species is to be changed, the keyword requires a supplemental record. This record is a line following the keyword in which the user must enter a value (1 or 2) for each tree species (see the example below).

Example: Changing the *Annosus* type for more than one tree species

Suppose all species except white fir (code 4) and Douglas-fir (code 3) are to be considered host to P-type Annosus root disease (code 1), the keyword would be:

```
RRHOSTS              0
    1    1    2    2    1    1    1    1    1    1    1
```

The '0' in the first field of the keyword indicates that more than one species is to be changed. The '1' or the '2' tells the model which disease type the corresponding tree species will be assigned.

The keyword **RRHOSTS** can also be used to change the disease type of only one tree species. In this case, the supplemental record is not used, and users specify the species code number (field 1) and the new disease type (field 2).

Example: Changing the Annosus root disease type for only one tree species

Suppose that the stand contains a tree species which is susceptible to S-type Annosus root disease but is not one of the 10 specified species in FVS (and thus will be given species code 11, or 'other'). By default, the tree species in the 'other' category will be assumed to be susceptible to P-type Annosus root disease. The keyword to change the Annosus root disease type from P-type (code 1) to S-type (code 2) for tree species 11 (field 1) is:

```
RRHOSTS        11        2
```

5.5.2 Root Radius

Root radius is dependent on the DBH and species of a tree. The size of the root radius affects the spread rate of centers and the infection rate of healthy trees within centers. Smaller root radii reduce the size of centers and the

number of infected trees. Using the keyword **SDIRMULT**, users can create a multiplier (ranging from 0.5 to 1.5) that further changes root radius based on the density of the stand. By default this multiplier is not present.

Field	Description	Default	
		Imp	**Met**
1	"Normal" Stand Density Index (SDI at which the multiplier should be 1).	369	826
2	Slope of the relationship between SDI and multiplier (negative slope means the multiplier is small when SDI is large or that areas in crowded stands have a smaller root system than expected).	-0.0033	-.0013
3-7	Not used.		

SDIRMULT   Allow the root radius to be modified by stand SDI.

Imp. = imperial units, Met. = metric units

   The assumption behind the default values in this keyword is that trees of similar DBH in dense stands (those with SDI greater than 369 [826 in metric]) will have a smaller root radius than those in a "normal" stand (SDI = 369 [or 826]) and that those in an open grown stand (SDI < 369 [< 826]) will have a larger root radius (*fig. 5.16*). To use the default conditions, the keyword must be entered with no values in the fields.

Example: Changing the root radius based on density

Suppose a user running the imperial version believed that the effect of density should go in the opposite direction (and be given a slope of 0.001, field 2), and that the SDI of a "normal" stand was actually 450 (*fig. 5.16*), then the keyword would be:

SDIRMULT   450   0.001

If a different user was running the metric version of the model and wanted to use the keyword to produce exactly the same effect, the keyword would be:

SDIRMULT   1112   0.0004

The effect of this change is shown in *figure 5.17*.
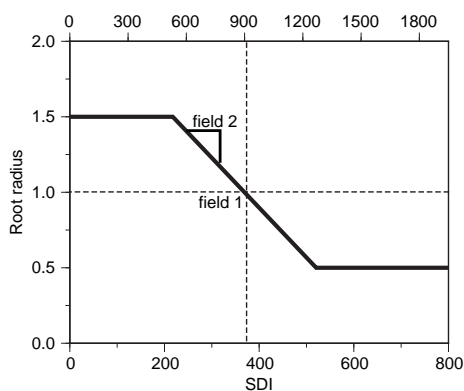
Figure 5.16 — Default curve for the SDI-based root radius multiplier, with the parts that can be changed with each field of the keyword labelled. Imperial units are used on the bottom x-axis and metric units are on the top axis.
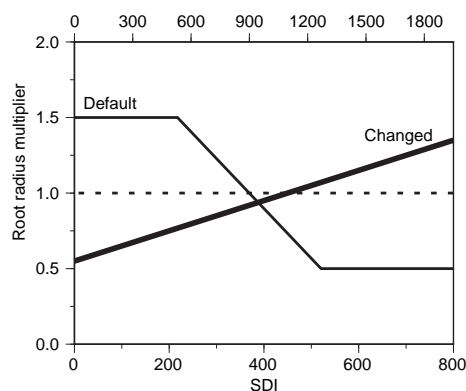
Figure 5.17 — Effect of changing the parameter values for the root radius multiplier. The parameter values used are those in the SDIRMULT keyword example. The default curve is shown for comparison. Notice that the metric SDI values are given on the top axis while the bottom axis contains the imperial values.

5.6 Random Numbers

The Western Root Disease Model uses random numbers in simulating the spread rates of centers and in calculating the infection that occurs inside centers. Each time a run is repeated with the same stand and the same keyword set, the results will be identical because the model will be choosing the same set of random numbers. To get some idea of the variability in behavior which results from the choice of random number, users should choose a different starting point for the random number generator using the keyword **RSEED**.

RSEED Select a new 'seed' value for the random number generator.		
Field	**Description**	**Default**
1	The new random number generator seed value (positive, odd integer).	889347
2-7	Not used	

5.7 Compressing the Root Disease Tree Lists

The root disease model tree lists can contain at most 500 tree records. This is a smaller size limit than in FVS (with no root disease model extension present) but is necessary to reduce the amount of memory used by the tree lists (see the detailed model description for more information about the format of WRDM3 tree lists). By default, the model keeps the tree list under 150 records. Users may change the number of tree records used in the model by using the keyword **RRCOMP**. If any planting or regeneration occurs in the model, the tree lists may exceed the specified tree limit, and compression will occur.

RRCOMP Maximum number of records in the tree list.		
Field	**Description**	**Default**
1	The maximum number of records in the tree list. A value ≤500 must be present.	150
2-7	Not used.	

6.0   Managing Root Disease
6.1 Introduction

Few options exist for managing root disease once it has entered a stand. Many of these options may, however, be simulated using FVS and root disease model keywords. *Table 6.1* lists several techniques, and

Table 6.1 — Options for managing root disease and their implementation in FVS.[1]

Effect	Technique	Keywords
Inoculum removal	removing (pushing) stumps "push-over" harvest	**PSTUMP** FVS harvest keywords and **PSTUMP**
Species change	plant less susceptible species increase time before regeneration	FVS harvest and regeneration keywords
Inoculum avoidance	plant trees away from infection	Cannot be modelled (but may be approximated by using FVS regeneration keywords to plant at a lower than normal density).
Chemical agents	use chemicals to prevent infection	**BORATE** (*Annosus* only)

[1] Many of the effects and techniques in this table are based on those listed in the *Root Disease Management Guidebook* published by the BC Ministry of Forests and BC Environment (1995).

the keywords that can be used to perform the operations. Example keyword sets are given below to illustrate the different techniques.

Users should always be wary of thinning root diseased stands, especially those containing Armillaria root disease and Annosus root disease. Thinning may often increase root disease in the stand because it allows the disease to spread more rapidly through the root systems of the trees that were cut and may introduce new infection courts. Some of this effect may be countered by some of the management techniques below.

6.2 Inoculum Removal

Inoculum removal is just that: removing the inoculum, in the form of infected roots, from the soil. This can be done by pushing stumps currently present in the stand (i.e., stumps that were not necessarily created by a harvest that year or any year), or by harvesting and removing the stumps as part of the same operation. In both cases, the keyword **PSTUMP** must be used while in the second case, a harvest must first be done in FVS. Note that the **PSTUMP** keyword affects all dead infected trees whether they are cut stumps or snags. The keyword specifies the year or cycle in which stumps are pushed and the proportion of stumps above a certain size to remove. *Figure 6.1* shows an example of the effect of removing stumps.
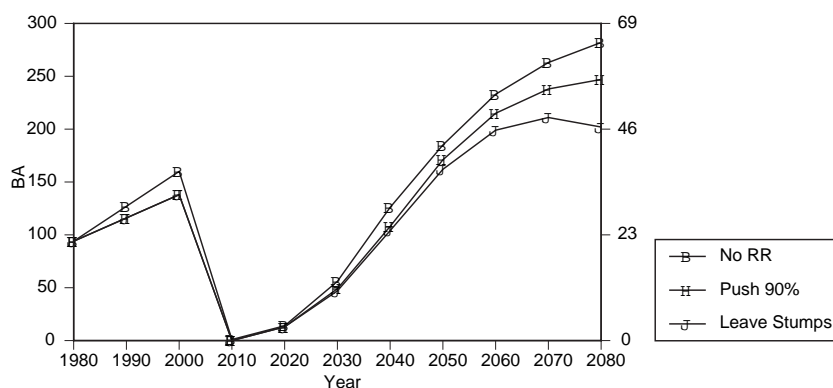
Figure 6.1 — The effect of inoculum removal. Three runs are shown here: no root disease (■), leaving the infected stumps in the stand (●) and pushing 90 percent of the infected stumps (▲). The stand was projected to be clear-cut in 2000 and planted with Douglas-fir. 90 percent of stumps were pushed (see example). Metric units (sq. m/ha) are given on the right y-axis and imperial units (sq. ft./acre) are on the left y-axis.

PSTUMP   Simulate stump pushing to remove infected stumps.

Field	Description	Default
1	Year in which stump pushing is to occur (calendar year or cycle number).	1
2	Proportion of stumps to be removed.	1.0
3	Minimum stump diameter (DBH of the tree that left the stump) for stump pushing (inches or cm).	0.0
4-7	Not used.	

Example: Inoculum removal

Suppose that in 2000 a stand is clear-cut and the stumps and large roots of the cut trees are to be removed. The keywords would be (see the FVS keyword guide for information about harvest keywords):

THINABA   2000   0.0
RDIN
miscellaneous root disease model keywords
PSTUMP   2000   0.9   0.0
END

Note that 90 percent of *all* diseased stumps and infected standing dead trees in the stand will be removed by this keyword, including those which were in the stand before the harvest.

6.3 Species Change

Tree species differ in their response to the various root diseases. Some trees are highly susceptible, while others are more resistant. This is especially true for Annosus root disease, in which tree species are susceptible only to S- or P-type *Annosus,* but not to both. The relative susceptibility of the different tree species defined by the default values is listed in the appendix. Examples of very susceptible and resistant species are listed in *table 6.2.*

There are two methods for implementing a species change:

1.   Regenerate only with more resistant species (*fig. 6.2*).

2.   Do not allow any regeneration on the stand for several years, i.e., long enough for the inoculum to leave the site (*fig. 6.3*). This is considered a species change because other species (grasses, etc.) will use the site in the interim.

Table 6.2 — Most resistant and susceptible tree species for each root disease type. These are based on the default values for the Inland Empire and the Southern Interior variants. When more than one species is listed, they have the same (or very similar) default values.

	Annosus		*Armillaria*	*Phellinus*
	S-type	P-type		
Most resistant	any P-type host	any S-type host	Western red cedar	Western red cedar
Most susceptible	Larch, Douglas-fir, Spruce, true fir	Ponderosa pine	True firs, Douglas-fir	Douglas-fir, Grand fir, Alpine fir
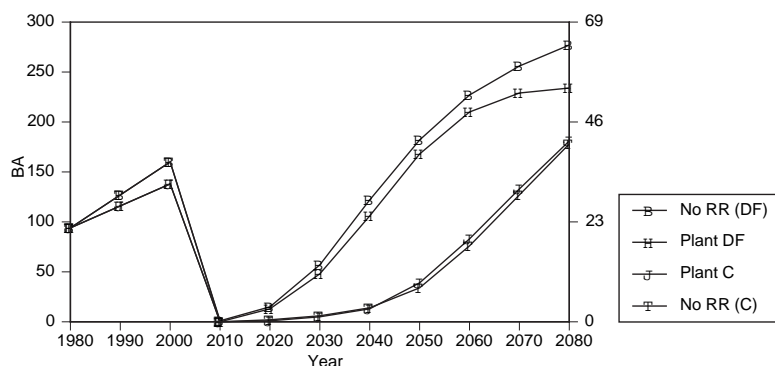
Figure 6.2 — Effect of planting different species after a clear-cut. Four runs are shown here: no root disease and planting Douglas-fir (–■–), no root disease and planting red cedar (–❑–), *Phellinus weirii* **and planting Douglas-fir (–▲–), and** *Phellinus weirii* **and planting red cedar (–●–). Notice that the root disease has little effect on the red cedar (a more resistant species), and more effect on Douglas-fir (a fast-growing but susceptible species). Metric units (sq. m/ha) are given on the right y-axis, and imperial units (sq. ft./acre) are on the left y-axis.**

Example: Species change by planting a more resistant tree species

Suppose that in 2000 a stand infected with *Phellinus weirii* is clear-cut and red cedar, a relatively resistant species, is planted. No root disease management keywords are necessary. See FVS and Establishment model keyword guides for information about these keywords.

```
THINABA      2000     0.0
ESTAB        2000
PLANT        2003     6        400
TALLYONE     2007
END
RDIN
RRTYPE       4
```
miscellaneous root disease model keywords
```
END
```

Example: Species change by increasing the regeneration delay

Suppose that in 2000 a stand infected with Armillaria root disease is clear-cut and no planting occurs for 30 years, at which time, Douglas-fir is planted (code 3). No root disease management keywords are necessary. See FVS and Establishment model keyword guides for information about these keywords.

```
THINABA      2000     0.0
ESTAB        2025
PLANT        2030     3        400
TALLYONE     2037
END
RDIN
RRTYPE       3
```
miscellaneous root disease model keywords
```
END
```

The delayed planting has an additional effect in the model. During the period in which no trees are in the stand, the model starts reducing the size of the remaining centers (see the Model Description). At the time of planting, all centers may have disappeared, which means the disease has disappeared, or they may just have
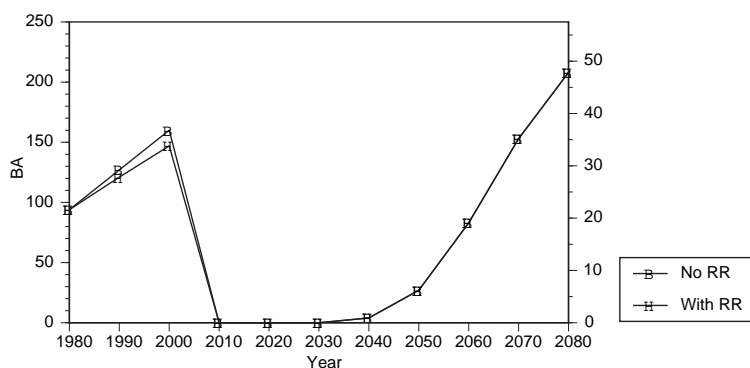
Figure 6.3 — Effect of planting several years after a clear-cut. Two runs are shown here: no root disease (–■–) and Armillaria root disease (▲–). In both cases, the harvest and planting keywords were those shown in the example. The 30-year delay in planting gives the stand a chance to become free of root disease (so the runs overlap in the graph). Metric units (sq. m/ha) are given on the right and imperial units (sq. ft./acre) are on the left y axis.

been reduced in size, which will also reduce the amount of infection which occurs after planting. Species change is the only mechanism by which centers will disappear.

Note that the model does consider the effect of other competing vegetation such as grasses or shrubs on the establishment success of the delayed planting. Additional site preparation may be required. In addition, in natural systems natural regeneration may occur during the period in which planting is delayed. If the trees that are regenerated naturally are susceptible to the root disease, they may carry the disease until the stand is planted. This would likely remove the benefits to the delayed planting.

6.4 Other

The remaining two management options are: inoculum avoidance and chemical application. Inoculum avoidance would be done in the field by planting trees far away from root disease infected stumps so that, ideally, the root systems of the stump and the new tree would not overlap. Since the root disease model does not model the location of each tree and stump, this option is not possible to simulate in the model. It may, however, be simulated to some degree by telling FVS to plant at a lower density. Then, when the root disease model simulates root-to-root infection, it will be less likely to place two root systems overlapping. The model will likely still overestimate the amount of root disease infection occurring after the planting, if planting crews in the field can indeed accurately determine the location and extent of inoculum.

Special Keyword for Annosus root disease

Chemical application is simulated in the model as borate application on stumps through the use of the **BORATE** keyword. Borate can be applied to stumps after harvesting to reduce colonization by Annosus root disease spores. By default, no borate application occurs, but using the keyword **BORATE**, the user can simulate this management action. In the keyword, the user must indicate the minimum size stump and the proportion of these stumps which will receive borate treatment. These parameters can be changed in any cycle, hence borate can be applied after one harvest but not after a second. In the model, borate application has a large impact on the number of centers in the stand but has little effect on the stand dynamics, at least for the first several decades (*fig. 6.4*).
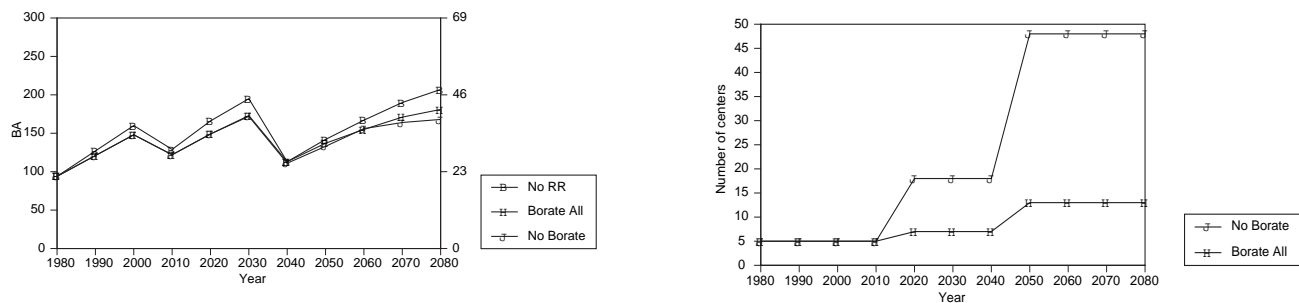
Figure 6.4 — Effect of borate application on basal area (left) and number of centers (right). The model was run using the keywords in the borate example, with the exception of the second BORATE keyword (so that borate application will be done every time there is a cut). Three runs are shown: no root disease (■), S-type Annosus root disease present with no borate (●), and S-type Annosus root disease present with borate application after both thinnings (▲). Note that since the borate was only 80 percent effective, the number of centers increases even with the borate application. In the graph on the left, metric units (sq. m/ha) are given on the right y-axis and imperial units (sq. ft./acre) are on the left y-axis.

BORATE   Simulate borate application to reduce number of new centers after a cut.

Field	Description	Default Imp	Met
1	Year in which to change the parameters (cycle number).	1	1
2	Proportion of newly cut stumps to receive borate treatment.	0.95	0.95
3	Minimum stump diameter for borate treatment (inches or cm).	12	30.5
4-7	Not used.		

Imp. = imperial units, Met. = metric units.

It is not necessary to use the same cycle numbers in the thinning and borate keywords. This is because the cycle number in **BORATE** indicates when the parameter values change, not when borate treatment occurs.

Example: Applying borate

Suppose that a thinning from below occurred in cycles 3 and 6, and that borate treatment was to occur after the first thinning only. The keywords would be (see the FVS keyword guide for details on harvesting keywords):

```
THINBBA      3       90
THINBBA      6       90
RDIN
```
miscellaneous root disease model keywords
```
BORATE       1       .8      14
BORATE       5       0       0
END
```

The same effect would occur by changing the first borate cycle number to be any integer between 1 and 3 and the second to be any integer between 4 and 6.

Note that borate application is reported as "DONE" in the activity scheduler in the main output file in the cycle when parameter values are changed, not in the cycle in which borate is actually applied.

7.0 Output

Several output files provide information specific to the Western Root Disease Model, version 3.0.

Some of these files are printed automatically while others can be requested using one of the five relevant root disease model keywords (*table 7.1*). Example output files are provided and described in the following sections.

Many of the keywords used for producing output (except **RRDOUT**) must be followed by the **OPEN** keyword.

Table 7.1 — Keywords controlling the model output tables.

Section	Keyword	Function	Default file number (field 1)
7.2	**RRECHO**	Print summary table to separate file without headers	24
7.3	**RRDOUT**	Print detailed output (to main output file)	Not used
7.4	**BBOUT**	Print bark beetle information.	27
7.5	**SMCOUT**	Print center spread rate Monte Carlo results.	26
7.6	**INFSIMS**	Print and control inside infection Monte Carlo results.	25 (field 3)

OPEN	**Open a file for printing output.**	
Field	**Description**	**Default**
1	File unit number (20-35)	24
2	Handling of blanks within a record: 0=spaces are zeros, 1=spaces are nulls.	0
3	File status: 0=unknown, 1=new, 2=old, 3=fresh (if file exists, delete and create new).	3
4	File record length (1-132)	132
5-7	Not used.	
Suppl. Record	**Required.** Name of file to be opened.	

Example: Opening a file for output

Suppose a user wishes to print the summary output information to a separate file called "SUMMARY.OUT"; the required keywords are:

```
RRECHO      24
OPEN        24
SUMMARY.OUT
```

Further examples are given in the sample keyword set in Section 8.1.

In the following sections, sample output files are shown for both imperial and metric units. It is important to notice that the only difference between the files is in the headings; otherwise, all columns contain the same sort of information. The output files that have been chosen also demonstrate the difference between the output files when they are reporting different root disease types. The output files will show a variety of cases: both types of Annosus root disease, Armillaria root disease, or *Phellinus weirii*.

7.1 Input Information

The first section of the main output file ("Options selected by input") contains a listing of each keyword in the keyword file and a description of the values in each parameter field. It also gives other information such as whether bark beetles were selected by default, whether the stand is being run as one center, and any errors that occurred while reading the keywords.

The next section of input information is entitled "Summary of root disease information read in on input." If the **RRTREIN** keyword was used, this section reports the number of infected and uninfected tree records and infected stump records inside root disease centers of each disease type. It also lists the number of resinous and non-resinous infected stumps by size class and disease type (input either using **STREAD** or **RRTREIN**, *tables 7.2* and *7.3*). If, after running the model, the results given in later tables seem unusual, these sections provide good opportunities to check the input information and data.

Notice that there are two types of information under the heading "Summary of Disease Information Read in on Input" (*tables 7.2* and *7.3*). The first few lines of this output give the number of records that were in the inventory that had these characteristics (i.e. 2 infected tree records, 49 uninfected records, and 0 stumps in the first half of *table 7.2*). The second part of the output summarizes the number of stumps that are present initially (not the density). These will include the stumps in the stump records and the stumps entered under the **STREAD** keyword.

Table 7.2 — Summary of root disease information read in on input (imperial). In this example, the model is being simulated with both P- and S-type Annosus root disease, although the only stumps in the inventory were in S-type Annosus root disease.

```
-------------------------------------------------------------------------------------------------------------

          SUMMARY OF ROOT DISEASE INFORMATION READ IN ON INPUT
-------------------------------------------------------------------------------------------------------------


     DISEASE TYPE: P
     NUMBER OF INFECTED TREE RECORDS IN DISEASE PATCHES=        2.
     NUMBER OF UNINFECTED TREE RECORDS IN DISEASE PATCHES=     49.
     NUMBER OF INFECTED STUMP RECORDS IN DISEASE PATCHES=       0.
     NUMBER OF INFECTED STUMPS
     SIZE CLASS     RESINOUS      NON-RESINOUS
     ------------------------------------------------

      0- 12"            0.             0.
     12- 24"            0.             0.
     24- 48"            0.             0.
     48-100"            0.             0.
       >100"            0.             0.
     DISEASE TYPE: S
     NUMBER OF INFECTED TREE RECORDS IN DISEASE PATCHES=       16.
     NUMBER OF UNINFECTED TREE RECORDS IN DISEASE PATCHES=     97.
     NUMBER OF INFECTED STUMP RECORDS IN DISEASE PATCHES=       5.
     NUMBER OF INFECTED STUMPS
     SIZE CLASS     RESINOUS      NON-RESINOUS
     ------------------------------------------------

      0- 12"            0.           100.
     12- 24"           50.             0.
     24- 48"            0.             0.
     48-100"            0.             0.
       >100"            0.             0.
-------------------------------------------------------------------------------------------------------------
```

Table 7.3 — Summary of root disease information read in on input (metric). In this example, the model is being simulated with Armillaria root disease (disease type "A"), and both infected stumps and infected trees were present in the inventory.

```
-------------------------------------------------------------------------------------------------------------

          SUMMARY OF DISEASE INFORMATION READ IN ON INPUT
-------------------------------------------------------------------------------------------------------------


     DISEASE TYPE: A
     NUMBER OF INFECTED TREE RECORDS IN DISEASE PATCHES=      153.
     NUMBER OF UNINFECTED TREE RECORDS IN DISEASE PATCHES=    213.
     NUMBER OF INFECTED STUMP RECORDS IN DISEASE PATCHES=      20.
     NUMBER OF INFECTED STUMPS
     SIZE CLASS     RESINOUS      NON-RESINOUS
     ------------------------------------------------

      0- 30 CM        506.            28.
     30- 61 CM          0.             0.
     61-122 CM          0.             0.
    122-254 CM          0.             0.
      >254 CM           0.             0.
-------------------------------------------------------------------------------------------------------------
```

7.2 Standard Output

The standard output table contains the summary information about the status of root disease in the stand. For the root disease type(s) present, the model reports the number of centers, the area in root disease, and the average spread rate, as well as the density of live infected and uninfected trees and the density and basal area of dead infected trees and stumps. A more detailed description of each column is provided below, and examples are given in *tables 7.4* and *7.5*. Note that all densities in this table are based on the area in root disease only.

Table 7.4 — Standard root disease output table, with headings and in imperial units. Both Annosus root disease types are present in this stand, so information about both disease types is printed in the table. Had only S-type been present, for example, the P-type rows would not be printed.

```
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                                    GENERAL ROOT DISEASE MODEL
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

             SUMMARY STATISTICS FOR ROOT DISEASE AREAS (PER ACRE BASED ON DISEASED AREA ONLY)
-------------------------------------------------------------------------------------------------------------
          DISEASE STATISTICS          DEAD TREE CHARACTERISTICS        LIVE TREE CHARACTERISTICS
                                      STUMPS        LOSSES
                                                 FROM DISEASE
                ---------------------------   -------------  --------------   -------------------------------------
                                                            NO OF  VOLUME     UNINF    INFECTED      OVERALL
                       NO    DISEASE  SPREAD           BA/   TREES  LOSSES    NO OF   NO OF   AVE    MERCH  BA/      IDENTIFIERS
                       OF    AREA     RATE    TOTAL   ACRE  KILLED  CU FT     TREES   TREES  %ROOTS   CU FT ACRE
YEAR   AGE   TYPE   CENTS   ACRES    FT/YR   /ACRE   SQFT   /ACRE   /ACRE     /ACRE   /ACRE INFECTED  /ACRE  SQFT   STAND IDMGMT ID
-------------------------------------------------------------------------------------------------------------
1990   100    P      5     1.03     .00     4.8     3.9     .0      .0       64.2    64.2    9.5     2336.  100.   MIXED  NONE
1990   100    S      5     1.04     .00     6.3     7.7     .0      .0      118.6   118.6   11.7      325.   36.   MIXED  NONE
2000   110    P      5     1.18     .50    70.0    33.3   65.8   874.4       57.9     4.5   38.2     2101.   78.   MIXED  NONE
2000   110    S      5     1.10     .19     5.9     7.3  102.3   112.8      109.5    24.8   48.6      525.   37.   MIXED  NONE
2010   120    P      5     1.50     .77    35.9    40.0   18.0   536.1       39.7     2.5   38.4     1420.   54.   MIXED  NONE
2010   120    S      5     1.22     .30    40.2    18.9   19.8    55.0       97.2    12.1   50.7      442.   29.   MIXED  NONE
2020   130    P      5     1.84     .77    27.4    38.3   12.4   277.8       31.7     1.8   39.7     1311.   49.   MIXED  NONE
2020   130    S      5     1.31     .27    22.0    10.7   12.9    33.7       89.7     8.6   36.8      481.   30.   MIXED  NONE
2030   140    P      5     2.11     .56    26.6    35.6    7.9   222.3       25.1     1.9   37.8     1189.   43.   MIXED  NONE
2030   140    S      5     1.45     .29    15.8     8.4   12.5    53.5       88.2    10.4   47.6      678.   36.   MIXED  NONE
-------------------------------------------------------------------------------------------------------------
```

Table 7.5 — Standard root disease output table, with headings and in metric units. Only Phellinus weirii is present in this stand, and is identified by the "W" in the column "TYPE." This output table also shows an example of the entire 2-ha stand being within a single disease center (the number of centers is 1, and the spread rate is 0).

```
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                                    GENERAL ROOT DISEASE MODEL
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

            SUMMARY STATISTICS FOR ROOT DISEASE AREAS (PER HECTARE BASED ON DISEASED AREA ONLY)
-------------------------------------------------------------------------------------------------------------
          DISEASE STATISTICS          DEAD TREE CHARACTERISTICS        LIVE TREE CHARACTERISTICS
                                      STUMPS        LOSSES
                                                 FROM DISEASE
                ---------------------------   -------------  --------------   -------------------------------------
                                                            NO OF  VOLUME     UNINF    INFECTED      OVERALL
                       NO    DISEASE  SPREAD           BA/   TREES  LOSSES    NO OF   NO OF   AVE    MERCH  BA/      IDENTIFIERS
                       OF    AREA     RATE    TOTAL   ACRE  KILLED  CU FT     TREES   TREES  %ROOTS   CU FT ACRE
YEAR   AGE   TYPE   CENTS   HA       M/YR    /HA     SQ M   /HA     /HA       /HA     /HA  INFECTED  /HA    SQ M   STAND IDMGMT ID
-------------------------------------------------------------------------------------------------------------
1992    26    W      1     2.00     .00   267.0     4.8     .0      .0      1431.0   217.0   56.6      26.   18.   SUGAR  NONE
2002    36    W      1     2.00     .00      .1      .0  231.1    19.0       911.9   390.3   18.0     107.   28.   SUGAR  NONE
2012    46    W      1     2.00     .00      .3      .0   57.6     6.4       687.9   424.6   32.6     179.   34.   SUGAR  NONE
2022    56    W      1     2.00     .00   224.5     6.7  191.7    56.7       390.3   462.2   24.8     213.   33.   SUGAR  NONE
2032    66    W      1     2.00     .00   183.2     6.4  158.4    55.8       197.4   457.8   27.8     234.   31.   SUGAR  NONE
-------------------------------------------------------------------------------------------------------------
```

Year: The first year of the cycle for which the information is given (unless otherwise specified below).

Age: Stand age. This will be the same as the age in the summary stand output table.

Disease Statistics:

Type: The type of root disease for which the information is given:

> P   P-type Annosus root disease
> S   S-type Annosus root disease
> A   Armillaria root disease
> W   *Phellinus weirii* (the W comes from *weirii*)

No. of Cents:

The number of centers in the stand. Note that if there are several centers, or if the centers are large, parts of centers may overlap.

Disease Area:

Area in root disease centers (acres or hectares). This is the area in the stand that is considered to be within centers (overlapping areas are counted only as being within one center). This is not necessarily the same as the amount of area containing inoculum (*fig. 1.2*).

Spread Rate:

The rate of spread of the edge of centers (ft/year or m/year) in the previous cycle. For example, if using 10-year cycles, then the spread rate printed in the year 2000 is for the period 1990-1999, and is the spread used to get from the area printed in 1990 to the area printed in 2000. This means that the spread rate in the first year will always be 0.

Dead Tree Characteristics:

Stumps:

> Total: Density of dead infected trees and stumps within root disease centers.
> BA: Basal area (sq.ft./acre or sq.m/ha) of these dead infected trees and stumps.

Losses from Disease:

> No. of Trees Killed: Density of trees killed by root disease only. This number does not include any trees killed by bark beetles, windthrow, or other agents (trees/acre or trees/ha).

Volume Losses: The total volume of the trees killed by root disease only (cu ft/acre or cu m/ha).

Live Tree Characteristics:

Uninf: Density of uninfected host trees within centers (trees/acre or trees/ha).

Infected:

> No. of Trees: Density of trees infected by this root disease type (trees/acre or trees/ha).
> Avg. percent Roots Inf: The average percentage of the root radius of live infected trees that is colonized by root disease.

Overall:

> Merch: Merchantable cubic ft/acre or cubic m/ha of live trees within centers.
> BA: Basal area (sq.ft./acre or sq.m/ha) of live trees within centers.

Identifiers:

Stand ID: Stand identification given in the FVS keywords.

Mgmt ID: Management identification given in the FVS keywords.

Each of the categories describing trees considers only host trees inside disease centers. Therefore, if the entire stand is being run as one center, and non-host trees are present in the stand (such as when simulating only one Annosus root disease type when trees that are susceptible to the other type are present), the density of trees may not be the same as that in the standard FVS summary table.

This output table is always printed at the end of the main FVS output file and is *not* under user control.

Using the **RRECHO** keyword, users may request that a machine-readable version of this information (i.e., no headings, no blank lines, and values always present for both Annosus root disease types) be printed in a separate file. This is useful as input for statistical and graphical software packages.

7.3 Detailed Output

A more detailed root disease output table (*tables 7.6* and *7.7*) can be requested using the keyword **RRDOUT**. This information is also printed in the main FVS output file below the standard root disease output information and contains column headings. All information in this table is applicable within root disease centers only. Columns are self-explanatory but are described below.

Year: The initial year of the cycle.
Type: Root disease type
                P P-type Annosus root disease
                S S-type Annosus root disease
                A Armillaria root disease
                W *Phellinus weirii* (the W comes from *weirii*)
Area: Area (acres or hectares) inside centers of the appropriate disease type.
SP: Tree species. There may be several species of trees within one disease type, and the information for each species will be listed separately.
Killed Trees: DBH distribution of trees killed by root disease. This is given as a percentile distribution which lists the DBH which is greater than *x* percent of the trees. For example, if the 90 percent DBH = 15.8, then 90 percent of the trees are 15.8 or smaller.
Total: The total density (trees/root diseased acre [ha]) of this species of tree killed by root disease.
Alive Trees: DBH distribution of living (infected or uninfected) trees within root disease centers.
Uninfected: Density of uninfected trees (trees/root diseased acre [ha]).
Infected: Density of infected trees (trees/root diseased acre [ha]).
% roots infected: Percentage of the root radius of infected trees that is infected.

Table 7.6 — Example detailed output file (imperial). In this example, both Annosus root disease types are present, but each disease type contains only one species of tree. If other species were present, they would be listed under the appropriate disease type (see table 7.7).

```
 * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                          WESTERN ROOT DISEASE MODEL DETAILED OUTPUT VERSION 1.0
 * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

                                STAND ID= MIXED       MANAGEMENT ID= NONE
                                STAND ATTRIBUTES  INSIDE ROOT DISEASE PATCHES

-------------------------------------------------------------------------------------------------------
       ROOT                KILLED TREES                               ALIVE TREES
     DISEASE        %TILE POINTS BY DBH (INCHES)    TOTAL    %TILE POINTS BY DBH (INCHES)    TOTAL    TOTAL
    ----------   -------------------------------   KILLED  -------------------------------- UNINFECTED INFECTED %ROOTS
YEAR TYPE AREA  SP  10   30   50   70   90  100   TREES/    10   30   50   70   90  100   TREES/  TREES/ INFECTED
                                                   ACRE                                      ACRE    ACRE
-------------------------------------------------------------------------------------------------------
1990  P   1.0
             PP  .0   .0   .0   .0   .0   .0    .0   4.7  6.0  8.2 10.8 16.2 50.0   64.2   64.2   9.54
      S   1.0
             WF  .0   .0   .0   .0   .0   .0    .0   2.0  2.0  3.0  3.7  7.8 41.0  118.6  118.6  11.71
-------------------------------------------------------------------------------------------------------
2000  P   1.2
             PP 5.6  6.9  9.2 10.7 15.8 20.8  65.8   5.9  7.4  9.8 13.5 22.0 51.1   57.9    4.5  38.15
      S   1.1
             WF 2.1  2.1  2.1  3.9  6.5  7.4 102.3   2.1  2.1  3.9  7.0  9.8 43.2  109.5   24.8  48.63
-------------------------------------------------------------------------------------------------------
2010  P   1.5
             PP 6.5  7.6 10.2 11.8 17.6 52.3  18.0   6.6  8.9 11.3 15.2 21.2 52.3   39.7    2.5  38.39
      S   1.2
             WF 2.2  2.2  3.9  4.9  8.6 15.2  19.8   2.2  2.2  4.5  5.4 10.5 44.8   97.2   12.1  50.67
-------------------------------------------------------------------------------------------------------
2020  P   1.8
             PP 7.0  8.2 11.1 12.6 16.9 53.0  12.4   7.3  9.6 12.5 16.4 22.4 53.0   31.7    1.8  39.68
      S   1.3
             WF 2.3  2.3  5.1  6.0  8.2 18.6  12.9   2.3  2.3  5.1  6.1 11.6 46.8   89.7    8.6  36.77
-------------------------------------------------------------------------------------------------------
2030  P   2.1
             PP 7.5  9.4 12.0 13.4 18.2 53.9   7.9   7.9 11.5 13.4 17.4 23.8 53.9   25.1    1.9  37.80
      S   1.4
             WF 2.5  2.5  5.6  5.9  9.6 20.4  12.5   2.5  2.5  5.6  6.8 12.9 48.1   88.2   10.4  47.58
-------------------------------------------------------------------------------------------------------
```

Table 7.7 — Example detailed output file (metric). Armillaria root disease is being simulated. Several different species of trees are present in the stand.

```
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                      WESTERN ROOT DISEASE MODEL DETAILED OUTPUT VERSION 1.0
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                         STAND ID= SUGAR92     MANAGEMENT ID= NONE
                        STAND ATTRIBUTES  INSIDE ROOT DISEASE PATCHES
```

| | | | | | KILLED TREES %TILE POINTS BY DBH (CMS) | | | | | | TOTAL KILLED TREES/HA | ALIVE TREES %TILE POINTS BY DBH (CMS) | | | | | | TOTAL UNINFECTED TREES/HA | TOTAL INFECTED TREES/HA | %ROOTS INFECTED |
YEAR	TYPE	AREA	SP	10	30	50	70	90	100		10	30	50	70	90	100			
1992	A	2.0																	
			WP	.0	.0	.0	.0	.0	.0	.0	11.0	15.0	15.0	17.0	23.0	23.0	7.0	.5	50.00
			L	.0	.0	.0	.0	.0	.0	.0	7.0	11.0	13.0	17.0	21.0	35.0	7.0	1.0	60.00
			DF	.0	.0	.0	.0	.0	.0	.0	7.0	9.0	11.0	13.0	15.0	23.0	1244.0	202.5	56.92
			WH	.0	.0	.0	.0	.0	.0	.0	5.0	7.0	9.0	13.0	17.0	55.0	69.5	5.5	53.64
			C	.0	.0	.0	.0	.0	.0	.0	5.0	7.0	9.0	11.0	19.0	63.0	57.0	.5	50.00
			LP	.0	.0	.0	.0	.0	.0	.0	13.0	13.0	17.0	17.0	17.0	17.0	1.5	.0	.00
			S	.0	.0	.0	.0	.0	.0	.0	5.0	7.0	7.0	9.0	13.0	15.0	45.0	7.0	50.71
2002	A	2.0																	
			WP	6.4	6.4	6.4	6.4	6.4	6.4	.5	12.0	18.8	22.3	23.2	27.6	32.1	2.4	3.9	10.01
			L	3.9	3.9	11.3	11.3	11.3	11.3	1.0	8.8	13.6	18.2	20.0	24.7	36.4	5.3	.6	3.23
			DF	6.2	9.4	12.3	14.9	19.1	27.6	216.6	8.6	13.0	14.6	17.4	22.7	31.4	749.0	379.4	18.36
			WH	4.0	4.4	4.4	5.6	5.6	9.0	5.5	8.3	11.5	16.1	17.8	24.7	60.6	60.9	3.6	4.87
			C	5.9	5.9	5.9	5.9	5.9	5.9	.5	5.9	8.2	10.3	14.0	22.1	65.4	52.6	1.5	1.00
			LP	5.9	5.9	5.9	5.9	5.9	5.9	.0	14.8	14.8	20.1	20.1	20.1	20.1	1.2	.1	.00
			S	6.6	8.1	11.2	11.4	12.6	16.6	7.0	7.7	9.3	10.9	11.9	17.0	19.5	40.5	1.1	13.34
2012	A	2.0																	
			WP	14.4	14.4	14.4	14.4	14.4	14.4	.2	17.6	19.9	25.7	26.4	31.4	40.9	1.9	3.7	31.22
			L	10.6	10.6	10.6	10.6	10.6	10.6	.0	10.7	16.7	21.7	22.7	28.0	37.9	4.2	.5	6.03
			DF	11.9	12.5	15.1	17.7	20.8	21.1	56.9	12.0	16.5	18.2	21.5	26.2	37.9	542.3	412.3	33.11
			WH	6.9	6.9	6.9	7.9	13.2	13.2	.2	10.7	17.8	20.4	22.2	29.8	62.3	53.4	4.7	8.18
			C	6.9	6.9	6.9	7.9	13.2	13.2	.0	7.1	11.4	13.4	18.7	30.2	67.6	48.4	1.8	8.43
			LP	6.9	6.9	6.9	7.9	13.2	13.2	.0	18.6	21.7	21.7	21.7	21.7	21.7	.8	.2	.00
			S	13.4	13.4	13.4	13.4	13.4	13.4	.2	10.0	12.9	13.4	15.4	19.6	21.5	36.9	1.4	20.30

7.4 Bark Beetle Output

Detailed information about bark beetle activity is available through the keyword **BBOUT**. This information is printed in a separate file (named using the keyword **OPEN**), and contains information about the species, size, and type of tree killed in each year (*tables 7.8* and *7.9*). Since beetles can kill trees inside and outside of disease centers, the output table reports the number of trees killed in the stand, not the density of trees. No information about unattacked species is printed.

If no beetle activity occurred in a cycle, the output file will contain the initial year of the cycle and the words "no beetle kill" (*tables 7.8* and *7.9*). If beetles were present in any cycle, the output will consist of groups of three rows: one set for each species attacked. The first row in each set is labeled "in-inf" and contains information about the infected trees inside disease centers that were killed. The second row, labeled "in-uninf," contains the number of uninfected trees within centers, while the third row, "outside," contains the number of killed trees outside of centers. A description of each column follows:

Period Ending: The first year of the cycle following a potential beetle attack (so 2000 means the cycle from 1990-1999).

Tree Species: The species number of trees that were attacked. If a species is not mentioned, it was not attacked.

Disease Status: The type of tree that was attacked (row 1: inside, infected; row 2: inside centers but uninfected; row 3: outside centers).

DBH class: The density of trees killed in each species and tree location (inside a center infected, inside a center and uninfected, or outside a center) and as in 5-inch (13-cm) DBH classes.

Row Total: The total density of trees killed in each species and tree location (inside, infected, inside uninfected or outside centers). The area used for each density calculation is the area relevant to the type of tree, i.e., in rows 1 and 2 (trees inside centers), the density is calculated from the area inside centers, while in row 3, the area is that outside of centers.

Species Total: The total density of trees killed for each species. Note that this density is calculated on the total stand area, while the other densities are calculated on the basis of the relevant area.

Total Before
Attack: The total density of trees in each species and tree location. This is included so that the user can determine what proportion of trees of any type are being killed. Again, the area used in the density calculations is the area relevant to the type of tree in that row (inside or outside of centers).

Note that this output is for all types of bark beetles combined. If more than one bark beetle type was active on the same species in a cycle, the information printed for that species would contain the resulting impact of both beetle types. The activity summary in the main output file lists which beetle types were and were not active in a given year.

Table 7.8 — Bark beetle output file (imperial). In this example, bark beetle type 4 was active on species 10 (ponderosa pine), and bark beetle type 3 was active on species 4 (grand fir).

```
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                                    GENERAL ROOT DISEASE MODEL
                        TREES PER ACRE KILLED BY BARK BEETLES IN EACH TIME PERIOD
-----------------------------------------------------------------------------------------------------------
Period   Tree     General                  DBH Class (in inches)                      Row     Species   Total
Ending   Species  Status   ---------------------------------------------------------  Total   Total     Before
(year)                      0-<5   5-<10  10-<15  15-<20  20-<25  25-<30   30+                           Attack
-----------------------------------------------------------------------------------------------------------
2000                        no beetle kill

2010     4        in-inf    .00    12.23   4.18    1.00    .00     .56     .29         18.24             120.45
                  in-uninf  .00     .00     .00     .00    .00     .00     .00          .00                9.03
                  outside   .00     .00     .00     .00    .00     .00     .00          .00      1.82     233.92

         10       in-inf    .00     .00     .59     .08    .47     .84     .81         2.78              68.29
                  in-uninf  .00    11.71   4.47    2.92    .33     .47     .58        20.49              34.16
                  outside   .00     2.04    .80     .45    .05     .07     .09         3.51      5.49     125.72

2020     4        in-inf    .00     4.23   3.73     .27    .00     .07     .13         8.42             118.37
                  in-uninf  .00     .00     .00     .00    .00     .00     .00          .00                6.30
                  outside   .00     .00     .00     .00    .00     .00     .00          .00       .84     227.72

         10       in-inf    .00     .00    1.10     .23    .54     .10     .18         2.15              59.50
                  in-uninf  .00     6.83   5.78    3.41    .82     .37     .65        17.85              35.64
                  outside   .00     1.55   1.33     .59    .14     .06     .11         3.78      5.41     117.78

2030     10       in-inf    .00     .00     .29     .38    .86     .08     .21         1.82              58.42
                  in-uninf  .00     5.57   6.19    3.47   1.29     .27     .73        17.53              37.76
                  outside   .00     1.43   1.51     .67    .24     .05     .14         4.03      5.57     109.42
```

Table 7.9 — Bark beetle output file (metric). In this example, bark beetle type 1 was active on species 7 (lodgepole pine), and bark beetle type 3 was active on species 4 (grand fir).

```
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
                                    GENERAL ROOT DISEASE MODEL
                         TREES PER HA KILLED BY BARK BEETLES IN EACH TIME PERIOD
-----------------------------------------------------------------------------------------------------------
Period   Tree     General                   DBH Class (in cm)                         Row     Species   Total
Ending   Species  Status   ---------------------------------------------------------  Total   Total     Before
(year)                      0-<13  13-<25  25-<38  38-<51  51-<64  64-<76   76+                          Attack
-----------------------------------------------------------------------------------------------------------
1991     7        in-inf    .00     7.28   24.00    .00    .00     .00     .00        24.28             242.83
                  in-uninf  .00     3.52   18.03    .00    .00     .00     .00        21.55             215.53
                  outside   .00     .00    15.83    .00    .00     .00     .00        15.83     23.32    458.78

2001     4        in-inf    .00     .00   100.01   17.64   .00     .00     .00       117.65             133.67
                  in-uninf  .00     .00     .00     .00    .00     .00     .00          .00                .00
                  outside   .00     .00     .00     .00    .00     .00     .00          .00      23.53      .00

         7        in-inf    .00     4.60   18.38    .00    .00     .00     .00        22.98             229.78
                  in-uninf  .00     2.23    9.37    .00    .00     .00     .00        11.60             115.98
                  outside   .00     .00    32.70    .00    .00     .00     .00        32.70     33.17    326.96

2011     7        in-inf    .00     .00    10.65    .00    .00     .00     .00        10.65             106.60
                  in-uninf  .00     .00     5.65    .00    .00     .00     .00         5.65             313.33
                  outside   .00     .00    25.34   1.31    .00     .00     .00        26.65     23.68    523.15
```

7.5 Spread Rate Output (Advanced)

Another optional output table, which is requested using the keyword **SMCOUT**, prints the results of the Monte Carlo simulations of center spread (see Chapter 4, Section 2.4.1 of this guide for details about this simulation). This information is printed in a separate file (named using the keyword **OPEN**), with column headings (*tables 7.10* and *7.11*). Each year of output for each disease type present consists of three lines. Note that although only the first 10 simulation results are printed (columns labelled #1-#10), the average and the standard deviation of the spread rates are calculated from all simulations.

Year: The last year of the cycle in which the spread rate was applied.

Type: The root disease type:

        P   P-type Annosus root disease

        S   S-type Annosus root disease

        A   Armillaria root disease

        W   *Phellinus weirii* (the W comes from *weirii*)

Num: The number of Monte Carlo simulations which were done in the model.

Avg: The average spread rate (ft/year or m/year) from the simulation results. Note that this average may be different from the spread rate listed in the standard output table because the standard output table prints the average of the spread rates that were applied. (See the Detailed Model Description for details on this calculation).

SD: The standard deviation of the spread rate.

Dens: The density of uninfected trees in the fringe around the outside of centers.

#1-10:   Information about the first 10 simulations. If fewer than 10 simulations are done, some of the columns will be blank.

   Line 1: the calculated spread rate.

   Line 2: the number of uninfected trees that were placed into the simulated area.

   Line 3: the quadratic mean diameter of the trees in the simulation.

Table 7.10 — Example spread rate simulation output (imperial). This example is for a stand which contains both S- and P-type Annosus root disease.

```
*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

                              ANNOSUS ROOT DISEASE MODEL
                        SPREAD RATE MONTE CARLO SIMULATION RESULTS
-----------------------------------------------------------------------------------------------------------------------------------
YEAR  TYPE NUM   AVG   SD    DENS      # 1      # 2      # 3      # 4      # 5      # 6      # 7      # 8      # 9      #10
-----------------------------------------------------------------------------------------------------------------------------------
1999   P   10   .50   .36  128.30     .80      .06     1.05      .39      .32      .95      .59      .28      .00      .54
           NUM TREES IN MC SIM.        19       24       20       17       16       26       15       19       20       17
           QMD OF TREES IN SIM.       10.4      8.8     14.6     10.1      8.4     17.7     10.7     10.2      9.1     12.0

1999   S   10   .19   .18  237.21     .00      .37      .11      .31      .09      .53      .00      .16      .27      .02
                                       17       22       23       16       21       20       15       19       23       26
                                       3.7      5.4      5.7      4.8      7.0      7.7      3.6      7.1      4.7      5.3

2009   P   10   .77   .24  128.27     .84     1.07      .89      .37      .56      .89      .74      .95      .41      .95
                                       27       19       30       19       21       26       20       22       17       24
                                      13.9     14.5     15.7     10.7     10.4     12.5     13.3     15.4     10.6     14.2

2009   S   10   .30   .17  236.56     .15      .31      .11      .24      .30      .28      .61      .22      .57      .17
                                       18       24       21       20       23       19       19       17       20       18
                                       4.4      6.2      6.0      6.1      6.0      6.1     10.9      4.7      9.1      5.0

2019   P   10   .77   .28  109.03     .98     1.00      .67      .20      .65      .97      .76     1.11      .50      .87
                                       18       22       19       19       19       23       19       18       18       22
                                      15.0     13.8     10.7     12.4     11.9     13.0     14.2     20.5     11.6     12.6

2019   S   10   .27   .17  233.37     .20      .34      .49      .45      .36      .44      .03      .16      .25      .00
                                       20       22       21       21       21       19       17       23       20       19
                                       5.0      5.8      6.6      6.8      6.1      6.2      4.5      5.5      5.6      5.1

2029   P   10   .56   .35  105.98     .00      .65      .87      .56      .70      .85      .59      .00     1.02      .39
                                       18       23       23       16       21       21       23       18       17       21
                                      14.1     12.2     14.4     12.0     15.6     13.7     15.0     12.7     16.6     13.4

2029   S   10   .29   .26  231.59     .22      .18      .73      .00      .06      .62      .26      .00      .52      .37
                                       20       19       24       20       20       21       19       19       24       20
                                       5.9      6.6     12.9      6.2      6.3     13.0      6.0      5.3     10.2      6.5
```

Table 7.11 — Example spread rate simulation output (metric). This is for a stand which contains Armillaria root disease ("A")

```
*  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

                              GENERAL ROOT DISEASE MODEL
                        SPREAD RATE MONTE CARLO SIMULATION RESULTS
-----------------------------------------------------------------------------------------------------------------------------------
YEAR  TYPE NUM   AVG   SD    DENS      # 1      # 2      # 3      # 4      # 5      # 6      # 7      # 8      # 9      #10
-----------------------------------------------------------------------------------------------------------------------------------
2001   A   10   .14   .08  1648.2     .05      .11      .02      .20      .21      .14      .04      .17      .23      .23
           NUM TREES IN MC SIM.        21       21       14       19       23       18       14       18       26       22
           QMD OF TREES IN SIM.       11.3     10.8     12.2     11.4     13.8     12.7      9.6     12.7     13.1     11.3

2011   A   10   .21   .08  1237.8     .22      .27      .25      .26      .21      .16      .00      .26      .25      .22
                                       20       22       22       29       17       22       10       24       22       22
                                      15.8     15.7     20.3     14.7     16.8     14.9     14.6     15.2     14.7     14.9

2021   A   10   .25   .04  1008.6     .25      .21      .26      .28      .23      .29      .29      .24      .26      .16
                                       18       14       19       20       17       25       21       19       16       17
                                      18.6     19.6     21.1     19.3     17.6     17.1     22.8     19.4     18.7     20.3
```

7.6 Inside Infection Output (Advanced)

Output showing the results of the (optional) (Monte Carlo simulation of infection within centers can be requested using the **INFSIMS** keyword (see Section 5.1 for keyword details). This information is printed to a separate file which contains column headings (*tables 7.12* and *7.13*). Each year of output for each disease type present consists of two lines. As in the center spread rate output file, although only the first 10 simulations results are printed (columns labelled #1-#10), the average and the standard deviation of the number of trees becoming infected are calculated from all simulations.

Year: The last year of the cycle in which the infection was calculated and applied.

Type: The root disease type:

         P   P-type Annosus root disease

         S   S-type Annosus root disease

         A   Armillaria root disease

         W   *Phellinus weirii* (the W comes from *weirii*)

Num: The number of Monte Carlo simulations which were done in the model.

Avg: The average number of trees that become infected.

SD: The standard deviation of the number of trees that become infected.

#Uninf: Total number of uninfected host trees within centers.

#1-10:   Information about the results of the first 10 simulations.

     Line 1:   the number of uninfected trees which become infected.

     Line 2:   the number of inoculum sources (infected trees and stumps) which were put into a simulation plot.

Any inoculum source can potentially infect any number of live trees, provided that the live tree's root system overlaps the inoculum. Thus, the number of uninfected trees which become infected may either be greater than or less than the number of inoculum sources.

Table 7.12 — Example output file from the Monte Carlo simulation of infection within centers (imperial). This example is for a stand which contains both S- and P-type Annosus root disease.

```
 * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

                              WESTERN ROOT DISEASE MODEL
                      INSIDE CENTER INFECTION SIMULATION RESULTS
-----------------------------------------------------------------------------------------------------
YEAR  TYPE  NUM  AVG   SD   #UNINF   # 1    # 2    # 3    # 4    # 5    # 6    # 7    # 8    # 9    #10
-----------------------------------------------------------------------------------------------------
1999   P    10   7.   1.    66.     11.    5.     9.     7.     6.     4.     9.     9.     7.     5.
                                    53     54     52     49     50     49     54     55     44     52
1999   S    10   10.  1.    123.    10.    11.    6.     9.     13.    6.     10.    10.    11.    12.
                                    49     50     45     49     52     46     50     53     54     54

2009   P    10   12.  1.    68.     13.    13.    12.    16.    13.    11.    8.     13.    10.    10.
                                    58     56     55     57     55     58     57     59     57     56
2009   S    10   16.  2.    120.    6.     13.    14.    17.    21.    21.    14.    22.    18.    14.
                                    21     22     19     20     23     22     22     22     19     18

2019   P    10   5.   0.    60.     5.     4.     6.     5.     5.     5.     6.     4.     8.     7.
                                    49     48     51     48     46     49     52     50     49     47
2019   S    10   11.  1.    118.    12.    9.     14.    12.    8.     11.    13.    14.    10.    13.
                                    38     36     35     36     37     33     33     39     34     33

2029   P    10   5.   1.    58.     9.     5.     5.     3.     3.     4.     6.     4.     5.     7.
                                    46     47     46     47     46     48     48     51     48     50
2029   S    10   6.   1.    117.    6.     5.     4.     6.     3.     11.    3.     7.     6.     6.
                                    21     22     22     24     22     31     26     26     23     25

2039   P    10   3.   0.    53.     2.     3.     2.     3.     2.     2.     3.     4.     3.     5.
                                    51     55     56     52     53     53     52     53     51     52
2039   S    10   12.  1.    128.    12.    11.    12.    11.    14.    9.     10.    9.     15.    13.
                                    24     25     22     23     26     21     22     22     23     23
-----------------------------------------------------------------------------------------------------
```

Table 7.13 — Example output file from the Monte Carlo simulation of infection within centers (metric). This example is for a stand which contains Phellinus infection.

```
 * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

                              WESTERN ROOT DISEASE MODEL
                      INSIDE CENTER INFECTION SIMULATION RESULTS
-----------------------------------------------------------------------------------------------------
YEAR  TYPE  NUM  AVG   SD   #UNINF   # 1    # 2    # 3    # 4    # 5    # 6    # 7    # 8    # 9    #10
-----------------------------------------------------------------------------------------------------
2001   W    10   994.  22.  2838.   961.   950.   979.   1098.  983.   936.   923.   969.   1026.  1115.
                                    27     31     27     32     29     29     28     31     30     33

2011   W    10   493.  20.  1863.   398.   464.   465.   611.   518.   487.   514.   435.   478.   554.
                                    12     13     11     19     16     13     15     12     13     17

2021   W    10   643.  19.  1401.   647.   609.   702.   644.   547.   708.   663.   613.   576.   717.
                                    38     36     42     38     34     40     37     35     35     43
-----------------------------------------------------------------------------------------------------
```

8.0 Sample Keyword Files

This section contains two sample keyword files, showing how some of the keywords can be used. Note that the first example is in Imperial units and the second example uses metric units. Both use the Inland Empire variant.

　　　Both examples are discussed in the same format. The keyword file is listed first, with line numbers for easy reference (although note that line numbers are not part of an input keyword file). Each line containing a root disease model keyword is described more fully. Finally, several pages list the output from the FVS main file. This output file describes the parameters that have been read from the example keyword file.

8.1　File 1: Create Output Files, Enter Stumps, and Change Defaults (Imperial)

This keyword file can be used to create many of the output tables shown in Section 7. It is not the simplest example since it is specifically designed to demonstrate how to create the more common output files. This set of keywords provides information to the FVS base model about the stand, then initializes the root disease (as both P- and S-type Annosus root disease) and specifies that only bark beetle types 3 and 4 should be active. Each line in this keyword set is described more fully in the page facing the example.

　　　Some other points that are demonstrated in this keyword set are:
1. Entering stumps which were not in the tree list (see the **STREAD** keyword, lines 14 and 15).
2. Turning off the default bark beetles and changing some of the default values for bark beetles to occur (see **BBTYPE3**, line 17 and **BBTYPE4**, line 18).
3. Changing some of the default values for root disease and stand information (see lines 11-13, **SAREA** and **RRINIT**).

```
 1.      NUMCYCLE     10
 2.      STDINFO     509              100     225              52      42
 3.      DESIGN       -1      1      999.9            0
 4.      INVYEAR    1990
 5.      STDIDENT
 6.      MIXED
 7.      DELOTAB       1
 8.      DELOTAB       2
 9.      RDIN
10.      RRTYPE        1      2
11.      SAREA        10.0
12.      RRINIT        0.0   5.0                           1.00    1
13.      RRINIT        0     5.0                           1.00    2
14.      STREAD       10     2      5.0     1      4
15.      STREAD        4     2      6.5     2      6
16.      BBCLEAR
17.      BBTYPE3                     8       5                    0.10
18.      BBTYPE4
19.
20.      RRDOUT
21.      RRECHO       24
22.      OPEN         24
23.      RRSUM.OUT
24.      BBOUT        27
25.      OPEN         27
26.      BEETLE.OUT
27.      END
28.      PROCESS
29.      STOP
```

Line #	Description
1	The number of cycles to simulate the model. Each cycle represents 10 years.
2-6	Miscellaneous FVS keywords giving information about the stand.
7-8	Instructions to FVS not to print certain output tables.
9	Begin reading the root disease model keywords. All keywords that are between **RDIN** and **END** (line 27) *must* be root disease model keywords.
10	Root disease being simulated is *Annosus*, both S- and P-type.
11	Stand area is set to 10 acres.
12-13	Initialize the root disease area for each disease type to be five centers with an area of 1 acre. Default values are used for the initial density of uninfected and infected trees inside centers.
14-15	Initialize some infected stumps with the following characteristics: 5 diameter class 2 ponderosa pine stumps (code 10) which have been dead for 4 years, and 6.5 diameter class 2 white fir stumps (code 4) which have been dead for 6 years.
16	Turn off the default bark beetle types.
17	Request Type 3 bark beetles, with a different threshold criterion.
18-19	Request Type 4 bark beetles at the default values. Notice the blank line (line 19) which must be present as a space holder for the supplemental records.
20	Print the detailed root disease output table. This will be printed to the main output file.
21-23	Print the root disease summary table in machine readable format to a separate file. Notice that the **OPEN** keyword is use to open the file "RRSUM.OUT" for printing.
24-26	Print the bark beetle output table. Notice that the **OPEN** keyword is used to open the file "BEETLE.OUT" for printing.
27	End of the root disease model keywords. All keywords which follow are not part of the root disease model.
28-29	Process the stand, run the model, and then stop

The first part of the main output file is shown on the following pages.

```
1         FOREST VEGETATION SIMULATOR VERSION 6.2 — INLAND EMPIRE PROGNOSIS 12-15-1995    11:41:55
----------------------------------------------------------------------------------------------------------
                                  OPTIONS SELECTED BY INPUT
----------------------------------------------------------------------------------------------------------
KEYWORD         PARAMETERS:
----------------------------------------------------------------------------------------------------------
NUMCYCLE   NUMBER OF CYCLES= 10
STDINFO    FOREST-LOCATION CODE= 118; HABITAT TYPE=260; AGE= 100; ASPECT AZIMUTH IN DEGREES= 225.;
           SLOPE= 5 percent ELEVATION(100'S FEET)= 52.0; LATITUDE IN DEGREES= 42.
DESIGN     BASAL AREA FACTOR= -1.0; INVERSE OF FIXED PLOT AREA= 1.0; BREAK DBH= 999.9
           SEE "OPTIONS SELECTED BY DEFAULT" FOR PLOT COUNTS AND SAMPLING WEIGHT.
INVYEAR    INVENTORY YEAR= 1990
STDIDENT
           STAND ID= MIXED
DELOTAB    TABLE NUMBER 1  SPECIFIED.  STAND COMPOSITION TABLE WILL BE DELETED.
DELOTAB    TABLE NUMBER 2  SPECIFIED.  SAMPLE TREE TABLE WILL BE DELETED.
RDIN       GENERAL ROOT DISEASE KEYWORDS:
RRTYPE     P TYPE AND S TYPE WILL BE SIMULATED.
SAREA      STAND AREA = 10.00 ACRES
RRINIT     ROOT DISEASE IS P TYPE
           ROOT DISEASE INITIALIZATION KEYWORD; ROOT DISEASE CENTERS ASSIGNED RANDOMLY
           INITIALIZATION WILL BE WITH USER-SUPPLIED DATA UNLESS THE RRTREIN KEYWORD IS USED IN THE RUNSTREAM
           NUMBER OF CENTERS= 5
           50 percent OF TREES/ACRE IN THE DISEASED AREAS ARE INFECTED
           50 percent OF TREES/ACRE IN THE DISEASED AREAS ARE UNINFECTED
           PROPORTION ROOTS INFECTED= .10 ;DISEASE AREA = 1.00 ACRES
RRINIT     ROOT DISEASE IS S TYPE
           ROOT DISEASE INITIALIZATION KEYWORD; ROOT DISEASE CENTERS ASSIGNED RANDOMLY
           INITIALIZATION WILL BE WITH USER-SUPPLIED DATA UNLESS THE RRTREIN KEYWORD IS USED IN THE RUNSTREAM
           NUMBER OF CENTERS= 5
           50 percent OF TREES/ACRE IN THE DISEASED AREAS ARE INFECTED
           50 percent OF TREES/ACRE IN THE DISEASED AREAS ARE UNINFECTED
           PROPORTION ROOTS INFECTED= .10 ;DISEASE AREA = 1.00 ACRES
STREAD     5.0 P TYPE STUMPS OF DIAMETER CLASS 2 OF SPECIES 10 AND 4 AGE ADDED.
STREAD     6.5 S TYPE STUMPS OF DIAMETER CLASS 2 OF SPECIES 4 AND 6 AGE ADDED.
BBCLEAR    NO BARK BEETLES WILL BE ACTIVE
BBTYPE3    TYPE 3 BARK BEETLE TO BE ATTEMPTED IN DATE/CYCLE= 1; SPECIES = 4.;  MINIMUM DBH=10.00 INCHES
           MINIMUM ELIGIBLE STEMS FOR EVENT= 10. STEMS/ACRE ;  MORTALITY RATE = .88
           MINIMUM ROOT DISEASE INFECTION= .30
BBTYPE4    TYPE 4 BARK BEETLE IS ON EVERY YEAR SPECIES =10.;  MINIMUM DBH= 4.00 INCHES
           MINIMUM ELIGIBLE STEMS FOR EVENT= 1. STEMS/ACRE ; INFECTED MORTALITY= .750
            MINIMUM ROOT DISEASE INFECTION= .40 UNINFECTED-WITHIN-PATCH MORTALITY= .30
           UNINFECTED-FRINGE MORTALITY= .15 UNINFECTED-NON-PATCH MORTALITY= .01
RRECHO     MACHINE READABLE OUTPUT ON LOGICAL UNIT 24
OPEN       DATA SET REFERENCE NUMBER = 24; BLANK=ZERO; STATUS=FRESH
           MAXIMUM RECORD LENGTH (IGNORED ON SOME MACHINES) = 132; FILE FORM= 1 (1=FORMATTED, 2=UNFORMATTED)
           DATA SET NAME = RRSUM.OUT
BBOUT      DETAILED BARK BEETLE MORTALITY OUTPUT ON LOGICAL UNIT 27
OPEN       DATA SET REFERENCE NUMBER = 27; BLANK=ZERO; STATUS=FRESH
           MAXIMUM RECORD LENGTH (IGNORED ON SOME MACHINES) = 132; FILE FORM= 1 (1=FORMATTED, 2=UNFORMATTED)
           DATA SET NAME = BEETLE.OUT
END        END OF ROOT DISEASE KEYWORDS
PROCESS    PROCESS THE STAND.
   ----------------------------------------------------------------------------------------------------


   ----------------------------------------------------------------------------------------------------
```

```
                                 OPTIONS SELECTED BY DEFAULT
      ------------------------------------------------------------------------------------------------
TREEFMT     (I4,T1,I7,F6.0,I1,A3,F4.1,F3.1,2F3.0,F4.1,I1,3(I2,I2),2I1,I2,2I3,2I1)
DESIGN      BASAL AREA FACTOR= -1.0; INVERSE OF FIXED PLOT AREA= 1.0; BREAK DBH= 999.9
            NUMBER OF PLOTS= 9; NON-STOCKABLE PLOTS= 0; STAND SAMPLING WEIGHT= 9.00000


      ------------------------------------------------------------------------------------------------
                         SUMMARY OF DISEASE INFORMATION READ IN ON INPUT
      ------------------------------------------------------------------------------------------------
            DISEASE TYPE: P
            NUMBER OF INFECTED STUMPS
            SIZE CLASS      RESINOUS    NON-RESINOUS
            ----------------------------------------
             0- 12"           0.            0.
            >12- 24"          5.            0.
            >24- 48"          0.            0.
            >48-100"          0.            0.
              >100"           0.            0.
            DISEASE TYPE: S
            NUMBER OF INFECTED STUMPS
            SIZE CLASS      RESINOUS    NON-RESINOUS
            ----------------------------------------
             0- 12"           0.            0.
            >12- 24"          0.            7.
            >24- 48"          0.            0.
            >48-100"          0.            0.
              >100"           0.            0.


      ------------------------------------------------------------------------------------------------
CALIBRATION STATISTICS:
                                                    PP      --
                                                    ----    ----
NUMBER OF RECORDS PER SPECIES                        45      16
NUMBER OF RECORDS WITH MISSING HEIGHTS              32      12
NUMBER OF RECORDS WITH BROKEN OR DEAD TOPS           0       0
NUMBER OF RECORDS WITH MISSING CROWN RATIOS         35      15
NUMBER OF RECORDS AVAILABLE FOR SCALING
THE DIAMETER INCREMENT MODEL                         9       1
RATIO OF STANDARD ERRORS
(INPUT DBH GROWTH DATA : MODEL)                    1.14    1.00
WEIGHT GIVEN TO THE INPUT GROWTH DATA WHEN
DBH GROWTH MODEL SCALE FACTORS WERE COMPUTED        .75     .00
INITIAL SCALE FACTORS FOR THE
DBH INCREMENT MODEL                                 .75    1.00
NUMBER OF RECORDS AVAILABLE FOR SCALING
THE SMALL TREE HEIGHT INCREMENT MODEL                0       0
INITIAL SCALE FACTORS FOR THE SMALL TREE
HEIGHT INCREMENT MODEL                             1.00    1.00
NUMBER OF RECORDS WITH MISTLETOE                     0       0
```

8.2 File 2: Thin, Plant, and Push Stumps (Metric)

This keyword file gives examples of harvesting and planting. A highly susceptible species is removed preferentially and a more resistant species is planted. Stump pushing is done to remove the diseased stumps. All values are given in metric units.

In this example, instructions are first given to FVS to harvest and plant. *Armillaria* is the root disease being simulated, and the disease information is read from the tree list (**RRTREIN**). Some additional output files are requested.

```
1.      NUMCYCLE           10
2.      METRIC
3.      INVYEAR          1990
4.      STDINFO           104                 26
5.      DESIGN                        4       999        8
6.      STDIDENT
7.      SUGAR1
8.      THINABA          2001         20        1.00
9.      SPECPREF         2001          3        99
10.     ESTAB            2001
11.     PLANT            2003          6       250       99
12.     TALLYONE         2008
13.     END
14.     NOAUTOES
15.     ECHOSUM
16.     DELOTAB             1
17.     DELOTAB             2
18.     RDIN
19.     RRTYPE              3
20.     SAREA               4
21.     RRINIT              0        30                              1.2
22.     RRTREIN
23.     RRDOUT
24.     PSTUMP           2001        0.9      15.0
25.     BBOUT              27
26.     OPEN               27
27.     BEETLE.OUT
28.     RRECHO             24
29.     OPEN               24
30.     RRSUM.OUT
31.     END
32.     PROCESS
33.     STOP
```

Line #	Description
1	The number of cycles to simulate the model. Each cycle represents 10 years.
2	Tell the model that all input and output will be in metric units.
3-7	Miscellaneous FVS keywords giving information about the stand.
8-9	FVS thinning keywords which ask the model to thin from above to 20 sq.m./ha basal area, preferentially selecting Douglas-fir (species code 3).
10-14	Establishment model keywords to plant 250 trees/ha of species 6 (western red cedar) directly after the harvest. Also, turn off the automatic regeneration model.
15	Print the FVS summary table in a machine readable form in a separate output file.
16-17	Instructions to FVS not to print some of the FVS tables.
18	Begin reading the root disease model keywords. All keywords that are between **RDIN** and **END** (line 31) must be root disease model keywords.
19	Root disease type is *Armillaria* (code 3). Notice that this keyword is one of the first root disease model keywords used.
20	Stand area is set to 4 ha.
21	Initialize the centers and their area. **RRINIT** places 1.2 acres of root diseased area into 30 centers. Notice that field 7 is left blank. Thus, the model will assume that the initialization is for the current disease type: *Armillaria*.
22	Read the infected trees and stumps from the inventory. Use the severity codes to set the initial infection levels for each tree.
23	Print the detailed root disease output table.
24	Push all diseased stumps greater than 15 cm in diameter, with a 90 percent efficiency.
25-30	Print the results from bark beetles to a file titled "BEETLE.OUT", and the machine readable root disease output to the file titled "RRSUM.OUT".
31	End of the root disease model keywords. In the main output file, note that after the **END** keyword, the model prints information about the values used for the bark beetles which are active by default.
32-33	Process the keywords, run the model, and stop.

The first part of the main output file is shown on the following pages.

```
1   FOREST VEGETATION SIMULATOR     VERSION 1.0b — INTERIOR DOUGLAS FIR PROGNOSIS     12-13-1995  23: 7:10
-------------------------------------------------------------------------------------------------------------
                                        OPTIONS SELECTED BY INPUT
-------------------------------------------------------------------------------------------------------------
KEYWORD       PARAMETERS:
-------------------------------------------------------------------------------------------------------------
NUMCYCLE      NUMBER OF CYCLES= 10
METRIC        INPUT AND OUTPUT UNITS ARE METRIC
INVYEAR       INVENTORY YEAR= 1990
STDINFO       FOREST-LOCATION CODE= 104; HABITAT TYPE= 260; AGE= 26; ASPECT AZIMUTH IN DEGREES= 0.; SLOPE=
              5 percent ELEVATION(METERS)= 1158.2; LATITUDE IN DEGREES= 45.
DESIGN        BASAL AREA FACTOR= 9.2; INVERSE OF FIXED PLOT AREA= 4.0; BREAK DBH= 999.0
              SEE "OPTIONS SELECTED BY DEFAULT" FOR PLOT COUNTS AND SAMPLING WEIGHT.
STDIDENT
              STAND ID= SUGAR1
THINABA       DATE/CYCLE= 2001; RESIDUAL= 20.00; PROPORTION OF SELECTED TREES REMOVED= 1.000
              DBH OF REMOVED TREES WILL RANGE FROM .0 TO 999 CMS, AND
              HEIGHT OF REMOVED TREES WILL RANGE FROM .0 TO 999.9 METERS.
SPECPREF      DATE/CYCLE= 2001; SPECIES= DF  (CODE= 3); THINNING SELECTION PRIORITY= 99.
ESTAB         REGENERATION ESTABLISHMENT OPTIONS:
              DATE OF DISTURBANCE= 2001
PLANT         DATE/CYCLE= 2003; SPECIES= CW  (CODE= 6); TREES/HA= 250.;  PERCENT  SURVIVAL= 99.00
              AGE= .0; AVE. HEIGHT= .0; SHADE CODE= .0
TALLYONE      DATE/CYCLE= 2008; DATE OF DISTURBANCE= 2001.
END           END OF ESTABLISHMENT KEYWORDS
NOAUTOES      TALLIES AND INGROWTH WILL NOT BE ADDED AUTOMATICALLY.

              STOCKADJ IS SET TO ZERO, AND NO SPROUTING WILL BE SIMULATED.
DELOTAB       TABLE NUMBER 1  SPECIFIED.  STAND COMPOSITION TABLE WILL BE DELETED.
DELOTAB       TABLE NUMBER 2  SPECIFIED.  SAMPLE TREE TABLE WILL BE DELETED.
RDIN          GENERAL ROOT DISEASE KEYWORDS:
RRTYPE        ARMILLARIA WILL BE SIMULATED.
SAREA         STAND AREA = 4.00 HA
RRINIT        ROOT DISEASE IS ARMILLARIA

              ROOT DISEASE INITIALIZATION KEYWORD; ROOT DISEASE CENTERS ASSIGNED RANDOMLY

              INITIALIZATION WILL BE WITH USER-SUPPLIED DATA UNLESS THE RRTREIN KEYWORD IS USED IN THE
              RUNSTREAM
              NUMBER OF CENTERS= 30

              50 percent OF TREES/HA IN THE DISEASED AREAS ARE INFECTED

              50 percent OF TREES/HA IN THE DISEASED AREAS ARE UNINFECTED

              PROPORTION ROOTS INFECTED= .10 ;DISEASE AREA = 1.20 HA
RRTREIN       ROOT DISEASE INITIALIZATION IS FROM TREELIST
RRDOUT        DETAILED ROOT DISEASE OUTPUT WILL BE PRINTED
PSTUMP        DATE/CYCLE= 2001;  EFFICIENCY = .90; MIN SIZE = 15.00 CMS DBH
BBOUT         DETAILED BARK BEETLE MORTALITY OUTPUT ON LOGICAL UNIT 27
OPEN          DATA SET REFERENCE NUMBER = 27; BLANK=ZERO; STATUS=FRESH
              MAXIMUM RECORD LENGTH (IGNORED ON SOME MACHINES) = 132; FILE FORM= 1 (1=FORMATTED, 2=UNFORMATTED)
              DATA SET NAME = BEETLE.OUT
RRECHO        MACHINE READABLE OUTPUT ON LOGICAL UNIT 24
OPEN          DATA SET REFERENCE NUMBER = 24; BLANK=ZERO; STATUS=FRESH
              MAXIMUM RECORD LENGTH (IGNORED ON SOME MACHINES) = 132; FILE FORM= 1 (1=FORMATTED, 2=UNFORMATTED)
              DATA SET NAME = RRSUM.OUT
END           END OF ROOT DISEASE KEYWORDS
******* WARNING: NO BARK BEETLES WERE SPECIFIED AND  THE BBCLEAR KEYWORD WAS NOT USED.
                        BARK BEETLES ARE ON USING THEIR DEFAULT VALUES AS FOLLOWS
BBTYPE1       TYPE 1 BARK BEETLE IS ON EVERY YEAR. SPECIES =10.;  MINIMUM  DBH=20.32 CMS
              MINIMUM ELIGIBLE STEMS FOR EVENT = 371. STEMS/HA; MORTALITY RATE = .100
BBTYPE3       TYPE 3 BARK BEETLE IS ON EVERY YEAR SPECIES = 4.;  MINIMUM  DBH=25.40  CMS
              MINIMUM ELIGIBLE STEMS FOR EVENT= 25. STEMS/HA;  MORTALITY RATE = .88
              MINIMUM ROOT DISEASE INFECTION= .30
```

```
BBTYPE4      TYPE 4 BARK BEETLE IS ON EVERY YEAR SPECIES = 10.;  MINIMUM DBH= 10.16  CMS
             MINIMUM ELIGIBLE STEMS FOR EVENT= 2. STEMS/HA ; INFECTED MORTALITY= .750
             MINIMUM ROOT DISEASE INFECTION= .40 UNINFECTED-WITHIN-PATCH MORTALITY= .30
             UNINFECTED-FRINGE MORTALITY= .15 UNINFECTED-NON-PATCH MORTALITY= .01
PROCESS      PROCESS THE STAND.


 --------------------------------------------------------------------------------------------------
                              OPTIONS SELECTED BY DEFAULT
 --------------------------------------------------------------------------------------------------
TREEFMT      (I4,T1,I7,F6.0,I1,A3,F4.1,F3.1,2F3.0,F4.1,I1,3(I2,I2),2I1,I2,2I3,2I1)
DESIGN       BASAL AREA FACTOR= 9.2; INVERSE OF FIXED PLOT AREA= 4.0; BREAK  DBH= 999.0
             NUMBER OF PLOTS= 8; NON-STOCKABLE PLOTS= 0; STAND SAMPLING WEIGHT= 8.00000


 --------------------------------------------------------------------------------------------------
                                   ACTIVITY SCHEDULE
 STAND ID= SUGAR1          MANAGEMENT ID= NONE
 --------------------------------------------------------------------------------------------------
 CYCLE DATE  EXTENSION   KEYWORD   DATE   PARAMETERS:

 ----- ----  ---------   -------   ----
 --------------------------------------------------------------------------------------------------
 1    1990
             RDIS      BBTYPE1   1990    10.00    20.32   370.65     .10     .00
             RDIS      BBTYPE3   1990     4.00    25.40    24.71     .88     .30     .00
             RDIS      BBTYPE4   1990    10.00    10.16     2.47     .75     .40     .30    .15    .00
 2    2000
             BASE      THINABA   2001    20.00     1.00      .00  999.00     .00  999.00
             BASE      SPECPREF  2001     3.00    99.00
             RDIS      PSTUMP    2001      .90    15.00
             ESTB      PLANT     2003    14.83   101.17    99.00     .00     .00     .00
             ESTB      TALLYONE  2008  2001.00

 3    2010
 4    2020
 5    2030
 6    2040
 7    2050
 8    2060
 9    2070
10    2080
 --------------------------------------------------------------------------------------------------
```

```
------------------------------------------------------------------------------------------------------------
                          SUMMARY OF DISEASE INFORMATION READ IN ON INPUT
------------------------------------------------------------------------------------------------------------
           DISEASE TYPE: A
           NUMBER OF INFECTED TREE RECORDS IN DISEASE PATCHES=    153.
           NUMBER OF UNINFECTED TREE RECORDS IN DISEASE PATCHES=  213.
           NUMBER OF INFECTED STUMP RECORDS IN DISEASE PATCHES=    20.
                NUMBER OF INFECTED STUMPS
           SIZE CLASS    RESINOUS     NON-RESINOUS
           -----------------------------------------
             0- 30 CM     1012.          56.
            >30- 61 CM       0.           0.
            >61-122 CM       0.           0.
           >122-254 CM       0.           0.
              >254 CM       0.           0.


------------------------------------------------------------------------------------------------------------
   CALIBRATION STATISTICS:

                                              PW      LW      FD      HW      CW      SE      PL
                                              --      --      --      --      --      --      --

   NUMBER OF RECORDS PER SPECIES              16      16     221      53      44      33       3
   NUMBER OF RECORDS CODED AS RECENT MORTALITY  5       0       8       5       0       1       1
   NUMBER OF RECORDS WITH MISSING HEIGHTS     11      16     212      48      44      32       2
   NUMBER OF RECORDS WITH BROKEN OR DEAD TOPS   0       0       0       0       0       0       0
   NUMBER OF RECORDS WITH MISSING CROWN RATIOS 11      16     213      48      44      32       2
   NUMBER OF RECORDS AVAILABLE FOR SCALING
   THE DIAMETER INCREMENT MODEL                0       0       0       0       0       0       0
    RATIO OF STANDARD ERRORS
    (INPUT  DBH GROWTH DATA : MODEL)         1.00    1.00    1.00    1.00    1.00    1.00    1.00


   WEIGHT GIVEN TO THE INPUT GROWTH DATA WHEN
   DBH GROWTH MODEL SCALE FACTORS WERE COMPUTED  .00     .00     .00     .00     .00     .00     .00


   INITIAL SCALE FACTORS FOR THE
   DBH INCREMENT MODEL                        1.00    1.00    1.00    1.00    1.00    1.00    1.00


   NUMBER OF RECORDS AVAILABLE FOR SCALING
   THE SMALL TREE HEIGHT INCREMENT MODEL       0       0       0       0       0       0       0


   INITIAL SCALE FACTORS FOR THE SMALL TREE
   HEIGHT INCREMENT MODEL                     1.00    1.00    1.00    1.00    1.00    1.00    1.00
   NUMBER OF RECORDS WITH MISTLETOE            0       0       0       0       0       0       0
```

9.0 References

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Goheen, E.M.; Thompson, M.K. n.d. **User friendly user's guide to the western root disease model**. Version 1.1. Portland, OR: USDA Forest Service; 49 p. and appendix.

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Chapter 3

Pointers for Using the Western Root Disease Model

Ellen Michaels Goheen[1]   Matthew K. Thompson[2]

Assessing Current Conditions

What Is Important to the Western Root Disease Model

The impacts of root diseases on forest stands vary considerably depending upon the root disease(s) present, inoculum loads, the area of the stand with diseased roots, configuration of root disease patches, host species, size, and distribution, site characteristics, and other factors. Root disease impacts as described by WRDM3 outputs will also vary depending upon how initial conditions are configured in the model. Certain model components are more sensitive than others; knowledge of how these components drive the model should guide how information used to describe the initial conditions of root disease is gathered in the field.

The WRDM3 is most sensitive to the root disease being simulated. Basic model functions that control infection, tree mortality, inoculum survival, and inoculum decay differ depending upon whether the user is modeling laminated root rot, Armillaria root disease, or P-type or S-type Annosus root disease. It is therefore important to know which root disease occurs in the stands being modeled.

How initial root disease conditions in the field are described for the model is also critical. The most important component of root disease initialization is the area inside root disease centers: the proportion of the stand that is inside centers. In general, the greater the area inside centers, the greater impact the disease will have.

If root disease occurs in distinct centers or patches, accurately estimating the area inside the patches is more important than counting the actual number of patches. However, when acres in root disease are equal, very high numbers of centers may have a greater impact on stand dynamics than low numbers, under some stand conditions. Where distinct patches occur, the numbers of infected and uninfected trees inside the patches have little impact on stand dynamics, particularly in mixed species and mixed age stands. Defaults for these entries in the keyword (**RRINIT**) for root disease initial conditions are adequate. If local knowledge indicates that distinct patch patterns are associated with particular root disease/site combinations, efforts to inventory root disease can then be focused on evaluating the area in root disease rather than individual tree characteristics. For example, laminated root rot is frequently found in distinct centers in Douglas-fir stands west of the Cascade Mountains in Oregon and Washington. Therefore, in west-side Douglas-fir stands, estimating root disease area would be a more powerful and efficient inventory method than collecting individual tree disease information.

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If root disease is confined to only a portion of a stand, a post-inventory stratification of the stand into root-diseased and non-root-diseased portions that are simulated separately may provide more realistic outputs. In the WRDM3, root disease centers are randomly placed within a stand unless coordinates are provided. By simulating the strata separately, root disease impacts will be more accurately accounted for in the root diseased portion of the stand, and the "healthy" portion of the stand will not be unnecessarily affected.

When root disease occurs in numerous tiny centers or when the edges of centers are not readily discernible on the ground, the stand should be modeled as one root disease patch. Then, having an accurate estimate of the numbers of infected and uninfected trees becomes critical. Accuracy of the model run will be further improved if individual tree information regarding root disease infection and severity are obtained in the field and included (via **RRTREIN**) in the run. Dead trees with root disease should be included in the tree list to serve as inoculum and adjacent live trees need to be rated for root disease severity. Severity ratings include determining if trees are within 30 feet (10 meters) of known root disease, if they are infected but asymptomatic, or if they are infected and symptomatic.

Acquiring Root Disease Information

In the Western United States, several techniques are used to assess root disease impacts. These include many types and intensities of ground-based surveys as well as interpreting aerial photography to estimate root disease severity. Some of the methods have been developed specifically to acquire the information needed to describe initial root disease conditions for the WRDM3. Regardless of origin, a shared objective of these strategies is to reasonably describe root disease infection levels in a stand.

When information on root disease distribution is not available prior to the survey, comprehensive approaches to root disease survey are necessary. A common approach is to systematically examine a stand, mapping the extent and area in root disease, combined with plot-based sampling of the characteristics of live and dead trees. The mapping distinguishes distinct centers from scattered infection. Plot locations can be geographically tied to root disease centers. Sampling individual trees provides damage and severity information that can be input into the model as a part of the tree list.

Care must be taken that both the mapping and plot grids are intense enough to discern unevenly distributed root disease centers. Sampling intensities used to gather tree characteristics in healthy stands will likely be less than adequate for root diseased stands. To efficiently and economically combine an intensive root disease examination with a standard stand inventory, two sampling grids can be used. A standard plot grid is used to gather information on live and dead trees to supply information to the treelist. These plots can provide the height and growth information that is time-consuming, and therefore expensive, to gather. A more intensive grid is then overlaid on the stand to sample trees in those areas where root disease occurs. Only information necessary to determine proportions of infected and uninfected trees is collected. By using this method, more plots are taken, but efforts are focused in portions of the stand of interest.

Often stand inventory data are available but do not contain root disease information. A systematic walk-through of the stand can provide the necessary root disease information: the area affected and the distribution of centers. The walk-through can also be used to gather information on inoculum sources, such as numbers of infected stumps, that might otherwise not be gathered during the stand inventory.

Interpretation of aerial photography may be used to assess root disease conditions. This procedure is most useful where root disease is the predominant cause of tree mortality seen in the photos and where root disease occurs in a scattered distribution such that the entire stand is considered a single center. Stands are assigned root disease severity ratings on the basis of the number of dead trees in the photographs. These ratings are translated into proportions of infected and uninfected trees and incorporated into inventory keywords. Ground-truthing the severity ratings and other assumptions regarding root disease characteristics is a vital part of this methodology. The intensity of ground-truthing that is adequate will depend on the variability of the forest stands surveyed.

As mentioned in the previous section, any information that can indicate whether root disease occurs in distinct patches or as numerous small centers can help to focus the inventory effort. If scattered infection is

found in certain stand types, such as with S-type Annosus root disease in mixed conifer stands, tree level information is important. Surveys can be designed that focus on intensive sampling of trees and stumps infected by root disease. If discrete patches are the norm, mapping strategies for root disease inventory are more important. Root disease specialists with knowledge of local conditions may be able to provide guidance.

A basic description of root disease initial conditions is essential to a realistic WRDM3 simulation. However, more information is not necessarily better. Data acquisition efforts should be selective; they should take into account the sensitivity of the model to different initialization components, information on local conditions supplied by area experts, and how initialization keywords interact with one another.

Incorporating Information on Current Conditions into a Western Root Disease Model Simulation

It is possible to execute a successful simulation using the WRDM3 without providing information on the actual root disease conditions that exist in the stand of interest. The model has default values that describe a stand of a certain size with a particular configuration of root disease centers. However, running the model without entering information about actual root disease conditions is not recommended. It is highly unlikely that these values represent the actual conditions for your stand. The better the user can describe initial conditions according to available information, the more realistic the output from the run.

There are several root disease inventory keywords to choose from depending upon the type of information available. The user must also be aware that some keywords override others and that keywords used in different combinations have different results.

Essential Inventory Keywords

SAREA: Specifies the stand area. Root disease is simulated spatially; **SAREA** provides boundaries for spread.

RRINIT: Describes initial root disease conditions including the number of root disease centers in the stand, the area that is affected, and the level of infection within that area.

RRTYPE: Designates the root disease being simulated.

RRTREIN: Specifies that the model should look to the tree-level data for specific root disease information. Proportion of infected and uninfected trees inside the centers will come from the treelist. Root infection levels will be based on root disease severity ratings given to individual trees. **RRTREIN** should be used only if root disease information was collected and stored with individual tree data.

Helpful Inventory Keywords

STREAD: Allows the user to enter inoculum sources not included in the treelist. Infected or dead trees and stumps are categorized by species and diameter class. The number entered is the total number for the area, not the density.

PLREAD: Lists the plots (by number) inside root disease centers from which to read individual tree-level damage information from the treelist. The model will ignore all tree-level information on plots not listed.

PLOTINF: Lists the plots (by number) inside the centers and the proportions of infected trees in each plot. This keyword should be used only if **RRTREIN** is not available.

Inventory Keyword Combinations

RRTREIN, RRINIT:

Values calculated from stand examination data where tree-level root disease information is known (when **RRTREIN** is used) will override values entered in **RRINIT**. The number of uninfected and infected trees per acre will be calculated from the tree data. The proportion of root system infected will be based on the root disease severity rating assigned to a tree and the species of tree.

RRINIT, PLREAD:

When **RRINIT** is used in combination with **PLREAD**, the model will use the area in root disease provided by **RRINIT**. If the user does not know the area in root disease, a "-1" can be placed in the field designated for area in root disease in **RRINIT**. The area in root disease will then be calculated as a proportion of the total area based on the proportion of plots infected out of the total number of plots.

PLREAD, RRTREIN:

PLREAD must be combined with **RRTREIN**. **RRTREIN** provides the information that **PLREAD** needs to determine infection levels inside centers.

PLOTINF, RRTREIN, PLREAD:

PLOTINF should NOT be used with **RRTREIN**. If information in **RRTREIN** is available, **PLREAD** should be used. **PLOTINF** is not as powerful a keyword as **PLREAD** combined with **RRTREIN** because it is based on an estimate of the proportion of infected trees, rather than the actual trees that are infected.

Examples of Initializing Root Disease Conditions

The stand of interest encompasses 32 acres. In the field, a walk-through examination provides information on current root disease conditions. Laminated root rot is present in five distinct centers. The centers encompass 7 acres. Information from local pathologists suggests that the default, a 10 percent average root infection level, is low for the area; 45 percent average root infection represents the local conditions better.

Within the WRDM3, the keywords **SAREA** and **RRINIT** are used to describe current conditions. SAREA equals 32 acres. Input to **RRINIT** includes that the root disease centers are located randomly (there is no information on coordinates of individual root disease centers available), the number of centers is 5, no information was collected on the number of infected and uninfected trees per acre inside the centers (defaults are used), the average percent root infection is 0.45, the number of acres with root disease is 7, and the disease simulated is laminated root rot (type 4).

The portion of the keyword set that directs the WRDM3 looks like this:

```
RDIN
RRTYPE      4
SAREA       32
RRINIT      0       5       (blank)  (blank)  .45      7        4
END
```

In another area, a 45-acre stand is intensively inventoried. Root disease centers are well represented by the plot data. Root disease damage codes and appropriate severity levels are designated for individual trees. Additional information on infected stumps outside of plots was also collected during the inventory. Four laminated root rot centers totaling 16 acres were found.

WRDM3 inventory keywords used are **SAREA**, **RRINIT**, **RRTREIN**, and **STREAD**.

RDIN							
RRTYPE	4						
SAREA	45						
RRINIT	0	4	(blank)	(blank)	.1	16	4
RRTREIN							
STREAD	4	1	45				
STREAD	2	1	33				
STREAD	4	2	11				
STREAD	4	3	5				
END							

A 39-acre stand is examined. Tree-level root disease information is not collected; however, an effort is made to estimate the proportion of trees affected by root disease on every plot. Root disease pockets are mapped in relation to stand inventory plots. Three laminated root disease centers were found, each of which is associated with a different inventory plot (Plots 1, 5, and 11), and within each plot, 30 percent of the trees are estimated to be infected. Based on the map, the three plots are estimated to represent a total of 9 acres.

WRDM3 keywords used to represent these current conditions are **SAREA**, **RRINIT**, and **PLOTINF**. **PLOTINF** tells the model the proportion of trees, on a given plot, that are infected.

RDIN							
RRTYPE	4						
SAREA	39						
RRINIT	0	3	(blank)	(blank)	.1	9	4
PLOTINF		4					
	1	0.30					
	5	0.30					
	11	0.30					
-999							
END							

Adjusting Model Functions

The functions inside the WRDM3 that describe mortality and growth loss, spread rate, inoculum survival, etc. are based on best estimates for West-wide averages, or are specific to locations where reliable data were available at the time the model was built. Outputs based on defaults are not meant to represent conditions on all sites. Local conditions may differ. Species susceptibility or site factors may not be well represented by model defaults. However, the model can be adjusted to more closely represent these differences.

Most of the functions that guide model behavior can be modified using keywords. By adjusting one or more of these keywords, changes in model behavior may better reflect local conditions. For example, in some areas, Armillaria root disease readily kills ponderosa pine in all age and size classes. In other locations, ponderosa pine is little affected and would be a good species to plant when managing Armillaria root disease. When modeling Armillaria root disease in areas where ponderosa pine is a resistant species, defaults specific to ponderosa pine can be changed. These may include increasing the time required for ponderosa pine trees to die, increasing the proportion of colonized root system necessary for ponderosa pine death, and making it more difficult to transmit the fungus from one ponderosa pine root system to another.

Model-modifying keywords should be used with caution. Some are much more powerful than others; small adjustments in certain keywords have large effects on model output. There are logical combinations of keywords and combinations that override one another. Model adjustments should be based on experience and local information. Local root disease specialists should be consulted to determine under which circumstances, and to what degree, these adjustments need to be made. West-wide efforts are underway to calibrate the model for local conditions. In many cases, data are available to support adjustments; in other situations, default values are adequate.

The keywords listed below are frequently used to modify model functions:

INFKILL: In the model, trees die before their entire root system becomes colonized by the root disease-causing fungus. The proportion of colonized root system necessary for tree death differs for each root disease fungus and each tree species. **INFKILL** controls this proportion. The larger the proportion, the more fungal colonization required for tree death, and hence, the longer trees live.

INFMULT: Infection probability describes how well root disease is transmitted from one tree to another, assuming root system overlap. This probability is controlled by **INFMULT** and is specific to root disease and tree species. **INFMULT** is the most powerful model-modifying keyword to use to reflect changes in species susceptibility.

TTDMULT: The time-to-death multipliers in the model describe how long it takes for a tree to reach the proportion of root system infection required for death from the time it first becomes infected. These multipliers are specific to root disease and tree species. They are controlled by the keyword **TTDMULT**.

Other model-modifying keywords are available. They are not as powerful as the ones described above. These other keywords control specific equations in the model such as how inoculum decays (**INOCLIFE**), the minimum number of years the inoculum is present (**INOCSPAN**), and the proportion of root system infected after death (**INFCOLO**).

Modeling Complexes

Modeling Stands with Multiple Root Diseases

In many stands, more than one root disease is present. However, with the exception of Annosus root disease where both P-type and S-type can be modeled simultaneously, the WRDM3 can simulate only one root disease at a time. Model behavior is different depending upon which fungus is being modeled.

Modeling the effects of root disease complexes can be done by using combinations of keywords that modify model assumptions to fit the root disease dynamics of the complex. Any reference to root disease type becomes academic. Infection parameters, inoculum lifespan, species susceptibility, etc. are adjusted to represent how the fungi work together. Calibration data or experience with local conditions are required to be successful. Local experts can provide guidance on which keywords to use and how to adjust them to represent stand conditions.

Bark Beetles

Bark beetles are often found in association with root diseased trees; beetles are attracted to trees with reduced vigor. They can also affect root disease dynamics by killing trees. Tree death reduces stand density and, thus, influences root disease spread. Bark beetles may also cause mortality that is not related to root disease; the beetle activity is triggered when stand density thresholds are exceeded or by sudden increases in down wood.

The WRDM3 offers several options for including bark beetle activity in stand simulations with root disease. Bark beetles that are dependent on density and/or root disease operate at all times during a simulation, unless they are turned off using the keyword **BBCLEAR**. Bark beetles that respond to windthrow will be included in the run if windthrow occurs and other parameters are met. Both endemic and outbreak populations of bark beetles can be simulated.

The user should examine the assumptions associated with bark beetle activity to determine whether defaults used to describe each bark beetle type in the model (**BBTYPE 1-4**) correspond to known behavior of local bark beetle populations. Entomologists with bark beetle expertise should be consulted. Bark beetle parameters can be easily changed by adjusting the keyword specific to the bark beetle type to be modified (**BBTYPE 1-4**). The user can change minimum tree diameters associated with bark beetle attack, threshold stand densities, threshold down tree densities, the proportion of root system infected that triggers bark beetle attack, as well as species susceptibility and mortality rates. But, unless there is good reasoning behind it, bark beetle functions, as with all other model functions, should remain at default settings during simulations.

Windthrow

Major blowdown events can be simulated within the WRDM3. The keyword **WINDTHR** is used to set how soon windthrow occurs in the run and the proportion of trees affected. The user designates a minimum threshold of trees to be windthrown. This keyword must be present to activate bark beetles requiring windthrow (**BBTYPE2**).

Chapter 4

Detailed Model Description

Sarah J. Beukema[1] **Werner A. Kurz**[2] **Julee Greenough**[3]

This chapter is organized into four sections. Section 1 discusses some of the model's basic concepts and definitions. The second section describes details of root disease dynamics. The final two sections describe other options in the model: bark beetles, windthrow, and management options. This chapter explains the functions contained in the Western Root Disease Model, version 3.0. For instructions explaining how to use the model, see Chapter 2, How to Use the Western Root Disease Model, Version 3.0.

1.0 Basic Concepts
1.1 Order of Calculations
Both FVS and the Western Root Disease Model operate on the same time step or "growth cycle." In each cycle, after FVS predicts the amounts of growth and mortality and before it applies them to the tree records, the root disease model simulates the dynamics of root disease and other agents and adjusts the FVS-predicted growth and mortality values to account for impacts from bark beetles, root disease, and windthrow. *Table 1.1* presents the basic order of calculations in the model.

1.2 Tree Lists
The root disease model keeps track of stand information using a variety of tree lists. The structure and number of records in the standard FVS list of live trees is replicated three times. The content of each element in each new tree list varies depending on its disease status. These new tree lists are:
- Trees outside root disease centers (as trees per acre [or hectare] of area outside centers);
- Trees which are uninfected but which are inside a center (as number of trees); and
- Infected trees inside centers (as number of trees), stratified by the source of infection (from a center expanding or from being infected inside a center).

For each of these lists, the model also keeps track of the species, dbh, and root radius of each element. When Armillaria root disease or *Phellinus* are simulated, all tree species are potential hosts to the disease. For Annosus root disease, each tree species is capable of being host to only one of the two Annosus root disease types (S or P). A list of the number of dead infected trees and stumps stratified by Annosus root disease type (if Annosus root disease is being simulated), wood type (resinous or non-resinous), and diameter size class is also maintained (*table 1.2*). Note that the model does not distinguish between dead trees and stumps.

Since the model must update infection levels in both live infected trees and dead infected trees and stumps based on either age or time since death, the list of live infected trees contains information about

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Table 1.1–Order of calculations in the Western Root Disease Model, including sections of FVS. Italicized activities are part of FVS.

Read all keywords and inventory
Establish initial root disease conditions

For Each Growth Cycle
    Apply stand management

    Apply borate to newly created stumps (Annosus root disease only)
    Calculate spore infection of stumps (Annosus root disease only)
    Update dead infected list and stump list

    Estimate normal growth and mortality for each tree list element
    Compute radial extent of roots
    Calculate effects from bark beetles and windthrow
    Update dead infected tree list
    Push stumps
    Calculate new infection within centers
    Calculate new centers (from spore infection, if Annosus root disease is present)
    Spread or shrink centers (including the "jump" after harvesting)
    Update infection levels
    Calculate actual tree mortality and growth
    Update all tree lists
    Decay the inoculum in dead infected trees and stumps

    Call Establishment Model
    Update Stand Attributes (by applying the growth and mortality rates)
    Display Indicators

End Growth Cycle Loop

Table 1.2–Stratification of dead infected trees and stumps. This list is further stratified by year of death (not pictured here).

Disease Type[*]	Resinous	Diameter size class				
		0-12 in. [0-30.5 cm]	>12-24 in. [>30.5-61 cm]	>24-48 in. [>61-122 cm]	>48-100 in. [>122-254 cm]	>100 in. [> 254 cm]
P	yes					
	no					
S	yes					
	no					

*Annosus root disease only

the year in which infection occurred, and the list of dead trees and stumps retains the year that the infected tree died.

All dead trees (i.e., not just dead infected trees) are recorded in an array for potential use outside the root disease model (e.g., in the simulation of snag dynamics). This array contains information about the number of trees that died, the "official" cause of death (root disease, bark beetles, windthrow, or "natural" causes), and whether the tree was infected at the time of death. This array is not used or manipulated at any point within the root disease model.

Note for Annosus Root Disease

When Annosus root disease is simulated, information about newly created, uninfected stumps is maintained for two cycles after a harvest, for use by the spore model (see Section 2.6). These lists contain the same information as the list with dead infected trees and stumps. After 20 years the information in these lists is either discarded or, if stump infection occurred, added to the list of dead infected trees and stumps.

Transfer between the various lists occurs through harvesting, infection, and mortality. A pictorial summary of the processes is shown in *figure 1.1*.

1.3 Representation of Roots, Centers, and Stands

The root disease model makes several simplifying assumptions about roots, centers, and stands. These simplifications are designed to capture the essence of the geometry but still retain some generality and ease of calculation.
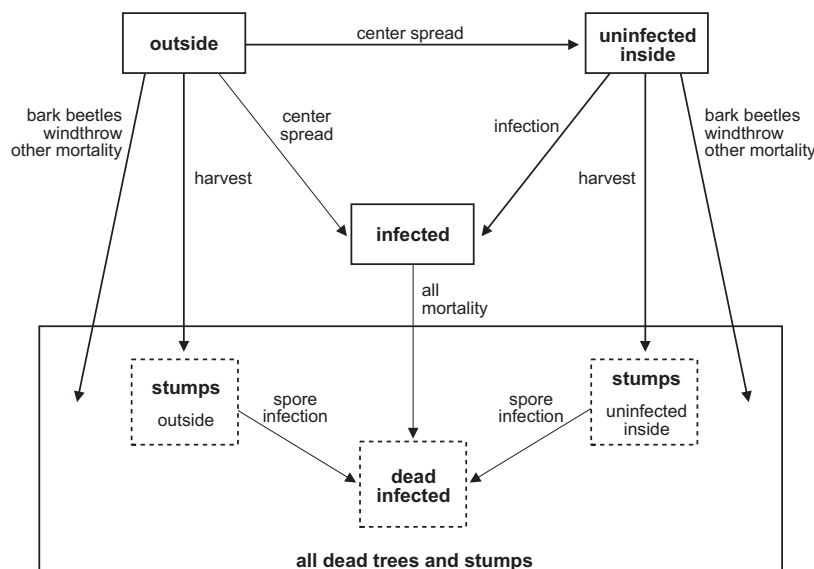
Figure 1.1–Mechanisms which transfer trees between tree lists (shown in bold). "Other mortality" mechanisms are those not predicted by the root disease model. The "All dead" list includes those trees contained in the Dead Infected list and the two stump lists. Note that not all uninfected trees which are harvested will become spore-infected, and only stumps created during a simulation with Annosus root disease present can potentially become infected.

1.3.1 Roots

The model assumes that in each tree, the extent of all roots large enough to become infected by root disease is modeled as a circle with the stem of the tree as its center. The radius of this circle is a linear function of dbh for trees greater than 3.5 inches [8.9 cm] dbh:

$$Radius = F1 * F2 * dbh$$

where

Radius	is the root radius in feet;
F1	is an FVS parameter which is normally equal to 1.0;
F2	is an FVS species-specific parameter which equals 14.26 for all species except western hemlock (14.5) and western red cedar (9.35); and
dbh	is the dbh in *feet* (i.e., inches/12) or *meters* (i.e., cm/100).

For trees less than 3.5 inches [8.9 cm] dbh, the root radius depends on tree height and stand basal area:

$$\text{(Imperial)}\ Radius = e^{(0.6\ \ln(HT)+0.4\ \ln(BA)\text{-}0.81)}$$

$$\text{or (Metric)}\ Radius = e^{(0.6\ \ln(HT)+0.4\ \ln(BA)+2.75)}$$

where

Radius	is the root radius in feet or meters;
HT	is the height in feet or meters; and
BA	is the stand basal area in sq.ft./acre or m^2/ha.

These equations both assume that the roots are growing under some average condition. Since the root radius may be different in stands which are more or less crowded than average, the model includes a keyword, **SDIRMULT,**[4] which allows users to have the root radius change as the density of the stand changes. This keyword invokes a multiplier which depends on the Reineke's stand density index (SDI) (Reineke 1933) and which ranges from 0.5 to 1.5 (*fig. 1.2*). When this keyword is used at the default values, the root radius will be larger in less dense stands, and smaller in denser stands, where the "normal" density is defined by the users. The maximum and minimum values of the multiplier are not under user control.
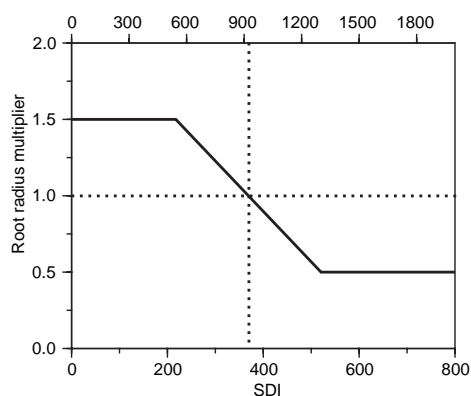
Figure 1.2–Root radius multiplier activated using the SDIRMULT keyword. The bottom axis is in imperial units (trees/acre) and the top axis is in metric units (trees/hectare).

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[4] All model keywords are listed in bold. They are explained in detail in Chapter 2, How to Use the Western Root Disease Model, Version 3.0.

Since root systems are defined as circles, infection levels and the amount of inoculum in the stand are defined by the length of the root radius that is infected in live trees, dead trees, and stumps. This method for defining infection means that while the proportion of the radius that is infected increases linearly, the amount of area that is considered infected increases quadratically (*fig. 1.3*). Section 2 contains detailed descriptions of the dynamics of the infection.
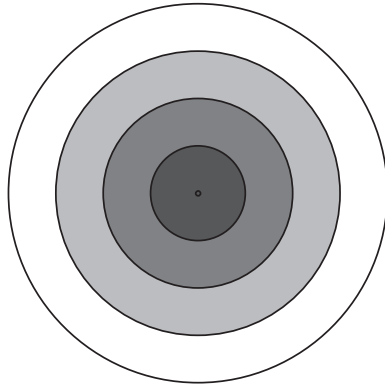
Figure 1.3–Area within a root system that is infected. Lighter shading indicates areas infected in more recent time steps. Notice that each concentric ring is the same width (the radius increases linearly), but the area represented by each ring increases as the distance from the center of the circle increases (i.e., the area increases quadratically.)

1.3.2 Centers

A second model assumption is the definition of a root disease center. Centers are assumed to be circles encompassing the outermost point of infection, i.e., the perimeter of the infected root systems. Note that this definition may be different from the one used often in the field in which the center boundaries are drawn by connecting stems of infected trees. This assumption has two ramifications. The first is that the area inside root disease centers may be much larger when calculated by the model than what is seen in the field (*fig. 1.4*). The second is that while the center is considered to be one large infection zone, it has a certain level of inoculum (as represented by infected live trees, dead trees, and stumps) which may be patchy. Thus it is possible for a center to cover 2 acres, for example, with two old stumps whose infected roots each have a 2-foot radius as the only source of inoculum (*fig. 1.5*). The stand would seem heavily
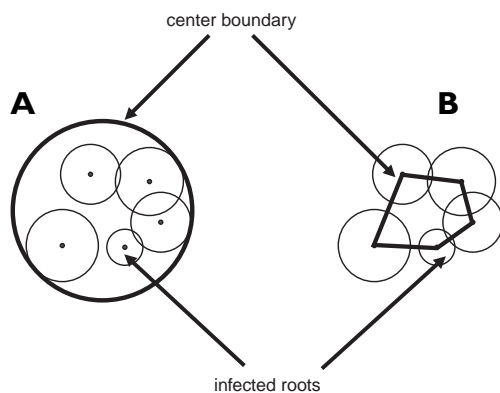
Figure 1.4–Boundary of a center. The heavy line indicates the edge of the center (i.e., the area inside the area defined by the line represents the area inside centers), the black dots are the stems of trees, and the light circles are the extent of the root disease in each tree. (A) Calculation of the boundary by the model. (B) One method of calculating the boundary in the field.
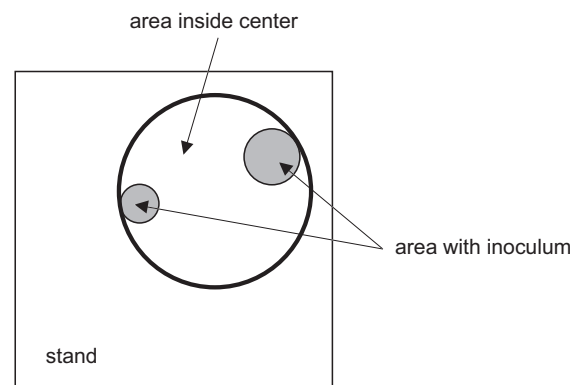
Figure 1.5–Difference between the center area and area with inoculum. The square represents the stand boundary, the heavy circle outlines the center boundary, and the shaded circles show the area with inoculum.

infected from the amount of area inside the center but would actually contain very little inoculum or potential for infecting healthy trees.

The disease centers are defined by their location in the stand and their size. Location is defined by assigning coordinates to the mid-point of each center either randomly by the model or specified by the user at the time of initialization. The size of each center is entirely defined by its radius. Any center may overlap other centers or may extend outside the stand boundary (*fig. 1.6*); the model accounts for the actual area inside centers in the stand correctly (see Section 2.4 for details). For Annosus root disease, when both types of root disease are in the stand, S- and P-type Annosus root disease centers are maintained separately.
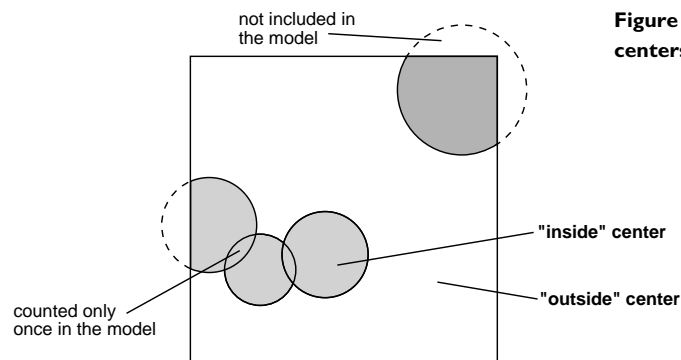
Figure 1.6– Areas considered inside centers. Notice that some centers extend outside the stand, and other centers overlap.

Throughout all reports, the part of the stand infected by root disease (of the type of interest) is referred to as "inside" (as in inside a disease center), while the part of the stand not infected by that root disease is termed "outside" (*fig. 1.6*). For example, for Annosus root disease, a tree that is an S-type host is considered "inside" if it is within an S-type center, but is considered "outside" in all other areas of the stand, including areas which are inside P-type centers.

1.3.3 Stands

All stands are represented as squares. Stand dimensions (measured in feet or meters) are used for two purposes: for calculating the total area in root disease centers inside the stand and for placing centers into the stand. While the mid-point of each center must be inside the stand, part of a center may extend outside of the stand boundaries. The part outside the stand is not considered as part of the root disease area in the model. Thus, when calculating the total area inside centers, the model needs to know the location of the edges of the stand so as not to account for any of the area outside of the stand. The model also needs to know the stand's dimensions when determining the location of centers (as assigned by the user or by the random number generator) to ensure that the mid-point of the center is within the stand.

Users should be aware of some of the consequences of manually placing centers in a stand. Most stands in the field are not actually squares so a center which is inside the stand in the field may be outside the stand in the model. The model will change the coordinates of any centers which are outside of the stand to be on the stand border (*fig. 1.7*). As a consequence, the area inside centers may not be preserved. A center which is on the border will have less area inside the stand than the center that was totally within the original non-square stand.

1.4 Effect of Infection

Root disease affects trees in three ways: by reducing their height and diameter growth, by increasing their susceptibility to other agents (bark beetles and windthrow), and ultimately by killing the trees. The effect of the root disease on growth is a function of the proportion of the root radius infected (*fig. 1.8*):

$$Growth = -2 * infection + 1 \qquad \text{if } infection \leq 0.5$$
$$= 0 \qquad \text{if } infection > 0.5$$

where

> *Growth* is the proportion of growth that is realized; and
> *infection* is the proportion of the root radius that is infected.

This proportion of growth realized is applied to the height and diameter growth increments predicted by FVS. Since a FVS tree record may be made up of a mixture of infected and uninfected trees, the amount that a record actually grows is the average of the height or diameter increment for each tree in the record.
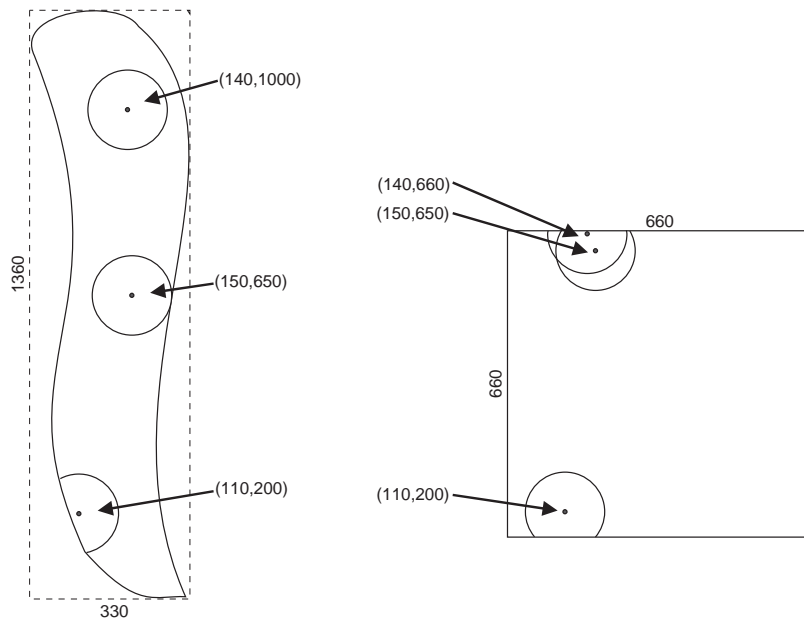
Figure 1.7–Caveats when placing centers in a stand. On the left, a non-square stand with three centers. On the right, the model's square representation of the same stand. Notice the new location of the uppermost center. Also notice that the stand in the model will have less area in root disease because of the overlap in the two centers near the top edge of the stand.
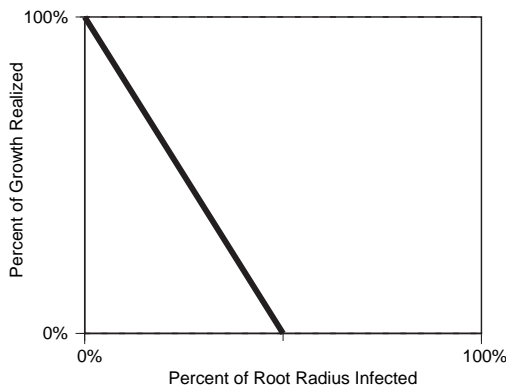
Figure 1.8–Percentage of growth realized in infected trees.

1.5 Mortality Reconciliation

Both the root disease model and FVS predict mortality. FVS calculates an expected probability of mortality for each tree record in the tree list at the beginning of each growth cycle. The FVS mortality functions were, in theory, developed from data that include all causes of tree death, including root disease, bark beetles, and windthrow. Because the root disease model explicitly calculates the mortality from these sources, and because the FVS-predicted mortality is a minimum value, the actual mortality applied must be a combination of the mortality predicted by the two models.

The two estimates of mortality are reconciled on a record-by-record basis. FVS mortality applies to the entire tree record. The root disease model identifies, for each record, trees that are infected, uninfected inside centers, or outside centers (by definition uninfected). The model calculates a specific mortality rate for each category of trees. The objectives of the reconciliation process are to apply the mortality differentially to each category while killing at least as many trees in the entire record as the background mortality predicted by FVS.

Two cases can apply: total mortality predicted by FVS can either be greater than (or equal) or less than that predicted by the root disease model.

1. FVS mortality is greater than (or equal to) root disease model mortality

For infected trees, the root disease model first applies the greater of the root disease or FVS predicted mortality. Then it applies the remaining mortality to trees outside centers and, if necessary, to uninfected trees inside centers. If the mortality of infected trees predicted by the root disease model is greater than that predicted by FVS, then the mortality of uninfected trees must be reduced in proportion (except when bark-beetles or windthrow caused mortality of uninfected trees that was greater than that predicted by FVS). For example, imagine a record of 36 trees, 12 in each of the three categories. FVS predicted a mortality of 9 trees, i.e., 25 percent of the record. For infected trees, the FVS prediction of mortality is 12*0.25 = 3 trees. Assume that the root disease model predicted that 7 of the 12 infected trees died, and that there was no mortality of uninfected trees due to bark beetles or windthrow (*table 1.3*). First, 7 of the 12 infected trees are killed. The total mortality predicted by FVS was 9, so 2 more trees must be selected from the uninfected trees inside or outside centers. Since the stand density is higher outside centers, the remaining mortality is first applied to trees outside centers. FVS predicted that 25 percent or 3 of the trees outside centers would die, but in this case only 2 trees would be killed according to the model. None of the uninfected trees inside centers would be affected.

2. FVS mortality is less than root disease model mortality

As in the previous example, the root disease model first applies the greater of the root disease or FVS-predicted mortality to infected trees. Then it applies the remaining mortality to trees outside centers and, if necessary, to uninfected trees inside centers. For example, imagine a record of 36 trees, 12 in each of the three categories. FVS predicted a mortality of 9 trees, i.e. 25 percent of the record. The FVS prediction for mortality of infected trees is 12*0.25 = 3 trees. Assume that the root disease model predicted that 7 of the 12 infected trees died, and that 4 trees outside centers and 2 uninfected tree inside centers were killed by bark-beetles (*table 1.4*). Since total mortality predicted by the root disease model is greater than that predicted by FVS, the mortality predicted by the root disease model in each category of trees will be applied.

Table 1.3–Example of mortality reconciliation when FVS predicts higher mortality than the root disease model.

	Total	Infected	Inside-Uninfected	Outside
Number of trees	36	12	12	12
FVS-predicted mortality	9	3	3	3
Root disease-predicted mortality	7	7	0	0
Applied mortality	9	7	0	2

Table 1.4–Example of mortality reconciliation when FVS predicts lower mortality than the root disease model.

	Total	Infected	Inside-Uninfected	Outside
Number of trees	36	12	12	12
FVS-predicted mortality	9	3	3	3
Root disease-predicted mortality	13	7	2	4
Applied mortality	13	7	2	4

2.0 Root Disease Dynamics

2.1 Introduction

The root disease model simulates the dynamics of root disease in a tree's root system from the time of infection, through the spread of the disease across the root system, to the complete decay of the inoculum (*fig. 2.1*). Infection can occur in live trees through contact with inoculum or in stumps through spores. Each step is explained in more detail below.

2.2 Initial Infection in the Stand

The two principal options for simulating stand dynamics with the model are stand establishment on bare ground or starting with an existing stand. A new stand is established through planting or natural regeneration and the inoculum originates from infected stumps remaining from the previous stand (entered either using a keyword or through the tree list). When the model is used to simulate an existing stand, infection can be initialized in many different ways (see Chapter 2, Section 3). Accurately portraying the existing status of the root disease in the actual stand in the model is both difficult and important. In the field, trees will show a variety of infection levels: some trees will have recently been infected, others may have just been killed by the disease, and others will have infection levels between these stages. Depending on how the model is initialized, the model will attempt to capture some of this heterogeneity of infection levels.

2.2.1 Initializing from the Tree List

The root disease can be initialized using information in the tree list, either disease code information, plot information, or both. When the keyword **RRTREIN** is used, codes in the tree list identify infected tree
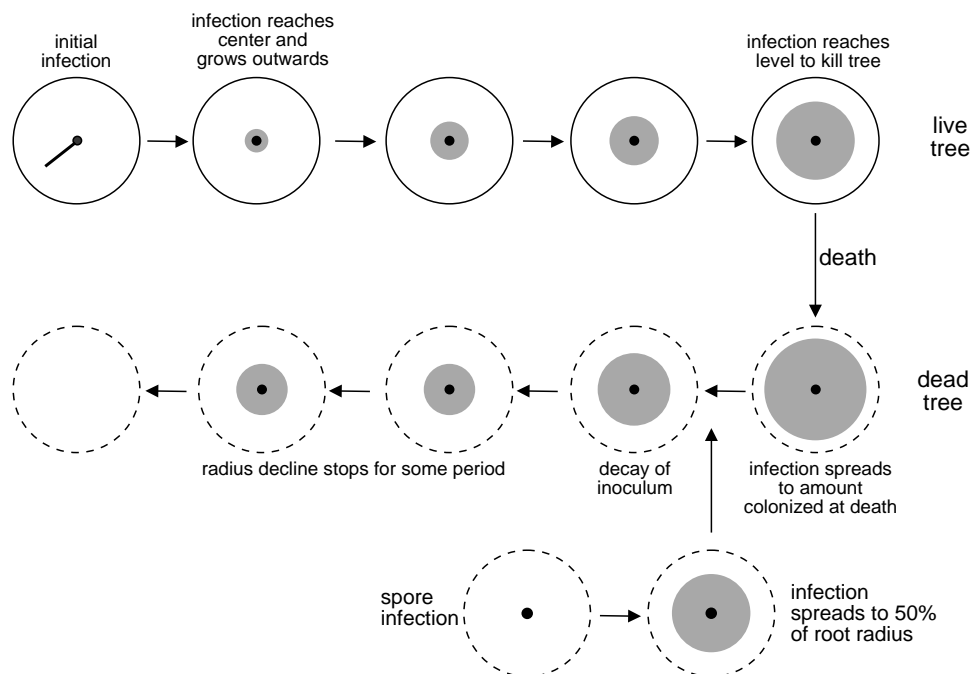
Figure 2.1–Summary of the dynamics of root disease. The first row is for a live tree, and the second and third are for a dead tree or stump. In all cases, infection is represented by the shaded area, the stem or stump by a black dot, and the maximum extent of the root system by the outermost circle. Note that spore infection occurs only for Annosus root disease.

records. All other records are assumed to be uninfected, either inside or outside of centers. If **PLREAD** is used, the model assumes that all the records in the plots listed in the keyword are inside centers. Those records that do not have root disease damage codes will be assumed to be uninfected. All records which are in plots not identified in the keyword are assumed to be uninfected trees outside disease centers (even if a disease code is present, i.e., the disease codes are ignored).

When **PLREAD** is used, each element in the FVS tree list represents trees in only one of the root disease model tree lists. To account for density correctly, the model scales each of the root disease model tree lists by the ratio of the stand area to appropriate area (area inside centers for tree lists inside centers and disease-free area for the outside tree list). This keyword allows the model to have different stand densities inside and outside centers. The Appendix for Chapter 4 shows the equations which adjust the densities in each of the tree lists, and provides users with an example.

2.2.2 Choosing Trees to Infect (When No Damage Codes are in the Tree List)
The choice of which tree records to infect becomes more complicated when **RRTREIN** is not present and the model is initialized via the keyword **RRINIT.** This keyword allows users to define the amount of area within centers and the proportion of trees in centers which are infected or uninfected. The model assumes that the distribution of infected trees by species should be based in part on the likelihood of becoming infected so that, all else being equal, the center should contain more infected trees of a species which has a high probability of being infected. Next, the model uses the average time from infection to death for the trees (by species) in the center; species with long times to death will be more likely to be represented as infected in the center than those whose time to death is very short. Combining this information, the model calculates the number of trees of each species to be infected in diseased areas. A more detailed explanation (with equations and examples) is given in the Appendix for Chapter 4.

2.2.3 Degree of Infection

Trees may initially be infected at different levels. When **RRTREIN** is used, the severity code connected with the damage code determines the initial proportion of root radius that is infected (see Chapter 2 for the exact definition of each severity code). The severity codes define a proportion relative to the amount infected at death; thus the same severity code may lead to different proportions of infected root radii in different species.

If information about the damage or severity codes is unavailable and the keyword **RRINIT** or **PLOTINF** was used, the infection level is assigned differently. Users may define the average proportion of root radius which is infected in the keyword **RRINIT**. For each tree record which is infected initially, the root disease model will choose a proportion infected from a distribution about the defined root radius. The average proportion of root radius infected will usually be close to the requested value (see the root disease summary table in the main output file), but deviations occasionally occur because of the random component. Assigning a range of initial infection levels assures some variability in the timing of the death of infected trees. This avoids a peak in mortality near the beginning of the model simulation, which is created by a cohort of trees infected at identical levels.

2.3 Spread of Infection Within a Center

2.3.1 Infection within Root Disease Centers

Live trees become infected through root contact with sources of inoculum (modeled as the infected portion of the root systems of either live or dead infected trees and stumps). Because FVS is not spatially explicit, the root disease model does not know the location of trees in the stand. To estimate the likelihood of becoming infected, the model explicitly simulates a small portion of the stand (with average characteristics of inside centers). The locations of a representative sample of live infected and uninfected trees and dead infected trees and stumps (*fig. 2.2*) are assigned at random. The sample plot is used to estimate the new infections resulting from root contacts. The results from these simulations are then applied to the entire stand.
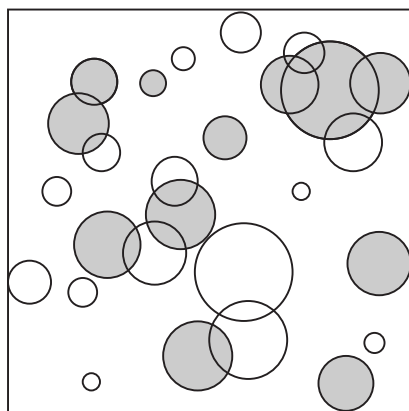
Figure 2.2–Example sample plot used for calculating infection rates inside centers. The shaded circles are the sources of inoculum (the infected roots of live and dead infected trees and stumps), while the open circles are the root systems of uninfected trees.

For each disease type, the sample plot is set up with representative trees. In order to control execution time, the model attempts to simulate 20 trees, and adjusts the area which is simulated accordingly (so a dense stand would use a smaller plot than a less dense stand). The model estimates the number of trees from each record in each infected tree list (live and dead infected) that should be placed into the plot, based on the target number of trees (20), and the resulting plot area. Then, the number of trees equal to the integer number of trees in each entry is placed in the simulated plot. If there is a fractional number of trees remaining, a random number is drawn which determines whether to include another tree from that

element. If the random number is less than the fractional number, another tree will be added. For example, if the model computes that an element should contribute 3.4 trees, 3 trees would be added, and there would be a 40 percent chance of including one more tree (because in a uniform random number generator 40 percent of the number will be less than 0.4, the fractional number of remaining trees).

At the time these inoculum trees are chosen, they are also randomly assigned an X and Y coordinate. The model then loops over each tree in the inside uninfected live tree list with the appropriate disease type, placing each one in the simulation plot.

2.3.2 Probability of Infection

Infection can occur when the infected portion of the root system of a diseased tree contacts the root system of a healthy tree. The probability of infection, given a single contact, varies among tree species and root disease species (*table 2.1*) and can be controlled using the **INFMULT** keyword (*table 2.2*).

The probability of infection is defined to be the probability in a 10-year period: *i.e.,* in 10 years, what is the probability that a tree becomes infected, given that its root system contacts the infected portion of the root system of an infected live or dead tree? The model properly adjusts the probabilities of infection if a time step other than 10 years is simulated. (This was not the case in earlier versions of the model). Thus, considering infection rates only and assuming no additional effects from the change in time step, if the model was simulated in 5-year steps, the same amount of infection should occur after 30 years as when simulating in 10-year steps.

Table 2.1–Examples of parameters defining root disease dynamics for Annosus root disease (A), Armillaria root disease (Ar) and laminated root rot (Ph). The parameters given here are those used in the Inland Empire and Southern Interior variants of FVS. Details on these parameters for other species and other variants can be found in the Appendix for Chapter 2.

Species	Prob. of infection			Relative time to death			Prop. of root radius infected at death			Prop. of root radius colonized after death			Wood type[1]
	A	Ar	Ph	A	Ar	Ph	A	Ar	Ph	A	Ar	Ph	
White pine	0.4	0.1	0.1	1.0	1.8	3.0	0.6	0.3	0.8	0.8	1.0	0.8	R
Larch	0.4	0.05	0.2	1.0	2.0	1.5	0.9	0.85	0.6	0.95	1.0	0.6	R
Douglas-fir	0.4	0.5	0.4	1.0	1.0	1.0	0.8	1.0	0.3	0.95	1.0	0.3	R
Grand fir	0.5	0.6	0.4	1.5	0.75	1.0	0.8	0.75	0.85	0.9	1.0	0.85	NR
Western hemlock	0.5	0.1	0.2	1.75	0.9	1.5	0.8	0.8	0.8	0.9	1.0	0.8	NR
Western red cedar	0.0	0.1	0.02	1.0	1.2	1.0	1.0	0.8	0.85	1.0	1.0	0.85	R
Lodgepole pine	0.4	0.2	0.1	1.5	1.8	3.0	0.5	0.8	0.8	0.75	1.0	0.8	R
Spruce	0.4	0.5	0.2	1.0	1.1	1.1	0.9	0.6	0.8	0.95	1.0	0.8	NR
Alpine fir	0.5	0.5	0.4	1.5	0.75	1.0	0.8	0.8	0.75	0.9	1.0	0.75	NR
Ponderosa pine	0.5	0.2	0.1	0.5	1.8	3.0	0.5	0.8	0.65	0.75	1.0	0.65	R
Other	0.0	0.1	0.4	1.0	0.9	1.5	1.0	0.6	0.8	0.86	1.0	0.8	NR

[1]R = resinous, NR = non-resinous

Table 2.2–Keywords used to change the parameters defining root disease dynamics. Each of these keywords uses essentially the same format (see Chapter 2). Note that these keywords will rarely be used by users other than pathologists.

Parameter	Disease type	Probability of infection	Relative time to death	Proportion of root radius infected at death	Proportion of root radius colonized after death
Keyword	**RRHOSTS**	**INFMULT**	**TTDMULT**	**INFKILL**	**INFCOLO**

2.3.3 Multiple Overlaps

For each tree, the model determines the number of overlaps between the uninfected root system and the infected root system, the length of each overlap, and the probability of no infection occurring, given the number of overlaps:

$$Pno = (1 - Pinf)^{overlaps}$$

where:

        Pno   is the probability of no infection occurring;
        Pinf   is the probability of infection occurring at a single contact in the cycle (*table 2.1*); and
       overlaps   is the number of infected root systems which contact this uninfected one.

This information is then averaged within a tree record to determine the likelihood that the tree has been infected.

2.3.4 Location of Infection

For each newly infected tree, the model also assigns the initial amount of infection if the two root systems overlap. The model assumes that the point of infection is the contact point closest to the centers of the uninfected tree (*fig. 2.3*, example A). In the subsequent years, the infection will first travel to the center of the tree and then spread in concentric circles throughout its root system. The model assigns a negative proportion of root radius (-*r*) to indicate that the infection is growing towards the center. At this stage, the tree does not infect its neighbors. In some cases, the center of the uninfected tree is surrounded by the inoculum from the infected neighbor (*fig. 2.3*, example B). If this is the case, the model assumes that the infection has reached the center of the uninfected tree and has spread outward to infect the proportion (*r*) of its root system.

    The entire process of determining the new infection of trees within a center is by default done only once each cycle for each disease type. The keyword **INFSIMS**, however, allows the users to specify that the process be repeated within a cycle and that the average infection rates are calculated from multiple simulations. Output information about the results from each simulation is also available with this keyword. Sensitivity analyses indicate that in most conditions a single simulation is adequate. In low-density stands, users may want to increase the number of simulations to 5 or 10 (*fig. 2.4*).
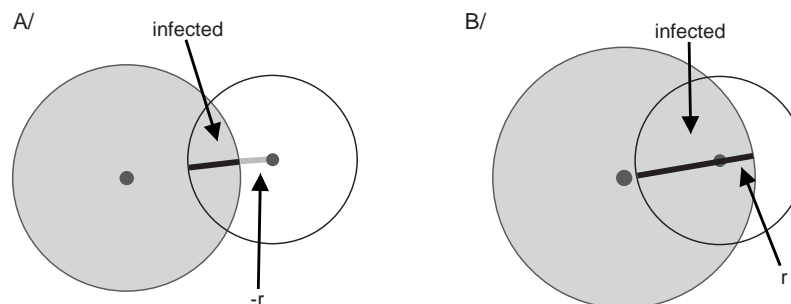
Figure 2.3–Radius that is considered infected when root overlap and infection occur. The shaded circle is an infected root system, and the open circle is an uninfected root system. The heavy black line represents the radius of the uninfected root system that becomes infected. In both cases, the distance from the center of the uninfected tree to the perimeter of the infected tree represents the newly infected root-radius. (A) The overlap did not include the center, so the tree is given a negative radius of infection, -r. (B) The overlap included the stem, and the tree is given a positive radius of infection, r.

New infections occuring inside centers
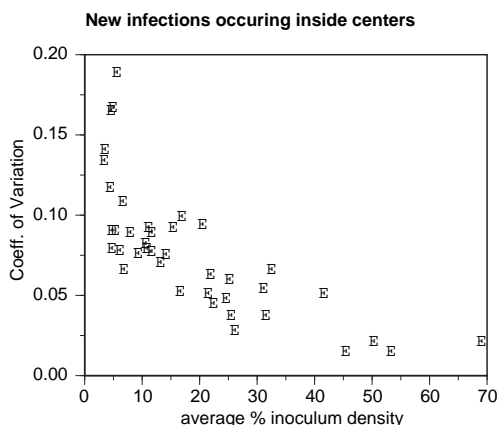
Figure 2.4–Coefficient of variation of the new infections in stands with different inoculum densities. The inoculum density is the percentage of total stems that are infected (live and dead) inside centers.

2.3.5 Progress of Infection Through a Live Root System

Infection can occur at any point along the root system. If the infection occurs outside the center of the root system, the disease must grow inwards toward the center along the radius. The tree cannot infect others until infection has reached its center. Once a tree is infected at its center, the model assumes that root disease spreads through the root system from the stem of the tree, radiating outwards in concentric rings (*fig. 1.3*).

The rate at which the disease spreads through the root system of an infected tree is determined from the number of years it takes root disease to kill a tree (a function of dbh, tree species, and root disease type, *table 2.1*), the root radius of the tree (primarily a function of dbh and tree species, see Section 1.3.1) and the proportion of the root radius that must be infected to cause death (function of tree species and root disease type, *table 2.1*). The equation which relates these is

$$Rate\ of\ spread\ =\ \frac{(Root\ Radius)*(Proportion\ infected\ at\ death)}{Time\ to\ death}$$

Thus, increasing only the root radius or the proportion of the root radius at which the tree dies will increase the rate at which the disease spreads through the root system (because the disease will have farther to travel in the same amount of time). Even though the time to death increases with increasing dbh, the rate of spread through the root system also changes with dbh. *Figure 2.5* shows this for several tree species and different tree diameters.
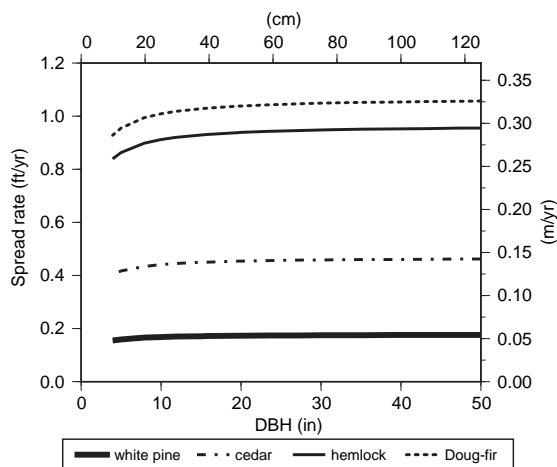
Figure 2.5–Rate of spread of the infection through root systems. Each species has a different time-to-death multiplier, and some have different parameters used in the calculation of root radius. This example was created using parameters for Armillaria root disease from the Inland Empire variant of the WRDM3. Metric units are given on the top axis (dbh in cm) and on the right axis (spread rate in m/yr), while Imperial units are on the left axis and the bottom axis.

Time-to-death, i.e., the number of years it takes for root disease to kill a tree, is defined as the length of time it takes the disease to grow from the center of the root system to the proportion of the root radius at which the tree dies. The number of years to death is a linear function of dbh (*fig. 2.6*) and is defined relative to a basic curve which is the reference curve for all tree species and root disease types. This basic curve is defined such that a 4-inch [10 cm] dbh tree will take 5 years to die and a 35.4-inch [90 cm] dbh tree will require 40 years, with linear interpolation between these points. The time to death varies for different tree species and different root disease types and is defined using a multiplier which is applied to the basic curve (*table 2.1*). Ponderosa pine, for example, when infected with Annosus root disease, takes half as long to die as predicted by the reference curve (as indicated by the 0.5 as the relative time to death), so the values would be 2.5 years for a 4-inch [10 cm] dbh ponderosa pine and 20 years for the 35.4-inch [90 cm] ponderosa pine. This multiplier can be controlled using the keyword **TTDMULT** (*table 2.2*) and can be changed for all species. The effect of changing the time to death is explored in Section 2.5.
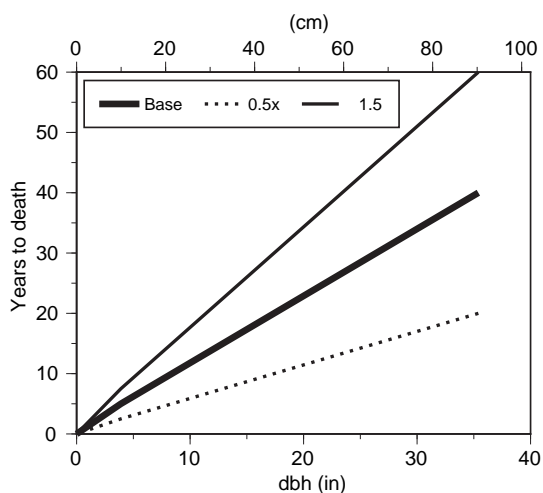
Figure 2.6–Number of years from infection at the center to death for the base curve (e.g., Douglas-fir), for a species which takes half as long to die (e.g., ponderosa pine with Annosus root disease), and for a species which takes 50 percent longer to die (e.g., larch with *Phellinus*).

Each species of tree has a different tolerance to root infection and will be killed at different degrees of infection. Trees die when a pre-defined proportion of their root radius is infected (*table 2.1*). After death the disease will continue to spread for a short time, until a pre-determined amount of the root system is colonized. The default values (*table 2.1*) vary for the different root disease species (*table 2.3*). Note that the proportion of the root radius which is infected at death is changed by the user (using the keyword **INFKILL**), the proportion of the root radius infected after death does not change automatically; users must make the change using the **INFCOLO** keyword. The effect of changing the proportion of the root radius infected at death is explored in Section 2.5.

Table 2.3—Amount that each root disease will spread through the root system after death.

Root disease	Amount of spread after death
Annosus	50 pct of the remaining root system
Armillaria	100 pct of root system
Phellinus	No spread

2.4 Spread of Root Disease Centers

2.4.1 Calculating the Spread Rate

Root disease centers can expand by infecting trees that were previously outside disease centers but whose roots now contact infected roots. Therefore, the rate of spread of centers is based on the size, density, and species of host trees *outside* of centers. Stands with large numbers of host trees likely contain trees whose roots extend into the center and become infected, increasing the chance of the center spreading.

As with the simulation of new infection within a center, the calculation of the spread rate of the center is based on a spatially explicit simulation of a small portion of the stand. In this case, the model simulates the dynamics of infection within the plot for a number of years and calculates the distance traveled by the disease in that time period. This simulation is repeated several times (default is 10), and the resulting spread rates are applied to centers as discussed below.

For the spatially explicit simulation, trees are selected from the list of live trees outside disease centers in the same way that trees were selected in the inside center simulation (Section 2.3.1). These trees are placed in the plot either randomly or on an almost uniform grid. In general, the random pattern (the default) is most useful here since grid patterns of planted trees rarely occur, especially when there is some natural regeneration. This flexibility, however, allows users to investigate the effects of different distribution patterns on the spread of root disease through the stand. Users can change the distribution pattern at any time in the root disease model run by using the keyword **TDISTN**.

The bottom border of the spatially explicit plot represents the edge of the root disease center and is assumed to be infected (*fig. 2.7*). Therefore, any tree whose roots overlap this border can become infected with some probability (*table 2.1*). In all cases of infection, the disease must grow to the stem of the tree before radiating outwards in concentric circles. The trees are not infectious until the disease has reached the center of the root system. In each time step of the spatially explicit simulation, the radius of infection in each infected tree is updated, and some trees may die. Each live non-infectious tree (uninfected trees or those where the disease has not reached the center) in the simulation is checked against each of its overlapping neighbors to see if the neighbor can infect it. If the tree is uninfected and in contact with infection, it can become infected with some probability for each tree contacted. If the tree is already infected, the new source of overlap may cause it to be infected at some point closer to the center of the tree. This new point of contact will cause a new infection on the tree with the usual probability, thus potentially accelerating the rate at which infection reaches the stem. All the basic parameters used for tracking infection in trees (as in *table 2.1*) are used in the spread rate simulations.

This spatially explicit sub-model is simulated for twenty 5-year time steps or until the infection has reached the opposite side of the simulation plot. In either case, the spread rate (in feet/year or meters/year) is calculated as the distance traveled (in feet or meters) divided by the number of years that it took to get there (*fig. 2.7*). A separate spread rate is calculated for each disease type. During this spatially explicit Monte Carlo simulation, trees themselves do not grow.
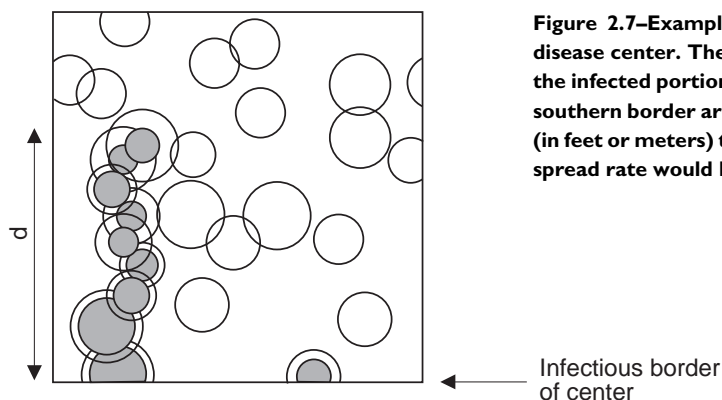
Figure 2.7–Example of a plot used to calculate the spread rate of a disease center. The circles define root systems. The shaded sections are the infected portions of the root systems. Notice that the trees along the southern border are infected. The distance "d" is the maximum distance (in feet or meters) that the disease traveled in the simulation time, so the spread rate would be d/year.

Infectious border of center

The entire calculation of spread rate is normally performed 10 times. Each resulting spread rate is remembered. Using the **SPREAD** keyword, users can control the number of Monte Carlo simulations (to a maximum of 50), and apply the average spread rate to each center or apply each of the spread rates that were calculated from each simulation to a different center (see below). Output on the results from the simulations is available with the **SMCOUT** keyword.

The spread rate is based only on the density and root system size of host trees outside of centers. By default the size of the root system of a tree is independent of the density of the stand. The keyword **SDIRMULT** (Section 1.3.1) modifies the root radius of a tree on the basis of the total density of the stand. This is particularly important for S- and P-type Annosus root disease, where the total stand density is composed of both host and non-host tree species. The spread rate simulation model cannot distinguish between a low-density, pure host stand, and a high-density stand with a low proportion of host (*fig. 2.8*). The keyword **SDIRMULT** thus accounts for some of the effects of non-host trees on host trees. When this keyword is used, the spread rate will be different in stands with the same density of host but with different overall stand density.
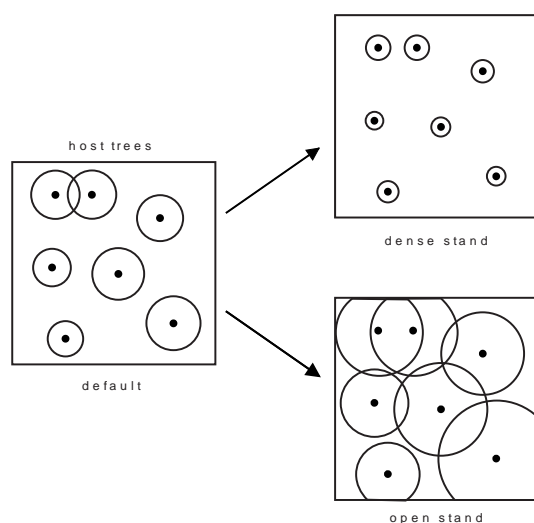
Figure 2.8–Effect of SDIRMULT on root system size. In the diagram, each circle represents the root system of a host tree. With the SDI effect on root radius, the trees in the diagram have either a smaller root system (in a dense stand) or a larger root system (in a more open stand) than would be predicted by the basic root radius equation. The effect is drawn more extreme than would actually occur.

2.4.2 Spreading the Centers

The amount of spread (in feet or meters) is determined by multiplying the spread rate (feet/year or meters/year) by the model time step (the cycle length, in years). The spread is applied by increasing the radius of centers by this amount.

As mentioned above, two methods exist for applying spread rates. The first is that the average spread rate of all the Monte Carlo simulations is applied to each center. This method is based on the assumption that since the model does not know which trees are in which center, the size of each center is not important, and all can spread with the average rate. The second is that different spread rates (based on the simulated values) are assigned to each center. This is based on the assumption that having different centers spread at different rates will result in a more accurate portrayal of the dynamics of the area in root disease in the stand. This method also is more likely to allow some centers to stop spreading for some time. Two methods exist for assigning the individual spread rate simulation results to different centers, based on the number of simulations and the number of centers:

1. The number of centers is at least as large as the number of simulations. In this case, each spread rate is applied to a center until all the spread rates have been used, and the process is repeated until all the centers have a spread rate. For example, if the stand had 14 centers (labeled *C1, C2, … , C14*) but only 10 spread rates (represented as *s1, s2, … , s10*) were

calculated, the spread rates that would be used would be: $C1 = s1$, $C2 = s2$, …, $C10 = s10$, $C11 = s1$, … , $C14 = s4$. This method preserves the range of values that occurred from the spread-rate simulations, but it may not preserve the mean.

2. The number of centers is less than the number of simulations. In this case, averages of the spread rates are calculated such that all spread rates are used and each is used in only one average. For example, if the stand had 3 centers but 10 Monte Carlo simulations (represented by $s1$, $s2$, … ,$s10$) were done, the spread rates that were used would be: average[$s1,s2,s3$], average[$s4,s5,s6$], average[$s7,s8,s9,s10$]. This method preserves the mean of the Monte Carlo simulation results, but may not preserve the range of values. Also, any zero spread rates that occurred will likely be lost during the averaging.

Two constraints are considered when applying spread rates. The first is that centers which received a zero spread rate in the previous cycle are more likely to receive a zero spread rate in the current cycle, provided one exists. The second is that centers which are shrinking in this time step (see Section 2.8) are not assigned a spread rate from these calculations, and are not included in the number of centers when determining which method to use.

2.4.3 Calculating Infected Area

As the centers expand, they may start to overlap other centers of the same disease type or they may extend outside the boundaries of the stand. When describing the total area in root disease, the model ignores any areas outside the stand and avoids double accounting of the areas within multiple disease centers. The total area within root disease centers of each type is estimated by laying a fine grid over the stand and determining how many cells of this grid lie inside each disease type's centers (*fig. 2.9*). The proportion of points in the grid that fall inside the centers of each type is a measure of the proportion of the stand that is infected by this type. The number of grid cells is always the same, regardless of the size of the stand. This means that the area within centers is more accurately calculated in smaller stands, in which the grid cell size is smaller.
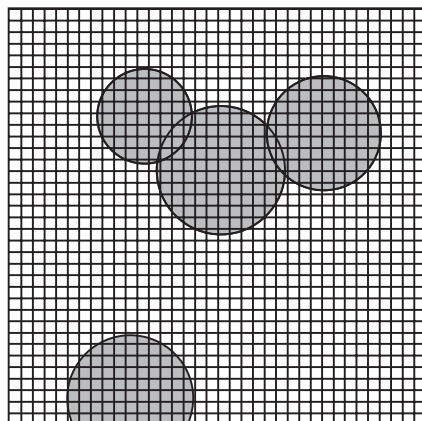
Figure 2.9–Method for calculating total area inside centers. Each grid cell is marked as 'inside' (shaded), or 'outside' (unshaded), and the proportion of cells 'inside' the grid is used to determine the proportion of the stand area infected.

2.4.4 Infecting New Trees

New trees are infected on the basis of the increase in diseased area. The model processes each element of the appropriate disease type in the live, outside (uninfected) tree list to determine the number of trees that have moved from being outside all centers of that disease type to inside the center. A proportion of these (equal to the probability of becoming infected, *table 2.1*) is considered to be infected at the center of the tree's root system. The remaining new trees inside centers are uninfected. For example, suppose that the centers expanded to include an additional 0.1 acres, and that an outside tree record had 100 trees/ acre. Of these, $100*0.1 = 10$ trees would now be inside centers. If the probability of becoming infected was 30 percent, then 3 trees ($10*0.3$) would be infected and the remaining 7 trees would be uninfected.

Trees infected by expanding centers are always infected at the stem, i.e. the mid-point, of their root system, and they are immediately infectious. Unlike infection occurring within root disease centers (Section 2.3), the disease does not need to travel to the stem base before radiating outwards. The assumption behind this is that centers expand only after the infection has crossed past the stem of the tree. Therefore, by definition, trees that were infected through center expansion are infected at the stem.

2.4.5 Center Expansion After a Harvest

At the time of a clearcut, the model assumes that each disease center is surrounded by a ring of trees whose roots have just been infected (those trees whose stems would be inside the disease center after the center expands). When these trees are cut, the infection will spread very rapidly through the root systems of these trees; in effect, causing the center to "jump" in size. The model simulates this effect by estimating the mean diameter of all root systems outside of disease centers at the time of the cut and using this as the distance by which the radii of all disease centers increase.

This option can be controlled using the **RRJUMP** keyword. This keyword also allows users to change the number of root diameters by which the center expands. The default behavior is different for each root disease (*table 2.4*) and is active only for Armillaria root disease.

Table 2.4–Defaults for the jump in center size after a clear-cut for each root disease. The distance multiplier defines the increase in center radius as a multiple of the mean root system diameter of the trees outside centers.

Root disease	Jump occurs?	Distance Multiplier
Annosus	No	not applicable
Armillaria	Yes	1
Phellinus	No	not applicable

2.5 Summary of the Effects of Parameters

Root disease dynamics in live trees are almost entirely determined from three parameters: the probability of infection, the time from infection at the stem base to death, and the proportion of the root radius that is infected at death. These parameters control, among other functions, the number (or rate) of new infections in the stand, the amount of mortality, and the area of root disease.

To demonstrate the effects of these parameters, a series of simulations was performed with the model. The simulations changed each parameter independently from the others in the following way:

- no change,
- double the time to death,
- double the probability of infection (to a maximum of 1.0), and
- halve the proportion of the root radius which is infected at death.

The runs were done on six different types of stands, representing a range of conditions (*table 2.5*). Each stand was 10 acres, 5 of which were inside Armillaria root disease centers. All other parameters and assumptions, except those specifically mentioned, were at default values. Each simulation lasted for 50 years (5 cycles). At the end of the simulation, the effect of each parameter change was assessed on a number of different root disease indicators. The summary of the effects of changing the parameters is given in *table 2.6*.

2.5.1 Time-to-Death

When the time to death is increased, the obvious effect is that trees take longer to die, so less mortality occurs, and the density of currently infected trees is higher (i.e., the infected trees are living rather than

Table 2.5–Types of stands used in the simulations. The pine stand contained only ponderosa pine, the fir stand contained Douglas-fir, and the mixed-species stand contained Douglas-fir, grand fir, western hemlock, and ponderosa pine.

| | Species | | |
| | Single | | |
	Pine	Fir	Mixed
Even-aged			
Young	✘		
Older	✘	✘	✘
Uneven-aged	✘		✘

*Table 2.6–Effect of **increasing** the given parameter. A '-' means that the indicator was decreased relative to the run on the same stand but with no change in parameter values, a '+' means that the indicator increased, an '=' means that the indicator displayed essentially no change (but the value in brackets indicates the direction of what little change occurred), and the '?' means that the result was inconclusive. Note that simulations which examined the effect of the proportion of the root radius infected at death simulated a decrease in infection level. The results were therefore reversed before being entered in the table.*

Indicator: Increase in:	Root disease area	Mortality from root disease	New infections	Number of infected trees
Time to death	−	−	−	+
Probability of infection	= (+)	+	+	+
Infected radius at death	+	+	+	?

dead). Two secondary effects also occur. The first is that the proportion of uninfected trees which become infected is lower ("new infections" in *table 2.6*) because, although there are more live trees which are infected, less of their root system is infected. For example, suppose that, after 6 years, a tree has 6 feet of infected root radius using the default time-to-death values. When the time to death is doubled, the same tree would have only 3 feet of its root radius infected. This reduction in root radius causes a 75 percent reduction in area infected (*table 2.7*). Roots from uninfected trees will be less likely to contact the smaller area containing the infection.

The other secondary effect is that centers are generally smaller when the time-to-death is increased, assuming the dynamic spread rate model is used. This occurs because spread rate of centers is calculated on the basis of the basic parameters defined above (see Section 2.4.1 for details about spread rate calculations). If the disease is traveling slower inside individual trees, fewer trees are dying, and fewer new infections are occurring, the disease will spread more slowly throughout the stand.

Table 2.7–Example of the effect of doubling the time to death on the area with infected roots. This example is for a 10-inch dbh tree which uses the basic time-to-death curve (i.e., the multiplier is 1.0). Rate of spread inside the root system is estimated assuming that most of the radius is infected at death.

	Time-to-death (yr)	Rate of spread (ft/yr)	Radius infected after 6 years (ft)	Area of infected roots (ft^2)
Default	11.7	1.0	6	113.1
Double	23.4	0.5	3	28.3

2.5.2 Probability of Infection

Increasing the probability of infection means that more infection will occur in each time step, especially as centers spread. This higher infection rate will lead to higher disease-caused mortality. It will also generally mean that there will be more live infected trees in the stand at any time step (even if the trees are all the same age). A less intuitive effect is that the higher probability of infection has little impact on center spread and center area. There are two reasons for this. First, when the spread rate calculation is performed, only the farthest distance traveled in the simulation is used to calculate the rate of spread. Increasing the number of infected trees does not guarantee that the disease will travel farther in the specified direction. Second, not all probabilities were doubled because many default probabilities were greater than 0.5, and the maximum possible probability was 1.0. The magnitude of the changes in center area may have been small because some probabilities were not increased by as much. It is likely that a greater impact would be noticed if the probabilities of infection were decreased (halved). What little impact on center area occurred caused an increase in center area.

2.5.3 Infected Radius at Death

The proportion of the radius infected at death controls the amount of live inoculum in the stand. Decreasing the proportion of the radius which is infected at death has a similar effect to increasing the time to death. In both cases, the disease will travel a shorter distance along the root radius in the same amount of time (*table 2.8*), leading to less area containing inoculum from infected roots. However, some important differences arise. The change in proportion of root radius infected at death does not necessarily change the number of live trees which are infected because infected trees will die in the same number of years. Decreasing the radius at which death occurs results in the stand containing a much smaller area of inoculum from living trees. Infection, when it occurs, will occur later and will occur primarily from the dead trees. If *Phellinus* were being simulated instead of Armillaria root disease, even fewer new infections would occur because, with *Phellinus*, the disease does not continue to expand through the roots after the tree has died. To maximize the effect of changing the infected radius at death, it would be useful to also adjust the parameter which controls the amount of the root system infected *after* death.

Table 2.8–Example of decreasing the radius which is infected at death. This example is for a tree which takes 10 years to die. Note that table 2.6 shows the effect of increasing the infected root radius.

	Radius infected at death (ft)	Rate of spread (ft/yr)	Radius infected after 6 years (ft)	Area of infected roots (ft^2)
Default	10	1.0	6	113.1
Halved	5	0.5	3	28.3

2.6 Creation of New Centers: Annosus Root Disease Only

Root disease centers are created in two ways: at model initialization using keywords (see Chapter 2, Section 3), and from Annosus root disease spores infecting freshly-cut, uninfected stumps. After a stand entry, uninfected stumps anywhere in the stand may be colonized with spores from the appropriate Annosus root disease type. Only infected stumps which are above a diameter limit are simulated by the model. Some of these newly infected stumps are outside of all centers, and, in the second time step after infection, may create new centers (*fig. 2.10*). The coordinates for each new center are chosen at random, with the constraint that the new center must be outside of all existing centers. The radius for the new center is set to 50 percent of the stump's root radius, similar to the proportion of the root radius that is considered to be infected. All large, spore-infected stumps inside centers are added to the main list of dead infected trees and stumps 20 years after creation. Thus they increase the amount of inoculum without affecting the area with root disease.

spore-infected stumps
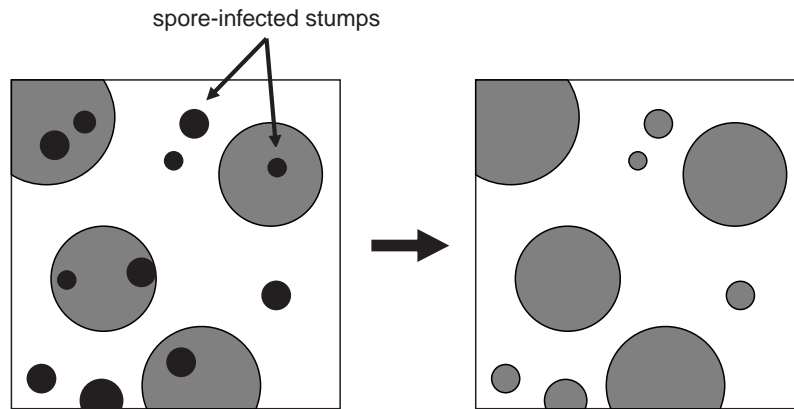
Figure 2.10–Centers created from spore infection. The light shading in the left figure are the old centers, while the darker circles are the spore-infected stumps. Those stumps outside of centers become new centers (right figure). The original centers also have increased inoculum due to the newly infected stumps.

The spore model has the potential of creating a large number of small centers, especially if the stumps are large and the proportion of stumps becoming infected is high. To avoid excessively long execution times, the model allows a maximum of 200 centers, 100 in each disease type. If the spore model attempts to create more than 100 centers in a disease type, the area of an existing center will be increased to include the area which normally would have been in the new center.

Spore-created centers are different from other centers for the first time step after creation. Infected trees die slower within this center (by default three times as slow), and the probability of infection from root overlap is only 50 percent of the value in other centers. Since the model does not know which trees are in which centers, it cannot track mortality and infection rates by center. Thus, the infection and mortality rates which are actually used in the model are weighted by the amount of area in spore-created or other centers, by disease type.

In nature, small stumps usually do not become active root disease centers. To capture this effect users can control the minimum diameter at which stumps can potentially create centers, and the proportion of these stumps which become infected using the keyword **SPORE**. The mortality and infection rate multipliers can also be adjusted in this keyword. Since the spore model is active by default, new centers may be created each time a cut occurs on large trees. Spore infection may be de-activated by setting the proportion of stumps becoming infected to 0. This, and any other change in spore model parameters, may be made in any cycle.

Spores can create centers only for Annosus root disease. New centers cannot be created if Armillaria root disease or *Phellinus* is being simulated.

2.7 Dynamics of Infection Within Dead Trees and Stumps

Once an infected tree has died from any cause, the roots are assumed to be at maximum colonization within a year. The proportion of the root radius colonized after death is a function of tree species and root disease type (*table 2.1*). The default values for the proportion colonized after death for each species are defined as given in *table* 2.3, and can be modified using the **INFCOLO** keyword. The only exception to this is that stumps that have been infected from spores (Annosus root disease only) are assumed to have 50 percent of their root radius infected, regardless of the tree species. This assumption is not under user control.

The model assumes that inoculum decays at a constant rate, and represents this by reducing the radius of the infected roots. When the remaining root radius has decreased such that mainly the stump itself is left, the radius of infection is held constant for a number of years. Thus, the inoculum remains active close to the stump for the longest period of time.

The default decay rate is given by the linear equation:

$$decay = a * radius + b$$

where:

decay	is the decay rate (feet/year or meters/year);
radius	is the radius of the infected root system (feet or meters), and
a and *b*	are root disease-specific constants shown in *table 2.9*.

This rate of decay is applied until the inoculum is reduced to the amount given by the linear equation:

$$radius = c * dbh + d$$

where:

radius	is the radius of the infected root system (feet or meters);
dbh	is the dbh associated with the infected stump (inches or centimeters); and
c and *d*	are root disease-specific constants shown in *table 2.9*.

Finally, the inoculum stays at this level for a number years, determined by:

$$years = g * dbh + h$$

where:

years	is the radius of the infected root system (feet or meters);
dbh	is the dbh associated with the infected stump (inches or centimeters); and
g and *h*	are root disease-specific constants shown in *table 2.9*.

All constants, including the values governing decay rate, are controlled using the keyword **INOCLIFE**.

Table 2.9–Default constants for inoculum decay, by root disease species.

	a	*b*	*c*	*d*	*g*	*h*
(Imperial)	*ft decay /yr /ft radius*	*ft/yr*	*ft/inch*	*feet*	*yr/inch*	*yr*
Annosus	0.02212	1.2032	0.01667	0	2	0.0
Armillaria	0	1	0.297	0	1.1111[*]	0.0[*]
					0.5556	6.6667
Phellinus	0	1	0.2377	0	1.1111[*]	0.0[*]
					0.5556	6.6667
(Metric)	*m decay /yr /m radius*	*m/yr*	*m/cm*	*m*	*yr/cm*	*yr*
Annosus	0.02212	0	0.3667	0	0.79	0.0
Armillaria	0	0.3048	0.0356	0	0.4374[*]	0.0[*]
					0.2187	6.6667
Phellinus	0	0.3048	0.0285	0	0.4374[*]	0.0[*]
					0.2187	6.6667

[*]The first value is for trees < 12 inches [30.5 cm] dbh, while the second is for trees ≥ 12 inches [30.5 cm] dbh.

For Annosus root disease, the values given in *table 2.9* were derived using the following assumptions. The root radius at which the decline in infected root radius stops is (by default) equal to twice the diameter of the stump (when measured in feet), so a 15-inch (1.25-foot) stump will stop declining when the root radius reaches 2.5 feet. The number of years that the length of the infected root radius stops decreasing is also equal to twice the diameter (when measured in inches). For example, if a dead tree has

a dbh of 15 inches, then the infected portion of the root system will not change for 30 years. After this period, the stump and the remainder of its infected root system disappear. For Armillaria root disease and *Phellinus*, the initial decay of the inoculum (as defined by infected root radius) is independent of tree or stump size (*a=0*).

Resinous vs. Non-resinous

The constants in the equation for the decay rate are for resinous tree species only (see *table 2.1* for species assignments). In non-resinous tree species, the decay rate will be faster by a third. For example, suppose a tree of a resinous species has an inoculum decay rate of 1.5 feet/year. A non-resinous tree with the same infected root radius will use a decay rate of 1.5 / 0.75 = 2.0 feet/year. All the other decay constants (as defined in *table 2.9*) are unchanged. Thus, the roots of a non-resinous tree will stop decaying sooner than the roots of a resinous tree of the same size, and the overall lifespan of the inoculum in the non-resinous tree will be shorter (*fig. 2.11*).
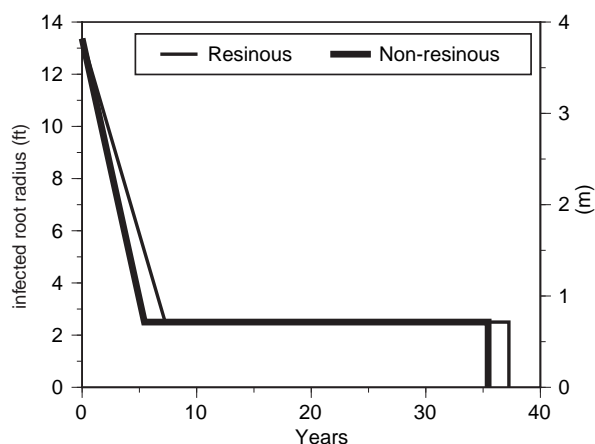
Figure 2.11–Comparison between the inoculum decline of a resinous and a non-resinous tree of the same size. This example is for Annosus root disease, but the difference in behavior is similar for Armillaria root disease and *Phellinus*. Imperial units are on the left y axis (ft) and metric units are on the right y axis (m).

Minimum Lifespan

Under most circumstances, inoculum decays according to the equations and parameters above. The model contains an option, however, which specifies the minimum amount of time that the inoculum must be present (*table 2.10*). If the default parameters above predict that the inoculum would live for less than the minimum number of years, the initial decay rate is reduced so that the inoculum will be present for the full period (*fig. 2.12*). If the inoculum is predicted to live longer than the minimum time, the decay rate remains unchanged from the predicted value. By default, only *Phellinus weirii* uses this option.

Table 2.10–Default minimum lifespan of inoculum for each disease type.

Root disease	Minimum lifespan (years)
Annosus	0
Armillaria	0
Phellinus	20
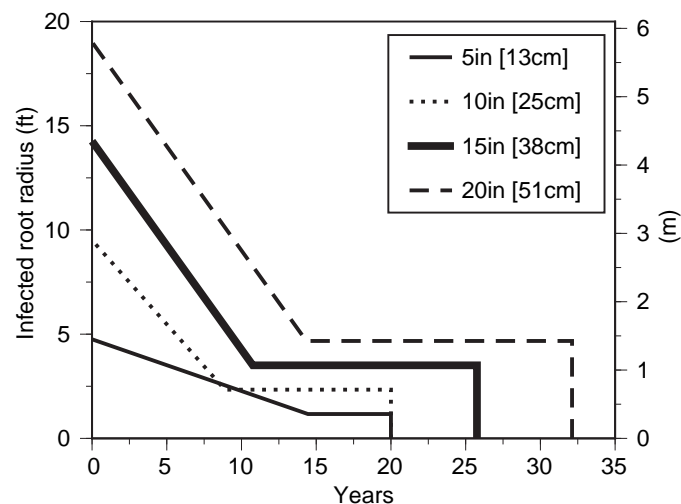
Figure 2.12–Comparison between the decay of *Phellinus* **inoculum in trees of different sizes. Note that the smaller two trees (5 and 10 inches) have a slower, initial decay rate than the larger two trees (15 and 20 inches).**

2.8 Shrinking Centers

Occasionally a stand has fewer live trees within centers than it has centers. When this condition occurs, some centers must not contain any live trees, although they may still contain some dead infected trees and stumps. Assuming no new infection, these centers will start to shrink as the inoculum decays, and the centers may disappear (*fig. 2.13*).

Shrinking occurs in three stages:

1. An initial rapid decline in which the decrease in center radius is proportional to the reduction in root radius of stumps and dead trees at the perimeter of the center.
2. A period when the center radius remains constant. This conservatively assumes that the biggest stumps in the center are at the edge of the center, and that they have reached the stage in which the size of their root systems are remaining constant. During this period the inoculum potential inside the center continues to decrease as smaller stumps inside the center decay completely.
3. The center disappears as all stumps completely decay.

The model does not know which stumps are in which centers. Since big resinous stumps take longer to decay than smaller stumps, the model chooses the biggest stump in the stand and calculates the stages of shrinking based on this stump's decay pattern. The model chooses the smallest centers to start shrinking, since by their size, they are less likely to have any live trees in them.

If stand conditions change (such as new trees being planted) so that there would be enough live trees to have at least one tree per center, all shrinking centers will be eligible to start spreading. In some cases (see description of spread rate calculations above), only some of the centers will start spreading again. The model chooses the biggest centers to start spreading, since these will be more likely to have a higher level of inoculum present and to infect new trees.
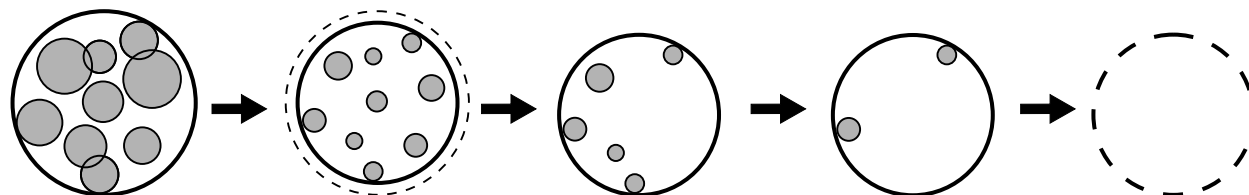
Figure 2.13–Diagram of a shrinking center. The heavy circle represents the center boundary, and the shaded circles are the inoculum surrounding infected stumps. The dotted lines show where the center boundary used to be.

3.0 Other Agents

3.1 Bark Beetles

Four functional types of bark beetle can be simulated in the model. The differences between the four types are described in detail below and are summarized in *table 4.1* of Chapter 2. Each type of bark beetle is controlled by a separate keyword. The user may implement any combination of types of beetles in any time step, including using multiple versions ("varieties") of any type of bark beetle. For example, the user may want to have Type 1 beetles cause 20 percent mortality when there are 100 trees/acre above the dbh limit but cause 60 percent mortality when there are more than 200 trees/acre above the dbh limit. The same type of beetle can also act on more than one species of tree. These scenarios can be achieved by entering the keyword for that beetle type two or more times with different parameter values. The model will implement up to 33 beetle varieties in each growth cycle.

The model evaluates the criteria for each beetle type (or variant) before any mortality has been applied. Thus, in any time step the threshold conditions for any bark beetle are not affected by mortality caused by preceding bark beetle types. For any beetles that meet or exceed the thresholds, the model then calculates the mortality occurring on each element of each live tree list for each beetle variety. The mortality that is actually applied is the maximum mortality that would occur on any tree list element (i.e., bark beetle mortality is not additive within tree list elements; see *table 3.1*).

By default, stand conditions are re-evaluated for a possible outbreak of each beetle variety in every growth cycle after the first cycle specified by the beetle's keyword. However, the keywords for each beetle type provide an option to inactivate all current varieties of that type of beetle after the specified growth cycle. If some of the varieties affected by this procedure are to remain potentially active, their keywords must be re-entered for the following growth cycle (see Chapter 2).

Bark beetle types 1, 3, and 4 are active by default in the model. The keyword **BBCLEAR** turns off all bark beetles. Type 2 is not active by default and must be entered individually.

Table 3.1–Application of bark beetle mortality to trees. This table assumes that all the bark beetles were active in the same time step on the same species of trees. The number in each cell is the percentage mortality predicted for the trees of that type. Numbers in bold are the mortalities which were actually applied.

dbh (in.)	Outside			Inside Uninfected			Infected			
	< 4	4 - 8	> 8	< 4	4 - 8	> 8	< 4	4 - 8	>8 -10	> 10
Type 1	0	0	**10**	0	0	10	0	0	10	10
Type 3	0	0	0	0	0	0	0	0	0	**88**
Type 4	0	**1**	1	0	**30**	**30**	0	**75**	**75**	75
Applied	0	1	10	0	30	30	0	75	75	88

Type 1 Beetles

In the event of an outbreak, Type 1 bark beetles apply the same mortality rate to all host trees larger than a threshold diameter (dbh). The user may choose to trigger the outbreak by either the density (trees/acre [stems/hectare]) of host trees larger than the threshold diameter, or the current stand density index (SDI) which considers all species and all sizes of trees present. Whichever measure is chosen, the user may further specify either that it is calculated for areas outside centers only or that it is averaged over the entire stand, and that it is calculated for either live trees only or for all trees that were alive within the last 2 years. An outbreak will be triggered when the resulting value is greater than a specified threshold.

The defaults for Type 1 beetles are that they will kill 10 percent of all ponderosa pine more than 8 inches [20.32 cm] dbh whenever the density of such trees exceeds 150 live stems/acre [371 live stems/ha] over the stand as a whole. The keyword **BBTYPE1** will change the default parameters, and the **DNSCALC**

keyword changes the method of calculating the threshold value. Type 1 bark beetles are active by default in the model. Examples of Type 1 beetles are western pine beetle (*Dendroctonus brevicomis*) on ponderosa pine and mountain pine beetle (*D. ponderosae*) on lodgepole pine.

Type 2 Beetles

Like Type 1 beetles, Type 2 beetles apply the same mortality rate to all host trees larger than a threshold dbh. However, Type 2 beetles are triggered by the density of host trees that are windthrown in the current time step and that are larger than this dbh. The actual mortality rate that occurs in the event of an outbreak depends on the number of windthrown trees: provided that enough live trees are available, a specified number of trees will be killed by the beetle for each windthrown host tree that was larger than the threshold dbh. The user inputs this "number of trees to kill for each tree windthrown," not the actual mortality rate. If the number of trees to kill is more than the number of live trees available, then all host trees above the threshold dbh will be killed.

The defaults for Type 2 beetles are that they will kill 0.88 Douglas-fir for every windthrown Douglas-fir, of any size, whenever the density of windthrown Douglas-fir exceeds 10 stems/acre [24.7 stems/ha] over the growth cycle. The keyword to change these defaults is **BBTYPE2**. Type 2 bark beetles are *not* active by default in the model, and, even if requested, they will occur only if windthrow has been scheduled for the same time step. An example of a Type 2 beetle is Douglas-fir beetle (*D. pseudotsugae*) on Douglas-fir.

Type 3 Beetles

Type 3 bark beetles affect only those host trees that are larger than a threshold dbh *and* have a sufficient proportion of their root radius infected with root disease. The outbreak is triggered by the density of live trees with these characteristics in the root disease areas that infect the host species. In the event of an outbreak, a specified mortality rate is applied to all trees that met the criteria.

The defaults for Type 3 beetles are that they will kill 88 percent of all white fir (or grand fir in some FVS variants) larger than 10 inches [25 cm] dbh and with more than 30 percent of their root radius infected with root disease. Mortality will occur whenever the density of such trees exceeds 10 live stems/acre [24.7 trees/ha] in root disease areas. The keyword to change these defaults is **BBTYPE3**. Type 3 bark beetles are active by default in the model. An example of a Type 3 beetle is fir engraver (*Scolytus ventralis*) on white or grand fir.

Type 4 Beetles

Like Type 3 beetles, Type 4 beetles are triggered by the density of sufficiently large host trees that have a sufficient proportion of their root system infected with root disease. However, any such trees that were alive within the last 2 years, and not just currently living trees, contribute to triggering an attack of a Type 4 beetle. Furthermore, Type 4 beetles may apply different mortality rates to the trees that exceed the threshold dbh in each of the following categories:

1. Trees that have more than the threshold proportion of their root radius infected (i.e., "inside-infected" trees).
2. Trees that have less than the threshold proportion of their root radius infected but are inside a root disease area of the type that infects the beetle's host (i.e., "inside-uninfected" trees and inside-infected trees with low infection levels).
3. Trees that are outside of root disease areas of the type that infects the beetle's host, but are within a distance *d* of such areas (i.e., "fringe" trees), where *d* is the average root diameter of all the trees outside of those disease areas that are susceptible to that type of root disease.
4. Trees that are more than the distance *d* from root disease areas of the type that infects the beetle's host (i.e., "outside" trees).

Before applying mortality rates, the model must determine which trees fall into each of the four categories. Categories 1 and 2 can be calculated from the knowledge of the trees inside centers and their infection levels. Fringe trees (category 4) are determined differently, since the model does not have any spatial representation of the trees in the stand. The model calculates the average root diameter of all trees outside centers that are susceptible to the disease type of the center. This distance is *d*. This value is then used to determine the amount of area that would fall within *d* of the center boundary, i.e., the torus surrounding the center. Finally the model uses the density of trees outside centers to determine which trees will be in this fringe area. Thus before the bark beetles attack the trees, the density of trees in the fringe is the same as in the rest of the area outside centers. "Outside" trees are all remaining trees outside centers.

The defaults for Type 4 beetles are that they will attack ponderosa pine greater than 4 inches [10.2 cm] dbh when there is at least one [2.5] such tree[s] with more than 40 percent of the root radius infected per acre [hectare] of disease area. The resulting mortality rates will be 75 percent for "inside-infected" trees, 30 percent for "inside-uninfected" trees, 15 percent for "fringe" trees, and 1 percent for "outside" trees. The keyword to change these defaults is **BBTYPE4**. Type 4 bark beetles are active by default. An example of a Type 4 beetle is mountain pine beetle (*D. ponderosae*) on ponderosa pine.

3.2 Windthrow

The windthrow model simulates major blowdown events and can affect all live trees, whether or not they are infected. Once the model knows the magnitude of the event (defined as the proportion of dominant and codominant stems to windthrow), it can allocate the effect between species according to their relative susceptibility to windthrow, and then among individuals of a species.

The windthrow model operates on all stems which are considered to be dominant or codominant. Trees are defined as dominant or codominant if the basal area percentile for their tree record is greater than or equal to 80 percent. Therefore, the total number of susceptible stems is the sum of all trees that meet this dominance criterion. The number of stems to windthrow is a proportion of the total susceptible stems. At this point, one of two conditions are possible:

1. The number of stems to windthrow is less than a minimum value. Windthrow will not occur in that time step, and the windthrow model will be called each time step until the number of stems to windthrow is above the minimum value.
2. The number of stems to windthrow exceeds the threshold value. In this case, windthrow will occur, and the effects will be allocated among the various stems.

Once windthrow has occurred, it will not occur again, unless the user has entered the keyword again for a later cycle.

Allocating the effects among the different tree records is a three-step procedure. First, the number of stems of each species that will be windthrown is calculated as:

$$S_S = \frac{E_s R_s}{\sum\limits_{j=l}^{nsp} E_j R_j}$$

where

S_s is the number of stems of species *s* to windthrow;
E_s is the number of eligible stems of species *s* to windthrow; and
R_s is the relative susceptibility of species *s* to windthrow (default is 1 for all species);
nsp is the total number of species; and
$\sum E_j R_j$ is the sum over all species (*j=1 to nsp*) of the number of eligible stems of species *j* times the relative susceptibility of species *j*.

Second, the number of stems to windthrow from each tree record *i* of each species *s* is computed by:

$$M_{S,i} = \frac{S_n N_{s,i} L_{s,i} \left(1 + P_{s,i}\right)}{\displaystyle\sum_{k=l}^{t} S_s N_{s,k} L_{s,k} \left(1 + P_{s,k}\right)}$$

where

$M_{s,i}$ is the number of stems in tree record *i* to windthrow;
$N_{s,i}$ is the number of stems in tree record *i*;
$L_{s,i}$ is the crown length of tree record *i* expressed as a percentage of total height;
$P_{s,i}$ is the proportion of the root radius of tree record *i* infected by root disease; and
t is the number of tree records in the tree list;
k is a record counter for summing over the number of records.

This calculation assumes that stems with a larger proportional crown length are more susceptible to windthrow, and that stems with greater root disease infection are more prone to windthrow.

Third, the model determines the number of stems that tip over as opposed to snapping off. Infected windthrown stems which tip over are assumed to remove the major portion of their root system from the soil, and therefore cannot continue to spread the root disease. Infected windthrown stems that snap off become infected stumps and can continue to serve as an inoculum source. In the model, the probability of a stem being uprooted is equal to the proportion of its root system that is infected, so that more heavily infected trees are more likely to tip over than to break off.

The **WINDTHR** keyword controls the windthrow model. It specifies the proportion of dominant and codominant stems which are windthrown and the minimum number of eligible stems for windthrow to occur.

4.0 Management

The root disease model contains two management actions (borate application and stump removal) that are specific to the model. All the usual FVS-level stand management options are also available and may affect root disease development.

4.1 Borate (Annosus Root Disease Only)

When Annosus root disease is in the stand, the user can simulate the application of borate to newly created stumps. Borate application reduces the number of stumps that are eligible for colonization by spores and thus reduces the number of new disease centers and the spread of root disease. If the spore sub-model is not being used, then borate application has no effect. Also, if most of the stand is already inside root disease centers, the application will have less effect than in a stand with less root disease. Finally, borate application has the biggest effect on large diameter stumps: those that have the potential to create a relatively large disease center and to contribute significantly to the inoculum in the stand.

Borate is applied in the year that the harvest occurs. Using the **BORATE** keyword, users must specify the minimum stump diameter for borate to be applied (current default is 12 inches [30.5 cm]), and the proportion of stumps on which the borate treatment prevents colonization (current default is 95 percent). These values may be changed in any year, and the treatment with the specified parameters will be used for all harvests until the values are changed again. By default, borate application does *not* occur. Once requested, borate application occurs with each harvest unless the proportion of stumps on which the treatment is successful is set to 0.

4.2 Stump Removal

Pushing stumps removes stumps with root disease**.** A proportion of all infected stumps of all ages are removed. Using the keyword **PSTUMP**, users can specify in which year or cycle to remove the stumps, and what proportion of stumps above a given size is removed. By default, stump removal does *not* occur. If stump removal is requested, the default is that all stumps will be removed.

4.3 Regeneration

Adding new trees to a stand is a standard FVS option through use of the Establishment Model (Ferguson and Crookston 1991), and in some variants is a default condition. In the Root Disease Model, when new trees are added (as part of FVS), all the trees are uninfected. They are placed both inside and outside of centers in proportion to the size of the relative areas. New trees are "immune" to the infection in the time step in which they are planted, and will not show up in the root disease model-specific output until the subsequent time step.

5.0 References

Ferguson, D.E.; Crookston, N.L. 1991. **User's guide to version 2 of the Regeneration Establishment Model: part of the Prognosis model**. Gen. Tech. Rep. INT-279. Ogden, UT: Intermountain Research Station, Forest Service, U.S. Department of Agriculture; 34 p.

Reineke, L.H. 1933. **Perfecting a stand density index for even-aged forests**. Journal Agricultural Research 46:627-638.

Chapter 5

A Comparison Between Western Root Disease Model Predictions and Real Data

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Introduction

How accurate are the WRDM3's simulations of the impacts of root disease and bark beetles on forest stands? The WRDM3 was not derived from empirical data, instead it is based upon a group effort to capture a complex biological system through a series of assumptions. Although its design makes intuitive sense to the forest pathologists and entomologists who created it, does it make reasonable predictions of the impacts of root disease on stand development?

To determine whether the model is accurately simulating the impacts of root disease on forest stands, we ran the model in many different types of stands under heavy, moderate, and light infection levels. We tested every keyword to see if the response from the model made intuitive sense. These behavior analyses (Zhang and others, 1997, Beukema and Kurz 1995) increased our confidence in the model's ability to predict the impacts of root disease in a reasonable manner.

To quantitatively test the model, comparisons of model predictions to data from permanent plots are useful. In this analysis we compared model predictions to data from permanent plots, tracking the impact of Annosus root disease in fir stands. We entered the data from 1981, the year of plot establishment, into the model, ran the model for a 13-year simulation period, and compared the output to the data from our most recent year of data (1994). Unfortunately, we could use only 26 plots, but for this limited data set we found that the S-type Annosus functions of the WRDM3 are, on average, making accurate predictions.

Methods

Pest Damage inventory plots measured in 1981 were remeasured in 1994. The 0.1-acre plots in fir stands on the Stanislaus and Eldorado National Forests are centered around trees that died in 1972-73. In 1981, tree species, diameter at breast height (dbh), height, crown ratio, and root disease severity were recorded and trees tagged and stem mapped.

In 1994, these plots were revisited, and all inventory measurements required by the USDA Forest Service, Pacific Southwest Region (USDA FS 1994) were recorded. Tree numbers were matched so actual growth measurements could be determined from 1981 to 1994. In some cases, a 1994 plot tree could be matched to a tree in the 1981 plot, but diameter was not measured on that tree in 1981 (in 1981 the tree was smaller than 10 cm, or not picked up by the 5 BAF prism). For these trees the 1981 dbh was determined by subtracting the plot average dbh growth from its 1994 dbh. On 20 plots, there occurred one or more instances of a tree recorded as dead in 1994 that could not be matched with a 1981 tree record. In these cases,

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the plot was dropped from the analysis. One other plot was discarded because the stand conditions were not characteristic of fir stands in the Sierra Nevada.

For the remaining 26 plots, the 1981 data were translated and processed with the Forest Vegetation Simulator (FVS) with and without the Western Root Disease Model. Default values were used for all parameters of the Western Root Disease Model. In order to eliminate variation due to inaccurate height measurements, the Pacific Southwest Region height dubbing routines in FVS were used to assign heights to both the 1981 and 1994 data sets.

The changes in tree mortality and basal area from 1981 to 1994 were calculated from the actual plot data and compared to the 1994 predicted values from the FVS summary table. Mortality in trees per acre, increase in basal area in square feet per acre, and volume killed in cubic foot mortality per acre were compared.

Results and Discussion

The average actual mortality calculated from the data over the 13-year period was 657 cu. ft. of mortality per acre, from 35 trees per acre. On average, the model predicted 650 cu. ft. of mortality per acre from 49 trees per acre. Average increase in plot basal area from 1981 to 1994 was predicted to be 23 sq. ft. per acre; the actual plot average was 29 sq. ft. per acre.

We also ran the FVS model without the WRDM3 extension for comparison. Without the WRDM3, running the Western Sierra Nevada (WESSIN) variant of the FVS model overpredicted growth by 20 sq. ft. per acre (41 percent) underestimated the mortality by 497 cu. ft. per acre (76 percent) and 17 trees per acre (49 percent).

Mortality and basal area were simulated for each plot, and the results were averaged (see *tables 1* and *2* for individual plot values). The model did not accurately predict the mortality on a plot-by-plot basis. The plots are very small, which makes the model simulations more variable: one tree killed or not killed on a plot is a high percentage of the volume of a very small plot.

These plots come from a small geographic area, and it is unknown how well they represent Annosus root disease in other areas. It tests only the functions of S-type *Annosus*; the functions for P-type *Annosus*, *Armillaria* and *Phellinus* are significantly different and need to be analyzed separately. We are currently performing a similar analysis in P-type *Annosus* infecting ponderosa pine in northeastern California.

Only 26 plots were analyzed, a small number on which to base the accuracy of a model, but at least in this project area the WRDM3 on average made an accurate prediction of the impact of Annosus root disease in fir stands after 13 years of development. When making runs with the WRDM3, it is best to plan the analysis and review the results with a forest pathologist or entomologist familiar with pathogens and insect activity in the analysis area.

Summary

Simulations of 26 permanent plots in fir stands infected with Annosus root disease (caused by *Heterobasidion annosum*) demonstrate that the Forest Vegetation Simulator with the Western Root Disease Model is, on average, accurately predicting mortality for 13 years. Data from 1981 were processed using the Forest Vegetation Simulator (FVS)—with and without the Western Root Disease extension model— then compared to measurements made in 1994/95. The 0.1-acre plots, from the Pest Damage Inventory on the Stanislaus and Eldorado National Forests, are centered around dead true firs infested with Annosus root disease. Enlargement of tree mortality centers has been mapped and monitored at these plots from 1981 to 1995. On average, the actual mortality calculated from the data over the 13-year period was 657 cu. ft. mortality per acre. The FVS model with the Western Root Disease Model predicted 650 cu. ft. per acre. The FVS model without the root disease model underpredicted mortality, calculating mortality at 160 cu ft. per acre.

Table 1—Individual plot data for mortality and basal area change for a 13-year interval (1981-1994) on 26 Annosus root disease plots in fir stands in the Sierra Nevada.

Plot numbers	Trees per acre		Basal area		Change in mortality	Change in basal area	Volume mortality[1]
	1981	1994	1981	1994			
			$ft^2/acre$		trees/acre	$ft^2/acre$	ft^3
6 St055	360	320	259	325	40	66	410
7 St077	280	230	109	140	50	31	370
8 St070	80	50	52	47	30	-5	390
9 St050	140	110	47	65	30	18	130
11 St105	130	110	276	253	20	-23	2240
13 St126	170	170	139	181	0	42	0
14 St127	250	240	92	150	10	58	20
15 St114	170	160	137	161	10	24	180
16 St120	220	212	107	120	8	13	447
17 St086	410	380	312	307	30	-5	2300
18 St024	250	200	337	348	50	11	650
20 St034	350	280	99	140	70	41	130
21 St038	170	140	153	144	30	-9	1230
31 El002	200	120	232	162	80	-70	3260
32 El023	320	310	208	208	10	0	3400
64 El018	80	70	126	151	10	25	140
65 St058	240	240	197	249	0	52	0
67 St056	330	310	186	247	20	61	60
71 St047	290	260	222	280	30	58	36
72 St045	250	210	241	277	40	36	100
73 St080	270	260	136	207	10	71	10
81 St081	410	290	216	269	120	53	730
83 St111	110	100	148	195	10	47	30
84 St119	150	140	90	156	10	66	0
86 St125	350	310	302	373	40	71	140
87 St091	510	410	212	245	100	33	680
Averages	250	217	178	208	35	29	657

[1]Volume mortality uses 1981 dimensions of trees that died during the period, per acre.

Table 2—Western Root Disease Model predictions for mortality and basal area change from 1981 to 1994 (13 years) on 26 Annosus root disease plots in fir stands in the Sierra Nevada.

Plot numbers	Annosus Off[1]			RRINIT[2,3]			RRTREIN[3,4]		
	Δ[5] in mortality	Δ in basal area	Volume mortality[6]	Δ in mortality	Δ in basal area	Volume mortality[6]	Δ in mortality	Δ in basal area	Volume mortality[6]
	trees/acre	*ft²/acre*	*ft³*	*trees/acre*	*ft²/acre*	*ft³*	*trees/acre*	*ft²/acre*	*ft³*
6 St055	59	65	538	65	51	1768	64	54	1489
7 St077	8	55	23	23	45	105	21	43	105
8 St070	2	31	16	14	15	212	15	4	326
9 St050	5	45	16	39	19	296	32	23	178
11 St105	6	38	198	16	24	252	20	18	323
13 St126	6	40	54	23	37	54	6	38	54
14 St127	9	55	26	14	54	26	9	55	26
15 St114	6	51	56	49	5	938	38	31	202
16 St120	8	65	51	44	27	667	37	17	831
17 St086	45	54	423	77	2	1556	87	-31	2690
18 St024	26	27	420	46	15	657	43	21	478
20 St034	12	60	32	81	28	227	87	17	283
21 St038	6	45	58	24	20	416	26	18	513
31 El002	6	67	125	55	-17	1955	77	-33	2079
32 El023	12	41	70	98	13	250	86	11	304
64 El018	2	50	85	15	16	896	21	35	221
65 St058	8	39	50	31	34	83	27	34	93
67 St056	29	52	168	41	49	192	34	51	179
71 St047	26	52	260	72	11	1169	42	41	286
72 St045	32	45	333	48	40	320	37	44	337
73 St080	9	77	49	47	37	756	46	36	694
81 St081	49	44	324	104	9	796	104	-7	1032
83 St111	4	38	78	26	-5	1180	19	15	472
84 St119	6	47	42	49	11	584	42	-2	791
86 St125	39	50	402	65	29	805	67	19	1044
87 St091	57	51	254	105	18	728	125	-6	1081
Averages	18	49	160	49	23	650	47	21	620

[1]"Annosus off" means tree data for 1981 were projected for 13 years using the WESSIN (Western Sierra Nevada Variant) of the Forest Vegetation Simulator with the Western Root Disease Model turned off.

[2]"RRINIT" displays results of Western Root Disease Model simulations; root disease was entered into the model using the RRINIT keyword.

[3]Plots are run as 0.1-acre stands, with one fir-type Annosus root disease center, 30-foot radius (0.065 acre).

[4]"RRTREIN" displays results from simulation done with the Western Root Disease Model, with the root disease information read from the plot inventory information using the RRTREIN keyword.

[5]Δ = change

[6]Volume mortality is taken from FVS summary table and applies to the whole plot.

References

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Chapter 6

Root Disease and the Western Root Disease Model in British Columbia

Sarah J. Beukema[1] **Werner A. Kurz**[2] **John McLaughlin**[3]

Introduction

This chapter gives an overview of the use of the Western Root Disease Model Version 3 (WRDM3) in southeastern British Columbia (BC) for the benefit of current and potential model users in BC. This chapter will:

- Give an overview of the history of the development and testing of the model and of the involvement of BC pathologists,
- Compare this model to Tree and Stand Simulator/ROTSIM,
- List some of the BC-specific features of the model, and
- Discuss some of the applications and limitations to using the model in BC.

After reading this chapter, readers should have a better understanding of the applicability of the WRDM3 to ecosystems in southeastern BC, and of some of the issues relating to its use. Descriptions of how to use the model and details of model behavior will not be provided because they are available in other chapters.

Root diseases, especially those caused by *Armillaria ostoyae* and *Phellinus weirii* (laminated root rot), are common throughout the Kamloops and Nelson Forest Regions (Morrison and others 1992; *fig. 1*). In some areas, more than 50 percent of the stands surveyed contain some level of identifiable root disease. Armillaria root disease is found in many different biogeoclimatic ecosystem classification zones (BEC) (Meidinger and Pojar 1991, Pojar and others 1987) whereas laminated root rot is found only in the Interior Douglas-fir (IDF) and Interior Cedar Hemlock (ICH) zones *(table 1).* Neither of the root diseases is found in the Ponderosa Pine zone (PP) or in the higher elevations of the Englemann Spruce Subalpine Fir (ESSF) zones (Morrison 1997). *Heterobasidion annosum* occasionally occurs in the cool, wet ICH zones in the Nelson region (Braumandl and Curran 1992) but is not of major concern in BC.

These diseases create serious complications for forest management, especially since the recent introduction of the Forest Practices Code which specifies forest management guidelines in British Columbia (Government of British Columbia 1995). For example, the Code calls for Silviculture Prescriptions and Stand Management Prescriptions to identify the forest health implications of conducting planned silviculture treatments (e.g., clear-cut vs. partial cut or juvenile spacing). Likewise, restraint on timber harvesting arising from the need to manage for other forest values (e.g., scenery, wildlife, cultural heritage) has resulted in the reduction of the Annual Allowable Cut (AAC). The degree to which this AAC reduction can be mitigated through treatment of sites infected with root disease must be quantified.

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Phellinus weirii   *Armillaria ostoyae*
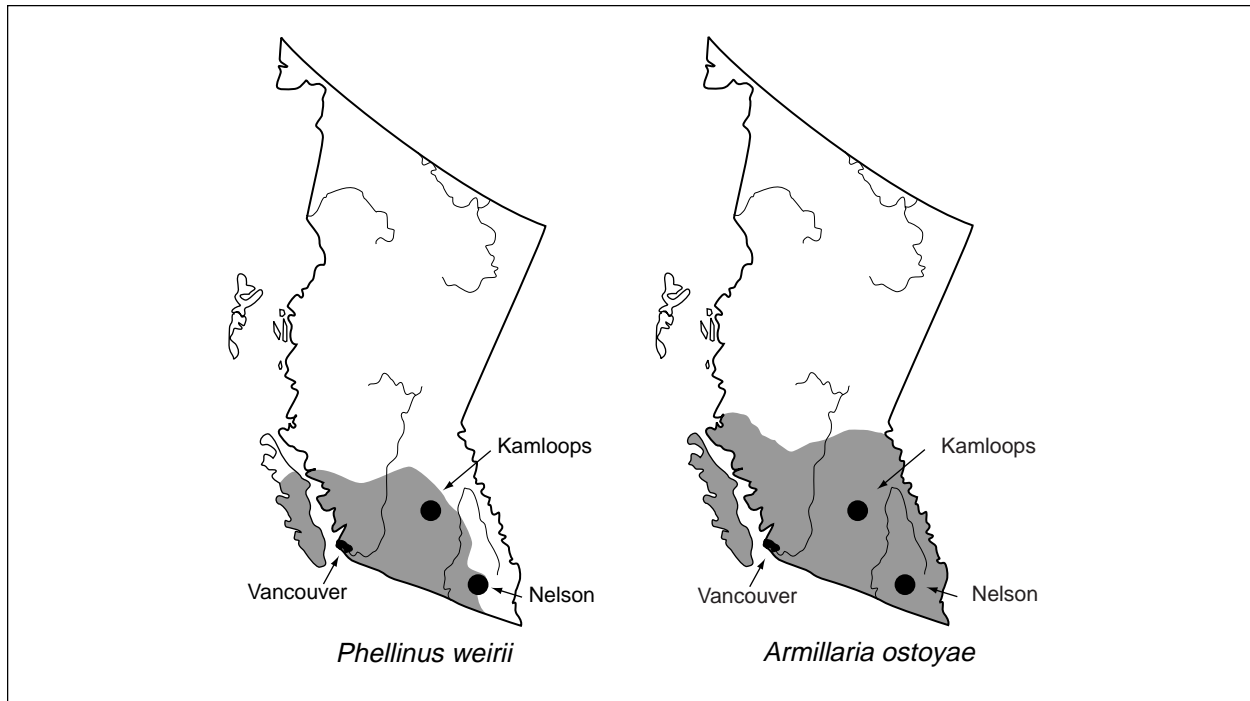
Figure 1—Extent of *Phellinus weirii* **and** *Armillaria ostoyae* **in British Columbia (from Morrison and others 1992)**

Table 1—Summary of distribution of **Armillaria ostoyae** *and* **Phellinus weirii,** *by BEC[1] zones, in the Kamloops Forest Region and the Nelson Forest Region, BC. In the Kamloops Forest Region, an '***X***' marks those zones with moderate to severe infestations (Lloyd and others 1990). In the Nelson Forest Region, an '***X***' indicates those zones with "probable and persistent incidences" (Braumandl and Curran 1992, Morrison 1997, Norris 1997).*

	ESSF	MS	SBS	ICH	IDF	PP
Kamloops Region						
A. ostoyae	**X**[2]	**X**	**X**	**X**	**X**[3]	
P. weirii				**X**	**X**[3]	
Nelson Region						
A. ostoyae[4]	**X**[5]	**X**	na[6]	**X**	**X**	
P. weirii			na	**X**	**X**	

[1]The BEC zones listed here are: ESSF = Englemann Spruce-Subalpine Fir, MS= Montane Spruce, SBS = Sub-boreal Spruce, ICH = Interior Cedar Hemlock, IDF = Interior Douglas-fir, and PP = Ponderosa Pine (Pojar and others 1987, MacKinnon and others 1992).

[2]Only known in the dv and wc subzones.

[3]Not known in (or speculated to be in) the xh1 and xh2 subzones.

[4]Listed as a "broad spectrum agent" infecting all common tree species.

[5]Lower elevations only.

[6]na = zone does not exist in the Nelson Forest Region.

For these and other reasons, the ability to model the behavior and impact of root disease in southeastern BC was recognized as a priority by the BC Ministry of Forests, and funding was allocated to assist in model development.

Addressing forest health issues with extensions to the Forest Vegetation Simulator (FVS) was an attractive solution because FVS is widely used in the United States and many add-on tools are available that address forest health, stand visualization, wildlife/habitat relationships, and other issues at the stand and landscape level. Two forest health extensions to FVS were used in the United States to simulate the dynamics of root disease and its interaction with forest management activities: the Western Root Disease Model version 1.0 (WRDM) (Stage and others 1990), which simulates root disease caused by *Phellinus weirii* or *Armillaria ostoyae*, and the Annosus Root Disease/Bark Beetle Model (Beukema and others 1995), which evolved from the WRDM1. Following the recommendations from a workshop with model users and pathologists from the United States and Canada, the British Columbia Ministry of Forests decided to fund the merger of these models into a single model: the WRDM3.

Forest health extensions to the FVS, such as the WRDM3, have been developed over a number of years using a workshop approach (Holling 1978). These workshops brought together pathologists, entomologists, silviculturalists, and others to identify the important relationships to be included in the model and to review model behavior. Several pathologists from BC participated in initial workshops in which the first version of the model was created (the Western Root Disease Model, Version 1) (Stage and others 1990), and have been involved in workshops developing the current version. With the advent of the SI (Southern Interior) variant of FVS, a variant applicable to a range of ecosystems in the Kamloops and Nelson Forest Regions, interest from BC pathologists has increased. Upon completion of model development, pathologists from BC and the United States defined a series of stand conditions and stand management scenarios to be used in behavior analyses of the model. The results of these simulations have been reviewed by the pathologists. Although the model behavior was generally endorsed, it was also realized that the development and testing of default parameter sets applicable to specific regions are important.

Root Disease Models

With the introduction of the WRDM3 into BC, two root disease models are supported by the BC Ministry of Forests: the WRDM3 and ROTSIM (Bloomberg 1988). Each model is an extension to a different base model that is used to simulate the growth and yield of trees. ROTSIM is an extension to the Tree and Stand Simulator (TASS; Mitchell 1975), a distance-dependent, even-aged growth model that simulates pure-species stands *(table 2)*. Mixed-species stands are simulated as smaller blocks of the pure species independently and in proportion to the species distribution in the mixed stand. Results are then combined to obtain per hectare estimates. The WRDM3 is an extension to FVS (Wykoff and others 1982), a distance-independent, even or uneven-aged growth model that simulates pure or mixed species stands. The Southern Interior (SI) variant of FVS is applicable to ecosystem types in British Columbia's southern interior regions. Both base models allow users to simulate different types of thinning and harvest options.

The two root disease models simulate the dynamics of the root disease using different approaches *(table 2)*. ROTSIM has a detailed, three-dimensional representation of the uninfected and *Phellinus weirii*-infected portions of root systems of trees and the location of these trees in the stand. Users of the WRDM3 can select one of three root diseases. The model carries information about the average species composition, size distribution, and density of trees inside and outside root disease centers. In both root disease models, the root disease will affect the growth and survival of infected trees.

The Kamloops and Nelson Forest Regions contain many uneven-aged and multi-species stands, and have large areas infected with Armillaria root disease. For these regions, therefore, the WRDM3 is the more useful of the two models because of the ability of the base model to portray these types of stands. For areas in which there are mostly even-aged stands and for which TASS has been calibrated, ROTSIM may be the more appropriate choice.

Table 2—Comparison between main components of the WRDM3 and ROTSIM. A brief comparison of the base tree growth and yield model used with each (FVS or TASS) is also included.

	Root disease model	
	WRDM3	ROTSIM
Species	*Armillaria ostoyae,* *Phellinus weirii,* *Heterobasidion annosum,* some representation of bark beetles	*Phellinus weirii*
Centers	Root disease centers contain average stand densities and inoculum levels.	Root disease centers are self forming, due to spatial modeling of entire stand
Disease spread	Simulations of probability of root contact based on tree species, root radius and stand density	Root contact as estimated from the number of root elements per cubic meter of soil.
Root systems	Root systems are two-dimensional circles	Root systems modeled in three dimensions
Management actions	Stump removal Borate application	Stump removal
Stand types	Pure or mixed species Even or uneven-aged 11 species—interior only, No hardwoods	Pure or mix-prorated species Even-aged 7 tree species
Growth model	FVS Distant independent Diameter driven Individual tree growth is adjusted to account for relative position in stand. Root disease reduces tree growth and increases mortality.	TASS Distance dependent Height driven Individual tree growth is adjusted to account for competition from neighbors. Root disease reduces tree growth and increases mortality.
Actions modelled	Thinning and harvesting Planting	Thinning and harvesting Planting, Pruning
Region	Southern Interior	Province-wide

Use of the WRDM3 in British Columbia
Model Features Unique to the BC Version

The biology of the trees and root diseases in southeastern BC is similar to those in the adjacent states (Idaho, Montana, and eastern Washington). Thus, the WRDM3 is the same model as that linked to the Northern Idaho variant of FVS used by the USDA Forest Service with the exception that all input and output are in metric units.

To facilitate use of the model, the BC Ministry of Forests has developed a user-friendly interface. This interface will allow users to select from options that they are familiar with (such as BEC zone, thinning terminology, etc.) and will create the appropriate annotated keyword files. In addition, this front end will make the cross-reference between the BEC zone entered by the user to the U.S. Daubenmire habitat classification system (Daubenmire and Daubenmire 1968) used inside the model.

Potential Applications

The root disease model produces output on a number of variables, with various levels of detail about the stand or root disease. As such, it is designed to be used for a wide variety of purposes, including (but not limited to): research, designing silviculture prescriptions, and providing input to the development of timber supply reviews. For example, the model can be used to project how a stand will respond to various treatments under different assumptions about root disease. Detailed results about a stand are available, or the results from many stands can be processed outside FVS to get summary information.

The model can be run with different options. If data are available, the model can simulate existing stands from the time the inventory information was obtained. Users also have the option of running 'bareground' simulations, as can be done with WinTIPSY (the Windows version of the Table Interpolation Program for Stand Yields; Mitchell and others 1995) and the Variable Density Yield Prediction System (VDYP) (Anon. 1995).

In BC, the WRDM3 (and FVS) has been used to explore partial harvesting scenarios in areas that may be subject to a decline in wood supply (Robinson and Kurz 1996). Simulations explored the response of mean annual increment (MAI) to combinations of partial harvest entry age, re-entry age, and basal area removed, with different assumptions about root disease levels. In addition, post-processed output from the model was subsequently used with FSSIM, an optimizing landscape projection model used by the BC Ministry of Forests to conduct timber supply analyses at the district level.

Data Requirements

To run the root disease model (and FVS) from existing stands, some basic information about the stand and site is required. At a minimum, this information must include lists of representative trees with their species, diameter at breast height (dbh), and sample weight. Some knowledge about the measure of disease incidence in the stand is also necessary. The model will yield more realistic results if more information, such as site information (BEC unit, slope, elevation, aspect), height, crown ratio, disease status, and recent growth increments, is included as part of the input data. Note that the SI variant of the model uses site information (not site index) to modify growth projections.

Current standard surveys do not supply the necessary model input data *(table 3),* and some modifications to these methods are necessary to provide at least the minimum input data required for the model. For example, when a pixel survey is done, some information about the live trees in the stand can also be collected (using prism sweeps or more detailed plot exams). New surveys suitable for collecting data for partial cutting and for meeting the data requirements of existing and future models are under development by the Ministry.

Table 3—Brief summary of the types of data collected by standard surveys used in BC. Note that the only data mentioned in the table are those that are part of the minimum information needed for running FVS and the WRDM3.

Survey method	Collected	Not collected / Comments
Stocking	Species and density, some root disease information	dbh
Free-growing	Species and density, some root disease information	dbh
Pre-stand tending	Species, number, dbh (by size class) Disease damage	dbh usually not accurate Survey method is being phased out
Timber cruise	Data about commercial species of merchantable size	No information collected on other species or other sizes.
Multi-story silviculture survey	Percent species by crown layer, some root disease information	dbh
Pixel	Distribution and severity of disease	No detailed stand information

Opportunities to Improve

Although the WRDM3 has many uses in BC, some obstacles to more general use remain:

• Few long-term data sets which include information on both the living uninfected trees and the root-disease-infected trees and stumps are available in BC. This situation has limited the amount of model calibration and testing that can be done with the model. Current model calibration has focused on behavior analyses of the model that are reviewed for 'reasonableness' by local pathologists.

• Many stands in the region contain significant numbers of hardwood species, which are not included in the Southern Interior variant of the FVS model at the present time. This limits the use of the WRDM3 model in these stands. In addition, no brush and shrub species, which act as a host for *A. ostoyae*, are included in the model, which may result in underestimates of the impact of the root disease in early successional stands.

• It is not uncommon to find Armillaria root disease and laminated root rot in the same stand, infecting the same species of trees. The WRDM3 cannot accommodate more than one root disease type in a stand (with the exception of S- and P-type Annosus root disease), independent of whether the root disease is infecting the same tree species. Although it is possible to revise the model to accommodate multiple root diseases in the same stand, it is uncertain whether the biological understanding about the interactions of different root disease species is adequate to parameterize such a revised model.

Future steps in WRDM3 model development and validation are needed to establish and expand the usefulness of the model in BC. These include:

• Addressing some of the obstacles listed above (such as performing additional simulations and comparing the results to expert opinion and data, promoting the development of long-term data sets, adding hardwood species to both the root disease model and the base model, and developing a version of the model that includes the ability to model more than one root disease in the same stand);
• Adding other root diseases (such as Tomentosus root rot);
• Refining existing biological relationships in the model and adding new ones (such as increasing the "flushing" effect that occurs after a stand entry and adjusting the parameters of the root disease relative to the vigor of the tree);
• Adding additional management treatment options (such as "pop-up" spacing);
• Further refinement of the user-friendly front-end.

Conclusions

The WRDM3 is the first growth and yield model that simulates stand dynamics in mixed species, even or uneven-aged stands that are affected by root diseases in southeastern BC. The model simulates the impact of root disease on stand dynamics, including reduction in growth rates, increased mortality, changes in species composition, and increased disease levels after a stand entry. The model has been tested for selected ecosystem types in these regions and its behavior is generally considered reasonable

by expert reviewers. The lack of long-term plot data in managed and unmanaged stands with and without root disease precludes more formal model calibration and validation at this time.

Acknowledgments

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Appendices

Index of Keywords[1]

[1] Page numbers in boldface type indicate where keyword is defined.

Glossary of Abbreviations

A: Armillaria root disease

Ann: Annosus root disease

approx.: approximately

Arm: Armillaria root disease

ave: average

ba: basal area

BC: British Columbia

BEC: biogeoclimatic ecosystem classification zone

cents: centers

cm: centimeters

cu: cubic

dbh: tree diameter measured at breast height

Dens: density

ft: feet

FVS: Forest Vegetation Simulator

ha: hectares

ID: identifier

IMP: imperial units

in: inches

in-uninf: tree is inside root disease center, but is uninfected

in-inf: tree is inside root disease center and is infected

m: meters

MAI: mean annual increment

MC: monte carlo

met: metric units

merch: merchantable

na: not applicable

no: number

nr: non-resinous

Num: number

outside: tree is outside root disease center and is therefore uninfected

%tile: percentile

p. pine: ponderosa pine

Phel.:   laminated root disease caused by *Phellinus weirii*

prob: probability

prop: proportion

P-type: Biologial species of Annosus root disease that damages pine, juniper, incense cedar and other tree species.

QMD: quadratic mean diameter

r: resinous

ROTSIM: Root Rot Simulation model developed in BC and used with the Tree and Stand Simulator (TASS)

RR: root rot

SD: standard deviation

SDI: Stand density index

SI: Southern Interior variant of FVS (used in British Columbia)

SIM: simulation

SORNEC: Southern Oregon Northeastern California variant of FVS

sp: tree species

sq. ft.:   square feet

S-Type: Biological species of Annosus root disease that damages true fir, giant sequoia and other tree species.

uninf: uninfected

US: United States

W: laminated root disease caused by *Phellinus weirii*

WESSIN: Westside Sierra Nevada variant of FVS

WRDM3:   Western Root Disease Model, Version 3.0

x: times

yr: year

List of Default Values by Tree Species and Variant

Western Root Disease Model Species Tables

Variants and Associated Species Table

Variant	Species Code (as represented in tree data and output)										
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
Inland Empire	WP	L	DF	GF	WH	C	LP	S	AF	PP	OTH
Southern Interior	*PW*	L	*FD*	*BG*	*HW*	C	*PL*	S	*BL*	*PY*	*OTH*
S.Cen.Oregon/NE Calif.	WP	SP	DF	WF	MH	IC	LP	S	RF	PP	OTH
Eastern Montana	WB	L	DF	GF	WH	C	LP	S	AF	PP	OTH
East Cascades	WP	WL	DF	SF	C	GF	LP	ES	AF	PP	OTH
Blue Mountains	WP	WL	DF	WF	WH	GF	LP	ES	AF	PP	OTH
Western Sierra Nevada	OC	SP	DF	WF	GS	IC	BO	JP	RF	PP	TO

Species Abbreviation Table

The non-italicized abbreviations are for all variants except the Southern Interior (SI) (BC) variant. The species abbreviations for this SI variant are given in italics next to the main abbreviation.

Species Abbreviation		Species Name	Species Abbreviation		Species Name
AF	*B or BL*	Alpine Fir	MH		Mountain Hemlock
AS		Aspen	OC		Other conifers
BO		Black Oak	OH		Other hardwood
BS		Blue Spruce	OS		Other softwood
C	*C*	Western Red cedar	OTH		Other species
CB		Corkbark Fir	PP	*PY*	Ponderosa Pine
CW		Cottonwood	RF		Red Fir
DF	*FD or F*	Douglas-fir	S	*S*	Spruce
ES		Engelmann Spruce	SF		Pacific Silver Fir
GF	*BG*	Grand Fir	SP		Sugar Pine
GS		Giant Sequoia	TO		Tanoak
IC		Incense-cedar	WB		Whitebark Pine
J		Juniper	WF		White Fir
JP		Jeffrey Pine	WH	*HW*	Western Hemlock
L	*L*	Larch	WL	*LW or L*	Western Larch
LM		Limber Pine	WP	*PW*	White Pine
LP	*LP*	Lodgepole Pine	WS		White Spruce

Keyword Defaults by Species and Variant

INFCOLO

This keyword defines the proportion of the root system that is colonized **after** death (Section 5.3 of Chapter 2).

Variant	Species Code (as represented in tree data and output)										
	1	2	3	4	5	6	7	8	9	10	11
ANNOSUS											
Inland Empire	0.8	0.95	0.95	0.9	0.9	1.0	0.75	0.95	0.9	0.75	0.86
Southern Interior	0.8	0.95	0.95	0.9	0.9	1.0	0.75	0.95	0.9	0.75	0.86
S.Cen.Oregon/NE Calif.	0.8	0.8	0.95	0.9	0.9	0.95	0.75	0.95	0.9	0.75	0.86
Eastern Montana	0.8	0.95	0.95	0.9	0.9	1.0	0.75	0.95	0.9	0.75	0.86
East Cascades	0.8	0.95	0.95	0.9	0.9	0.9	0.75	0.95	0.9	0.75	0.86
Blue Mountains	0.8	0.95	0.95	0.9	0.9	0.9	0.75	0.95	0.9	0.75	0.86
Western Sierra Nevada	0.9	0.8	0.95	0.9	0.95	0.95	0.0	0.75	0.9	0.75	0.0
ARMILLARIA											
Inland Empire	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Southern Interior	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
S.Cen.Oregon/NE Calif.	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Eastern Montana	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
East Cascades	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Blue Mountains	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
Western Sierra Nevada	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
PHELLINUS											
Inland Empire	0.8	0.6	0.3	0.85	0.8	0.85	0.8	0.8	0.75	0.65	0.8
Southern Interior	0.8	0.6	0.3	0.85	0.8	0.85	0.8	0.8	0.75	0.65	0.8
S.Cen.Oregon/NE Calif.	0.8	0.6	0.3	0.3	0.8	0.85	0.8	0.8	0.3	0.65	0.8
Eastern Montana	0.8	0.6	0.3	0.85	0.8	0.85	0.8	0.8	0.75	0.65	0.8
East Cascades	0.8	0.6	0.3	0.85	0.8	0.85	0.8	0.8	0.75	0.65	0.8
Blue Mountains	0.8	0.6	0.3	0.3	0.8	0.85	0.8	0.8	0.75	0.65	0.8
Western Sierra Nevada	0.8	0.6	0.3	0.3	0.8	0.85	0.8	0.8	0.9	0.65	0.8

INFKILL

This keyword defines the proportion of the root system that is colonized **at** death (Section 5.3 in Chapter 2).

Variant	Species Code (as represented in tree data and output)										
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
ANNOSUS											
Inland Empire	0.6	0.9	0.9	0.8	0.8	1.0	0.5	0.9	0.8	0.5	1.0
Southern Interior	0.6	0.9	0.9	0.8	0.8	1.0	0.5	0.9	0.8	0.5	1.0
S.Cen.Oregon/NE Calif.	0.6	0.6	0.9	0.8	0.8	0.9	0.5	0.9	0.8	0.5	1.0
Eastern Montana	0.6	0.9	0.9	0.8	0.8	1.0	0.5	0.9	0.8	0.5	1.0
East Cascades	0.6	0.9	0.9	0.8	1.0	0.8	0.5	0.9	0.8	0.5	1.0
Blue Mountains	0.6	0.9	0.9	0.8	0.8	0.8	0.5	0.9	0.8	0.5	1.0
Western Sierra Nevada	0.75	0.6	0.9	0.8	0.9	0.9	0.0	1.0	0.8	0.5	0.0
ARMILLARIA											
Inland Empire	0.3	0.85	1.0	0.75	0.8	0.8	0.8	0.6	0.8	0.8	0.6
Southern Interior	0.3	0.85	1.0	0.75	0.8	0.8	0.8	0.6	0.8	0.8	0.6
S.Cen.Oregon/NE Calif.	0.3	0.85	1.0	0.3	0.75	0.85	0.8	0.6	0.75	0.8	0.6
Eastern Montana	0.8	0.85	1.0	0.75	0.8	0.8	0.8	0.6	0.8	0.8	0.6
East Cascades	0.3	0.85	1.0	0.65	0.8	0.75	0.8	0.6	0.8	0.8	0.6
Blue Mountains	0.3	0.85	1.0	0.3	0.8	0.75	0.8	0.6	0.8	0.8	0.6
Western Sierra Nevada	0.8	0.85	1.0	0.3	0.8	0.85	0.8	0.8	0.75	0.8	0.6
PHELLINUS											
Inland Empire	0.8	0.6	0.3	0.85	0.8	0.85	0.8	0.8	0.75	0.65	0.8
Southern Interior	0.8	0.6	0.3	0.85	0.8	0.85	0.8	0.8	0.75	0.65	0.8
S.Cen.Oregon/NE Calif.	0.8	0.6	0.3	0.3	0.8	0.85	0.8	0.8	0.3	0.65	0.8
Eastern Montana	0.8	0.6	0.3	0.85	0.8	0.85	0.8	0.8	0.75	0.65	0.8
East Cascades	0.8	0.6	0.3	0.85	0.8	0.85	0.8	0.8	0.75	0.65	0.8
Blue Mountains	0.8	0.6	0.3	0.3	0.8	0.85	0.8	0.8	0.75	0.65	0.8
Western Sierra Nevada	0.8	0.6	0.3	0.3	0.8	0.85	0.8	0.8	0.9	0.65	0.8

INFMULT

This keyword defines the probability of infection, given root contact (Section 5.3 in Chapter 2).

Variant	Species Code (as represented in tree data and output)										
	1	2	3	4	5	6	7	8	9	10	11
ANNOSUS											
Inland Empire	0.4	0.4	0.4	0.5	0.5	0.0	0.4	0.4	0.5	0.5	0.0
Southern Interior	0.4	0.4	0.4	0.5	0.5	0.0	0.4	0.4	0.5	0.5	0.0
S.Cen.Oregon/NE Calif.	0.4	0.4	0.4	0.5	0.5	0.5	0.4	0.4	0.5	0.5	0.0
Eastern Montana	0.4	0.4	0.4	0.5	0.5	0.0	0.4	0.4	0.5	0.5	0.0
East Cascades	0.4	0.4	0.4	0.5	0.0	0.5	0.4	0.4	0.5	0.5	0.0
Blue Mountains	0.4	0.4	0.4	0.5	0.5	0.5	0.4	0.4	0.5	0.5	0.0
Western Sierra Nevada	0.45	0.4	0.4	0.5	0.5	0.5	0.0	0.5	0.5	0.5	0.0
ARMILLARIA											
Inland Empire	0.1	0.05	0.5	0.6	0.1	0.6	0.2	0.5	0.5	0.2	0.1
Southern Interior	0.1	0.05	0.5	0.6	0.1	0.6	0.2	0.5	0.5	0.2	0.1
S.Cen.Oregon/NE Calif.	0.1	0.1	0.5	0.6	0.1	0.5	0.2	0.5	0.5	0.2	0.1
Eastern Montana	0.1	0.05	0.5	0.6	0.1	0.6	0.2	0.5	0.5	0.2	0.1
East Cascades	0.1	0.05	0.5	0.6	0.6	0.6	0.2	0.5	0.5	0.2	0.1
Blue Mountains	0.1	0.05	0.5	0.6	0.1	0.6	0.2	0.5	0.5	0.2	0.1
Western Sierra Nevada	0.1	0.1	0.5	0.6	0.1	0.1	0.0	0.1	0.5	0.2	0.2
PHELLINUS											
Inland Empire	0.1	0.2	0.4	0.4	0.2	0.02	0.1	0.2	0.4	0.1	0.4
Southern Interior	0.1	0.2	0.4	0.4	0.2	0.02	0.1	0.2	0.4	0.1	0.4
S.Cen.Oregon/NE Calif.	0.1	0.1	0.4	0.4	0.4	0.4	0.1	0.2	0.4	0.1	0.4
Eastern Montana	0.1	0.2	0.4	0.4	0.2	0.02	0.1	0.2	0.4	0.1	0.4
East Cascades	0.1	0.2	0.4	0.4	0.02	0.2	0.1	0.2	0.4	0.1	0.4
Blue Mountains	0.1	0.2	0.4	0.4	0.2	0.2	0.1	0.2	0.4	0.1	0.4
Western Sierra Nevada	0.4	0.1	0.4	0.4	0.4	0.4	0.0	0.02	0.4	0.1	0.1

RRHOSTS

This keyword allows users to change the default Annosus root disease type to which the tree species is host (Section 5.5 in Chapter 2). This keyword can be used only for *Annosus*.

Variant	Species Code (as represented in tree data and output)										
	1	2	3	4	5	6	7	8	9	10	11
Inland Empire	1	2	2	2	2	2	1	2	2	1	1
Southern Interior	1	2	2	2	2	2	1	2	2	1	1
S.Cen.Oregon/NE Calif.	1	1	2	2	2	1	1	2	2	1	1
Eastern Montana	1	2	2	2	2	2	1	2	2	1	1
East Cascades	1	2	2	2	2	2	1	2	2	1	1
Blue Mountains	1	2	2	2	2	2	1	2	2	1	1
Western Sierra Nevada	1	1	2	2	2	1	1	1	2	1	1

TTDMULT

This keyword gives a multiplier for the basic time-to-death function (Section 5.3 in Chapter 2).

Variant	Species Code (as represented in tree data and output)										
	1	2	3	4	5	6	7	8	9	10	11
ANNOSUS											
Inland Empire	1.0	1.0	1.0	1.5	1.75	1.0	1.5	1.0	1.5	0.5	1.0
Southern Interior	1.0	1.0	1.0	1.5	1.75	1.0	1.5	1.0	1.5	0.5	1.0
S.Cen.Oregon/NE Calif.	1.0	1.0	1.0	1.5	1.75	1.75	1.5	1.0	1.5	0.5	1.0
Eastern Montana	1.0	1.0	1.0	1.5	1.75	1.0	1.5	1.0	1.5	0.5	1.0
East Cascades	1.0	1.0	1.0	1.5	1.0	1.5	1.5	1.0	1.5	0.5	1.0
Blue Mountains	1.0	1.0	1.0	1.5	1.75	1.5	1.5	1.0	1.5	0.5	1.0
Western Sierra Nevada	1.0	1.0	1.0	1.5	1.75	1.75	99.0	0.5	1.5	0.5	99.0
ARMILLARIA											
Inland Empire	1.8	2.0	1.0	0.75	0.9	1.2	1.8	1.1	0.75	1.8	0.9
Southern Interior	1.8	2.0	1.0	0.75	0.9	1.2	1.8	1.1	0.75	1.8	0.9
S.Cen.Oregon/NE Calif.	1.8	1.8	1.0	0.75	0.9	0.9	1.8	1.1	0.75	1.8	0.9
Eastern Montana	1.8	2.0	1.0	0.75	0.9	1.2	1.8	1.1	0.75	1.8	0.9
East Cascades	1.8	2.0	1.0	0.75	1.0	0.75	1.8	1.1	0.75	1.8	0.9
Blue Mountains	1.8	2.0	1.0	0.75	0.9	0.75	1.8	1.1	0.75	1.8	0.9
Western Sierra Nevada	0.9	1.8	1.0	0.75	0.9	0.9	99.0	0.2	0.75	1.8	1.8
PHELLINUS											
Inland Empire	3.0	1.5	1.0	1.0	1.5	1.0	3.0	1.1	1.0	3.0	1.5
Southern Interior	3.0	1.5	1.0	1.0	1.5	1.0	3.0	1.1	1.0	3.0	1.5
S.Cen.Oregon/NE Calif.	3.0	3.0	1.0	1.0	1.5	1.5	3.0	1.1	1.0	3.0	1.5
Eastern Montana	3.0	1.5	1.0	1.0	1.5	1.0	3.0	1.1	1.0	3.0	1.5
East Cascades	3.0	1.5	1.0	1.0	1.0	1.0	3.0	1.1	1.0	3.0	1.5
Blue Mountains	3.0	1.5	1.0	1.0	1.5	1.0	3.0	1.1	1.0	3.0	1.5
Western Sierra Nevada	1.5	3.0	1.0	1.0	1.5	1.5	99.0	10	1.0	3.0	3.0

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Detailed Calculation of Initial Root Disease
Density Calculation Using Disease Codes

Density Calculation Using RRTEIN

The keyword **RRTREIN** is used to tell the model to read disease codes from the tree list. These codes identify tree records that contain some root disease. The model assumes that each record represents a density of trees that covers the entire stand. Thus, each record represents trees inside centers (either infected or uninfected, depending on the presence or absence of a disease code) and trees outside centers. The densities of trees in both locations (inside and outside centers) are assumed to be the same. Thus for each record, the model sets:

$$Infected = RecordDensity \qquad or\ Infected = 0$$
$$UnInf = 0 \qquad or\ UnInf = RecordDensity$$
$$Outside = Infected + UnInf$$

where:

Infected	is the density of infected trees inside centers (trees/acre or trees/hectare);
UnInf	is the density of uninfected trees within centers (trees/acre or trees/hectare);
Outside	is the density of uninfected trees outside centers (trees/acre or trees/hectare);
RecordDensity	is the density of the current record;

The overall stand density is equal to the sum of the density for each record.

Density Calculation Using PLREAD

The keyword **PLREAD** is always used in conjunction with **RRTREIN**. When **PLREAD** is used, each record is either entirely within a center or outside of a center, and those records within centers are further identified as infected or uninfected. However, initial density as determined by FVS is calculated as the density of the record over the whole stand. Thus, the model scales each record in the tree lists by the ratio of the total area in the stand to the area in root disease centers, using one of the following equations

$$Infected = RecordDensity_{inf} * StandArea / RRArea$$
$$UnInf = RecordDensity_{un} * StandArea / RRArea$$
$$Outside = RecordDensity_{out} * StandArea / (StandArea - RRArea)$$

where:

RecordDensity	is the density of the current record, either infected (*inf*), uninfected inside centers (*un*), or outside centers (*out*);
StandArea	is the total area of the stand; and
RRArea	is the area inside root disease centers.

The overall stand density is then calculated either by summing the total *RecordDensity* or by summing the total density in each list (infected, uninfected, and outside center) and using the following formula:

$$StandDensity = \frac{(Infected_{tot} + UnInf_{tot}) * RRArea + Outside_{tot} * (StandArea - RRArea)}{StandArea}$$

Comparison of using RRTREIN and PLREAD

Imagine a stand with 10 plots, each of which has two tree records. Four of the plots contain one tree record with disease codes, and in these plots the density is 15 trees/acre for each record. When the keyword **PLREAD** is used, these four plots are considered to be inside centers. The remaining six plots have no disease codes, have 25 trees/acre for each record and are considered outside centers when using **PLREAD**.

Plot No.	1	2	3	4	5	6	7	8	9	10
No. Records	1	1	1	1	1	1	1	1	1	1
Disease Code	yes	yes	yes	yes	no	no	no	no	no	no
Density of each record	15	15	15	15	25	25	25	25	25	25
No. Records	2	2	2	2	2	2	2	2	2	2
Disease Code	no	no	no	no	no	no	no	no	no	no
Density of each record	15	15	15	15	25	25	25	25	25	25

Next assume that the stand is 10 acres, with 3 acres inside disease centers. Using the above formulas, and summing across all records, the resulting densities can be calculated and are:

	Infected	Uninfected	Outside	Total Stand
RRTREIN only	60	360	420	420
RRTREIN & PLREAD	200	200	429	420

Choosing the Trees to Infect (detailed explanation)

When the keyword **RRINIT** is used for setting initial infection levels, the steps for calculating which tree records will be infected are:

1. Place trees in centers. This is done by determining how much of the stand is inside root disease centers, and then placing that proportion of each tree record inside centers. For example, if centers cover 30 percent of the stand, 30 percent of each tree record will be inside a center.

2. Determine the relative proportion of trees of each species which should be infected. This is calculated using the formula:

$$PropInf_{sp} = \frac{Pinf_{sp} * AvgTTD_{sp}}{\sum_{sp}^{11} Pinf_{sp} * AvgTTD_{sp}}$$

where:

$PropInf_{sp}$	is the proportion of trees of species sp which should be infected;
$Pinf_{sp}$	is the probability of infection for species sp; and
$AvgTTD_{sp}$	is the average time to death for the trees of species sp which are present in the center.

When Annosus root disease is being simulated, the denominator of the equation is based only on the species which are host to the same disease type. For the other root diseases, all trees are host so all species would be considered.

For example, imagine a hypothetical stand with nine tree records, three each for ponderosa pine, lodgepole pine, and incense cedar. Each species has one record that is 5 inches dbh, one that is 10 inches and one that is 20 inches, and each record within a species contains the same number of trees. Given the basic time to death of an infected tree (i.e., a tree with a time-to-death multiplier of 1) is: 6.12 years for a 5-inch tree, 11.69 years for a 10-inch tree, and 22.84 years for a 20-inch tree, with an average time to death of 13.55 years, and using Armillaria root disease in the Inland Empire variant, the following calculations can be made:

Species	$Pinf$	TTD mult.	$AvgTTD$	$Pinf*TTD$	$PropInf$
Basic		1.0	13.55		
Ponderosa pine	0.2	1.8	24.39	4.88	0.39
Lodgepole pine	0.6	0.75	10.16	6.10	0.48
Incense cedar	0.1	1.2	16.26	1.63	0.13
Total				12.61	1.00

3. Determine the density of trees of each species in the center which should be infected. The pieces of information required for this step are: the total number of trees inside centers, the proportion of each species to be infected (from step 2 above), and the proportion of trees in the center which should be infected.

$$NumInf_{sp} = NumTrees * PropCenterInf * PropInf_{sp}$$

where:

$NumInf_{sp}$	is the desired number of trees of species sp infected;
$NumTrees$	is the total number of trees inside the center of a disease type;
$PropCenterInf$	is the proportion of the center which should be infected; and
$PropInf_{sp}$	is the proportion of each species to be infected (from step 2).

For example, consider the stand in step 2. If there were 75 trees and 30 percent of the trees in centers were to be infected, then 8.8 ponderosa pine trees would be infected, 10.8 lodgepole pine, and 2.9 incense cedar.

	Ponderosa Pine	Lodgepole Pine	Incense Cedar	Total
Number of Trees	30	15	30	75
$PropInf_{sp}$	0.39	0.48	0.13	1
$NumInf_{sp}$ @ 30 percent	8.8	10.8	2.9	22.5
Actual Number Infected	8.8	10.8	2.9	22.5

If too few trees of a species are present in the center, then all of the trees of that species will be infected and the remainder of the 'desired' number of trees will be distributed evenly among the other species. If the stand in the previous example were to be 50 percent infected, the model would want to initialize 18 lodgepole pine as infected. However, since the centers contain only 15 lodgepole pine, all of them will be infected and the remaining three will be divided equally between the two remaining species (ponderosa pine and incense cedar).

	Ponderosa Pine	Lodgepole Pine	Incense Cedar	Total
Number of Trees	30	15	30	75
$PropInf_{sp}$	0.39	0.48	0.13	1
$NumInf_{sp}$ @ 50 percent	14.6	18	4.9	37.5
Actual Number Infected	16.1	15	6.4	37.5

4. Infect the trees. A proportion of each tree record inside centers will be infected on the basis of the proportion calculated from the number infected in step 3. The proportion is applied across all size classes; the size variation of trees within centers is accounted for in the calculation of time to death, since small trees die faster than large ones.

In the first example given in step 3, 8.8 ponderosa pine out of 30 total will be infected. Thus 29 percent (8.8/30) of each ponderosa pine record will be considered infected. A similar calculation can be done for the lodgepole pine and the incense cedar.

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