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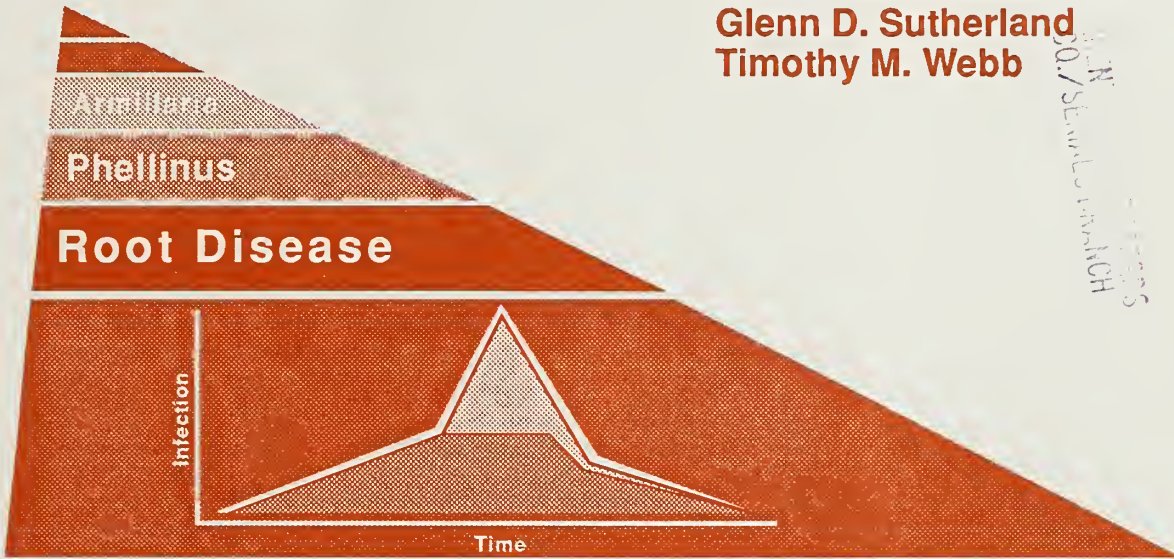
User's Manual for Western Root Disease Model

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RESEARCH SUMMARY

Effects of *Armillaria* spp. or *Phellinus weirii* on stand dynamics are represented by the Western Root Disease Model. This model, which operates in conjunction with the Prognosis Model for Stand Development, can be used to evaluate effects of a wide assortment of silvicultural practices, including stump removal for disease reduction. The model was developed through a series of workshops designed to elicit information about the disease process from many experts on the biology of the root diseases and their hosts. Forest land managers also participated in the workshops to provide their insight into the values and resources being affected.

This publication contains model applications, a brief description of how the model is formulated, and documentation of the keyword procedures for using the model.

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INTRODUCTION

Tree root diseases pervade forested lands of the United States. Timber losses caused by root diseases have been estimated to average nearly 240 million cubic feet per year (Smith 1984). Root diseases typically originate from infected stumps of previous stands and spread to root systems of other trees in the immediate vicinity (Thies 1984; Wargo and Shaw 1985). The ability of these diseases to survive for many years in roots and stumps and to spread in stands throughout a rotation (possibly without early detection) imposes constraints on the management prescriptions available for regenerating stands (Bloomberg and others 1980). Management practices such as transplanting of trees, deep planting, partial cutting, fire prevention, or excessive removal of understory biomass may initiate or enhance the spread of one or more root diseases (Wargo 1980). Other practices, including use of disease-resistant tree species, trenching around infection centers, and careful cutting and commercial thinning methods, are known to reduce root disease impacts (Shaw and Roth 1978).

In response to managers' concerns for lack of information about the future development of diseased stands, a model was designed to predict the spread and impact of pathogenic *Armillaria* spp. or *Phellinus weirii* (Murr. [Gilbn.]) in mixed species, multiaged stands in the Western United States. The model was developed through a series of workshops in which the knowledge of many experts on the biology and management of root diseases was captured (Brookes 1985 and appendix I). With this information, and after several rounds of refinement, the model was produced; it currently operates in conjunction with the Prognosis Model for Stand Development. Details on the process of model development appear in Shaw and others (1985), Eav and Shaw (1987), and McNamee and others (1985).

The combined Prognosis/Root Disease Model can be used with existing forest inventories to evaluate possible outcomes of silvicultural prescriptions and root disease control activities for sites where root disease may influence stand development. Its uses include long-term planning for management of stands affected by root disease and for highlighting potential uncertainties and research needs for better understanding of root disease dynamics and effects.

To model effects of silviculture on root-disease organisms, and their effects on stand dynamics, requires a model of stand development that can represent stands of mixed species and ages. Furthermore, the stand model should represent the species and sizes of regeneration that are expected to fill openings created by tree mortality. The Stand Prognosis Model described by Stage (1973) and Wykoff and others (1982) has these capabilities. In addition, it is extensively used for examining and evaluating alternative stand management practices in the Western United States. The Prognosis Model is intended to produce estimates of realizable yield. Growth statistics calculated by the model include the average effects of factors such as climatic variation, past management activities, and pest damage as they are applied to the individual tree classes that make up the stand. One or more "extensions" to the Prognosis Model must be used to explicitly include interactions

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between the stand and events such as establishment of regenerating stands, pest outbreaks, and understory development.

At present, the Root Disease Model is linked to the Prognosis Model. Once during each of the Prognosis growth cycles, which span about 10 years of simulated time, the Root Disease Model calculates rates of spread of the disease and numbers of trees within diseased areas that become infected. Then reductions in growth and increases in mortality are passed to the Prognosis Model to be used in updating tree attributes. At the end of each cycle, a summary of disease conditions is produced, as well as the usual descriptions of stand volume, accretion, and mortality produced by the base Prognosis Model.

When the stand is primarily composed of conifer regeneration of less than 3 inches diameter at breast height (d.b.h.), the usual Prognosis cycles are too long to capture the rapid dynamics of the disease process. In this case, a "miniature" version of the Root Disease Model is invoked with shorter time steps. This submodel is termed the "Carryover Model" because it serves to bridge the gap in modeling the transition from a mature stand to the reestablished stand at time of root closure.

Ecological Scope

The pathogens covered by this model, pathogenic *Armillaria* spp. and *P. weirii*, are widely distributed in forests of Western North America (fig. 1). Where these distributions overlap with the area covered by an existing variant of the Prognosis Model (fig. 1), the Root Disease Model can be used. However, when used with variants for which the regeneration establishment component (Ferguson and Crookston 1984) has not been implemented, projections will not include natural regeneration. When the stand is cut, the user must simulate regeneration through some sort of planting. In this manual, the examples will be based on the Inland Empire variant, which has a regeneration establishment component.

In addition to effects of pathogenic *Armillaria* spp. or *P. weirii*, the model includes interactions with damage caused by windthrow of trees in the stand and with three types of bark beetles. The bark beetle types are defined by their role in the dynamics of the root disease process. The three types are (1) dependent only on the density of susceptible stems, (2) dependent upon windfallen stems as refugia for the beetle population, and (3) dependent upon stems infected by root disease.

Management Actions Represented

The model can evaluate both direct control of root disease and a wide variety of silvicultural treatments, which may have indirect effects on the course of the disease.

Direct Control of Root Disease—The Root Disease Model implements only one management action specifically used for control of root disease, that of removal of inoculum by "pushing" infected stumps and their root systems (or by fumigation). This option can be requested in a specific year, with a factor specifying the efficiency with which roots are removed and the minimum dead tree/stump diameter for removal. This practice is an accepted management alternative in certain stands but should not be considered as feasible in all cases. A pathologist should be consulted to evaluate the possibility of using this option rather than selecting a resistant species, as described below.

Silvicultural Treatment—The silvicultural options available with the Prognosis Model can also be invoked to analyze alternative methods for indirect control of root disease. Regeneration systems to be simulated can span the full range from single-tree selection to clearcutting. In addition to the harvest of existing trees, new stands can be introduced following site preparation by natural regeneration or by planting. Of these, modification of species composition of regenerated stands through planting or choice of regeneration systems is the most effective means of avoiding root disease problems.

Figure 1—Locations covered by Prognosis variants. Shading indicates where either *Armillaria* spp. or *Phellinus weirii* is considered to be a management problem.

Data Required

The model is designed to start with sample inventories of actual stands. For example, the compartment examination procedure described by Stage and Alley (1972) and in USDA Forest Service Handbook 2409.21h R1 (1986) can supply the necessary stand data if augmented to include stumps infected with root disease.

In addition to the customary tree size attributes, the model uses information on the frequency of tree infection by root disease. This value can be compiled by the model from disease status codes of the individual sample trees or supplied by the user from an overall estimate based on an independent sample of the stand. The Root Disease Model also uses data on the area of the stand and the sizes and distribution of diseased centers to initiate the simulation. The model can start from bare ground by invoking the regeneration establishment component or from the description of the existing stand contained in the list of trees sampled in the inventory. Proportions of trees infected and proportions of roots infected within diseased areas can be supplied in the aggregate or by specifying disease status of each tree in the sample inventory.

APPLICATIONS IN PLANNING AND MANAGEMENT

The Root Disease Model is potentially an important pest model. Root diseases affect a significant area of the West, more than 3 million acres in northern Idaho and western Montana alone (Smith 1984). *Phellinus weirii* and *Armillaria* spp. which are represented in this model are the major pathogens in those States (James and others 1984) and in Oregon and Washington (Hadfield and others 1986). In addition, effects of *Annosus* root disease may be approximated by making changes in the parameters through use of the keywords of this model (Shaw and others 1989).

Root diseases strongly influence stand prescriptions. Stand losses can exceed 50 percent or more at rotation age. Therefore, projections of stand volumes that do not account for disease effects can be greatly inflated. Even so, short-term effects can be subtle and easily underestimated. The loss of only a few trees per acre a year, many of which are salvaged for firewood or fall down from decay in a relatively short time, makes it difficult to recognize the magnitude of the problem. Silviculturists can learn from gaming with the model how past practices may have exacerbated the root disease problem and how prescribed treatments may reduce future losses.

The Root Disease Model may also be useful because the disease process is predictable. Although the model is still relatively new and untested, and many aspects of disease behavior are incompletely known, root disease, once established in a stand, is persistent. Tree killing and disease center enlargement continue at a relatively slow but predictable rate compared with certain other pests that are sporadic and unpredictable in occurrence and intensity. Empirical data to accurately assess these relationships are scarce. Therefore, outputs from the model should be used in a qualitative sense to evaluate alternative management prescriptions rather than as a precise quantitative estimator of future root disease impacts. However, output from the model will provide a "best guess" based on expert opinion and is likely to be more realistic than estimates by less experienced personnel. How important these best guesses are has been explored through model sensitivity analyses (McNamee and Sutherland 1986).

Stand Level

Because the model predicts stand growth and yield under different stand treatments and disease intensities, the results can be used to formulate stand prescriptions that will meet specified objectives and to communicate the treatment effects to interdisciplinary team members, line officers, and others. The model may be used at any stage of stand development. However, it may be most valuable for planning the regeneration phase because the greatest opportunity to influence root disease occurs at that time.

The most frequent approach to management of root disease problems in timber stands is regeneration to site-suited tree species that are disease tolerant. The model can be used to compare the effects of variations of this approach, as well as others. For example, the following options may be considered:

1. A clearcut, seed-tree cut, or shelterwood cut followed by regenerating to disease-tolerant species, or a mixed stand with a predominance of tolerant species.
2. Overstory removal from an understory that might be disease susceptible, tolerant, or a mixture of the two.
3. A clearcut and stump removal, followed by planting of a disease-susceptible but otherwise preferred species.
4. No treatment, or a deferred treatment.

We recommend that two other simulations be included even if those actions are not contemplated because they provide baselines against which other treatments can be compared:

1. Harvest without stump treatment, followed by natural regeneration, even if it consists of susceptible species. Simulate with the Root Disease Model operating.
2. Harvest, followed by planting of preferred species, ignoring root disease considerations. Simulate without the Root Disease Model operating.

In precommercial stands the model also may be used to evaluate effects of different treatment alternatives. Treatment options at this phase might include precommercial thinning, using various leave tree species and spacing rules, deferred or no treatment, and destroying the existing stand to replace with a disease-tolerant species.

Forest Level

Long-term planning for sustained yield requires that the yield potential of existing stands be estimated unbiasedly. All too often, inventories of young stands do not adequately describe the root-disease status. As a consequence, their future contribution to forest yield is seriously overestimated if they consist of susceptible species growing on infested sites. In the judgment of some managers, omission of pest effects may have resulted in plans that, in reality, are infeasible.

Representation of root disease impacts on long-term plans requires three elements:

1. An inventory that identifies those sites on which root disease can be expected to cause losses. Guides for classifying sites with respect to the risk of loss from root disease could be developed for some areas from information in Byler and others (in press), McDonald and others (1987), Williams and Marsden (1982).

2. A model such as this one for representing effects of proposed management activities on future yields that includes interactions between tree growth and mortality and the dynamics of the root pathogens.

3. A structure for a planning model that permits site-specific yield forecasts to be used in developing solutions to the yield scheduling problem. Stage and others (1986) suggested one such structure.

To be effective, all of the yield-estimating procedures used in a given planning solution should include pest effects. Otherwise, the solution would favor harvesting of stands with higher potential yield, even if those stands are, in their own right, also susceptible to damage by various pests.

Multistand Analysis

The model has the potential for describing disease effects and evaluating alternative treatment strategies at intermediate planning levels.

A strategy for reducing pest-caused losses for compartments or entire watersheds is to select high-risk stands for immediate harvest and defer treatment in low-risk stands. Root Disease Model simulations on stands of different ages, species composition, stocking, and disease condition could be used to set harvesting priority. Thus, mortality that would otherwise occur in high-loss stands would be captured and the growth potential of the site realized by regenerating to species tolerant of disease.

The Root Disease Model also has potential at the multistand level when implementing forest plans. The desired future vegetative conditions to achieve the mix of products and values identified in the plans remain to be specified. By projecting growth and development of many stands in an analysis area, effects of root disease and various treatments can be displayed. Stands can be scheduled for treatment in a sequence that best meets the management objectives. For example, treatments could provide a mix of stands at different successional stages, spaced in a manner that would meet visual management objectives, provide for big game hiding cover (Canfield and others 1986), thermal cover, and browse (Moeur 1985) yet provide a flow of timber products as well.

Crow Creek Stand— An Example

To illustrate use of this modeling system, we will develop a simulation for a stand in the Crow Creek drainage on the Lolo National Forest. This 51-acre stand is about 130 years of age, growing on a *Thuja/Clintonia* habitat type at an elevation of 3,300 feet. When the stand was examined in 1983, it consisted of grand fir, larch, redcedar, and Douglas-fir. *Armillaria* occurred on two of the seven inventory plots. One possible scenario for management of this stand is to harvest the existing trees

in 2003, burn the slash, and plant larch. On this productive habitat, there will also be substantial natural regeneration, but largely comprising grand fir and Douglas-fir, which, in this habitat, are susceptible to damage from root rot. Therefore, a cleaning at age 10 favoring larch will remove most of the natural regeneration. The Prognosis Model keywords and data representing the Crow Creek inventory are listed in table 1. Portions of this input that contain information specific to the Root Disease Model are shaded.

Table 1—Keywords for the Root Disease and the Prognosis Models as they occurred in the Prognosis Model input file for a stand in Crow Creek on the Lolo National Forest

```
STDIDENT
164581202025 CROW CREEK DATA-R1-ROOT DISEASE
COMMENT
        - RRSETB - TEST ROOT DISEASE MODEL
        - TYPE OF STAND - INVENTORY
        - ROOT DISEASE - ARMILLARIA
        - 7 PLOTS, 2 WITH RD
        - RANDOM CENTERS
END
TREELIST          1.
DESIGN           40.0      300.0        5.0        7.0        0.0        1.0
STDINFO          16.0      530.0      130.0        2.0        1.0       33.0
INVYEAR        1983.0
GROWTH            0.0        5.0
NUMCYCLE         20.0
NOTRIPLE
THINDBH        2003.0        1.0       99.0        1.0
TIMEINT           3.0        5.0
TIMEINT           4.0        5.0
TIMEINT           5.0        5.0
TIMEINT           6.0        5.0
TIMEINT           7.0        5.0
TIMEINT          20.0        5.0
ESTAB          2003.0
BURNPREP       2004.0       80.
PLANT          2005.0        2.0      500.0       80.0
TALLYONE       2007.0
TALLYTWO       2012.0
RESETAGE       2005.        0.0
HTADJ          2005.0        2.0        1.5
END
SPECPREF       2008.0        2.0       -2.0
THINBTA        2013.0     1000.0
RRIN
SAREA            51.0
PLREAD
  1
  5
-999
RRTYPE            1.0
RRINIT            0.0        3.0                                0.4       21.00
RRTREIN
STREAD
    3   25.0   10.0
    4   15.0   25.0
    3    5.0  100.0
-999
CARRY             1.0        4.0        0.02
SPREAD            1.0
PSTUMP         2003.0        0.8        3.0
RRJUMP            1.0
RSEED         11188.0
RRDOUT
END
```

```
TREEFMT
(13X,I4,T1,I5,T28,F2.0,T25,I1,T33,A2,F3.1,F2.1,3X,F3.0,T43,F3.0,T54,
F2.0,T46,I1,T48,3(I2,I1),T22,I1,T22,I1)
TREEDATA        5.0
1645812020252 001  10  0  0 12 OPP217 5175 9652611  0  01250 040S 592000
1645812020252 001  20  0  0 13 ODF214 7 5210752611  0  02700 0 0    0000
1645812020252 001  30  0  0 16 ODF184 0  010200610  0  00 00 0 0    0000
1645812020252 0011010  0  0 11 OGF 3310 26 1783611  0  01 00 0 0    0000
1645812020252 0011020  0  0 11 ODF  1 0 18   263611  0  01 00 0 0    0000
1645812020252 0011030  0  0 11 OGF  1 0 15   153611  0  01 00 0 0    0000
1645812020252 0011040  0  0 51 OGF  1 0 22   154611  0  00 00 0 0    0000
1645812020252 0011050  0  0101 ODF  1 0 31   055611  0  00 00 0 0    0000
1645812020252 0011060  0  0 74 ODF  1 0 31   055902611 00 00 0 0    0000
1645812020252 002  10  0  0 12 ODF 95 7 52 5453  0  0  01 00 0 5E 530000
1645812020252 002  20  0  0 12 ODF 61 3 46 4343  0  0  01 00 0 0    0000
1645812020252 002  30  0  0 11 OGF 5711 37 5073  0  0  01 00 0 0    0000
1645812020252 002  40  0  0 12 ODF 59 3 45 3844  0  0  00 00 0 0    0000
1645812020252 0021010  0  0 11 OGF  1 0 23   254  0  0  01 00 0 0    0000
1645812020252 0021020  0  0201 OGF  1 0 22   154  0  0  00 00 0 0    0000
1645812020252 0021030  0  0 54 OGF  1 0 22   054  0  0  00 00 0 0    0000
1645812020252 003  10  0  0 13 OL 354 310313952972452  02 00 025SE531000
1645812020252 003  20  0  0 12 OL  57 9 53 5453601  0  01 00 0 0    0000
1645812020252 003  30  0  0 12 OLP 83 4 57 6733601  0  01 00 0 0    0000
1645812020252 0031010  0  0 11 OC   9 0 25   774601  0  01 00 0 0    0000
1645812020252 0031020  0  0 11 OGF  1 0 15   165601  0  01 00 0 0    0000
1645812020252 0031030  0  0501 OGF  1 0 22   065601  0  00 00 0 0    0000
1645812020252 0031040  0  0 61 OC   1 0 25   265601  0  00 00 0 0    0000
1645812020252 0031050  0  0 44 ODF  1 0 31   145601  0  00 00 0 0    0000
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1645812020252 0041010  0  0 14 OLP 39 3 43 5233902  0  02 00 0 0    0000
1645812020252 0041020  0  0 11 ODF 14 0 40 1164  0  0  01 00 0 0    0000
1645812020252 0041030  0  0 11 OGF 14 0 38   854  0  0  01 00 0 0    0000
1645812020252 0041040  0  0 11 ODF  1 0 38   654  0  0  01 00 0 0    0000
1645812020252 0041050  0  0 11 OGF  1 0 20   264  0  0  01 00 0 0    0000
1645812020252 0041060  0  0451 OGF  1 0 22   055  0  0  00 00 0 0    0000
1645812020252 0041070  0  0201 ODF  1 0 31   055  0  0  00 00 0 0    0000
1645812020252 005  10  0  0 19 OWP134 0  0 8700960610  00120 0 5NE550000
1645812020252 005  20  0  0 12 OL 396 310315022453971  02200 0 0    0000
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1645812020252 005  40  0  0 19 OL 236 0  013400960610  00 00 0 0    0000
1645812020252 005  50  0  0 15 OC 256 4 50 8464456981  02 00 0 0    0000
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1645812020252 0051050  0  0 62 OC   5 0 25   655611  0  00 00 0 0    0000
1645812020252 006  10  0  0 12 OGF138 5 8810334991  0  01200 0 5N 530000
1645812020252 006  20  0  0 12 OGF12312 72 9234451  0  00 00 0 0    0000
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(con.)

Table 1 (Con.)

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1645812020252 006   50   0   0 13 0L 132 4 9911223454   0  02 00 0 0    0000
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1645812020252 006   70   0   0 11 0L 160 310311443   0   0  00 00 0 0    0000
1645812020252 006   80   0   0 11 0GF2151510012342   0   0  01 00 0 0    0000
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1645812020252 007   50   0   0 13 0WP340 4  015532453   0  00 00 0 0    0000
1645812020252 007   60   0   0 11 0C 43914 7511853   0   0  02 00 0 0    0000
1645812020252 007   70   0   0 12 0C 39919 7511653   0   0  00 00 0 0    0000
1645812020252 007   80   0   0 12 0C 31715 5011053   0   0  00 00 0 0    0000
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1645812020252 007  130   0   0 19 0GF118 0  0 9000960   0   0  00 00 0 0    0000
1645812020252 007  140   0   0 12 0DF253 3 5213043   0   0  02 00 0 0    0000
1645812020252 007  150   0   0 12 0L 337 410314942   0   0  00 00 0 0    0000
1645812020252 007  160   0   0 13 0C 32312 5011053452   0  00 00 0 0    0000
              -999
PROCESS
STOP
```

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PREPARING A SIMULATION

The Root Disease Model is controlled, and its parameter values modified, through 27 keywords similar in structure and use to those in the Prognosis keyword system (Wykoff and others 1982). A submittal system that interactively assists the user to prepare the necessary sequence of keywords and tree data has been a useful adjunct to the Prognosis Model. A system for users of pest models, including the Western Root Disease Model, is fully integrated with the above system for growth and yield models (Gladden 1989; Sleavin 1989).

The Keyword System

Root Disease Model keywords allow users to:

1. Control program execution, including the nature of root disease processes simulated, and the interaction with other agents.
2. Describe initial conditions of the stand and its disease status.
3. Specify management prescriptions to be invoked.
4. Change critical factors, particularly those that can be habitat-specific or dependent on the source of new trees; and to assume static rates and probabilities for one or more of the processes governing root disease dynamics.
5. Investigate effects of bark beetles and windthrow on root disease dynamics.

The Root Disease Model is invoked by inserting a sequence of root-disease keywords into the sequence of keywords for a normal Prognosis simulation. These keywords may be inserted by editing a Prognosis runstream or by using a submittal system such as that described in the next section.

The first keyword in the Root Disease Model control section is always RRIN, and the list is always terminated by the keyword END. Root Disease keywords must be kept together as a discrete unit. Also, they must not be inserted into the middle of another model extension list of keywords (such as the regeneration establishment model keywords). As in the Prognosis Model, all keywords are left justified in the first 10 characters of the record. If required, the next six 10-character fields (the parameter fields) may be used to add numeric data. Numeric data should include a decimal point or be right-justified in the field.

Users of the Forest Service Growth and Yield Submittal System on the Data General (Sleavin 1989) can generate the Western Root Disease Model keywords by choosing the keyword "PEST" from the Main Keyword Entry Screen. When the keyword PEST is selected, the Pest Model Submittal System (Gladden 1989) is invoked. A menu of pest models available for the particular variant of Prognosis is the first screen displayed. From this menu of pest models, the user can select the "WESTERN ROOT DISEASE MODEL."

Once the Western Root Disease Model is invoked, the system displays this model's Main Keyword Entry Screen, which gives the user the following options:

1. Program Execution Options
2. Root Disease Inventory Options
3. Root Disease Management Options
4. Model Modification Options
5. Other Agent Options
6. Process All Root Disease Keyword Groups
7. Add, Replace, or Delete a Keyword
8. Display All Entered Keywords
9. Exit Main Keyword Entry Screen

The last three of these options are shared by several other pest models served by the same submittal system. With the selection of a group, the system displays the appropriate keywords in that group for processing.

The main advantage of the submittal system is that it lets the user run the model without having to be concerned with formats of keyword parameters. In addition, users do not have to learn job control language and file assignment protocol for the USDA National Computer Center's computers in Fort Collins, CO, where the model resides. Formatting of keywords and all necessary job control language statements are handled by the submittal system. Furthermore, the system performs some checks for values entered to prevent logical errors and ensure that mandatory keywords are present in the keyword file.

Controlling Program Execution

The keywords that control program execution accomplish three general tasks. The RRIN and END keywords signal the beginning and ending of root disease-specific keywords. COMMENT is used to print out a more detailed description of the run. Finally, the RRDOUT and RRECHO keywords serve to control the format and amount of output generated by the model. The keywords for both the Root Disease Model and Prognosis are written to an output file.

RRIN   The RRIN keyword is actually a Prognosis model keyword, signifying that the Root Disease Model is to be called. All following keywords, up to the END keyword, must be Root Disease Model keywords. Use of this keyword with the Root Disease Model is mandatory.

COMMENT   This allows the user to enter a comment describing the root disease scenario being specified. This comment, entered on supplemental records, can be as many lines as the user wishes and is printed as part of the regular output provided by the Root Disease Model. The final supplemental record must contain "END." If such a supplemental record is not provided, keywords that follow will be assumed to be part of the comment and not processed as keywords. This "END" is not to be mistaken for the END keyword that signifies the end of the root disease keywords.

Supplemental Records

The supplemental records that follow this keyword form the comment statement.

DEFAULT: No comment statement is provided.

RRDOUT   This keyword allows the user to get more detailed output from the Root Disease Model. More detailed output will be provided if the keyword is present.

Field 1:   This field contains the file reference number on which the detailed output will be provided. If this field is blank, a value of 22 is assumed.

DEFAULT: No detailed output is provided. If the keyword is provided with blank fields, detailed output will be directed to file-reference number 22.

RRECHO   The summary output is usually written with headers at the beginning that describe the output. Often, a user wishes to make a series of simulation runs and store the output from all scenarios for later analysis. In this case, headers are not needed. The RRECHO keyword allows the user to print out a machine-readable root disease summary table with no headings, in addition to the normal root disease summary output.

Field 1: This field contains the file reference number on which the machine-readable summary output is to be written. The default value is 24.

DEFAULT: No machine-readable output is printed.

END This keyword signifies the end of the root disease keywords. No field entries are needed. This keyword *must* be provided. Otherwise, all Prognosis Model keywords that may follow will be taken as invalid Root Disease keywords and not processed.

Entering Inventory Data

The Prognosis Model is initialized with a list of individual tree and stand characteristics from stand inventories. Sample-tree data are used in conjunction with a description of the sampling design to estimate stand statistics such as volume per unit area. Other information about sample trees (total height, crown ratio, past growth increment) and about the site (slope, aspect, elevation, and habitat type) may be optionally provided by the user.

The Root Disease Model is capable of defining initial root disease conditions using stand examination data that describe the root disease status of sample trees and stumps. The model summarizes number of infected and uninfected trees per acre inside root disease areas, number of trees per acre outside of root diseased areas (all of which are assumed to be noninfected), and the number, size, and type of stumps. When stand examination data do not include the disease status of sample trees, initial root disease conditions may be found through variables entered by user-supplied keywords, which define how the initial conditions for root disease are to be specified.

The RRTYPE keyword specifies the fungal species causing root disease in the stand. The model will not simulate infection by *Armillaria* spp. and *P. weirii* in the same stand at the same time. RRINIT indicates the configuration of the root disease centers within the stand and may also be used to enter the number of diseased and healthy trees within centers.

Alternatively, the disease status of individual trees may be entered for each sample tree as part of the information on the input tree list if the RRTREIN keyword is present. If the stand being represented with the RRTREIN keyword has been inventoried with a number of subplots, the numbers identifying those subplots that are in disease centers are entered with the PLREAD keyword. In addition, the total area of the stand is given by the SAREA keyword; this information is used to calculate tree densities inside root disease centers. If stumps are inventoried in the stand, then the STREAD keyword can be used to initialize the number and attributes of infected stumps.

Many Root Disease Model keywords require a tree species to be designated. An index between 1 and 11 identifies the conifers represented in the Prognosis Model. Conifer species indicated by the index may vary with different geographic variants of Prognosis. For the Inland Empire variant, the index corresponds to the following species:

1. Western white pine (*Pinus monticola*)
2. Western larch (*Larix occidentalis*)
3. Douglas-fir (*Pseudotsuga menziesii*)
4. Grand fir (*Abies grandis*)
5. Western hemlock (*Tsuga heterophylla*)
6. Western redcedar (*Thuja plicata*)
7. Lodgepole pine (*Pinus contorta*)
8. Engelmann spruce (*Picea engelmannii*)
9. Subalpine fir (*Abies lasiocarpa*)
10. Ponderosa pine (*Pinus ponderosa*)
11. Mountain hemlock (*Tsuga mertensiana*)

Indices for other Prognosis Model variants are in the documentation of those variants.

RRTYPE: This keyword allows the user to specify the root disease type to be simulated.

Field 1: The value in this field should be a 1 or a 2. If it is 1, *Armillaria* is simulated. If it is 2, *P. weirii* is simulated. Any other value in field 1 will cause an error message to be printed and *Armillaria* will be simulated.

DEFAULT: *Armillaria* will be simulated.

SAREA This keyword defines the stand area to be simulated in the Root Disease Model and recalculates the dimensions of the stand as a square.

Field 1: This field contains the new stand area in acres that is to be simulated. A value in field 1 that is not positive will cause an error to be printed and the stand area to be set to 100 acres.

DEFAULT: The stand area is 100 acres.

We cannot overemphasize the importance of defining the stand area and root disease type to be simulated before other root disease conditions are defined. These two variables should be defined for the scenario before the conditions described with the other keywords can be meaningful.

If root disease is scattered throughout the stand, then one should consider starting the simulation with the area in root disease equal to stand area. However, when that option is used, or if spread has been sufficient to engulf the entire stand, spread-rate estimates become meaningless.

RRINIT This keyword indicates configuration of root disease centers. The user has two options. In the first, the user specifies the total area in root disease and the number of centers. Then, the model will randomly locate the root disease centers throughout the stand. Centers will be circles of equal size, calculated as the total area in root disease divided by the number of centers. The alternative is to provide a list of root disease centers with the X and Y coordinates of each center and its radius. If RRTREIN is not used, fields 3 and 4 of this keyword also provide information on the number of healthy and diseased trees within the root disease centers.

Field 1: This field specifies whether initial coordinates of root disease centers are to be assigned randomly or read in. If it has value = 0, root disease coordinates are chosen randomly. If it has value = 1, root disease center attributes are read in with supplemental records. The default value of 0 is used if no value is entered in this field.

Field 2: This field specifies the total number of root disease centers to be located in the stand. If attributes of root disease centers are to be read in (field 1 = 1), several supplemental records (equal to the value in field 2) are expected to follow. The number of centers cannot exceed 100. If field 2 exceeds 100, an error message is printed and the number of centers is set to 100.

Field 3:   This field contains the number of infected trees per acre in the root disease centers. If no value is supplied, a default value of 50 percent of average stand density (trees per acre) will be used. If this value is to be obtained from the inventory tree list (indicated by the RRTREIN keyword), then the value in this field will be ignored.

Field 4:   This field contains the number of uninfected trees per acre in the root disease centers. If no value is supplied, a default value of 50 percent of average stand density (trees per acre) will be used. If this value is to be obtained from the inventory tree list (indicated by the RRTREIN keyword), then the value in this field will be ignored.

Field 5:   This field contains the average level of root infection on infected trees. It should be a number between 0 and 1 (which indicates 100 percent infection). All infected trees read in field 3 are given this infection level. The default value of 0.1 is used if no value is entered in this field.

Field 6:   This field specifies the total acres in root disease and is only read if root disease centers are to be assigned randomly (field 1 = 0). In this case, the area of each root disease center is equal to field 6 divided by field 2.

Supplemental Records

Supplemental records are expected following this keyword if the root disease centers are to be read in (field 1 = 1). Each supplemental record contains all necessary information for one center and is read in with format 3F7.1: X-coordinate of the center in feet, Y-coordinate of the center in feet, and radius of the center in feet. An error will appear if either the X or Y coordinate of a center is outside the linear dimensions of the stand (assumed to be square) and the coordinate will be set to the linear dimension of the stand (on the edge of the stand). It is therefore important to define the total stand area with the SAREA keyword before using this keyword.

DEFAULT: Center locations assigned randomly, total center area is 25 percent of stand area, with 20 centers of equal size.

Fields 3 and 4 for the RRINIT keyword and the tree defect and damage codes entered on the individual-tree inventory data used in conjunction with the RRTREIN keyword provide the same kind of information to the model. However, the two alternatives may give somewhat different results during the first few periods of growth. When infection status is entered with RRINIT, all trees in the stand represented by a particular tree record in the sample are assumed to be divided between infected and uninfected in the same proportions. However, when status is indicated separately for each sample tree, differences in the infected proportions of the many sizes and species of trees in the stand are possible. Which alternative is more realistic depends on the adequacy of the sample of trees in the inventory input. For small samples, perhaps less than 40 trees, RRINIT may be better. With larger samples, the RRTREIN option should be more realistic.

RRTREIN   This keyword is used when initial disease conditions are included in the attributes of individual trees in the list of trees. Disease conditions of the sampled trees are described by three pairs of descriptors. Any one of the three may contain the root disease condition of the tree. The remaining two can be used to describe other insect, disease, or damage symptoms. Although arbitrary, the usual ordering is by importance. The first variable in each pair identifies the presence of a particular damaging agent. The second variable describes the severity of the condition. Any tree less than 5 inches d.b.h. and with a severity of 1 is not considered as infected. Default values of these codes are taken from specifications in the Forest Service Handbook FSH 2409.21h R1 Field Instructions for Stand Examinations (1986).

Agent	Code	Severity	Code
Armillaria	61	Tree within 30 feet of tree with deteriorating crown or killed by root disease.	1
P. weirii	62	Pathogen or diagnostic symptoms detected.	2
		Crown deterioration	3

The tree class information used in the Root Disease Model corresponds to the tree history information used in the Prognosis Model (variable ITH). When the Root Disease Model is active, the tree class information should be read into the Prognosis Model variable ITH. Tree class codes 6 and 7 identify trees that have died 5 years ago or less. Tree class codes 8 and 9 represent trees that have died more than 5 years ago.

Stumps, in the context of the Root Disease Model, are cut stumps or trees that are dead and infected with root disease. For example, a tree with a tree class of 6 and a damage code of 61 would be classified and processed as an infected stump. Stumps can also be added to the Root Disease Model in another way when using the tree list information. Trees that were infected by root disease and cut in previous rotations are identified by entering a tree height of 1.5 for the Prognosis Model variable THT. These trees are classified and processed as stumps and then discarded. Finally, additional stumps can be added to the root disease model when using RRTREIN keyword by using the STREAD keyword. When the Root Disease Model is used with initial user-supplied information, stumps can only be added to the model using the STREAD keyword.

PLREAD   This keyword, which is used only in conjunction with RRTREIN, indicates which subplots within the stand contain root disease. This keyword should be used when modeling a stand that contains both relatively large, identifiable areas of root disease and areas unaffected by root disease. Its absence, but with RRTREIN present, indicates that the stand is to be modeled as a single root disease center. No parameter fields are read in conjunction with this keyword. The user is, however, expected to provide supplemental records that contain the subplot identification of plots in diseased centers.

Supplemental Records

Each supplemental record should contain one number in I4 format. This is the diseased subplot number. A –999 entered at the end of the list of diseased subplot numbers indicates that all the disease

STREAD   This keyword is used to initialize stumps within the root diseased areas of the stand. A stump, in the context of the Root Disease Model, is defined as an infected tree that is killed by any means. The tree can be a stump formed by cutting, a dead standing tree, or a tree that has been snapped off by wind. The important attribute of these stumps is that they were formed by trees that were infected by root disease at the time of their death by whatever cause. These stumps will serve as inoculum sources from which infection will spread through the simulation. No parameter fields are read in conjunction with this keyword. However, the user is expected to provide supplemental records that contain necessary stump information.

Supplemental Records

Each supplemental record should contain three numbers in format I4,2F6.1. The first field contains the index of the tree species tabulated previously. Species identification is important because stumps of heartwood species are assumed to decay more slowly than stumps of nonheartwood species. Douglas-fir, all pines, western redcedar, and western larch are classified as heartwood species; the remainder are classified as nonheartwood species. The second field is the stump diameter in inches, taken at one foot above ground. The third field is the number of stumps of the given heartwood class and diameter. This number should be given as the total number of stumps of this type in the root diseased area, and not the number of stumps per acre. A –999 entered in the first four columns of the supplemental record indicates that all the stump list information has been read. This supplemental record must be provided; otherwise, keywords that follow will be assumed to be part of the stump list information and not processed as proper keywords.

subplot information has been read. This supplemental record must be provided; otherwise, keywords that follow will be assumed to be part of the subplot list and not processed as proper keywords.

When the RRINIT keyword is used and STREAD keyword omitted, the model assumes there are no stumps present. When the RRTREIN keyword is used, stump information can be entered into the model directly from the input tree list even though the STREAD keyword is omitted. Stump information may also be entered into the model from both the input tree list and the STREAD keyword when RRTREIN is used.

For our Crow Creek example, examination of aerial photos indicates that 21 of the 51 acres in the stand are in three root disease centers. Note that the proportion of infested area is greater than indicated by the proportion (2/7) of infested plots. Because the status of root disease was recorded for each tree in the inventory, the RRTREIN keyword will be used. However, because there are relatively few plots in the diseased portions of the stand, an additional list of infected stumps will be supplied by the STREAD keyword.

The Crow Creek data are similar to standard Forest Service Region 1 stand exam data. Tree damage codes are in columns 48-50, 51-53, and 54-56. Up to three damage types or agents can be recorded. The first two columns are the agent or cause, the last is the severity. When the data were taken the following were allowable root disease codes:

60 ROOT DISEASE

61 Shoestring root rot (*Armillaria* spp.)

62 Yellow laminated root rot (*P. weirii*)

63 Brown cubical rot (*Polyporous schweinitzii, Coniphora puteana*)

64 White rot (*Heterobasidion annosum, Poria subacida*)

65 Black stain root disease (*Verticicladiella* sp.)

Severity Codes:

1. Tree within a disease center or within 30 feet of a tree or stump that is symptomatic or killed by root disease.
2. Root disease confirmed by stain, decay, or other signs or symptoms.
3. Root disease crown symptoms.

Specifying Management Options

The only management action that is specific to root disease is pushing stumps, specified by the PSTUMP keyword. Although fumigation of stumps is a possibility for reducing inoculum, for the present, its effects can be approximated by varying the parameters of PSTUMP. Other silvicultural options that can influence the dynamics of root disease, such as species choices when planting or thinning, are invoked by using the options in the base Prognosis Model.

PSTUMP   This keyword simulates a stump-pushing event in a particular year of the rotation. Stump pushing can only occur once in a scenario.

Field 1:   The year in which stump pushing is to occur.

Field 2:   The stump-pushing efficiency. This is the proportion of stumps that will be removed by the stump-pushing activity. The default is an efficiency of 1.0. An error message will appear if the entry in field 2 is less than 0 or greater than 1, and the default will be retained.

Field 3:   The minimum stump diameter for stump pushing. All stumps of this diameter and greater will be removed with the efficiency provided in field 2. If left blank, the minimum stump d.b.h. is set to 0 inches and all stump sizes will be removed with the efficiency provided in field 2.

Interactions With Other Damaging Agents

Action of other agents in influencing mortality inside root disease centers is controlled by the BBTYPE1, BBTYPE2, BBTYPE3, and WINDTHR keywords. These keywords simply switch on the potential for a bark beetle or windthrow event to occur. The event will not occur before the specified cycle year and will not occur if conditions are inappropriate. Thus, a user could specify a cycle year of 1991 on the keyword line but not have the event occur until 2021 because conditions from 1991 to 2021 were not suitable for the event to occur. Each of the BBTYPE keywords uses an index of tree species in field 2.

BBTYPE1   This keyword specifies a type 1 bark beetle event. Examples of type 1 bark beetles are mountain pine beetle (*Dendroctonus ponderosae*) on lodgepole pine and western pine beetle (*D. brevicomis*) on ponderosa pine. The user specifies a year and intensity to switch this other agent on. The type 1 bark beetle model is switched off after one outbreak has occurred.

Field 1:   This field specifies the earliest year that an outbreak can occur. This field must be specified, there is no default value for year.

Field 2:   This field specifies the tree species eligible for attack by the bark beetle and should be a number between 1 and

11, inclusive, which is the tree species index applicable to your variant of the Prognosis Model. If the field is left blank, the default is 7, which is lodgepole pine in the Inland Empire variant.

Field 3: This field specifies the minimum d.b.h. (in inches) of trees that will be considered eligible for attack by the bark beetle. The default is a d.b.h. of 8 inches.

Field 4: This field specifies the minimum density of eligible trees as specified by fields 2 and 3, which must be present before an outbreak can occur. The default density is 10 eligible trees per acre.

Field 5: This field specifies the mortality rate that will be applied to all eligible trees if an outbreak occurs. The default rate is 0.85 for all eligible trees.

BBTYPE2   This keyword specifies a type 2 bark beetle event. An example of type 2 bark beetle is Douglas-fir beetle (*D. pseudotsugae*) on Douglas-fir. The user specifies a year and intensity to switch on this agent. A type 2 bark beetle outbreak can occur only if a windthrow event of a sufficient size also occurs. An error message is printed if the BBTYPE2 keyword is provided without the WINDTHR keyword, although the WINDTHR keyword does not have to precede the BBTYPE2 keyword. The mortality of live trees is determined by the number of windfallen trees that are of the size and species specified as host for this bark beetle. The number of live trees killed by the bark beetle is only slightly fewer than the number of host trees wind-thrown. For example, if 12 Douglas-fir trees of the size specified were wind-thrown, then 11 more live trees could be attacked and killed by the beetle. This action is dependent on there being a sufficient number of eligible stems remaining after windthrow for bark beetle attack. The type 2 bark beetle model is switched off after one outbreak has occurred.

Field 1: This specifies the earliest year an outbreak can occur. A year must be specified. There is no default value.

Field 2: This field specifies the tree species elgible for attack by the bark beetle and should be a number between 1 and 11, inclusive, which is the tree species index applicable to your variant of the Prognosis Model. Default is 3, which is Douglas-fir in the Inland Empire variant.

Field 3: This field specifies the minimum d.b.h. (in inches) of trees that will be considered eligible for attack by the bark beetle. The default is 10 inches d.b.h.

Field 4: This field specifies the minimum density of eligible trees as specified by fields 2 and 3, which must be windthrown in the same or prior year within the same time step as this bark beetle event. The default density is 10 eligible trees per acre.

Field 5: This field specifies the mortality rate that will be applied to all eligible trees if an outbreak occurs. The default rate is 0.88 for all eligible trees.

BBTYPE3   This keyword specifies a type 3 bark beetle event, which kills trees infected by root disease. Fir engraver (*Scolytus ventralis*) on grand fir is an example of this type. The user specifies a year and intensity to switch on this agent. Because the pattern of action for type 3

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beetles is determined by the density of trees with greater than a specified level of root damage, the model remains active once it is switched on.

Field 1: This specifies the year that is the earliest an outbreak can occur. A year must be specified. There is no default.

Field 2: This field specifies the tree species eligible for attack by the bark beetle and should be a number between 1 and 11, inclusive, which is the tree species index applicable to your variant of the Prognosis Model. The default is 4, which for the Inland Empire variant corresponds to grand fir.

Field 3: This field specifies the minimum d.b.h. (in inches) of trees that will be considered eligible for attack by the bark beetle. The default is 10 inches d.b.h.

Field 4: This field specifies the minimum density of eligible trees as specified by fields 2 and 3 that must be present before an outbreak can occur. The default is 10 trees per acre.

Field 5: This field specifies the mortality rate that will be applied to all eligible tree records if an outbreak occurs. The default mortality rate is 0.88 for all eligible trees.

Field 6: This field specifies the minimum proportion of roots that must be infected for trees to be eligible for attack by this beetle. Trees with a lower infection level are not eligible for attack. The default is 0.30 proportion of the root system infested.

WINDTHR   This keyword specifies a windthrow event. The user specifies a year and intensity to switch on this agent. The windthrow model is switched off after an event has occurred. Both uninfected and infected trees are wind-thrown.

Field 1: This specifies the earliest year a windthrow event can occur. A year must be specified. There is no default value.

Field 2: The value in this field specifies the proportion of eligible stems that can be wind-thrown. In a sense, it is a measure of the magnitude of the event. Only dominant and codominant trees of any species (the largest 20 percent in the diameter distribution) are subject to windthrow events. The proportion of these trees to be wind-thrown should be specified. The default is zero, which will result in no trees wind-thrown.

Field 3: This field specifies the minimum density of eligible trees per acre necessary for a windthrow event. The default is zero, and the windthrow event will be independent of the density of eligible stems.

CONSIDERATIONS WHEN USING THE COMBINED MODELS

There are several items that users of this model should consider when deciding how to develop a scenario.

Root Disease Dynamics

Many of the functional relationships that describe how live root systems become infected, how trees are killed, and the progress of infection through roots are based on our current best understanding of root disease pathology. However, default

values for the number of years required to kill trees, lifespan of effective inoculum, and the percentage of a root system that is infected at the time of tree death are representative of conditions in stands in the Inland Empire Region of the Western United States. These values (appendix II) should be adjusted through keywords for other Regions.

Carryover of Root Disease

The carryover model is used to predict the persistence of root disease between rotations in the same stand. There are some restrictions on its use in the current version of the model. First, the carryover model can span only four time steps prior to the time specified for evaluation of carryover. Second, these time steps should be of equal length. Third, the new regeneration affecting the carryover (in addition to the stumps) will be visible to the model only if the regeneration establishment model has been invoked by the user with new trees entering the tree list during the 20 years following the harvest. These options include natural regeneration and planting. Another keyword, TDISTN, should be considered when the planting option is used.

INTERPRETING MODEL OUTPUT

Information in earlier sections of this guide will enable users to prepare scenarios for simulation by the Root Disease and the Prognosis Models. Outputs from the combined models are presented in tables that summarize information on the conditions in the stand during the period covered by the projection. Outputs from the Root Disease Model are:

1. A summary listing of the options specified by keyword and any associated values in effect for the simulation. These include both Root Disease Model and Prognosis Model keywords and are written to the Prognosis Model output file.

2. A table representing the summary statistics for root disease areas. This table displays conditions within the diseased portion of the stand and is written to the Prognosis Model output file.

3. A detailed output file that describes species-specific consequences of root disease infection on tree growth and mortality. These data are written to a separate output file when requested by the keyword RRDOUT.

4. A machine readable file containing all the information in the root disease summary table except table headings. This file is created only when requested by the keyword RRECHO.

The descriptions below focus largely on outputs specific to the Root Disease Model. Prognosis outputs are shown for comparative purposes only; a guide to their interpretation appears in Wykoff and others (1982).

Table of Keywords

Root Disease Model keywords and their parameters that define the scenario are listed with Prognosis Model keywords (table 2). The listing is designed to include only the keywords and their parameters that have been specified in the input data set. If some of the parameters are "out of bounds," warning messages will appear in this table. This listing is intended to help verify that the projection is based on the intended actions as well as to facilitate problem solving. This table is printed on the same file as the Root Disease summary table (table 2). The listing is designed to include only the parameters and options in effect for the simulation; not all possible keywords are listed.

In the example (table 2), keywords for the Root Disease Model begin with RRIN and end with END. These two keywords are left-adjusted in the table. The other Root Disease Model keywords are printed between these and are indented two positions to the right. The parameter values for each keyword are printed after the keyword; some are default values. For example, the parameters for PSTUMP are year (2003), efficiency (0.8), and minimum stump diameter, (3.0). No parameter value was entered for RRDOUT, so the default 22 is printed.

Table 2—Keywords and parameters for the Root Disease Model as reported in the Prognosis Model output file for a stand in Crow Creek on the Lolo National Forest

```
        STAND GROWTH PROGNOSIS SYSTEM      VERSION 6.0 -- INLAND EMPIRE      01-22-1990  10:41:37

--------------------------------------------------------------------------------------------------

                                    OPTIONS SELECTED BY INPUT

--------------------------------------------------------------------------------------------------

KEYWORD    PARAMETERS:
-------

STDIDENT

           STAND ID= 16458120        2025 CROW CREEK DATA-R1-ROOT DISEASE

COMMENT

           - RRSETB - TEST ROOT DISEASE MODEL
           - TYPE OF STAND - INVENTORY
           - ROOT DISEASE - ARMILLARIA
           - 7 PLOTS, 2 WITH RD
           - RANDOM CENTERS

END

TREELIST   DATE/CYCLE=   1; DATA SET REFERENCE NUMBER =  3.; HEADING SUPPRESSION CODE = 0.
           (0=WITH HEADING. OTHER VALUES=SUPPRESS HEADING).

DESIGN     BASAL AREA FACTOR= 40.0; INVERSE OF FIXED PLOT AREA=  300.0; BREAK DBH=   5.0
           SEE "OPTIONS SELECTED BY DEFAULT" FOR REMAINING DESIGN CARD PARAMETERS.

STDINFO    FOREST-LOCATION CODE=   116; HABITAT TYPE=530; AGE=   130; ASPECT AZIMUTH IN DEGREES=  45.; SLOPE=   10.%
           ELEVATION(100'S FEET)= 33.0; LATITUDE IN DEGREES=  45.
           HABITAT TYPE MAPPED TO 530 FOR THIS PROJECTION.

INVYEAR    INVENTORY YEAR= 1983

GROWTH     DIAMETER GROWTH DATA TYPE CODE= 0.    5 YEAR MEASUREMENT PERIOD;
           HEIGHT GROWTH DATA TYPE CODE  = 0.    5 YEAR MEASUREMENT PERIOD;
           MORTALITY MEASUREMENT PERIOD  = 5

NUMCYCLE   NUMBER OF CYCLES= 20
```

(con.)

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Table 2 (Con.)

NOTRIPLE	
THINDBH	DATE/CYCLE= 2003; SMALLEST DBH= 1.0; LARGEST DBH= 99.0; PROPORTION OF SELECTED TREES REMOVED= 1.000
TIMEINT	CYCLE= 3; PERIOD LENGTH= 5
TIMEINT	CYCLE= 4; PERIOD LENGTH= 5
TIMEINT	CYCLE= 5; PERIOD LENGTH= 5
TIMEINT	CYCLE= 6; PERIOD LENGTH= 5
TIMEINT	CYCLE= 7; PERIOD LENGTH= 5
TIMEINT	CYCLE= 20; PERIOD LENGTH= 5
ESTAB	REGENERATION ESTABLISHMENT OPTIONS:
	DATE OF DISTURBANCE= 2003
BURNPREP	DATE/CYCLE= 2004; % GROUND= 80.0
PLANT	DATE/CYCLE= 2005; SPECIES= 2.; TREES/ACRE= 500.; % SURVIVAL= 80.00
TALLYONE	DATE/CYCLE= 2007; DATE OF DISTURBANCE=2003.
TALLYTWO	DATE/CYCLE= 2012; DATE OF DISTURBANCE=2003.
RESETAGE	DATE/CYCLE= 2005; NEW AGE= 0.
HTADJ	DATE/CYCLE= 2005; SPECIES NUMBER= 2.; ADJUSTMENT VALUE= 1.5000
END	END OF ESTABLISHMENT KEYWORDS
SPECPREF	DATE/CYCLE= 2008; SPECIES= 2.; THINNING SELECTION PRIORITY= -2.
THINBTA	DATE/CYCLE= 2013; RESIDUAL= 1000.00; PROPORTION OF SELECTED TREES REMOVED= 1.000
	DBH OF REMOVED TREES WILL RANGE FROM .0 TO 999.0 INCHES, AND
	HEIGHT OF REMOVED TREES WILL RANGE FROM .0 TO 999.0 FEET.

(con.)

Table 2 (Con.)

RRIN   ROOT DISEASE KEYWORDS:

SAREA   STAND AREA =   51.00 ACRES

PLREAD   DISEASE SUBPLOTS READ IN
            DISEASED PLOTS=   1   5

RRTYPE   ROOT DISEASE SIMULATED IS ARMILLARIA

RRINIT   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=   3; INFECTED TREES/ACRE IN DISEASED AREAS =   100.00
            UNINFECTED TREES/ACRE IN DISEASED AREAS = 100.00 ;PROPORTION ROOTS INFECTED= .40 ;DISEASE AREA =   21.00 ACRES

RRTREIN   ROOT DISEASE INITIALIZATION IS FROM TREELIST

STREAD   STUMPS READ IN FROM KEYWORD FILE; SUMMARY OF TOTAL NUMBER OF STUMPS IN STAND REPORTED BELOW

CARRY   DYNAMIC CARRYOVER MODEL. MINIMUM SPREAD=   .00 FT/YR MODEL CALLED   4 CYCLES AFTER MANAGEMENT

SPREAD   DYNAMIC SPREAD MODEL

PSTUMP   DATE/CYCLE= 2003; EFFICIENCY = .80;   MIN SIZE =   3.00 INCHES DBH

RRJUMP   ROOT DISEASE AREA WILL JUMP OUT 1.00 RADII UPON CUT

RSEED   SEED TO REINITIALIZE RANDOM NUMBER GENERATOR= 11188.00

RRDOUT   DETAILED ROOT DISEASE OUTPUT ON LOGICAL UNIT   22

END   END OF ROOT DISEASE KEYWORDS

TREEFMT   (I3X.I4,T18.I4,T28.F2.0,T30.I1,T33.A2.F3.1.F2.1,3X,F3.0.T43,F3.0.T54,
            F2.0.T46.I1,T48.3(I2,I1),T22,I1,T63.I2,I3,I3,I1,I1)

TREEDATA   DATA SET REFERENCE NUMBER= 5

PROCESS   PROCESS THE STAND.

                                                                              (con.)

22

Table 2 (Con.)

OPTIONS SELECTED BY DEFAULT

DESIGN   BASAL AREA FACTOR= 40.0; INVERSE OF FIXED PLOT AREA= 300.0; BREAK DBH=   5.0
          NUMBER OF PLOTS=   7; NON-STOCKABLE PLOTS=   0; STAND SAMPLING WEIGHT=   1.00000

SUMMARY OF ROOT DISEASE INFORMATION READ IN ON INPUT

NUMBER OF   INFECTED TREE RECORDS IN DISEASE PATCHES=   6.
NUMBER OF UNINFECTED TREE RECORDS IN DISEASE PATCHES=   13.

NUMBER OF STUMPS

SIZE CLASS	HEARTWOOD	NON-HEARTWOOD
0- 12"	100.	0.
12- 24"	3.	25.
24- 48"	11.	0.
48-100"	0.	0.
>100"	0.	0.

**Root Disease
Summary Table**

The key information in the root disease summary output file is a table of changes within the area infected by root disease. The summary output from the Root Disease Model (table 3) is designed to illustrate a number of important indicators of root disease effects in diseased areas of the stand:

1. Measure of the extent of root disease infection, including the number of infection centers, the mean annual spread rate in feet per year, and the total acres of the stand with root disease.

2. The number of infected stumps and the basal area of those stumps (in square feet per acre).

3. The number of trees per acre killed by root disease in the current growth cycle and the timber volume loss represented by those trees (in cubic feet per acre). Note that the number of trees killed by other agents (if called) are not included here; those losses will be reflected in the stand averages summarized by Prognosis.

4. The number of uninfected trees per acre within disease centers.

5. The number of infected trees per acre in the centers and the average percentage of their root systems that are infected.

6. Economic indicators of the volume (cubic feet per acre), and total basal area (square feet per acre) of live trees in diseased areas.

Column headings in table 3 describe the information in general. Column 1 is the year of the end of the growth cycle. Column 2 is stand age; this age is relevant only if one sets the age in the Prognosis keywords, or resets it in the case of a harvest. Column 3 is the number of root disease centers in the stand. This value is set by a keyword (RRINIT, RRTREIN, or PLREAD). It is reset only if the carryover model is called. Root disease centers merging to form fewer, but larger, centers through time are handled elsewhere in the model on an area-infected basis.

Column 4 is the total area of the stand with root disease. Column 5 is the rate of spread of the disease over the past growth cycle; this is always positive. Reduction of the area in root disease by removal of infected stumps (if PSTUMP is invoked) occurs at the beginning of the growth cycle. Spread rate is calculated from the remaining infected stumps after that removal.

The next four columns are dead tree characteristics, which describe trees killed by root disease. The first of these columns is the number of stumps per acre infected with root disease. Zeros may occur in this column for two reasons. At the start of a simulation the history of the past growth period is undefined. When the infection rate is less than one tree per acre per year in the past cycle, a zero is shown. The next column is the basal area of infected stumps per acre. The last two columns are the number of trees per acre killed and the cubic volume of these trees for the past growth cycle.

Following the summary of dead tree characteristics is a summary of live trees in diseased portions of the stand. First is the number of noninfected trees per acre, then the number of infected trees per acre. After a harvest these values are incorrect. Until the carryover model is finished, newly infected trees are missed by the root disease model when writing this table. Small trees once infected also die within the growth cycle so they may not be seen as infected and alive. The next column is the simulated percentage of the root system infected for all infected trees in the stand. It serves primarily as an index to model performance. This is followed by the merchantable cubic foot volume per acre in the diseased portion of the stand at the end of the cycle. Newly infected trees on the edge of the disease centers are included. The basal area for this same set of trees appears in the next column.

Stand and management identifiers, as specified in the Prognosis keywords, are also listed in this table. All root disease outputs are aggregated across tree species in the root diseased portions of the stand.

As discussed elsewhere in this manual, the most straightforward indicator of the extent of root disease in a stand is the total area within root disease centers. The number of infection centers is presented primarily to verify the initial inventory

Table 3—A summary of conditions within the diseased proportion of the stand as reported in the Root Disease Model output file for a stand in Crow Creek on the Lolo National Forest

```
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
*                         ROOT DISEASE MODEL        VERSION 1.0                *
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
```

SUMMARY STATISTICS FOR ROOT DISEASE AREAS

| | | | DISEASE STATISTICS | | | DEAD TREE CHARACTERISTICS STUMPS | | | | LIVE TREE CHARACTERISTICS | | | OVERALL | | IDENTIFIERS | |
| | | NO OF | DISEASE AREA | SPREAD RATE | TOTAL | BA/ ACRE | NO OF TREES | VOLUME LOSSES | UNINF NO OF TREES | INFECTED NO OF TREES | AVE %ROOTS | MERCH CU FT | BA/ ACRE | | |
YEAR	AGE	CENTS	ACRES	FT/YR	/ACRE	SQFT	KILLED	CU FT /ACRE	/ACRE	/ACRE	INFECTED	/ACRE	SQFT	STAND ID	MGMT ID
1983	130	3	20.93	.00	7.	4.	0.	0.	5258.	78.	40.0	6523.	200.	16458120	NONE
1993	140	3	21.44	.48	9.	14.	269.	163.	3838.	71.	56.1	6349.	203.	16458120	NONE
2003	150	3	21.56	.10	56.	65.	416.	16835.	2709.	17.	37.3	4242.	148.	16458120	NONE
2008	5	3	23.99	.01	13.	22.	323.	33.	2930.	0.	.0	0.	28.	16458120	NONE
2013	10	3	24.01	.04	3.	12.	2.	0.	2908.	0.	.0	0.	35.	16458120	NONE
2018	15	3	24.01	.01	3.	11.	0.	0.	876.	0.	.0	0.	11.	16458120	NONE
2023	20	3	24.01	.03	3.	11.	0.	0.	859.	0.	.0	0.	33.	16458120	NONE
2028	25	86	6.65	.09	3.	11.	4.	1.	840.	2.	65.8	75.	63.	16458120	NONE
2038	35	86	7.44	.11	1.	4.	30.	132.	758.	3.	80.2	728.	119.	16458120	NONE
2048	45	86	7.73	.18	0.	0.	7.	22.	626.	2.	72.5	1984.	164.	16458120	NONE
2058	55	86	10.20	1.01	1.	2.	29.	127.	491.	23.	53.2	3582.	212.	16458120	NONE
2068	65	86	15.16	1.77	11.	23.	50.	914.	356.	43.	50.1	4898.	234.	16458120	NONE
2078	75	86	19.54	1.63	28.	68.	47.	1943.	272.	37.	52.9	4689.	208.	16458120	NONE
2088	85	86	22.29	1.47	46.	88.	35.	1724.	209.	29.	53.8	4278.	180.	16458120	NONE
2098	95	86	25.28	1.98	27.	45.	16.	214.	169.	32.	58.9	5462.	200.	16458120	NONE
2108	105	86	27.57	1.77	20.	35.	19.	1271.	140.	27.	58.7	5530.	190.	16458120	NONE
2118	115	86	30.37	2.50	25.	55.	16.	1262.	117.	24.	54.8	5531.	180.	16458120	NONE
2128	125	86	31.94	1.61	21.	50.	11.	1030.	98.	21.	57.3	5493.	170.	16458120	NONE
2138	135	86	34.44	2.43	17.	46.	10.	1192.	87.	18.	54.5	5582.	165.	16458120	NONE
2148	145	86	36.47	2.31	15.	41.	8.	880.	76.	16.	54.5	5918.	165.	16458120	NONE
2153	150	86	37.74	3.46	15.	53.	5.	930.	70.	17.	46.0	5613.	156.	16458120	NONE

and to illustrate the outcome of carryover after a cut. No attempt is made by this version of the model to merge overlapping centers, although overlaps are taken into account when calculating the area infected with disease. In addition, the number of centers is prevented from increasing beyond 100 for the stand.

Interpretation of entries in the output tables for periods between a stand harvest and execution of the carryover model requires some special considerations. After the carryover model produces an estimate of the number of new disease centers (displayed in the output tables), the number of new centers remains constant until either the carryover model is called again or the area in root disease goes to zero. That is, although those centers may be spreading and coalescing, the model output does not display the "effective" number of disease centers. Thus, the number of root disease centers has meaning only for the cycle following completion of the carryover model; a more general indicator of root disease infection in stands is simply the total area in root disease. At present, the output tables (tables 3 and 4) do not accurately reflect disease conditions of the regeneration until after carryover has been executed. To check that CARRY has been executed, refer to the Activity Summary listed by Prognosis Event Monitor (Crookston 1985) just after the Summary Yield Tables.

Some comparisons will likely be made between the Root Disease Model summary, table 3, and the summary from the Prognosis Model, table 5. The critical issue to remember is that the Prognosis summary is for the entire stand including both the portion infested with root disease, and the portion uninfested. Infested area changes from one projection cycle to the next.

The Prognosis Model summary contains several columns of data that correspond directly to entries in the Root Disease Model summary table. In table 5 these are the columns labeled YEAR, AGE, TREES/ACRE, BA/ACRE, MERCH CU FT, ACC, and MOR. The first two columns should be identical to the first two columns in table 3. The third column refers to the number of live trees per acre; in table 3 this number is broken down into live noninfected and live infected trees per acre. The merchantable cubic foot volume per acre is the same measurement in both tables, except for the area to which the value applies. Both accretion (ACC) and mortality (MORT) appear in the Prognosis Model summary, but only mortality from root disease appears in the output table for the Root Disease Model. If the mortality level for the Prognosis Model is greater than that for the Root Disease Model, the Prognosis Model level is used in both tables.

Conditions in uninfested proportions of the stand can be obtained from these two tables by taking the values from table 5 and converting them to totals for the entire stand area and converting values from table 3 to a total for the area infested at that growth cycle. The stand total minus the disease area total is then divided by the area of the stand that is uninfested to get a per acre value for that part of the stand.

A second copy of the summary table can optionally be written to a supplementary output unit as specified with the RRECHO keyword. This copy of simulation results can be used as input to other analyses.

Detailed Output Table

Use of the RRDOUT keyword causes a more detailed output table to be printed (table 4). This table displays some measures of the effects of root disease on attributes of each tree species in diseased areas. At the time of stand inventory, and at the end of each cycle, the number of trees killed during that cycle and the number of alive uninfected and alive infected trees are displayed. In addition, five percentile classes for tree d.b.h. are presented, along with the size of the largest tree in each class for both the trees killed by root disease and live trees. This detail is intended to illustrate species-specific growth effects in the root-diseased areas of the stand.

The detailed output table is written to a separate file from all other model output. This output is controlled by the keyword RRDOUT. The additional information that is not in the root disease summary output table is the breakdown by size classes within species of the frequency and condition of trees within the root disease centers.

Table 4—A detailed summary of tree conditions within the diseased proportion of the stand by tree size class by species as reported in the Root Disease Model output file (RRDOUT) for a stand in Crow Creek on the Lolo National Forest

```
ROOT DISEASE MODEL EXTENSION    VERSION 1.0

STAND ID= 16458120    MANAGEMENT ID= NONE

STAND ATTRIBUTES INSIDE ROOT DISEASE PATCHES
```

	AREA IN ROOT DISEASE		KILLED TREES %TILE POINTS BY DBH (INCHES)						TOTAL TREE	ALIVE TREES %TILE POINTS BY DBH (INCHES)						TOTAL UNINFECTED	TOTAL INFECTED	% ROOTS
		SP	10	30	50	70	90	100	TREES/ACRE	10	30	50	70	90	100	TREES/ACRE	TREES/ACRE	INFECTED
YEAR	DISEASE																	
1983	20.9	WP	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.0	.00
		L	.0	.0	.0	.0	.0	.0	.0	39.6	39.6	39.6	39.6	39.6	39.6	2.3	2.6	.00
		DF	.0	.0	.0	.0	.0	.0	.0	.1	.1	.1	.1	.1	.1	2700.0	8.0	.00
		GF	.0	.0	.0	.0	.0	.0	.0	.1	1.7	3.3	3.3	3.3	3.3	1350.0	59.4	.00
		C	.0	.0	.0	.0	.0	.0	.0	.5	25.6	25.6	25.6	25.6	25.6	1055.6	.0	.00
		LP	.0	.0	.0	.0	.0	.0	.0	.5	25.6	25.6	25.6	25.6	25.6	.0	.0	.00
		S	.0	.0	.0	.0	.0	.0	.0	4.9	4.9	4.9	4.9	4.9	4.9	150.0	.0	.00
		PP	.0	.0	.0	.0	.0	.0	.0	4.9	4.9	4.9	4.9	4.9	4.9	.0	7.8	.00
2003	21.6	WP	5.3	5.3	5.3	5.3	5.3	5.3	.0	34.8	34.8	34.8	34.8	34.8	34.8	.0	.0	7.92
		L	37.0	37.0	37.0	37.0	37.0	37.0	18.6	41.8	41.8	41.8	41.8	41.8	41.8	3.4	2.5	25.78
		DF	28.3	28.3	28.3	28.3	28.3	28.3	197.5	28.3	28.3	28.3	28.3	28.3	28.3	1208.4	6.7	65.18
		GF	1.8	1.8	24.6	24.6	24.6	24.6	142.4	1.8	24.6	24.6	24.6	24.6	24.6	609.9	.2	60.87
		C	35.9	35.9	35.9	35.9	35.9	35.9	40.0	50.2	50.2	50.2	50.2	50.2	50.2	803.5	1.0	31.62
		LP	4.6	4.6	5.9	7.0	9.2	9.2	.9	4.6	4.6	5.9	5.9	9.2	9.2	2.9	.4	20.56
		S	5.7	5.7	5.7	5.7	5.7	5.7	16.3	5.7	5.7	5.7	5.7	5.7	5.7	81.1	.0	.00
		PP	5.7	5.7	5.7	5.7	5.7	5.7	.0	5.7	5.7	5.7	5.7	5.7	5.7	.0	6.4	13.48

(con.)

Table 4 (Con.)

2008 24.0

L	5.7	5.7	5.7	5.7	5.7	.0	.4	.4	.4	.4	.4	.4	537.8	.0	.00
DF	1.5	1.5	1.9	1.9	1.9	70.6	1.5	1.5	1.5	1.5	1.5	1.9	1084.7	.0	.00
GF	2.0	2.0	2.0	2.0	2.2	244.3	.9	.9	2.0	2.2	2.2	2.2	534.0	.0	.00
C	1.7	1.7	1.7	1.7	1.7	8.2	1.7	1.7	1.7	1.7	1.7	1.7	692.1	.0	.00
LP	1.7	1.7	1.7	1.7	1.7	.0	.5	.5	.5	.5	.5	.5	74.7	.0	.00
S	1.7	1.7	1.7	1.7	1.7	.0	.4	.4	.4	.4	.4	.4	5.1	.0	.00
PP	1.7	1.7	1.7	1.7	1.7	.0	.6	.6	.6	.6	.6	.6	1.7	.0	.00

2028 6.7

L	1.9	2.3	2.3	2.8	2.8	.0	2.3	2.9	3.4	6.3	7.6	7.8	467.1	.9	60.21
DF	2.1	2.6	5.0	5.0	5.0	1.0	2.1	2.6	5.0	5.0	5.0	5.0	81.1	.0	.00
GF	1.3	2.9	3.9	5.5	5.5	2.0	1.3	1.3	2.1	7.5	7.5	7.5	116.3	1.0	71.44
C	.9	1.0	1.3	3.4	3.4	.1	.9	.9	1.3	3.4	3.4	3.4	88.4	.0	.00
LP	1.5	2.9	2.9	2.9	2.9	.5	1.5	2.0	2.9	3.2	3.2	3.2	72.9	.0	27.91
S	.4	.9	1.0	1.1	1.1	.1	.4	.4	.9	1.0	1.1	1.1	12.1	.0	.00
PP	.4	.9	1.0	1.1	1.1	.0	3.4	3.4	3.4	3.4	3.4	3.4	1.7	.0	24.60

2153 37.7

L	15.2	15.7	21.7	25.5	25.5	1.2	11.6	13.8	19.9	19.9	23.0	28.3	51.9	10.5	50.41
DF	9.1	11.8	13.0	13.0	13.0	.1	8.2	11.8	15.7	18.5	18.5	18.5	.5	.4	47.71
GF	31.3	31.3	31.3	31.3	31.3	3.3	22.6	31.3	31.3	31.3	31.3	31.3	1.1	4.6	35.15
C	3.2	8.7	18.1	18.1	18.1	.1	3.7	4.5	4.8	4.8	18.1	18.1	15.8	.9	50.53
LP	6.0	10.6	11.7	11.7	11.7	.0	6.0	8.5	9.5	11.7	11.7	11.7	.3	.1	15.59
S	2.5	2.6	3.5	3.5	3.5	.0	3.5	4.0	4.0	4.0	4.2	4.2	.2	.0	70.89
PP	2.5	2.6	3.5	3.5	3.5	.0	7.8	7.8	7.8	7.8	7.8	7.8	.0	.0	10.04

Table 5—A summary for the entire stand as reported in the Prognosis Model output file for a stand in Crow Creek on the Lolo National Forest

STAND GROWTH PROGNOSIS SYSTEM   VERSION 6.0 -- INLAND EMPIRE   01-22-1990 10:43:08

SUMMARY STATISTICS (PER ACRE OR STAND BASED ON TOTAL STAND AREA)

		START OF SIMULATION PERIOD									REMOVALS				AFTER TREATMENT					GROWTH THIS PERIOD			MAI
YEAR	AGE	NO OF TREES	BA	SDI	CCF	TOP HT	QMD	TOTAL CU FT	MERCH CU FT	MERCH BD FT	NO OF TREES	TOTAL CU FT	MERCH CU FT	MERCH BD FT	BA	SDI	CCF	TOP HT	RES QMD	PERIOD YEARS	ACCRE PER	MORT YEAR	MERCH CU FT
1983	130	8349	242	791	255	113	2.3	9151	8022	37853	0	0	0	0	242	791	255	113	2.3	10	209	89	61.7
1993	140	6118	293	868	333	117	3.0	10354	9220	43160	0	0	0	0	293	868	333	117	3.0	10	144	68	65.9
2003	0	4528	282	793	310	123	3.4	10195	9151	42883	742	10157	9151	42883	11	54	31	7	.7	5	56	1	.0
2008	5	4241	57	217	130	12	1.6	313	0	0	0	0	0	0	57	217	130	12	1.6	5	55	0	.0
2013	10	4196	80	284	175	17	1.9	587	0	0	3196	563	0	0	5	21	9	17	.9	5	20	0	.0
2018	15	946	18	64	29	23	1.9	125	0	0	0	0	0	0	18	64	29	23	1.9	5	58	0	.0
2023	20	930	47	138	66	27	3.1	416	0	0	0	0	0	0	47	138	66	27	3.1	5	101	1	.0
2028	25	912	84	219	108	34	4.1	920	325	1011	0	0	0	0	84	219	108	34	4.1	10	161	4	.0
2038	35	845	173	385	190	43	6.1	2495	1640	6410	0	0	0	0	173	385	190	43	6.1	10	265	21	.0
2048	45	706	265	522	268	56	8.3	4936	4251	20134	0	0	0	0	265	522	268	56	8.3	10	205	46	.0
2058	55	579	300	556	294	65	9.7	6523	5896	29365	0	0	0	0	300	556	294	65	9.7	10	183	83	.0
2068	65	457	308	541	294	72	11.1	7524	7014	35250	0	0	0	0	308	541	294	72	11.1	10	143	121	.0
2078	75	363	293	496	274	78	12.2	7745	7330	36959	0	0	0	0	293	496	274	78	12.2	10	133	127	.0
2088	85	290	274	450	252	84	13.2	7802	7441	37592	0	0	0	0	274	450	252	84	13.2	10	157	74	.0
2098	95	242	279	441	252	89	14.5	8632	8297	42680	0	0	0	0	279	441	252	89	14.5	10	144	113	.0
2108	105	204	271	417	241	94	15.6	8943	8636	44804	0	0	0	0	271	417	241	94	15.6	10	112	121	.0
2118	115	172	256	385	224	99	16.5	8847	8572	44756	0	0	0	0	256	385	224	99	16.5	10	116	113	.0
2128	125	147	245	360	212	102	17.5	8873	8616	45474	0	0	0	0	245	360	212	102	17.5	10	117	119	.0
2138	135	128	234	338	200	106	18.3	8854	8612	45773	0	0	0	0	234	338	200	106	18.3	10	132	104	.0
2148	145	112	230	324	194	111	19.4	9138	8901	47501	0	0	0	0	230	324	194	111	19.4	5	105	177	.0
2153	150	104	219	307	183	112	19.6	8781	8553	45722	0	0	0	0	219	307	183	112	19.6	0	0	0	.0

For the most part, column and row headings are sufficient to interpret the contents of this table. Realize that the table summarizes by time steps the conditions at the end of a growth cycle and the changes that took place within the past cycle.

The first section of the table is for the base year (usually inventory). For this point in time, a breakdown of tree density is presented for live trees but not for mortality. Instead, a section of zeros is printed because the model does not summarize periodic mortality in the time before the date of inventory.

The size class breakdown within a species is by five percentile classes. Diameter distributions between species may vary greatly and are sometimes based on a small number of sample trees. A detailed diameter distribution is available as a Prognosis option. However, this distribution is for the entire stand, not just the area in root disease. Thus, the Prognosis summary will differ from the breakdown within the root-diseased portion of the stand. Following harvest and reestablishment, and prior to the time at which the Carryover Model is invoked, values for trees killed per acre represent newly established trees being infected and killed by the normal Root Disease Model within the infection centers as they existed at the time of the cut. During this interval (such as in table 4, in year 2008) there are no entries for total infected trees, or percentage of roots infected. After the Carryover Model is run, the model will have a set of new infection centers and an estimate of number of trees infected and percentage of roots infected. From that point on, this table represents the new area infected.

HOW THE MODEL WORKS

The Root Disease Model simulates the epidemiology of pathogenic *Armillaria* spp. or *P. weirii*. The model simulates spatial relationships between location of infected stumps and infected and uninfected live trees to predict the spread of infection in the stand. Persistence of infection between rotations is also simulated. The major relationships captured in the model are the susceptibility of trees to infection, vulnerability of trees to death once infected with root disease, effects of windthrow and attack by bark beetles, disease related growth reduction, and inoculum dynamics in infected trees and stumps. Physical and biological agents that may influence the dynamics of root disease incidence can optionally be included in the simulation.

The parameters used as defaults in the model reflect our best current understanding of *Armillaria* and *P. weirii* epidemiology in the Inland Empire region of the western United States. These parameters can be adjusted using keywords to more accurately reflect particular pathogenicities and stand conditions (appendix II).

The dynamics and impact of root disease in a stand projection is modeled in roughly six major parts:

1. Representation of root disease centers at the start of a simulation.
2. Simulation of the effects of other mortality agents on trees inside root disease centers.
3. Simulation of the spread of root disease centers.
4. Dynamics of the infection of trees inside root disease centers.
5. Estimation of the "carryover" of root disease from one stand through a harvest to a new stand with new infection centers.
6. Calculation of mortality inside root disease centers and growth effects due to root disease.

Brief descriptions of each of these phases will serve as background for describing input requirements, interpretation of output, and understanding model behavior. For additional detail, refer to McNamee and others (1989).

Representation of Root Disease Centers at Start of Simulation

The Prognosis Model represents the stand by a list of sample tree records. Each record in the list represents a number of trees in the stand with identical attributes. The number of trees per unit area represented by each record at the time of inventory is determined by the sample design. In addition to the number of trees, each record includes the species of the tree and its d.b.h., height, and crown ratio.

After Prognosis compiles the stand inventory and prescriptions for selected management actions, the root disease inventory is used to characterize diseased portions of the stand. Inventory data can be generated in two ways: (1) exclusively through keywords specified by the user, or (2) a combination of keywords specified by the user and data obtained directly from the input tree list used by Prognosis. Regardless of the method used, the following information is needed:

1. The number and size of root disease centers and their locations (unless a random distribution of locations is assumed).
2. The number of infected and uninfected trees within root disease centers (input through keyword or supplied directly from tree list) and the average proportion of root systems infected on infected trees (always keyword supplied).
3. A list of infected stumps (including infected dead trees) inside the root disease centers, and their sizes. This stump information can be entered through keywords, read directly from the tree list, or both for a given scenario.

In the model, the stand is assumed to be square and infection centers within it are assumed to be circular. The total density of infected and uninfected trees of each tree record inside the disease centers is computed from the input tree list or from the keyword, RRINIT, supplied by the user.

The proportion of root systems colonized on infected trees at the time of inventory can be defined by the user. Once simulation begins, this proportion is calculated separately for each tree, and thus the average for all infected trees will change.

Dead tree and stump information is summarized from the input tree list, from a user specified keyword, or both. Dead trees and stumps, in the context of the Root Disease Model, are defined as any tree that died infected with root disease, whatever the cause of death. The model assumes that trees uninfected with root disease at the time of death do not become inoculum sources. The remaining dead trees or stumps can be a whole standing tree, a standing bole, or a bole that has been snapped off. These dead trees and stumps act as inoculum sources for root disease in the infection centers.

Following the initialization of stand conditions and extent of root disease within the stand, the summary of the initial inventory is completed and the stand projection begins.

Effects of Other Agents

Effects of windthrow and bark beetles on tree mortality may be simulated if desired. These agents interact with the root disease process primarily by influencing inoculum levels and potential disease spread. For example, trees killed by bark beetles can become *Armillaria* inoculum only if they were infected by the fungus prior to death. The killing by beetles of uninfected trees near disease centers could slow disease spread because the model assumes that these root systems will not become inoculum. The other agents submodel is actually a collection of separate models, each of which simulates the action of one type of agent on trees in the stand. These models require the user to specify timing and severity of the event.

Through keywords the user can specify the occurrence of one or more of these agents during any desired cycle year of the projection. The user specifies the earliest year in which the other agent of interest can occur. If the required conditions are not appropriate in that cycle, the agent remains potentially active until conditions are appropriate, and then the event occurs. Only one incident of BBTYPE 1 and BBTYPE2 is permitted.

Windthrow of Trees—The windthrow model simulates major blowdown events in infection centers. Dominant and codominant trees are wind-thrown if the density of eligible stems exceeds a user-defined minimum. For infected trees that are wind-thrown, the model determines the number of stems that tip over, removing their root systems from the soil, as opposed to snapping off and thus leaving the root system in the ground. This decision is based on the proportion of the root systems that are infected. Windfallen stems that tip over do not further contribute to the spread of root disease. Infected trees that are snapped off are entered in the dead tree/stump list and become inoculum sources for root disease.

Bark Beetle Interactions—The current version of the other agents submodel simulates three types of bark beetle-stand interactions:

Type 1 beetles—An outbreak of type 1 beetles occurs when the density of susceptible trees of a given species and minimum diameter exceeds a user-defined minimum. Mountain pine beetle attacking lodgepole pine stands is used as the prototype interaction from which parameters for type 1 interactions are set. Mountain pine beetle and western pine beetle attacking ponderosa pine are also type 1 interactions.

Type 2 beetles—These depend on trees wind-thrown in the current time step. An outbreak occurs if the number of windfallen stems of a suitable size exceeds a user-specified minimum. Standing live trees are also attacked in proportion to their density and the density of wind-thrown trees that are attacked. The user must also specify a windthrow event with a type 2 bark beetle interaction. Douglas-fir beetle attacking Douglas-fir is used as the prototype type 2 beetle interaction from which defaults are set.

Type 3 beetles—An outbreak of type 3 beetles occurs if the density of a given tree species with sufficient size and proportion of their root systems infected exceeds a user-defined minimum density. That is, this type of beetle interaction is dependent on root disease infection, and tree species, size and density. Each of these can be specified by the user. Fir engraver attacking grand fir is used as the prototype type 3 interaction from which parameters are estimated.

In all of these bark beetle-stand interactions, the infected trees that are killed by an outbreak are added to the dead tree/stump list to act as inoculum.

Spread of Infection Centers

The spread of infection centers can be simulated dynamically or it can be set to a predefined rate by the user. If the latter option is chosen, the user specifies the annual rate (feet per year) at which to expand infection centers. If the dynamic spread model is chosen (the default), then the spread rate is simulated in the following way:

Figure 2 shows the basic relationship of how live root systems become infected, trees are killed, and infection spreads in dead roots. The average portion of a root system that is colonized when a tree dies is a function of the pathogen and tree species. The number of years it takes for a given root disease pathogen to kill a tree is a function of tree species and size.

The time necessary to kill a Douglas-fir tree on Douglas-fir habitat in the interior region of the Western United States is defined by the relationship shown in figure 3. This relationship is modified for other species, pathogens, and habitat types, as shown in the figure, but assumes that all trees react to infection in a similar way until their d.b.h., and hence their time-to-death exceeds some minimum.

Following tree death, fungal spread through the root system depends on the species of pathogen. *Armillaria* is assumed to colonize the entire root system within 5 years. *Phellinus weirii* is assumed to be unable to colonize the rest of the root system after death. But *P. weirii* inoculum on dead trees and stumps is assumed to have a minimum lifespan of 20 years. There is no minimum lifespan for *Armillaria* on dead trees and stumps. The maximum lifespan of inoculum is a function of stump size and tree species (fig. 4). Tree species are grouped into

heartwood and nonheartwood types. Species with heartwood include Douglas-fir, pines, western redcedar, and western larch. Nonheartwood species are true firs, hemlocks, and spruce. Inoculum is assumed to decay at a rate that reduces the radial extent of infected root systems by 75 percent during the first one-third of the lifespan. Remaining infected roots are assumed to decay at a steady rate over the remaining two-thirds of their lifespan.
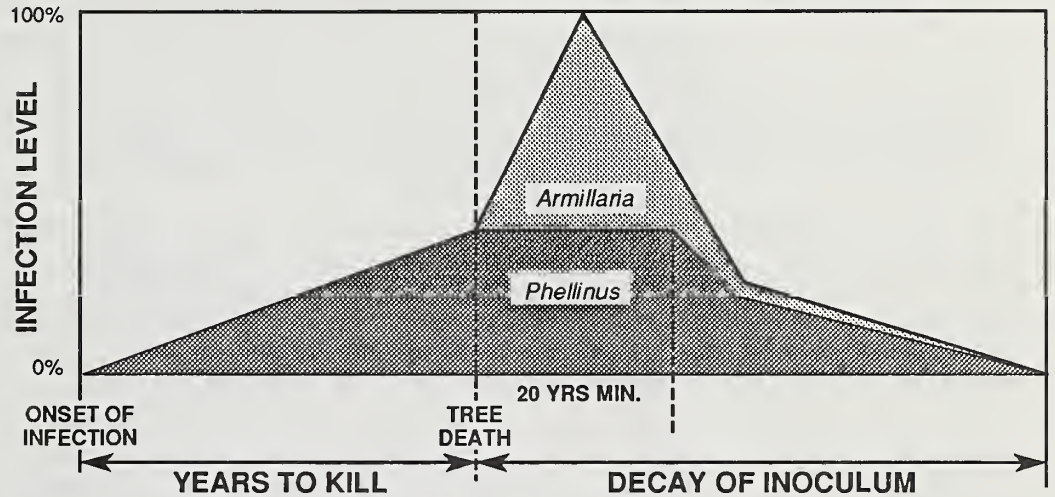

Figure 2—Patterns of pathogen spread and inoculum development in a single root system. Time scales depend on tree species.
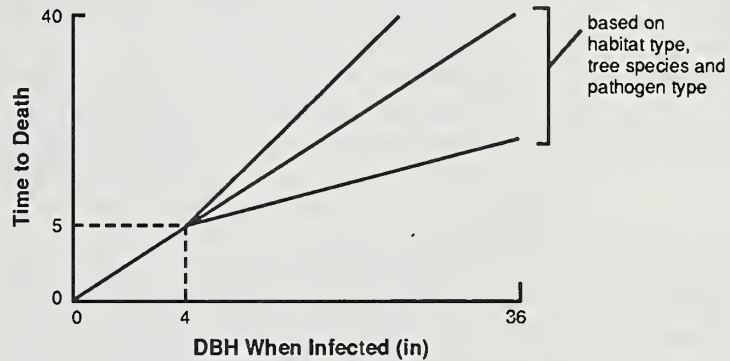
Figure 3—Time required from infection by *Armillaria* to tree death for Douglas-fir on a Douglas-fir habitat type.
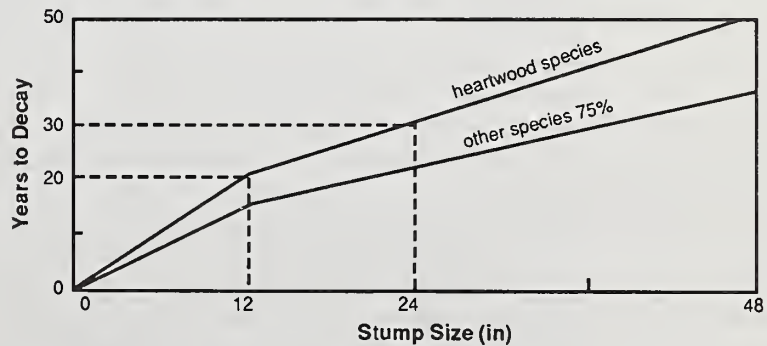
Figure 4—Lifespan of inoculum for various tree species infected with *Armillaria*; see text for desciption.

Spread rate is calculated by explicitly simulating a small portion of the stand for a number of years and averaging the spread rate of root disease over that period. Trees are selected from the tree list in proportion to their density in the stand and placed in a small "test plot" in either a random pattern (the default) or a square grid pattern with a small, positive amount of "error" in tree placement. These spatial patterns can be used to simulate the spread of root disease in stands under conditions ranging from natural regeneration in the stand to a plantation with little or no natural regeneration. Spread is simulated by increasing the area of infection of each infected root system using the relationship shown in figure 2, then checking to see whether this root system contacts any uninfected root systems. If they do, the uninfected trees contacting the infected trees become infected at a rate equal to the probability of pathogen transmission on contact (dependent on tree species and root disease pathogen). For simplicity, degree of root overlap is ignored in the estimation of probability—the probability is the same whether one or more systems come into contact.

Spread rate is converted to an increase in the radius of each disease center for the current growth cycle. These increased radii are then converted into an increase in total root disease area in the stand for that cycle, taking into account the overlaps between centers. The average spread rate is converted to an annual rate expressed in feet per year for the summary output display.

Old infection centers are assumed to expand at the time of the cut if the root disease pathogen is *Armillaria*. This is because many of the root systems at the edge of the infection center have just become infected with root disease, and *Armillaria* is assumed to completely colonize these root systems after tree death. The user can specify, through a keyword option (RRJUMP), by how many root-system diameters the center will expand after a cut.

Infection Dynamics Inside Centers

Not all trees inside infection centers develop root disease. This part of the model simulates pathogen transmission from infected to uninfected trees within the infection centers.

A representative sample of inoculum (infected stumps) is placed on the plot in a similar way to the live trees for the spread model above. Then trees from the tree list are distributed randomly on this test plot in proportion to their density. The number of newly infected trees inside infection centers is estimated, depending on the proportion of the root systems of each tree that contacts inoculum sources and the probability of infection from that contact.

Carryover of Root Disease to a New Stand

This model component represents our best, albeit incomplete, understanding of the ways in which root disease centers are affected by the harvest of trees and subsequent regeneration of a new stand. For example, the integrity of root disease centers from the old stand may break down after a clearcut. The disease in the new stand may arise from only a few isolated inoculum sources within the previously infected area. Or the centers may remain essentially whole after the clearcut. Or centers in the new stand may rapidly coalesce and expand from essentially the old boundaries. These possibilities are part of a continuum that is determined by the density of inoculum, the composition of the original stand, and the composition of the regenerating stand.

The user has two options for specifying how carryover of root disease is to be modeled. The user can simply set the expected probability of new center initiation and the expected number of new infection centers created after carryover. This option, termed the "static" carryover model, is the default. The second option uses the same relationships for disease spread and pathogenicity used by the main Root Disease Model to estimate carryover of disease from one stand to the next. This option is called the "dynamic" carryover model. Its operation is discussed more fully below.

The carryover model calculates the probability of infection persisting from the time of the cut through to the time of root closure in the new stand. This is done by

reconstructing conditions at the time of the cut and keeping track of the probabilities of infection persisting from the original stumps and from young trees that become infected through contact with old infected stumps or other infected trees. The time step used by the carryover model for this reconstruction is 5 years. This submodel uses the same relationships as those used in the estimation of root disease spread and infection. After the simulation of carryover is completed, the probability of infection persisting is converted into an estimate of the number of new infection centers. The model allows up to 100 new centers to be created from carryover; these new centers are randomly distributed within the boundaries of the old infection centers.

Mortality and Growth Effects Inside Centers

The final part of the Root Disease Model is to reconcile the mortality from root disease and other agents, and growth effects due to root disease in infected trees, with stand averages calculated by Prognosis. These rates are then passed back to Prognosis.

Trees outside root disease centers and uninfected trees inside root disease centers can suffer mortality from causes represented by Prognosis and other agents, while infected trees inside the root disease centers can suffer mortality from causes represented by Prognosis, other agents, and root disease. The model assumes that the total mortality on any tree class will be the maximum of the mortality predicted by Prognosis or the mortality predicted by the combined effect of root disease or other agents.

Root disease infection can affect both diameter and height increment and is modeled as a function of the proportion of the root system colonized by root disease. These relationships are applied only to infected trees; the actual growth increments for each Prognosis tree record are a weighted average of the separate growth increments of the three categories of trees represented by each record: infected inside centers, uninfected inside centers, and trees outside centers. Finally, the Root Disease Model updates the attributes in the dead tree/stump list, and passes control back to Prognosis. The projection continues as Prognosis updates the attributes of the trees in the stand, calculates tree volumes, compiles the tables that display projected stand conditions, and if required, begins the next cycle. At the conclusion of the projection, the Prognosis stand tables are displayed as are the tables summarizing conditions within root disease centers.

Linkage to Prognosis Model and Limitations

Coastal forest conditions were included in development of the Root Disease Model. At this time, however, a Prognosis Model variant has not been developed for coastal forests. This Root Disease Model could be linked to other stand growth models in addition to Prognosis Model. The essential requirements are:

1. A list of trees in the stand, with each tree representing a number of trees per acre on a sampling basis.
2. A regeneration component to add new trees as growing space is released by mortality or harvest.
3. A procedure for compressing the tree list to make space for the new trees.

The limited length of the tree list (500 tree records) imposes some limitation on the representation of the root disease process. The most serious limitation is the necessity of having each tree record represent trees both infected and uninfected, and both inside and outside root disease centers. The consequence of this limitation is that tree attributes such as crown ratio, height increment, and diameter increment must be maintained using weighted averages of the values for trees in each condition. However, this limitation does not apply at the start of the simulation if the disease status of each tree in the inventory is supplied using the RRTREIN option. A further consequence of having each tree record represent trees in all disease conditions is that their growth rates (before modification for effects of infection) are based on overall stand stocking.

An alternative model formulation that would remove this limitation would be to maintain each annulus of spread as an independent stand. Such a formulation would be possible with the Parallel Processing Extension of the Prognosis Model (Crookston and Stage in press). At this time, however, we do not believe that the improved resolution would be justified in view of the other approximations of the disease process implicit in the rest of this model.

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APPENDIX II—REAL WORLD VS. THE MODEL: CHANGING MODEL ASSUMPTIONS

These keywords offer the user flexibility in exploring the dynamics of the model by altering important keywords (the INFKILL, INFMULT, INOCSPAN, RRJUMP, RRMINK, TDISTN, and TTDMULT keywords) and modifying the simulation of important processes such as the spread of disease centers, and carryover between rotations (the SPREAD and CARRY keywords). The RSEED keyword allows the user to vary the random numbers used by the model in calculating spread rate and the dynamics of infection inside root disease centers.

CARRY Specifies the type of carryover model to be simulated (static or dynamic). The default is that a static carryover model is simulated.

  Field 1: Contains either a 0 or 1. If 0 is entered or field is left blank, a static carryover model is assumed and an entry in field 3 will be read, specifying the fixed probability of forming new disease centers. If 1 is entered, the dynamic carryover model is assumed and field 3 will be searched for the minimum spread rate at root closure.

  Field 2: This contains the number of Prognosis growth cycles after harvesting (thinning or clearcutting) that the carryover model will be called. The default is four cycles. Additional harvesting within the delay interval will, in turn, delay the execution of CARRY.

  Field 3: The entry in field 3 depends on whether the user invokes a static or dynamic carryover model. If field 1 is 0 or blank, a static carryover model is being invoked and field 3 contains the probability of forming new disease centers. The default is a probability of 1.0. An error message will appear if the entry in field 3 is less than 0 or greater than 1, and the default probability will be retained. If field 1 contains 1, the dynamic carryover model will be simulated and field 3 should contain the minimum rate of disease spread at root closure.

  Field 4: Field 4 is only examined if the user has specified a static carryover model. Field 4 contains the number of new disease centers in the entire stand that will be formed when the carryover model is invoked. From one to 100 centers can be established in this way. The default value of three centers will be used if the user specifies less than one or greater than 100 centers.

  DEFAULT: Static spread model called four growth cycles after every stand thinning, including clearcutting.

INFKILL Infection through a root system proceeds until a threshold proportion of the root system is infected and the tree dies. This keyword allows the user to modify the proportion of the root system that is infected at the time of death.

  Field 1: This field defines for which type of root disease the proportions are to be specified. A value of 1 specifies *Armillaria*, 2 specifies *P. weirii*. Any other value entered on this line will cause an error message to be printed and the *Armillaria* type to be assumed.

However, if the disease specified in this field differs from that specified by the RRTYPE keyword, this keyword will be ignored.

Field 2: The value entered in this field, if between 1 and 11 inclusive, specifies that a single proportion of roots infected at death value is to be changed and indicates the tree species index to be changed. Any other value indicates that all proportions of root infection at death are to be changed, and a supplemental record is to be provided with the new values.

Field 3: This field is only examined if field 2 has a value between 1 and 11 inclusive. It contains the new proportion of root systems infected at death for the species indexed in field 2.

Supplemental Records

A supplemental record is expected if the proportion of roots infected at death is to be changed for all species (Field 2 is not a number between 1 and 11 inclusive). Format for this supplemental record is 11F5.2.

DEFAULT:

Species abbrev.	WP	L	DF	GF	WH	C	LP	S	AF	PP	OTH
Species index	1	2	3	4	5	6	7	8	9	10	11
Armillaria	0.3	0.85	0.8	0.8	0.8	0.75	0.3	0.75	0.3	0.3	0.3
P. weirii	0.85	0.75	0.8	0.6	0.8	0.75	0.85	0.65	0.60	0.85	0.8

INFMULT This keyword allows the user to change the probabilities of disease transmission given that the vertical projections of the infected and uninfected root systems overlap. As one example of the use of this keyword, the user may change infection probabilities for each tree species to represent differences in various habitats.

Field 1: This field contains the year in which the probabilities of infection modified with this keyword are to take effect. This allows the user to change these parameters once during the simulation. The user must put the year in field 1 on all INFMULT keywords that refer to probabilities of infection changed at some point during the simulation. The year in which the probabilities of infection are changed is the date specified on the last INFMULT keyword that has a year in field 1.

Field 2: This field defines for which type of root disease the probabilities are to be specified. A value of 1 specifies *Armillaria*, 2 specifies *P. weirii*. Any other value entered on this line will cause an error message to be printed and *Armillaria* to be assumed. However, if the disease specified in this field differs from that specified by the RRTYPE keyword, this keyword will be ignored.

Field 3: The value entered in this field, if between 1 and 11 inclusive, specifies that a single probability of infection is to be changed and indicates the tree species index to be changed. Any other value indicates that all probabilities are to be changed and a supplemental record is to be provided with the new probabilities.

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Field 4: This field is only examined if field 3 has a value between 1 and 11 inclusive. It contains the new probability of infection for the species indexed in field 3.

Supplemental Records

A supplemental record is expected if all probabilities are to be changed (field 3 is not a number between 1 and 11 inclusive). Format for this supplemental record is 11F5.2.

DEFAULT:

Species abbrev.	WP	L	DF	GF	WH	C	LP	S	AF	PP	OTH
Species index	1	2	3	4	5	6	7	8	9	10	11
Armillaria	0.1	0.05	0.5	0.6	0.1	0.1	0.2	0.5	0.5	0.2	0.1
P. weirii	0.1	0.2	0.4	0.4	0.2	0.02	0.1	0.2	0.4	0.1	0.4

INOCSPAN This keyword specifies the minimum lifespan, in years, of inoculum for the two root disease types.

Field 1: This field contains the minimum lifespan of the *Armillaria* root disease type.

Field 2: This field contains the minimum lifespan of the *P. weirii* root disease type.

DEFAULT: 0 years for the *Armillaria* type and 20 years for the *P. weirii* type.

RRCOMP Prognosis tree list arrays are 1,350 records long. In an effort to conserve computer memory requirements but maintain good representation of trees inside disease centers, the root disease tree lists are 500 records long. Because of a one-to-one correspondence between the Prognosis and Root Disease tree lists, the Prognosis tree lists can never contain more than 500 records when using the root disease extension. Compression of the tree lists occurs whenever the number of records exceeds 500. This keyword allows the user to specify the maximum size of the tree lists for the scenario to be between one and 500 records. Compression will occur automatically whenever the tree list length is about to exceed (because of new regeneration) the user-defined maximum. There is a tradeoff to be aware of in that a shorter tree list is quicker to process but compression is expensive. It is advisable to compress the tree list to about 200 elements if a large number, near 500, tree records are read in and regeneration is to occur. This will minimize the number of times the compression routine will have to be called. Two precautions: (1) Be sure to include the NOTRIPLE Prognosis keyword to avoid immediately undoing the effect of the RRCOMP action, and (2) be sure not to introduce an RRCOMP action between the time of a harvest and the subsequent timing of the CARRY keyword.

Field 1: The maximum size of the tree list. The tree list is compressed to this number whenever its length approaches this number. An error message will appear if the value of field 1 is blank or is greater than 500 and the maximum size of the tree list will be set to 150 records.

DEFAULT: 150 records.

RRJUMP	Root disease spreads through trees around the edge of centers when the stand is thinned or clearcut. This keyword allows the user to specify the extent to which root disease will expand outward when centers are cut.

> Field 1: This field contains the number of root-system diameters by which the centers will expand upon cutting. The model computes the average root system diameter of all trees in the stand, and the centers will move out this distance multiplied by the value contained in parameter field.
>
> DEFAULT: Centers will expand one mean root radius upon cutting.

RRMINK	It is assumed that modifiers of the mortality and infection dynamics of trees infected with either *Armillaria* or *P. weirii* are effective at all tree sizes. This keyword allows the user to relax this assumption (see also the TTDMULT keyword and fig. 3).

> Field 1: This field contains a time-to-death below which the modifiers specified by the TTDMULT keyword do not influence mortality and infection dynamics for trees infected by *Armillaria*. This field should contain a value. If it is blank, the minimum time to death is set to 0 years.
>
> Field 2: This field contains a time-to-death below which the modifiers specified by the TTDMULT keyword do not influence mortality and infection dynamics for trees infected by *P. weirii*. This field should contain a value. If it is blank, the minimum time to death is set to 0 years.
>
> DEFAULT: The time to death below which the modifiers do not influence mortality and infection dynamics is 0 inches for both *Armillaria* and *P. weirii*.

RSEED	This keyword allows the user to change the seed value used in starting the model random number generators. The random number generators are used in the dynamic simulation of spread rate, as well as in the dynamics of infection inside root disease centers.

> Field 1: The new seed value. This can be any positive integer number less than the maximum number allowed on the particular computer. The default value is 855998726.

SPREAD	Specifies the type of spread model to be simulated (static or dynamic).

> Field 1: Contains either a 0 or 1. If 0 is entered or is left blank, a static spread model is assumed and an entry in field 2 will be read, specifying the fixed annual spread rate. If 1 is entered, dynamic spread model is used.
>
> Field 2: The fixed annual spread rate. This field is only examined if field 1 is blank or contains 0.
>
> DEFAULT: Static spread model, with a spread rate of 1.0 ft per year.

TDISTN   Spread of root disease between trees depends on the spatial distribution of trees in the stand. The distribution can be random or gridded, as in a plantation. This keyword allows the user to specify the initial tree distribution and the tree distribution after some point in the simulation.

Field 1:   This field contains the year in which the distribution will change from that specified in field 2 to the other. This is particularly useful when, for example, a stand is to be cut and turned into a plantation.

Field 2:   This field is used to specify the current tree distribution. If field 2 is blank or contains a 0, the tree distribution is assumed to be random. If field 2 contains a 1, the tree distribution is set to regular spacing. All other entries in the parameter field are ignored and the default, a random distribution, is used.

Field 3:   This field contains the standard deviation about the mean distance between trees in a regular, or lattice, distribution. This is useful in those cases when a stand is to be established with planting, but natural regeneration is allowed in the stand.

DEFAULT: The tree distribution is assumed to be random.

TTDMULT   This keyword allows the user to change the time-to-death multipliers for root disease mortality. These multipliers permit the user to vary the time-to-death for each tree species. (See also the RRMINK keyword and fig. 3.)

Field 1:   This field contains a year in which the time-to-death multipliers modified with this keyword are to take effect. This allows the user to change these parameters once during the simulation. The user must put the year in field 1 on all TTDMULT keywords that refer to time-to-death multipliers changed at some point during the simulation. The year in which the time-to-death multipliers are changed is the date specified on the last TTDMULT keyword that has a year in field 1.

Field 2:   This field defines for which type of root disease the multipliers are to be specified. A value of 1 specifies *Armillaria*, while a value of 2 specifies *P. weirii*. Any other value entered on this line will cause an error message to be printed and the *Armillaria* type to be assumed. However, if the disease specified in this field differs from that specified by the RRTYPE keyword, this keyword will be ignored.

Field 3:   The value entered in this field, if between 1 and 11 inclusive, specifies that a single multiplier is to be changed and indicates the tree species index to be changed. Any other value indicates that all multipliers are to be changed and a supplemental record is to be provided with Format 11F5.2 for the new multipliers. Indices for tree species are given in the rightmost column of table 4 of Wykoff and others (1982).

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Field 4:   This field is only examined if field 3 has a value between 1 and 11 inclusive. It contains the new multiplier for the tree species indexed in field 3.

Supplemental Records

A supplemental record is expected if all multipliers are to be changed (field 3 is not a number between 1 and 11 inclusive). Format for this supplemental record is 11F5.2.

DEFAULT:

Species abbrev.	WP	L	DF	GF	WH	C	LP	S	AF	PP	OTH
Species index	1	2	3	4	5	6	7	8	9	10	11
Armillaria	1.8	2.0	1.0	0.75	0.9	1.2	1.8	1.1	0.75	1.8	0.9
P. weirii	3.0	1.5	1.0	1.0	1.5	10.	3.0	1.1	1.0	3.0	1.5

APPENDIX III—KEYWORD SUMMARY AND DEFAULT VALUES

This summary lists all the keywords and their associated parameter fields for the Root Disease Model. Default values exist for all program options. Keywords need only be used if the desired action differs from the default action. Page number of detailed description of each keyword appears in parentheses beneath the keyword.

Summary of Keyword Specific to Root Disease Model Extension

Keyword	Parameter fields					
	1	2	3	4	5	6

Program execution options

COMMENT
(10)   Supplemental records, as many as desired until END in the first 3 columns is read.

END
(11)

RRDOUT   logical unit number
(10)   for detailed output

RRECHO   logical unit number
(10)   for machine
          readable output

RRIN
(10)

Root disease inventory options

PLREAD
(14)   Supplemental Records: 1 record for each subplot in disease center. Subplot number in I4 format corresponding to the subplot identifier on the tree records. A subplot identifier of –999 indicates end of subplot supplemental records.

Keyword	1	2	3	4	5	6
RRINIT (12)	type of root disease initialization (random/fixed)	no centers in stand	number infected trees per acre in disease centers	number uninfected trees per acre in disease centers	proportion of root systems colonized	total area in root disease centers (acres)

Supplemental Records, if initialization is fixed, 1 record for each center noted in field 2 of RRINIT keyword, (3F7.1) X-coordinate of center, Y-coordinate of center, radius of center.

RRTREIN
(14)

RRTYPE   root disease
(12)   type

SAREA   stand area
(12)   (acres)

STREAD
(15)   Supplemental records containing following information are needed for STREAD keyword, (I4,2F6.1) tree species, stump diameter, number of stumps. –999 in first 4 columns signals end of plot information.

(con.)

Keyword	1	2	3	4	5	6
			Parameter fields			

Root disease management options

Keyword	1	2	3	4	5	6
PSTUMP (16)	year of stump pushing	proportion of stumps removed	minimum stump diameter to be removed			

Model modification options

Keyword	1	2	3	4	5	6
BBTYPE1 (16)	first year beetle infestation can occur	tree species to infest	minimum DBH to infest	minimum No. of eligible stems	proportion of eligible stems killed	
BBTYPE2 (17)	first year beetle infestation can occur	tree species to infest	minimum DBH to infest	minimum No. of eligible stems	proportion of eligible stems killed	
BBTYPE3 (17)	first year beetle infestation can occur	tree species to infest	minimum DBH to infest	minimum No. of eligible stems	proportion of eligible stems killed	minimum proporation of roots infected in eligible stems
CARRY (40)	type of carryover (static or dynamic)	No. growth cycles after stand entry that carryover model is called	(static model) probability of forming new centers (dynamic model) minimum spread rate	(static model) number of new centers to form (dynamic model) not used		
INFKILL (40)	tree species to modify	root infection at death				

Supplemental records, if field 1 of INFKILL keyword is ≤0 or >11, all species changed, (11F5.2) Root infection at death for all species.

Keyword	1	2	3	4	5	6
INFMULT (41)	year multiplier takes effect	root disease type	tree species to modify	species multiplier		

Supplemental records, if field 3 of INFMULT keyword is ≤0 or >11, all species changed, (11F5.2) Probabilities of infection for all species.

Keyword	1	2	3	4	5	6
INOCSPAN (42)	years for *Armillaria*	years for *P. weirii*				
RRCOMP (42)	No. records to which tree list is compressed					

(con.)

	Parameter fields					
Keyword	1	2	3	4	5	6

Model modification options (Con.)

Keyword	1	2	3	4	5	6
RRJUMP (43)	No. of root-system diameters to expand centers after cut					
RRMINK (43)	years to death for *Armillaria*	years to death for *P. weirii*				
RSEED (43)	alternative seed value for random number generators					
SPREAD (43)	type of spread (static or dynamic)	annual spread rate (for static spread)				
TDISTN (44)	year in which tree spatial distribution changes to other type	tree spatial distribution of initial stand (random or uniform)	standard deviation of uniform distribution			
TTDMULT (44)	year multiplier takes effect	root disease type	tree species to modify	species multiplier		

Supplemental records, if field 3 of **TTDMULT** keyword is ≤0 or >11, all species changed, (11F5.2) Time-to-death multipliers for all species.

Keyword	1	2	3	4	5	6
WINDTHR (18)	first year windthrow can occur	proportion of eligible stems to windthrow	minimum No. of eligible stems necessary for windthrow event			

Default values for Keywords;

COMMENT, END, PLREAD, and RRIN have no defaults

Keyword	Default values by field					
	Field 1	Field 2	Field 3	Field 4	Field 5	Field 6
BBTYPE1	YYYY[a]	7[b]	8.0	10.0	0.85	—
BBTYPE2	YYYY[a]	3[b]	10.0	10.0	0.88	—
BBTYPE3	YYYY[a]	4[b]	10.0	10.0	0.88	0.30
CARRY	0	4	1.0[c]	3.0[d]	—	—
INFKILL	1	—[e]	—	—	—	—
INFMULT	YYYY[a]	1	—[f]	—	—	—
INOCSPAN	0	20	—	—	—	—
PSTUMP	YYYY[a]	1.0[g]	0.0	—	—	—
RRCOMP	150	—	—	—	—	—
RRDOUT	22	—	—	—	—	—
RRECHO	24	—	—	—	—	—
RRINIT	0	20[h]	0.5[i]	0.5[i]	0.1[g]	25
RRJUMP	1.0	—	—	—	—	—
RRMINK	0	0	—	—	—	—
RRTREIN	(Keyword has no parameter fields)					
RRTYPE	1	—	—	—	—	—
RSEED	855998726	—	—	—	—	—
SAREA	100	—	—	—	—	—
SPREAD	0	1.0	—	—	—	—
STREAD	(Keyword has no parameter fields)					
TDISTN	YYYY[a]	0	—	—	—	—
TTDMULT	YYYY[a]	1	—[j]	—	—	—
WINDTHR	YYYY[a]	0.0[g]	0.0[g]	—	—	—

[a]The four-digit YYYY is specified as a calendar year.

[b]The tree species value must be a number between 1 through 11, inclusive, which is the Prognosis tree species index.

[c]If field 1 = 0, then a static carryover model is invoked with a default of 1.0 in field 3. If field 3 is specified by the user, the value must be a number between 0.0 and 1.0, inclusive. If field 1 = 1, then the dynamic carryover model is invoked with a default of 0.0 feet per year in field 3 as a minimum spread rate.

[d]This field is only used if field 1 = 0. The number of new centers must be between 1 through 100, inclusive.

[e]A supplemental record is expected if the proportion of roots infected at death are to be changed for all species (value other than 1 through 11 inclusive, entered in field 1). Format for this supplemental record is 11F5.2.

[f]A supplemental record is expected if the probabilities of infection are to be changed for all species (value other than 1 through 11 inclusive, entered in field 2). Format for this supplemental record is 11F5.2.

[g]The value must be a number between 0.0 and 1.0, inclusive.

[h]The number of root disease centers must be between 1 and 100, inclusive.

[i]If RRTREIN is not present, fields 3 and 4 will default to 0.5 of average stand density.

[j]Supplemental record is expected if all multipliers are to be changed (value other than 1 through 11, inclusive, entered in field 2). Format for this supplemental record is 11F5.2.

Effects of pathogenic *Armillaria* spp. or *Phellinus weirii* on stand dynamics are represented by the Western Root Disease Model. This model, which operates in conjunction with the Prognosis Model for Stand Development, can be used to evaluate effects on stand generation and growth of a wide assortment of silvicultural practices, including stump removal for disease reduction. This publication contains model applications, a brief description of how the model is formulated, and documentation of the keyword procedures for using the model.

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