

User Friendly User's Guide To the Western Root Disease Model

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based on original written by
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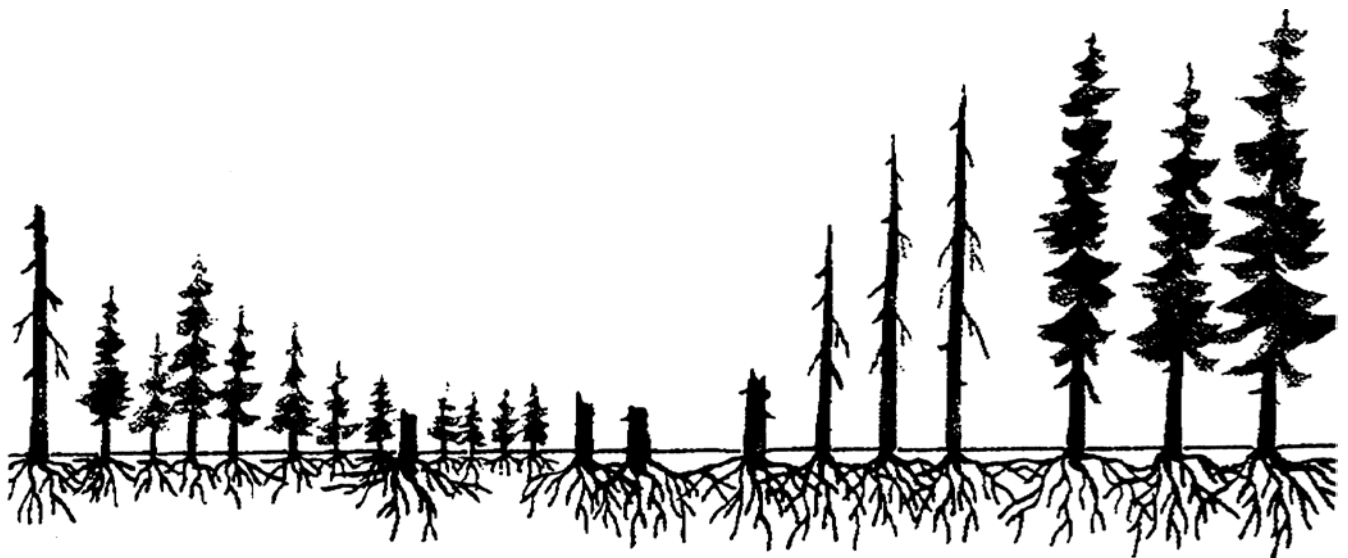


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Introduction



Cautions, Philosophy, and Words of Wisdom by the Authors

Why did we write this? A constant stream of comments that the root disease model is too difficult to use, too cumbersome, doesn't represent local conditions, or requires too much information upfront that is difficult or expensive to collect, has driven the point home. We had to make this model easier to use. We weren't about to change the model itself. It's a strong model, built of the best information we have. We didn't think our job was to explain in great detail what happens inside the black box. Instead, we wanted to let the users know the easiest way to get around the system as it exists. What are the critical information needs that must be gathered from the field? Which keywords are more useful than others? What happens when you use certain keywords in combination with others? When should you "tweak" the model functions by using inputs other than the defaults? In our insect and disease model training classes we emphasize these types of questions, but the audience of root disease model users is still a relatively small one. Hopefully, the following information can reach a wider group.

And now for a little discussion about models in general. Many not-so-nice things have been said about using models and there are still many skeptics. If you are using this guide, you probably have bought into the idea of modeling forest vegetation. You may, however, be in the position of needing to convince others about models. This can be difficult. "Why use a model when you can get the advice of knowledgeable people?" they say... And then there are always those comforting phrases such as "Garbage in, garbage out" or "All models are bad, but some are useful." It's hard to argue isn't it? The most important thing to keep in mind is that models like the Western Root Disease Model are tools to help the user compare alternatives -- something models do well because they produce consistent answers. Any two experts you go to for advice might give you two different answers to a question because they are working from different assumptions. In the Western Root Disease Model the assumptions that are behind model behavior are explicit; they are laid out for all to see. But there is no doubt that the answers the model gives will always be better when users can provide information to fit the model more closely to their local conditions.

So, if you have root disease in your stand, within your watershed, or in your planning area and you want to understand how the composition, stocking levels, and structure of the vegetation will be altered by the activity of the fungi, plunge into FVS and use the Western Root Disease Model. Give the model the best information you have on the current conditions for your area. If you don't know, seek out your local pathologist and ask for help with survey methods, input parameters, and using the model itself. Don't be shy; you would be surprised how excited some people get about rotten roots!¹

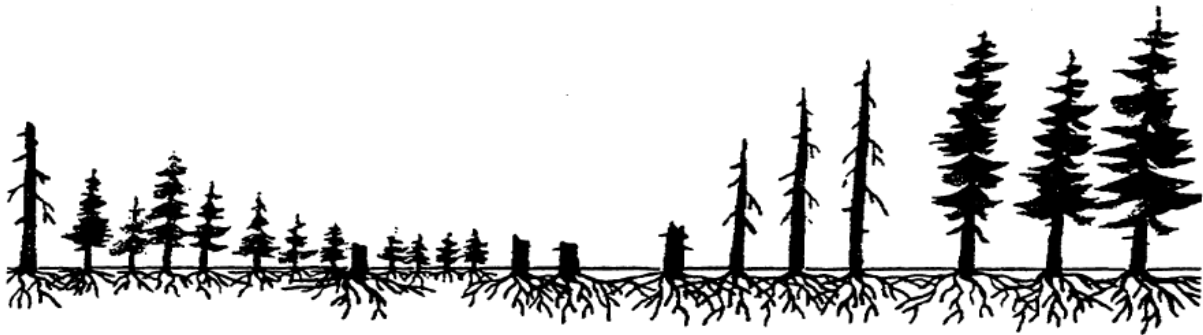
¹ This User's Guide is a compilation of training materials and examples that have helped those using the Western Root Disease Model to understand its basic principles. It is meant to be used in combination with other published material and in no way replaces those documents.

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Chapter 1

What You Need To Get Started



Do you have the current installation of the Forest Vegetation Simulator?

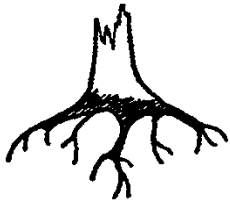


If you are planning to use the Western Root Disease Model, (WRDM) you must have the current installation of the Forest Vegetation Simulator (FVS). The installation package for Microsoft Windows based PCs is available for download from the Forest Management Service Center, Forest Vegetation Simulator website (<http://www.fs.fed.us/fmssc/fvs/>). The WRDM is included in most western FVS variants and if available will be offered through the options in the Suppose FVS interface after you have selected the variant and added your data to the simulation.

The following FVS variants currently have the WRD model attached:

- Blue Mountains (BM)
- Central Idaho (CI)
- Central Rockies (CR)
- East Cascades (EC)
- Eastern Montana (EM)
- Inland Empire (IE)
- Klamath Mountains (NC)
- Kootenai / Kaniksu / Tally Lake (KT)
- Pacific Northwest Coast (PN)
- Southern Oregon / Northeast California (SO)
- Tetons (TT)
- Utah (UT)
- West Cascades (WC)
- Western Sierras (WS)

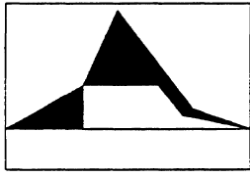
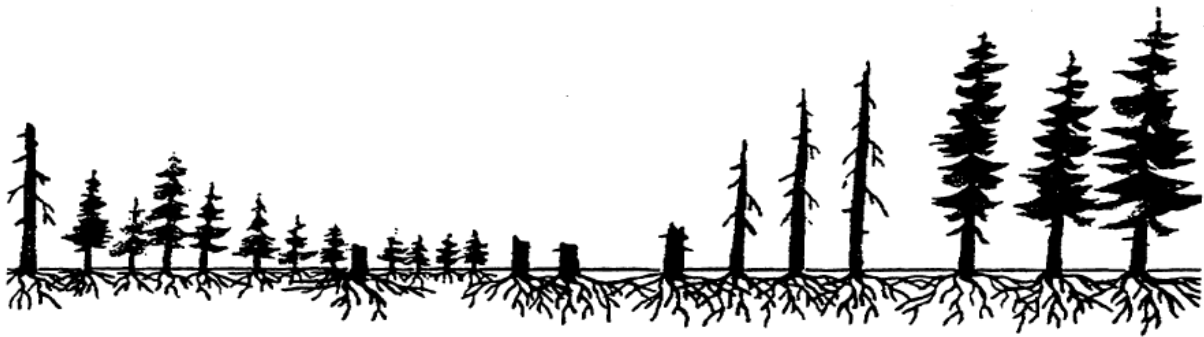
Invoking the Western Root Disease Model



As you build your FVS run using Suppose, you can access WRD model options for your stand projection including disease model initialization, reporting, modifying growth and mortality impacts, and disease management options via several avenues. Keywords can be accessed directly through the “Add Keywords” button and then selecting the appropriate option in the left pane to display the WRD keywords in the right pane. Additional WRD Model option screens have also been developed that in some cases involves multiple related keywords so that the user does not have to deal with them individually. Those are found through the “Select Management”, “Select Output” and “Select Modifiers” buttons at the top of the main Suppose screen. If at any time you wish to see the keywords associated with an item in the Suppose “Simulation file contents” or an option entry screen as they will appear in the keyword file, use the Suppose “Simulation Preparation” dropdown option “View Component Keywords”.

Chapter 2

How the Model Works



Without going into nauseating details and numerous equations, the user should have an idea of the basic principles and underlying assumptions that went into building the WRDM.

Many groups of root disease researchers, extension specialists, silviculturists, growth and yield specialists and programmers met over several years to bring together their best knowledge and estimates of how two root diseases, Armillaria root disease and laminated root rot caused by *Phellinus sulphurascens* could be modeled in the environment of the existing growth and yield model, now known as the Forest Vegetation Simulator. Then a second endeavor to create a second model for P-Type and S-Type Annosus ensued. These two extensions were used, maintained and improved for several years and then the two were combined into the single model we have today that can represent all four root diseases. The functions were built with data and observations gathered over the western United States and Canada. All projections will be improved by understanding the biology and behavior of these root diseases in your local area.

Basics

The Western Root Disease Model currently models four root diseases: Armillaria root disease caused by *Armillaria ostoyae*, laminated root rot caused by *Phellinus sulphurascens*, Heterobasidion root disease in pines (P-Type annosus and Heterobasidion root disease in firs (S-Type annosus). What is known about species susceptibility is reflected in how easily infection and colonization of roots occurs, how quickly the fungus spreads from tree to tree, and how quickly trees die. Tree size and stand density are also factors.

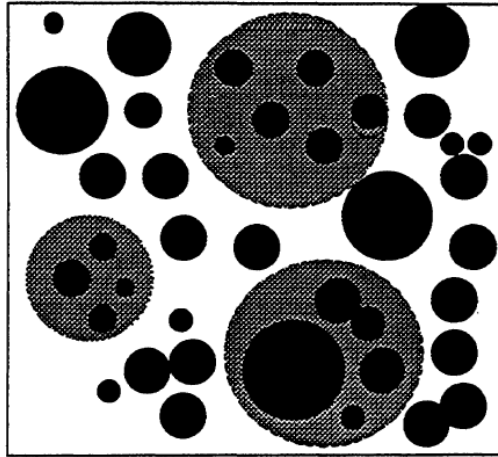


Figure 1. Trees (solid circles) and root disease centers (hatched areas) in a WRDM stand.

The model assumes that the stand is a square and that the root systems of trees are round, with the root radius length related to tree diameter at 4.5 feet above the ground (diameter at breast height, DBH). Root disease centers are also round (Fig. 1).

The spatial distribution and size distribution of trees inside root disease centers changes from cycle to cycle. The base model, FVS, does not keep track of individual trees or where those trees are located. It is therefore impossible to track one tree with root disease from the beginning of the projection to the end. But that's okay. Remember, what you are looking for is relative differences between runs, not absolute numbers.

Spread Inside Centers

Based on the tree data or the additional information provided via keywords, a certain number of trees/acre are assigned root disease with some proportion of their root system infected (Fig. 2a). The fungus grows within those root systems (Fig. 2 b,c) until a critical proportion is reached - that which is necessary for tree death. The proportion of root system infected necessary for a tree to be killed is dependent upon which fungus is being modeled and which tree species is infected. It is assumed that trees die before their entire root system is colonized; therefore the proportions in the controlling functions are always less than 1.00.

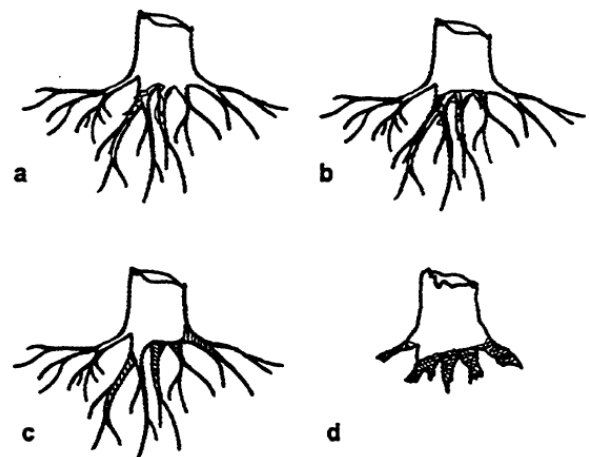


Figure 2. Progression of root infection a-d.

How long it takes a particular tree to die is dependent upon its size, species, and the root disease (Fig. 3). The larger the tree at time of initial infection, the longer it takes to die.

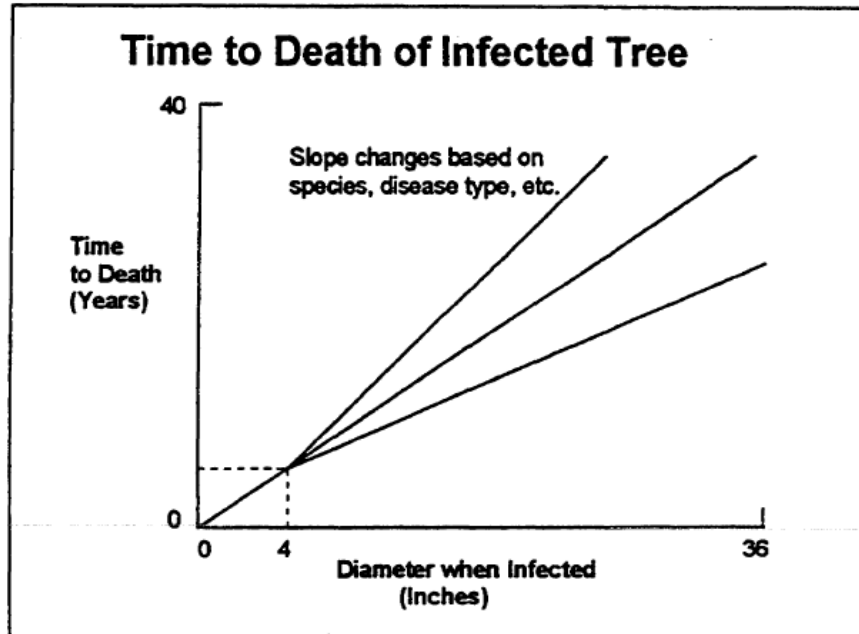


Figure 3. Time required from infection to tree death.

The root disease-causing fungi modeled by the WRDM remain viable, protected inside root material, for decades. So once a tree dies, the model must maintain the inoculum on the site for several years. If a tree dies that has Armillaria root disease (Fig. 4), inoculum will increase until the entire root system of the tree is colonized. If a tree dies due to Heterobasidion, the inoculum will increase an additional 5 to 25% of the root system, but will not go to 100% like Armillaria. Across all species represented by the model, the minimum Heterobasidion post-death colonization is 75% and maximum is 95%.

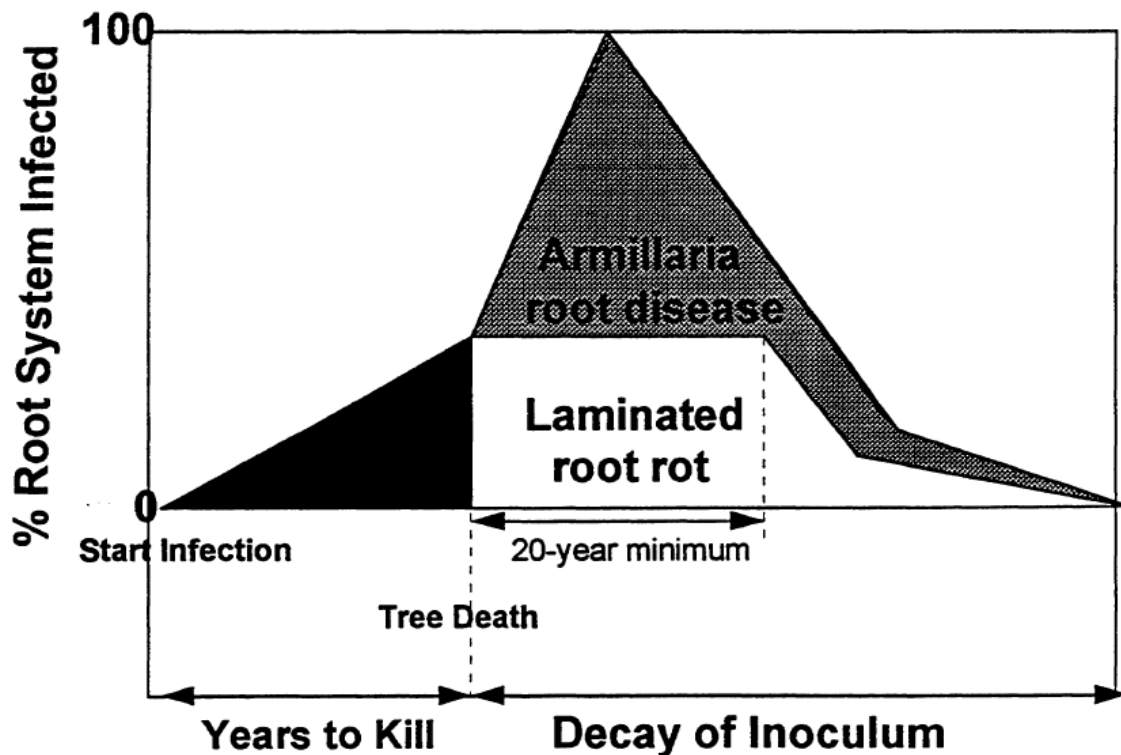


Figure 4. How inoculum develops in a single root system. The time scale is dependent upon tree species.

When laminated root rot occurs, no further colonization of the root system takes place after a tree has died (Fig. 4). However, *P. sulphurascens* inoculum does not immediately start to decline. The fungus is assumed to have a minimum lifespan of 20 years before it decreases and the proportion of root system infected begins to decline. As with Armillaria, the actual lifespan of viable fungal inoculum is dependent upon tree species and size.

Once peaked, the infection level will immediately begin to decrease. Meanwhile, the dead tree's root system itself begins to decay (Figs. 2d and 5). The maximum lifespan of the inoculum is a function of species and stump size. Small trees will support inoculum for fewer years than larger trees.

Heartwood/resinous species will take longer to decay than non-heartwood/non-resinous species.

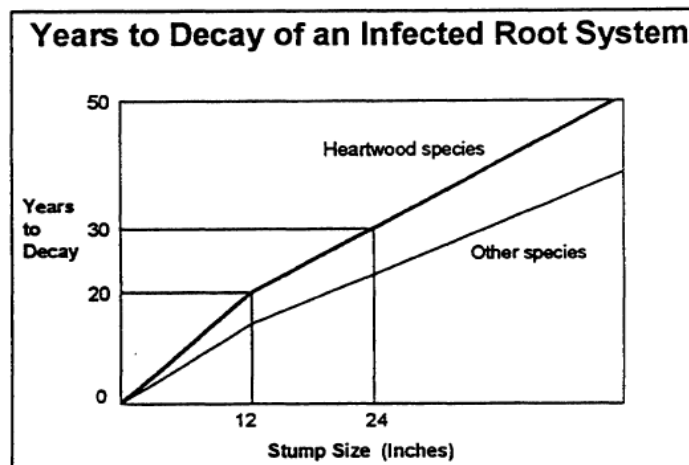


Figure 5. Lifespan of inoculum in tree species by species type.

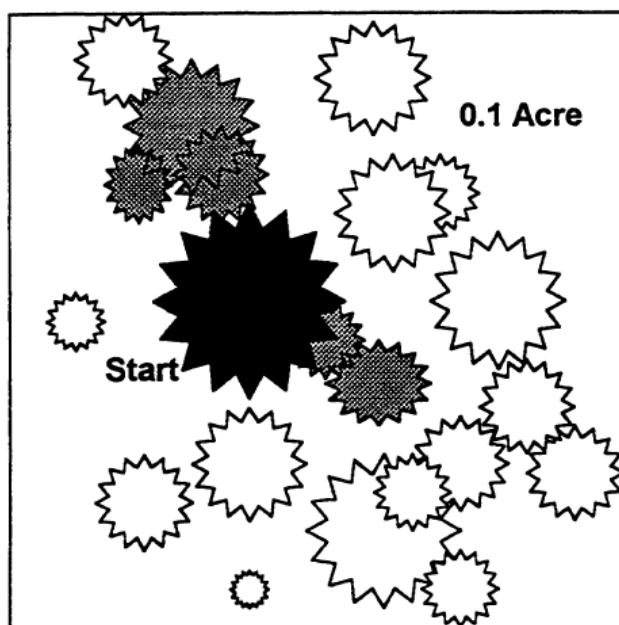


Figure 6. Spread of root disease inside centers across susceptible host roots.

Meanwhile, root disease spreads to uninfected trees inside centers according to their susceptibility. Each species is assigned a probability of infection that indicates how well the particular fungus will infect and colonize the roots. So as the model run progresses, trees inside centers will continue to become infected and die.

Spread Outside Centers

Root disease centers increase in size as roots of infected trees on the perimeter of the centers come into contact with roots of susceptible hosts outside those centers. In the model, this may happen in one of two ways: 1) via a *static* spread rate that is user supplied, or 2) by a *dynamic* spread rate that is calculated based on tree density.

Static Spread

The static spread rate is the simplest way to model an increase in the size of centers. The user supplies a spread rate, such as 1 foot per year. The centers increase at that rate (Fig.7) regardless of root system size or placement. The increase in root disease center area is reflected as a consistent increase in acreage from cycle to cycle. The static spread rate may be appropriate when trees are uniformly distributed in stands, such as orchard or plantation settings.

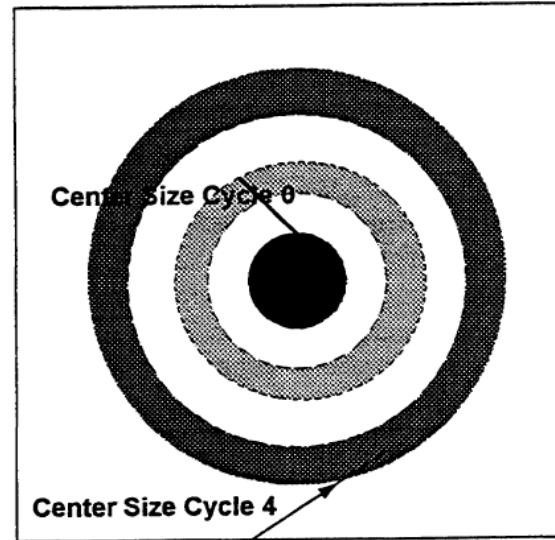


Figure 7. Static spread rate of a root disease center over 4 cycles. Spread is consistent with a user specified input rate.

Dynamic Spread

Dynamic spread rates reflect changes from cycle to cycle as root systems grow and trees die (Fig. 8). When the dynamic spread rate is used, the model draws a sample of trees from the tree list and randomly places those trees and their corresponding root systems in a 0.1 acre cell (Figs. 9 a-d). The model puts the fungus on one side of the cell and allows it to spread across the root systems that are in contact with each other for 10 years. How fast this happens depends upon functions and parameters inside the model that are associated with species susceptibility. Depending on the arrangement of root systems, the fungus will reach a certain distance in that time period. Trees are selected and placed in the cell several times and the distance traveled is calculated each time. An average of these distances is then used to determine how far root disease will move in one cycle. Since the treelist changes from cycle to cycle as trees grow or die, spread rate changes from cycle to cycle (Fig. 8). This explains why spread rates can vary so much

in the output tables. The dynamic spread rate will paint a more realistic picture of root system/fungal dynamics, particularly in mixed age and species stands.

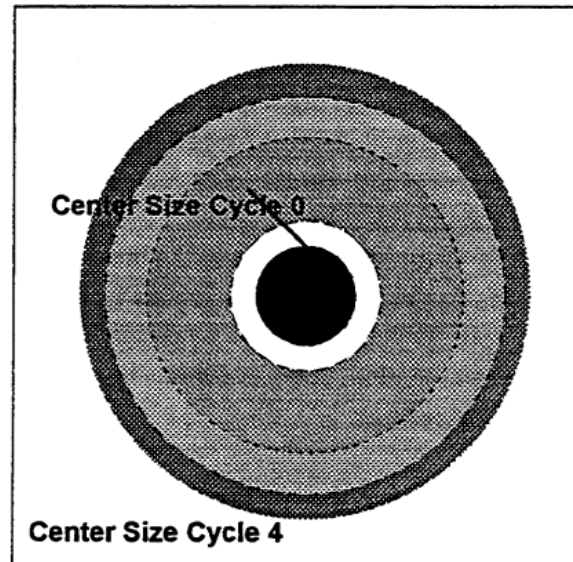


Figure 8. Dynamic spread rate used in a 4 cycle FVS run. Spread rate changes from cycle to cycle.

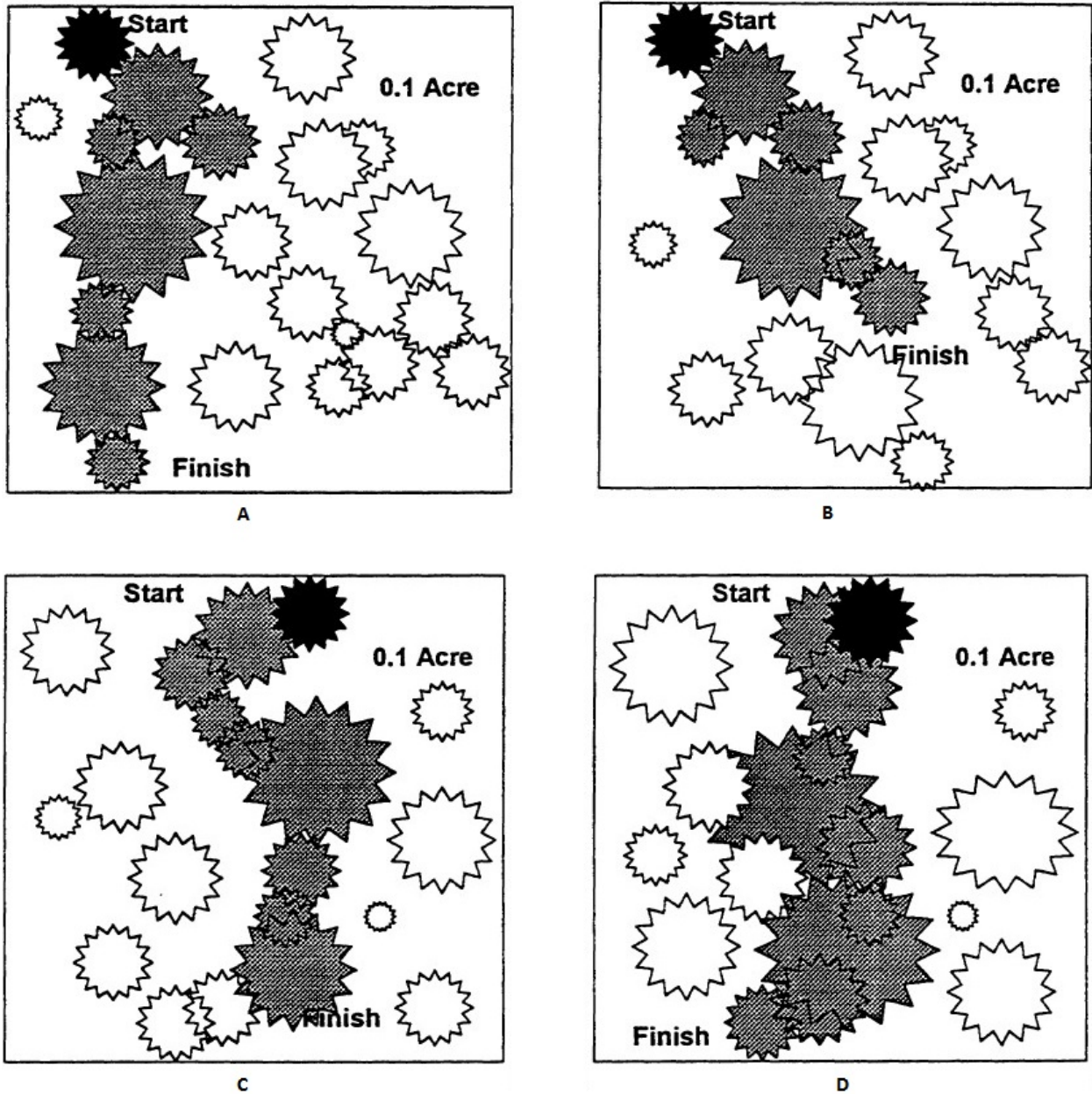


Figure 9. Trees are randomly placed in a .1 acre cell and the fungus spreads tree to tree over a 10 year period. The distance traveled within that time is tracked by the model. This action is repeated several times and the average is used as the rate of spread of centers. In B and C, the fungus does not travel as far as in A or D due to random tree placement. This allows for changes in spread rates from cycle to cycle.

One of the things the WRDM cannot do is coalesce overlapping centers into large mega-centers (Fig. 10). The number of centers that a model run ends with, even if it is 300 years later, will be the same number that it started with, unless cutting occurs. What does happen is that the area inside each center increases-perhaps even to the point of having the original centers take over the entire stand. The area in root disease will never exceed the size of the stand.

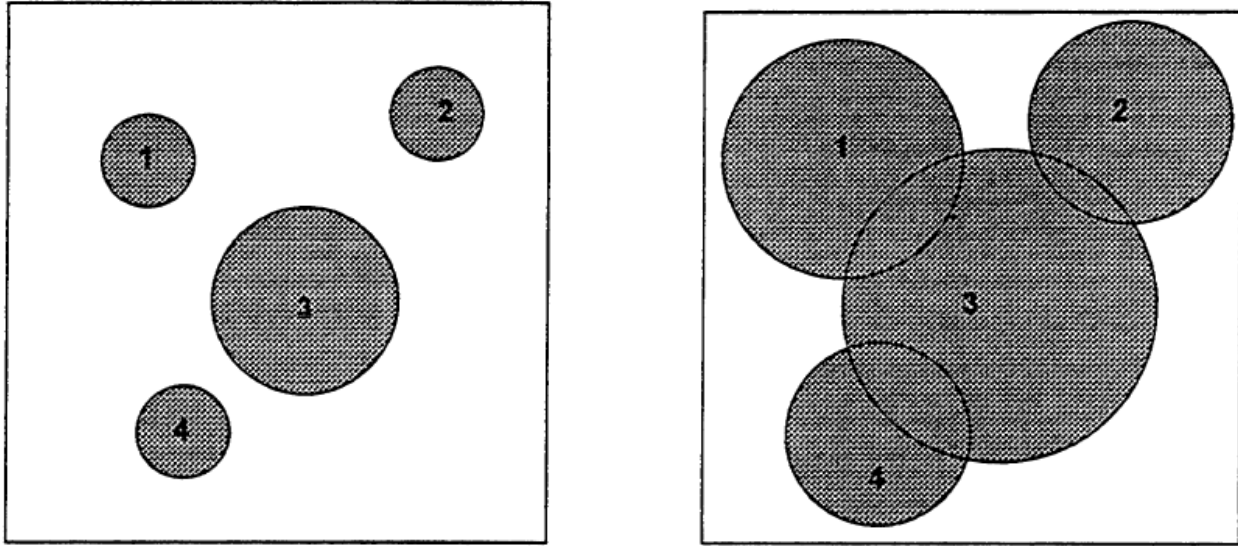


Figure 10. Four distinct root disease centers occurring in cycle 0 remain distinct in model outputs several cycles later even though the centers have coalesced in the field.

Mortality and Growth

The WRDM is constantly interacting with the functions in the FVS base model. FVS provides the WRDM with information on new trees that are planted or trees that are harvested. The WRDM provides FVS with information on trees that are killed by root disease. Since FVS has its own mortality functions, it is essential that the two models interact to avoid killing trees twice! When the root disease model causes mortality, that mortality is compared with the FVS-based mortality. The larger mortality value of the two is then used.

The WRDM also modifies the diameter and height growth predictions of root disease-infected trees. Diameter growth modifications are based on the proportion of root systems infected (Fig. 11). Growth values are not affected until a certain proportion of the root system has become infected. Growth decreases as the proportion of root system infected increases, until trees reach the infection level where mortality occurs. Height growth impacts are directly related to diameter growth reductions.

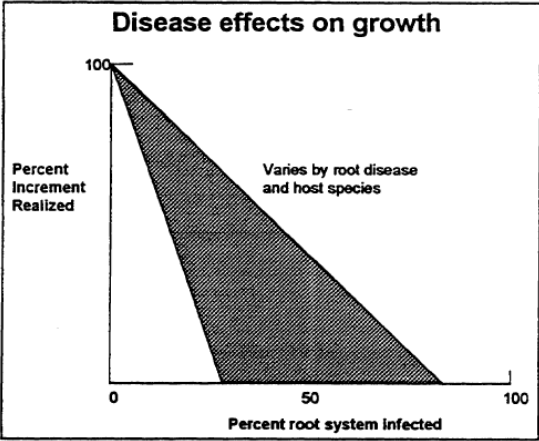


Figure 11. Growth reduction occurs after a certain proportion of the root system is colonized.

Cutting and Harvests

Root disease conditions may change as a result of harvesting or management actions in an infected stand. The model has mechanisms built into it which maintains, to some degree, root disease on the site. How much root disease is maintained is based on how much inoculum was present in the trees at the time they were cut. The species composition of the stand and their relative susceptibilities, the species that are regenerated in the stand and their relative susceptibilities along with any stump management (stump removal or borate application) all contribute to the continuation and intensity of the disease as the FVS projection continues.

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

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

During the regeneration of a stand, 5 year cycles should be used. The shorter cycle length is used because the first 10-20 years in a regenerating stand are critical in terms of transmitting root disease and the dynamics of the infection/colonization process would be lost in a 10 year cycle. Too much is happening! In a single species stand, the mortality of the regeneration may not occur as expected. In a mixed species stand, the mortality (or survival) of one or more species may be impacted in a manner that alters the long term stand composition in an unexpected manner. Now, just because the long term results are unexpected does not mean they are wrong. Additionally, just because the results of a simulation are reasonable for one location does not mean the same results for a different location are also reasonable. It is very important to consult a forest pathologist who is familiar with the root diseases and their behavior in the location where you are working. A few tests were performed using the Inland Empire variant, which has the full establishment model. During this modelling exercise, very minor species in the establishment model added to the stand after a thinning activity were able to remain as minor components (just a few trees per acre) when the cutting activity was followed with four 5-year cycles as opposed to the default 10-year cycles. When the cutting activity was followed with 10-year cycles, the minor species ingrowth did not remain as components of the stand.

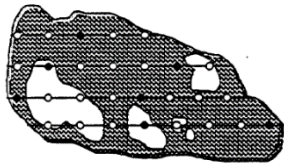
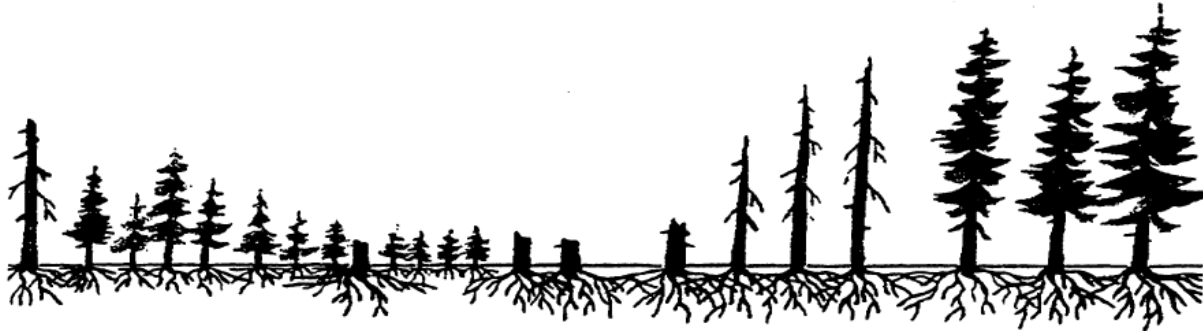
When modeling Heterobasidion root disease, new disease centers will be created due to spores infecting newly cut host stumps. The rate and size of stumps that will be infected and ultimately create new centers is controllable by the user with the **SPORE** keyword. The default

behavior for both P-Type and S-Type is a 10% infection rate of stump diameters 14 inches and larger. The root system radius of these stumps that become colonized still goes to 50% of the root radius the tree had prior to being cut. The root system and decline of inoculum will occur at the standard rate. The likelihood of disease transmission based on root contact in spore initiated disease centers is just half that of the original disease centers in the stand. Additionally, the time-to-death parameter for newly infected trees in spore initiated disease centers is increased by a factor of three.

Now, with a little information about the root disease situation in your area, you are ready to run!

Chapter 3

Root Disease Inventory: Assessing Current Conditions



There is no getting around it; one of the weakest links in assessing the effects of root disease on vegetation over time is inadequate information about the root disease conditions that currently exist. We could write a book on why that is (root diseases are sometimes difficult to identify, crews are inadequately trained in identification, estimating area affected is not built into stand examination procedures, “we don’t do root disease”, we’ve heard it all). What we would rather do is provide some helpful hints on how to acquire the needed information, with the best payoff on your dollar.

You need to provide the model with some basic information on the configuration of root disease in the stand. Without this information, the model will use default values. If the default values do not adequately represent your actual conditions, you cannot expect the model results to reflect a realistic potential future condition.

What happens when root disease centers in your stand are readily delineated—that is, you are comfortable with the idea that you have distinct root disease pockets?

Helpful Hint #1:

The WRDM is VERY sensitive (in other words, you will see relatively large differences in outputs when you change these parameters relatively slightly) to:

- **Infected Area**
- **Number of Centers**
- **Distribution of Centers**

(Fig. 13 and 14)

The larger the area affected, the more quickly the remainder of the stand will be colonized; the greater the number of centers, the more the perimeter to spread from, and thus a faster increase

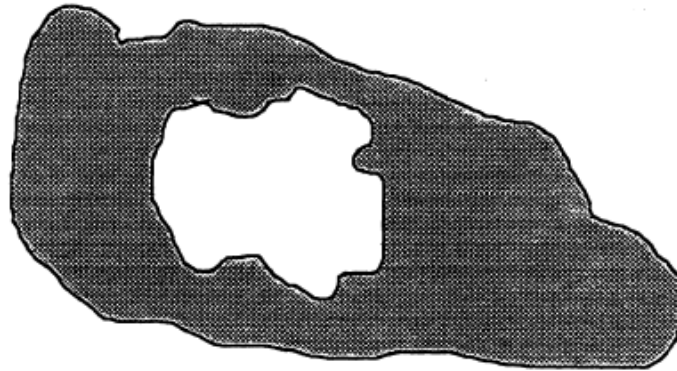
of root disease (Fig 13). Root disease centers are distributed randomly by the WRDM, unless the user specifies differently. If "real" conditions are such that root disease is confined to a portion of the stand, then the healthy portion of the stand may be shortchanged (fewer trees, more mortality, slower growth, etc.) if it is modeled as though it had root disease (Fig 14). On the other hand, the diseased portion of the stand may grow better, according to the model, than it would in reality because less root disease was placed there by the random draw.

The WRDM is not as sensitive (you must make significant changes in these input parameters to see significant changes in outputs) to:

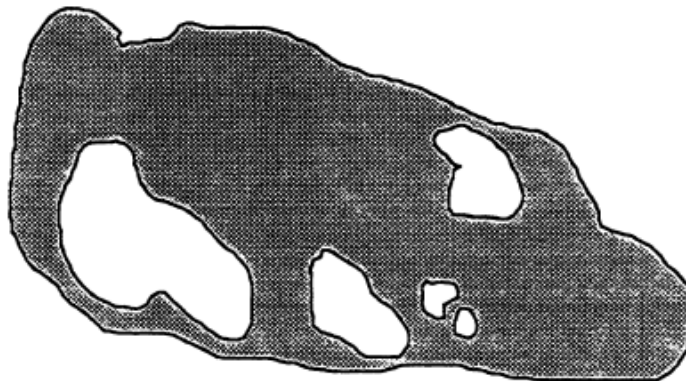
- **Numbers of trees infected vs uninfected inside centers**
- **Average percent root system infected**

(Fig. 15)

So, if inventory resources are limited, or you already have an existing stand exam that supplies you with adequate live tree information and you cannot afford to send the crew back in to do another complete exam, ***spend your effort identifying where the centers are and estimating how big they are***. This is probably most effectively done by sketching in the pockets on a gridded map of the stand as you move from one stand exam plot to another. After all, you have to walk that line anyway; you might as well pay attention to what is happening to the vegetation between plots. Then use the model defaults for uninfected versus infected trees per acre within centers.



1 Center



5 Centers

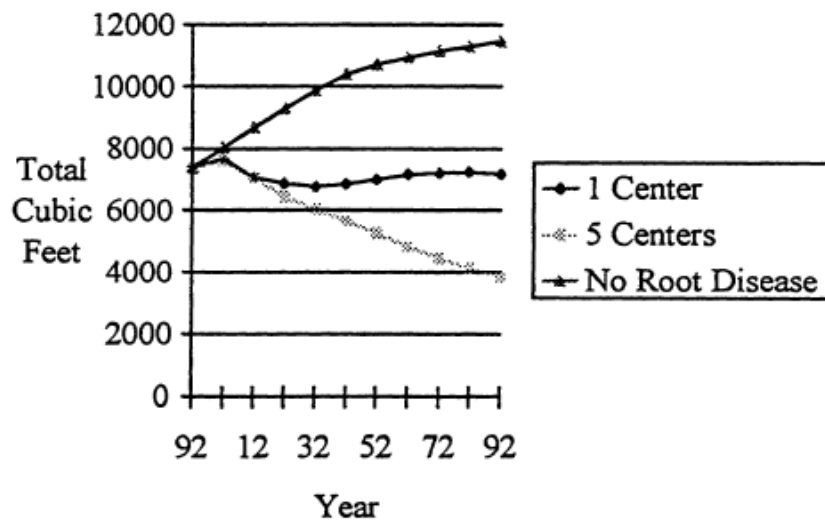


Figure 12. Three FVS runs were made with this stand. The upper line in the graph indicates results in total cubic feet for the stand over 100 years, without any root disease. The middle line depicts results when the root disease area is distributed in 1 distinct center and the bottom line shows what happens when that same area in root disease is modeled as 5 distinct centers.

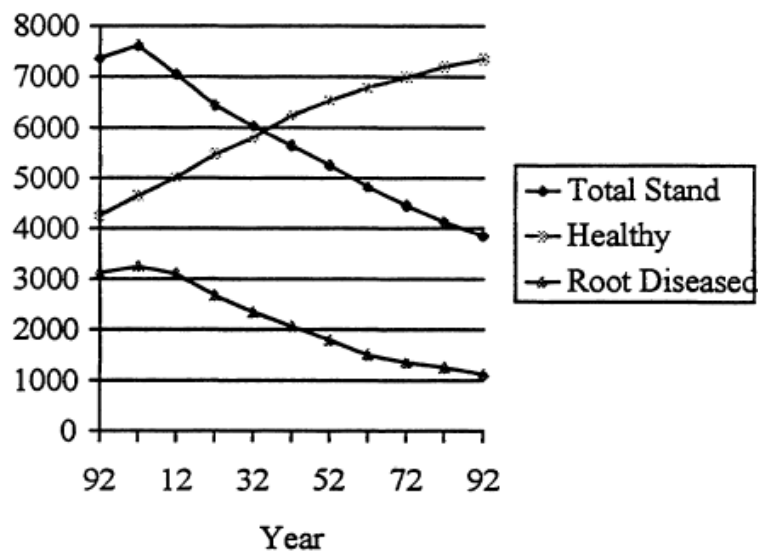
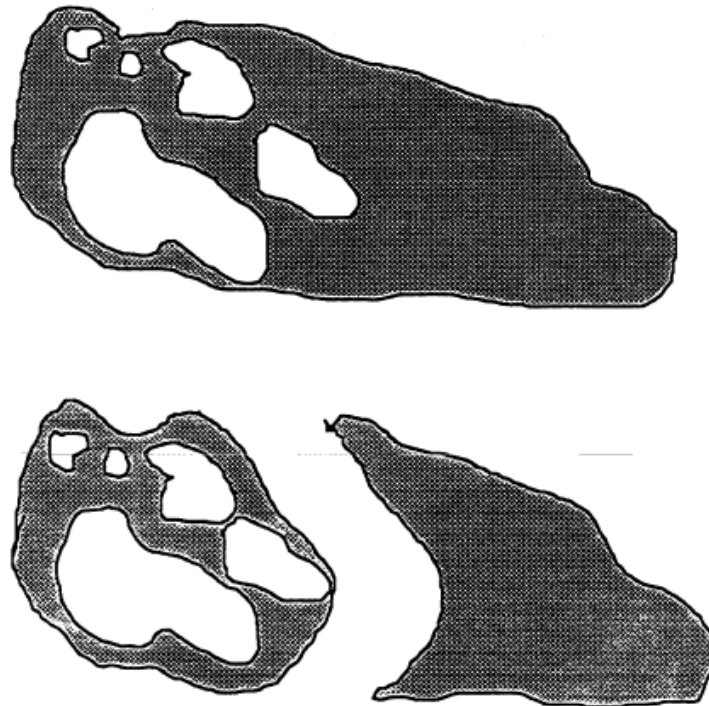


Figure 13. In this stand, the root disease is concentrated in one portion of the stand. Making an FVS run with 5 root disease centers that the model randomly places, results in the output labelled Total Stand. Splitting the stand into Healthy and Root Diseased portions and running them separately will result in a more realistic output. The healthy portion of the stand will not be penalized for having root disease and the root disease impacts will be more accurately simulated.

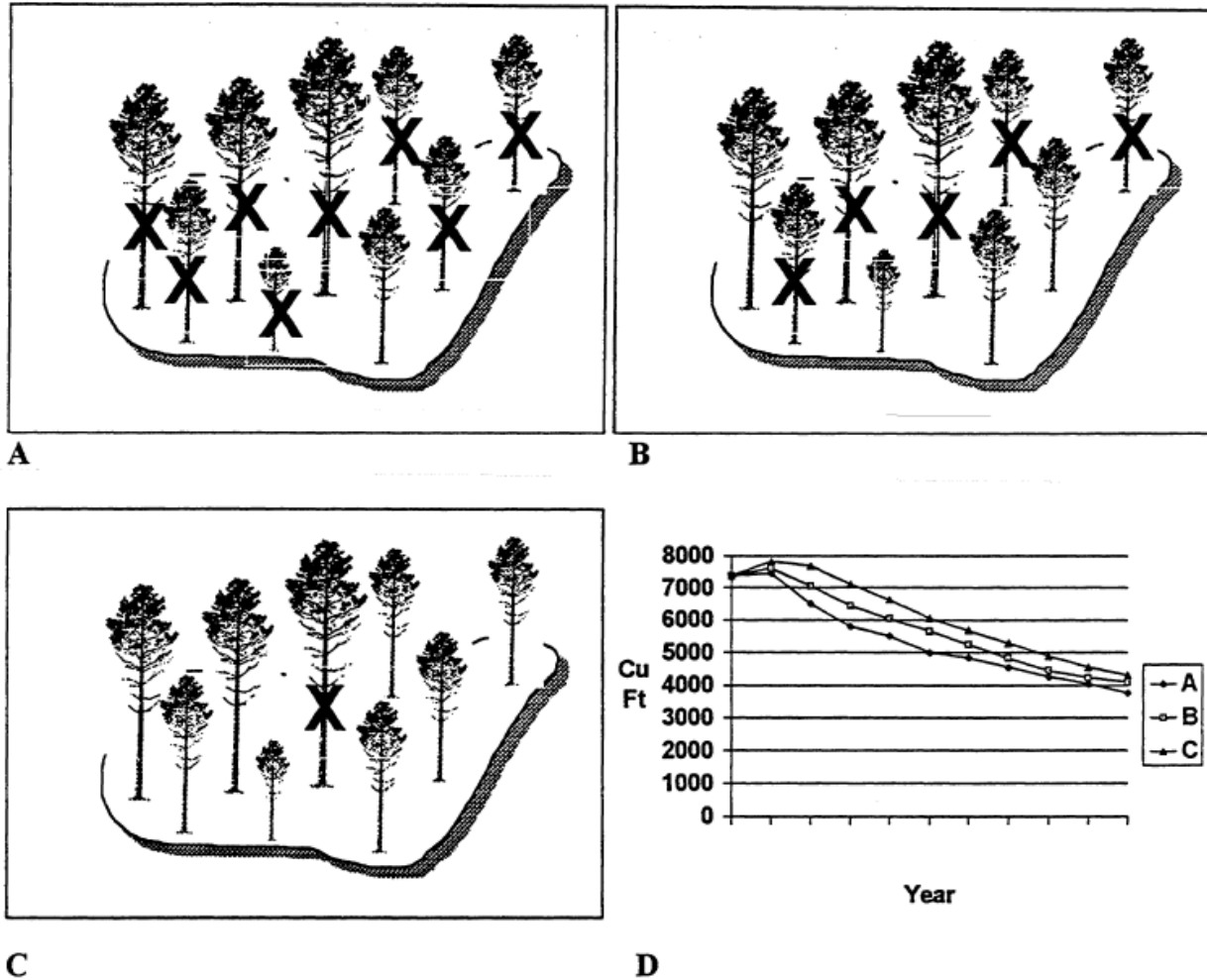


Figure 14. Three FVS runs are made in a stand with 5 root disease centers. In each run the ratio of infected (trees with X's) to uninfected trees per acre is altered while all other parameters are kept the same. In A, the ratio is 9:1 infected to uninfected trees; in B, the ratio is 4.5:4.5; and in C, the ratio is set at 1:9. Differences in relative outputs, portrayed in D, (Total Cubic Feet) are relatively small.

What happens when root disease is so scattered that individual centers seem impossible to delineate?

Helpful Hint #2:

Talk to your local pathologist, or get to know the root disease conditions by stand type. You might find that root disease is so scattered over an area it is impossible to map where one center ends and the next begins. Or, your pathologist may fill you in on information they have about how extensive inoculum is in non-symptomatic trees. As such, you may be better off running the entire stand as a single center, with root disease area equal to stand area. **THEN, information on the number of infected trees versus uninfected trees becomes much more critical.** Your stand exam

plots must represent the root disease conditions that are out there. That means, care must be taken to identify those trees with identifiable root disease AND those trees within 30 feet of known root disease which are considered susceptible species. In this case, the defaults used by the model for uninfected versus infected trees may not be adequate.

How can surveying methods be improved to gather better information?

Helpful Hint # 3:

If you can afford the Rolls Royce (Land Rover, or Infiniti) of stand examinations, tighten up your sampling intensity so that you are able to pick up information about sporadically distributed root disease pockets in your data. For most situations, a 1 plot per 5 acre intensity will not provide you with the root disease data you need. That sampling intensity was designed to give you confidence about your healthy tree information. So, work out a compromise in sampling where you don't spend extra money and time acquiring expensive information (tree heights, ages, growth), but you do gather extra data on root disease area. Here is one sampling scheme that we've used in the Pacific Northwest:

- 1) Lay a grid over the area to be sampled (Fig. 16) indicating the locations of routine stand examination plots where data is gathered according to standard procedures. Data acquired on these plots include species, diameters, crown ratio, crown class, damage and severity, and a sample of ages, heights, and growth.

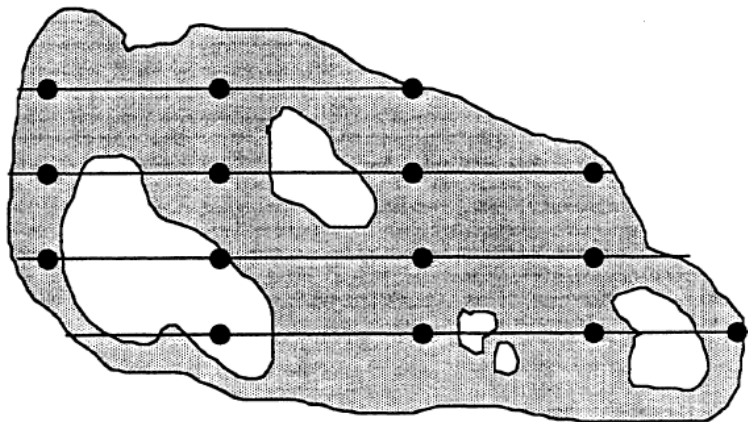


Figure 15. Grid of lower intensity plots used to gather "green tree" information.

- 2) Lay another grid over the same area that is more intensive (Fig.17). Use these additional or supplemental plots to gather data on root disease areas when those pockets are encountered. Tally the plot trees according to the same sampling instructions as the standard plots (BAF or fixed area) but only gather the ESSENTIAL information about them such as species and root disease damage and severity codes. Use this supplemental information to beef up your estimate of uninfected vs infected trees inside the centers. The supplemental plots also ensure that stopping at a point on the ground and looking carefully around that plot center for root disease will make your map of root disease area more accurate

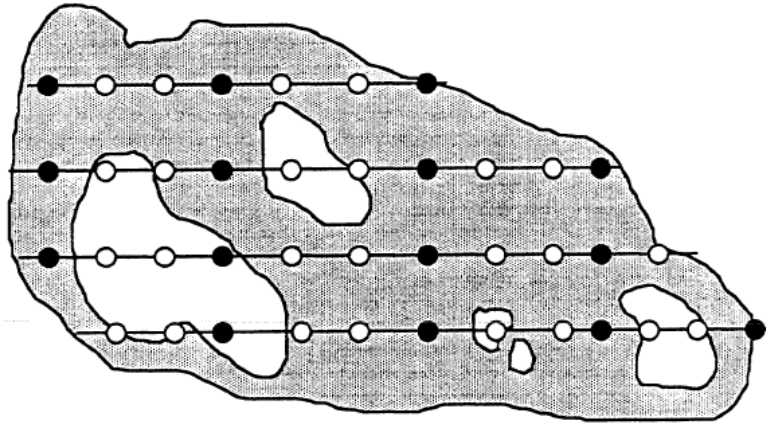


Figure 16. Intensive grid with “green tree” plots in black and supplemental plots in white. Supplemental plots provide additional information on root disease in this particular stand.

Whether it comes from plot data, walk through examinations, or the advice of experts, there is no getting around the need for good root disease data. For your model run to be meaningful, you must have some idea of which disease you are dealing with, where the root disease is, how it is distributed, and what species are being affected

Damage and Severity Codes

The WRD model does recognize and process damage and severity codes on the input FVS tree records. So, if you have the luxury to collect and use root disease information at the tree level, you will need to use the appropriate damage and severity codes shown in the table below. The damage code 60 is a non-specific root disease code, whereas the code 61, 62 and 64 are specific and indicate Armillaria, Phellinus and Heterobasidion (both P-type and S-type), respectively. The significance or importance of using the specific root disease codes is dependent on the needs and uses of the data. As far as the model is concerned, if you use the RRTREIN keyword instructing the model to process and use the root disease damage codes that are present in the input tree records, it will handle the damage codes exactly as specified. Therefore, if the non-specific code of 60 is used, the tree records with that code will be recognized by the model as diseased regardless of the disease type specified (RRTYPE keyword) for the model run. If the specific codes are used, those codes will be recognized by the WRD model only when the corresponding root disease type is being modeled. If input FVS tree records contain damage codes of 61, the trees with that code will only be recognized as diseased when the modeled disease type is Armillaria. Those same trees (damage code 61) will be interpreted as disease-free if the modeled disease type is changed to Phellinus or Heterobasidion .

The severity codes indicate the suspected or visible level of root disease infection on the tree. The severity codes, of which there are only four, all get translated to a proportion of root system

infected. The specific proportion of infected root system is based on the proportion of root system infection causing death that is assigned for the tree species. A severity code of 00 or 01 indicates that the tree is not showing outward signs or symptoms of root disease, but is within 30 feet of an obviously infected tree. Additionally, the size of the tree affects its classification when assigned a severity code of 00 or 01 where trees with DBH 5 inches or less are classified as uninfected but within a disease center. That places their likelihood of future infection higher because it will become infected by the inside disease center spread instead of by disease center expansion. Trees with DBH 5+ inches are suspected of having been infected by the disease, just not displaying symptoms yet. This level of infection is placed at 10% of the proportion of the root system infection that causes death for the tree species. Severity code 02 is given to trees on which root disease symptoms have been detected. This level of infection is placed at 65% of the proportion of the root system infection that causes death for the tree species. The Severity code of 03 is given to trees that are showing root disease symptoms and crown deterioration. This level of severity is translated to 75% of the proportion of root system infection that causes death of this tree species.

Damage Code	Severity Code	Description
60	N/A	Non-specific root disease
61	N/A	Armillaria
62	N/A	Phellinus
64	N/A	Annosus (both P-type and S-type)
N/A	00,01	Within 30 feet of root disease infected tree. (10% lethal infection*)
N/A	02	Symptoms of root disease detected. (65% lethal infection)
N/A	03	Symptoms of root disease and crown deterioration detected. (75% lethal infection)
N/A	N/A	* Additional root disease severity code notes: Sev 01 and DBH <=5.0 interpreted as uninfected small tree inside disease center. Sev 00 or 01 and DBH >5.0 interpreted as infected large tree.

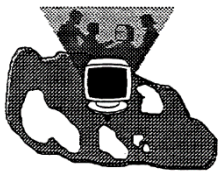
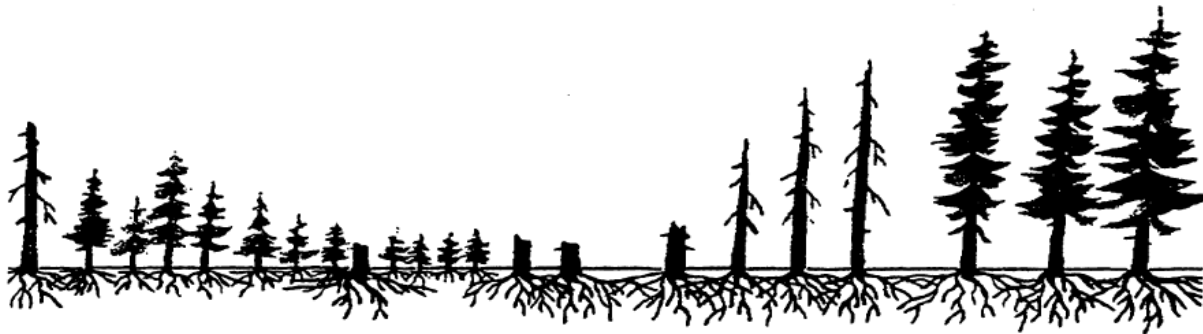
Illustration 1. Input data damage and severity codes recognized by Root Disease Model.

There is one final and critical detail you must ensure is in place in order for the WRD model to process the damage and severity codes on the input tree records; one more instance where keyword order is important. The WRD model keywords must be processed prior to FVS processing the input tree records. The default behavior of Suppose when assembling the keywords for a projection is to place the block of keywords that reads the input data as the first item. The problem with this is that FVS processes the tree records prior to the WRD model being instructed to process the damage codes. The WRD model does not recognize that is the case and does not issue an error when the RRTREIN keyword is processed. The resolution to this is simple, but the user must be aware and manually perform the action. In the “Simulation file contents” pane of Suppose, under the group “All Stand” there is an item labeled “From Database” which contains the keywords that direct the reading of the stand and tree data from the input database. You need to

move this down to the end of the keyword list. Select the item "From Database" and click button "Cut". It is very important that you keep this item associated with all the stands in the run. Under the group "All", select the last item in the list and click button 'Paste "From Database"', then select "After". Now, the keywords that instruct FVS to read the input data will be processed after the WRD model knows that it needs to interpret the damage and severity codes during this process.

Chapter 4

Root Disease Inventory: Choosing Model Keywords



It is possible to execute a successful run of the WRDM without providing any information on the root disease conditions that currently exist in the stands you are interested in. The model has default values built in, but these may or may not make any sense when you consider the actual conditions. There are also several inventory keywords to choose from depending on the type of information you have. Be aware that some keywords override others and that keywords used in different combinations may alter the results.

What are the basic inventory keywords and their defaults?

SAREA:

The Stand Area in acres. The default value is **100 acres**.

RRTYPE:

The root disease type by species. Currently the WRDM allows you to choose between Armillaria root disease caused by the fungus *Armillaria ostoyae*, laminated root rot caused by *Phellinus sulphurascens*, or Heterobasidion root disease (S-type or P-type) caused by *Heterobasidion irregulare* or *H. occidentale*. The model will default to **Armillaria root disease**. If all three root diseases occur within the same stand, you must choose between them. You cannot run all diseases at once.

RRHOSTS:

When running Heterobasidion root disease, each tree species represented in the FVS variant is assigned as host to P-Type or S-Type or designated non-host to the disease. The default host assignments can be changed and if you choose to do so, this reassignment must take place prior to the WRD model initialization. Simply put, the RRHOSTS keyword must precede the RRINIT keyword in the keyword list.

RRINIT:

Initializes current stand conditions. You are asked to provide information on:

Root disease center placement: If you have coordinates which locate individual root disease centers, you may enter them here. Otherwise, the model will randomly scatter centers throughout the stand. The default is **random**.

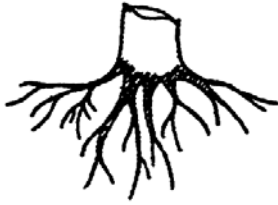
Number of centers: Enter the number of root disease pockets you found as a result of the field examination. If it was difficult to distinguish where one pocket stopped and another started, you may be better off running the entire stand, or that portion of the stand, as one center. The default is **20 centers**.

Number of infected trees per acre inside root disease centers: If you have information on the density of infected trees per acre inside the centers, you may enter it here. You can enter either the actual number of trees OR the percentage of the total. This may be obtained by separately inventorying the root disease pockets or it may come from the treelist (see RRTREIN keyword). The model will calculate **50% of the average stand density (inside and outside centers)** and enter that number as the default value.

Number of uninfected trees per acre inside root disease centers: As above, if you have separated out the information on stand density inside and outside disease centers, this is the place to enter the number of uninfected trees per acre you have calculated for inside the centers or the percentage of the total. Or, you can have the model supply this figure from the treelist (see RRTREIN). The model will calculate **50% of the average stand density (inside and outside centers)** and enter that as the default value.

The two fields above (infected and uninfected trees) are used by the model to calculate a proportion of trees infected inside centers. If you believe that 30% of the trees are infected and 70% are uninfected, enter 30 and 70 in the fields OR enter the actual numbers.

Level of root system infected: You may supply information on the average proportion of infected root systems for trees in the stand. (*HOW AM I SUPPOSED TO KNOW THAT??*) The model will take the proportion you provide, designate it as the mean of a truncated binomial distribution (*WHAT??*) and randomly assign a number from that distribution to infected trees within centers. The model can also obtain these proportions from the treelist (See RRTREIN). The default value is **10%**.



Before you ask where to procure the x-ray vision allowing you to see underground at the root systems or what sorts of statistical mumbo-jumbo is going on, relax, and remember this is a model. A lot of great minds, and some who have just looked at a large number of dead tree root systems (maybe they should get a life...) arrived at averages or defaults that they feel work. Your local pathologist can provide you with information on when defaults are appropriate, and if not, what numbers to plug in by species, plant associations, root disease type, etc.

Total acres in root disease: Enter the number of acres in root disease. The default value is **25% of the total stand area (SAREA) entered as number of acres.**

RRTREIN:

If you have tree data which includes information on the status of root disease on individual trees, -that is, you recorded root disease damage and severity codes during the stand examination-- you can use **RRTREIN** to direct the model to use this information; otherwise, the root disease damage and severity codes will not be processed. Values calculated from stand examination data (using **RRTREIN**) will override values entered with **RRINIT**.

When using **RRTREIN**, a very short report will be written to the main FVS output file directly following the FVS Activity Schedule report. It will report the number of tree records having damage codes indicating root disease infection; tree records not having a root disease damage code will be reported as uninfected; and tree records marked as dead (tree history code 7 or 9) and having a root disease damage code will be reported as infected stumps. These numbers are record counts and not the trees per acre values represented by the tree records.

Following the tree record report is a report of infected stumps. These values are for the entire stand; therefore, the values depend on the stand area defined by the **SAREA** keyword. They will include input data of dead tree records with root disease damage codes as well as additional diseased stumps included by the use of the **STREAD** keyword. The stump count entered on the **STREAD** keyword is the raw number of stumps in the entire stand and not a per acre value. It is unaffected by the **SAREA** keyword.

Table of root disease information read from input shown below is for a stand of 100 acres in size. The top portion of the table is simply record counts from the input tree data records having root disease damage codes present and the bottom portion reports the infected stumps in 5 broad size classes for the entire stand.

SUMMARY OF DISEASE INFORMATION READ IN ON INPUT

DISEASE TYPE: A
NUMBER OF INFECTED TREE RECORDS IN DISEASE PATCHES=
26.
NUMBER OF UNINFECTED TREE RECORDS IN DISEASE PATCHES=
23.
NUMBER OF INFECTED STUMP RECORDS IN DISEASE PATCHES=
2.

NUMBER OF INFECTED STUMPS

SIZE CLASS	RESINOUS	NON-RESINOUS
0- 12"	303.	0.
12- 24"	99.	0.
24- 48"	0.	0.
48-100"	0.	0.
>100"	0.	0.

Illustration 2. Summary of root disease information from processing of input data damage and severity codes.

The **number of infected trees per acre inside root disease centers** will come directly from the list of trees with root disease damage codes. The **number of uninfected trees per acre** will be calculated from those trees which do not have root disease damage codes. The **level of root system infected** will be based on the root disease severity rating given to individual trees and on tree species. If a tree has a **Severity Code 1** (within 30 feet of known root disease) recorded, the level of root system infected will be a random value chosen from a truncated binomial distribution based on a mean of **10%** of that species infection level at death. If **Severity Code 2** (pathogen or diagnostic symptoms detected) is attached to a given tree, the level of root system infected on that tree will be a random value chosen from a distribution based on a mean of **65%** of that species infection level at death. With a **Severity Code of 3** (pathogen detected AND symptomatic crown) associated with a given tree, the level of root system infected is a random value chosen from a distribution based on a mean of **75%** of that species infection level at death.

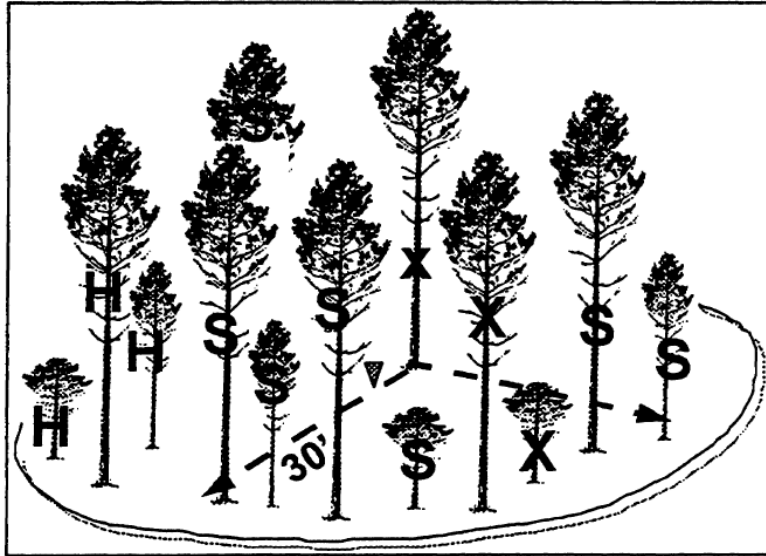
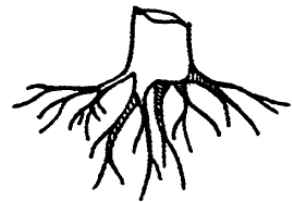


Figure 17. Trees with X's indicate Severity Code 3. Trees within 30' of X trees are suspect trees and are given a Severity Code of 1 during stand examinations and inventories. Trees with H are outside the 30' perimeter and are considered healthy.

For example: In the model, a Douglas-fir with a damage code indicating Armillaria root disease and a Severity Code of 3 will have somewhere in the statistical neighborhood of 60% of its root system infected. That's because the root system infection level at time of tree death for a Douglas-fir with Armillaria root disease is 0.80 and $0.80 * 0.75 = 0.60$ (INFKILL controls the species-specific infection level at time of death within the model). If that same Douglas-fir was given a severity code of 2, its level of root system infected would be approximately 52% ($0.80 * 0.65 = 0.52$).



On the other hand, if a ponderosa pine was given a severity code of 3, its level of root system infected would be much different. The proportion of root system infected at death for a ponderosa pine with Armillaria root disease is 0.30. Therefore the level of root system infected would be approximately 22.5% ($0.30 * 0.75 = 0.225$).

PLREAD:

This keyword allows you to designate (by plot number) which plots in a stand examination are within root disease centers. Once these plots are listed, the model will use the tree data only from these designated plots to provide information to RRINIT. Any trees with root disease codes in the treelist which are NOT on identified plots will be ignored.

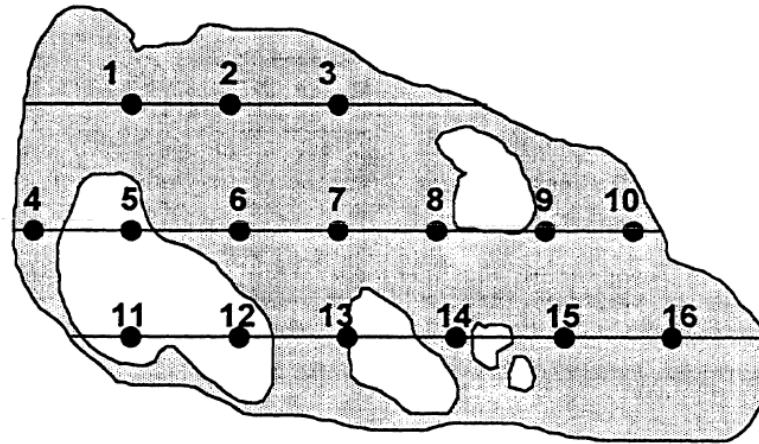
Important: If the keyword PLREAD is used, the keyword RRTREIN should also be included in the keyword set.

Here's how it works: The **infected trees per acre inside the root disease centers** will be calculated from trees with root disease damage codes that are located within the identified plots. The **uninfected trees per acre inside root disease centers** will be calculated from those trees inside identified plots that do not have root disease damage codes attached to them. The level of root system infected will be based on Severity codes attached to trees within the identified plots in the manner described in RRTREIN. The total acres in root disease will be based on the stand area multiplied by the proportion of plots that are identified as within root disease centers.

For example (Fig. 19): 16 stand exam plots are systematically placed within a 51 acre stand. Four of the plots fall within root disease centers; plots numbered 5, 11, 12 and 13 are typed in when PLREAD is used. The model will calculate that this stand has a root disease area of 12.75 acres based on $51 * \frac{4}{16} = 12.75$.

CAUTION: If you use the keyword PLREAD, the model will always calculate area in root disease from the proportion of infected plots to healthy plots. Even if you type the number of infected acres into RRINIT, it will be overridden by the calculated acres.

So, you must be thinking to yourself, when should I use PLREAD? Don't I risk giving up information about a sensitive variable (Area infected) to get information about a relatively insensitive variable (Number of trees uninfected versus infected)? The most appropriate time to use PLREAD is when you run the entire stand as 1 center. If you have more than 1 center in the stand, you are better off providing your own estimate of area affected.



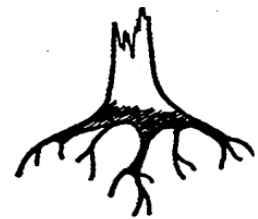
A

B PLREAD
 5
 11
 12
 13

Figure 18. A indicates where root disease pockets are located (white areas) in a stand where 16 Stand Examination plots were installed. B indicates how the keyword PLREAD would look within a WRDM keyword stream.

STREAD:

The keyword STREAD allows the user to supply additional information about fungal inoculum that might not otherwise be picked up during standard stand examination procedures. For example, if crews were instructed to check stumps (not normally considered in routine stand exams) to see if they were colonized by the root disease fungi and collect data about those stumps, this keyword allows the user to include that information when describing initial conditions. If standing dead material was not considered in the exam, information about that inoculum might also be entered here. If a standard stand exam was completed without root disease information, any additional exams or walk-through survey data on infected stumps and standing dead can be included. Just remember that the WRDM calls anything that is dead and still has its roots in the ground a stump.



Tree (stump) Species to Infect: Enter the species of the stump or snag.

Use the Help screen (Shift-F1) to obtain a list of species codes appropriate for the FVS variant you are working with.

Stump Diameter Class Code: You can group the stumps by diameter classes.

- Code 1 = up to 12" diameter
- Code 2 = 12 – 24" diameter
- Code 3 = 24 – 48" diameter
- Code 4 = 48 – 100" diameter
- Code 5 = 100"+ diameter

Number of Stumps in Infested Area: Enter the number of additional infected stumps to include in the run. *Note: this is the number of total inoculum sources you are adding, NOT the stumps per acre.*

REALITY CHECK:

Getting the Information into the Model

- 1) You have a stand examination for an area that adequately reflects tree measurement data. You know there was no information collected regarding root disease in the exam (the crew left the office without their pulaskis) yet you know that root disease occurs commonly within this plant association.

You build a FVS run and include the WRDM via Suppose interface options, either by the Model Modifiers, Modify Western Root Disease Model, Initialize Root Disease screen or with individual keywords (SAREA, RRTYPE and RRINIT) and accept default parameters for Armillaria root disease, since you have no specific information to provide. When you look at the keyword set, you will see one or more groups of keywords bracketed by the keywords RDIN and END, indicating WRDM keywords.

What does the Model do?

The stand will be 100 acres in size with either 1 or 20 Armillaria root disease centers occupying 25 acres. The model will randomly place the center(s) in the 100 acres. Within those centers, 50% of the trees per acre will be infected and the remaining 50% will be healthy. All infected trees will have a small percentage of their root system infected (approximately 10%).

The keyword stream should look like this:

FVS keywords

-
-
-

RDIN

.

(Western Root Disease Model keywords)

.
 END
 ●
 more FVS keywords
 ●
 ●
 Process
 Stop

CAUTION: DO NOT TRY THIS AT HOME! Why? We rarely recommend data-free analyses when making resource management decisions. Know something about the conditions in which root diseases operate in your area. Model behavior is different depending upon which fungus you are dealing with. Also, the model is fairly sensitive to how the root disease is distributed (is it one big center or many small ones?) and to the amount of area affected. You may find that the proportion of the stand affected is much smaller for certain vegetative conditions than others. So, get out there, walk around, and come back with better base information!

2) With the appropriate map, you determine that the area of the stand you are interested in is 32 acres. In the field, pulaski in hand, a walkthrough examination provides you with information on current root disease conditions. Laminated root rot has created 5 root disease centers. These centers total 5 acres in size. You also put a call in to your local pathologist who tells you that 10% root infection levels is low for the vegetative conditions you are modelling. She suggests that you use 45% as an average root infection level.

In the FVS run, you modify the Initialize Root Disease entry in Suppose or the individual keywords **SAREA**, **RRTYPE** and **RRINIT**. **RRTYPE** is set to 4 to indicate phellinus (laminated root rot). The number of centers is 5. You do not have individual tree information so you must use the default values for the number of infected and uninfected trees per acre inside the centers. Average root infection is 45%. Finally, the acres in root disease is 5. You now have a much better picture of the current conditions, and the numbers that come out of the model should better reflect reality.

The FVS keyword stream looks like this:

FVS keywords
 ●
 ●
 RRIN
 SAREA 32
 RRTYPE 4
 RRINIT 0 5 (blank) (blank) .45 5 4
 End
 ●
 more FVS keywords
 Process
 Stop

3) You are flush with money for new stand examinations, and your crew has gone through an intensive course to learn to recognize and identify root diseases. You know that the stand is 45 acres in size. The exam is intensive enough that root disease pockets are adequately represented in the plot data. Root disease damage codes with the appropriate severity ratings are collected during the stand exam. The crew collected information on infected stumps on the plots (stumps are usually ignored by stand exam procedures). The crew also drew a map of 4 root disease pockets as they walked through the stand. They estimated from the grid that the pockets represent 16 acres. You can use the default for proportion of root system infected in this plant association.

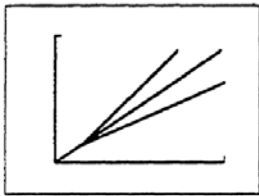
The WRDM keywords look like this:

```

RRIN
RRTYPE      4
RRINIT      0      4      (blank)      (blank)      .300      16.00      4
SAREA      45.0
RRTREIN
STREAD      4      1      45
             2      1      22
             4      2      11
             4      3      5
End

```

Chapter 5 When to Adjust Model Parameters



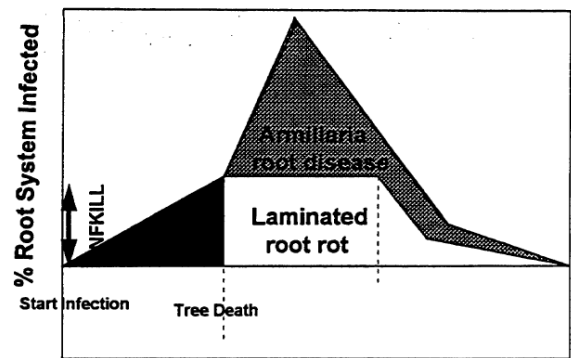
If you keep in mind that the WRDM was built in a large think tank of pathologists, silviculturists, and programmers, you will realize that the functions that spread and intensify root disease in a stand are based on best estimates, west-wide averages, or are specific to a location where reliable data were available. By its very nature, the output based on defaults is NOT meant to represent conditions on all sites. You can modify most of the functions which guide root disease behavior through keywords. Adjusting these keywords may bring reality to the model projection.

For example, Armillaria root disease very effectively kills ponderosa pine of all shapes and sizes at some locations on the east side of Washington and Oregon. In other locations, ponderosa pine is very tolerant of Armillaria root disease. In fact, it is recommended as a preferred species for managing this disease. If you are modeling the effects of Armillaria root disease on ponderosa pine where ponderosa pine tolerates the fungus, you can adjust the model functions for ponderosa pine so that the proportion of root system infected that is required for a tree to die is greater than the default and that the time it takes to reach this critical proportion is longer. You can also make it more difficult for transmission of the fungus from one root system to the next.

The following keywords are frequently used to modify model functions because they have the greatest effects on model behavior:

INFKILL:

Every tree species has a certain proportion of root system that must be colonized by the root disease-causing fungus before that tree species dies. The keyword INFKILL controls that proportion. Default values reflect broad scale resistance among species and may vary between root diseases. To change these values, the user defines the root disease that is modelled (Heterobasidion S-type, Heterobasidion P-



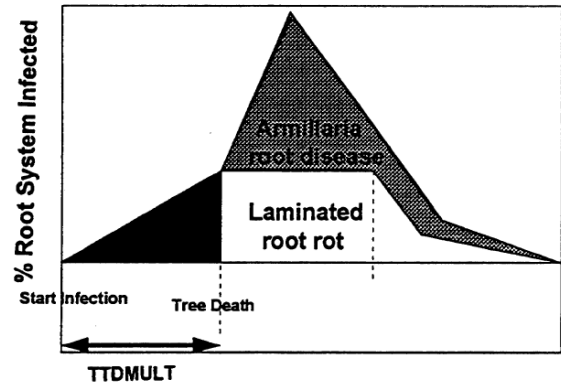
type, Armillaria root disease or laminated root rot) and then designates the tree species to modify. If only 1 species requires changing, the FVS numeric or two-character alpha code for that tree species is entered. Then the new critical proportion is entered. (If a list of variant-appropriate species and their default proportions is needed, the keyword with species and proportion fields blank can be entered. The complete species list with associated values will be written in the FVS output when the run is executed.) If more than one species is modified, the user should enter **ALL** or **0** in the species field and enter the value for each species in order separated by commas. This is referred to as the supplemental record and can span more than one line (record) in the keyword file. So, just do it in a format that makes it easy for you to track, maybe values for 10 species per line.

INFMULT:

INFMULT essentially controls infection probability, or how easily disease is transmitted from one tree to another if their root systems overlap. It is the most important keyword to tweak if you need to adjust species susceptibility as you move from location to location, from plant association to plant association. As with INFKILL, this keyword can be adjusted by root disease type and for one or more species.

TTDMULT:

The user can change the time to death multipliers for a given species by using this keyword. In other words, how long from when a tree first becomes infected until it reaches the proportion of root system infected required for a tree to die is altered. So if, in a given location, a species can be infected but seems to take longer to die than what the default models (it “stands up better to the fungus”), that can be represented.



The keyword has similar properties to INFMULT and INFKILL, allowing you to change values for individual species or all species at one time with the use of a supplemental record. It does require that you choose a date at which to apply the value change. In this way, if changes in susceptibility result from stand activities such as harvest or fire, the user has the opportunity to control the timing of these changes.

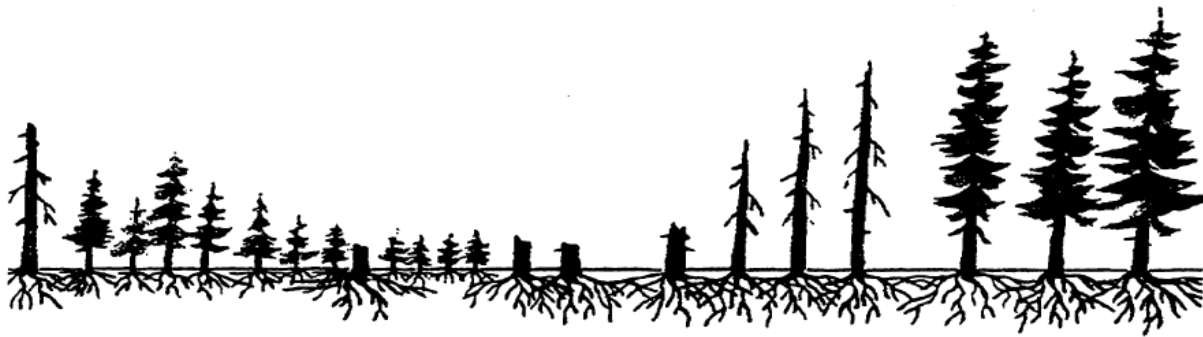
Other model modifying keywords exist. They are not as powerful as the ones mentioned above, but they do control specific equations within the WRDM.

CAUTION! Modifying the WRDM may be entirely appropriate as we move among different stand conditions in the Region. BUT this should **NOT** be done in a vacuum. We do not advocate making arbitrary changes to the model modifiers without good reason. We strongly suggest that you work with your local pathologist to determine under what circumstances and to what degree, these adjustments are made.

Pathologists monitor root disease on a series of permanent plots located throughout Washington, Oregon, Idaho and Montana for the specific purpose of validating model behavior and calibrating the model to local conditions. Most of these plots were established through the Westwide Pest Trends-Impacts Plot Project, which started in 1990. For information on the location of plots and the kinds of vegetation data being gathered, contact your local pathologist.

Chapter 6

Default Model Parameters



The Western Root Disease Model parameters the user can modify directly via keyword, or modify the affect with a multiplier, are shown in Appendix C. These are straight forward values which allow the user to understand the direction and magnitude that a change to a value will have on the behavior of the model. The user should first look at the appropriate variant species list in Appendix B to determine the appropriate species to reference in the Appendix C tables which are species and disease specific parameter default values.

Within the Western Root Disease Model there are 40 individual tree species recognized. This does not cover all tree species represented by FVS in all variants to which the WRD model is attached. So, where there are not direct matches for the FVS species, a surrogate WRDM species is used, one that exhibits similar root disease effects. Each tree species is assigned to a specific Heterobasidion root disease type (P-type or S-type) or non-host. Both P-type and S-type Heterobasidion use the same default disease characteristics parameters but due to the tree-species specificity of P-type and S-type, they are maintained, modeled and reported separately by the WRD model. The FVS variants species mappings for the WRD model for all variants which have this extension available are shown in Appendix B: Variant Species Lists at the end of this document.

All tree species represented in the root disease model are considered host to armillaria and phellinus. A category of non-host to disease is not maintained for armillaria and phellinus. The degree to which a tree species is susceptible or affected by either disease is reflected in the disease characteristics parameters assigned. Those basic parameters are: likelihood of infection (INFMULT), level of infection causing death (INFKILL), the relative time to death (TTDMULT), and level of root colonization by the disease after death (INFCOLO). The colonization of root system after a tree's death is a representation of the tree specie's ability to advance or propagate the disease to other nearby trees.

Chapter 7

Other Challenging Situations



The WRDM is designed to account for root disease behavior after harvesting stands and also to depict the effects of other agents such as bark beetles or windthrow. Doing so requires that the user understand how the functions work, what information is required, and their strengths and weaknesses.

Bark Beetles



In the real world, that is the forested one, bark beetles are often found in association with root diseased trees. Some bark beetles, such as fir engraver beetle (*Scolytus ventralis*) or Douglas-fir beetle (*Dendroctonus pseudotsugae*), maintain endemic population levels by attacking trees weakened because of root disease infection. In these situations it is appropriate to model the effects of bark beetles along with that of root disease. The WRDM allows this, with certain limitations. The WRDM is also designed to model certain types of bark beetles such as mountain pine beetle (*Dendroctonus ponderosae*) that are not as closely associated with root disease-infected trees.

Bark beetles are divided into 4 distinct groups or **TYPES**. The keywords which control their activity are found within WRDM keywords, NOT FVS keywords.

TYPE 1: Designed to represent mountain pine beetle on lodgepole pine and western pine beetle on ponderosa pine. It is triggered by stand density and tree diameter. This type of bark beetle event is not dependent on root diseased trees. The keyword **BBTYPE1** allows the user to set up the stand conditions that control the bark beetle activity. You can define the earliest year in which the bark beetle outbreak occurs (the default is 1), the tree species involved (default is lodgepole pine), the minimum DBH of trees eligible for attack (default is 8 inches), the minimum density of the eligible trees that must be present for the outbreak to occur (10 trees per acre (TPA) is the default value), and the mortality rate applied to all eligible trees (85% of eligible trees is the default). So, add the keyword **BBTYPE1** to your WRDM keyword set if you are interested in seeing how beasts like mountain or western pine beetles operate under your stand conditions. Once an outbreak has occurred, there is an option for recurrence, if the trigger conditions are again met later in the simulation.

TYPE 2: Designed to represent Douglas-fir beetle on Douglas-fir. This bark beetle event will only take place if a windthrow event occurs. (See the following discussion on windthrow.) Douglas-fir beetle populations build up in stands after major windthrow events and bark beetle behavior in the WRDM depends on the density of windthrown hosts. Even though you realize that endemic populations are associated with root disease pockets, *THAT IS NOT MODELED HERE!* This is intended to represent a bark beetle outbreak event. The input parameters for the keyword **BBTYPE2** are identical to those for **BBTYPE1**. The default values differ because these types of bark beetles have very different behavior. Once an outbreak has occurred, there is an option for recurrence, if the trigger conditions are again met later in the simulation.

TYPE 3: Designed to represent a bark beetle such as fir engraver that is very closely associated with root disease-affected trees. Once again the input parameters for the keyword **BBTYPE3** are similar to the other bark beetle types, and once again the default values are also very different. In addition to the information asked for in the other bark beetle keywords, **BBTYPE3** asks for information on the minimum proportion of roots infected to make trees eligible for attack (the default is 30%). Once an outbreak has occurred, there is an option for recurrence, if the trigger conditions are again met later in the simulation.

TYPE 4: Designed to represent a bark beetle such as fir engraver that is very closely associated with root disease-affected trees, but will also kill trees that have no root disease infection. The input parameters for the keyword **BBTYPE4** are much the same as the **BBTYPE3** keyword, but includes an additional mortality rate for eligible trees that have little or no root disease infection. IN ADDITION to the information asked for in the other bark beetle keywords, **BBTYPE3** asks for information on the minimum proportion of roots infected to make trees eligible for attack (the default is 30%). Once an outbreak has occurred, there is an option for recurrence, if the trigger conditions are again met later in the simulation.

The WRDM is the first of the insect and disease models to attempt a very simple form of multi-pest modeling. It's not perfect, but the reality is that in most cases, root diseases and other agents occur together in the same stands and sometimes their biologies are very interconnected. If you are dealing with mountain or western pine beetle in a more pure pine type and laminated root rot or Armillaria root disease do not occur in the stand you are modeling, or, if Douglas-fir beetle activity is a concern after a large windthrow event, it is more appropriate to use models specifically designed for those insects. Your local pathologist can put you in touch with the insect model expert for your area. (Don't be surprised if it is the same person!)

WINDTHROW

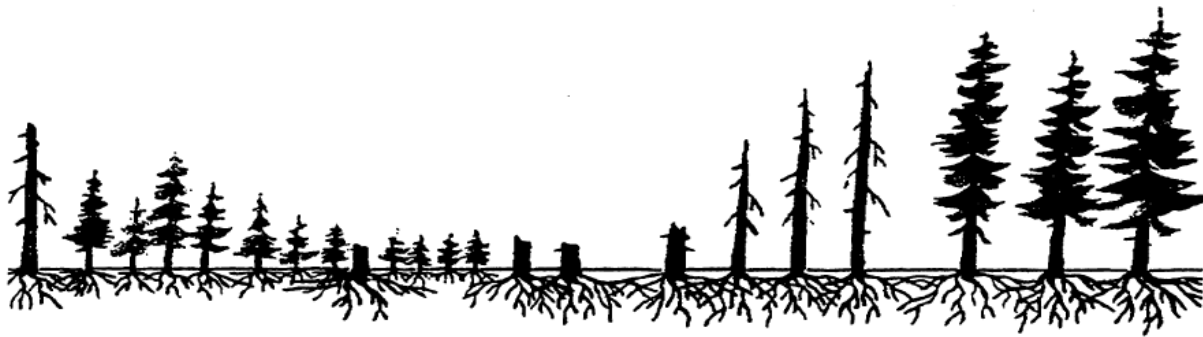
The WRDM also allows you to model windthrow. This may be particularly important when very long projections are made for stands in the Coast and Cascade Mountain Ranges where we know that wind events often occur. It is also essential to include windthrow when modeling a bark

beetle Type 2 outbreak (this bark beetle keyword requires a windthrow event in order to initiate).

The keyword **WINDTHR** is found within the WRDM keywords in the Other Agents group of keywords. When you include WINDTHR in the WRDM keyword set you must provide information on the earliest year or cycle that the windthrow can occur in (the default is 1), the proportion of stems that can be windthrown (0.0 is the default) and the minimum density of eligible trees necessary for windthrow to occur (default is 0.0). As you can see by the default values, you must have SOME idea of stand conditions where windthrow is likely to occur or it won't happen!

Chapter 8

Interpreting the Output



After all the hoops you have jumped through up to now, it is important to know where to find root disease information in the FVS output and how to interpret that information.

FVS output includes several indications that the WRDM has been included in the simulation.

- WRDM keywords and their values are included within the FVS “Options Selected by Input” section of the output.
- A summary table **specific to the root disease areas** is automatically generated.
- Detailed tables that are species specific can be generated by including the WRDM keyword **RRDOUT** in the WRDM keyword stream.
- The user can direct the WRD model to write these reports to the main FVS output file and/or the designated output database.

You may end up with more than you ever wanted to know about root disease in the stand. What is very important to remember is that root disease-specific output represents **only root diseased areas** in the stand--**NOT complete stand level information**. The stand level tables generated by FVS include the root disease areas. In order to know something about the healthy areas, that is the areas outside root disease pockets, you must work with both summary tables and use your subtraction skills.

Options Selected by Input:

Within the FVS output you will find all of the FVS keywords used in the simulation, including the WRDM keywords that were used to describe the initial root disease conditions in the stand. Root disease keywords start with **RDIN** and end with **END**. The input parameters you selected will all be reported and described. If the simulation results in stand characteristics that don't make sense to

you, check the keywords to make sure the root disease conditions are accurately portrayed. The example below has minor formatting modifications in order to print legibly on the page, but the content represents what you can expect to find in the main FVS output (.out) file which is a text file.

Another item of great importance with any FVS or extension option (keyword) that affects the processing of the input tree data, is the location within the keyword list. FVS processes the keywords in the order they exist in the keyword file. By default, Suppose places the input data reading keywords near the top of the keyword set. So, if an option/keyword that affects the processing of the input data occurs after the input data has already been read, it can't possibly influence the processing of the data. It is too late. What the user must do is relocate the data reading keywords to the end of the list. In Suppose, those keywords are identified in the **Simulation file contents** with the label **From Database**. Select the item **From Database** and Cut it, then select the last item in the **Group: All** section and Paste it. When prompted with options as to where to paste, select After. This will place the reading of the input tree data after all other FVS and extension options/keywords have been processed. In the sample FVS output below, the block of keywords DSNIN, STANDSQL, TREESQL and END would be relocated to precede the SPLABEL keyword.

```
FOREST VEGETATION SIMULATOR      VERSION 1778 -- INLAND EMPIRE EXPANDED
RV:04/07/16
```

```
04-29-2016  11:22:15
```

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

```
OPTIONS SELECTED BY INPUT
```

```
KEYWORD FILE NAME: ie_0023_Arm.key
```

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

```
KEYWORD      PARAMETERS:
```

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

```
COMMENT
```

```
Starting year for simulation is 2014
Ending year for simulation is   2114
Min and Max inventory years are 2014 2014
Common cycle length is         10
```

```
END
```

STDIDENT

STAND ID= 01160805050023
01160805050023 at Regional Training

Stand

SCREEN SUMMARY TABLE WILL BE PRINTED TO DATA SET REFERENCE NUMBER
6 AS RUN PROGRESSES.

STANDCN DATA BASE CONTROL NUMBER=212720010354

INVYEAR INVENTORY YEAR= 2014

NUMCYCLE NUMBER OF CYCLES= 10

DATABASE DATABASE KEYWORDS:

DSNIN DSN FOR INPUT CONNECTION IS FVS_Data.accdb
ODBC CONNECT STRING: DRIVER={Microsoft Access Driver (*.mdb,
*.accdb)};DBQ=C:\FVSData\Regional-Training\FVS_Data.accdb;UID=;PWD=
CONNECTION DATA BASE TYPE:ACCESS

STANDSQL STANDSQL COMMAND FOR INPUT CONNECTION: FVS_Data.accdb
SELECT *
FROM FVS_StandInit
WHERE Stand_CN= '%Stand_CN%'

STAND-LEVEL DATA BASE READ:
INV_YEAR: 2014
LONGITUDE: 115.4506
REGION: 1
FOREST: 16
DISTRICT: 8
COMPOSITE LOC: 116
LATITUDE: 47.5710

.
.
.

TREESQL TREESQL COMMAND FOR INPUT CONNECTION: FVS_Data.accdb
SELECT *
FROM FVS_TreeInit
WHERE Stand_CN= '%Stand_CN%'

COLUMN PROCESSING RESULTS:
STAND_CN WAS IGNORED
STAND_ID WAS IGNORED
STANDPLOT_CN WAS IGNORED
STANDPLOT_ID WAS IGNORED
PLOT_ID WAS BOUND
TREE_ID WAS BOUND

.

```

      .
      .
      PV_CODE          WAS BOUND
      TOPOCODE         WAS BOUND
      SITEPREP         WAS BOUND
      NUMBER ROWS PROCESSED:    53

END      END OF DATA BASE OPTIONS.

RDIN     WESTERN ROOT DISEASE MODEL OPTIONS:

RRRTYPE      ARMILLARIA    WILL BE SIMULATED.

SAREA      STAND AREA = 100.00 ACRES

RRINIT     ROOT DISEASE IS ARMILLARIA
           ROOT DISEASE INITIALIZATION KEYWORD; ROOT DISEASE CENTERS
ASSIGNED RANDOMLY
           INITIALIZATION WILL BE WITH USER-SUPPLIED DATA UNLESS THE
RRTREIN KEYWORD IS USED IN
           THE RUNSTREAM
           NUMBER OF CENTERS= 1
           50% OF TREES/ACRE IN THE DISEASED AREAS ARE INFECTED
           50% OF TREES/ACRE IN THE DISEASED AREAS ARE UNINFECTED
           PROPORTION ROOTS INFECTED=0.10 ;DISEASE AREA = 25.00 ACRES

END      END OF ROOT DISEASE KEYWORDS

***** WARNING: NO BARK BEETLES WERE SPECIFIED AND THE BBCLEAR KEYWORD
WAS NOT USED.
           BARK BEETLES ARE ON USING THEIR DEFAULT VALUES AS
FOLLOWS

BBTYPE1     TYPE 1 BARK BEETLE IS ON EVERY YEAR. SPECIES =10.; MINIMUM
DBH= 8.00 INCHES
           MINIMUM ELIGIBLE STEMS FOR EVENT = 150. STEMS/ACRE;
MORTALITY RATE = 0.100

BBTYPE3     TYPE 3 BARK BEETLE IS ON EVERY YEAR SPECIES = 4.; MINIMUM
DBH=10.00 INCHES
           MINIMUM ELIGIBLE STEMS FOR EVENT= 10. STEMS/ACRE ;
MORTALITY RATE = 0.88
           MINIMUM ROOT DISEASE INFECTION= 0.30

BBTYPE4     TYPE 4 BARK BEETLE IS ON EVERY YEAR SPECIES =10.; MINIMUM
DBH= 4.00 INCHES
           MINIMUM ELIGIBLE STEMS FOR EVENT= 1. STEMS/ACRE ;
INFECTED MORTALITY= 0.750
           MINIMUM ROOT DISEASE INFECTION= 0.40 UNINFECTED-WITHIN-PATCH
MORTALITY= 0.30

```



```
UNINFECTED-FRINGE MORTALITY= 0.15 UNINFECTED-NON-PATCH
MORTALITY= 0.01
```

```
RDIN WESTERN ROOT DISEASE MODEL OPTIONS:
RRDOUT DETAILED ROOT DISEASE OUTPUT WILL BE WRITTEN
BBOUT DETAILED BARK BEETLE MORTALITY OUTPUT WILL BE WRITTEN
END END OF ROOT DISEASE KEYWORDS
MGMTID
MANAGEMENT ID= ARM1
DATABASE DATABASE KEYWORDS:
END END OF DATA BASE OPTIONS.
SPLABEL STAND POLICY LABEL SET:
All, All_Stands, forest_type=221, Variant=IE
PROCESS PROCESS THE STAND.
```

Standard Output: Summary Statistics for Root Disease Areas

Whenever you run the WRDM you will receive a summary table that is specific to the root disease areas in the stand. You do not have to request this output. It indicates by cycle:

Disease Statistics

- Year of cycle
- Age of the Stand (based on FVS input)
- Disease type (P - Annosus P-type, S - Annosus S-type, A - Armillaria, W - Phellinus)
- Number of root disease centers
- Root disease area in acres
- Spread rate in feet per year. Note: If you are using the dynamic spread rate, this number should change somewhat from cycle to cycle. If you use a static spread rate, it should not.

Dead Tree Characteristics

- Stumps per acre. REMEMBER: the WRDM calls ALL dead infected trees "STUMPS" regardless of whether or not they were cut. So this column represents the density of dead infected material inside the root disease centers.
- Basal Area in square feet per acre of dead infected material (trees and stumps) inside the centers.
- Number of trees killed by root disease during the cycle.

- Volume losses in cubic feet per acre due to root disease.

Live Tree Characteristics

- Uninfected trees per acre inside the centers.
- Infected trees per acre inside centers. Note: if you supplied RRINIT with numbers or percentages, this number and the number of uninfected trees per acre should reflect that input in the starting year of the run.
- Average percent roots infected. The number appearing in the starting year should be the input you provided to RRINIT or the default value.
- Merchantable volume in cubic feet per acre represents that volume generated inside the root disease centers only.
- Basal area in square feet per acre represents live tree basal area inside centers.

Identifiers: (So you know which run is which when you compare outputs)

- Stand ID simply is the stand you are running according to the FVS input.
- Management ID is a 4-character identifier for the run that you provided using the MGMTID FVS keyword. We strongly recommend identifying different runs of the same stand using this keyword because it will appear in the Run Summary output.

```

*****
WESTERN ROOT DISEASE MODEL
*****
STAND ID= 01160805050023      MANAGEMENT ID= ARM1
SUMMARY STATISTICS FOR ROOT DISEASE AREAS (PER ACRE BASED ON DISEASED AREA ONLY)
-----
DISEASE STATISTICS      DEAD TREE CHARACTERISTICS      LIVE TREE CHARACTERISTICS
STUMPS      LOSSES FROM DISEASE
-----
NO OF      DISEASE      SPREAD      TOTAL      BA/      NO OF      VOLUME      UNINF      INFECTED      OVERALL
OF      AREA      RATE      /ACRE      ACRE      TREES      LOSSES      TREES      NO OF      NO OF      AVE      MERCH      BA/      NEWLY INFECTED
CENTS      ACRES      FT/YR      /ACRE      SQFT      /ACRE      /ACRE      /ACRE      /ACRE      TREES      %ROOTS      CU FT      ACRE      PROPORTION
YEAR      AGE      TYPE      /ACRE      /ACRE      /ACRE      /ACRE      /ACRE      /ACRE      /ACRE      /ACRE      /ACRE      /ACRE      /ACRE      INSIDE      EXPAND      TOTAL
-----
2014      0      A      1      24.85      0.00      0.0      0.0      0.0      0.0      183.0      183.0      11.4      5328.      186.      0.000      0.000      0.000
2024      10     A      1      25.10      0.53      4.2      6.6      112.1      68.8      137.8      109.8      21.6      5596.      188.      0.249      0.450      0.253
2034      20     A      1      25.58      0.63      35.2      49.3      82.4      1756.3      140.5      69.2      28.1      4490.      143.      0.323      0.446      0.328
2044      30     A      1      25.80      0.56      66.4      107.0      63.5      1822.8      99.1      31.8      47.5      2485.      80.      0.255      0.438      0.259
2054      40     A      1      26.12      0.83      58.7      109.1      53.6      1522.0      129.0      8.8      57.8      1169.      37.      0.321      0.432      0.324
2064      50     A      1      26.42      0.85      32.1      72.6      41.8      734.0      90.1      2.9      55.0      621.      20.      0.273      0.432      0.277
2074      60     A      1      27.04      0.90      9.4      30.6      16.3      312.2      126.3      1.9      38.0      567.      18.      0.146      0.429      0.163
2084      70     A      1      27.40      0.86      5.2      18.9      10.6      54.8      95.4      2.0      36.4      673.      20.      0.074      0.428      0.084
2094      80     A      1      27.64      0.91      3.0      10.5      2.8      80.0      137.9      1.5      35.2      729.      21.      0.017      0.426      0.025
2104      90     A      1      28.34      0.86      1.5      3.9      3.2      67.2      105.6      1.8      35.2      937.      27.      0.006      0.439      0.025
2114      100    A      1      28.69      0.94      1.3      3.7      3.6      61.6      175.6      2.2      36.1      1057.      29.      0.028      0.436      0.038

```

Species Specific Output

When you include the WRDM keyword **RRDOUT** in the run, you are requesting a detailed, cycle by cycle output table that provides you with information by tree species and diameter distribution for the root disease areas only. The output table includes:

- Disease type (P - Heterobasidion P-type, S - Heterobasidion S-type, A - Armillaria, W - Phellinus weirii).
- Area acres in root disease.

- Tree Species (FVS two-character abbreviations).

Killed trees.

- Percentile Points by DBH. Trees that die within the cycle are displayed by percentile distributions which indicate the dbh which is greater than that percentage of trees. In the example table below, in the year 2024, among the Douglas-fir (DF) killed during that cycle, 10 percent of the trees are .1 inch dbh or smaller, 30% of the trees are 0.3 inches dbh or smaller, 50% of the trees are 2.5 inches dbh or smaller, 70% of the trees are 2.7 inches dbh or smaller, 90% of the trees are 3.8 inches dbh or smaller, and the largest DF killed during the cycle was 11.4 inches dbh.
- Total trees killed per acre by species.

You can use the total number of trees in combination with percentile distributions to get a better picture of the numbers of trees that are being killed by species and size groups.

Alive Trees

- Percentile Points by DBH. Same as with the killed trees. This table includes both infected and uninfected living trees.
- Total Uninfected Trees per acre. The uninfected trees per acre by species for the root disease areas.
- Total Infected Trees per acre. The infected trees per acre by species for the root disease areas.
- Percent Roots Infected. The average percent of root system infected on infected trees.

```

*****
WESTERN ROOT DISEASE MODEL
*****
STAND ID= 01160805050023      MANAGEMENT ID= ARM1
DETAILED OUTPUT OF STAND ATTRIBUTES INSIDE ROOT DISEASE PATCHES
-----

```

YEAR	TYPE	AREA	ROOT DISEASE	SP	KILLED TREES				TOTAL KILLED TREES/ACRE	ALIVE TREES						TOTAL UNINFECTED TREES/ACRE	TOTAL INFECTED TREES/ACRE	% ROOTS INFECTED	
					%TILE	POINTS	BY DBH (INCHES)				%TILE	POINTS	BY DBH (INCHES)						
					10	30	50	70	90	100	10	30	50	70	90	100			
2014	A	24.9	DF	PP	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	2.2	3.5	15.1	26.1	183.0	121.7	12.09
					0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	61.3	9.95
2024	A	25.1	DF	PP	0.1	0.3	2.5	2.7	3.8	11.4	0.1	0.3	2.7	10.7	18.3	27.6	137.4	52.9	23.81
					0.0	0.0	0.0	0.0	0.0	0.0	12.0	12.6	15.7	19.3	21.6	31.8	0.5	56.8	19.51
2034	A	25.6	WL	DF	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.1	0.1	0.1	0.1	2.7	0.0	0.00
					0.1	0.6	3.9	12.1	18.6	24.0	0.1	0.1	0.6	4.1	18.5	29.4	130.6	37.4	30.58
					12.1	12.3	13.0	13.3	16.4	25.3	0.1	15.1	18.6	20.6	22.4	32.8	7.2	31.7	25.31
2044	A	25.8	WL	DF	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	1.7	0.0	0.00
					0.1	0.6	3.3	4.6	14.1	30.6	0.1	0.1	0.7	4.4	19.7	30.6	92.0	26.0	51.90
					12.8	15.8	19.1	21.5	22.7	26.2	0.1	0.1	18.9	20.5	27.1	33.9	5.4	5.8	27.35
2054	A	26.1	WL	DF	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	2.2	0.0	0.00
					0.1	0.8	3.8	16.0	20.4	31.5	0.1	0.1	0.1	0.3	4.9	31.5	112.8	8.2	60.39
					0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.1	0.1	0.1	0.1	2.2	0.0	0.00
					0.1	19.6	20.4	21.9	27.6	29.0	0.1	0.1	0.1	0.1	16.2	34.3	11.8	0.6	22.12
2064	A	26.4	WL	DF	0.1	0.1	0.1	0.3	0.3	0.3	0.1	0.1	0.1	0.3	0.3	0.3	1.4	0.0	0.00
					0.1	0.1	0.3	1.8	23.2	32.5	0.1	0.1	0.1	0.4	4.8	32.5	78.6	2.6	58.95
					0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	1.3	0.0	0.00
					0.1	0.1	0.1	0.5	33.1	34.5	0.1	0.1	0.1	0.5	16.7	34.5	8.8	0.3	15.61

2074	A	27.0	WL	0.1	0.1	0.1	0.4	0.5	0.5	0.0	0.1	0.1	0.1	0.1	0.1	0.5	6.8	0.0	0.00
			DF	0.1	0.1	0.6	2.2	23.5	34.1	15.6	0.1	0.1	0.1	0.3	2.3	34.1	108.1	1.4	44.65
			LP	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	3.0	0.0	0.00
			PP	0.1	0.1	0.1	0.5	13.8	35.4	0.5	0.1	0.1	0.1	1.1	21.5	35.4	8.5	0.4	15.68
2084	A	27.4	WL	0.1	0.1	0.1	0.1	0.6	0.7	0.0	0.1	0.1	0.1	0.1	0.3	0.7	4.3	0.0	0.00
			DF	0.1	0.1	0.3	0.9	5.9	35.9	10.2	0.1	0.1	0.3	0.6	4.4	35.9	82.4	1.5	42.65
			LP	0.1	0.1	0.1	0.1	0.4	0.4	0.1	0.1	0.1	0.1	0.1	0.4	0.4	1.7	0.0	0.00
			PP	0.1	0.5	1.0	13.7	20.1	36.2	0.3	0.1	0.5	1.0	14.5	23.6	36.2	7.0	0.5	16.97
2094	A	27.6	WL	0.1	0.1	0.1	0.1	0.1	1.0	0.0	0.1	0.1	0.1	0.1	1.0		4.9	0.0	0.00
			DF	0.1	0.5	1.5	6.3	23.4	36.5	2.6	0.1	0.1	0.1	0.3	1.8	36.5	125.0	1.1	41.59
			LP	0.1	0.1	0.1	0.1	0.1	0.7	0.0	0.1	0.1	0.1	0.1	0.7	0.7	2.1	0.0	0.00
			PP	1.1	14.0	14.7	17.3	24.4	37.0	0.2	0.5	1.1	2.2	16.8	24.8	37.0	5.9	0.4	17.37
2104	A	28.3	WL	0.1	0.1	0.1	0.1	0.3	1.1	0.0	0.1	0.1	0.1	0.1	0.3	1.1	3.1	0.0	0.00
			DF	0.1	0.1	0.5	2.5	21.4	37.3	3.0	0.1	0.1	0.3	0.7	3.5	37.3	95.7	1.3	42.02
			LP	0.1	0.1	0.1	0.4	1.0	1.0	0.0	0.1	0.1	0.1	0.4	1.0	1.0	1.2	0.0	0.00
			PP	2.7	15.1	19.0	22.7	25.8	37.6	0.2	1.2	1.9	14.7	20.5	26.0	37.6	5.6	0.5	14.92
2114	A	28.7	WL	0.1	0.3	0.3	0.3	0.5	1.3	0.0	0.1	0.1	0.1	0.3	0.5	1.3	3.0	0.0	0.00
			DF	0.1	0.1	0.5	1.5	20.3	38.3	3.5	0.1	0.1	0.1	0.1	1.4	38.3	164.3	1.7	42.69
			LP	0.4	0.6	0.6	0.6	0.6	1.4	0.0	0.1	0.1	0.1	0.4	0.6	1.4	1.8	0.0	0.00
			PP	2.2	15.5	21.9	25.3	28.7	38.1	0.1	0.1	1.7	14.5	20.1	26.4	38.1	6.5	0.5	13.83

Bark Beetle Output

When you include the WRDM keyword **BBOUT** in the run, you are requesting a report of the bark beetle activity included in the simulation. There are four types of bark beetle activity and each type is patterned after or intended to represent a different bark beetle with regard to root disease presence and intensity in the stand. These activities are identified by keywords BBType1, BBType2, BBType3 and BBType4. This detailed, cycle by cycle output table reports mortality information by tree species and diameter distribution in trees per acre for three tree categories. Those categories are: infected trees inside disease centers (in-inf), uninfected trees inside disease centers (in-uninf) and trees outside of disease centers (outside). These values can be a little difficult to interpret at a glance, because they are dealing with two different areas of the stand, infected area and uninfected area. The column, Species Total, is a trees per acre value representing the entire stand. So, unless you are running the simulation as having 100% of the stand in diseased area, the Species Total column holds the only number that can be related directly back to FVS Summary Statistics table which is also based on total stand area.

The bark beetle mortality report includes:

- Year of cycle
- Age of the Stand (based on FVS input)
- Tree Species (FVS two-character abbreviations).
- General Status (inside center infected, inside center uninfected, outside disease area)
- Trees per acre values in 6 DBH classes of 5" and a final class of 30" and larger
- Row Total TPA for each General Status category (based on disease and disease-free areas)
- Species Total TPA (based on total stand area)
- Total Before Attack for each General Status category (based on infected and uninfected areas)

 WESTERN ROOT DISEASE MODEL

 STAND ID= 01160805050023 MANAGEMENT ID= ARM1
 TREES PER ACRE KILLED BY BARK BEETLES IN EACH TIME PERIOD

Period Start (year)	Tree Species	General Status	DBH Class (in inches)							Row Total	Species Total	Total Before Attack
			0-<5	5-<10	10-<15	15-<20	20-<25	25-<30	30+			
2024			no beetle kill									
2034			no beetle kill									
2044	PP	in-inf	0.00	0.00	1.43	3.98	3.57	0.32	0.21	9.51		31.71
		in-uninf	0.00	0.00	0.16	0.11	0.09	0.01	0.00	0.38		7.22
		outside	0.00	0.00	0.27	0.19	0.15	0.01	0.01	0.63	3.00	61.17
2054	PP	in-inf	0.00	0.00	0.04	0.67	0.69	0.21	0.15	1.75		5.85
		in-uninf	0.00	0.00	0.15	0.10	0.09	0.02	0.00	0.36		5.43
		outside	0.00	0.00	0.25	0.17	0.16	0.04	0.01	0.63	1.01	57.15
2064	PP	in-inf	0.00	0.00	0.03	0.02	0.03	0.01	0.10	0.18		0.60
		in-uninf	0.00	0.00	0.16	0.10	0.12	0.03	0.01	0.40		11.81
		outside	0.00	0.00	0.23	0.14	0.19	0.04	0.01	0.61	0.61	60.01
2074			no beetle kill									
2084			no beetle kill									
2094			no beetle kill									
2104			no beetle kill									
2114			no beetle kill									

Chapter 9

Where To Find Help



The Forest Health Protection Staff are very interested in helping people understand and effectively use the Western Root Disease Model. Reaching help directly will be easier if you contact:

- Blakey Lockman (Forest Pathologist) Region 6, Regional Office (blockman@fs.fed.us)
- Kelly S. Burns (Forest Pathologist) Region 2, Regional Office (ksburns@fs.fed.us)
- Ellen Michaels Goheen (Plant Pathologist) SW Oregon(egoheen@fs.fed.us)
- James J. Jacobs (Forest Pathologist) Region 9, St. Paul, MN (jamesjjacobs@fs.fed.us)
- John Guyon (Plant Pathologist) Region 4, Regional Office (jguyon@fs.fed.us)

All of the insect and disease extensions are supported by **(someone at a location with phone number and e-mail address or a URL with contact information)**.

In addition to this User's Guide, other publications are available.

Beukema, S.J., W.A. Kurz, and J.A. Greenough. 1996. Western root disease model, version 3.0: detailed model description. Prepared by ESSA Technologies Ltd., Vancouver, B.C., 55 pp.

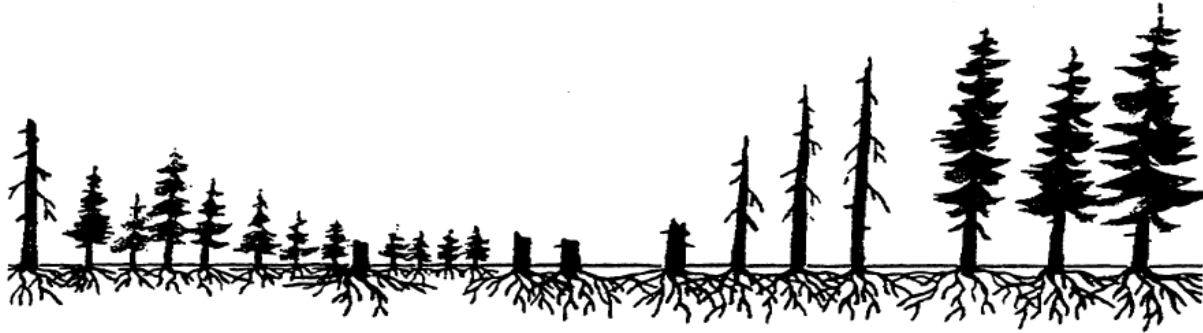
Dixon, Gary E. comp. 2002 (revised frequently). Essential FVS: A user's guide to the Forest Vegetation Simulator. Internal Rep. Fort Collins, CO: U.S. Department of Agriculture, Forest Service, Forest

Management Service Center. Gladden, J., L.R. David, and M.K. Thompson. 1992. Reference Guide for Western Root Disease Keywords. Ft. Collins, CO. USDA Forest Service. Forest Pest Management Methods Application Group. 18p.

Hadfield, J.S., D.J. Goheen, G.M. Filip, C.L. Schmitt, and R.D. Harvey. 1986 Root diseases in Oregon and Washington conifers. R6-FPM-250-86. Portland, OR. USDA Forest Service. Pacific Northwest Region. 27p.

- Marsden, M.A. 1992. Sensitivity analyses of the Western Root Disease Model to user-specified starting parameters. Res. Pap. RM-306. Fort Collins, CO. USDA Forest Service, Rocky Mountain Forest and Range Experiment Station. 20p.
- Marsden, M.A., B.B. Eav, and M.K. Thompson. 1993. Modeling initial conditions for root rot in forest stands: random proportions. Res. Note RM-524. Fort Collins, CO. USDA Forest Service, Rocky Mountain Forest and Range Experiment Station. 12p.
- Stage, A.L., C.G. Shaw III, M.A. Marsden, J.W. Byler, D.L. Renner, B.B. Eav, P.J. McNamee, G.D. Sutherland, T.M. Webb. 1990. User's Manual for Western Root Disease Model. GTR INT-267. Moscow, ID. USDA Forest Service, Intermountain Research Station. 49p.

Appendix A: Example Run

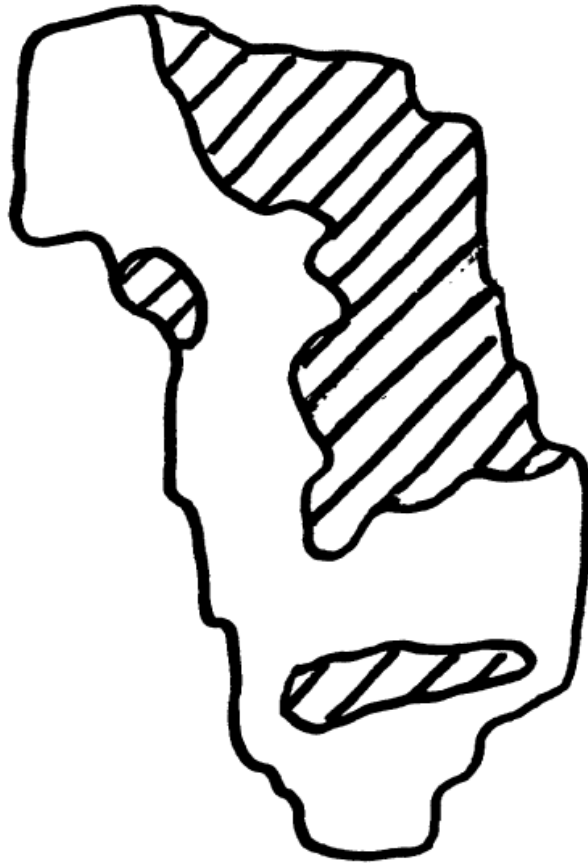


Example Run 1

Laminated Root Rot: Okanogan National Forest

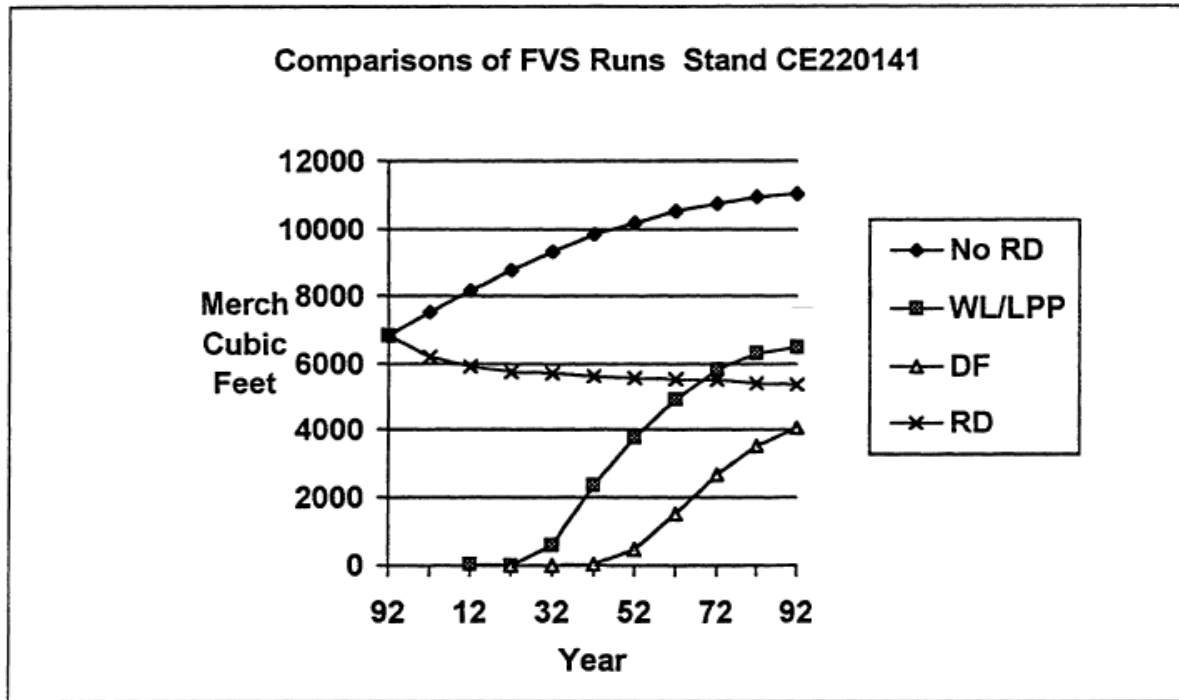
A 24-acre stand dominated by subalpine fir and Engelmann spruce and including western redcedar, Douglas-fir, lodgepole pine, and scattered quaking aspen is located on a cool moist site at 4500' elevation on the Okanogan National Forest in northcentral Washington. One large and two small pockets of laminated root rot, totaling 12 acres, were mapped during a stand examination.

The East Cascades variant of FVS with the WRDM extension was run for 10 cycles. Initial conditions for root disease were described using the keywords RRINIT, RRTYPE, SAREA, and STREAD. Dynamic spread was requested using SPREAD. A detailed output table was built using the keyword RRDOU.



Stand CE220141. Hatched areas are pockets of laminated root rot.

In the following graph, the previous FVS/WRDM run (**RD**) is compared with 1) an FVS run where root disease is ignored (**No RD**), 2) an FVS/WRDM run where the stand is harvested and planted back with Douglas-fir a highly susceptible species (**DF**), and 3) an FVS/WRDM run where the stand is harvested and planted with a mix of western larch and lodgepole pine, both of which are considered resistant to laminated root rot (**WL/LPP**).



Appendix B: Variant Species Lists



BLUE MOUNTAINS (BM)

-----FVS BM VARIANT-----	WRD MODEL SPECIES	ANNOSUS
# CD COMMON NAME	OR SURROGATE SP.	TYPE
1 WP WESTERN WHITE PINE	WHITE PINE (1)	P-TYPE
2 WL WESTERN LARCH	WESTERN LARCH (2)	S-TYPE
3 DF DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
4 GF GRAND FIR	GRAND FIR (4)	S-TYPE
5 MH MOUNTAIN HEMLOCK	MOUNTAIN HEMLOCK (11)	S-TYPE
6 WJ WESTERN JUNIPER	JUNIPER (26)	P-TYPE
7 LP LODGEPOLE PINE	LODGEPOLE PINE (7)	P-TYPE
8 ES ENGLEMAN SPRUCE	ENGELMANN SPRUCE (8)	S-TYPE
9 AF SUBALPINE FIR	SUBALPINE FIR (9)	S-TYPE
10 PP PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
11 OT OTHER	OTHER (30)	P-TYPE
12 LM LIMBER PINE	LIMBER PINE (23)	P-TYPE
13 PY PACIFIC YEW	PACIFIC YEW (38)	P-TYPE
14 YC ALASKA YELLOW CEDAR	YELLOW CEDAR (34)	S-TYPE
15 AS QUAKING ASPEN	APSEN (19)	NON-HOST
16 CW BLACK COTTONWOOD	COTTONWOOD (24)	NON-HOST
17 OS OTHER SOFTWOODS	OTHER SOFTWOODS (17)	P-TYPE
18 OH OTHER HARDWOODS	OTHER HARDWOODS (18)	NON-HOST

CENTRAL IDAHO (CI)

-----FVS CI Variant-----	WRD MODEL SPECIES	ANNOSUS
# CD COMMON NAME	OR SURROGATE SP.	TYPE
1 WP WESTERN WHITE PINE	WHITE PINE (1)	P-TYPE

2	WL	WESTERN LARCH	WESTERN LARCH (2)	S-TYPE
3	DF	DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
4	GF	GRAND FIR	GRAND FIR (4)	S-TYPE
5	WH	WESTERN HEMLOCK	WESTERN HEMLOCK (5)	S-TYPE
6	RC	WESTERN REDCEDAR	W. REDCEDAR (6)	S-TYPE
7	LP	LODGEPOLE PINE	LODGEPOLE PINE (7)	P-TYPE
8	ES	ENGLEMAN SPRUCE	ENGELMANN SPRUCE (8)	S-TYPE
9	AF	SUBALPINE FIR	SUBALPINE FIR (9)	S-TYPE
10	PP	PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
11	WB	WHITEBARK PINE	WHITEBARK PINE (22)	P-TYPE
12	PY	PACIFIC YEW	PACIFIC YEW (38)	P-TYPE
13	AS	QUAKING ASPEN	ASPEN (19)	NON-HOST
14	WJ	WESTERN JUNIPER	JUNIPER (26)	P-TYPE
15	MC	CURLLEAF MOUNTAIN- MAHOGANY	NON-HOST (40)	NON-HOST
16	LM	LIMBER PINE	LIMBER PINE (23)	P-TYPE
17	CW	BLACK COTTONWOOD	COTTONWOOD (24)	NON-HOST
18	OS	OTHER SOFTWOODS	OTHER SOFTWOOD (17)	P-TYPE
19	OH	OTHER HARDWOODS	OTHER HARDWOOD (18)	NON-HOST

CENTRAL ROCKIES (CR)

-----FVS CR VARIANT-----		WRD MODEL SPECIES	ANNOSUS
#	CD COMMON NAME	OR SURROGATE SP.	TYPE
1	AF SUBALPINE FIR	SUBALPINE FIR (9)	S-TYPE
2	CB CORKBARK FIR	CORKBARK FIR (21)	P-TYPE
3	DF DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
4	GF GRAND FIR	GRAND FIR (4)	S-TYPE
5	WF WHITE FIR	WHITE FIR (13)	S-TYPE
6	MH MOUNTAIN HEMLOCK	MOUNTAIN HEMLOCK (11)	S-TYPE
7	RC WESTERN REDCEDAR	W. REDCEDAR (6)	S-TYPE
8	WL WESTERN LARCH	WESTERN LARCH (2)	S-TYPE
9	BC BRISTLECONE PINE	PINYON PINE (33)	P-TYPE
10	LM LIMBER PINE	LIMBER PINE (23)	P-TYPE
11	LP LODGEPOLE PINE	LODGEPOLE PINE (7)	P-TYPE
12	PI PINYON PINE	PINYON PINE (33)	P-TYPE
13	PP PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
14	WB WHITEBARK PINE	WHITEBARK PINE (22)	P-TYPE
15	SW SOUTHWESTERN WHITE PINE	WHITE PINE (1)	P-TYPE
16	UJ UTAH JUNIPER	JUNIPER (26)	P-TYPE
17	BS BLUE SPRUCE	BLUE SPRUCE (20)	S-TYPE
18	ES ENGELMANN SPRUCE	ENGELMANN SPRUCE (8)	S-TYPE
19	WS WHITE SPRUCE	WHITE SPRUCE (25)	S-TYPE
20	AS QUAKING ASPEN	ASPEN (19)	NON-HOST

21	NC	NARROWLEAF COTTONWOOD	COTTONWOOD (24)	NON-HOST
22	PW	PLAINS COTTONWOOD	COTTONWOOD (24)	NON-HOST
23	GO	GAMBEL OAK	OTHER HARDWOOD (18)	NON-HOST
24	AW	ARIZONA WHITE OAK	BLACK OAK (29)	NON-HOST
25	EM	EMORY OAK	OTHER HARDWOOD (18)	NON-HOST
26	BK	BUR OAK	BLACK OAK (29)	NON-HOST
27	SO	SILVERLEAF OAK	BLACK OAK (29)	NON-HOST
28	PB	PAPER BIRCH	NON-HOST (40)	NON-HOST
29	AJ	ALLIGATOR JUNIPER	JUNIPER (26)	P-TYPE
30	RM	ROCKY MOUNTAIN JUNIPER	JUNIPER (26)	P-TYPE
31	OJ	ONESEED JUNIPER	JUNIPER (26)	P-TYPE
32	ER	EASTERN REDCEDAR	JUNIPER (26)	P-TYPE
33	PM	SINGLELEAF PINYON	PINYON PINE (33)	P-TYPE
34	PD	BORDER PINYON	PINYON PINE (33)	P-TYPE
35	AZ	ARIZONA PINYON PINE	PINYON PINE (33)	P-TYPE
36	CI	CHIHUAHUA PINE	PONDEROSA PINE (10)	P-TYPE
37	OS	OTHER SOFTWOODS	OTHER SOFTWOOD (17)	P-TYPE
38	OH	OTHER HARDWOODS	OTHER HARDWOOD (18)	NON-HOST

KOOTENAI (KT)

--FVS CI, KT, NI Variant---			WRD MODEL SPECIES	ANNOSUS
#	CD	COMMON NAME	OR SURROGATE SP.	TYPE
1	WP	WESTERN WHITE PINE	WHITE PINE (1)	P-TYPE
2	WL	WESTERN LARCH	WESTERN LARCH (2)	S-TYPE
3	DF	DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
4	GF	GRAND FIR	GRAND FIR (4)	S-TYPE
5	WH	WESTERN HEMLOCK	WESTERN HEMLOCK (5)	S-TYPE
6	RC	WESTERN REDCEDAR	W. REDCEDAR (6)	S-TYPE
7	LP	LODGEPOLE PINE	LODGEPOLE PINE (7)	P-TYPE
8	ES	ENGLEMAN SPRUCE	ENGELMANN SPRUCE (8)	S-TYPE
9	AF	SUBALPINE FIR	SUBALPINE FIR (9)	S-TYPE
10	PP	PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
11	OT	OTHER	OTHER (30)	P-TYPE

EASTSIDE CASCADES (EC)

-----FVS EC VARIANT-----			WRD MODEL SPECIES	ANNOSUS
#	CD	COMMON NAME	OR SURROGATE SP.	TYPE
1	WP	WESTERN WHITE PINE	WHITE PINE (1)	P-TYPE
2	WL	WESTERN LARCH	WESTERN LARCH (2)	S-TYPE

3	DF	DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
4	SF	PACIFIC SILVER FIR	P. SILVER FIR (16)	S-TYPE
5	RC	WESTERN REDCEDAR	W. REDCEDAR (6)	S-TYPE
6	GF	GRAND FIR	GRAND FIR (4)	S-TYPE
7	LP	LODGEPOLE PINE	LODGEPOLE PINE (7)	P-TYPE
8	ES	ENGELMANN SPRUCE	ENGELMANN SPRUCE (8)	S-TYPE
9	AF	SUBALPINE FIR	SUBALPINE FIR (9)	S-TYPE
10	PP	PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
11	WH	WESTERN HEMLOCK	WESTERN HEMLOCK (5)	S-TYPE
12	MH	MOUNTAIN HEMLOCK	MOUNTAIN HEMLOCK (11)	S-TYPE
13	PY	PACIFIC YEW	PACIFIC YEW (38)	P-TYPE
14	WB	WHITEBARK PINE	WHITEBARK PINE (22)	P-TYPE
15	NF	NOBLE FIR	NOBLE FIR (39)	S-TYPE
16	WF	WHITE FIR	WHITE FIR (13)	S-TYPE
17	LL	SUBALPINE LARCH	SUBALPINE LARCH (36)	S-TYPE
18	YC	ALASKA CEDAR	YELLOW CEDAR (34)	S-TYPE
19	WJ	WESTERN JUNIPER	JUNIPER (26)	P-TYPE
20	BM	BIGLEAF MAPLE	NON-HOST (40)	NON-HOST
21	VN	VINE MAPLE	NON-HOST (40)	NON-HOST
22	RA	RED ALDER	NON-HOST (40)	NON-HOST
23	PB	PAPER BIRCH	NON-HOST (40)	NON-HOST
24	GC	GOLDEN CHINKAPIN	NON-HOST (40)	NON-HOST
25	DG	PACIFIC DOGWOOD	NON-HOST (40)	NON-HOST
26	AS	QUAKING ASPEN	ASPEN (19)	NON-HOST
27	CW	BLACK COTTONWOOD	NON-HOST (40)	NON-HOST
28	WO	OREGON WHITE OAK	NON-HOST (40)	NON-HOST
29	PL	CHERRY AND PLUM SPECIES	NON-HOST (40)	NON-HOST
30	WI	WILLOW SPECIES	NON-HOST (40)	NON-HOST
31	OS	OTHER SOFTWOODS	OTHER SOFTWOOD (17)	P-TYPE
32	OH	OTHER HARDWOODS	OTHER HARDWOOD (18)	NON-HOST

EASTERN MONTANA (EM)

-----FVS EM VARIANT-----		WRD MODEL SPECIES	ANNOSUS
#	CD COMMON NAME	OR SURROGATE SP.	TYPE
-----		-----	-----
1	WB	WHITEBARK PINE	WHITEBARK PINE (22) P-TYPE
2	WL	WESTERN LARCH	WESTERN LARCH (2) S-TYPE
3	DF	DOUGLAS-FIR	DOUGLAS-FIR (3) S-TYPE
4	LM	LIMBER PINE	LIMBER PINE (23) P-TYPE
5	LL	SUBALPINE LARCH	SUBALPINE LARCH (36) S-TYPE
6	RM	ROCKY MTN JUNIPER	JUNIPER (26) P-TYPE
7	LP	LODGEPOLE PINE	LODGEPOLE PINE (7) P-TYPE
8	ES	ENGELMANN SPRUCE	ENGELMANN SPRUCE (8) S-TYPE
9	AF	SUBALPINE FIR	SUBALPINE FIR (9) S-TYPE

10	PP	PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
11	GA	GREEN ASH	OTHER HARDWOOD (18)	NON-HOST
12	AS	QUAKING ASPEN	ASPEN (19)	NON-HOST
13	CW	BLACK COTTONWOOD	COTTONWOOD (24)	NON-HOST
14	BA	BALSAM POPLAR	COTTONWOOD (24)	NON-HOST
15	PW	PLAINS COTTONWOOD	COTTONWOOD (24)	NON-HOST
16	NC	NARROWLEAF COTTONWOOD	COTTONWOOD (24)	NON-HOST
17	PB	PAPER BIRCH	OTHER HARDWOOD (18)	NON-HOST
18	OS	OTHER SOFTWOODS	OTHER SOFTWOOD (17)	P-TYPE
19	OH	OTHER HARDWOODS	OTHER HARDWOOD (18)	NON-HOST

INLAND EMPIRE (IE)

-----FVS IE VARIANT-----		WRD MODEL SPECIES	ANNOSUS
#	CD COMMON NAME	OR SURROGATE SP.	TYPE
1	WP	WESTERN WHITE PINE	WHITE PINE (1) P-TYPE
2	WL	WESTERN LARCH	WESTERN LARCH (2) S-TYPE
3	DF	DOUGLAS-FIR	DOUGLAS-FIR (3) S-TYPE
4	GF	GRAND FIR	GRAND FIR (4) S-TYPE
5	WH	WESTERN HEMLOCK	WESTERN HEMLOCK (5) S-TYPE
6	RC	WESTERN REDCEDAR	W. REDCEDAR (6) S-TYPE
7	LP	LODGEPOLE PINE	LODGEPOLE PINE (7) P-TYPE
8	ES	ENGLEMANN SPRUCE	ENGELMANN SPRUCE (8) S-TYPE
9	AF	SUBALPINE FIR	SUBALPINE FIR (9) S-TYPE
10	PP	PONDEROSA PINE	PONDEROSA PINE (10) P-TYPE
11	MH	MOUNTAIN HEMLOCK	MOUNTAIN HEMLOCK (11) S-TYPE
12	WB	WHITEBARK PINE	WHITEBARK PINE (22) P-TYPE
13	LM	LIMBER PINE	LIMBER PINE (23) P-TYPE
14	LL	SUBALPINE LARCH	SUBALPINE LARCH (36) S-TYPE
15	PI	PINYON PINE	PINYON PINE (33) P-TYPE
16	RM	ROCKY MTN JUNIPER	JUNIPER (26) P-TYPE
17	PY	PACIFIC YEW	PACIFIC YEW (38) P-TYPE
18	AS	QUAKING ASPEN	ASPEN (19) NON-HOST
19	CO	COTTONWOOD	COTTONWOOD (24) NON-HOST
20	MM	MOUNTAIN MAPLE	OTHER (30) P-TYPE
21	PB	PAPER BIRCH	OTHER (30) P-TYPE
22	OH	OTHER HARDWOODS	OTHER HARDWOOD (18) NON-HOST
23	OS	OTHER SOFTWOODS	OTHER SOFTWOOD (17) P-TYPE

NORTHERN CALIFORNIA / KLAMATH MOUNTAINS (NC)

-----FVS NC VARIANT-----		WRD MODEL SPECIES	ANNOSUS
#	CD COMMON NAME	OR SURROGATE SP.	TYPE
1	OS OTHER CONIFERS	OTHER CONIFERS (27)	P-TYPE
2	SP SUGAR PINE	SUGAR PINE (12)	P-TYPE
3	DF DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
4	WF WHITE FIR	WHITE FIR (13)	S-TYPE
5	MA MADRONE	OTHER (30)	P-TYPE
6	IC INCENSE CEDAR	INCENSE CEDAR (14)	P-TYPE
7	BO CALIFORNIA BLACK OAK	BLACK OAK (29)	NON-HOST
8	TO TANOAK	TANOAK/CHINKAPIN (32)	NON-HOST
9	RF RED FIR	RED FIR (15)	S-TYPE
10	PP PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
11	OH OTHER HARDWOOD	OTHER HARDWOOD (18)	NON-HOST

PACIFIC NORHTWEST COAST (PN)

-----FVS PN VARIANTS-----		WRD MODEL SPECIES	ANNOSUS
#	CD COMMON NAME	OR SURROGATE SP.	TYPE
1	SF PACIFIC SILVER FIR	P. SILVER FIR (16)	S-TYPE
2	WF WHITE FIR	WHITE FIR (13)	S-TYPE
3	GF GRAND FIR	GRAND FIR (4)	S-TYPE
4	AF SUBALPINE FIR	SUBALPINE FIR (9)	S-TYPE
5	RF CALIFORNIA RED FIR/ SHASTA RED FIR	RED FIR (15)	S-TYPE
6	SS SITKA SPRUCE	ENGELMANN SPRUCE (8)	S-TYPE
7	NF NOBLE FIR	NOBLE FIR (39)	S-TYPE
8	YC ALASKA CEDAR / WESTERN LARCH	YELLOW CEDAR (34)	S-TYPE
9	IC INCENSE CEDAR	INCENSE CEDAR (14)	P-TYPE
10	ES ENGELMANN SPRUCE	ENGELMANN SPRUCE (8)	S-TYPE
11	LP LODGEPOLE PINE	LODGEPOLE PINE (7)	P-TYPE
12	JP JEFFREY PINE	JEFFREY PINE (31)	P-TYPE
13	SP SUGAR PINE	SUGAR PINE (12)	P-TYPE
14	WP WESTERN WHITE PINE	WHITE PINE (1)	P-TYPE
15	PP PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
16	DF DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
17	RW COAST REDWOOD	REDWOOD (35)	S-TYPE
18	RC WESTERN REDCEDAR	W. REDCEDAR (6)	S-TYPE
19	WH WESTERN HEMLOCK	WESTERN HEMLOCK (5)	S-TYPE
20	MH MOUNTAIN HEMLOCK	MOUNTAIN HEMLOCK (11)	S-TYPE

21	BM	BIGLEAF MAPLE	NON-HOST (40)	NON-HOST
22	RA	RED ALDER	NON-HOST (40)	NON-HOST
23	WA	WHITE ALDER / PACIFIC MADRONE	NON-HOST (40)	NON-HOST
24	PB	PAPER BIRCH	NON-HOST (40)	NON-HOST
25	GC	GIANT CHINKAPIN / TANOAK	NON-HOST (40)	NON-HOST
26	AS	QUAKING ASPEN	ASPEN (19)	NON-HOST
27	CW	BLACK COTTONWOOD	NON-HOST (40)	NON-HOST
28	WO	OREGON WHITE OAK / CALIFORNIA BLACK OAK	NON-HOST (40)	NON-HOST
29	WJ	WESTERN JUNIPER	JUNIPER (26)	P-TYPE
30	LL	SUBALPINE LARCH	SUBALPINE LARCH (36)	S-TYPE
31	WB	WHITEBARK PINE	WHITEBARK PINE (22)	P-TYPE
32	KP	KNOBCONE PINE	KNOBCONE PINE (37)	P-TYPE
33	PY	PACIFIC YEW	PACIFIC YEW (38)	P-TYPE
34	DG	PACIFIC DOGWOOD	NON-HOST (40)	NON-HOST
35	HT	HAWTHORN	NON-HOST (40)	NON-HOST
36	CH	BITTER CHERRY	NON-HOST (40)	NON-HOST
37	WI	WILLOW	NON-HOST (40)	NON-HOST
38		---	NON-HOST (40)	NON-HOST
39	OT	OTHER	NON-HOST (40)	NON-HOST

SOUTH CENTRAL OREGON / NORTHEAST CALIFORNIA (SO)

-----FVS SO VARIANT-----	WRD MODEL SPECIES	ANNOSUS
# CD COMMON NAME	OR SURROGATE SP.	TYPE
---	-----	-----
1	WP WESTERN WHITE PINE	WHITE PINE (1) P-TYPE
2	SP SUGAR PINE	SUGAR PINE (12) P-TYPE
3	DF DOUGLAS-FIR	DOUGLAS-FIR (3) S-TYPE
4	WF WHITE FIR	WHITE FIR (13) S-TYPE
5	MH MOUNTAIN HEMLOCK	MOUNTAIN HEMLOCK (11) S-TYPE
6	IC INCENSE CEDAR	INCENSE CEDAR (14) P-TYPE
7	LP LODGEPOLE PINE	LODGEPOLE PINE (7) P-TYPE
8	ES ENGELMANN SPRUCE	ENGELMANN SPRUCE (8) S-TYPE
9	SH SHASTA RED FIR	RED FIR (15) S-TYPE
10	PP PONDEROSA PINE	PONDEROSA PINE (10) P-TYPE
11	WJ WESTERN JUNIPER	JUNIPER (26) P-TYPE
12	GF GRAND FIR	GRAND FIR (4) S-TYPE
13	AF SUBALPINE FIR	SUBALPINE FIR (9) S-TYPE
14	SF PACIFIC SILVER FIR	P. SILVER FIR (16) S-TYPE
15	NF NOBLE FIR	NOBLE FIR (39) S-TYPE
16	WB WHITEBARK PINE	WHITEBARK PINE (22) P-TYPE
17	WL WESTERN LARCH	WESTERN LARCH (2) S-TYPE

18	RC	WESTERN REDCEDAR	W. REDCEDAR (6)	S-TYPE
19	WH	WESTERN HEMLOCK	WESTERN HEMLOCK (5)	S-TYPE
20	PY	PACIFIC YEW	PACIFIC YEW (38)	P-TYPE
21	WA	WHITE ALDER	NON-HOST (40)	NON-HOST
22	RA	RED ALDER	NON-HOST (40)	NON-HOST
23	BM	BIGLEAF MAPLE	NON-HOST (40)	NON-HOST
24	AS	QUAKING ASPEN	ASPEN (19)	NON-HOST
25	CW	BLACK COTTONWOOD	COTTONWOOD (24)	NON-HOST
26	CH	BITTER CHERRY	NON-HOST (40)	NON-HOST
27	WO	OREGON WHITE OAK	NON-HOST (40)	NON-HOST
28	WI	WILLOW	NON-HOST (40)	NON-HOST
29	GC	GIANT CHINKAPIN	NON-HOST (40)	NON-HOST
30	MC	CURL-LEAF MOUNTAIN MAHOGANY	NON-HOST (40)	NON-HOST
31	MB	BIRCHLEAF MOUNTAIN MAHOGANY	NON-HOST (40)	NON-HOST
32	OS	OTHER SOFTWOODS	OTHER SOFTWOOD (17)	P-TYPE
33	OH	OTHER HARDWOODS	OTHER HARDWOOD (18)	NON-HOST

TETONS (TT)

-----FVS TT VARIANT-----		WRD MODEL SPECIES	ANNOSUS
#	CD COMMON NAME	OR SURROGATE SP.	TYPE
-----		-----	-----
1	WB WHITEBARK PINE	WHITEBARK PINE (22)	P-TYPE
2	LM LIMBER PINE	LIMBER PINE (23)	P-TYPE
3	DF DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
4	PM SINGLELEAF PINYON	PINYON PINE (33)	P-TYPE
5	BS BLUE SPRUCE	BLUE SPRUCE (20)	S-TYPE
6	AS QUAKING ASPEN	ASPEN (19)	NON-HOST
7	LP LODGEPOLE PINE	LODGEPOLE PINE (7)	P-TYPE
8	ES ENGLEMANN SPRUCE	ENGELMANN SPRUCE (8)	S-TYPE
9	AF SUBALPINE FIR	SUBALPINE FIR (9)	S-TYPE
10	PP PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
11	UJ UTAH JUNIPER	JUNIPER (26)	P-TYPE
12	RM ROCKY MOUNTAIN JUNIPER	JUNIPER (26)	P-TYPE
13	BI BIGTOOTH MAPLE	NON-HOST (40)	NON-HOST
14	MM ROCKY MOUNTAIN MAPLE	NON-HOST (40)	NON-HOST
15	NC NARROWLEAF COTTONWOOD	COTTONWOOD (24)	NON-HOST
16	MC CURLLEAF MOUNTAIN- MAHOGANY	NON-HOST (40)	NON-HOST
17	OS OTHER SOFTWOODS	OTHER SOFTWOOD (17)	P-TYPE
18	OH OTHER HARDWOODS	OTHER HARDWOOD (18)	NON-HOST

UTAH (UT)

-----FVS UT VARIANT-----		WRD MODEL SPECIES	ANNOSUS
#	CD COMMON NAME	OR SURROGATE SP.	TYPE
1	WB WHITEBARK PINE	WHITEBARK PINE (22)	P-TYPE
2	LM LIMBER PINE	LIMBER PINE (23)	P-TYPE
3	DF DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
4	WF WHITE FIR	WHITE FIR (13)	S-TYPE
5	BS BLUE SPRUCE	BLUE SPRUCE (20)	S-TYPE
6	AS QUAKING ASPEN	ASPEN (19)	NON-HOST
7	LP LODGEPOLE PINE	LODGEPOLE PINE (7)	P-TYPE
8	ES ENGELMANN SPRUCE	ENGELMANN SPRUCE (8)	S-TYPE
9	AF SUBALPINE FIR	SUBALPINE FIR (9)	S-TYPE
10	PP PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
11	PI COMMON PINYON	PINYON PINE (33)	P-TYPE
12	WJ WESTERN JUNIPER	JUNIPER (26)	P-TYPE
13	GO GAMBEL OAK	OTHER HARDWOOD (18)	NON-HOST
14	PM SINGLELEAF PINYON	PINYON PINE (33)	P-TYPE
15	RM ROCKY MOUNTAIN JUNIPER	JUNIPER (26)	P-TYPE
16	UJ UTAH JUNIPER	JUNIPER (26)	P-TYPE
17	GB BRISTLECONE PINE (Great Basin)	PINYON PINE (33)	P-TYPE
18	NC NARROWLEAF COTTONWOOD	COTTONWOOD (24)	NON-HOST
19	FC FREMONT COTTONWOOD	COTTONWOOD (24)	NON-HOST
20	MC CURLLEAF MOUNTAIN- MAHOGANY	NON-HOST (40)	NON-HOST
21	BI BIGTOOTH MAPLE	NON-HOST (40)	NON-HOST
22	BE BOX ELDER	NON-HOST (40)	NON-HOST
23	OS OTHER SOFTWOODS	OTHER SOFTWOOD (17)	P-TYPE
24	OH OTHER HARDWOODS	OTHER HARDWOOD (18)	NON-HOST

WESTSIDE CASCADES (WC)

-----FVS WC VARIANTS-----		WRD MODEL SPECIES	ANNOSUS
#	CD COMMON NAME	OR SURROGATE SP.	TYPE
1	SF PACIFIC SILVER FIR	P. SILVER FIR (16)	S-TYPE
2	WF WHITE FIR	WHITE FIR (13)	S-TYPE
3	GF GRAND FIR	GRAND FIR (4)	S-TYPE
4	AF SUBALPINE FIR	SUBALPINE FIR (9)	S-TYPE
5	RF CALIFORNIA RED FIR/ SHASTA RED FIR	RED FIR (15)	S-TYPE
6	---	NON-HOST (40)	NON-HOST

7	NF	NOBLE FIR	NOBLE FIR (39)	S-TYPE
8	YC	ALASKA CEDAR / WESTERN LARCH	YELLOW CEDAR (34)	S-TYPE
9	IC	INCENSE CEDAR	INCENSE CEDAR (14)	P-TYPE
10	ES	ENGELMANN SPRUCE	ENGELMANN SPRUCE (8)	S-TYPE
11	LP	LODGEPOLE PINE	LODGEPOLE PINE (7)	P-TYPE
12	JP	JEFFREY PINE	JEFFREY PINE (31)	P-TYPE
13	SP	SUGAR PINE	SUGAR PINE (12)	P-TYPE
14	WP	WESTERN WHITE PINE	WHITE PINE (1)	P-TYPE
15	PP	PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
16	DF	DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
17	RW	COAST REDWOOD	REDWOOD (35)	S-TYPE
18	RC	WESTERN REDCEDAR	W. REDCEDAR (6)	S-TYPE
19	WH	WESTERN HEMLOCK	WESTERN HEMLOCK (5)	S-TYPE
20	MH	MOUNTAIN HEMLOCK	MOUNTAIN HEMLOCK (11)	S-TYPE
21	BM	BIGLEAF MAPLE	NON-HOST (40)	NON-HOST
22	RA	RED ALDER	NON-HOST (40)	NON-HOST
23	WA	WHITE ALDER / PACIFIC MADRONE	NON-HOST (40)	NON-HOST
24	PB	PAPER BIRCH	NON-HOST (40)	NON-HOST
25	GC	GIANT CHINKAPIN / TANOAK	NON-HOST (40)	NON-HOST
26	AS	QUAKING ASPEN	ASPEN (19)	NON-HOST
27	CW	BLACK COTTONWOOD	NON-HOST (40)	NON-HOST
28	WO	OREGON WHITE OAK / CALIFORNIA BLACK OAK	NON-HOST (40)	NON-HOST
29	WJ	WESTERN JUNIPER	JUNIPER (26)	P-TYPE
30	LL	SUBALPINE LARCH	SUBALPINE LARCH (36)	S-TYPE
31	WB	WHITEBARK PINE	WHITEBARK PINE (22)	P-TYPE
32	KP	KNOBCONE PINE	KNOBCONE PINE (37)	P-TYPE
33	PY	PACIFIC YEW	PACIFIC YEW (38)	P-TYPE
34	DG	PACIFIC DOGWOOD	NON-HOST (40)	NON-HOST
35	HT	HAWTHORN	NON-HOST (40)	NON-HOST
36	CH	BITTER CHERRY	NON-HOST (40)	NON-HOST
37	WI	WILLOW	NON-HOST (40)	NON-HOST
38		---	NON-HOST (40)	NON-HOST
39	OT	OTHER	NON-HOST (40)	NON-HOST

WESTERN SIERRAS (WS)

-----FVS WS VARIANT-----	WRD MODEL SPECIES	ANNOSUS
# CD COMMON NAME	OR SURROGATE SP.	TYPE
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1	SP SUGAR PINE	SUGAR PINE (12)	P-TYPE
2	DF DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
3	WF WHITE FIR	WHITE FIR (13)	S-TYPE
4	GS GIANT SEQUOIA	GIANT SEQUOIA (28)	S-TYPE
5	IC INCENSE CEDAR	INCENSE CEDAR (14)	P-TYPE
6	JP JEFFREY PINE	JEFFREY PINE (31)	P-TYPE
7	RF CALIFORNIA RED FIR	RED FIR (15)	S-TYPE
8	PP PONDEROSA PINE	PONDEROSA PINE (10)	P-TYPE
9	LP LODGEPOLE PINE	LODGEPOLE PINE (7)	P-TYPE
10	WB WHITEBARK PINE	WHITEBARK PINE (22)	P-TYPE
11	WP WESTERN WHITE PINE	WHITE PINE (1)	P-TYPE
12	PM SINGLELEAF PINYON	PINYON PINE (33)	P-TYPE
13	SF PACIFIC SILVER FIR	P. SILVER FIR (16)	S-TYPE
14	KP KNOBCONE PINE	KNOBCONE PINE (37)	P-TYPE
15	FP FOXTAIL PINE	KNOBCONE PINE (37)	P-TYPE
16	CP COULTER PINE	KNOBCONE PINE (37)	P-TYPE
17	LM LIMBER PINE	LIMBER PINE (23)	P-TYPE
18	MP MONTEREY PINE	PONDEROSA PINE (10)	P-TYPE
19	GP GRAY PINE (OR CALIFORNIA FOOTHILL PINE)	KNOBCONE PINE (37)	P-TYPE
20	WE WASHOE PINE	KNOBCONE PINE (37)	P-TYPE
21	GB GREAT BASIN BRISTLECONE PINE	PINYON PINE (33)	P-TYPE
22	BD BIGCONE DOUGLAS-FIR	DOUGLAS-FIR (3)	S-TYPE
23	RW REDWOOD	REDWOOD (35)	S-TYPE
24	MH MOUNTAIN HEMLOCK	MOUNTAIN HEMLOCK (11)	S-TYPE
25	WJ WESTERN JUNIPER	JUNIPER (26)	P-TYPE
26	UJ UTAH JUNIPER	JUNIPER (26)	P-TYPE
27	CJ CALIFORNIA JUNIPER	JUNIPER (26)	P-TYPE
28	LO CALIFORNIA LIVE OAK	BLACK OAK (29)	NON-HOST
29	CY CANYON LIVE OAK	BLACK OAK (29)	NON-HOST
30	BL BLUE OAK	BLACK OAK (29)	NON-HOST
31	BO CALIFORNIA BLACK OAK	BLACK OAK (29)	NON-HOST
32	VO VALLEY OAK (OR CALIFORNIA WHITE OAK)	BLACK OAK (29)	NON-HOST
33	IO INTERIOR LIVE OAK	BLACK OAK (29)	NON-HOST
34	TO TANOAK	TANOAK/CHINKAPIN (32)	NON-HOST
35	GC GIANT CHINKAPIN	TANOAK/CHINKAPIN (32)	NON-HOST
36	AS QUAKING ASPEN	ASPEN (19)	NON-HOST
37	CL CALIFORNIA-LAUREL	NON-HOST (40)	NON-HOST
38	MA PACIFIC MADRONE	NON-HOST (40)	NON-HOST
39	DG PACIFIC DOGWOOD	NON-HOST (40)	NON-HOST
40	BM BIGLEAF MAPLE	NON-HOST (40)	NON-HOST
41	MC CURLLEAF MOUNTAIN-MAHOGANY	NON-HOST (40)	NON-HOST
42	OS OTHER SOFTWOODS	OTHER SOFTWOOD (17)	P-TYPE
43	OH OTHER HARDWOODS	OTHER HARDWOOD (18)	NON-HOST

Appendix C: Model Parameter Default Values



SPECIES LIST AND PRIMARY DISEASE MODEL PARAMETER DEFAULTS

column descriptions:

- Species index number
CD - Species alpha code
Common Name
Resinous - Resinous (R) / Non-resinous (-) designation
P - Species is host to Heterobasidion (aka Annosus) P-type
S - Species is host to Heterobasidion (aka Annosus) S-type
NONE - Species is not host to either Heterobasidion types
PNINF - Probability of infection upon contact (keyword
InfMult)
PKILL - Proportion of root radius infected which causes death
(keyword InfKill)
RLTTD - Relative time to death from initial infection (keyword
TTDMult)
PCOLO - Proportion of root radius colonized after death
(keyword InfColo)

To keep the tables as complete units on a single page, Heterobasidion default values are on the following page and the Armillaria and Phellinus default values are on next page.

Heterobasidion (Annosus) Default Values

#	CD	COMMON NAME	Res- inous	ANNOSUS TYPE			--Annosus both types---			
				P	S	NONE	PNINF	PKILL	RLTTD	PCOLO
1	WP	WHITE PINE	R	P			0.4	0.6	1.0	0.8
2	WL	WESTERN LARCH	R		S		0.4	0.9	1.0	0.95
3	DF	DOUGLAS-FIR	R		S		0.4	0.9	1.0	0.95
4	GF	GRAND FIR	-		S		0.5	0.8	1.5	0.9
5	WH	WESTERN HEMLOCK	-		S		0.5	0.8	1.75	0.9
6	RC	W. REDCEDAR	R		S		0.0	1.0	1.0	1.0
7	LP	LODGEPOLE PINE	R	P			0.4	0.5	1.5	0.75
8	ES	ENGELMANN SPRUCE	-		S		0.4	0.9	1.0	0.95
9	AF	SUBALPINE FIR	-		S		0.5	0.8	1.5	0.9
10	PP	PONDEROSA PINE	R	P			0.5	0.5	0.5	0.75
11	MH	MOUNTAIN HEMLOCK	-		S		0.5	0.8	1.75	0.9
12	SP	SUGAR PINE	R	P			0.4	0.6	1.0	0.8
13	WF	WHITE FIR	-		S		0.5	0.8	1.5	0.9
14	IC	INCENSE CEDAR	-	P			0.5	0.9	1.75	0.95
15	RF	RED FIR	-		S		0.5	0.8	1.5	0.9
16	SF	P. SILVER FIR	-		S		0.5	0.8	1.5	0.9
17	OS	OTHER SOFTWOOD	R	P			0.5	0.8	1.5	0.9
18	OH	OTHER HARDWOOD	-			N	0.0	1.0	1.0	1.0
19	AS	ASPEN	-			N	0.0	0.0	99.0	0.0
20	BS	BLUE SPRUCE	-		S		0.0	1.0	1.0	1.0
21	CB	CORKBARK FIR	-	P			0.0	1.0	1.0	1.0
22	WB	WHITEBARK PINE	R	P			0.4	0.6	1.0	0.8
23	LM	LIMBER PINE	R	P			0.0	1.0	1.0	1.0
24	CO	COTTONWOOD	-			N	0.0	0.0	99.0	0.0
25	WS	WHITE SPRUCE	-		S		0.0	0.9	1.0	0.95
26	JU	JUNIPER	-	P			0.4	0.5	0.5	0.75
27	OC	OTHER CONIFERS	-	P			0.45	0.75	1.0	0.9
28	GS	GIANT SEQUOIA	R		S		0.5	0.9	1.75	0.95
29	BO	BLACK OAK	R			N	0.0	0.0	99.0	0.0
30	OTH	OTHER	-	P			0.0	1.0	1.0	0.86
31	JP	JEFFREY PINE	R	P			0.5	0.5	0.5	0.75
32	TO	TANOAK/CHINKAPIN	R			N	0.0	0.0	99.0	0.0
33	PI	PINYON PINE	-	P			0.4	0.7	1.0	0.9
34	YC	YELLOW CEDAR	R		S		0.4	0.8	1.5	0.95
35	RW	REDWOOD	R		S		0.4	0.8	2.0	0.95
36	LL	SUBALPINE LARCH	-		S		0.4	0.8	1.5	0.95
37	KP	KNOBCONE PINE	-	P			0.4	0.7	1.0	0.9
38	PY	PACIFIC YEW	-	P			0.4	0.8	1.5	0.95
39	NF	NOBLE FIR	-		S		0.4	0.8	1.5	0.95
40	NH	NON-HOST	-			N	0.0	1.0	99.0	0.0

Armillaria ostoyae and Phellinus sulphurascens Default Values

#	CD	COMMON NAME	Res- inous	-----Armillaria-----				-----Phellinus-----			
				PNINF	PKILL	RLTTD	PCOLO	PNINF	PKILL	RLTTD	PCOLO
1	WP	WHITE PINE	R	0.1	0.3	1.8	1.0	0.1	0.85	3.0	0.8
2	WL	WESTERN LARCH	R	0.05	1.0	2.0	1.0	0.2	0.75	1.5	0.6
3	DF	DOUGLAS-FIR	R	0.5	0.8	1.0	1.0	0.4	0.8	1.0	0.3
4	GF	GRAND FIR	-	0.6	0.8	0.75	1.0	0.4	0.6	1.0	0.85
5	WH	WESTERN HEMLOCK	-	0.1	0.8	0.9	1.0	0.2	0.8	1.5	0.8
6	RC	W. REDCEDAR	R	0.1	0.75	1.2	1.0	0.02	0.85	10.0	0.8
7	LP	LODGEPOLE PINE	R	0.2	0.3	1.8	1.0	0.1	0.85	3.0	0.8
8	ES	ENGELMANN SPRUCE	-	0.5	0.75	1.1	1.0	0.2	0.65	1.1	0.8
9	AF	SUBALPINE FIR	-	0.5	0.8	0.75	1.0	0.4	0.6	1.0	0.75
10	PP	PONDEROSA PINE	R	0.2	0.3	1.8	1.0	0.1	0.85	3.0	0.65
11	MH	MOUNTAIN HEMLOCK	-	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.8
12	SP	SUGAR PINE	R	0.1	0.3	1.8	1.0	0.1	0.85	3.0	0.6
13	WF	WHITE FIR	-	0.6	0.8	0.75	1.0	0.4	0.6	1.0	0.3
14	IC	INCENSE CEDAR	-	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.85
15	RF	RED FIR	-	0.5	0.8	0.75	1.0	0.4	0.6	1.0	0.3
16	SF	P. SILVER FIR	-	0.6	0.8	0.75	1.0	0.4	0.6	1.0	0.85
17	OS	OTHER SOFTWOOD	R	0.1	0.3	1.8	1.0	0.1	0.85	3.0	0.8
18	OH	OTHER HARDWOOD	-	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.8
19	AS	ASPEN	-	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.75
20	BS	BLUE SPRUCE	-	0.5	0.75	1.1	1.0	0.2	0.65	1.1	0.65
21	CB	CORKBARK FIR	-	0.6	0.8	0.75	1.0	0.4	0.6	1.0	0.8
22	WB	WHITEBARK PINE	R	0.1	0.3	1.8	1.0	0.1	0.85	3.0	0.8
23	LM	LIMBER PINE	R	0.1	0.3	1.8	1.0	0.1	0.85	3.0	0.8
24	CO	COTTONWOOD	-	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.8
25	WS	WHITE SPRUCE	-	0.5	0.75	1.1	1.0	0.2	0.65	1.1	0.8
26	JU	JUNIPER	-	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.8
27	OC	OTHER CONIFERS	-	0.6	0.8	0.75	1.0	0.4	0.6	1.0	0.8
28	GS	GIANT SEQUOIA	R	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.8
29	BO	BLACK OAK	R	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.8
30	OTH	OTHER	-	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.8
31	JP	JEFFREY PINE	R	0.2	0.8	1.8	1.0	0.1	0.85	3.0	0.8
32	TO	TANOAK/CHINKAPIN	R	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.8
33	PI	PINYON PINE	-	0.1	0.8	0.9	1.0	0.4	0.8	1.5	0.8
34	YC	YELLOW CEDAR	R	0.1	0.8	0.2	1.0	0.02	0.85	10.0	0.8
35	RW	REDWOOD	R	0.1	0.8	10.0	1.0	0.02	0.85	10.0	0.8
36	LL	SUBALPINE LARCH	-	0.1	0.8	1.1	1.0	0.4	0.8	1.5	0.8
37	KP	KNOBCONE PINE	-	0.1	0.8	10.0	1.0	0.1	0.85	10.0	0.8
38	PY	PACIFIC YEW	-	0.1	0.8	0.2	1.0	0.02	0.85	10.0	0.8
39	NF	NOBLE FIR	-	0.4	0.8	0.75	1.0	0.4	0.6	1.0	0.8
40	NH	NON-HOST	-	0.0	1.0	99.0	1.0	0.0	1.0	99.0	0.8