

AN ABSTRACT OF THE THESIS OF

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Title: FACTORS AFFECTING INTER-TREE ROOT CONTACT AND THE TRANSMISSION
OF *PHELLINUS WEIRII* IN YOUNG-GROWTH DOUGLAS-FIR

Abstract approved: { **Redacted for Privacy**
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Groups of second-growth Douglas-fir (Mirb.) Franco were excavated in plots of two to six trees on two sites in the vicinity of Cowichan Lake, Vancouver Is., British Columbia. Eleven excavation plots provided 36 trees which could be studied in pairs (a total of 50 pairs) in order to ascertain the relation of root attributes and tree, stand and site characteristics to the extent of root contact occurring between pairs of trees.

Regression analysis was used to relate the combined root attributes of two trees jointly occupying the same soil space to the number of root contacts. Three contact types were recognized: tenuous (Type I), substantial (Type II-III) and apparent grafts (Type IV). Type I contacts were found to be positively related to root length and negatively related to root volume. Type II-III contacts were positively related to the number of roots. Type IV contacts were positively related to both root number and cross-sectional area.

Discriminant analysis was employed to determine the relation of various tree, stand and site factors to the probability of root contact. Three contact groups were defined: 1) no contact, tree-pairs for which no contacts occurred; 2) low contact incidence, tree-pairs with only Type I contacts and 3) high contact incidence, tree-pairs having both Type I and higher order root contacts. Inter-tree slope distance, DBH, effective rooting depth, soil gravel content and percent slope were all found to be significant.

The results of the discriminant analysis were incorporated into a model for spread of laminated root rot. The goal of the spread model is to characterize the behavior of the system in order to evaluate the influence of silvicultural options and environmental constraints on the ability of laminated root rot to spread from tree to tree.

The model consists of four submodels: tree growth and survival, root contact, infection and spread. Twenty-seven simulation runs were made to evaluate the effects of tree spacing, stand age and soil depth on the cumulative distribution of earliest time to bole infection under conditions of constant soil gravel content and percent slope. Three principle areas are identified in the model where better or more complete information is necessary before the model can be considered adequately specified. These are: time to fungal growth cessation following bole infection, the shape and location of the potential contact zone and the distribution of contacts within this zone and certain features of the spread behavior of *Phellinus weirii*. Numerical solutions for the relation between the tree, stand and site factors and the cumulative distribution of time to earliest bole infection were not attempted,

consequently. A qualitative analysis of the laminated root rot spread system's behavior was undertaken, however. The salient features of this analysis are:

- 1) the cumulative distribution function of earliest time to bole infection is a composite function consisting of two functions, one for each of two recognized phases in the distribution function.
- 2) the phases of the composite function can be physically interpreted as two relatively distinct infection waves; the first wave corresponds to primary infection from a source while the second represents secondary infection from adjacent trees.
- 3) the functional form of the phase I relation is given by the single process law while the form of phase II is given by a simple exponential expression and
- 4) all of the initial conditions studied influence the shapes, slopes and asymptotes of the two phases.

Factors Affecting Inter-Tree Root Contact and
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FACTORS AFFECTING INTER-TREE ROOT CONTACT AND
THE TRANSMISSION OF *Phellinus weirii* IN YOUNG-GROWTH DOUGLAS-FIR

I. INTRODUCTION

The prospect of a broadening impact of root disease on young growth timber management in the Pacific Northwest promises to create increasing demands upon forest managers faced with dwindling timber supplies. Though root disease has never taken on, and probably never will take on, catastrophic proportions in the region, the need to deal effectively with affected or threatened areas of timber production will continue to grow as the resource becomes progressively scarcer. In Oregon and Washington alone, it has been estimated that root rots account for an annual loss of approximately 1.4 million cubic meters in Douglas-fir (Childs and Shea 1967), 90 percent of this occurring in the westside Douglas-fir subregion. *Phellinus weirii* (Murr.) Gilbertson, alone, is responsible for an estimated annual loss of 0.90 million cubic meters in the subregion. Losses due to *Fomes annosus* (Fr.) Cooke and *Armillaria mellea* (Fr.) Karst account for the majority of the difference. Moreover, mortality and loss of growth potential in young-growth (2.25 million cubic meters) far exceeds that found in old-growth timber (0.92 million cubic meters) for all root rots in the region.

Current understanding of the epidemiology of root diseases in general has been derived from studies of the pathogens' biology. Little attention has been given to host and environmental factors that affect the spread of disease within a stand of trees. It has, however, been clearly demonstrated for *P. weirii* (Wallis and Reynolds 1965) and *F.*

annosus (Rishbeth 1950) that little or no mycelial growth away from roots occurs. As a result, growth within the soil is limited to the inner wood and bark surfaces of the host. This information has profound consequences: it suggests that the distribution of roots within a stand must exert a significant influence on the spread of root diseases. The latter observation is of particular significance in the case of both *F. annosus* and *P. weirii* by virtue of the apparent biological constraints on free mycelial growth through soil. On the other hand, it is possible that root distribution plays a less significant role in the epidemiology of *A. mellea* inasmuch as the ability to spread via rhizomorphs must also be taken into account.

This study has two major objectives: 1) to determine the types of factors that influence the potential for spread of *P. weirii* in second growth Douglas-fir and the manner in which they do so and; 2) to develop a model for inter-tree spread of laminated root rot in young-growth Douglas-fir.

The data which provided a basis for the analyses relevant to the first objective were obtained by hydraulic root excavations. The first objective is approached from two perspectives. First, the influence of various root attributes (for instance, volume, length) on both the numbers and types of contacts within a defined volume of soil is examined. This information could be readily incorporated into a model for inter-tree spread of laminated root rot. Such a model would take into account the actual root distributions of trees. The second aspect of the first objective concerns the influence of tree, stand and site factors on the probability of inter-tree root contact. The results of

the analyses related to this work constitute a contribution to the second objective of the study.

The epidemiological model developed here is a model for inter-tree spread of laminated root rot. This model represents a very simplified and idealized system involving tree-tree and tree-fungus interactions. The goal associated with this aspect of the study is to characterize the behavior of the system for the purpose of evaluating how silvicultural options and environmental constraints influence the propensity for spread of laminated root rot. Though greatly simplified, the modeling effort required a simulation approach. The model and simulator are covered in detail in RESULTS, part B.

The inter-tree spread model can easily be adapted for use as a submodel in a stand model for laminated root rot impact. Dr. W. J. Bloomberg (personal communication) has been developing such a stand model.

II. LITERATURE REVIEW

Early Taxonomic Work

Phellinus weirii (Murr.) Gilbertson, the cause of laminated root rot of Douglas fir, was originally described by Murrill (1914) as *Fomitoporia weirii* Murrill from a western red cedar specimen collected by Weir in 1912. In Murrill's 1914 publication, however, the fungus was renamed *Poria weirii* Murrill. Gilbertson (1974) has placed *P. weirii* in the genus *Phellinus*. *Phellinus weirii* was first described in the Pacific Northwest at the Dominion Laboratory of Forest Pathology in Victoria, B.C. from a specimen collected at the Lake Cowichan Forest

Experiment Station in 1928 (Mounce *et al.* (1940)). Upon comparing their own description to that of Murrill, the latter authors concluded that this specimen was either a variety of *P. weirii* or a closely related species. Cultural and decay characteristics were similar in many respects. The most obvious differences related instead to habit. For instance, the specimens described by Mounce *et al.* (1940) were found on Douglas-fir (*Pseudotsuga mengiesii*) and western hemlock (*Tsuga heterophylla*) and the sporophores were annual as opposed to perennial (as described by Murrill).

Distribution of the Disease

Subsequent to its discovery in the vicinity of Lake Cowichan, *P. weirii* was found throughout the southern half of Vancouver Island (Mounce *et al.* 1940). Bier and Buckland (1947) reported the fungus to be distributed ". . . as far north as the islands in Johnstone Strait, east in the lower Fraser Valley to Yale and from the interior at Revelstoke." Later work indicated that many stands in the Pacific Northwest have at least some incidence of laminated root rot (Childs 1955; Johnson 1976). The present known geographic range within the region extends from Central British Columbia, south to northern California and east to north Idaho (Childs 1970; Childs and Nelson 1971). Moreover, *P. weirii* has been reported from Japan (Aoshima 1953).

Hosts

Most major timber species in the Pacific Northwest are infected to some extent (Buckland and Wallis 1956; Shea 1968; Childs and Nelson 1971; Hadfield and Johnson 1977). Those that are especially susceptible include

silver fir (*Abies amabilis*), grand fir (*Abies grandis*), mountain hemlock (*Tsuga mertensiana*) and Douglas fir, while incense cedar (*Calocedrus decurrens*), ponderosa pine (*Pinus ponderosa*) and western red cedar (*Thuja plicata*) exhibit little or no susceptibility (Childs 1970, Hadfield and Johnson 1977; Filip and Schmitt 1979). Western hemlock is considered moderately susceptible.

Symptoms and Signs

The most prominent feature of stands infected by *Phellinus weirii* is the occurrence of stand openings as a result of mortality within the infection centers (Mounce *et al.* 1940, Childs 1960, 1970; Hadfield and Johnson 1977). While often limited to a few hundred square feet, openings may be up to an acre or more in extent (Wallis and Reynolds 1965; Childs 1960, 1970; Childs and Nelson 1971). Within an infection center, windthrown trees are a common feature. Typically they are in various states of decay, indicating that damage within the area has been occurring over an extended period. The direction of fall exhibits a distinctly random pattern in contrast to the uniform pattern associated with blowdown due to winter storms (Hadfield and Johnson 1977). Leaning trees are common toward the margin of a center (Childs 1960; Shea 1968).

Individual trees vary considerably in their degree of symptom expression prior to blowdown (Buckland *et al.* 1952; Buckland and Wallis 1956; Childs 1955; Hadfield and Johnson 1977). Wallis (1957) has noted that trees may remain apparently healthy and vigorous well into the advanced stages of root decay. As an extreme example, he cites the case

of a tree which, in 1955, had lost 100 percent of its live root system due to infection by *P. weirii* in spite of which leader growth had been 33.5 inches and 24.0 inches for the 1953 and 1954 growing seasons, respectively. The phenomenon was sufficiently common in the latter study that the author concluded that trees generally do not exhibit recognizable symptoms until at least 50 percent of the root system has been killed. Accordingly, it is not unusual to find trees recently wind-thrown or still standing whose root systems are severely infected yet show little or no crown symptoms (Buckland *et al.* 1952; Childs 1970).

When observable, indicators of infection are first a reduction in (leader and branch) growth followed by thinning and chlorosis of the foliage which is sometimes accompanied by the production of distress cone crops (Mounce *et al.* 1940; Bier and Buckland 1947; Childs 1960; Hadfield and Johnson 1977; Shea 1968). Tree death usually follows within a few years of such symptom expression; the foliage then turns a yellow to reddish-brown color (Mounce *et al.* 1940; Buckland *et al.* 1952; Childs 1970). Regardless of symptom expression prior to blowdown, the disease is readily diagnosed subsequently by the presence of root balls and the characteristic decay.

Incipient decay appears as a reddish-brown crescent or ring of stained wood in a transverse section through the bole or as a streak in longitudinal section (Mounce *et al.* 1940, Bier and Buckland 1947; Childs and Nelson 1971; Hadfield and Johnson 1977). Decay may extend up to 4 meters into the butt log of living trees. In later stages, the decay causes the wood to separate along the annual rings, imparting a distinctly laminated appearance, and to turn a yellowish to brown color.

Numerous small pockets are apparent in the decayed wood at this stage; they measure 0.5 by 1.0 mm and may be empty or filled with white mycelium. Brown, felt-like mycelial mats are often found between the laminations, in wood crevices or on the bark surface of roots. Using a 10 x hand lens, the characteristic setal hyphae of *P. weirii* can also be observed. Eventually the wood decomposes into a loose, stringy mass and still later only a hollow butt may remain, leaving only branch bases still more or less intact (Childs 1970).

Mounce *et al.* (1940) provide a detailed description of the sporophore. These are found on the undersides of down trees, uprooted stumps and rarely, on standing dead trees (Bier and Buckland 1947; Buckland *et al.* 1952; Hadfield and Johnson 1977). They are not found until the wood is well decayed and the tree has been dead for some time. Sporophores appear from late summer to early fall. In the Pacific Northwest, they are annual. Because they are only rarely produced, they are not considered a useful diagnostic tool (Childs 1960).

Susceptibility of and Damage to Douglas-fir.

Susceptibility of individual trees and the implications for fungal survival.

The earliest reports in the region make it clear that trees of all vigor classes are susceptible to laminated root rot (Mounce *et al.* Bier and Buckland 1947; Buchanan 1948). Buckland *et al.* (1952) concluded that all Douglas-fir trees over the age of six years were, for all practical purposes, equally susceptible, though the period between initiation of infection and death was quite variable among trees. Moreover,

this variation could not be accounted for even when the position of the initial infection (with respect to the bole) was taken into account. It was noted, however, (Buckland *et al.* 1952; Buckland and Wallis 1956) that variation in rate of symptom development might be related to degree of host resistance. "Resistant" trees may exhibit little or no symptom development due to: 1) confinement of *P. weirii* to the heartwood, 2) production of adventitious roots and 3) protection from wind within an intact stand. "Susceptible" trees, on the other hand, appeared to exhibit symptoms more or less in direct proportion to the percentage of dead sapwood.

Buckland *et al.* (1952) suggested that resistant trees could be expected to serve as an important source of inoculum in the next generation:

This waterproof, resin-soaked wood prevents the fungus from being drowned, greatly impedes its growth, protects the wood from further saprophytic colonization, and provides a habitat that enables the pathogen to survive over extended periods of time. p. 75

Wallis and Reynolds (1965) proffered a similar opinion. Childs' (1963) work suggested that, in half the cases studied, death could be ascribed to physiological causes associated with encroachment by *P. weirii* on the sapwood and that, in the remaining cases, the trees, though resistant, are windthrown due to deterioration of the root heartwood. Estimation of time of survival of the fungus in stumps range from 50 to 100 years (Buckland *et al.* 1952; Buckland and Wallis 1956; Childs 1955, 1963, 1970; Childs and Nelson 1971; Hadfield and Johnson 1977; Hansen 1976, 1979; Wallis 1957).

Trees lacking resistance, on the other hand, would be rapidly colonized with little associated resin production. Decay would then proceed rapidly, followed by rapid saprophytic displacement of *P. weirii* (Buckland *et al.* 1952). It must be emphasized, however, that the above was no more than speculative, being based for the most part on circumstantial evidence. Later, critical studies on inoculum survival are discussed in section F.

Factors influencing degree of stand damage.

Buckland *et al.* (1952) have characterized the relationship between stand development and the potential for disease transmission (and thus, also, damage) in a general way. Minimal damage can be expected in stands less than 20 years old since root system development is neither very intensive nor extensive and inter-tree root contact is thus limited. Later studies by McMinn (1963) on the root system structure of Douglas-fir confirm this view. Greatest damage, it was felt, could be expected in 20 to 60 year old stands. Subsequently, damage would begin to diminish as natural thinning reduced the frequency of root contact between the remaining crop trees. The basic pattern of this scenario is generally accepted; however, as experience with the natural history of *P. weirii*-infected stands accumulated, the upper limit for the period of maximum stand damage has been set as high as 150 years (Wallis and Reynolds 1967).

Of special interest to the current study is the following: "Fluxuations in rate of spread of the disease (and, hence, damage) can be attributed to the variation in number of root contacts." (Buckland *et al.*

1965, p. 73). Intuitively, it seems reasonable to suppose that as a stand develops (and so also the root systems of the trees that comprise that stand) the potential for root contact will increase up to some point. A quantitative understanding of how stand development influences this potential, and how soil and other site conditions act to modify it, has been lacking (Childs and Nelson 1971; Shea 1968; Wallis and Reynolds 1967). Stand age, stocking density, effective rooting depth, slope and rock content of the soil have all been suggested as factors that may be involved in determining the rate of disease spread and stand damage.

Two studies suggest a general relationship between site factors and disease development (Molnar *et al.* 1961; Schultz 1963). In both cases, greater damage was associated with shallower, rockier soils. This may be explainable in terms of McMinn's (1963) observations that:

On reaching an obstructing layer such as fragipan, bed-rock or cobbles and boulders, taproots and other elements of the deep-root system commonly proliferated into several branches. Such branches frequently followed the contour of the obstruction for several meters. (p. 117)

There is good reason to suppose that shallow, stony soils may enhance inter-tree root contact and facilitate the spread of disease. In this same study, McMinn also characterizes root system development as having two recognizable stages: an early, pioneer phase in which the main, structural roots grow rapidly outward and colonize the growing space and; a later phase, during which much of the root elongation is contributed by high order branches that more intensively colonize the site. McMinn further noted that, although lateral extent of rooting was closely

associated with crown width, overlap of rooting zones of adjacent trees was common even in the more central rooting zone about a tree. Increase in root contacts thus appears likely in the later stages of stand development. Schultz's (1963) work dealt specifically with stand and site factors influencing grafting among Douglas-fir trees. He found that grafting incidence increased as the stand developed with decreasing soil depth and with increasing stoniness and percent slope. It is reasonable to suppose that root contact in general is increased under the same circumstances and that the spread of disease is thus facilitated.

Red alder (*Alnus rubra*) assumes a controversial role as a possible deterrent to the survival of *P. weirii*. As such, it deserves consideration as an influence on damage to future stands of Douglas-fir. Its role in this regard is discussed in connection with general aspects of *P. weirii*'s survival below.

Assessment of stand damage.

Though it is clear that *P. weirii* is a destructive disease agent, the actual damage has proven difficult to assess. In part, the difficulties are attributable to the variation in symptom expression. A further unpredictable aspect of damage assessment which compounds the problem is the possibility of rapid population build-ups of bark beetles which may not only hasten the death of infected trees but healthy neighbors as well (Buckland and Wallis, 1956; Childs 1963, 1970; Childs and Nelson 1970; Wallis and Reynolds 1965).

In spite of these handicaps, a number of "rules of thumb" and principles have evolved which can aid in damage assessment. Childs (1955) reported that 50 percent of the trees within a half chain of an infected tree could be expected to be infected and that only a few would be found infected at a distance of a chain or more. A later study (Childs 1963), essentially confirmed these earlier findings. In his 1955 paper, Childs also suggested that: 1) when infection centers were common in small Douglas-fir pole stands, losses would be severe before the stand reached saw-timber size and 2) openings created by laminated root rot would not be effective in obtaining release of trees on the margin since they would be too heavily infected to take advantage of the increased availability of light and soil moisture, etc.

On the basis of stand reconstruction studies, Childs (1960) estimated that damage in poles and young saw-timber could be expected to double every 15 years. Along similar lines, Hadfield and Johnson (1977) state that damage to the current rotation will be at least as heavy as in the previous one. In general losses due to butt rot are small (Childs and Nelson 1971; Hadfield and Johnson 1977), especially when compared to losses due to mortality and reduced growth potential in young stands.

Initiation, Spread and Persistence of Infection.

Initial infection from stumps.

Buchanan (1948) was the first worker to associate infected stumps from the previous stand with the initiation of infection in the current one. Numerous workers have subsequently confirmed this relationship

(Buckland *et al.* 1952; Buckland and Wallis 1956; Childs 1955, 1963, 1970; Childs and Nelson 1971; Hadfield and Johnson 1977; Wallis 1957, 1962; Wallis and Reynolds 1965, 1967). A very recent study (Filip 1979) establishes some quantitative relationships between the frequency of infected stumps and mortality.

Persistence of disease.

The role of zone lines. Garrett (1970) has characterized a zone line as ". . . a boundary envelope of the fungal colony in the wood (which) is formed by a tissue of dark-coloured, sclerotoid and inflated fungal cells." (p. 167). Work by Hopp (1938) and Rishbeth (1951) indicates that zone lines are formed in response to gradual desiccation of the wood. A series of studies by Nelson (1964, 1967, 1969, 1973) on the biological significance of zone line formation by *P. weirii* produced the following conclusions:

- 1) Other conditions being favorable, zone lines do not form in the absence of competition. (1973)
- 2) Zone lines serve a general protective function, though highly competitive/antagonistic fungi can breach the barrier and displace *P. weirii*. (1964, 1973)
- 3) Zone line formation is more rapid in wood with advanced decay, but this does not contribute to the efficiency of the barrier. (1967).
- 4) Survival of *P. weirii* in wood improves with depth.

Support for the second conclusion can also be found in the work of Rishbeth (1951) on *F. annosus* and Bliss (1951) on *A. mellea*. With

respect to the last conclusion, Rishbeth (1951) suggested that alternate wetting and drying of wood promotes concomitant expansion and contraction which in turn leads to mechanical disruption of the zone line barrier. Thus the more constant environmental conditions at greater soil depths may favor survival in addition to the possible influence of fewer antagonists (Nelson 1967). The retreat of *F. annosus* down into a stump (Rishbeth 1951) and of *P. weirii* back into the stump (Hansen 1979) is accompanied by the formation of a succession of zone lines which Garrett (1970) has colorfully described as a "succession of rearguard actions" (p. 168).

The role of red alder and effects of fertilization. The use of red alder (*Alnus rubra*) in the Douglas-fir subregion either as an alternate crop or in mixture with Douglas-fir has attracted interest quite apart from any possible influence it may exert over *P. weirii*. Numerous studies point to favorable changes in understory composition (greater diversity and abundance of species), soil nitrogen content, foliar nitrogen content of associated crop trees, bulk density, organic matter content, moisture holding capacity and, as a result, site productivity (Franklin and Pechanec 1968, Tarrant *et al.* 1951; Bollen and Lu 1968; Tarrant 1961, 1968; Tarrant and Trappe 1961, 1971; Tarrant and Miller 1963).

Considerable attention has focused on the question of whether red alder's soil amending properties influence the survival of *P. weirii* (Trappe 1970a, 1970b, 1971; Trappe *et al.* 1973; Nelson *et al.* 1978). Changes in the soil microflora's composition have been clearly

demonstrated (Lu *et al.* 1968; Neal *et al.* 1968; Wicklow *et al.* 1974). In particular, species of both *Streptomyces* and *Trichoderma*, some of which are antagonistic to *P. weirii*, have been found in greater abundance under red alder stands. In spite of this, and soil biochemical changes induced by red alder (Li *et al.* 1967a, 1967b, 1969, 1970, 1972; Lu *et al.* 1968), evidence for a real effect of alder on the survival of *P. weirii* is contradictory. Nelson has found both positive (1968) and negative (1975b) effects on *P. weirii*'s survival in wood blocks buried under alder stands. Hansen (1975, 1976, 1979) found no evidence to suggest that survival of *P. weirii* in stumps was significantly reduced in the presence of alder. Similarly, the evidence for nitrogen fertilization as a means of reducing the pathogen's survival time is contradictory. Positive effects have been demonstrated by Nelson (1967, 1970, 1975a). Negative results have been obtained by Nelson (1970, 1975b) and Wallis and Reynolds (1974).

Long-term survival in stumps and roots. Wallis and Reynolds (1965) have examined the survival of *P. weirii* in roots. They found that roots inoculated up to one year after felling differed only slightly from inoculated roots of newly fallen trees in their suitability as a substrate for colonization. Survival in root segments, ranging in diameter from less than two cm. to more than eight cm., was also examined; average survival across all diameter classes was greater than 98 percent for the 8 year period. Similarly, in ten trees felled 11 years previously, "Eighty-two percent, including roots as small as 1.5 cm in diameter contained *P. weirii* mycelium . . ." (p. 6). Stump excavations by

Hansen (1976, 1979) indicate that:

- 1) there is a ". . . progressive retreat of *P. weirii* from infected roots toward the stump." (1979, p. 485)
- 2) little or no colonization of sound wood occurs subsequent to harvest and
- 3) there is a progressive decrease in the occurrence of ectotrophic mycelium with time from harvest (at 50 years, only 3 percent of 371 roots had surface mycelium compared to 42 percent of 489 roots after 20 years).

With respect to the first conclusion, it was found that "On sites regenerated to Douglas-fir, *P. weirii* was alive in 96%, 59% and 26% of the stumps after 20, 30, and 50 years, respectively." (p. 486) and that the mortality rate of the fungus within individual roots was even more pronounced. Hansen (1979) as well as Wallis and Reynolds (1965) suggest that the ability of *P. weirii* to cause infection after extended periods may be much less than the figures on fungal survival in the wood may suggest.

Means of spread.

The role of basidiospores. Basidiospores play no recognizable role in the spread of laminated root rot. Two extensive surveys (Buckland, Foster and Nordin 1949; Wright and Isaac 1956) indicated that almost no infection of stump surfaces or wounds occur as a result of basidiospore infection. In the latter study, 448 trees with a total of 1218 logging scars were examined. *P. weirii* was found in only four instances. Moreover, it was not clearly established in these instances

that the source of infection was not from below ground. Childs' work (1963) on the spatial relations of clones provided further evidence that the spread of laminated root rot was principally, if not entirely, occurring vegetatively. Further, when freshly cut stump surfaces were inoculated with *P. weirii* basidiospores, no stump infection was observed subsequently (Nelson 1971). Inoculation trials on wood discs in petri dishes were successful, however, (Nelson 1976b) and indicate that the failure of *P. weirii*'s basidiospores to act as effective dispersal agents may be attributable to a very low competitive ability.

Vegetative spread along roots. Mycelial growth of *Phellinus weirii* through the soil is severely restricted (Buckland *et al.* 1952, Wallis, 1962, 1976), growth being almost wholly confined to heartwood (and sapwood to varying degrees) and the bark surface of roots. The transmission of laminated root rot is thus limited to points of root contact. Wallis (1957) and Wallis and Buckland (1956) indicate that surface contact between roots is sufficient; grafting is not a prerequisite for transmission.

Ectotrophic growth of *P. weirii* is considerably faster than growth of the fungus through the wood (Wallis, 1957, 1962, Wallis and Reynolds 1965) and hence might be viewed as the rate determining event of the spread process. Ectotrophic growth was observed as much as two meters in advance of wood colonization in Douglas-fir and one meter in western hemlock. Ectotrophic growth in the distal direction is as great or greater than proximal growth; the respective averages are 20-25 cm/year and 10-20 cm/year on Douglas-fir (Wallis and Reynolds 1962). Several

other facets of growth were also brought out in the latter study: 1) death of the distal portion of an infected root was more common among small roots; 2) the rate of growth during the winter months was as great or greater than during summer months; 3) over a diameter range of 1 to 5 cm, size of the root had no apparent influence on rate of ectotrophic growth and; 4) penetration of large roots required a greater time interval (this being attributable to greater bark thickness).

In the course of his 1957 study, Wallis had observed numerous roots in relatively close proximity (20-50 mm) but saw no evidence for spread of disease across such distances, confirming earlier observations. A later, more detailed, study re-examined the potential for spread of laminated root rot over limited distances (Wallis 1976a). When inoculum blocks were placed two cm. from a live, intact root colonization occurred in 40 percent of the trials. At five cm, colonization fell to 20 percent while none occurred at a distance of 10 cm. In only one instance in all the above trials did bark penetration take place after 18 months, and this occurred in one of the two-cm distance trials. The potential for transmission over various types of materials was examined as well. Means of transmission, other than direct root to root spread included: 1) transmission across "bridges" of heartwood or bark (80% success after 24 months when the bridge joined a healthy root to an inoculum block up to maximum test distance of 10 cm and 100% success after 12 months when the bridge joined a healthy and diseased root up to a maximum test distance of 30 cm); 2) transmission via root surfaces of minor vegetation (no instances of infection were observed, though *P. weirii* had spread up to 15 cm along roots of salal and bracken

fern) and; 3) transmission across rock surfaces (again, no instances of infection but fungus observed growing up to five cm). Finally several tree species commonly associated with Douglas-fir were evaluated for the ability to transmit *P. weirii*. Ectotrophic growth on western hemlock was found to be generally slower than on Douglas-fir (also, Wallis and Reynolds 1965). Growth on western red cedar rarely exceeded a few centimeters, while on lodgepole, white and ponderosa pines growth was typically confined to the immediate site of inoculation 12 months after treatment.

III. MATERIALS AND METHODS

Description of Study Areas

The root excavation work was carried out at the British Columbia Ministry of Forests Lake Cowichan Experiment Station, located approximately 58 km northwest of Victoria, B.C. (48° 49' N 124° 08' W) on Vancouver Island. The experiment station is situated on the south arm of Cowichan Lake, approximately two miles west of the village of Lake Cowichan (fig. 1).

Thirteen plots were excavated in the immediate vicinity of the lake. Plots 1 through 9 were located on the south side of the lake (fig. 1) on the Mesachie Unit of the B.C. Forest Service Lake Cowichan Experiment Station. The elevation for all plots is approximately 175 m. The timber type is relatively uniform throughout the area and has been characterized as a *Pseudotsuga-Polysticum* association (McMinn 1960). Douglas-fir predominates in the overstory with scattered western red cedar and western hemlock and rarely, grand fir. The understory and

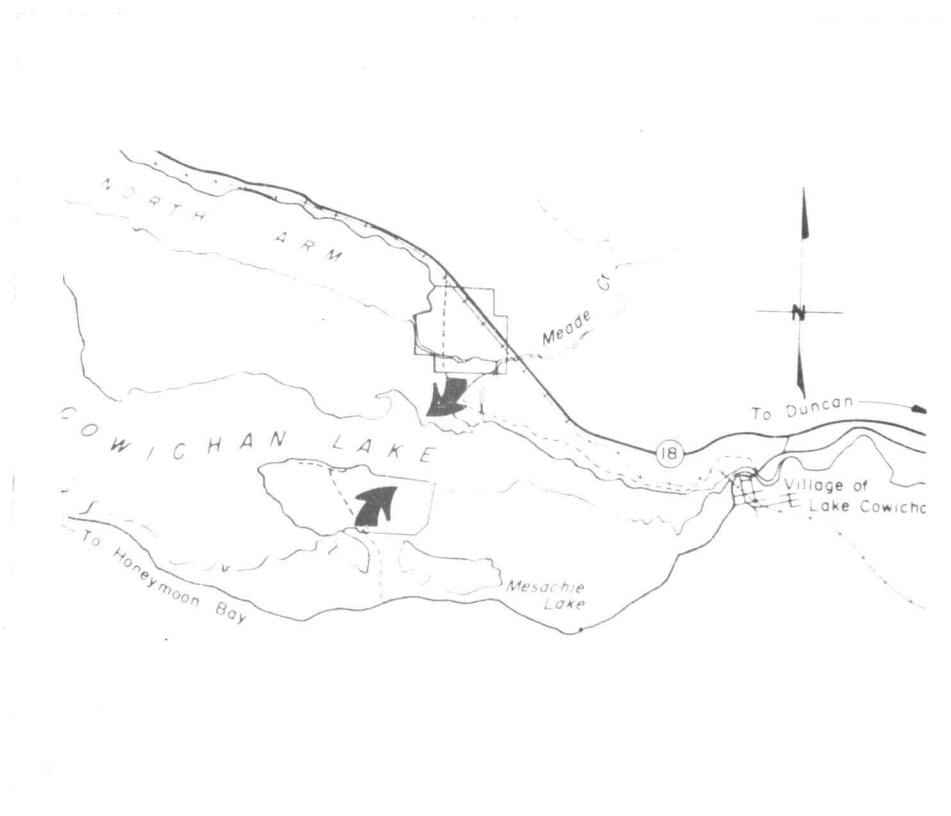


Figure 1. General locations of the excavation plots on the north and south sides of the south arm of Cowichan Lake.

reproduction are a mix of western red cedar and western hemlock. The shrub layer is dominated by sword fern but also includes Oregon grape as a major component. Vanilla leaf is the dominant herb. Stand characteristics for these plots, hereafter referred to collectively as the "south side plots," are summarized in Table I. A profile description based on Plot #9 and representative of all the south side is given in Table II.

Plots 10 through 13 were located across the lake on the north side of the south arm on B. C. Forest Products holdings (fig. 1) and will hereafter be referred to collectively as the "north side plots." Here, also, the timber type is uniform and corresponds to McMinn's (1960) description of the *Pseudotsuga-Gaultheria* association. Douglas-fir is the only tree species in the overstory, understory and reproduction layers in the plots. The shrub layer is almost exclusively salal which commonly attains a height of 1 m. The herb layer is extremely sparse to non-existent. Stand and site characteristics are summarized for the north side plots in Table III. A profile description for plot #12 is given in Table IV and, again, is reasonably representative of all the plots.

The two sites differ in productivity (Tables I and III). McMinn's (1960) study of water relations and their effect on forest type distribution indicated that the *Pseudotsuga-Gaultheria* association is characterized by more xeric summer conditions and the soils of this type are generally less fertile than those of the *Pseudotsuga-Polysticum* association. The close proximity of the north and south side plots should preclude any possibility of significant climatic differences between

TABLE I. SITE AND STAND CHARACTERISTICS FOR SOUTH SIDE PLOTS

	No. of Observations	Mean	S.E. of Mean	Minimum	Maximum
Tree height (m)	18	32.85	2.20	15.60	46.10
DBH (cm)	18	45.72	12.48	20.00	54.00
Age (years)	18	64.89	0.28	63.00	67.00
Gravel (cc/cu ft)	7	3094.14	136.05	2448.00	3617.00
Cobble (cc/cu ft)	7	741.86	142.32	370.00	1450.00
Soil depth (cm)	7	120.00	7.79	85.00	140.00
Slope (percent)	7	48.14	2.22	44.00	60.00

TABLE II: SOIL PROFILE REPRESENTATIVE OF SOUTH SIDE PLOTS

Horizon	Depth (cm)	Boundary	Color	Texture	Structure	Moist/wet Consistency
A ₀ F	2.0-1.0		dark brown	partially decomposed		
A ₀ H	1.0-0.0		dark brown	duff mull felty mor		
A ₂ (roots common)	0-9	clear smooth	rich brown	loam	weak-medium coarse to fine subangular blocky	friable slightly sticky slightly plastic
B (roots common)	9-37	abrupt wavy	red brown	coarse sandy loam	weak, fine subangular blocky	friable slightly sticky slightly plastic
B (roots common)	37-66	clear wavy	olive brown	gravel sandy loam	very weak, fine subangular blocky	very friable non-sticky non-plastic
B (roots sparse- absent)	66-110	--	olive brown	gravel sandy loam	structureless single gravel	loose non-sticky non-plastic

TABLE III. SITE AND STAND CHARACTERISTICS FOR NORTH SIDE PLOTS

	No. of Observations	Mean	S.E. of Mean	Minimum	Maximum
Tree height (m)	18	24.56	1.56	10.50	33.20
DBH (cm)	18	26.19	1.85	9.70	38.60
Age (years)	18	45.39	0.26	43.60	48.00
Gravel (cc/cu ft)	4	2465.00	172.52	2180.00	2940.00
Cobble (cc/cu ft)	4	1445.50	236.95	893.00	1946.00
Soil depth (cm)	4	96.25	6.88	80.00	110.00
Slope (percent)	4	40.00	1.87	35.00	44.00

TABLE IV: SOIL PROFILE REPRESENTATIVE OF NORTH SIDE PLOTS

Horizon	Depth (cm)	Boundary	Color	Texture	Structure	Wet/moist Consistency
A ₀ F	1.5-1.0		dark brown			
A ₀ H	1.0-0.0		dark brown	felty mor.		
A ₂ (roots common)	0-8	clear smooth	reddish brown	gravely, fine sandy loam	medium, weak crumb	very friable slightly sticky to non-sticky non-plastic
B (roots common)	8-16	clear smooth	reddish brown	gravely, fine sandy loam	medium, weak crumb	very friable slightly sticky to non-sticky non-plastic
B (roots common)	16-36	abrupt wavy	reddish brown	gravely, fine sandy loam	coarse, weak crumb to fine weak subangular blocky	very friable slightly sticky to non-sticky non-plastic
B (roots sparse to absent)	36-96+		slightly gleyed	(cobbly) gravely, fine sandy loam	structureless single gravel	loose non-sticky non-plastic

the two areas. It appears that it is the topographic and edaphic features and aspect of the sites which are determining the timber types. Moreover, comparing the profile descriptions in Tables II and IV, it would appear that soil depth and stoniness account for most of the differences in water holding capacity. Table V, from McMinn (1960), provides a summary of climatic data for the area.

Description of Data Collection

Plot selection criteria

The hydraulic excavation of trees used in the study was performed in the summer of 1979. Plots to be excavated were selected on the basis of three criteria. Close proximity to a reliable water supply was the primary concern. The vicinity of Lake Cowichan was selected (streams on the island rapidly dry up in late spring due to the limited snow pack). Another consideration of practical significance was slope. A minimum slope and the extent of unimpeded drainage for soil movement become particularly important in those instances where three or more trees were excavated as a group. Under such circumstances, it was necessary to move rather large volumes of soil. Overall, the plots selected had an average slope of approximately 40 percent. Finally, characteristics of individual trees were taken into account (Table I and III) in an attempt to include a range of these characteristics.

Excavation procedure

The general method of excavation has been described by McMinn (1963). The method employed in the current study differs from McMinn's

TABLE V: SUMMARY OF CLIMATIC DATA^a

Mean annual precipitation	225 cm
Mean summer precipitation	13 cm
Mean summer maximum temperature	29°C
Mean summer range	24°C
Mean winter minimum temperature	-8°C
Mean winter range	17°C

^afrom McMinn (1960)

in some respects, however. Except in one instance, no support was provided for stumps since enough surrounding or underlying soil was left in place to provide the necessary support. Additionally, the precise position of roots was not maintained by wire guys since the principal goal was to determine root contact and these could be noted and flagged accordingly as the excavation work was in progress.

Prior to actually initiating the excavation, all brush and ground cover was removed down to bare soil in the vicinity of the trees to be excavated. A pathway was cleared down the slope as well to provide free soil movement down slope.

The pump utilized for excavation was a Wajax Mark III which is a high pressure centrifugal pump with a capacity to deliver 225 gallons per minute at a nozzle pressure of 10 p.s.i. at 10 feet. Two members of the crew handled the hoses. Hose pressure could be varied by an adjustable nozzle. Generally, lower pressures were used to clear soil away from the roots and higher pressures used to clear accumulations of soil. The third crew member cleared large cobbles and stones from the pit and insured the unimpeded flow of soil down slope. The fourth member was engaged in observing the roots as they were uncovered in order to locate points of contact as soon after soil removal as possible and flag these points with ribbon for future reference. Typical excavations plots are depicted in Figures 2 and 3.

Root mapping procedure

Once all the plots had been excavated, the mapping was begun. The general mapping procedure was developed by Dr. W. J. Bloomberg (Pacific

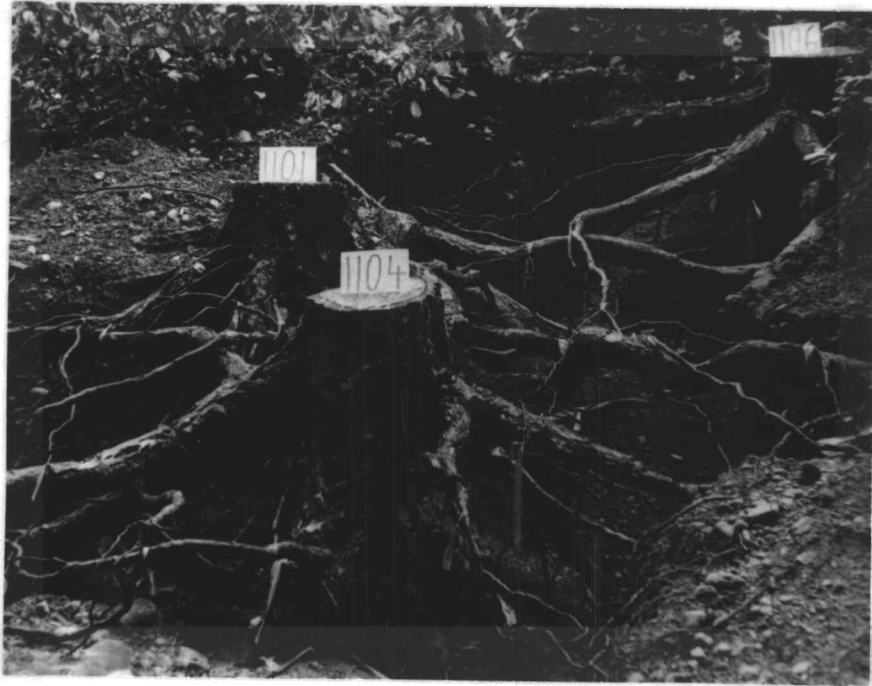


Figure 2. Example of an excavation plot.

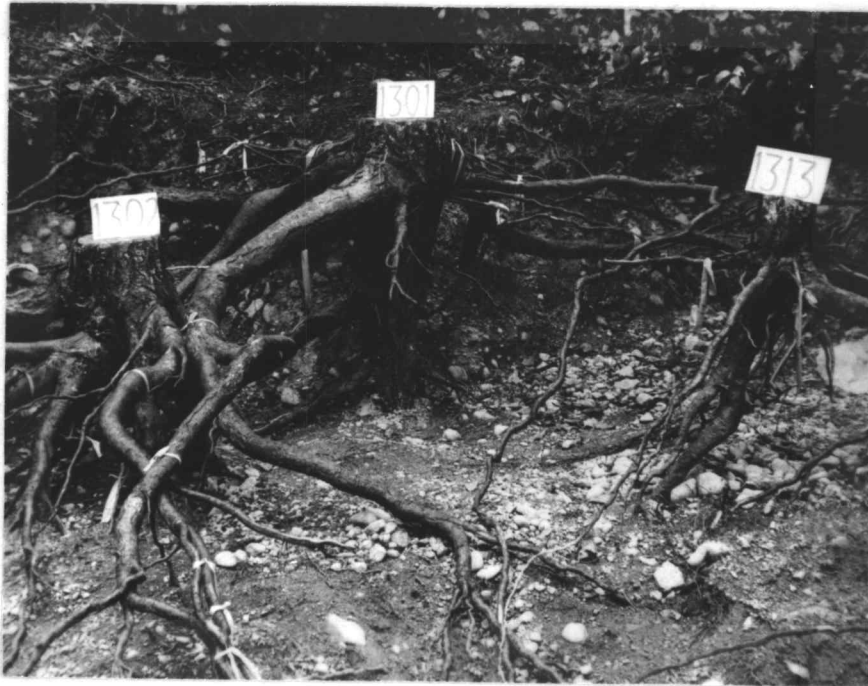


Figure 3. Example of an excavation plot.

Forest Research Lab, Victoria, B.C.). The method utilizes a system of root identification whereby roots are assigned to an order class determined by their point of origin. A root originating at the root collar, for instance would be classified as a primary root; a root originating at any point along the length of a primary would be assigned to the secondary root class, etc. Four root order classes were used in all, the highest order being a quaternary. Mapping proceeded in a hierarchical manner: all measurements were made on a primary root; next, the first secondary root would be measured; if present, the first tertiary on the latter secondary root would be measured, etc. At all measurement points, diameter, azimuth, horizontal distance and depth were recorded. Measurements were made at the origin, terminus and all intermediate points at which a significant change in any of the measurements occurred. Measurements were also made at all points of root contact whether these were inter- or intra-tree in nature.

Each contact was issued a code number to indicate tree of origin and a serial number as it was encountered in data collection. Upon re-encountering the later contact in the course of mapping another root, this code was recorded for the new root at the point of contact. These codes were converted into a new code to indicate the precise root with which contact was being made prior to keypunching.

The type of each contact was also recorded. Contact types are defined as follows:

Type 1 - a "simple" contact in which the roots were either touching or at least in very close proximity but which showed no physical indication of contact (Figure 4).

Type 2 - a contact evidenced by some deformation on at least one of the roots, indicating a confirmable and more substantial contact (Figure 5).

Type 3 - a contact in which either one root had grown around the other or along it for some distance, providing a still more substantial contact (Figure 5).

Type 4 - a graft, as determined by external evidence (Figure 6).

Roots were mapped out to minimum diameter of 0.6 cm. Roots with a diameter less than 0.6 cm at their point of origin were not mapped, but their frequency was recorded along each section of mapped root between measurement points. Hereafter, the word "roots" should be taken to mean roots larger than 0.6 cm.

Other information recorded included the type of root termination. Though no special use for this data was planned, it was deemed potentially useful in delineating the extent of excavation and has been used in this capacity in program ROOTMAP (see appendix B).

Plot data collection.

The most centrally located excavated tree was chosen as a reference tree and designated tree No. 1 on each excavation plot. The remaining excavated trees and all neighbors within 10 meters were numbered sequentially by starting at an azimuth aligned with the slope's aspect and proceeding clockwise around the plot. For each tree, horizontal and vertical distance and azimuth relative to tree No. 1 were recorded. Species, DBH, tree height and crown width were recorded for excavated trees. For neighboring, unexcavated trees, the species was also recorded.



Figure 4. A Type I contact.



Figure 5. Contact Types II and III. The two smaller roots flagged with ribbon form a Type II contact. The larger of the latter roots forms a Type III contact with the much larger root in the photograph. Note, particularly, the difference in the extent of surface contact between the two contact types.



Figure 6. A Type IV contact.

Analytical Methods and Programs

Preliminary data summarization was performed using two programs developed by Dr. W. J. Bloomberg (Pacific Forest Research Centre, Victoria, B.C.). Both programs report the number of roots, their length, cross-sectional area, volume and number of contacts of each type within specified unit volumes of soil. The first of the summarization programs reports the total quantities of the above root characteristics for two or more trees' root systems. The sum of two trees' root numbers, etc. were reported for a soil volume of 0.5 cubic meters (1.0 m wide x 1.0 m long x 0.5 m deep). Two auxiliary programs, SITEMAP (Appendix A) and ROOTMAP (Appendix B), were prepared by the author to facilitate the use of the data summarization program of Bloomberg. Program SITEMAP 1) produces summary plot data tables, 2) calculates inter-tree horizontal and vertical distances, 3) computes a crowding coefficient for each excavated plot tree and 4) produces a map of the excavation plot. Sample output is presented in Appendix A. Program ROOTMAP (Appendix B) utilizes a graphic device to draw out the root systems of all excavated plot trees. Sample output from plot No. 6 is presented in Figure 7.

Two types of analyses were used to study the effect of root characteristics on root contact. First, a univariate regression approach was used to determine the influence of total root number, total root length, total root cross-sectional area and total root volume on the total number of contacts in 0.5 cubic meter volumes of soil. The second approach examined the influence of these factors on the number of contacts by contact type. The SIPS (Rowe *et al.* 1978) interactive

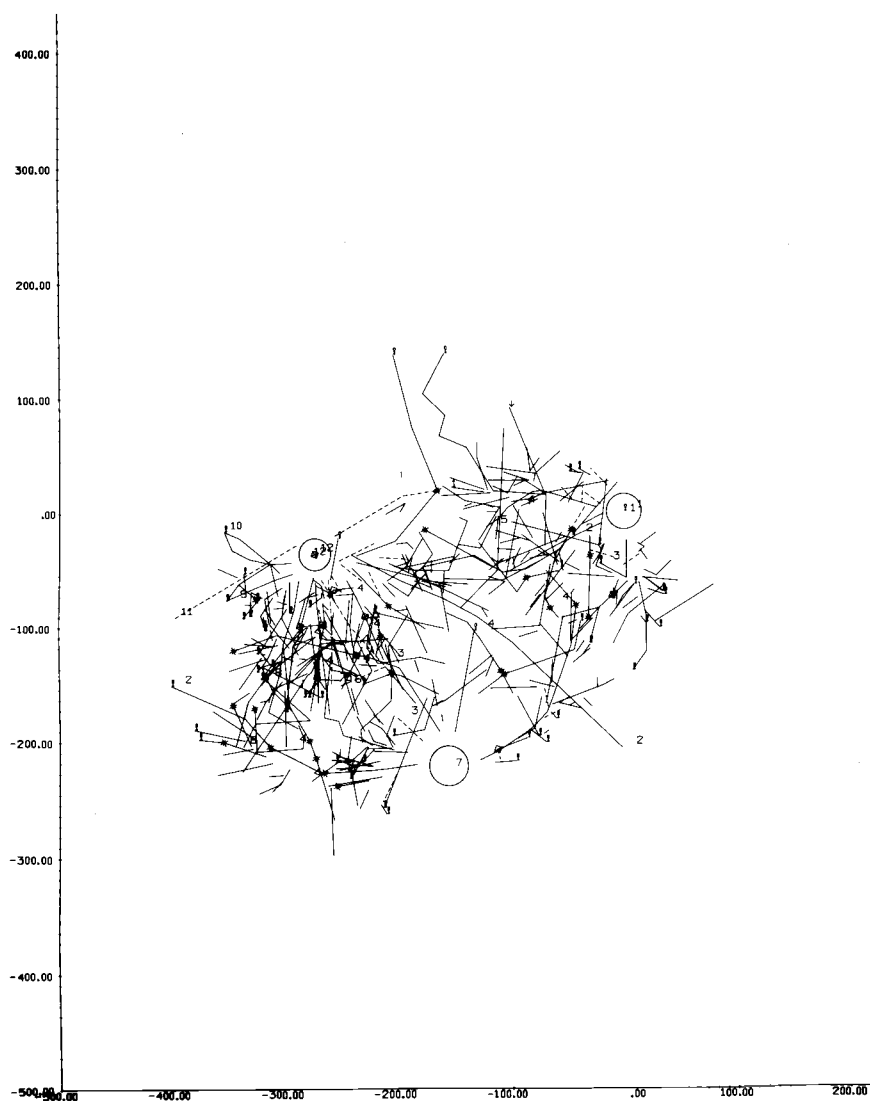


Figure 7. Map of the root systems of the trees on plot number one. Tree numbers appear within the circle representing the root collar. Numbers for the primary roots appear at the end of the root. Contact types are indicated with following symbols: Type I, an asterisk; Type II, a triangle; Type III, an open box and; Type IV, a box with an "x" in the center. Root termination types are indicated with the following symbols: normal termination, no symbol; root measured to limits of excavation, an exclamation mark and; root measured to point of break, a downward-directed arrow.

data analysis package was used for these analyses.

The second data summarization program (Bloomberg, Pacific Forest Research Centre) performs operations similar to the first but summarizes root characteristics for only a single tree. The latter program provides greater detail in that the various root attributes are reported by root order whereas in the former version the values reported are summed for the two (or more) trees over all root orders. The data derived from the individual-tree root attribute summarization was used together with output from program SITEMAP to study the influence of the tree, stand and site factors on the probability of inter-tree root contact. Program BMDØ7 (Biomedical Computer Programs 1977) was used for this analysis. The latter program performs a stepwise discriminant analysis. Two additional programs were prepared by the author to augment the discriminant analysis. Program PLOTDIS (Appendix C) produces a graphic device plot of the canonical variables generated by BMDØ7. Program RESPON (Appendix D) produces three-dimensional response surface plots (the response being the probability of no contact) for two to five predictor variables.

The results obtained from the discriminant analysis have been incorporated into a model for inter-tree spread of laminated root rot. The model is presented in detail in the Results, part B. A simulation program, SIMROT1, which is used to implement the model, is presented in Appendix E.

Documentation on the use of all programs prepared by the author is included in each appendix.

IV. RESULTS PART A

Analysis of Root Contact Frequency as a Function of Root

Attributes

Regression analysis was used to develop predictive equations for the number of contacts in a defined soil volume as a function of total root length (dm), total root cross-sectional area (dm^2), total root volume (dm^3) and total root number. The values for the above independent variables were obtained by summing a given attribute over all root orders of two trees within an 0.50 m^3 of soil ($1.0 \text{ m} \times 1.0 \text{ m} \times 0.50 \text{ m}$). For example, to obtain the total number of roots in a specific soil volume, the numbers of primary, secondary, tertiary and quaternary roots occupying that soil volume were summed for both trees. Two approaches to the analysis were taken. In the first, the total number of contacts served as the dependent variable in a univariate regression model.

The univariate regression for the total number of contacts was highly significant ($\alpha \ll 0.0001$) for the single-variable model using root number as the predictor. The correlation coefficient for this model is $r = 0.659$. An analysis of variance for the model is presented in Table VI. Regression coefficients and their standard errors and t-statistics are given in Table VII. The tests reported in Table VII (and Tables IX, XI and XIII) are two-sided. The significance level is reported as the highest level at which the variable is still significant without interpolating in the table. Root length, cross-sectional area, and volume were not significant once the variation due to root

Table VI. Analysis of variance for regression of total number of contacts on root number.

source	degrees of freedom	mean square	F value	significance level
total	278	6.385		
regression	1	770.195		
residual	277	3.628	212.29	<< 0.0001

Table VII. Regression coefficients and related statistics for the regression of total number of contacts on root number.

variable	regression coefficient	standard error	t value	significance level
constant	0.5688	0.1862	3.055	0.01
number	0.0671	0.0046	14.571	<< 0.0001

number was taken into account.

In the second approach, the number of contacts of each type were regressed on the same set of independent variables (length, cross-sectional area, volume and number). Preliminary analyses (not reported in detail here) indicated that none of the independent variables were significant in the regression on Type III contacts. These results led to a decision to combine the Type II and Type III contacts into a new compound type which will hereafter be referred to as Type II-III to emphasize its derivation from the original nomenclature. As a result only three contact types are used in the analyses that follow.

A test developed by Lawson (1940) was used to test for interdependence among the three contact types (I, II-III and IV). The nature of the test is expressed in the null hypothesis: $H_0: [P] = [I]$ where $[P]$ is the matrix of correlations among the three contact types and $[I]$ is the identity matrix. The test statistic is:

$$\chi^2 \approx N - 1 - \frac{(2p + 5)}{6} \sum_{i < j} r_{ij}^2$$

where:

N = the number of observations,

p = the number of dependent variables being tested,

r_{ij} = the correlation coefficient of the i^{th} and j^{th} variables.

Table VIII. Analysis of variance for regression of the number of Type I contacts on root length and volume.

source	degrees of freedom	mean square	F value	significance level
total	278	2.3169		
regression	2	61.0442		
residual	276	1.8913	32.38	< 0.0001

Table IX. Regression coefficients and related statistics for the regression of the number of Type I contacts on root length and volume.

variable	regression coefficient	standard error	t value	significance level
constant	0.5716	0.1385	4.128	< 0.0001
length	0.001277	0.000164	7.774	< 0.0001
volume	-0.00001369	0.00000586	-2.337	0.02

Table X. Analysis of variance for regression of the number of Type II-III contacts on root number.

source	degrees of freedom	mean square	F value	significance level
total	278	2.1721		
regression	1	129.7080		
residual	277	1.7117	75.77	<< 0.0001

Table XI. Regression coefficients and related statistics for the regression of the number of Type II-III contacts on root number.

variable	regression coefficient	standard error	t value	significance level
constant	-0.0019	0.1279	-0.015	> 0.80
number	0.0275	0.0032	8.705	< 0.0001

Table XII. Analysis of variance for regression of the number of Type IV contacts on root cross-sectional area and number.

source	degrees of freedom	mean square	F value	significance level
total	278	0.6467		
regression	2	31.3887		
residual	276	0.4239	74.05	<< 0.0001

Table XIII. Regression coefficients and related statistics for the regression of the number of Type IV contacts on root cross-sectional area and number.

variable	regression coefficient	standard error	t value	significance level
constant	-0.061587	0.063737	-0.966	0.60
x-section	0.000358	0.000051	6.975	< 0.0001
number	0.007200	0.001990	3.617	0.001

The calculated approximate chi-square statistic is 2.14 ($df = \frac{1}{2}p(p - 1) = 3$) which is not significant ($P < 0.50$). The test indicates that the correlation matrix cannot be shown to be significantly different from the identity matrix. In other words, the interdependence of the three dependent variables (Types I, II-III and IV) is very low.

Analyses of variance for the models with Types I, II-III and IV contacts as the dependent variables are given in Tables VIII, X and XII, respectively. Corresponding summaries of the regression coefficients, and their standard errors and t-statistics appear in Tables IX, XI and XIII. The results of these analyses can be summarized briefly. Both root length and volume are significant in the regression for the number of Type I contacts. The regression is highly significant ($\alpha < 0.001$), with a correlation coefficient of $r = 0.435$. The proportion of variation explained by length and volume is nonetheless very modest ($R^2 = 0.190$). Note particularly that the coefficient of volume is negative, indicating that Type I contacts are associated with smaller roots.

Root number is the only significant variable in the regression for Type II-III contacts (Tables X and XI). The regression is highly significant ($\alpha < 0.0001$), but again, the amount of variation explained is rather modest ($R^2 = 0.215$).

The number of Type IV contacts is a function of both root cross-sectional area and number (Tables XII and XIII). The regression is highly significant ($\alpha < 0.0001$). There is some improvement in predictive ability ($R^2 = 0.349$), though this is still modest.

It should be pointed out that root number and length are highly correlated ($r = 0.962$) as are root volume and cross-sectional area ($r = 0.941$). The correlations are sufficiently high that the correlated variables could readily be interchanged with little effect on the proportion of variation that is explained in the appropriate models.

Analysis of Root Contact Probability

Whereas, in the previous analysis, attention was focused on root characteristics that might influence root contact frequency in a defined volume (0.5 m^3) of soil, the analyses of this section deal with tree, soil and site factors that determine the extent of contact between a pair of trees. Attention focused on the variables shown in Table XIV, after a preliminary screening of a larger set of possibilities. Comments on units, etc. are included in the table. Two variables, however, require some explanation. The variable "angle" is the departure (in degrees) of a tree-pair from perfect alignment with the slope's aspect. Thus, "angle" represents a measure of relative slope position. The crowding index (referred to as "nearest neighbor coefficient" in program SITEMAP) was obtained by establishing four quadrants about a tree, selecting the nearest tree in each quadrant, dividing the square of the latter's DBH by its distance from the tree in question and summing the resulting indices over the four quadrants.

Discriminant analysis was employed as a means of relating the various tree stand and site factors to the probability of inter-tree root contact. Several group breakdowns were experimented with. Only the final version is presented. In the latter, three contact categories

Table XIV. Independent variables used in inter-tree contact discriminant analysis.

Variable	Comments
inter-tree slope distance	(cm)
$\ln (\text{DBH}_1 + \text{DBH}_2)$	the natural log of the sum of two trees' DBH
angle	see text
soil depth	(cm)
slope	(percent)
gravel content	(cc/cu. ft.)
cobble content	(cc/cu. ft.)
total rock content	(cc/cu. ft.)
crowding index	see text
number of roots per unit root volume	for each root order: the sum of the number of roots of both trees divided by the sum of the volumes of both

were established as a basis for grouping the data into contact groups:

- 1) no inter-tree contact (NOCON)
- 2) inter-tree contacts of Type I only (LOCON)
- 3) inter-tree contacts of Type I and higher orders (HICON)

A BMD (Biomedical Computer Programs 1977) stepwise discriminant analysis program (BMD07) was used in the analysis. Data on 50 pairs of trees was available as a basis for the analysis (Appendix F). The significant variables were inter-tree slope distance (which, for brevity will hereafter frequently be referred to simply as distance), $\ln(\text{DBH}_2 + \text{DBH}_1)$, effective rooting depth, gravel content of the soil and percent slope. The F-values for removal of discriminant variables from the full model are given in Table XV. The approximate F-statistic for overall model significance is $F = 4.84$ ($df = 10.86$) which is significant at the 0.001 level. In Table XVI, a matrix for inter-group significance is given. All contact types are significantly discriminated at the 0.05 level. Coefficients of the discriminant functions are given in Table XVII. The functions are used to compute the discriminant score, S_{ij} , for observation j with respect to group i . For details concerning the calculation of the posterior probability of group membership, the reader should refer to the BMD documentation.

The incidence of misclassification for each group is shown in Table XVIII. The later table provides some insight into the distinctness of each group. Note that the rate of misclassification is relatively low for the two groups, NOCON and HICON, their respective rates being 0.143 and 0.250. The intermediate group, LOCON, is still significantly dif-

Table XV. F-values for removal of significant variables from the full, 3-group^b discriminant model.

variable	F to remove	significance ^a
distance	14.37	<< 0.001
DBH	8.75	< 0.001
soil depth	3.49	0.05
gravel	4.99	0.025
slope	4.72	0.025

^adf = 2, 43

^bgroup definitions

1. NOCON - no inter-tree contact
2. LOCON - only type I contacts
3. HICON - type I and higher contact orders

Table XVI. Significance^a of group differences^b.

group	group	
	NOCON	LOCON
LOCON	0.005	
HICON	0.001	0.05

^adf - 5, 43

^brefer to (b) in Table XIV for group definitions

ferent from both of the latter groups in spite of a rather high rate of misclassification (0.555).

The canonical variables from the discriminant analysis are plotted in Figure 8 using program PLOTDIS (Appendix C). One can see in this figure the basis for the misclassifications shown in Table XVII. The groups NOCON and HICON are well segregated on the first canonical axis. The intermediate group LOCON is separated from the latter groups in the second dimension. Note, however, that five of the nine observations from the LOCON group are effectively "buried" in the transitional zone between the NOCON and HICON groups.

As an aid in interpreting the influence of the significant variables and the nature of their interactions, Figures 9 through 14 present the posterior probability of no contact as a function of the five discriminant variables. The distance is held constant at 300 cm. in all of the figures. Two variables are fixed at their respective mean values while the remaining two (which appear on the X and Y axes) are allowed to vary over the range of values shown in Table XIX.

Table XVII. Coefficients of the discriminant functions for the 3-group model.

coefficient for:	group		
	NOCON	LOCON	HICON
constant	-175.66739	-208.94675	-196.08026
distance	-0.06028	-0.07130	-0.07817
DBH	79.74764	87.02414	87.05154
soil depth	0.55168	0.59947	0.51809
gravel	-0.03389	-0.03912	-0.03662
slope	2.31630	2.69519	2.50904

Table XVIII. Incidence of group misclassification for the 3-group model.

group	number of cases classified into:		
	NOCON	LOCON	HICON
NOCON	18	0	3
LOCON	4	4	1
HICON	4	1	15

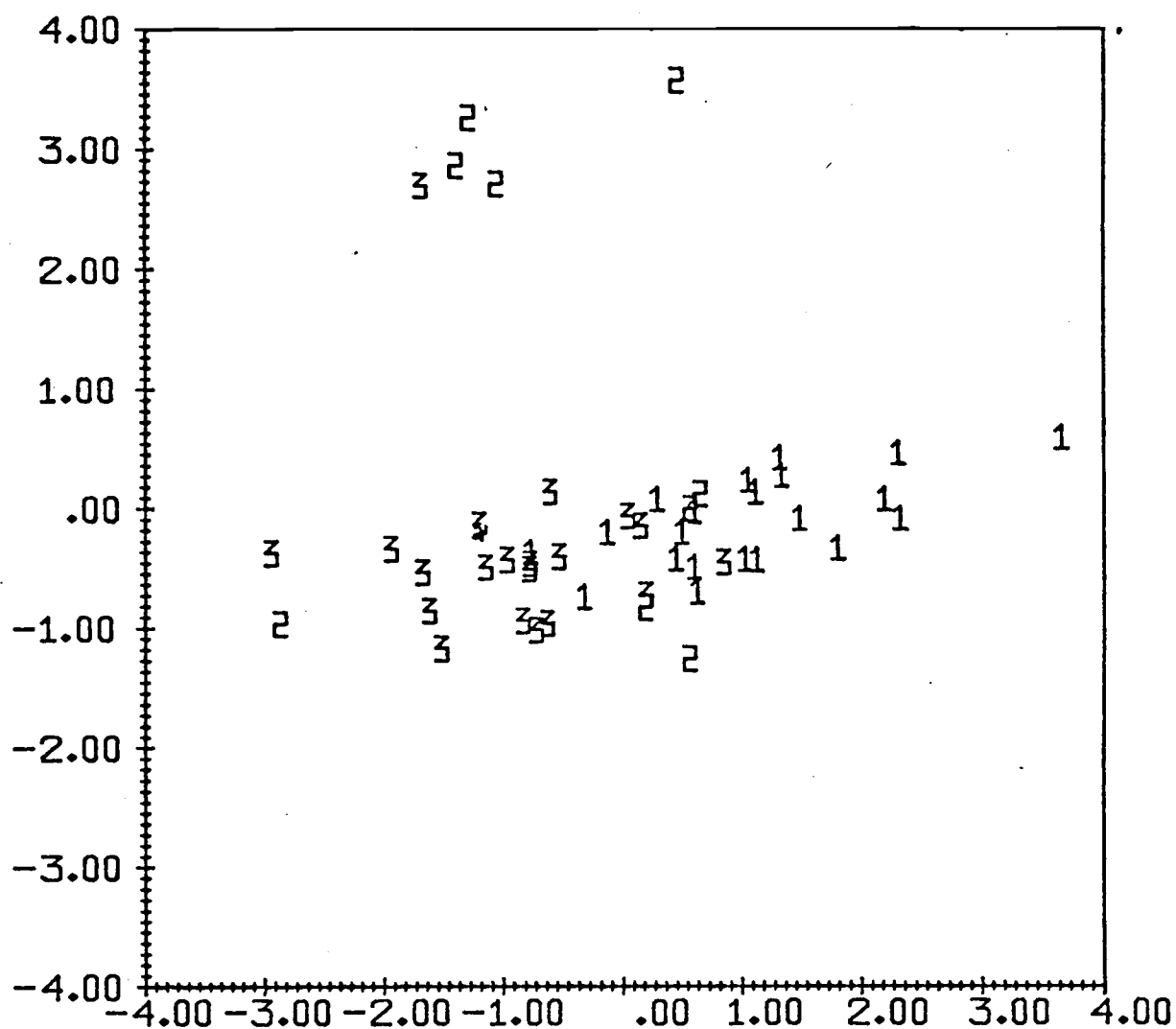


Figure 8. Plot of canonical variables^a from 3-group discriminant analysis.

^aPlotting code:

- 1 NOCON
- 2 LOCON
- 3 HICON

Table XIX. Values of independent variables used in Figures 9 through 14.^a

index	DBH ^b	soil depth (cm)	slope (percent)	gravel content (cc)
1	3.500	80.0	30.0	2000.0
2	3.625	85.0	33.0	2200.0
3	3.750	90.0	36.0	2400.0
4	3.875	95.0	39.0	2600.0
5	4.000	100.0	42.0	2800.0
6	4.125	105.0	45.0	3000.0
7	4.250	110.0	48.0	3200.0
8	4.375	115.0	51.0	3400.0
9	4.500	120.0	54.0	3600.0
mean	4.000	100.0	42.0	2800.0

^aThe index value in the table corresponds to the index used in labeling the axes.

^bDBH is defined to be $\ln(\text{DBH}_1 + \text{DBH}_2)$ where DBH_1 and DBH_2 are the actual DBH's (cm.) measured for the two trees.

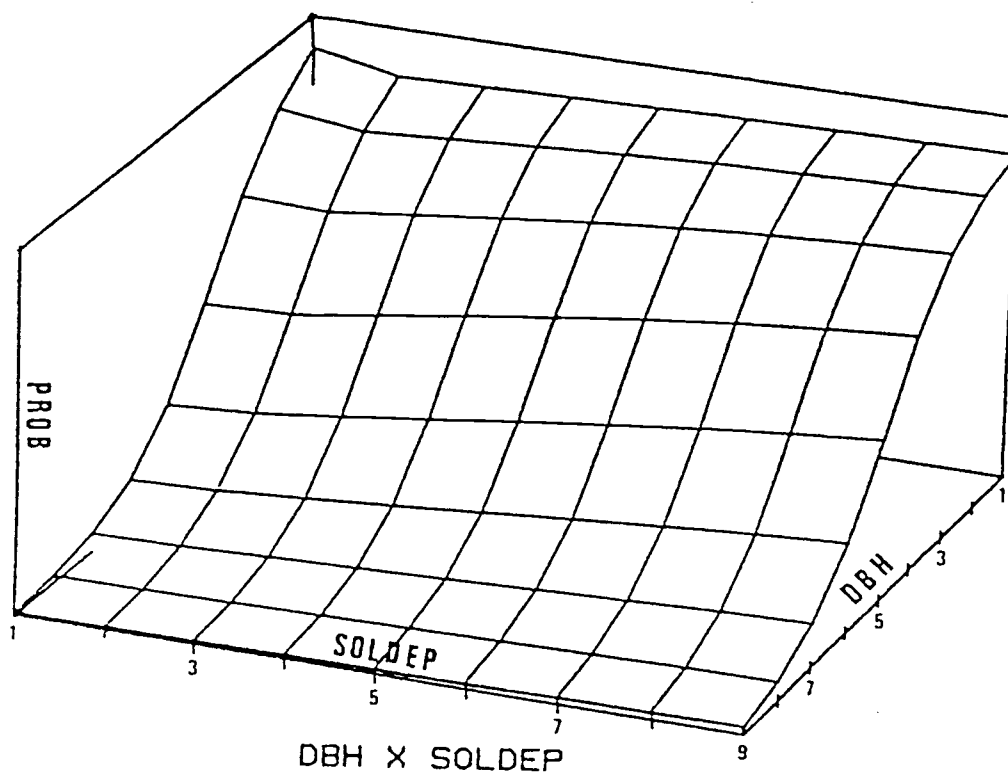


Figure 9. Posterior probability of no contact plotted over DBH and soil depth.^a

^aSee text for explanation of plotting procedure.

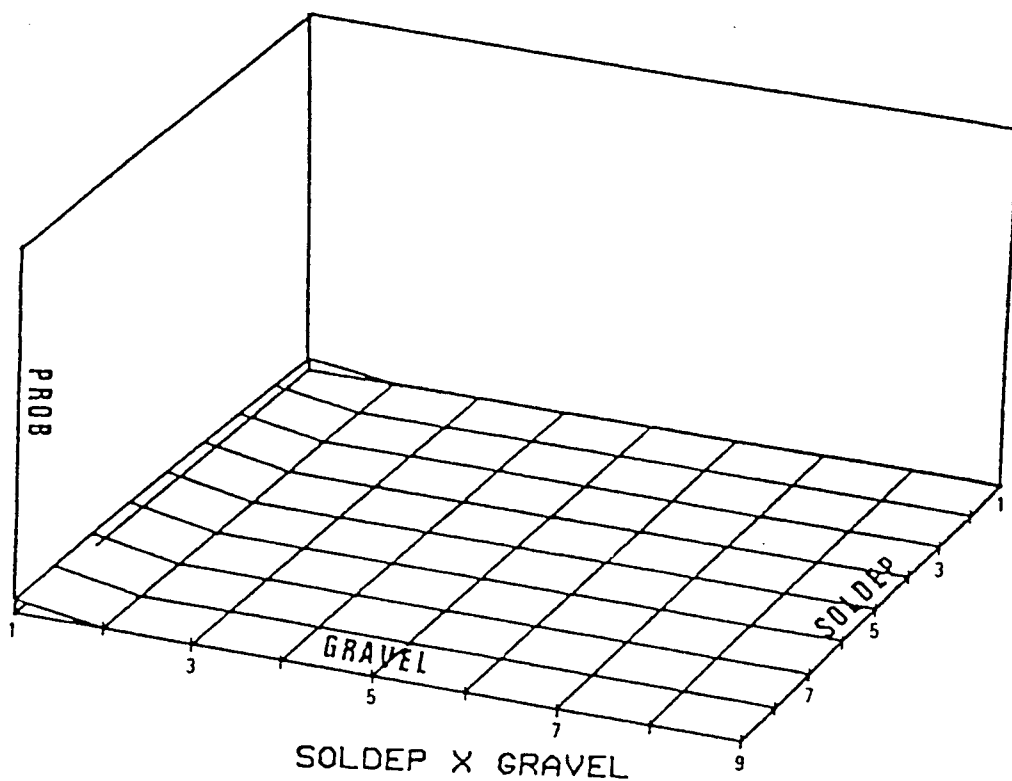


Figure 10. Posterior probability of no contact plotted over gravel content and soil depth.^a

^aSee text for explanation of plotting procedure.

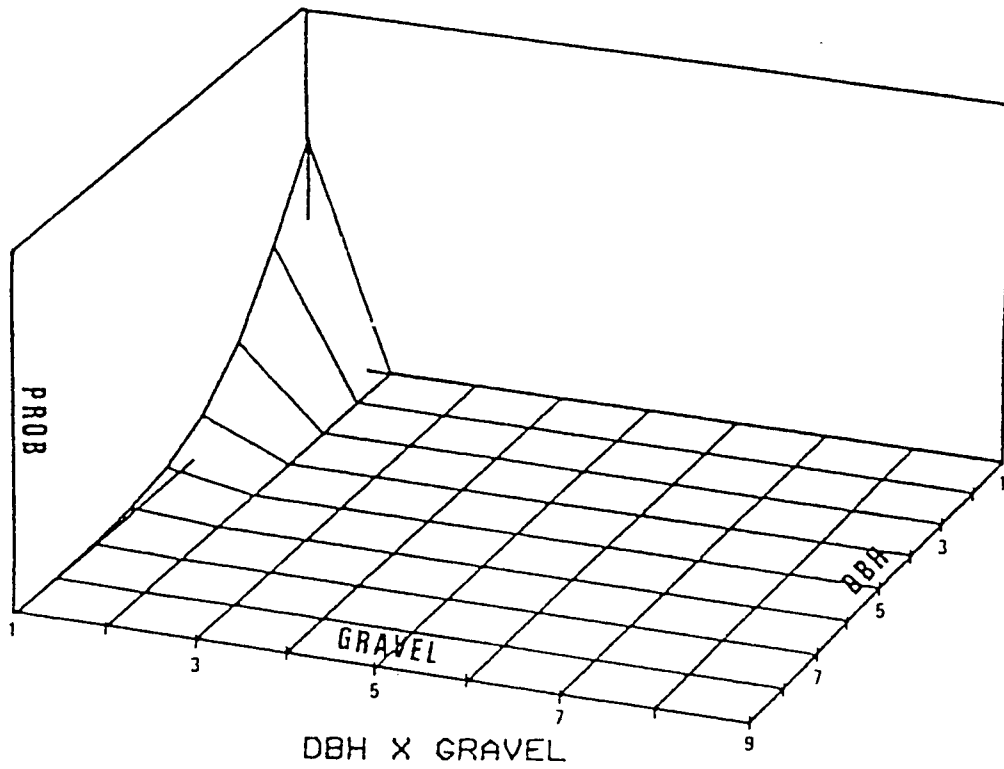


Figure 11. Posterior probability of no contact plotted over gravel content and DBH.^a

^aSee text for explanation of plotting procedure.

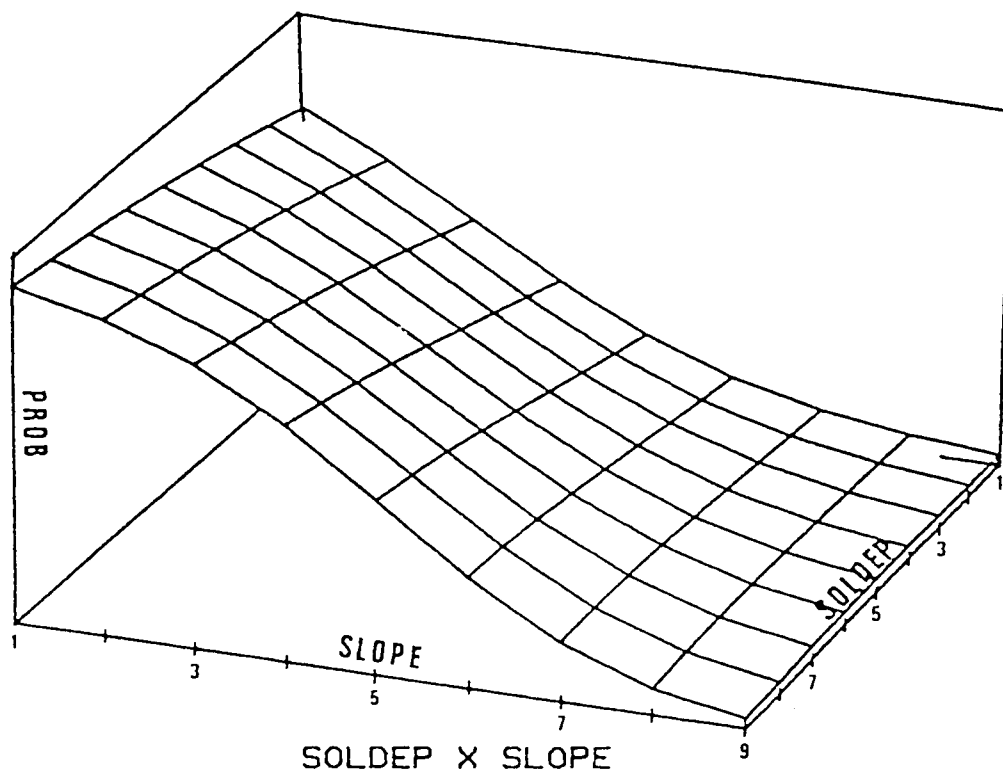


Figure 12. Posterior probability of no contact plotted over percent slope and soil depth.^a

^aSee text for explanation of plotting procedure.

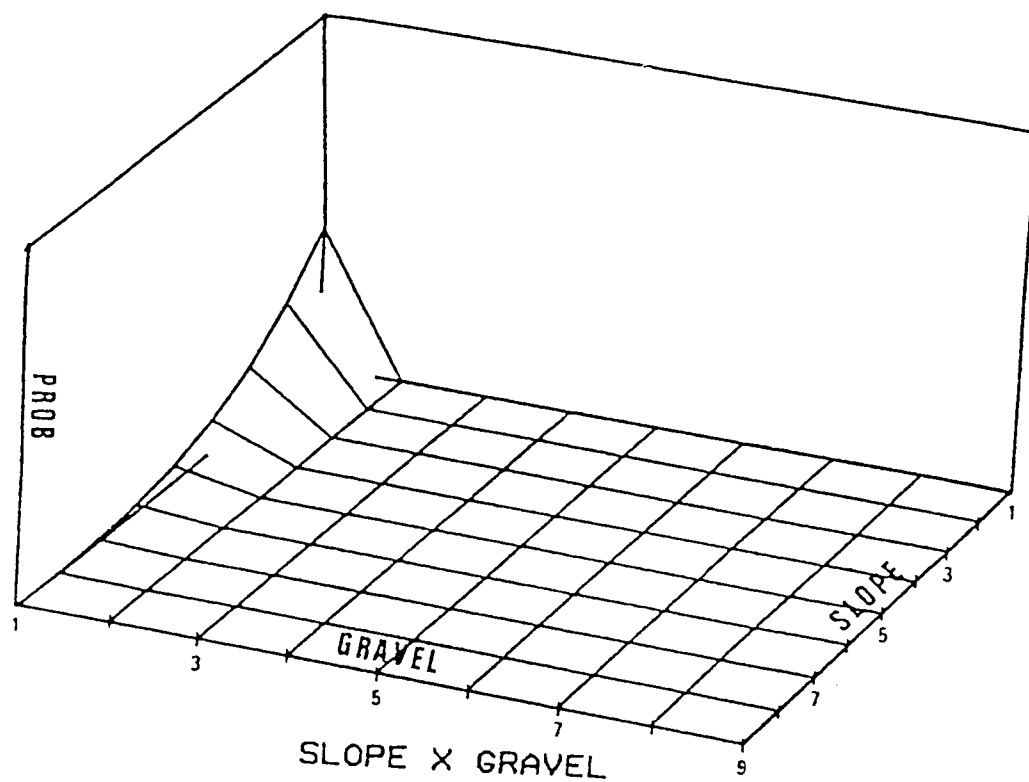


Figure 13. Posterior probability of no contact plotted over gravel content and percent slope.^a

^aSee text for explanation of plotting procedure.

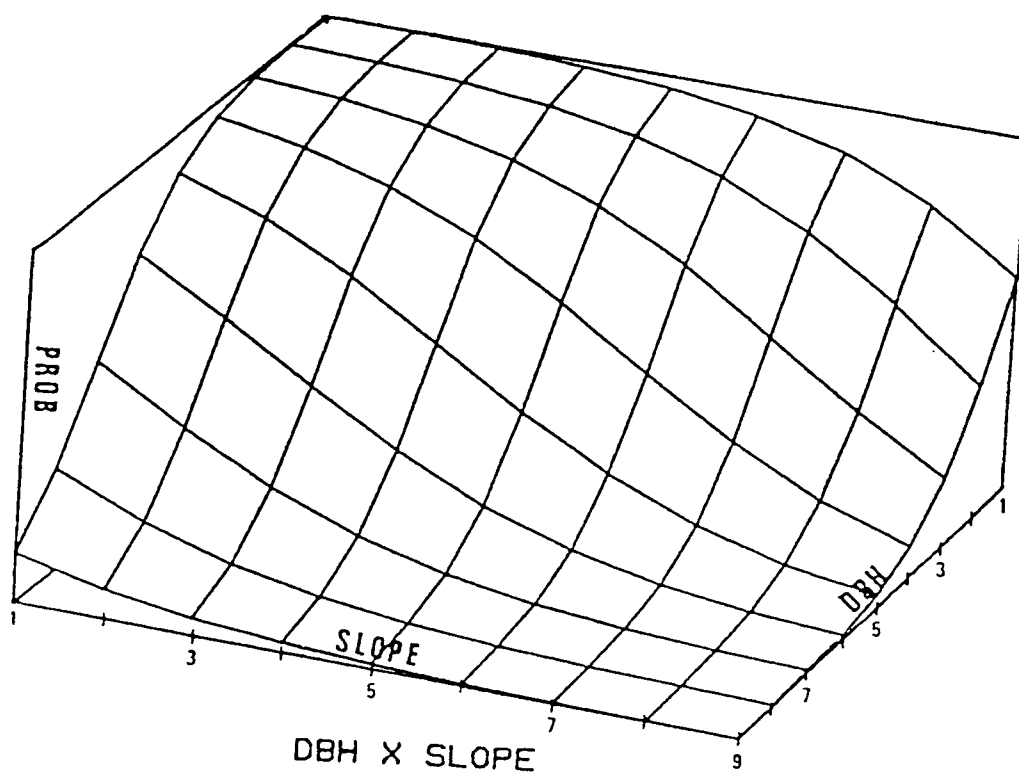


Figure 14. Posterior probability of no contact plotted over percent slope and DBH.^a

^aSee text for explanation of plotting procedure.

V. RESULTS PART B

A Model for Inter-tree Spread of *Phellinus weirii*

The objective of the model is to characterize the spread behavior of laminated root rot in terms of those tree, stand and site factors that are relevant to inter-tree root contact and, thus, also to spread of the disease. The goal associated with this objective is to provide a means for determining how silvicultural options and environmental constraints influence the spread of disease. The inter-tree spread model is, moreover, a submodel of a stand model for *P. weirii*-impact which has the broader goal of determining how these same tree, stand and site factors influence laminated root rot's impact on the timber yield of a site (Bloomberg, Pacific Forest Research Centre, Victoria, B.C.).

The basic, hypothetic structure for the inter-tree spread model is presented in Figure 15. The perspective is relative to the infection ability of an infected tree (or trees). The principle quantities associated with the model are differentiated into inputs and outputs and state variables. The space-time resolutions for the principle quantities are given in Table XX. It should be noted that the inputs represent permanent attributes of the system and are not subject to modification via a system-environment interaction.

The complexity of the model required a simulation approach. Certain of the input quantities have been fixed in order to limit the number of simulation runs required; the model deals specifically with the spread behavior of laminated root rot in a young-growth stand of site index

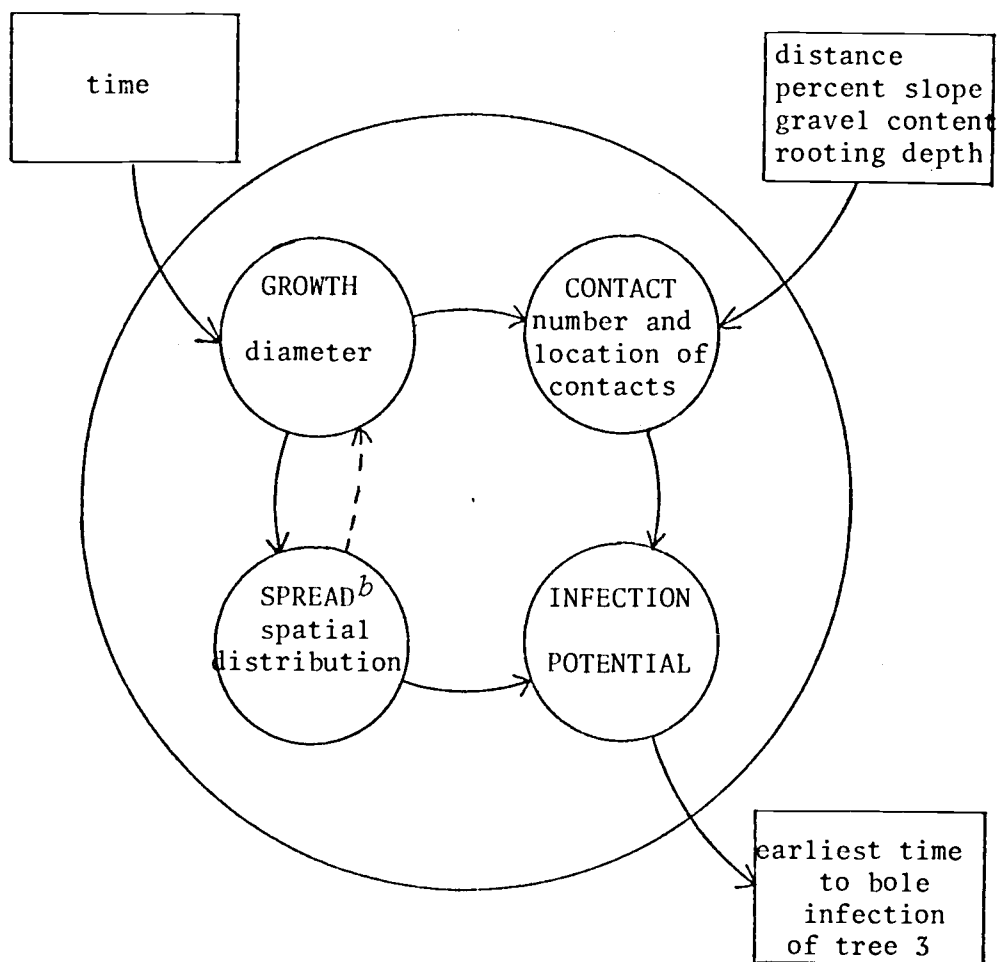


Figure 15. Hypothetic structure of the inter-tree spread model.^a

^aSubsystems are represented by the small circles and are identified by upper case letter. The principal state variable associated with each subsystem is identified with lower case letter. Input to the system consists of fixed environmental attributes. See Table XX for definition of time-space resolutions.

^bSee Figure 16.

Table XX. Time-space resolution of state variables, environmental attributes and system output.

variable	type	time-space resolution
tree diameter (dbh)	state variable in GROWTH sub- model	0.001 cm
number of contacts	state variable in CONTACT submodel	integer
spatial distribution of infection	state variable in SPREAD submodel	0.01 cm
infection condition of "targets"	state variable in INFECTION POTENTIAL submodel	positive or negative
inter-tree slope distance	environmental attribute	0.01 cm
percent slope	environmental attribute	1%
gravel content of soil	environmental attribute	1.0 cc/cu ft
effective rooting depth	environmental attribute	1.0 cm
time	environmental attribute	1.0 years
earliest time to bole infection of a "target" tree	system output	1.0 years

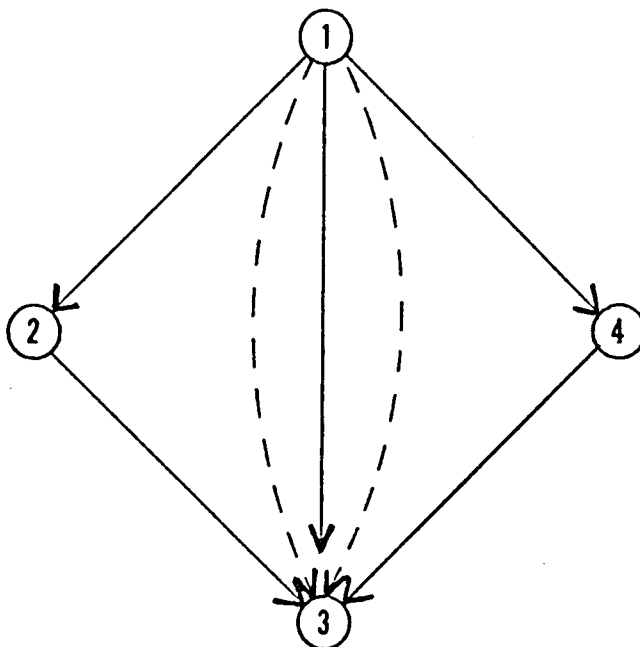


Figure 16. Numbering convention and arrangement of trees in program SIMROT2 (and possible infection pathways^a).

^aArrows in the figure illustrate possible pathways of fungal spread from tree 1 to tree 3.

- 1) solid arrows indicate paths that involve bole infection of trees 2 and 4
- 2) dashed arrows indicate paths that involve trees 2 and 4, but do not require spread from the bole of these trees

200 Douglas-fir; the percent slope and gravel content of the soil are set to 45 percent and 2500 cc./cu. ft., respectively. The simulation problem is thus reduced to finding a numerical solution for the relation between a limited set of input quantities (inter-tree slope distance, initial DBH, and soil depth) and the output quantities.

The contact subsystem (Figure 15) is further subdivided into an element that computes the probability of contact and an element that determines the number of contacts between a particular pair of trees. The behavior of both these elements is stochastic. The output of the model, in consequence, is not uniquely determined for a specific set of initial conditions: the time to initial root infection and the time to earliest bole infection are both expressed as cumulative distribution functions; the latter output is also presented as a density.

The simulation program, SIMROT2, is presented in Appendix E together with documentation on its use and a sample simulation run.

The basic algorithm is described below in order to characterize the nature of the spread model's submodels and draw attention to the latter's respective external quantities that provide a basis for subsystem couplings.

It is imperative that the reader bear in mind the very tentative nature of the model as described below. Several simplifications are introduced. Simplification, in some instances, is both intentional and desirable as a means of obtaining computational tractability. On the other hand, the process of system structural development has drawn the author's attention to significant information gaps with respect to

specifications of particular subsystems. It is, in fact, an important activity of the modeling process to explicitly identify these gaps in knowledge as a means of directing research along pathways fruitful to better understanding. Attention will therefore be drawn (in the DISCUSSION) to those model specifications for which better or more complete information is necessary. Simplifying assumptions have been supplied as necessary in order to produce a functional simulation model. The quantitative behavior of the model is certainly affected by these assumptions; however, it is still valid to qualitatively assess system behavior. That is, the general relation between input and output quantities can be deduced as well as the manner in which the input variables enter the relation.

Four trees, arranged equidistantly on the vertices of a diamond, are used in SIMROT2. It must be emphasized that the trees are equidistant on the slope and not on a horizontal projection from the slope. Refer to subroutine PLOTTYPE for details of establishing the X and Y coordinates of a tree's geographic center. Figure 16 illustrates the numbering convention and arrangement of trees in SIMROT2. Note that, although four trees are used in the simulation program, the output (i.e., earliest time to bole infection) is strictly with respect to tree 3. Trees 2 and 4 are included only to provide alternate pathways of spread from tree 1 (Figure 16).

Tree 1 is infected at the bole when simulation is initiated. The probability of contact between tree 1 and trees 2 through 4 is calculated at each time step until contact is established for a particular tree-pair (subroutine CONPROB). The algorithm for calculating the

probability of contact utilizes the results of the tree-group discriminant analysis of Results, Part A. The probability is computed as: $1.0 - (\text{probability of no inter-tree contact})$. Subroutine CONPROB is by-passed in subsequent time steps once contact is established for a particular pair of trees. A uniform random deviate is compared to the calculated probability of contact (subroutine PICKCON). Contact is established if the random deviate fails to exceed the probability of contact.

A zone of potential root contact is defined in subroutine CONTACT once contact has been established for a given pair of trees (lines 38 through 44). This zone represents that soil area between a pair of trees that contains the majority of inter-tree root contacts. The contact zone is defined to be a circular area whose origin lies at the midpoint of the line determined by the geographic centers of the root collars of the pair of trees in contact. The radius of the zone is a function of the trees' DBH. If, at time $t = 0$, the DBH is equal to that of a 20 year old stand, then the radius is 200.0 cm and increases to a maximum of 300.0 cm at time $t = 20$ (line 43). The radius of the contact zone is initially set equal to 300.0 cm and remains constant throughout the simulation if the trees' initial DBH is that of at least a 40 year old stand.

The number of contacts and their spatial location is also determined in subroutine CONTACT. A suitable expression for the total number of contacts between a pair of trees was obtained by discarding extreme observations from the discriminant analysis data (Appendix F). The resulting equation for total number of contacts (TNC) is:

$$\text{TNC} = 2.3544 + 0.2386 * \exp((\text{DBH}_1 * \text{DBH}_2) * \text{SLOPE} * \text{GRAVEL}) / ((\text{DIST} ** 2.0) * \text{SOLDEP} * 10.0))$$

where

CON = the total number of contacts for a specific tree-pair
 DBH₁ = diameter breast height of the first tree
 DBH₂ = diameter breast height of the second tree
 SLOPE = percent slope
 GRAVEL = cc. gravel/cu. ft. soil
 DIST = inter-tree slope distance and
 SOLDEP = effective rooting depth of the soil.

The determination of the number of contacts at a specific time step is performed in a two-stage process. The calculated number of contacts is a real number. Both the real number and its corresponding truncated integer are used in subsequent steps to determine when and how many new contacts should be added at a specific time step. Only the integer portion of the number is utilized, however, for purposes of creating new contacts. As an example, let the current number of contacts be 3. The calculated number could be any value in the interval [3.0, 4.0]. Now suppose that at time t, a tree-pair has 3 contacts and the actual calculated number is 3.41. At time t + 1, a new value is calculated to be 3.91. A uniform random deviate with range [0.0, 1.0] is compared to the difference in the calculated number of contacts at time t and time t + 1. In this example, the difference is 0.50; if the uniform random deviate fails to exceed the difference, then a new contact may be added. If the

deviate exceeds the calculated difference of 0.50, there is no possibility of a new contact. In the current example, suppose the first condition for adding a new contact is met: the deviate fails to exceed the difference. The value 3.91 is truncated to the integer value 3 and this number is compared to the integer value obtained at time t . If the integer value of the number of contacts at time $t + 1$ exceeds that for time t , a new contact will be added. In the example, this is not the case and no new contact is added. If, at time $t + 2$, the calculated number of contacts were 4.21 and the deviate again failed to exceed the difference (which is now $4.21 - 3.41 = 0.80$), then, upon truncation, the number of contacts would be 4 and the number of contacts for the pair of trees would be incremented. The value 4.21 is now retained as the last calculated number of contacts and is used in subsequent time steps to obtain the calculated difference.

The number of contacts added at time $t = 1$, and those added subsequently by the above process, are randomly located within the potential contact zone. The probability of selecting any particular point in the zone is equally likely (lines 41 through 50).

The spread of disease from a bole-infected tree progresses radially outward from the bole at a constant distal rate (subroutine SPREAD, lines 20 through 24). Prior to incrementing the extent of radial spread, the infection status of the bole-infected tree is evaluated. Extent of spread after bole infection is presumed to be a function of the infected tree's DBH at the present time step and the number of years since bole infection occurred (Table XXI). If the elapsed time since bole infection is greater than or equal to the specified value for the infected

Table XXI. Derivation of the coefficients for the spread decrement equation^a

diameter class (cm)	spread time after bole infection (yrs)	max. radial spread ^b (cm)	coefficient a	coefficient b ^c
dbh < 5.0	2	60	12.48	0.0167
5.0 ≤ dbh < 10.0	5	150	10.46	0.0067
10.0 ≤ dbh < 20.0	7	210	8.84	0.0048
20.0 ≤ dbh < 40.0	10	300	8.09	0.0033
40.0 ≤ dbh	15	450	9.60	0.0022

^adecrement = $a \cdot \exp(-b \cdot dt)$

^bmaximum radial spread is determined by spread time after bole infection and the distal rate of spread which, here, was assumed to be 30 cm/year

^cthe coefficient "b" equals the multiplicative inverse of the maximum radial spread

tree's diameter class, tree growth and fungal spread are arrested. (Table XXI and lines 121 through 129 of the main program).

Once fungal spread is arrested, the infection zone begins to contract (subroutine SPREAD). The annual decrement to the radial extent of infection is presumed to be a negative exponential function of the general form:

$$\text{decrement} = a \cdot \exp(-b \cdot dt)$$

where:

dt = number of years since arrest of spread and

"a" and "b" are determined by the diameter
class of the tree

The coefficient "b" is simply the multiplicative inverse of the maximum radial spread. The coefficient "a" (Table XXI) is obtained by integrating the spread decrement function over the time interval required for the infection to die back to the bole and then solving for "a" (see also lines 55 through 72 of subroutine spread for details of the algorithm). Each time the radial spread is decremented, the radius of the infection zone is evaluated. The tree is no longer considered infectious when the latter radius falls to or below zero.

Infection of a healthy tree by a bole-infected tree is ascertained by computing the distance between each of the former's contact points with the bole-infected tree and the geographic center of the latter's root crown. Each such computed distance is compared to the radial extent of infection from the bole-infected tree. If the radius of the

infection zone encompasses a contact point, that point is now considered to be infected (subroutine INFECT, lines 61 through 91). If tree 2 and/or tree 4 is infected through this process, that tree is now designated as a new source of infection. As new points of infection are acquired on tree's 2, 3 and 4, each is evaluated with respect to the time required for the new infection to reach the bole. Note particularly that tree 1 can infect any or all of the other trees by the process of radial spread described. This capability is diagrammed in Figure 16, the solid arrows indicating infection pathways from a bole-infected tree. Figure 16 also indicates that trees 2 and 4 can become bole-infected and subsequently infect tree 3 via the mechanism of radial spread described. Thus, tree 3 can become infected via three pathways that involve bole-infected sources of infection.

Two additional pathways, indicated by dashed arrows are also shown in Figure 16. These pathways represent an infection process that leads to the infection of tree 3 through trees 2 and 4 but does not require bole infections in the latter two trees. Prior to the establishment of a bole infection on either tree 2 or tree 4, the disease is presumed to spread in a linear fashion. Disease spread in this situation occurs along a line formed by the infected contact point and the geographic center of tree 2 or 4, as the case may be. The linear mode of growth is intended to represent spread of infection along an idealized radial root system. The proximal and distal rates of spread are specified by the user (direction is relative to the bole of the infected tree). The linear extent of infection is incremented annually. An infectious zone about this line is defined to be that area within 30.0 cm of any point

on the line (refer to lines 64 through 76 of subroutine INFECTION). Spread of infection may occur along several such lines on a given tree simultaneously.

Outward radial spread from the bole of tree 2 or 4 is initiated when one of the elongating "root" infections reaches the geographic center of the infected tree's root crown. Thereafter the spread of disease continues in two modes: both linearly as before, and now, also, radially outward. Whereas the limit of radial spread is predetermined by the diameter of the tree at the time of bole infection, no such constraint is automatically applied to distal, linear spread. A maximum distance for the latter form of spread must be input as a separate constraint by the user.

The simulation outputs (time to initial root infection and earliest time to bole infection of tree 3) constitute distribution functions in view of the stochastic nature of the contact submodel. The simulator is run 50 times for a specific set of initial conditions in order to generate these distributions.

The Simulations

Representative output from the simulator is presented in Appendix E, following the program listing for the model.

The distribution of earliest time to bole infection is presented both graphically and in tabular form for all initial conditions in Appendix G. It is important to note that the time scale of the abscissa in the graphs of Appendix G does not correspond exactly to the range of times shown in the corresponding tables. The values on the abscissa are

equal to the tabular values minus ten years. This rescaling was performed to increase the axis scale for improved viewing and to simplify some exploratory analyses (the rescaling of time to zero allowed the elimination of a translation parameter in a nonlinear regression analysis).

It was noted in the previous section that it was not feasible to consider the influence of all of the possible factors that might affect the distribution of earliest time to bole infection. The simulations consider the influence of inter-tree slope distance, the trees' diameter and effective rooting depth. Each of the latter variables represents an initial condition for the system; three levels of each variable are evaluated, thus twenty-seven simulation runs were required to study all possible combinations. The initial conditions for each simulation run are shown in Table XXII.

The reader should also recall that soil gravel content and percent slope are fixed at 2500 cc/cu. ft. and 45%, respectively.

A detailed analysis of the system's behavior and the influence of the initial conditions on this behavior is taken up in the discussion.

Table XXII. Initial conditions used in the simulations of SIMROT2.

Simulation number	Distance (cm)	(cm)	effective rooting depth (cm)
1	300.0	21.59	80.0
2	300.0	21.59	100.0
3	300.0	21.59	120.0
4	300.0	32.36	80.0
5	300.0	32.36	100.0
6	300.0	32.36	120.0
7	300.0	46.23	80.0
8	300.0	46.23	100.0
9	300.0	46.23	120.0
10	400.0	21.59	80.0
11	400.0	21.59	100.0
12	400.0	21.59	120.0
13	400.0	32.26	80.0
14	400.0	32.26	100.0
15	400.0	32.26	120.0
16	400.0	46.23	80.0
17	400.0	46.23	100.0
18	400.0	46.23	120.0
19	500.0	21.59	80.0
20	500.0	21.59	100.0
21	500.0	21.59	120.0
22	500.0	32.36	80.0
23	500.0	32.36	100.0
24	500.0	32.36	120.0
25	500.0	46.23	80.0
26	500.0	46.23	100.0
27	500.0	46.23	120.0

V. DISCUSSION

Interpreting the Root Contact Analyses Dealing with Contact Frequency in Specific Soil Volumes

The regression analyses of Results, Part A, are considered in this section. Discussion relevant to the discriminant analyses of Part A is taken up in the next section.

In the first analysis, the total number of contacts in 0.5 m^3 of soil was regressed against the sums of all roots' attributes for each pair of trees whose roots occupied that volume of soil. The results of the analysis were very clearcut: only the number of roots was significant (Tables VI and VII). Why only root number should appear as a significant variable is not immediately apparent.

One approach to the problem is to consider the role that root number plays in the separate regressions of the three contact types (I, II-III and IV) on the root attributes. First, recall that: 1) Type I contacts are a function of root length and volume (Tables VIII and IX), 2) Type II-III contacts are a function of root number (Tables X and XI) and; 3) Type IV contacts are a function of root number and cross-sectional area (Tables XII and XIII). It will greatly simplify the discussion to note, moreover, that root number and length are highly correlated ($r = 0.926$) as are root cross sectional area and volume ($r = 0.9412$). The correlations of the latter variable-pairs are sufficiently great that the two members of each pair can be thought of as interchangeable. Consequently, the proportion of variation due to root number will be quite comparable to that for root length. Similar conclusions apply to

interchanging variables in the regressions for Type II-III and Type IV contacts.

The foregoing conclusions are reflected in Table XXIII in which the variable-pairs length/number and cross-sectional area/volume are designated as "number" and "volume," respectively. The table shows the proportion of explainable variation (R_p^2) due to root "number" or "volume" in the regression equation for each contact type. R_p^2 , for the first variable to enter the model, is defined as:

$$\frac{R^2_{\text{reduced}}}{R^2_{\text{full}}}$$

and for the second variable as:

$$\frac{(R^2_{\text{full}}) - (R^2_{\text{reduced}})}{(R^2_{\text{full}})}$$

An asterisk following a table entry indicates that the variable was, for instance, actually root length instead of root number. It is clear from Table XXIII that root "number" figures vary prominently in the prediction of Type I and Type II-III contacts. If we further consider the proportion of contacts that are either Types I or II-III, the prominence of root number becomes even more apparent. The means of the root attributes were used to compute the number of contacts of each type in order to address this point. The means are:

length	795.38 dm/0.5 m ³ soil
cross-sectional area . . .	690.62 dm ² /0.5 m ³ soil
volume	11992.20 dm ³ /0.5 m ³ soil
number	31.96

Table XXIII. Proportion of explainable variation (R_p^2)^a due to root "number"^b and "volume"^c in the regression of each contact type.

model	proportion of explainable variation due to:	
	"number" ^b	"volume" ^c
Type I	0.9151*	0.0849
Type II-III	1.0000	0.0000
Type IV	0.0820	0.9180*

^aSee text for definition of R_p^2

^b"Number" indicates root number or, almost equivalent, length. An asterisk indicates that the calculated value of R_p^2 is actually based on length.

^cAnalogous to (b) above, but for volume and cross-sectional area.

The predicted number of contacts of each type was obtained by use of the regression coefficients in Tables IX, XI and XIII. The predicted values for each type are:

Type I	1.4242
Type II-III	0.8770
Type IV	0.4158

the sum of which is 2.7170. Thus, Types I and II-III contacts make up 85% of the total number of contacts. It is to be expected that factors which predominate in the equations for each of these contact types will also figure very prominently in the equation for the total number of contacts. It has been shown that root number (at least by inference in the case of Type I contacts) does, indeed, assume an important role in both the equation for Type I contacts and Type II-III contacts as seen in the values for R_p^2 .

It is also of interest to compare the predicted total number of contacts (2.7133, from the model for total number of contacts) with the sum of the predicted numbers of contacts of each contact type (2.7170). The two results compare remarkably well.

The independent variables in each of the equations for prediction of the number of contacts of each type also deserve some consideration. It has been noted that Type I contacts are a function of root length (or number) and volume. Recall (Materials and Methods) that Type I contacts were characterized as being tenuous in the sense that they were defined for roots that were at least in close proximity if not actually in physical contact. This type of contact was most noticeably associated with small roots (roots less than approximately 2.0

cm). Moreover, the relation between root volume (or cross-sectional area) and root length (or number) is relatively poor (R^2 = approximately 0.30). A plausible explanation for this fact is that even large numbers of small roots do not contribute much root volume to a soil volume compared to a few large roots. It is suggested, therefore, that it is small roots (which are more numerous and contribute to the total root length in a cell in disproportion to their volume) which contribute most to the number of Type I contacts. Note that the coefficient is negative for root volume. The smaller the root volume in a certain volume of soil, the more the number of Type I contacts becomes strictly a function of root length. Conversely, if greater root length (or number) is associated with larger root volumes, the number of Type I contacts is less.

Type II-III contacts are solely a function of root number. While it is not clear why root number should be the sole predictive variable, it can be noted that Type II-III contacts occupy a transitional zone, in a physical sense, between Types I and IV; Type I contacts are tenuous, Type II-III contacts are more substantial, while Type IV contacts (grafts, or apparent grafts) represent the "ultimate" contact. Corresponding with this, note that volume exerts a negative effect on the Type I end of this physical spectrum (Table IX) and a positive effect on the Type IV end (Table XIII). In the transitional zone of contact status (the Type II-III range of the spectrum), volume exerts no influence on the number of contacts (Table XI). Thus, there seems to be a clear correspondence.

Finally, one point requires comment in connection with Type I and Type IV contacts. It has been noted that Type I contacts are a function

of root number (positive relation) and root volume (negative relation). In contrast, the influence of both root number and volume on the number of Type IV contacts is positive. Thus, the influence of root number and volume in the regression for Type IV contacts is not strictly the converse of that seen in the regression for Type I contacts. Note, however, that the independent variables play contrasting roles in the two equations when one considers the contribution each makes to the total explainable variation in each model (Table XXIII).

A further question arises concerning which set of regression analyses is most relevant to the study of laminated root rot transmission. The predicted number of total contacts was shown to be nearly identical to the sum of the number of contacts of each type. There seems to be little advantage in the choice of model from the point of view of predicting the total number of contacts. Another point is worthy of consideration, however. Wallis (1957) and Wallis and Buckland (1956) have indicated that root contact is sufficient for disease transmission; grafting is not required. One may conclude from that that contact Types II-III and IV are probably functionally equivalent in terms of their ability to transmit laminated root rot. Type I contacts, in contrast, are distinct from the other types because of the tenuous aspect of this type of contact. Consequently, disease transmission should not be considered assured with Type I contacts. Wallis' (1976a) work on disease transmission across short soil distances suggests that the probability of transmission across Type I contacts might conservatively be estimated to be 0.50.

It becomes necessary to speak of effective contacts, if one takes the view that disease transmission is not assured in the case of Type I contacts. It is then advantageous to make use of the regression equations for the number of contacts for each type. It is possible, using the latter equations, to calculate the total number of effective contacts. The number of effective contacts, below, was computed using the mean values of the independent variables as before and assuming a transmission failure probability of 0.50 as suggested above:

effective Type I	0.7121
Type II-III	0.8770
Type IV	0.4158

the sum of which is 2.0049 effective contacts.

Factors Affecting Root Contact and Their Relation to Site Hazard

The results of the discriminant analysis indicate that the probability of inter-tree root contact: 1) increases with increasing DBH, percent slope and soil gravel content and; 2) decreases with increasing inter-tree slope distance and effective rooting depth. An important consideration, in view of these results, is whether or not the probability of inter-tree contact can be interpreted as an index of laminated root rot site hazard.

The analysis, of course, did not deal explicitly with the transmissibility of *Phellinus weirii* and its spread behavior needs to be considered. Wallis (1976a) has demonstrated that *P. weirii* does not grow through the soil to any appreciable extent. Moreover, dispersal via basidiospores is apparently non-existent (Nelson 1971). These obser-

vations indicate that spread is necessarily through root contacts (or is limited to small distances through the soil) and the latter are thus of paramount importance to the spread of laminated root rot. Wallis (personal communication) has indicated a belief that, given contact, transmission of disease between structural roots is extremely likely if not, in fact, wholly assured. The above discussion clearly lends support to the proposition that root contact potential may serve as a direct measure of spread potential.

Further support for the latter proposition can be found in some of the site hazard studies that deal with *Fomes annosus*. Kuhlman (1963) observed:

The findings suggest that less frequent root contact and failure of the fungus to colonize the tree root results in reduced losses on low hazard sites.

Kuhlman (1974) later asserted that frequency of root contact was the greatest single factor contributing to differences in annosus root rot site hazard. Factors that specifically increase root contact are: 1) shorter inter-tree distances (Hodges 1974); 2) limited effective rooting depth (Alexander and Skelly 1974; Alexander *et al.* 1975); 3) larger tree diameter (Grieg 1962) and 4) steeper slopes (Powers and Hodges 1970). Effective rooting depth may be limited by very sandy soil (Alexander and Skelly 1974) or simply a shallow profile development as often occurs on steep slopes. In the present study, there is reason to believe that steep slopes exert a further influence by an effect on the spatial distribution of the roots. It was observed in the course of the root excavations (but never quantified) that root systems tend

to become more asymmetrical on steeper slopes: roots tended to be more concentrated in the up- and downhill directions instead of evenly distributed about the bole (also McMinn 1963). This being the case, one might anticipate that relative slope position (Materials and Methods) would also influence the number of inter-tree root contacts. In fact, in preliminary discriminant analyses, relative slope position did appear as a significant variable: as the angle two trees made with the slope's aspect increased the probability of contact diminished.

The influence of soil gravel content might be interpreted as an effect on "effective rooting volume," analogous to effective rooting depth. In both instances, root systems have less volume available for root occupation and the chances of root contact would increase accordingly. Studies dealing specifically with the influence of soil characteristics on root form suggest another effect: increased stoniness seems to promote limited lateral root elongation accompanied by more profuse branching (Haasis 1921; Faulkner and Malcolm 1972). The discussion of the previous section brought out the significant influence of either root number or length on the number of Type I and Type II-III contacts. One can infer from this that soil gravel content will exert its greatest influence on the frequency of Types I and II-III contacts.

One variable which the present study did not deal with was soil texture for the simple reason that no significant variation in texture occurred among the study plots. The annosus root rot site hazard studies provide some insight into ways in which soil texture may affect site hazard. It is useful to consider these in relation to laminated root rot site hazard. Very sandy soils, it has already been noted,

limit the effective rooting depth, promoting shallow and extensive rooting (Alexander and Skelly 1974) and thus are associated with a higher incidence of root contact. At least in the Douglas-fir subregion of the Pacific Northwest, soils of sufficiently high sand content to produce an effect on rooting form are neither extensive nor common. It is the author's opinion that the soil textural variation that does occur in the subregion is, in general, not of sufficient magnitude to produce significant changes in root form and thus, also, root contact. The findings of Faulkner and Malcolm (1972) also support this contention.

Several of the annosus root rot studies have either suggested or demonstrated a further way in which soil texture may influence site hazard: sandy soils allow more effective spore percolation from the surface and increase the hazard of direct root infection (Kuhlman 1969; Alexander and Skelly 1974; Alexander *et al.* 1975; Froelich *et al.* 1965; and Froelich *et al.* 1966). This influence on laminated root rot site hazard would seem to be irrelevant. In addition, it has yet to be demonstrated that the natural variation in soil texture, pH, base saturation or even microflora has any tangible effect on either the spread or survival of *P. weirii*.

The probability of inter-tree root contact may be considered as one of three components of laminated root rot site hazard. A site hazard formula should include not only the probability of inter-tree root contact, but also a factor representing fungal spread potential and a factor expressing inoculum distribution. A study, already in progress, is examining the influence of isolate variation in *Phellinus*

weirii and site on the potential for spread along roots (Hansen, personal communication). Bloomberg (personal communication) has developed survey methods for evaluation of disease distribution.

Before the results of the present study can be incorporated into a site hazard rating system, it must be demonstrated that the coefficients of the discriminant functions are applicable throughout the Douglas-fir subregion. This could be accomplished most expeditiously by excavating trees on a number of additional sites, determining their contact groups and evaluating the frequency with which the current model correctly classifies the observations. If the success rate proves acceptable, the newly acquired data may be added to that provided in this study with the potential for improving the current model. Failure of the model to adequately classify the new observations into the appropriate contact groups would demonstrate the need to develop separate models for partitions of the subregion. The latter possibility seems unlikely however, given the general form of the model.

Implications and Assumptions of the Laminated Root Rot Inter-Tree Spread Model

It is important to understand the limitations and assumptions of the inter-tree spread model before taking up a discussion of the spread behavior revealed in the analysis of the model.

The pattern of spread was described in RESULTS, Part B. Spread from a bole infected tree is presumed to be radial in all directions outward from the bole whereas spread from a contact on a non-bole infected tree was assumed to be linear (the line being defined by the

location of the infected contact point and the center of the bole of the newly infected trees). Recall also that the model allows for differential rates of spread proximal and distal to the bole of an infected tree as well as a maximum growth mode. These simplifications of fungal spread behavior seem desirable and reasonable.

Closely related to spread behavior is the matter of time to cessation of radial spread following bole infection. No information concerning this facet of fungal behavior is available in the literature so the author provided what seemed to be a reasonable relation between DBH and time to cessation of fungal growth (Table XXI). Several points must be made in connection with these assumptions. First, annual DBH increment is presumed to be unaffected by the proportion of the root system that is infected. It is reasonable to hypothesize that the latter increment is some function of the proportion of infected root system and, in fact, work regarding this hypothesis is presently underway (Bloomberg, personal communication). Wallis' (1957) earlier work on the influence of infection on height growth demonstrated the marked insensitivity of height growth to the level of infection. Recall that at least half the root system was found to be infected prior to a noticeable influence on height growth. DBH is probably more sensitive than height growth, however. Nonetheless, in the context of this model, it would probably be sufficient to limit the influence of level of infection on DBH to that period following bole infection since, in the cases of trees 2 and 4, they are only being infected from a single source (tree 1) and it is likely that less than half, and perhaps much less than half, of their root systems are affected prior to bole

infection. Thus, an influence of level of colonization on DBH increment could be introduced to the model's algorithm to improve its realism. Moreover, it is convenient and probably reasonable to use the time of bole infection as a reference point. DBH increment at time $t + 1$ could then be expressed as a function of DBH at time t , the normal DBH increment at time t and the present level of infection (i.e., - years since bole infection).

Another problem of concern is the prescribed behavior of fungal spread. It is assumed in the model that proximal and distal spread proceed at constant rates, which, in the simulations, were both set to 30.0 cm per year. These rates exceed those reported by Wallis and Reynolds (1962). When rates of spread comparable to those reported by the latter were used, however, the rate of disease spread appeared to be unreasonably slow. One possible explanation is that these reported rates are not representative of all possible spread behavior. Wallis (1961) in connection with the latter proposition, observed that *Fomes annosus* grew much more rapidly along the bark surface (and within the wood) of severed, as opposed to intact, pine roots. Similarly Hodges (1974) found that on several susceptible pine species *F. annosus* grew at a rate of approximately 35 cm per year on living roots, but that on roots that had been recently killed, distal growth often was as much as 100 cm per year.

If, as the author suspects, the ectotrophic growth behavior of *P. weirii* is similar to that of *F. annosus*, then using the proximal and distal rates reported by Wallis and Reynolds (1962) would not reasonably reproduce the fungus spread behavior; its average rate of spread

would be considerably faster. Moreover, one might anticipate that the average rate of spread would differ among stands of different age classes.

There is an important connection between the time of fungal growth cessation following bole infection and the average rate of fungal spread discussed above. Small trees exhibit minimal fungal spread following bole infection (i.e., two year spread after bole infection in the case of trees with a diameter less than 5.0 cm). The extent of distal spread that would occur assuming an average rate of spread 30.0 cm per year would be roughly 60.0 cm at the time of growth cessation. If, on the other hand, we assumed that the fungus grew at a distal rate of 20.0 to 25.0 cm per year (as the data of Wallis and Reynolds suggest) and that at the time of root girdling a flush of distal fungal growth on the order of 100.0 cm occurred, then the total distal spread, assuming the latter growth flush was limited to a single year, would be approximately 140.0 to 150.0 cm. The average distal spread rate for the three year period would then be roughly 50.0 cm per year. Notice that in computing this average an extra year allowed for spread. In order to allow for the full 150 cm of spread, it would be necessary to either allow for an extra year of spread or account for the total spread in the two year period. The above example indicates that the average rate of fungal spread in a very young stand would be profoundly affected by a variation in assumed fungal behavior. The rate of spread of 30.0 cm per year used in the simulations of this study would seriously underestimate the rate of tree-to-tree spread if, in fact, fungal growth flushes accompanied death of the distal portion of a root.

The stands used in the simulations of this study were all at least 20 years old. If one examines the assumptions presented in Table XXI that deal with time to fungal growth cessation following bole infection, it will be seen that the minimum time is 10 years for the stands used in the simulations. Now, assume again that distal growth rate is 20.0 to 25.0 cm per year. At the end of ten years' time the fungus will have spread approximately 200.0 to 250.0 cm from the bole. If we now take into account a fungal growth flush of 100.0 cm and average the extra growth over the previous ten year period the average growth rate will be 30.0 to 35.0 cm per year.

Similar calculations can be performed for 20, 40 and 60 year old stands as used in the simulations of this study. These calculations are not carried out here. One can see, however, based on the assumed times to fungal growth cessation for the different diameter classes in Table XXI that when the fungal growth flush is distributed over the time to growth cessation that the impact of a flush on the annual distal spread increment becomes progressively smaller. Therefore, the rate of 30.0 cm per year was used throughout the simulations.

The basis for the spread behavior described above applies equally well to the concept of the infection zone that surrounds the pathogen's linear growth path during the interval between initial infection and bole infection. Recall that in the linear mode of spread, the model allows for an infection zone which encompasses that area within 30.0 cm of the distal and proximal limits of spread (and any intervening point). Now, imagine the path of spread as representing growth along a primary

root. As the fungus progresses along that root, it encounters and colonizes smaller lateral roots. The latter can probably be girdled rapidly due to their relatively small diameter. The distal portion of the root would then also die rapidly and the fungus could quickly colonize the distal portion. In the model this process is represented as an instantaneous event in effect. That is, it is assumed that, when infection has spread to some point "s" on the primary root, it has also spread to all root surfaces within 30.0 cm of that point. The concept of the infection zone about the linear path of fungal spread is a reasonable approximation to the extent that rapid colonization of dead, distal, lateral root surfaces is a reality.

The representation of the contact zone as a circular area whose center lies at the midpoint of the line joining the boles of two trees is also an oversimplification. Insufficient data were obtained in the present study to specify its parameters more accurately, however. Study of the root maps produced by program ROOTMAP (Appendix B) suggests that the location, size and shape of the contact zone are affected by all of the factors associated with the probability of inter-tree root contact. The following general functional forms are hypothesized:

$$\text{location} = f(\text{tree distance, DBH, slope})$$

$$\text{size} = f(\text{tree distance DBH, effective rooting depth, gravel content}) \text{ and}$$

$$\text{shape} = f(\text{DBH, slope}) \quad .$$

The simple influence of tree distance on the location of the zone's center is apparent in the definition of the zone (above): the center is

located at the midpoint of the line joining the two trees' boles. DBH and slope can be expected to affect location as well. As DBH of the source tree increases relative to the target tree, the location of the zone's center should shift toward the target tree. As slope increases (and therefore, also, root asymmetry) the location of the zone will move downslope.

The influence of all tree, stand and site factors on contact zone size is apparent.

Finally, DBH and slope should influence contact zone shape in a manner analogous to their effects on the location of the zone.

Within the contact zone it has been assumed that the distribution of contacts is random. Here, too, it is possible to hypothesize a general functional form for the distribution which would more realistically represent actual conditions:

$$f(x,y) = g(\text{DBH}, \text{slope}).$$

This expression implies that the distribution of contacts is, in some way, related to the shape of the contact zone and relative sizes of the trees. Intuitively, this relation seems appropriate. Examination of the root maps lends further support to this view.

Explication of System Behavior

A system is defined, from one perspective, in terms of its inputs, outputs and state variables and the relations between them (Klir 1969). The motivating hypothesis for study of the inter-tree disease spread

system is that the cumulative distribution of the earliest time to hole infection of an uninfected tree (that stands adjacent to an infected one) is functionally related to several tree, stand and site factors. In RESULTS, Part A, several factors were specifically identified which affect the probability of inter-tree root contact. The nature of disease spread in the case of laminated root rot suggests that these same factors will be an important influence in determining the rate of disease spread. Thus, the trees' diameters, inter-tree slope distance, the effective rooting depth, gravel content of the soil and the percent slope are all hypothesized to affect the cumulative distribution of earliest time to the infection. The influence of the first three factors on system behavior are considered here.

It is appropriate to first consider the general properties of the system as illustrated in the twenty-seven graphs of Appendix G, before considering the influence of each factor in detail. A careful study of each simulation plot suggests that the functional relation between the cumulative distribution of earliest time to hole infection and time is actually composed of two distinct functions. Simulation run 1 can be taken as a typical example. It can be seen in the graph (Appendix G and Figure 18) that the distribution curve up to year (actual time is 30 years) can be expressed by a general logistic function:

$$CDF = b_0 - \frac{1}{1 - \exp(b_1 + b_2 t + b_3 t^2)}$$

where: $b_0 = 0.30$ (the asymptote) and b_1 , b_2 and b_3 represent shape parameters.

The portion of of the curve from year 21 to year 26 could be described by a simpler relation:

$$\text{CDF} = 1 - b_1 e^{b_2 t}$$

If we examine other curves, however, (for instance, those of simulation runs 7, 8 and 9) it becomes apparent that the former function does not adequately represent all possible behavior in the lower region of the curve. The curve appears to take on a distinctly exponential character under some conditions. The lower portion of the distribution function, which for brevity will be referred to simply as phase I, requires a more general functional form such as that for the single process law:

$$\text{CDF} = b_1 + b_2 (t - b_3 b_4)^{b_4}$$

This functional relation would encompass all the forms of behavior evidenced in phase I of the graphs of Appendix G.

It is equally apparent from study of the graphs (Appendix G and Figures 17, 18 and 19) that the upper portion of the distribution function (phase II) can be adequately represented in all cases by the functional relation described for simulation run 1: that is, a simple exponential expression.

The composite function appears to be a fundamental property of the system. That it is a reasonable property to expect, can be concluded from a reexamination of Figure 16. During the early stages of the spread process, only tree 1 is infected. Only the primary infection path to tree 3 is available at the beginning of this period. Trees 2 and 4 are becoming infected in addition to tree 3, however, and it is probable that

they are contributing to the infection of tree 3 via the indirect pathways of spread (shown with dashed arrows) in the latter part of this period. Note that, in the model specifications, fungal growth on tree 1 is arrested at year 10 (or year 0 in the plots of Appendix G and Figures 17, 18 and 19) when the initial DBH is 21.59 cm. The extent of tree 1's influence either directly or indirectly on the distribution function of earliest time to bole infection is thus probably limited to phase I. As already noted, trees 2 and 4 have been infected in the meantime and these trees are responsible for a secondary wave of infection. Which wave predominates in a given simulation will depend, moreover, upon how rapidly the disease is spreading and this is determined by the initial conditions.

Exploratory non-linear regression were performed on a few of the simulation run results. Severe problems were encountered when trying to fit a curve with three or more parameters to only a few data points. The problem could be easily remedied by making several additional simulation runs for each set of initial conditions. There seems, however, little or no compelling reason to do so at the present time. The previous discussion on the limitations of the model make it clear that several aspects of the system's behavior require more accurate specification (such as the rates of proximal and distal spread, the size and location of the potential contact zone, and the distribution of contacts within the latter zone). Given these limitations, it seems appropriate to postpone the costly and time-consuming analyses required to accurately specify the system's behavior until improvements in the simulator can be made.

It is still reasonable to consider the general influence of the initial conditions on system behavior, limitations notwithstanding. Refinements incorporated into the model will certainly alter the distribution of time to bole infection, but should not materially alter the basic behavior as deduced from the general shapes of the curves in Appendix G.

The reader should refer back to Table XXII to reacquaint himself with the pattern of variation in the initial conditions of the system. The influence of soil depth on system behavior can be seen by examining the simulation run plots in triplets. For instance, runs 1 through 3 (Appendix G) have effective rooting depth of 80.0, 100.0 and 120.0 cm., respectively while, for all three plots distance and DBH are constant (3.0 m and 21.59 cm., respectively). Similarly, triplets of every third plot can be examined to discern effects of changes in DBH. The first such triplet would consist of plots 1, 4 and 7 representing initial DBH's of 21.59, 32.36 and 46.23 cm., respectively. Finally, triplets of every ninth plot can be examined to evaluate the influence of inter-tree slope distance (or, simply, distance) on the system's behavior, other conditions being equal.

Each factor will be treated separately in the following discussion to simplify the analysis. The general pattern of analysis will be to consider some appropriate triplet of simulation runs for a factor in detail and to subsequently generalize the conclusions obtained such that they are valid for all simulation run triplets.

The influence of effective rooting depth. The earlier discussion on the general properties of the system has already drawn attention to

one aspect of the influence of effective rooting depth: the shape and, to a lesser extent, the asymptote of the distribution function in phase I is influenced by depth. In simulation run 1, the shape of the curve in phase I is basically sigmoid in character. The same region of the curve in run 2 assumes a more obviously sigmoid character. There is a reduction in both the slope and the asymptote proceeding from run 1 to 2. The latter statement is also valid for a comparison of phase II between those two runs. If we next compare run 2 with run 3, it seems there is no practical difference in the behavior of the system as effective rooting depth increases past 100.0 cm.

Characterizing the general influence of effective rooting depth is considerably more difficult. It may be noted that the observations made concerning the triplet 1-2-3 apply equally well to the next two succeeding triplets [4-5-6 (distance = 3.0 m, DBH = 32.26, Figure 17) and 7-8-9 (distance = 3.0 m, DBH = 46.23)]. Although in the case of the triplet 7-8-9, phase I completely dominates the distribution function and asymptotes are equal to 1.0. It is apparent, however, when we examine runs 10 through 18 (distance = 4.0 m) that only in phase I is there a consistent effect of rooting depth and that as before their effect is only apparent in the first two runs of a triplet. There is essentially no difference in the phase II portions of the curves of each triplet in the sequence 10 through 18. Further, if we must examine runs 19 through 27, it can be seen that the influence of rooting depth disappears entirely. Clearly, the influence of rooting depth is conditional upon (distance = 3.0 m) effective rooting depth affects the asymptote, slope and shape of both phases of the CDF; 2) in runs 10 through 18

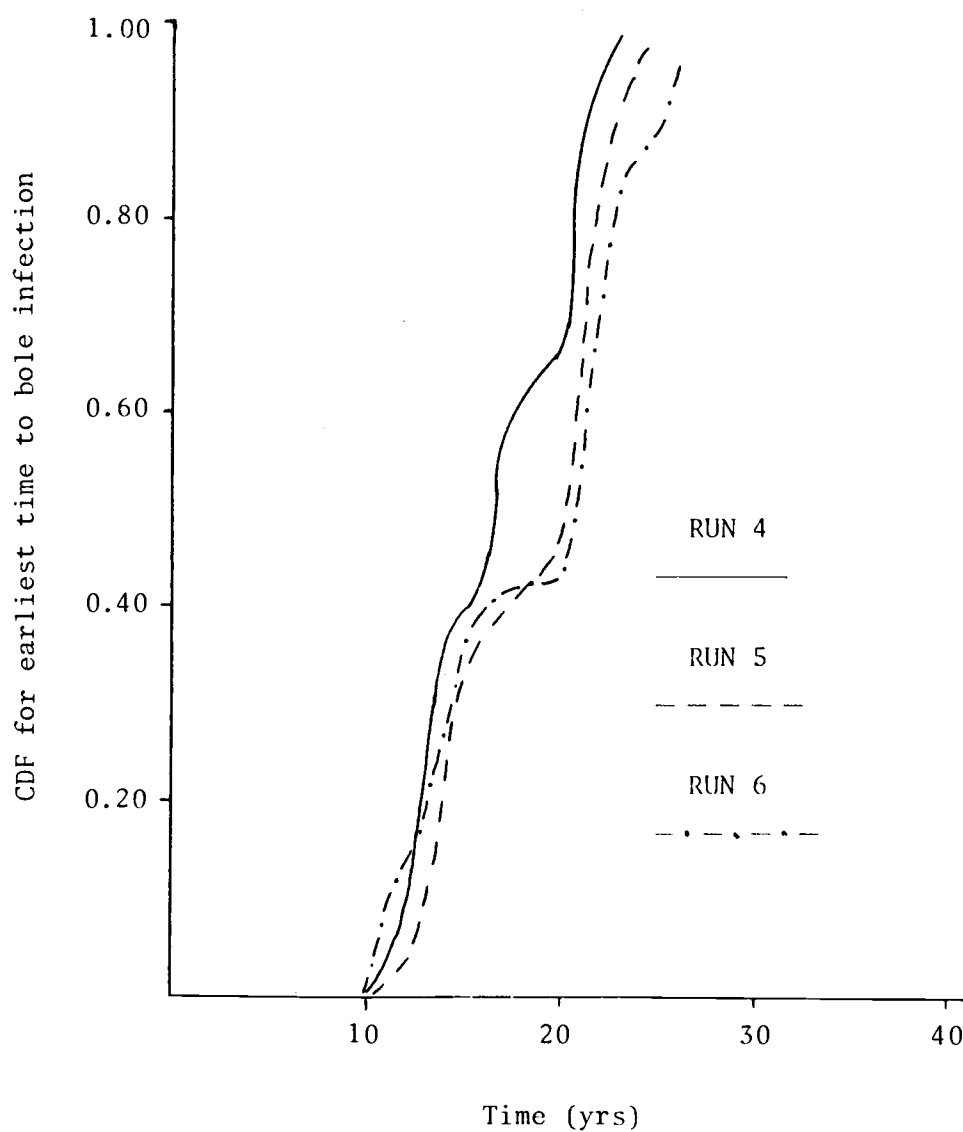


Figure 17. Influence of change in effective rooting depth on CDF for earliest time to bole infection.

Inter-tree distance = 300.0 cm.

Initial DBH = 32.36 cm.

Soil depths for simulation runs 4, 5 and 6 are 80.0, 100.0 and 120.0 cm., respectively.

(distance = 4.0 m) the same influences are seen only in phase I and 3) the runs 19 through 27 (distance = 5.0 m) an effect due to rooting depth is no longer evident.

The influence of initial stand DBH. The simple effects in increasing initial DBH can be seen in the triplets 1-4-7, 2-5-8, etc. We will start, again, by considering the specific effects seen in the 1-4-7 triplet (Figure 18). First, it can be noted that, in runs 1 and 4 of this triplet, phase I of each simulation run can be represented by the general logistic function. In the same triplet set, it can be seen also that the slope of the function in phase I increases sharply as one progresses from run 1 to 4 to 7. Further the asymptote of phase I increases dramatically as initial DBH increases. The asymptotes of phase I for runs 1, 4 and 7 are 0.30, 0.64 and 1.00, respectively. Similar trends are also seen in the triplets 2-5-8 and 3-6-9. Note, however, that a new phenomenon appears in run 7 (Figure 18) as well as runs 8 and 9. The composite function has been replaced by a single exponential one. The explanation becomes clear if we examine the trend in phase I asymptote changes due to increasing initial DBH: phase I assumes a progressively dominant role in the composite function as DBH increases. In view of the earlier discussion on the origin of the composite function, a shift to primary infection as the principle source of infection seems the most plausible explanation for the change in form of the cumulative distribution function of earliest time to bole infection. It is this interpretation which makes it necessary to replace the general logistic function with the single process function in phase I.

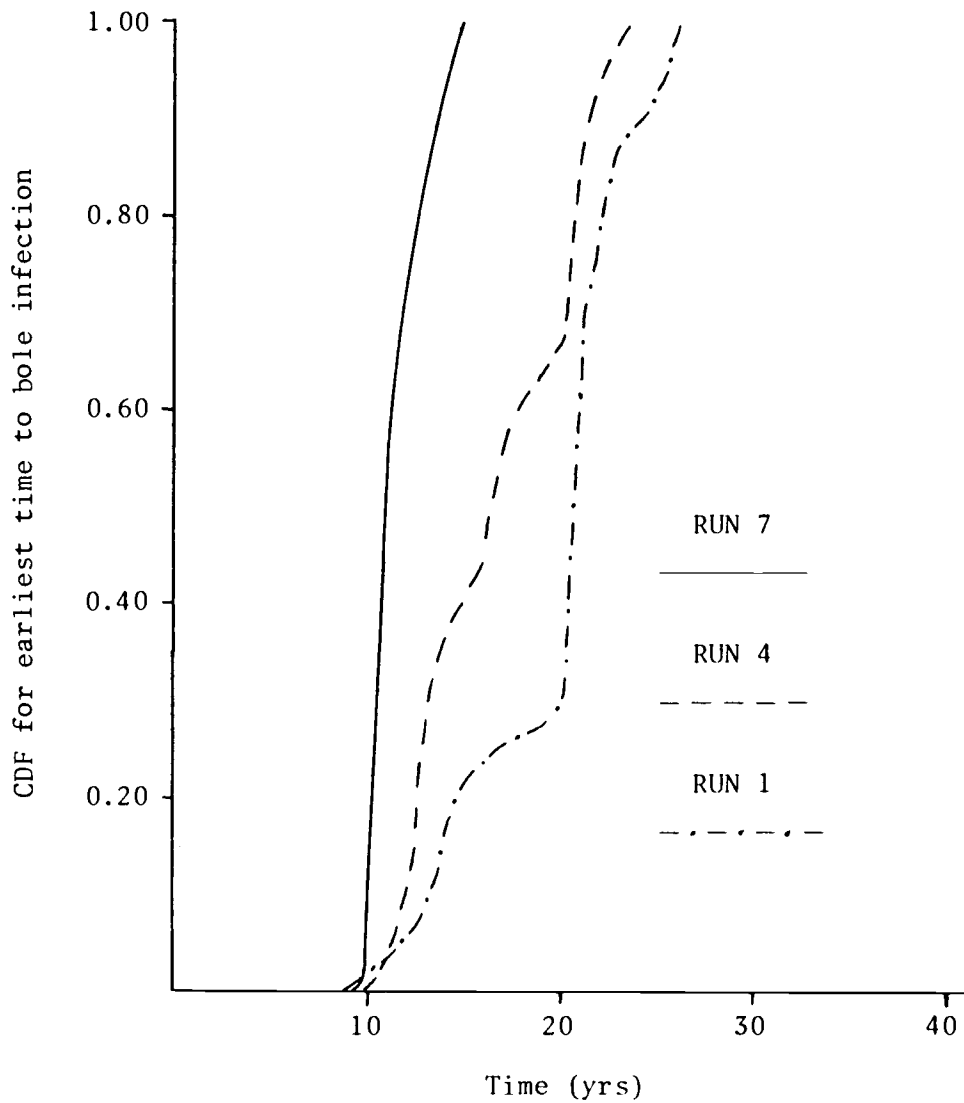


Figure 18. Influence of change in initial DBH on CDF for earliest time to bole infection.

Inter-tree distance = 300.0 cm.

Effective rooting depth = 80.0 cm.

Initial DBH's for simulation runs 1, 4 and 7 are 21.59, 32.36 and 46.23 cm., respectively.

The same basic pattern of DBH influence is visible in the triplets 10-13-16, 11-14-17 and 12-15-18. In these nine simulations, two additional observations can be made. First, in contrast with runs 1 through 9, phase I is characterized by a more strongly sigmoid function. The observations pertaining to change in slope and asymptote of the phase I curve remain valid nonetheless. Second, at the greater inter-tree slope distances, the asymptote of the phase II function is often less than 1.0 and an influence of DBH on this parameter is apparent: the asymptote increases with increasing DBH.

The influence of DBH on the cumulative distribution functions of runs 19 through 27 is anomalous. Examination of the appropriate triplets in this group will indicate that, in the phase I portion of the curves, the probability does not consistently increase but, rather, drops from the first in the set and then increases again in the third member of the triplet, returning to the approximate level at which it started in the first member of the set. No logical explanation presents itself to account for this model behavior. It would seem, however, that the departure from the expected pattern of influence is a result of a DBH x distance interaction. The pattern of influence of DBH on the phase II portion of runs 19 through 27 is, however, consistent with those described for the earlier cases.

The influence of distance. The influence of distance on the cumulative distribution of earliest time to bole infection can be studied by examining triplets of every ninth simulation run. Runs 7,16 and 25 (Figure 19) constitute one such triplet, as an example. Increasing

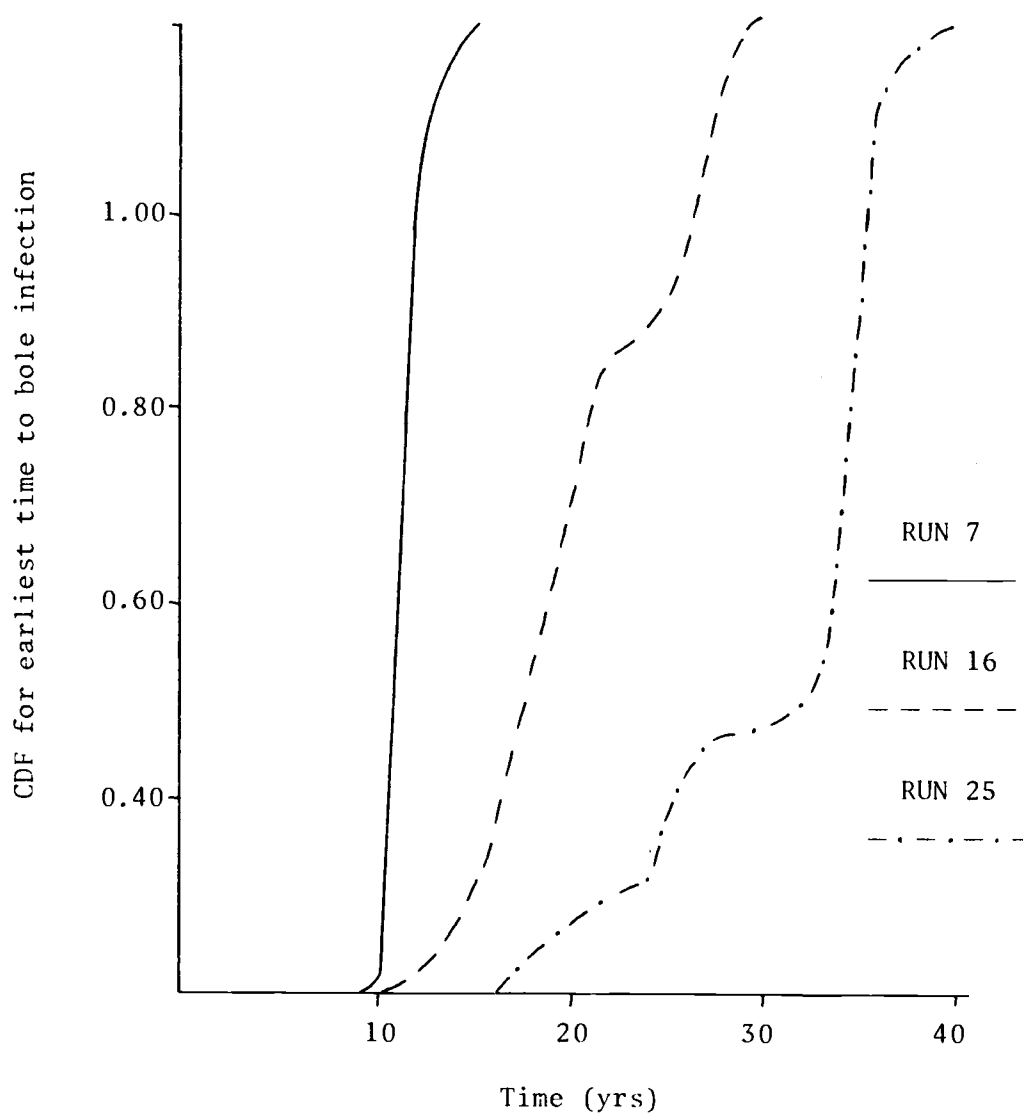


Figure 19. Influence of change in inter-tree distance on CDF of earliest time to bole infection.

Initial DBH = 46.23 cm.

Effective rooting depth = 80.0 cm.

Inter-tree distances for simulation runs 7, 16 and 25 are 300.0, 400.0 and 500.0 cm., respectively.

distance exerts an influence similar to increasing effective rooting depth. The magnitude of this effect is far stronger however.

Section summary. A detailed qualitative analysis of the influence of three initial conditions on system behavior has been presented. The salient features of this analysis are briefly summarized here:

- 1) the cumulative distribution function of earliest time to hole infection is actually a composite function consisting of two functions, one for each of the recognized phases,
- 2) the functional form of the phase I relation is given in the single process law while the form of phase II is given in a simple exponential expression,
- 3) the phases of the composite function can be physically interpreted as two relatively distinct infection waves; the first wave represents primary infection from a source, while the second represents secondary infection from adjacent trees and
- 4) all of the initial conditions can influence the shapes, slopes and asymptotes of each phase although the effect of rooting depth is strongly influenced by inter-tree distance.

VII. CONCLUSIONS AND SUMMARY

Relations Between the Number of Root Contacts in a Specific Soil Volume and Root Attributes in that Soil Volume

The number of root contacts between two trees that jointly occupy the same 0.5 m^3 of soil can be functionally related to the total root attributes of both trees in that volume of soil. The total number of contacts (TNC) is a simple function of the total number of roots (Tables VI and VII):

$$\text{TNC} = 0.5688 + 0.0671 (\text{number}).$$

The number of contacts of each type can also be related to the root attributes. Type I contacts are a function of both root length and volume (Tables VIII and IX):

$$\text{Type I} = 0.5716 + 0.001277 (\text{length}) - 0.00001369 (\text{volume}).$$

Type II-III contacts are a function of root number (Tables X and XI):

$$\text{Type II-III} = -0.0019 + 0.075 (\text{number}).$$

Type IV contacts are a function of root number and root cross-sectional area (Tables XII and XIII):

$$\text{Type IV} = -0.061587 + 0.0072 (\text{number}) + 0.000358 (\text{x-section}).$$

It was pointed out in the discussion that whether the total number of contacts was being predicted from the first of the above four equations or the total was obtained as the sum of the number of each contact type,

comparable answers would be obtained.

That the equation for total number of contact between two trees' roots in 0.5 m^3 of soil is properly a function of root number alone was demonstrated, in part, by a consideration of this factors contribution to the prediction of each contact type. It was seen that, since 1) root number and length are highly correlated ($r = 0.962$) and 2) root number accounts for a major proportion of the explainable variation in Type I contacts and all the explainable variations in Type II-III contacts and 3) Types I and II-III contacts represent 85.0 percent of the contacts in an "average" soil volume, the dependence of the total number of contacts on root number alone was a reasonable result.

The appropriateness of the relation for each contact type was also considered. Field observations made it obvious that Type I contacts were most commonly associated with the smaller, more numerous roots. This observation is plainly reflected in the equation for Type I contacts. The latter are a function of root length (and, hence, almost equivalently, root number) and volume. Root length was positively and volume negatively related to the number of Type I contacts. Type IV contacts were, to a great extent, a function of cross-sectional area (and, again, almost equivalently, root volume) and, to a much lesser extent, root number. It was quite apparent in the field that Type IV contacts were generally associated with larger roots, hence the significance of cross-sectional area to the relation. Finally, Type II-III contacts were portrayed as representing the "middle ground" in a physical continuum of contact associations where Type I and Type IV contacts represented the physical extremes. The appropriateness of the dependence of Type II-III contacts

on root number alone was inferred from this fact.

The Relation of Tree, Stand and Site Factors to the Probability of Inter-Tree Root Contact

The discriminant analysis on root contact probability revealed that it was possible to distinguish between the three contact categories NOCON, LOCON and HICON (described in RESULTS, Part A) on the basis of several attributes (Tables XV and XVI). Specifically, the probability of contact was seen to increase with increasing DBH, soil gravel content and percent slope and to decrease with increasing inter-tree slope distance and effective rooting depth.

The probability of contact may be incorporated into a site hazard index with a 0.0 to 1.0 scale. Few quantitative site hazard studies on forest pathogens are available for comparison. Those on *Fomes annosus*, however, indicate that tree size, inter-tree distance, effective rooting depth and percent slope are important factors in the spread of annosus root rot. Further, the latter factors appear to exert this influence via an affect on the probability of root contact. Factors such as soil stone content may not have been considered in the annosus root rot studies due to a lack of appreciable variation in these factors. Soil texture was not examined in the present study for this reason. The effects on site hazard due to soil texture or the presence of surface organic layers were related to an influence on spore percolation which, though meaningful to annosus root rot hazard, at the present time, appears irrelevant to the spread of laminated root rot.

A site hazard rating system should certainly include such factors as inter-tree root contact potential and intra-tree fungal spread potential which together could be used as an indication of inter-tree spread potential.

Moreover, inoculum distribution has a strong influence on future yield losses in stands of Douglas-fir affected by laminated root rot. A hazard index of practical use to the forest manager should incorporate data on the size and distribution of infection centers in addition to the potential for tree to tree spread from those centers.

Current Status of the Laminated Root Rot Spread Model

The laminated root rot spread model must be treated as hypothetical. Several important areas have been identified where data is lacking or incomplete.

Fungal spread time following bole infection was simply guessed at since no data were available on the subject (Table XXI). If or when information on spread times does become available, it will be necessary to modify the coefficients of the fungal spread decrement equation (Table XXI) which are based on these assumed times.

Insufficient data were available in the study to allow a precise specification of certain features in the contact submodel. The potential root contact zone is assumed to be circular and situated at the midpoint of a line defined by the geographic centers of the root collars of two trees. It is further assumed that the zone has a radius of 200.0 cm at age 20 and that the radius increases linearly to a maximum of 300.0 cm by age 40. Contacts are assumed to be randomly distributed

within the zone. All of the above assumptions are simply first approximations and more appropriate functional forms were discussed.

Finally, the rate of spread of *Phellinus weirii* along the roots was approximated as an average rate that takes into account fungal growth flushes that accompany death of the distal portion of a root following girdling by the fungus. The work of Hodges (1974) and Wallis (1961) on *Fomes annosus* suggests that this is reasonable.

The Relation of Tree, Stand and Site Factors to System Behavior as Revealed in the Simulations of SIMROT2

The ultimate modeling objective is to characterize the behavior of the system in a functional expression that relates rate of inter-tree disease spread to the several tree, stand and site factors. Practical reasons for not doing so at the present time have been offered. The latter arise from the hypothetical status of the simulation model.

Informational gaps notwithstanding, it has been possible to describe the fundamental properties of the system and the manner in which the various factors (inter-tree slope distance, initial DBH and effective rooting depth) influence behavior more specifically. The following points emerge from a consideration of the plots presented in Appendix G:

- 1) the cumulative distribution function of earliest time to bole infection is a composite function consisting of two functions, one for each of two recognized phases in the distribution function.
- 2) the phases of the composite function can be physically interpreted as two relatively distinct infection waves; the first

wave corresponds to primary infection from a source while the second represents secondary infection from adjacent trees,

- 3) the functional form of the phase I relation is given by the single process law while the form of phase II is given by a simple exponential expression and
- 4) all of the initial conditions studied influence the shapes, slopes and asymptotes of the two phases although the effect of rooting depth is strongly conditioned by inter-tree distance.

VIII. LITERATURE CITED

- Alexander, S. A. and J. M. Skelly. 1973. Disease incidence and disease severity in loblolly pine planted over two soil hazard types. In: Proc. IV Conf. in *Fomes annosus*. S.E. For. Exp. Sta., U.S.D.A., Dept. 17-22, Achville N.C. pp 184-191.
- Alexander, S. A.; J. M. Skelly and C. L. Morris. 1975. Edaphic factors associated with the incidence and severity of diseases caused by *Fomes annosus* in loblolly pine plantations in Virginia. *Phytopath.* 65(5):585-591.
- Aoshima, K. 1953. Wood-rotting *Poria* from Japan. *Rev. Appl. Myc.* 32:597-598.
- Bier, J. E. and D. C. Buckland. 1947. Relation of research in forest pathology to the management of second growth forests. I. *Poria weirii* root rot, an important disease affecting immature stands of Douglas-fir. *B. C. Lumberman* 31:49-51.
- Biomedical Computer Programs. 1977. Univ. of Cal. Press, Berkeley. 770 p.
- Bliss, D. E. 1951. The destruction of *Armillaria mellea* in citrus soils. *Phytopath.* 41:665-683.
- Bollen, W. B. and K. C. Lu. 1968. Nitrogen transformation in soils beneath red alder and conifer. In Biol. Alder, Proc. N. W. Sci. Assoc. Ann. Meeting, April 14-15, 1967, 141-148.
- Buchanan, T. S. 1948. *Poria weirii*: its occurrence and behavior on species other than cedars. *N. W. Sci.* 22:7-12.
- Buckland, D. C.; R. E. Foster and V. J. Nordin. 1949. Studies in forest pathology. VII. Decay in western hemlock and fir in the Franklin River area. *Can. J. Res. C.* 27:312-331.
- Buckland, D. C.; A. C. Molnar and G. W. Wallis. 1952. Yellow laminated root rot of Douglas-fir. *Can. J. Bot.* 32:69-81.
- Buckland, D. C. and G. W. Wallis. 1956. The control of yellow laminated root rot of Douglas-fir. *For. Chron.* 32(1):14-19.
- Childs, T. W. 1955. Synopsis of present information concerning *Poria weirii* root rot in Douglas-fir. U.S.D.A. For. Ser. P.N.W. For. & Range Exp. Sta. PNW-116.
- Childs, T. W. 1960. Laminated root rot of Douglas-fir. U.S.D.A. For. Ser., For. Pest Lft. No. 48, 6 p.

- Childs, T. W. 1963. *Poria weirii* root rot. *Phytopath.* 53(10):1124-1127.
- Childs, T. W. 1970. Laminated root rot of Douglas-fir in western Oregon and Washington. U.S.D.A. For. Ser., P.N.W. For. & Range Exp. Station, Rec. Paper PNW-102.
- Childs, T. W. and E. E. Nelson. 1971. Laminated root rot of Douglas-fir. U.S.D.A. For. Ser., For. Pest Leaflet No. 48, 7 pp.
- Childs, T. W. and K. R. Shea, 1967. Annual losses from disease in Pacific Northwest Forests. U.S.D.A. For. Ser. Resource Bull. PNW-20, 19 pp.
- Cyber. Complot User's Manual. 1979. Milne Computer, Oregon State University, 90 pp.
- Faulkner, M. E. and D. C. Malcolm. 1972. Soil physical factors affecting root morphology and stability of Scots pine on upland heather. *Forestry.* 45(1):23-36.
- Filip, G. M. 1979. Root disease in Douglas-fir plantations is associated with infected stumps. *PDR.* 63(7):580-583.
- Filip, G. M. and C. L. Schmidt. 1979. Susceptibility of native conifer to laminated root rot east of the Cascade range in Oregon and Washington. *For. Sci.* 25(2):261-265.
- Franklin, J. T. and A. A. Pechanec. 1968. Comparison of vegetation in adjacent alder, conifer and mixed alder-conifer communities. In: (J. M. Trappe; F. T. Franklin; R. T. Tarrant; G. M. Hansen, eds.) *Biology of Alder. Proceedings of a symposium held at Northwest Scientific Assoc. 40th Ann. Meeting. Pullman, WA, April 14-15, 1967.* U.S.D.A. For. Ser. P.N.W. For. & Range Exp. Sta.
- Froelich, R. C.; T. R. Dell and C. H. Walkinshaw. 1965. Factors associated with occurrence of *Fomes annosus* in pine plantations. *Phytopath.* 55(10):1058-1059.
- Froelich, R. C.; T. R. Dell and C. H. Walkinshaw. 1966. Soil factors associated with *Fomes annosus* in the Gulf states. *For. Sci.* 12(3):356-361.
- Garrett, S. D. 1970. Pathogenic root-infecting fungi. Cambridge Univ. Press, 294 p.
- Gilbertson, R. L. 1974. Fungi that decay Ponderosa pine. University of Arizona Press, Tucson, 197 p.

- Greig, B. J. W. 1962. *Fomes annosus* (Fr.) Coke. and other root-rotting fungi in conifer on ex-hardwood sites. *Forestry* 35(2):164-182.
- Haasis, F. W. 1921. Relation between soil type and root form of western yellow pine seedlings. *Ecol.* 2:292-303.
- Hadfield, J. S. and D. W. Johnson. 1977. Laminated root rot -- a guide for reducing and preventing losses in Oregon and Washington forests. U.S.D.A. For. Ser. P.N.W. Region.
- Hansen, E. 1975. *Phellinus* (*Poria*) *weirii* root rot in Douglas-fir -- alder stands 10-17 years old. U.S.D.A. For. Ser. Rec. Note, P.N.W. For. & Range Exp. Sta. No. PNW-250, 5 pp.
- Hansen, E. M. 1976. Twenty-year survival of *Phellinus* (*Poria*) *weirii* in Douglas-fir stumps. *Can. J. For. Res.* 6(2):123-128.
- Hansen, E. M. 1979. Survival of *Phellinus weirii* in Douglas-fir stumps after logging. *Can. J. For. Res.* 9(4):484-488.
- Hodges, C. S. Jr. 1974. Symptomatology and spread of *Fomes annosus* in Southern pine plantations. U.S.D.A. For. Ser. Rec. Pap., S.E. For. Exp. Sta. No SE-114, 10 pp.
- Hopp, H. 1938. The formation of coloured zones by wood-destroying fungi in culture. *Phytopath.* 28:601-620.
- Johnson, D. W. 1976. Incidences of disease in National Forest plantations in the Pacific Northwest. *PDR.* 60:883-885.
- Klir, G. J. 1969. An approach to general systems theory. Van Nostrand Reinhold Co., New York. 323 pp.
- Kuhlman, E. G. 1969. Survival of *Fomes annosus* spores in soils. *Phytopath.* 59:198-201.
- Kuhlman, E. G. 1973. Rate of infection of loblolly pine roots on high and low hazard sites by *Fomes annosus*. *Phytopath.* 63:444.
- Kuhlman, E. G. 1974. Variation in infection of loblolly pine roots on high and low hazard sites in the Southeastern United States. p. 179-183. In: Proc. IV Conf. in *Fomes annosus*. S.E. For. Exp. Sta., U.S.D.A., Dept. 17-22, Achville N.C.
- Lawley, D. N. 1940. The estimation of factor loadings by the method of maximum likelihood. *Proc. Roy. Soc. Edinburgh.* 60:64-82.
- Li, C. Y.; K. C. Lu; E. E. Nelson; W. B. Bollen and J. M. Trappe. 1969. Effect of phenolic and other compounds on growth of *Poria weirii* in vitro. *Microbios.* 3:305-311.

- Li, C. Y.; K. C. Lu; J. M. Trappe and W. B. Bollen. 1967a. Effect of pH and temperature on growth of *Poria weirii* in vitro. U.S.D.A. For. Ser. Pac. N. W. For. & Range Exp. Sta. Res. Note No. PNW-66.
- Li, C. Y.; K. C. Lu; J. M. Trappe and W. B. Bollen. 1967b. Selective nitrogen assimilation by *Poria weirii*. Nature. (London) 213(507B):814.
- Li, C. Y.; K. C. Lu; J. M. Trappe and W. B. Bollen. 1968. Enzyme nitrate reductase of some parasitic fungi. U.S.D.A. For Ser. Res. Note PNW-79 PNW For. & Range Expt. Sta.
- Li, C. Y.; K. C. Lu; J. M. Trappe and W. B. Bollen. 1970. Inhibition of *Poria weirii* and *Fomes annosus* by linoleic acid. For. Sci. 16(3):329-330.
- Li, C. Y.; K. C. Lu; J. M. Trappe and W. B. Bollen. 1972. *Poria weirii* inhibiting and other phenolic compounds in roots of red alder and Douglas-fir. Microbios 5:65-68.
- Lu, K. C.; C. S. Chen, and W. B. Bollen. 1968. Comparison of microbial populations between red alder and conifer soils. 173-178. In: (J. M. Trappe, J. F. Franklin, R. F. Tarrant and G. M. Hansen, eds.) Biology of Alder. Proc. of a Symposium held at N.W. Sci. Assoc. 14th Annual Meeting, Pullman, WA, April 14-15, 1967, 292 pp.
- McMinn, R. G. 1960. Water relations and forest distribution in the Douglas-fir region of Vancouver Island. Can. Dept. Agr., For. Biol. Div., Pub. 1091, 71 pp.
- McMinn, R. G. 1963. Characteristics of Douglas-fir root systems. Can. J. Bot. 41:105-122.
- Molnar, A. C.; G. W. Wallis, and R. G. McMinn. 1961. Survey of *Poria (weirii)* rot in second-growth Douglas-fir stands. Bi-m. Prog. Rep. For. Ent. Path. Br. Dep. For. Can. 17(2):3-4.
- Mounce, I.; J. E. Bier and M. K. Nobles. 1940. A root-rot of Douglas-fir caused by *P. weirii*. Can. J. Bot. 18:522-533.
- Murrill, W. A. 1914. An enemy of western red cedar. Mycologia 6:93-94.
- Neal, J. L. Jr.; K. C. Lu, W. B. Bollen and J. M. Trappe. 1968. A comparison of rhizosphere microfloras associated with mycorrhizae of red alder and Douglas-fir. 179-184. In: (J. M. Trappe, J. F. Franklin, R. F. Tarrant and G. M. Hansen, eds.) Biology of Alder. Proc. of a Symposium held at N.W. Sci. Assoc. 14th Annual Meeting, Pullman, WA, April 14-15, 1967, 292 pp.

- Nelson, E. E. 1964. Some probable relationships of soil fungi and zone lines to survival of *P. weirii* in buried wood blocks. *Phytopath.* 54(1):120-121.
- Nelson, E. E. 1967. Factors affecting survival of *Poria weirii* in small buried cubes of Douglas-fir heartwood. *For. Sci.* 13(1):78-84.
- Nelson, E. E. 1968. Survival of *Poria weirii* in conifer, alder and mixed conifer/alder stands. U.S.F.S. Res. Note. Pac. N. W. For. and Range Exp. sta. No. PNW-87, 5 pp.
- Nelson, E. E. 1969. Occurrence of fungi antagonistic to *Poria weirii* in a Douglas-fir forest soil in western Oregon. *For. Sci.* 15(1):49-54.
- Nelson, E. E. 1970. Effects of nitrogen fertilizer on survival of *P. weirii* population of soil fungi and aerobic actinomycetes. *N.W. Sci* 44(2):102-106.
- Nelson, E. E. 1971. Invasion of freshly cut Douglas-fir stumps by *Poria weirii*. U.S.F.S. Res. Note Pac. N.W. For and Range Exp. sta. No. PNW-144, 5 pp.
- Nelson, E. E. 1973. Observation on the formation of zone lines in wood by *Poria weirii*. P.N.W. For. and Range Expt. Sta. Research note PNW-210.
- Nelson, E. E. 1975a. Survival of *P. weirii* in wood buried in urea-amended forest soil. *Phytopath* 65:501-502.
- Nelson, E. E. 1975b. Survival of *Poria weirii* on paired plots in alder and conifer stands. *Microbios.* 12:155-158.
- Nelson, E. E. 1976a. Effect of urea on *Poria weirii* and soil microbes in an artificial system. *Soil Biology and Biochem.* 8(1):51-53.
- Nelson, E. E. 1976b. Colonization of wood disks initiated by basidiospores of *Phellinus weirii*. *For. Sci.* 22(3):407-411.
- Nelson, E. E.; C. M. Hansen; C. W. Li and J. M. Trappe. 1978. The role of red alder in reducing dosser from laminated root rot. U.S.D.A. For. Ser. Gen. Tech. Rep. PNW-70. Utilization and Management of Alder, Proceedings of a Symposium held at Ocean Shores, WA, April 25-27, 1977.
- PLOTLIB Reference Manual. 1979. Milne Computer Center, Oregon State University, 47 pp.

- Powers, H. R. Jr., and W. J. A. Hodges Jr. 1970. Annosus root rot in eastern pines. For. Pest Lflt., U.S.D.A. No. 76, 8 p.
- Rishbeth, J. 1950. Observation on the biology of *Fomes annosus*, with particular reference to East Anglican pine plantations. I. The outbreaks of disease and ecological status of the fungus. Ann. Bot. 14:365-382.
- Rishbeth, J. 1951a. Observation on the biology of *Fomes annosus* with particular reference to East Anglican pine plantations. Ann. Bot. 15:221-246.
- Rowe, K.; R. Brenne,; J. A. Barnes and K. Ewert. 1978. Statistical interactive programming system (SIPS). Dept. of Stat., Oregon State U., 109 pp.
- Schultz, R. P. 1963. Occurrence of stump callusing in second-growth Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco). Masters Thesis, Oregon State University.
- Shea, K. R. 1968. Poria root rot: problems and progress in the Pacific Northwest. In: (T. A. Toussoun; R. V. Bega; P. E. Nelson eds.) Second Int. Symp. on Factors Determining the behavior of plant pathogens in soil in conjunction with First Int. Congress of Plant Path., part IV.
- Tarrant, R. F. 1961. Stant development and soil fertility in a Douglas-fir -- red alder plantation. For. Sci. 7:238-246.
- Tarrant, R. F. 1968. Some effects of alder on the forest environment In: (J. M. Trappe; F. T. Franklin; R. T. Tarrant; G. M. Hansen, eds.) Biology of Alder. Proceedings of a symposium held at Northwest Scientific Asso. 40th Ann. Meeting. Pullman WA, April 14-15, 1967. U.S.D.A. For. Ser. P.N.W. For. & Range Exp. Sta.
- Tarrant, R. F.; L. A. Isaac and R. F. Chandler, Jr. 1951. Observation on litter fall and foliage nutrient content of some Pacific Northwest tree species. J. For. 49:914-915.
- Tarrant, R. F. and R. E. Miller. 1963. Accumulation of organic matter and soil nitrogen beneath a plantation of red alder and Douglas-fir. Proc. Soil Sci. Soc. Amer. 27:231-234.
- Tarrant, R. F. and J. M. Trappe. 1971. The role of *Alnus* in improving the forest environment. Plant and Soil (Spec. Vol.):335-348.
- Trappe, J. M. 1970. Regulation of soil organism by red alder, a potential biological system for control of *Poria weirii*. In: (A. B. Berg, ed.) Managing young forests in the Douglas-fir region. Symposium held June 15-18, 1970. Oregon State Univ., Corvallis, OR 97331.

- Trappe, J. M. 1970. Regulation of soil organisms by red alder: A potential biological system for control of *Poria weirii*. In: (Berg, A. B. ed.) Managing young forests in the Douglas-fir region. Symposium June 15-18, 1970. Oregon State Univ., School of Forestry, Corvallis, OR 97331.
- Trappe, J. M. 1971. Biological control-forest diseases. Ann. Meeting of W. For. Pest Comm., W. Fors. and Conserv. Assoc., Spokane, WA, Nov. 30, 1971.
- Trappe, J. M.; C. Y. Li; K. C. Lu and W. B. Bollen. 1973. Differential response of *Poria weirii* to phenolic acids from Douglas-fir and red alder roots. For. Sci. 19(3):191-196.
- Wallis, G. W. 1957. *Poria weirii* root rot of Douglas-fir. Canada Dept. Agr. Interior Rep. 28 pp.
- Wallis, G. W. 1961. Infection of Scots pine roots by *Fomes annosus*. Can. J. Bot. 39:109-121.
- Wallis, G. W. 1962. Initiation and spread of the root rot fungus *Poria weirii* in second-growth stands of Douglas-fir. Proceedings of the 28th Session of the Can. Phytopath Soc., Ottawa.
- Wallis, G. W. 1976. Growth characteristics of *Phellinus (Poria) weirii* in soil and on root and other surfaces. Can J. For. Res. 6: 229-232.
- Wallis, G. W. and G. Reynolds. 1962. Inoculation of Douglas-fir roots with *Poria weirii*. Can. J. Bot 40(5):637-645.
- Wallis, G. W. and G. Reynolds. 1965. The initiation and spread of *Poria weirii* root rot of Douglas-fir. Can. J. Bot. 43(1):1-9.
- Wallis, G. W. and G. Reynolds. 1967. *Poria (weirii)* root rot in Douglas-fir in British Columbia. For. Pest Leaflet For. Insect. Dis. Surv. Can. No. 3, 5 pp.
- Wallis, G. W. and G. Reynolds. 1974. Urea and nitrate fertilizers found to inhibit root rot. Bi-monthly Res. Notes 30:25-26.
- Wicklow, M. C.; W. B. Bollen and W. C. Denison. 1973. Comparison of soil microfungi in forty year-old stands of pure alder, pure conifer mixtures. Soil Biol. & Biochem. 6:73-78.
- Wright, E. and L. A. Isaac. 1956. Decay following logging injury in western hemlock, sitka spruce, and tree firs. U.S.D.A. Tech Bull. 1148, 34 pp.

APPENDICES

APPENDIX A

Documentation for the use of program SITEMAP and
program listing with sample output

Program Use

Program SITEMAP performs several functions: 1) general plot information is summarized; 2) inter-tree distances and angles are computed; 3) crowding coefficients are computed and; 4) a map of the plot is produced. Multiple plots can be produced in a single run.

Data Input

The general form of the input is: 1) a control card that specifies the number of plots to be summarized and plotted; 2) a plot description card that provides general plot information and the number of tree data cards to read and; 3) individual tree data cards. The input format for each card is presented in Table IA.

The algorithm of the program requires that tree #1 have horizontal and vertical distances of 0.0. All other plot trees are located relative to tree number 1 by providing the horizontal distances and compass bearing from tree #1.

Program Output

Sample output follows the program listing. With the exception of the nearest neighbor coefficient, all output quantities should be self-explanatory. The former, also referred to in the text as the crowding index, is obtained by establishing four quadrants about a given plot tree, selecting the nearest tree in each quadrant, dividing the square of the latter's DBH by its distance from the given plot tree and summing the resulting indices over the four quadrants.

TABLE IA. Input format for data

CARD	VARIABLE	FORMAT ^a
CONTROL	no. of plots	I2
PLOT	plot number	I2
	no. plot trees	I2
	aspect of slope	F4.0
	percent slope	I2
	soil type ^b	I1
	soil depth	I3
	vegetation type ^b	I1
TREE	tree number	I2
	tree species ^c	A1
	DBH	F5.1
	height	I4
	crown width	I4
	horizontal distance ^d	I4
	vertical distance ^d	I4
	azimuth ^d	I3
	age	I3

^athe complete card format is as follows:

```
CONTROL (I2)
PLOT    (2I2, 2X, F4.0, 2X, I2, 2X, I1, 2X, I3, 2X, I1)
TREE    (14X, I2, 1X, A1, 1X, F5.1, 4(1X, I4), 2(1X, I3))
```

^buser's arbitrary integer code

^crefer to format 103 of subroutine MAPRIN for letter codes to species

^drelative to tree number one

```

PROGRAM SITEMAP(INPUT,OUTPUT,TAPES,TAPES)
DIMENSION IPIC(73,97),X(20),Y(20),V(20),SPLIST(20),DBHVEC(20)
COMMON IPIC,SPLIST
INTEGER SPEC,SPLIST

READ(5,100) ITOTAL
100 FORMAT(I2)

SET UP LOOP FOR ITOTAL NUMBER OF SITES TO BE PLOTTED

MM=LICAL
DO 10 I=1,MM
  READ(5,101) NSITE,NTREES,ASPECT,ISLOPE,ISLTP,ISLOEP,IVGTYP
101 FORMAT(2I2,2X,F4.0,2X,I2,2X,I1,2X,I3,2X,I1)

WRITE MAP TITLE AND SUMMARY OF PLOT DATA

WRITE(6,102) NSITE,NTREES,ASPECT,ISLOPE,ISLTP,ISLOEP,IVGTYP
102 FORMAT(1SITE NUMBER#,1X,I2//NUMBER OF PLOT TREES#,4X,I2,5X,
11IF TREE IS IN PLOT, MAPPED WITH AN ASTERISK) //ASPECT#,17X,F5.0,
15X, (TOP OF MAP ALIGNED WITH ASPECT) //PERCENT SLOPE#,12X,I2//
1 SOIL TYPE#,16X,2X//SOIL DEPTH#,1X,I3//VEGETATION TYPE#,11X,I1)

WRITE TITLE FOR DATA SUMMARY

DO 30 J=1,5
  WRITE(6,107)
30 CONTINUE
107 FORMAT(7)
  WRITE(6,103)
103 FORMAT(10X,1X, TREE NO.,3X, SPECIES#,5X, AGE#,5X, DBH#,5X, HEI
1GHT#,3X, CROWN WIDTH#,3X, HORIZ. DIST.#,3X, AZIM#,3X, VERT. DIST.#
1,3X, XMAP#,3X, YMAP#)

CLEAR IS SUBROUTINE TO ERASE IPIC ARRAY FOR NEXT SITE PLOT RUN
CALL CLEAR

SET UP INNER LOOP TO READ IN ONE TREE'S DATA

M=NTREES
DO 20 J=1,M
  READ(5,104) NTREE,SPEC,DBH,HT,ICROWNID,ICRODIS,IVCIS,IAZIM,IAGE
104 FORMAT(14X,I2,1X,A1,1X,F5.1,+(1X,I1),2(1X,I3))
  HT=FLOAT(HT)
  ICROWNID=FLOAT(ICROWNID)
  ICRODIS=FLOAT(ICRODIS)
  VJCIS=FLOAT(IVCIS)
  AZIM=FLOAT(IAZIM)
  AGE=FLOAT(IAGE)

CALCULATION OF ADJUSTED AZIMUTH (REFERRED TO WS ANGLE)
THIS ADJUSTMENT PRODUCES MAP WITH ASPECT ORIENTED TOWARD
TOP OF MAP.

ANGLE=ASPECT-(AZIM-90.0)

XCOORD AND YCOORD ARE FUNCTIONS.
NX AND NY DIVIDED BY 40 FOR MAP SCALE

ANG=ANGLE/57.1
X(J)=XCOORD(ICRODIS,ANG)
Y(J)=YCOORD(ICRODIS,ANG)
V(J)=VERDIS
NX=IFIX(X(J)+0.5)*0.04
NY=IFIX(Y(J)+0.5)*0.04
DBHVEC(J)=DBH
SPLIST(J)=SPEC

WRITE OUT TABLE OF RAW DATA AND CALCULATED MAP COORDINATES

WRITE(6,105) NTREE,SPEC,AGE,DBH,HT,ICROWNID,ICRODIS,AZIM,VERDIS,
X(J),Y(J)
105 FORMAT(1,13X,I2,9X,A1,9X,F3.0,4X,F5.1,5X,F5.0,6X,F5.0,10X,F5
1.0,7X,F4.0,5X,F3.0,5X,F3.2,2X,F3.2)

POINT IS SUBROUTINE TO CONVERT X AND Y COORDINATES INTO INDICES
FOR THE MAPPING ARRAY IPIC.

CALL POINT(NX,NY,SPEC)
20 CONTINUE

WRITE OUT TITLE FOR TABLE OF HORIZONTAL DISTANCES BETWEEN
ALL EXCAVATED TREE PAIRS.

```

```

      DO 40 J=1,5
        WRITE(6,107)
      40 CONTINUE
      WRITE(6,105)
106 FORMAT(10TABLE OF INTER-TREE HORIZONTAL AND VERTICAL DISTANCES 1
      1 NO AZIMUTH
      1 ST.#,3X,#VERT. DIST.#,3X,#AZIM.#)
      SUBROUTINE DISTAN COMPUTES AND PRINTS ABOVE DISTANCES
      CALL DISTAN(X,Y,V,M)
      DO 50 J=1,5
        WRITE(6,107)
      50 CONTINUE
      CALL COEFF(X,Y,SPLIST,DBHVEC,NTREES,NSITE)
      SUBROUTINE BORDER MODIFIES CONTENTS OF IPLOT TO PLACE BORDER
      AROUND THE MAP.
      CALL BORDER
MAPIN IS ACTUAL MAPPING SUBROUTINE
      CALL MAPIN
      10 CONTINUE
      STOP
      END
      SUBROUTINE CLEAR
      CLEARS IPLOT MAPPING ARRAY.
      COMMON IPLOT(73,97)
      DATA NBLANK/0/
      DO 10 I=1,73
        DO 20 J=1,97
          IPLOT(I,J)=NBLANK
        20 CONTINUE
      10 CONTINUE
      RETURN
      END

      FUNCTION XCOORD(HORDIS,ANG)
      COMPUTATION OF X COORDINATES FOR ALL TREES
      RELATIVE TO TREE NO. 1 AT 0,0
      XCOORD=HORDIS*COS(ANG)
      RETURN
      END

      FUNCTION YCOORD(HORDIS,ANG)
      YCOORD=HORDIS*SIN(ANG)
      RETURN
      END

      SUBROUTINE POINT(NX,NY,SPEC)
      THIS ENTERS A SINGLE POINT CALCULATED FROM X AND Y
      COORDINATES INTO IPLOT.
      COMMON IPLOT(73,97)
      INTEGER SPEC
      TEST WHETHER POINT IS IN RANGE.
      IF(ABS(NX).GT. 48) GO TO 99
      IF(ABS(NY).GT. 36) GO TO 99
      X AND Y COORDINATES CONVERTED TO IPLOT FORM.
      IPLOT(NY+37,NX+49)=SPEC
      RETURN
      99 WRITE(6,101) NX,NY
      101 FORMAT(2***INVALID POINT***2.2I12)
      RETURN
      END

      SUBROUTINE BORDER
      PLACES BORDER AROUND MAP.
      TREE NO. 1 IS CENTERED ON (0,0).
      PLUS SIGNS MARK TWO METER INTERVALS.

```

```
COMMON IPICT(73,97)
```

```
DATA NPLUS/2.2/
```

```
DATA NDOT/1.2/
```

```
I=1
```

```
GO TO 10
```

```
IF (L.NE. 1) GO TO 1
```

```
N=1
```

```
NN=1
```

```
SWITCH=1.0
```

```
GO TO 5
```

```
1 IF (L.NE. 2) GO TO 2
```

```
N=73
```

```
SWITCH=1.0
```

```
NN=1
```

```
GO TO 5
```

```
2 IF (L.NE. 3) GO TO 3
```

```
N=1
```

```
NN=1
```

```
SWITCH=0.0
```

```
GO TO 5
```

```
3 N=1
```

```
NN=97
```

```
SWITCH=0.0
```

```
5 CONTINUE
```

```
IF (L.LE. 2) GO TO 6
```

```
MEND=73
```

```
GO TO 7
```

```
6 MEND=97
```

```
GO TO 7
```

```
7 CONTINUE
```

```
DO 20 I=1,MEND
```

```
IF (SWITCH.EQ. 0.0) N=I
```

```
IF (SWITCH.EQ. 1.0) NN=1
```

```
IF (L.LE. 2) GO TO 8
```

```
MEND=3
```

```
GO TO 3
```

```
8 MEND=4
```

```
IF (MEND.EQ. 3) GO TO 12
```

```
ITEST=I/4
```

```
ITEST=ITEST*4
```

```
13 IF (ITEST.EQ. 1) GO TO 11
```

```
IPICT(N,NN)=NDOT
```

```
GO TO 20
```

```
12 ITEST=I/3
```

```
ITEST=ITEST*3
```

```
GO TO 13
```

```
11 IPICT(N,NN)=NPLUS
```

```
20 CONTINUE
```

```
10 CONTINUE
```

```
RETURN
```

```
END
```

```
SUBROUTINE MAPPRIN
```

```
PRINTS MAP FOR THE NTH SITE
```

```
COMMON IPICT(73,97)
```

```
WRITE(6,101)
```

```
101 FORMAT(1P1P)
```

```
DO 20 I=1,73
```

```
II=74-I
```

```
WRITE(6,102) (IPICT(II,J), J=1,97)
```

```
102 FORMAT(1P,15X,97A1)
```

```
20 CONTINUE
```

```
WRITE(6,103)
```

```
103 FORMAT(1P,20X,1P,MAP SCALE: 4 HOR. UNITS=1.0 METERS,
```

```
1P,20X,31X,23 VERT UNITS=1.0 METERS,
```

```
1P,20X,20X,EXCAVATED TREES MAPPED WITH ASTERISK,/,
```

```
1P,20X,20X,OTHER TREES DESIGNATED AS FOLLOWS:/,
```

```
1P,20X,20X,GOUGLAS FIR.....G,/,
```

```
1P,20X,20X,WESTERN HEMLOCK.....H,/,
```

```
1P,20X,20X,RED ALDER.....A,/,
```

```
1P,20X,20X,GRAND FIR.....F,/,
```

```
1P,20X,20X,BIG LEAF MAPLE.....M,/,
```

```
1P,20X,20X,RED CEDAR.....C,/,
```

```
RETURN
```

```
END
```

```
SUBROUTINE DISTAN(X,Y,V,M)
```

```
COMPUTATION OF HORIZONTAL AND VERTICAL DISTANCES FOR ALL  
EXCAVATED TREE PAIRS AND THEIR CORRESPONDING AZIMUTHAL DEPART. COSINES.
```

```
DIMENSION HOR2(20),X(20),Y(20),V(20),VERT(20)
```

```

      DIMENSION COSINE(20), IFILE(20), JFILE(20), ANGLE(20)
      COMMON IPLOT(73,97), SPLIST(20)
      INTEGER SPTST, SPLIST
      DATA SPTST/2,2/
      K=1
      DO 10 I=1,4
        DO 20 J=1,4
          IF(SPLIST(I).NE.SPTST.OR.SPLIST(J).NE.SPTST) GO TO 20
          IF(I.GE.J) GO TO 20
          COMPUTATION OF HORIZONTAL DISTANCE BETWEEN TREE I AND TREE J.
          HORIZ(K)=SQRT((X(I)-X(J))**2.+ (Y(I)-Y(J))**2.)
          COMPUTATION OF VERTICAL DISTANCE FOR SAME PAIR.
          VERT(K)=V(I)-V(J)
          COMPUTATION OF AZIMUTHAL DEPARTURE COSINES (IN DEGREES) FOR THE SAME.
          COSINE(K)=ABS(Y(I)-Y(J))/HORIZ(K)
          ANGLE(K)=ACOS(COSINE(K))
          IFILE(K)=I
          JFILE(K)=J
          K=K+1
        20 CONTINUE
      10 CONTINUE

      K=K-1
      WRITE(6,101) (IFILE(K), JFILE(K), HORIZ(K), VERT(K), ANGLE(K), N=1, K)
101  FORMAT(20F7.4,12F7.4,12F10.2,4F10.2,5X,F7.2)
      RETURN
      END
      SUBROUTINE COEFF(X,Y,SPLIST,DSHVEC,NTREES,VSITE)
      DIMENSION X(20),Y(20),SPLIST(20),DSHVEC(20)
      DIMENSION NNTREE(20)
      INTEGER SPLIST,SPTST,QUACH
      DATA SPTST/2,2/

      NEAREST NEIGHBOR COEFF. COMPUTED AS THE SUM (DSH**2./HORIZIS)
      SUM IS OVER THE NEAREST TREE IN EACH OF THE FOUR CARTESIAN QUADRANTS.

      WRITE(6,102) N=SITE
102  FORMAT(20NEAREST NEIGHBOR COEFFICIENTS FOR TREES ON PLOT#,1X,I2/
      120F7.4,12F10.2,5X,2COEFF,4X,2NEAREST TREES,1)
      DO 10 I=1,NTREES
        IF(SPLIST(I).NE.SPTST) GO TO 10
        SET UP INNER LOOP TO ALLOW SELECTION OF NEAREST NEIGHBOR IN EACH QUAD.
        SUMNN=0.0
        DO 20 II=1,4
          L=0
          QUACH=J
          DO 30 J=1,NTREES
            IF(I.EQ.J) GO TO 30
            IF(L.EQ.4) GO TO 2
            IF(L.EQ.3) GO TO 3
            IF(L.EQ.2) GO TO 4
            IF(X(J).LE.X(I).OR.Y(J).LE.Y(I)) GO TO 30
            TDIST1=SQRT((X(I)-X(J))**2.+ (Y(I)-Y(J))**2.)
            L=L+1
            IF(L.NE.1) GO TO 1
            TDIST2=TDIST1
            QUACH=J
            GO TO 30
            IF(TDIST1.GT.TDIST2) GO TO 30
            TDIST2=TDIST1
            QUACH=J
            GO TO 30
            IF(X(J).GT.X(I).OR.Y(J).LT.Y(I)) GO TO 30
            GO TO 5
            IF(Y(J).GE.X(I).OR.Y(J).GE.Y(I)) GO TO 30
            GO TO 5
            IF(X(J).LT.X(I).OR.Y(J).GT.Y(I)) GO TO 30
            GO TO 5
          30 CONTINUE
          IF(QUACH.EQ.0) GO TO 6
          SUMNN=SUMNN + (DSHVEC(QUACH))**2./TDIST2
          NNTREE(II)=QUACH
        20 CONTINUE
      10 CONTINUE

```



```
WRITE(6,103) I,SUMNN,(NNT-EE(K),K=1,4)  
103  FUEMAT(2,13A,I2,7X,F8.2,5X,4I3)  
10  CONTINUE  
    RETURN  
    END
```

SITE NUMBER 1
 NUMBER OF PLOT TREES 13 (IF TREE IS IN PLOT, MAPPED WITH AN ASTERISK)
 ASPECT 351. (TOP OF MAP ALIGNED WITH ASPECT)
 PERCENT SLOPE 66
 SOIL TYPE 0
 SOIL DEPTH 125
 VEGETATION TYPE 1

TREE NO.	SPECIES	AGE	DBH	HEIGHT	CROWN WIDTH	HORIZ. DIST.	AZIM	VERT. DIST.	XMAP	YMAP
1	*	64.	26.0	2250.	0.	0.	0.	0.	0.00	0.00
2	H	0.	15.5	0.	0.	490.	54.	-97.	436.61	233.35
3	A	0.	29.0	0.	0.	640.	89.	-37.	533.06	279.41
4	A	0.	29.2	0.	0.	505.	63.	-52.	476.63	166.89
5	A	0.	31.9	0.	0.	1050.	34.	115.	1027.77	-214.90
6	A	66.	23.4	217.	0.	360.	102.	19.	334.84	-122.17
7	A	0.	34.2	0.	0.	770.	116.	77.	639.22	-423.30
8	A	0.	20.0	1560.	0.	190.	128.	34.	132.16	-136.51
9	O	0.	26.0	0.	0.	680.	176.	131.	-48.26	-670.21
10	A	0.	26.1	0.	0.	316.	220.	62.	-237.22	-211.78
11	A	67.	20.7	206.	0.	249.	265.	26.	-238.53	-71.44
12	O	0.	20.7	0.	0.	516.	270.	-21.	-510.45	75.50
13	A	0.	33.4	0.	0.	366.	271.	-16.	-363.04	60.21

TABLE OF INTER-TREE HORIZONTAL AND VERTICAL DISTANCES AND AZIMUTH

TREE PAIR	HORIZ. DIST.	VERT. DIST.	AZIM.
1, 6	360.00	-19.03	1.22
1, 8	190.00	-34.03	.77
1, 11	249.00	-20.00	1.28
6, 8	206.97	-15.00	1.50
6, 11	579.39	-7.00	1.48
8, 11	376.36	6.00	1.43

NEAREST NEIGHBOR COEFFICIENTS FOR TREES BY PLOT 1

TREE NO.	COEFF.	NEAREST TREES
1	7.34	2 3 11 13
6	9.19	5 7 9 1
8	10.03	0 7 10 1
11	13.72	1 10 0 13

APPENDIX B

Documentation for the use of program
ROOTMAP and program listing

Program Use

Program ROOTMAP utilizes the COMLOT (Milne Computer Center, O.S.U. 1979) plotting library to produce a map of the root system of one or more trees. The program produces a two dimensional drawing that indicates: 1) the spatial distribution of the roots; 2) the type of root (normal versus adventitious); 3) the location of inter-tree root contacts, designated by type (see Materials and Methods) and; 4) the manner in which a root terminates.

Program Input

All input is read from TAPE 1. The run control variables are described briefly in Table IB where they are listed by the appropriate read format and by the order in which they are read. The variables, with one or two exceptions, are specific to COMLOT and the reader should refer to the COMLOT manual for more detailed information.

Program Output

Each tree's root system is mapped in its entirety. The primary roots are numbered at their endpoints, but all higher order roots are unidentified. Adventitious roots are distinguished as a class by plotting them with a dashed line instead of a solid one (Table BI, note h). Map symbols for contact type and root termination type are given in notes (j) and (k) respectively in Table BI.

TABLE BI. Run control variables for Program ROOTMAP

STATEMENT	VARIABLE	FORMAT	COMMENTS
1 ^a	ICODE	I2	specifies the type of plotting device
	ICODEG	I2	if ICODE = 3, the device used is a Gerber plotter. ICODEG specifies which Gerber ("BIG" or "little") is to be used
	MODEL	I4	if ICODE = 1, the device used is a TEKTERMINAL. MODEL specifies which type of terminal is being used.
3 ^b	XLENMM	F10.2	length of the X and
	YLENMM	F10.2	Y axes in mm
	XLENUN	F10.2	length of the X and
	YLENUN	F10.2	Y axes in user's units
	XBIAS	F10.2	width of lower map
	YBIAS	F10.2	border and left map border, respectively (in mm).
5 ^c	NCHAR	I2	number of characters in the map title
	MITTLE	3A10	map title is limited to 30 characters
6 ^d	NCHAR	I2	number of characters in the note at bottom of map
	NOTE	2A10	NOTE has been used to indicate the scale of the map
7 ^e	ASPECT	F10.2	the compass bearing of the plot's aspect. The plot is produced so that the aspect is always oriented toward the top of the map. North is indicated in the map's lower right corner.

Table BI. (continued)

STATEMENT	VARIABLE	FORMAT	COMMENTS
9 ^f	NTREE	A10	the tree number
	DIAM	F10.2	the tree's diameter
	AORG	F10.2	X-coordinate of the tree's geographic center
	BORG	F10.2	Y-coordinate of the tree's geographic center
	ASPECT	F10.2	this is the same value as in statement #7
12 ^g	NTREE	A2	the tree number
	NPRIME	A2	root numbers
	NSEC	A2	for each root
	NTER	A2	type
	NQUAT	A2	
	DIST	F3.2	horizontal distance to a measurement point, "p" on a given root
	ANGLE	F3.0	compass bearing to point "p"
	IRTYP ^h	I1	a value of 1 indicates the root is adventitious
	NCONTYP ^j	I1	the contact type at point "p"
	NTRTYP	A2	
	NTERM ^k	L1	the termination type of a root

^aformat for statement #1 is (2I2, I4)

^bformat for statement #3 is (6 F10.2)

^cformat for statement #5 is (I2, 8X, 3A10)

^dformat for statement #6 is (I2, 8X, 2A10)

^eformat for statement #7 is (F10.2)

Table BI. (continued)

^fformat for statement #9 is (A10, 4 F10.2)

^gformat for statement #12 is (2X, 5A2, 2(1X, F3.0), 13X, 11, 4X, 11, 1X, A2, 9X, 11)

^hThe designation for an adventitious root must appear in the first line of data for a given root. It need not be repeated thereafter.

ⁱThe contact types are defined in Materials and Methods. The following symbols are used to indicate contact types:

TYPE I - an asterick
 TYPE II - a triangle
 TYPE III - an open box
 TYPE IV - a box with an "x" inside

^kNTERM contains a root termination code. The code number, their meanings and the corresponding map symbols are given below:

CODE	DESCRIPTION	MAP SYMBOL
0	root measured to minimum diameter	no symbol
2	root measured to limit of excavation	exclamation mark
3	root measured to point of break	downward arrow


```

PROGRAM ROOTMAP(INPUT,OUTPUT,TAPE1=INPUT,TAPE10=OUTPUT)
DIMENSION MTITLE(25), NOTE(25), NVCONT(25), NVTERM(25)
DIMENSION NDFOP(25)
COMMON/DATA1/VDIST(25),VANGLE(25)
COMMON/DATA2/APLOT(25),YFLOT(25)
COMMON/DATA3/LABELS(5),NBLANK
DATA NORTH/'N'/
DATA NBLANK/' '/
DATA NQUEST/'?'/
DATA NEXCLAM/'!'/

C
C READ RUN CONTROL INFORMATION.
C ICCDE SPECIFIES THE GEARS. ICCDEG SPECIFIES THE LITTLE OR BIG.
C
5000 READ(1,1) ICCDE,ICCODEG,MODEL
1 FORMAT(2I2,14)
IF(=CF(1) .NE. 0.0) GO TO 1004
CALL PLOTTYPE(ICCDE)
IF(=CCDE .EQ. 1) GO TO 8
IF(=CCDEG .EQ. 2) GO TO 2
CALL GTYPE(6H LITTLE)
GO TO 4
2 CALL GTYPE(3H BIG)
GO TO 4
6 CALL TKTYPE(MODEL)
CALL ERASE
4 CALL METRIC

C
XLENMM IS LENGTH OF X AXIS IN MM.
XLENUN IS NO. OF UNITS ON X AXIS.
SIMILAR FOR THE Y PARAMETERS.
XFACT AND YFACT ARE SCALE PARAMETERS.
C
3 READ(1,3) XLENMM,YLENMM,XLENUN,YLENUN,XBIAS,YBIAS
3 FORMAT(6F10.2)

C
C COMPUTE THE X AND Y SCALE FACTORS.
C
WIDTH=XLENMM+XBIAS
HEIGHT=YLENMM + 2.3*YBIAS
CALL SIZE(WIDTH,HEIGHT)
XFACT=XLENMM/XLENUN
YFACT=YLENMM/YLENUN
ALOW=XLENUN/2.0
YLOW=YLENUN/2.0

C
CALL SCALE(XFACT,YFACT,XBIAS,YBIAS,XLOW,YLOW)

C
C DRAW AN X AND Y AXIS AND PLACE BORDER AROUND THE MAP.
C
XHIGH=ABS(ALOW)
YHIGH=ABS(YLOW)
XORG=ALOW
YORG=YLOW

C
CALL AXISL(XLOW,XHIGH,XORG,YLOW,YHIGH,YORG,25.0,100.0,10,10,1,1,
11.0,1.0,0.0,0)

C
CALL PLOT(XLOW,YHIGH,0,0)
CALL PLOT(XHIGH,YHIGH,1,0)
CALL PLOT(XHIGH,YLOW,1,0)

C
C X AND Y TITLE ARE USER UNIT COORD. OF LOWER LEFT CORNER OF FIRST LETTER IN A
C STRING. DEGREES IS ANGLE TO PRINT MESSAGE AT.. LABELS HOLDS MESSAGE.
C
5 READ(1,5) NCHAR,(MTITLE(I),I=1,3)
5 FORMAT(12,8X,3A10)
C
CALL CLEARLB
C
X=XLOW
Y=YHIGH + 25.0
DO 20 I=1,3
LABELS(I)=MTITLE(I)
20 CONTINUE
CALL SYMBOL(X,Y,0.0,15.0,NCHAR,LABELS)

C
CALL CLEARLB
C
5 READ(1,6) NCHAR,(NOTE(I),I=1,2)
5 FORMAT(12,8X,2A10)
X=XLOW
Y=YLOW - 50.0
DO 30 I=1,2

```

```

      LABELS(1)=NOTE(1)
3C CONTINUE
C      CALL SYMBOL(X,Y,0.0,15.0,NCHAP,LABELS)
C
C      INDICATE NORTH AT BOTTOM OF THE MAP.
      X=XHIGH - 50.0
      Y=YLOW - 50.0
      CALL PLOT(X,Y,0,0)
      Y=YLOW - 100.0
      CALL PLOT(X,Y,1,0)
C      AORG AND BORG ARE CONVERTED TO PHYSICAL MAP UNITS (MM) TO LOCATE
C      THE ORIGIN FOR SUBSEQUENT ROTATION.
      AORG=A*XFACT + XLENMM/2.0 + XBIAS
      BORG=B*YFACT + YLENMM/2.0 + YBIAS
      CALL ORIGIN(AORG,BORG)
      HEAD(1,7)=ASPECT
      7 FORMAT(F10.2)
      DEGREES=ASPECT
      CALL ROTATE(DEGREES)
      X=0.0
      Y=0.0
      CALL PLOT(X,Y,0,0)
      X=0.0
      Y=20.0
      CALL PLOT(X,Y,1,0)
C
C      CALL SYMBOL(X,Y,0.0,6.0,1,NORTH)
C
C      START READING TREE DATA.
C
C      CALL ALPHAS
1000 HEAD(1,9)=NTREE,DIAM,AORG,BORG,ASPECT
      CALL VECTORS
      9 FORMAT(A10,F10.2)
C      CHECK FOR AN END OF FILE. IF YES CALL PLOT END.
C      NEXT CHECK FOR DOUBLE EOF AT END TO INDICATE LAST PLOT.
      IF(EOF(1) .NE. 0.0) GO TO 50
C
C      TREE COORDINATES ARE GIVEN IN USER UNITS. THESE MUST BE TRANSLATED INTO
C      PHYSICAL MAP UNITS TO LOCATE ORIGIN.
      AORG=AORG*XFACT + XLENMM/2.0 + XBIAS
      BORG=BORG*YFACT + YLENMM/2.0 + YBIAS
      CALL ORIGIN(AORG,BORG)
C
C      THE STUMP CENTER IS NOW LOCATED AND ROTATION LEAVES LOCAL ORIGIN PROPERLY
C      ORIENTED.
C
C      DRAW A CIRCLE TO REPRESENT THE STUMP
C
C      XRAD=DIAM/2.
C
C      NOW THE PHYSICAL MAP UNITS ARE CONVERTED BACK TO USER UNITS.
      AORG=0.0
      BORG=0.0
C
      BACKDEG=-DEGREES
      CALL CIRCLE(AORG,BORG,0.0,360.0,ARAD,XRAD,0.10)
C
      X=AORG
      Y=BORG
      CALL SYMBOL(X,Y,BACKDEG,6.0,10,NTREE)
C
C      BEGIN READING ROOT TYPES AND POLAR COORD.
C
1001 M=1
      NSETVEC=0
      HEIGHT=10.0
      CALL MARKH(HEIGHT)
      CALL ALPHAS
      FEAL(1,12)=NTREE,NPFIME,NSEC,NTERT,NQUAT,CIST,ANGLE,IRTYP,
      1,CONTYP,ITRTYP,INTERM
      12 FORMAT(2X,5A2,2(1X,F3.0),13X,I1,4X,I1,1X,A2,9X,I1)
      NSETVEC=IRTYP
      CALL VECTORS
      TREE=NTREE
      IF(IRTYP .EQ. 1) CALL DASHES

```

```

      IFR,ME=NPRI ME
      YSEL=NSEC
      ITERS=NTEFT
      IQUAT=NQUAT
      VDIST(1)=DIST
      VANGLE(1)=-(ANGLE - 90.0)
      NVCONT(1)=NCONTYP
      NVTERM(1)=NTERM
C
      NDROP(1)=NTATYP
1002  N=M + 1
      CALL ALPHAS
      READ(1,12) NTFEE,NPRI ME,NSEC,NTER T,NQUAT,DIST,ANGLE,IR TYP,
      INCONTYP,NTR TYP,NTERM
      CALL VECTORS
      IF(NSETVEC.EQ. 1) CALL DASHES
C
      IF(NTFEE.EQ. NBLANK) GO TO 54
      IF(NTFEE.NE. ITFEE) GO TO 1003
      IF(NPRI ME.NE. IPRIME) GO TO 1003
      IF(NSEC.NE. ISEC) GO TO 1003
      IF(NTER T.NE. ITER T) GO TO 1003
      IF(NQUAT.NE. IQUAT) GO TO 1003
      VDIST(M)=DIST
      VANGLE(M)=-(ANGLE - 90.0)
      NVCONT(M)=NCONTYP
      NVTERM(M)=NTERM
      NDROP(M)=NTR TYP
      GO TO 1002
1003  BACKSPACE 1
      CALL RECTANG(M)
      Y=XPLT(1)
      Y=YPLT(1)
C
      A,Y AT THIS POINT ARE THE COORD. OF START OF A ROOT. SERIES OF #IFS# FOR
      SETTING MARK ARE USED HERE TO CODE CONTACT POINTS AS FOLLOWS
      ACCT GRAFT.....BOX WITH X INSIDE
      EXTENSIVE.....OPEN BOX
      MODERATE.....TRIANGLE
      CASUAL.....ASTERISK
C
      I MARK=0
      IF(NTFEE.EQ. NDROP(1)) GO TO 59
      IF(NVCONT(1).EQ. 0) GO TO 59
      IF(NVCONT(1).EQ. 4) I MARK=25
      IF(NVCONT(1).EQ. 3) I MARK=17
      IF(NVCONT(1).EQ. 2) I MARK=19
      IF(NVCONT(1).EQ. 1) I MARK=21
59    CALL PLOT(A,Y,0,I MARK)
      GO TO 2,M
      I MARK=0
      IF(NTFEE.EQ. NDROP(1)) GO TO 600
      IF(NVCONT(1).EQ. 0) GO TO 600
      IF(NVCONT(1).EQ. 4) I MARK=25
      IF(NVCONT(1).EQ. 3) I MARK=17
      IF(NVCONT(1).EQ. 2) I MARK=19
      IF(NVCONT(1).EQ. 1) I MARK=21
600  X=XPLT(1)
      Y=YPLT(1)
      CALL PLOT(X,Y,1,I MARK)
60    CONTINUE
C
      THIS SERIES OF #IFS# IS USED TO SELECT A TERMINATION CHARACTER FOR ROOTS.
      CODING FOR NTERM: STAR FOR BROKEN ROOT, ARROW FOR OUT OF PLOT
C
      IF(NVTERM(M).EQ. 3) CALL SYMBOL(A,Y,BACKDEG,6.0,1,NQUEST)
      IF(NVTERM(M).EQ. 2) CALL SYMBOL(X,Y,BACKDEG,6.0,1,NEXCLAM)
      X=X + 5.0
      Y=Y + 5.0
      IF(I SEC.NE. NBLANK) GO TO 56
      NRUCT=IPRI ME
      BACKDEG=-DEGREES
      CALL SYMBOL(A,Y,BACKDEG,6.0,2,NRUCT)
56    IF(NTFEE.EQ. NBLANK) GO TO 1000
      GO TO 1001
50    CALL PLOTENI
      CALL ENDFILE
      GO TO 5000
1004  STOP
      END
      SUBROUTINE CLEARLB
      COMMON/ DATA3/ LABELS(5),NBLANK
      DO 10 I=1,5
      LABELS(I)=NBLANK

```

```

10 CONTINUE
   RETURN
   END

C
   SUBROUTINE RECTANG(M)
   DIMENSION RVANGLE(20)
   COMMON/DATA1/VDIST(20),VANGLE(20)
   COMMON/DATA2/APLOT(20),YPLT(20)
   M=M-1
   DO 20 I=1,M
   IF(VANGLE(I).EQ.0.0)VANGLE(I)=360.0
   RVANGLE(I)=VANGLE(I)/57.296
   APLOT(I)=VDIST(I)*COS(RVANGLE(I))
   YPLT(I)=VDIST(I)*SIN(RVANGLE(I))
20 CONTINUE
   RETURN
   END

```

APPENDIX C

Documentation for use of program
PLOTDIS and program listing

Program Use

Program PLOTDIS utilizes the COMLOT graphics library (Milne Computer Center, O.S.U. 1979) to produce two-dimensional plots of the canonical variables generated by a discriminant analysis program. The plots may be produced on a TEKTERMINAL and/or a Gerber plotting device.

Program Input

Run control variables are supplied conversationally. The plot data are read from TAPE 1. The run control variables are described briefly in Table CI. The latter variables are specific to COMLOT; the reader should refer to the COMLOT manual for more detailed information. The structure of the program requires that the canonical scores, corresponding to a particular discriminant group, be listed together as a group. The X and Y coordinates of the canonical variables are read with the following format: (2 F10.2).

Program Output

The program produces a plot measuring five inches on a side (Figure 8 in Results, part B). No legend is produced in the program, however, so the user must keep track of how each group is identified.

TABLE CI. Run control variables for Program PLOTDIS

VARIABLE	FORMAT	COMMENTS
ICODE	integer (free)	Specifies the plotting device. Refer to COMLOT user's manual for code values.
NGROUPS	integer (free)	the number of groups (from the discriminant analysis) to be plotted
ID(I)	integer (free)	the numeric code that will be used to identify the I th group on the plot
NQUANT(I)	integer (free)	the number of canonical scores to be plotted for the I th group
HEIGHT	real (free)	the height of the group identification characters that will be plotted

```

PROGRAM PLOTDIS(INPUT,OUTPUT,TAPE1,TAPE10=OUTPUT)
DIMENSION ID(4),NGUANT(4),X(50),Y(50)
PRINT *,#WHAT IS THE VALUE FOR ICODE#,
READ *,ICODE
PRINT *,#HOW MANY GROUPS DO YOU WANT TO PLOT#,
READ *,NGROUPS
DO 10 I=1,NGROUPS
PRINT *,#WHAT IS THE ID CODE FOR GROUP#,I,
READ *,ID(I)
PRINT *,#HOW MANY OBSERVATIONS FOR GROUP#,I,
10 READ *,NGUANT(I)

C
C INITIALIZE THE PLOTTER AND DRAW AXES
C
CALL PLOTTYPE(ICODE)
IF(ICODE.EQ.1) GO TO 1
CALL GTYPE(SHLITTLE)
IF(ICODE.NE.2) GO TO 2
1 CALL TKTYPE(4010)
2 CALL ERASE
CALL SIZE(9.0,11.0)
CALL SCALE(0.625,0.625,2.5,3.0,-4.0,-4.0)
CALL AXISL(-4.0,4.0,-4.0,-4.0,4.0,-4.0,1.0,1.0,10,10,1.1,1.0,1.0
1,0.25,0)
CALL PLOT(-4.0,4.0,0.0)
CALL PLOT(4.0,4.0,1.0)
CALL PLOT(4.0,-4.0,1.0)
CALL ALPHAS
PRINT *,#HOW BIG DO YOU WANT THE DATA MARKS#,
READ *,HEIGHT
CALL POINTS
CALL MARKH(HEIGHT)
DO 20 I=1,NGROUPS
IMARK=ID(I)
M=NGUANT(I)
READ(1,100) (X(J),Y(J), J=1,M)
100 FORMAT(2F10.4)
CALL LINE(X,Y,IMARK,M)
20 CONTINUE
CALL PLOTEND
STOP
END

```


APPENDIX D

Documentation for use of program
RESPONS and program listing

Program Use

Program RESPONS utilizes the PLOTLIB (Milne Computer Center, O.S.U. 1979) and COMLOT (Milne Computer Center, O.S.U. 1979) libraries to produce three-dimensional plots. The dependent variable may be either the posterior probability of group membership derived from a discriminant analysis, or some dependent variable, Y, from a regression problem. In the case of plots involving the posterior probability of group membership, only the probability of belonging to one of the groups is actually plotted. The number of groups which the program can accommodate is limited to five. In the regression mode, the program will plot either a single dependent variable or up to five dependent variables whose values are functions of the same set of predictors (i.e., - a multivariate application).

Program Input

Data input to the program is supplied both conversationally and from TAPE 1. The run control information is supplied conversationally; the variables used are described in Table DI. These variables, with the exception of NGROUPS, are specific to PLOTLIB; therefore, the user should consult the PLOTLIB manual for detailed explanation of each variable. Note, particularly, that NGROUPS (Table DI) has two distinct meanings depending upon the context in which it is used. When using program RESPONS in the discriminant analysis mode, NGROUPS refers to the number of discriminant groups and thus indicates the number of sets of discriminant function coefficients that need to be read (one function

per group). In the regression mode, NGROUPS refers to the number of sets of regression coefficients that need to be read (one function per dependent variable).

TAPE 1 contains the following: 1) an "m" by 9 array of predictor values at which the functions are to be evaluated ("m" being the number of predictor variables; "m" can be 2 to 4); 2) a set of "n" functions corresponding to either "n" discriminant groups or "n" dependent variables, Y ("n" must be at least 2 for the discriminant application and in either case must be no greater than 5) and; 3) a set of labels for the plots (the label is limited to 10 characters). The following points should also be noted regarding the contents of TAPE 1: 1) each of the "m" predictor variables must have 9 values that increase by constant increments from element (m, 1) to (m, 9); 2) in the discriminant analysis application, the prior probability of group membership is listed as the last variable in the set of discriminant function coefficients (refer to format statement 1000). The formats for predictor values, function coefficients and plot labels are given in Table DII.

Program Output

The program has been designed to produce a set of plots so that one may examine how pairs of predictor variables interact to influence the response variable. The number of plots required is a simple problem of combinations in the discriminant analysis application: if only two predictor variables are used, a single plot is produced; if three predictor variables are used, three plots are required (three items taken two at a time) and; if four predictors are used, six plots are required.

In order to look at the interaction of any two variables, the balance must be held constant. In RESPON, the nonvarying predictors for a specific plot are set to their mean values (the mean being the 5th element of the "m" by 9 data matrix). In the case of a five-variable model, the value of the fifth predictor must be supplied conversationally and thus is always treated as a constant. The five-variable model produces six plots instead of ten since the fifth variable is treated as a constant. The number of plots produced in the regression application is equal to nC_2^m where "m" and "n" are defined as above. Thus, four regression functions with three independent variables would require 12 plots.

There is no provision in the program for labeling axes, though, as noted, the plot itself can be labeled. The convention for assignment of axes is given in Table DIII.

TABLE DI. Conversational variables used in
program RESPONS.

VARIABLE	TYPE	COMMENTS
ICODE	integer	selects the appropriate graphics device
WIDTH	real	sets the size of the plot (in inches)
HEIGHT	real	
PROBTYP	integer	specifies mode: if PROBTYP = 1, problem is a regression type
ZMIN	real	the minimum and maximum values, respectively on the Z axis (the dependent variable is plotted on the Z axis)
ZMAX	real	
NGROUPS	integer	the number of discriminant groups or the number of regression functions
NEWSHOT	integer	a flag used to indicate that the user wants to redo the last plot
X5BAR	real	the value will only be requested if 5 predictor variables are used in the function(s)
M	integer	an index to select the appropriate variable pairs for each plot (see Table DIII)
MODEL	integer	model number of TEKTERMINAL if used

TABLE DII. Variables read from TAPE 1.

VARIABLE	FORMAT	COMMENTS
X(m, 9)	4 F10.2 ^a	m x 9 array of values of m predictors
C(n, J) P(n)	7 F10.5 ^a	C(n, J) is an array of function coefficients where n equals the number of functions and J = m + 1 if a constant appears in the functions. P(n) is an array of prior probabilities which is only used in the discriminant analysis mode. Note that in the latter mode, P(n) follows the last function coefficient (see format statement 1000).
NCHAR	I2 ^b	number of characters in label for plot
LABELS	A10 ^b	plot title

^athis is the complete format statement

^bthe complete format statement for NCHAR and LABELS is: (I2, 8X, A10)

TABLE DIII. Axis assignemnt by plot number
for program RESPON.

PLOT NUMBER	VARIABLES ^a	VALUE OF M ^b
1	1 (x) 2 (y)	1
2	1 (x) 3 (y)	2
3	2 (x) 3 (y)	3
4	1 (x) 4 (y)	4
5	2 (x) 4 (y)	5
6	3 (x) 4 (y)	6

^a axis assignment is indicated in parentheses

^b "M" is the index that appears in Table XVIII

```

PROG FAN RESPON (INPUT, OUTPUT, TAPE1, TAPE2)
INTEGER PFO3TYP
COMMON/DATA1/XBAR(4), X5BAR, NVAR, NGRUPS, PFO3TYP, L, NPLT
COMMON/DATA2/X(9,4), DX, DY, DZ, ZMIN, ZMAX
COMMON/DATA3/PROB(9,9), PRCBM-N(3), PROBMAX(3)
COMMON/DATA4/C(3,8), C(5,1), Y(3,1)
COMMON/DATA5/DEP(9,9), DEPMIN(9), DEPMAX(9)
COMMON/FLT/ICODE, WIDTH, HEIGHT, NCHAR, LABELS(3), MODEL, IRATE, LUN

NPLT=0
NEXTY=0
ITEST=0
LUN=10
IRATE=2400
MODEL=0

```

C INPUT RUN CONTROL INFORMATION

```

PRINT *, 'WHAT IS THE VALUE FOR ICODE?',
READ *, ICODE
IF (ICODE .NE. 1 .AND. ICODE .NE. 4) GO TO 21
PRINT *, 'WHAT IS THE MODEL NUMBER FOR THE TEXTERMINAL?',
READ *, MODEL
21 PRINT *, 'WHAT ARE THE WIDTH AND HEIGHT?',
READ *, WIDTH, HEIGHT

PRINT *, 'IF THIS IS A REGRESSION PROBLEM TYPE 4 1?',
READ *, PFO3TYP
IF (PFO3TYP .NE. 1) GO TO 3
PRINT *, 'WHAT ARE THE VALUES FOR ZMIN AND ZMAX?',
READ *, ZMIN, ZMAX
9 PRINT *, 'HOW MANY GROUPS ARE THERE?',
READ *, NGRUPS
PRINT *, 'HOW MANY VARIABLES ARE BEING USED?',
READ *, NVAR
IF (NVAR .GT. 4) GO TO 6
N=NVAR
GO TO 5
6 N=4
5 DO 10 I=1,3
10 READ(1,100) (X(I,J), J=1,N)
100 FORMAT(10F10.2)
IF (N .EQ. 2) GO TO 7
DO 20 I=1,N
20 XBAR(I)=X(5,I)

IF THIS IS A DISCRIMINANT FUNCTION PROBLEM:
READ IN THE CONSTANTS FOR THE DISCRIM. FUNCTIONS. THE FIRST SET ARE FOR
THE CONTACT GROUP. *P* IS THE RESPECTIVE PRIOR PROBABILITY.
IF THIS IS A REGRESSION PROBLEM, READ THE NUMBER OF REGRESSION FUNCTIONS.
7 NN=NVAR + 1
DO 1000 I=1,NGRUPS
1000 READ(1,101) (C(I,J), J=1,NN), P(I)
105 FORMAT(7F10.5)
IF (ITEST .EQ. 0) GO TO 2

1 PRINT *, 'CONTINUE (Y OR N)?',
READ 19, ANSI
19 FORMAT(A1)
IF (ANSI .EQ. 'N') GO TO 4
PRINT *, 'WANT TO TAKE ANOTHER SHOT AT THIS ONE?',
READ 18, NEWSHOT
18 FORMAT(A1)
IF (NEWSHOT .EQ. 'Y') NEXTY=1
2 PRINT *, 'WHAT ARE THE VALUES FOR DX, DY, DZ?',
READ *, DX, DY, DZ
IF (NVAR .EQ. 5) PRINT *, 'WHAT IS THE VALUE FOR X5BAR?',
IF (NVAR .EQ. 5) READ *, X5BAR
IF (NEXTY .EQ. 1) GO TO 3

#M# INDICATES THE NUMBER OF COMBINATIONS REQUIRED:
FOR TWO VARIABLE MODELS, M=1
FOR THREE VARIABLE MODELS, M=1,2,4
FOR FOUR OR FIVE VARIABLE MODELS, M=1 TO 6.

PRINT *, 'WHAT IS THE VALUE FOR M?',
READ *, M

C
READ(1,101) NCHAR, LABELS(1)
101 FORMAT(I2,8X,A10)

C SURFACE CALCULATES THE POSTERIOR PROBABILITY OF AN OBSERVATION HAVING
COME FROM THE CONTACT GROUP. THE VALUE *P53* IS PLOTTED OVER

```


TWO OF THE VARIABLES WHILE THE REST ARE HELD CONSTANT.

```

3 CALL ERASE
IF(NEXTTRY.EQ. 1) GO TO 8
IF(PPROBTYP.NE. 1) GO TO 8
IF(NPLOT.GT. 8) GO TO 11
NPLOT=NPLOT + 1
GO TO 8
11 PRINT *, 'THE LAST PLOT WAS FOR FUNCTION', NPLOT
PRINT *, 'ARE YOU READY TO INCREMENT FUNCTION INDEX (Y OR N)?'
READ 17, ANS1
17 FORMAT(A1)
IF(ANS1.EQ. 'N') GO TO 8
NPLOT=NPLOT + 1
8 CONTINUE
CALL SURFACE(4)
NEXTTRY=0
GO TO 1
4 STOP
END

```

```

SUBROUTINE SURFACE(4)
INTEGER PROBTYP
COMMON/DATA1/XBAR(4), X5BAR, NVAR, NORDUPS, PROBTYP, L, NPLOT
COMMON/DATA2/X(3,4), DX, DY, DZ, ZMIN, ZMAX
COMMON/DATA3/P(3,9), PROSMIN(9), PROSMAX(9)
COMMON/DATA4/Z(5,6), P(5), Y(9,4)
COMMON/DATA5/DEP(9,9), DEPMIN(9), DEPMAX(9)
COMMON/DATA6/NN
COMMON/PLT/ISIZE, WIDTH, HEIGHT, NCHAR, LABELS(8), MODEL, IRATE, LUN

```

INITIALIZE THE ARRAY DEP

```

DO 70 I=1,9
DO 80 J=1,3
DEP(I,J)=0.0
80 CONTINUE
70 CONTINUE

```

```

IF(NVAR.GT. 4) GO TO 17
NN=NVAR
GO TO 18
17 NN=4

```

THE IF #N# STATEMENTS THAT FOLLOW ARE DESIGNED TO SELECT THE APPROPRIATE VARIABLE COMBINATIONS FOR EACH GRAPH.

```

18 IF(M.GT. 1) GO TO 2
L=0
1 L=L + 1
DO 10 I=1,3
Y(I,1)=X(L,1)
Y(I,2)=X(L,2)
IF(NVAR.EQ. 2) GO TO 10
Y(I,3)=XBAR(3)
IF(NVAR.EQ. 3) GO TO 10
Y(I,4)=XBAR(4)
10 CONTINUE
GO TO 12

```

```

2 IF(M.GT. 2) GO TO 4
L=0
3 L=L + 1
DO 20 I=1,9
Y(I,1)=X(L,1)
Y(I,2)=XBAR(2)
Y(I,3)=X(I,3)
IF(NVAR.EQ. 3) GO TO 20
Y(I,4)=XBAR(4)
20 CONTINUE
GO TO 12

```

```

4 IF(M.GT. 3) GO TO 6
L=0
5 L=L + 1
DO 30 I=1,9
Y(I,1)=XBAR(1)
Y(I,2)=X(L,2)
Y(I,3)=X(L,3)
IF(NVAR.EQ. 3) GO TO 30
Y(I,4)=XBAR(4)
30 CONTINUE
GO TO 12

```

```

6 IF(M.GT. 4) GO TO 8
L=0
7 L=L + 1

```

```

      DO 40 I=1,3
        Y(I,1)=X(L,1)
        Y(I,2)=X3AR(2)
        Y(I,3)=X3AR(3)
        Y(I,4)=X(I,4)
      40 CONTINUE
      GO TO 12

      8 IF(M.GT. 5) GO TO 101
      L=L+1
      DO 50 I=1,3
        Y(I,1)=X3AR(1)
        Y(I,2)=X(L,2)
        Y(I,3)=X3AR(3)
        Y(I,4)=X(I,4)
      50 CONTINUE
      GO TO 12
101 L=L+1
      DO 60 I=1,3
        Y(I,1)=X3AR(1)
        Y(I,2)=X3AR(2)
        Y(I,3)=X(L,3)
        Y(I,4)=X(I,4)
      60 CONTINUE

      NOW BEGIN THE COMPUTATION FOR THE RESPONSE VARIABLE.
      IF 3 REGRESSION, CALL REGRESS
      IF DISCRIMINANT FUNCTION, CALL DISCRIM.
      12 IF(PROBTYP.NE. 1) GO TO 19
      CALL REGRESS
      GO TO 21
      19 CALL DISCRIM

      21 IF(L.EQ. 3) GO TO 13
      IF(M.EQ. 1) GO TO 1
      IF(M.EQ. 2) GO TO 3
      IF(M.EQ. 3) GO TO 5
      IF(M.EQ. 4) GO TO 7
      IF(M.EQ. 5) GO TO 9
      GO TO 11
      13 IF(PROBTYP.EQ. 1) GO TO 22

      CALL SURFAC3(PROB,0.0,0.4,0.9,0.3,0.3,0.9,0.0,2.0,DX,DY,DZ)
      GO TO 23
      22 CALL SURFAC3(DEP,0.0,0.0,0.9,0.0,0.4,0.3,ZMIN,ZMAX,DX,DY,DZ)
      23 WRITE(2,102) LABELS(1)
      102 FORMAT(10X,/,#MINIMA AND MAXIMA FOR THE X VARIABLE IN#,2X,A10,2X,/,
      1 INTERACTION#)
      WRITE(2,103)
      103 FORMAT(10X ELEMENT#,5X,#MIN. VALUE#,5X,#MAX. VALUE#)

      IF(PROBTYP.EQ. 1) GO TO 24
      WRITE(2,104) (I,PROBMIN(I),PROBMAX(I),I=1,3)
      GO TO 25
      24 WRITE(2,104) (I,DEPMIN(I),DEPMAX(I),I=1,3)
      25 CONTINUE
      104 FORMAT(10X,/,#X,12,4X,2(F12.6,5X)))
      RETURN
      END

      SUBROUTINE DISCRIM
      DIMENSION S(3,1,9)
      COMMON/DATA1/X3AR(4),X53AR,NVAR,NGROUPS,PROBTYP,CINPLOT
      COMMON/DATA2/X(9,4),DX,DY,DZ,ZMIN,ZMAX
      COMMON/DATA3/PRC3(9,3),PRCBMIN(9),PRCBMAX(9)
      COMMON/DATA4/C(5,6),P(5),Y(9,4)
      COMMON/DATA5/DEP(9,9),DEPMIN(9),DEPMAX(9)
      COMMON/DATA6/NN
      COMMON/PLT/ICODE,WIDTH,HEIGHT,NCHAR,LABELS(9),MODEL,IKATE,LUN

      SUM=0.0
      DO 70 I=1,NGROUPS
        DO 80 J=1,3
          DO 90 K=1,3
            S(I,J,K)=0.0
          90 CONTINUE
        80 CONTINUE
      70 CONTINUE

      DO 110 K=1,3
        DO 120 N=1,NGROUPS
          DO 130 I=1,NN
            S(N,L,K)=S(N,L,K) + C(N,I+1)*Y(K,I)
          130
        120
      110

```

```

C      S(N,L,K)=S(N,L,K) + C(N,I)
C      IF(NVAR .EQ. 5) S(N,L,K)=S(N,L,K)+C(N,6)*X53AR
120    SUM=SUM + EXP(S(N,L,K))*P(N)
C      PROB(L,K)=P(1)*(EXP(S(1,L,K)))/SUM
C      NOW FIND THE MIN AND THE MAX FOR EACH VALUE OF L.
C      IF(K .EQ. 1) GO TO 14
C      IF(PROB(L,K) .LE. PROBMAX(L)) GO TO 15
14    PROBMAX(L)=PROB(L,K)
C      IF(K .GT. 1) GO TO 16
C      PROBMIN(L)=PROB(L,K)
C      GO TO 16
15    IF(PROB(L,K) .GE. PROBMIN(L)) GO TO 16
C      PROBMIN(L)=PROB(L,K)
16    PROB(L,K)=2.0*PROB(L,K)
110  CONTINUE
      RETURN
      END
C      SUBROUTINE REGRESS
C      COMMON/DATA1/XBAR(4),X53AR,NVAR,NGROUPS,PROBTYP,L,NPLOT
C      COMMON/DATA2/X(3,1),BX,BY,BZ,ZMIN,ZMAX
C      COMMON/DATA3/PROB(9,9),PROBMIN(9),PROBMAX(9)
C      COMMON/DATA4/C(5,6),P(5),Y(3,4)
C      COMMON/DATA5/DEP(9,9),DEPMIN(9),DEPMAX(9)
C      COMMON/DATA6/NN
C      COMMON/PLT/ICODE,WIDTH,HEIGHT,NCHAR,LABELS(6),MODEL,IRATE,LUN
C      BEGIN OUTER LOOP TO COMPUTE DEP
C      DO 30 K=1,9
C      DO 40 I=1,NN
40    DEP(L,K)=DEP(L,K) + C(NPLOT,I+1)*Y(K,I)
C      DEP(L,K)=DEP(L,K) + C(NPLOT,1)
C      IF(NVAR .EQ. 5) DEP(L,K)=DEP(L,K) + C(NPLOT,6)*X53AR
C      NOW FIND THE MIN AND THE MAX FOR EACH VALUE OF K ARRAY.
C      IF(K .EQ. 1) GO TO 14
C      IF(DEP(L,K) .LE. DEPMAX(L)) GO TO 15
14    DEPMAX(L)=DEP(L,K)
C      IF(K .GT. 1) GO TO 30
C      DEPMIN(L)=DEP(L,K)
C      GO TO 30
15    IF(DEP(L,K) .GE. DEPMIN(L)) GO TO 30
C      DEPMIN(L)=DEP(L,K)
30  CONTINUE
      RETURN
      END

```

APPENDIX E

Documentation of the use of
program SIMROT2 (or ROOTROT, in listing) with
program listing and sample output

Program Use

SIMROT2 is a simulation program designed to implement the laminated root rot spread model, described in detail in Results, part B.

Program Input

Data input to SIMROT2 is both conversational and read from TAPE 1. The variables supplied conversationally are described in Table EI while those read from TAPE 1 are described below. Only one of the input variables supplied conversationally requires amplification. VAR(I), as noted in the table, is the value of the Ith variable used in both the calculation of probability of contact and the number of contacts for a tree-pair at a specific time step. The program is designed so that VAR(1) is always inter-tree slope distance and VAR(2) is always some function of a pair of trees' DBH's. VAR(3) through VAR(5) presently correspond with the percent slope, soil gravel content and effective rooting depth, respectively (main program, line 28). The order, or even the choice of these three variables, can be modified providing corresponding alterations are made in the equation used to calculate the number of contacts for a pair of trees (subroutine CONTACT, lines 25, 26, 29, 30).

A 91-element array of DBH's is supplied on TAPE 1. The first element should correspond to the mean DBH of a 20 year old stand while the last element should correspond to the mean DBH of a 110 year old stand. This implies that the sum of the initial stand age (NAGE) and the

maximum number of timesteps must never exceed 110. The DBH array is read in F10.2 format.

The coefficients of the discriminant functions follow the DBH array on TAPE 1. The ordering of the coefficients of a specific function must correspond to the order of the variables as they appear in the DATA statement on line 28 of the main program. The format statement (7 F10.4) allows for a constant, five coefficients and the associated prior probability of group membership. The coefficient of the NO-CONTACT group's discriminant function should always be read in first; the order of presentation of the other two groups is immaterial.

Program Output

A sample simulation run is included following the program listing. This output should be self-explanatory. Output, as shown here, appears on TAPE 2. Plots are produced on TAPE 3. The first plot corresponds to the cumulative distribution of initial infection while the second plot corresponds to the cumulative distribution and density of time to earliest bole infection. The two curves associated with the CDF and the density are plotted with a "C" and "D," respectively. The plots for the sample run are not included here.

TABLE BI. Conversational variables supplied to SIMROT2

VARIABLE	TYPE	COMMENTS
PROX	real	the proximal spread rate of the fungus (direction is relative to an infected tree's root crown)
DISTAL	real	the distal spread rate of the fungus
DISTMAX	real	the maximum possible distance the fungus can spread distally along a "root" (see Results, Part B for details)
NTMAX	integer	the maximum number of time steps
NAGE	integer	stand age at start of simulation
SPACING	real	inter-tree slope distance
SLOPE	real	the percent slope (note that this value is asked for twice)
VAR(I)	real	value of the I th variable used in computing the probability of contacts and the calculated number of contacts

```

1      PROGRAM ROOTROT (INPJ1=64, OUTPUT=64, TAPE1=64, TAPE2=64, TAPE3)
COMMON/DATA1/NUMSOR,VAR(5),NT,NUMSOR1,SLOPE,CISTMAX
COMMON/DATA2/NUMIAR(4),ISSJURCE(4),ITARGET(4,4)
5      COMMON/DATA3/X(4),Y(4),SPRRAD(4),NDEATH(4)
COMMON/DATA4/INIT0,NEBIT(4),INOTINF(4)
COMMON/DATA5/O3HINIT(4),O3H(4),IDEAD(4)
COMMON/DATA6/TREEDIS(4,4)
COMMON/DATA7/PROBCON(4,4)
10     COMMON/DATA8/C(3,6),P(3)
COMMON/DATA9/NCUNPT(4,4)
COMMON/DATA10/AFFIRM(4,4)
COMMON/DATA11/CON1(4,4)
COMMON/DATA13/CONPTX(4,4,12)
COMMON/DATA14/CONPTY(4,4,12)
15     COMMON/DATA15/SORTARG(4,4)
COMMON/DATA18/NPTINF(4,4,12)
COMMON/DATA19/CO SANG(4,4,12)
COMMON/DATA20/SI NANG(4,4,12)
COMMON/DATA21/XPINE(4,4,12)
20     COMMON/DATA22/YDINF(4,4,12)
COMMON/DATA23/YPINF(4,4,12)
COMMON/DATA24/YDINF(4,4,12)
COMMON/DATA25/MAX(4,4,12)
25     DIMENSION CUMCP(50),CUMCCP(50),DENSITY(50),XINT(10),INT(10)
DIMENSION VARNAME(5),NEBITMP(50),DIAM(91),PROPINF(50)
DOUBLE PRECISION JSEED,PROBCON,USEED1
INTEGER AFFIRM,SORTARG,VARNAME
DATA VARNAME/'OIST#','O3H#','SLOPE#','GRAVEL#','SOLOEF#'/
30     NEXT=0
NGROUPS=3
NVAR=5

C      DSEED1=0.0
C
35     C INPUT RUN CONTROL INFORMATION.
C
PRINT *, 'ENTER THE PROXIMAL SPREAD RATE #,'
READ *, PROX
PRINT *, 'ENTER THE DISTAL SPREAD RATE #,'
40     READ *, DISTAL
PRINT *, 'ENTER THE MAXIMUM DISTAL SPREAD#,'
READ *, OISTMAX
100    READ(1,100) (DIAM(I), I=1,91)
45     FORMAT(F10.2)
N=NVAR + 1
DO 30 J=1,NGROUPS
30     READ(1,102) (C(J,K), K=1,N),P(J)
102    CONTINUE
50     1000 FORMAT(7F10.4)
PRINT *, 'ENTER THE TIME LIMIT #,'
1000   READ *, NIMAX
PRINT *, 'ENTER THE INITIAL TREE AGE #,'
55     READ *, NAGE
PRINT *, 'ENTER THE TREE SPACING (IN CM.) #,'
READ *, SPACING
TREEDIS(1,2)=SPACING
TREEDIS(1,3)=SPACING
TREEDIS(1,4)=SPACING
TREEDIS(2,3)=SPACING
60     TREEDIS(4,3)=SPACING
PRINT *, 'ENTER THE PERCENT SLOPE#,'
READ *, SLOPE
CALL PLOTPE (SPACING)
CALL DIAMSET (DIAM,NAGE)
65     DO 40 I=1,50
CUMCP(I)=0.0
CUMCCP(I)=0.0
DENSITY(I)=0.0
NEBITMP(I)=0
70     PROPINF(I)=0.0
40     CONTINUE
DO 70 I=3,NVAR
70     PRINT *, 'VARIABLE #, I, # IS #, VARNAME(I), #. VALUE IS #,'
READ *, VAR(I)
75     PRINT *, 'A VALUE FOR DSEED IS REQUIRED.#'
PRINT *, 'THIS IS USED IN 30TH SUBR. PICKCON AND CONTACT#'
PRINT *, 'ENTER THE VALUE FOR JSEED #,'

```



```

      READ *,OSEED
      OSEED1=OSEED
      NRUN=NRUN + 1
80      WRITE(2,104) NRUN
      104 FORMAT(21,104) ***** RUN #,I2, *****
      1#/,5X, #FIXED DISCRIM. VARIABLE LIST#/,8X, #NAME#,5X, #VALUE#,/
85      WRITE(2,105) (VARNAM(I),VAR(I), I=3,NVAR)
      105 FORMAT(2,105)
      WRITE(2,107) SLOPE,SPACING
      107 FORMAT(2,107) SLOPE#,84,F8.2,/, # TREE SPACING#,1X,F8.2)
      WRITE(2,108) OSEED1
90      108 FORMAT(2,108) SEED NUMBER FOR SUBROUTINES PICKCON AND CONTACT#,1X,320
      1.2)
      WRITE(2,103) PROX,DISTAL,NAGE
      103 FORMAT(2,103) PROXIMAL SPREAD RATE#,5X,F8.2,/, # DISTAL SPREAD RATE#
      1.7X,F8.2,/, # INITIAL TREE AGE#,5X,18)
95      DO 90 I=1,5
      90 WRITE(2,106)
      106 FORMAT(2,106)
      DO 120 MMM=1,50
      NT=0
      IAGE=NAGE
      CALL RESET(NOUT)
      1002 NT=NT + 1
      IAGE=IAGE + 1
      CALL DBHINC(DIAM,NAGE)
      DO 130 I=1,NUMSOR
      NSOURCE=ISOURCE(I)
      IF(ICEAD(NSOURCE).EQ. 1) GO TO 130
      IF(INCTINF(NSOURCE).EQ. 1) GO TO 130
      N=NUMTAR(I)
      DO 135 J=1,N
      IF(AFFIRM(I,J).EQ. 1) GO TO 8
      CALL CONPROB(I,J,NEAT,NVAR,NGROUPS)
      CALL PICKCON(I,J,OSEED)
      IF(AFFIRM(I,J).EQ. 0) GO TO 135
      CALL CONTACT(I,J,CONBAR,OSEED,IAGE)
115      135 CONTINUE
      130 CONTINUE
      DO 140 I=1,NUMSOR
      ITEST=ISOURCE(I)
      IF(ICEAD(ITEST).EQ. 1) GO TO 11
      IF(INOTINF(ITEST).EQ. 1) GO TO 140
      NDIFF=NT - NEBIT(ITEST)
      IF(NDIFF .GE. 2 .AND. DBH(ITEST) .LE. 5.0) GO TO 9
      IF(NDIFF .GE. 5 .AND. DBH(ITEST) .LE. 10.0) GO TO 9
      IF(NDIFF .GE. 7 .AND. DBH(ITEST) .LE. 20.0) GO TO 9
125      IF(NDIFF .GE. 10 .AND. DBH(ITEST) .LE. 40.0) GO TO 9
      IF(NDIFF .GE. 15 .AND. DBH(ITEST) .GT. 40.0) GO TO 9
      GO TO 11
      9 ICEAD(ITEST)=1
      NDEATH(I)=NT
      GO TO 140
130      11 CALL SPREAD(I,PROX,DISTAL)
      CALL INFECT(I,NOUT,PROXINF,PROX,DISTAL)
      140 CONTINUE
      NEBITMP(MMM)=NEBIT(3)
      NUMSOR=NUMSOR1
135      IF(NT.EQ. NTMAX) GO TO 120
      C
      GO TO 1002
140      120 CONTINUE
      T=0.0
      CP=0.0
      WRITE(2,109)
      109 FORMAT(2,109) CUMULATIVE DISTRIBUTION OF INITIAL INFECTION BY YEAR#)
      DO 160 I=1,NTMAX
      T=T + PROXINF(I)
145      160 CONTINUE
      NEND=0
      DO 165 I=1,NTMAX
      IF(PROXINF(I).EQ. 0.0) GO TO 2
      CP=CP + PROXINF(I)/50.0
      CUMCP(I)=CP
150      2 WRITE(2,110) I,CP
      NEND=NEND + 1
      IF(CP.GT. 0.9999) GO TO 5

```



```

      AMIN=XMEAN - 4.0*STDEV
      XINT(1)=XMIN
      DO 200 I=2,8
235      XINT(I)=XINT(I-1) + STDEV
      200 CONTINUE
      DO 210 I=1,8
      INT(I)=0
240      210 CONTINUE
      DO 220 I=1,50
      A=FLOAT(NB3:TMP(I))
      IF(A.EQ.0.0) GO TO 220
      DO 230 J=2,9
      IF(A.GT.XINT(J)) GO TO 230
245      INT(J-1)=INT(J-1) + 1
      GO TO 220
      230 CONTINUE
      220 CONTINUE
      WRITE(2,115) XMEAN,STDEV
250      115 FORMAT(20, 'MEAN TIME TO EARLIEST BOLE INFECTION',1X,F
      15.2,/,/,17X, 'STANDARD DEVIATION',2X,F5.2)
      WRITE(2,116)
255      116 FORMAT(20, 'FREQUENCY TABLE',/,/, 'FROM' TO 'NO. OCCURRENCES')
      117 FORMAT(2,117) (AINT(I),AINT(I+1),INT(I), I=1,8)
      C
      CALL PLOTAC(CUMCP,NEND)
      CALL PLOTB(CUMCCP,DENSITY,KEND)
      PRINT *, 'DO YOU WANT TO MAKE ANOTHER RUN (Y OR N)?',
260      READ 113,ANSI
      113 FORMAT(A1)
      IF(ANSI.NE.'Y') GO TO 14
      NEXT=NEXT + 1
      GO TO 1000
265      14 STOP
      END

```

```

1      SUBROUTINE PLOTYPE(SPACING)
      COMMON/DATA1/NUMSOR,VAR(5),NT,NUMSOR,SLOPE,DISTMAX
      COMMON/DATA3/X(1),Y(1),SPRAD(4),NOEAT(4)
5      COMMON/DATA6/TREEDIS(4,4)
      ALPHA=45.0*SLOPE/5729.58
      X(1)=1000.0
      Y(1)=1000.0
      X1=SPACING*COS(0.5235988)
      Y1=SPACING*SIN(0.5235988)*COS(ALPHA)
10      X(2)=X(1) - X1
      Y(2)=Y(1) + Y1
      X(3)=X(1)
      Y(3)=Y(1) + SPACING*COS(ALPHA)
      X(4)=X(1) + X1
      Y(4)=Y(1) + Y1
15      RETURN
      END

```

```

1      SUBROUTINE DIAMSET(DIAM,NAGE)
      COMMON/DATA5/D3HINIT(4),DBH(4),IDEAO(4)
      DIMENSION DIAM(91)
5      DO 10 I=1,4
      D3HINIT(I)=DIAM(NAGE-19)
10      CONTINUE
      RETURN
      END

```

```

1      SUBROUTINE RESET (NOUT)
COMMON/DATA1/NUMSOR,VAR(5),VT,NUMSOR1,SLOPE,DISTMAX
COMMON/DATA2/NUMTAR(4),ISOURCE(4),ITARGET(4,4)
5     COMMON/DATA3/X(4),Y(4),SPRRAD(4),NDEATH(4)
COMMON/DATA4/INITO,NESIT(4),INOTINF(4)
COMMON/DATA5/D3HINIT(4),DBH(4),ICEAD(4)
COMMON/DATA6/TREEDIS(4,4)
COMMON/DATA7/PROBCON(4,4)
10    COMMON/DATA9/NCUNPT(4,4)
COMMON/DATA10/AFFIRM(4,4)
COMMON/DATA11/CON1(4,4)
COMMON/DATA13/CONPTX(4,4,12)
COMMON/DATA14/CONPTY(4,4,12)
COMMON/DATA15/SORTARG(4,4)
15    COMMON/DATA18/NPTINF(4,4,12)
COMMON/DATA19/COSANG(4,4,12)
COMMON/DATA20/SINANG(4,4,12)
COMMON/DATA21/APINF(4,4,12)
COMMON/DATA22/XDINF(4,4,12)
20    COMMON/DATA23/YPINF(4,4,12)
COMMON/DATA24/YDINF(4,4,12)
COMMON/DATA25/MAX(4,4,12)
INTEGER AFFIRM,SORTARG
DOUBLE PRECISION PROBCON
25    NCUT=0
NRESID=0
NUMSOR=1
NUMSOR1=1
DO 10 I=1,4
30    ISOURCE(I)=0
NDEATH(I)=0
DBH(I)=DBHINIT(I)
INOTINF(I)=0
35    IDEAD(I)=0
NESIT(I)=0
SPRRAD(I)=0.0
DO 20 J=1,4
40    PROBCON(I,J)=0.0
CON1(I,J)=0.0
NCONPT(I,J)=0
AFFIRM(I,J)=0
SORTARG(I,J)=0
DO 30 K=1,12
45    CONPTX(I,J,K)=0.0
CONPTY(I,J,K)=0.0
COSANG(I,J,K)=0.0
SINANG(I,J,K)=0.0
NPTINF(I,J,K)=0
50    XPINF(I,J,K)=0.0
XDINF(I,J,K)=0.0
YPINF(I,J,K)=0.0
YDINF(I,J,K)=0.0
MAX(I,J,K)=0
55    30    CONTINUE
20    CONTINUE
10    CONTINUE
ISOURCE(1)=1
NUMTAR(1)=3
ITARGET(1,1)=2
60    ITARGET(1,2)=3
ITARGET(1,3)=4
NUMTAR(2)=1
NUMTAR(3)=1
ITARGET(2,1)=3
65    ITARGET(3,1)=3
RETURN
END

```

```

1  SUBROUTINE CONPROB (I,J, NEXT, NVAR, NGROUPS)
COMMON/DATA1/NUMSOR, VAR(5), NT, NUMSOR1, SLOPE, DISTMAX
COMMON/DATA2/NUMTAR(4), ISOURCE(4), ITARGET(4,4)
5  COMMON/DATA5/D3HINIT(4), D3H(4), IDEAD(4)
COMMON/DATA6/TREEDIS(4,4)
COMMON/DATA7/PROBCON(4,4)
COMMON/DATA8/C(3,6), P(3)
10  DIMENSION S(10)
DOUBLE PRECISION PROBCON
N=ITARGET(I,J)
NSOURCE=ISOURCE(I)
SUM=0.0
DO 30 K=1, NGROUPS
15 30  S(K)=0.0
CONTINUE
VAR(1)=TREEDIS(NSOURCE,N)
VAR(2)=ALOG(D3H(NSOURCE) + D3H(N))
DO 40 K=1, NGROUPS
20 40  L=1, NVAR
S(K)=S(K) + C(K,L+1)*VAR(L)
50  CONTINUE
S(K)=S(K) + C(K,1)
SUM=SUM + EXP(S(K))*P(K)
25 40  CONTINUE
PROBCON(I,J)=1.0 - P(1)*EXP(S(1))/SUM
RETURN
END

```

```

1  SUBROUTINE PICKCON (I, J, DSEED)
COMMON/DATA2/NUMTAR(4), ISOURCE(4), ITARGET(4,4)
COMMON/DATA7/PROBCON(4,4)
5  COMMON/DATA10/AFFIRM(4,4)
DOUBLE PRECISION DSEED,0, PROBCON
INTEGER AFFIRM
D=DGBUFS(DSEED)
10  IF (PROBCON(I,J) .GT. D) AFFIRM(I,J)=1
1  RETURN
END

```

```

1  SUBROUTINE REMRES(I)
COMMON/DATA1/NUMSOR, VAR(5), NT, NUMSOR1, SLOPE, DISTMAX
COMMON/DATA2/NUMTAR(4), ISOURCE(4), ITARGET(4,4)
5  COMMON/DATA4/INITO, NEBIT(4), INOTINF(4)
COMMON/DATA5/D3HINIT(4), D3H(4), IDEAD(4)
COMMON/DATA9/NSOUPPT(4,4)
NSOURCE=ISOURCE(I)
INOTINF(NSOURCE)=1
10  IDEAD(NSOURCE)=0
RETURN
END

```

```

1  SUBROUTINE CONTACT(I,J,CONBAR,DSEED,IAGE)
COMMON/DA11/NUMSOR,VAR(5),NT,NUMSOR1,SLOPE,DISTMAX
COMMON/DA12/NUMTAR(4),ISOURCE(4),ITARGET(4,4)
5  COMMON/DA13/X(4),Y(4),SPRAD(4),NDEATH(4)
COMMON/DA15/D3HINIT(4),D3H(4),IDEAD(4)
COMMON/DA16/TREEDIS(4,4)
COMMON/DA19/NCNPT(4,4)
COMMON/DA111/CON1(4,4)
10  COMMON/DA113/CONPTX(4,4,12)
COMMON/DA114/CONPTY(4,4,12)
COMMON/DA119/COSANG(4,4,12)
COMMON/DA120/SINANG(4,4,12)
COMMON/DA121/XPINF(4,4,12)
15  COMMON/DA122/XOINF(4,4,12)
COMMON/DA123/YPINF(4,4,12)
COMMON/DA124/YOINF(4,4,12)
DOUBLE PRECISION DSEED
ROIST=300.0
20  IF(NCNPT(I,J).EQ. 12) GO TO 1
MSOURCE=ISOURCE(I)
MTARGET=ITARGET(I,J)
VAR(1)=TREEDIS(MSOURCE,MTARGET)
VAR(2)=D3H(MSOURCE)*D3H(MTARGET)
25  IF(NCNPT(I,J).NE. 0) GO TO 2
CON1(I,J)=2.3544 + 0.2335*EXP((VAR(2)*VAR(3)*VAR(4))/((VAR(1)*VAR(
11))*VAR(5)*10.0))
NCON2=FIX(CON1(I,J))
GO TO 3
30  2 CON2=2.3544 + 0.2386*EXP((VAR(2)*VAR(3)*VAR(4))/((VAR(1)*VAR(1))*V
1AR(5)*10.0))
CONDIFF=CON2 - CON1(I,J)
CONTEST=GGUBFS(DSEED)
IF(CONTEST.GE. CONDIFF) GO TO 1
35  NCON2=FIX(CON2)
3 IF(NCON2.GT. 12) NCON2=12
IF(NCON2.LE. NCNPT(I,J)) GO TO 1
KK=NCNPT(I,J) + 1
CIRLOCX=(X(MSOURCE) + X(MTARGET))/2.0
CIRLOCY=(Y(MSOURCE) + Y(MTARGET))/2.0
40  DO 30 K=KK,NCON2
RANANG=GGUBFS(DSEED)*2.0*3.14159
IF(IAGE.GE. 40) GO TO 4
ROIST=5.0*FLCAT(IAGE) + 100.0
45  4 RANDIST=ROIST*GGUBFS(DSEED)
CONPTX(I,J,K)=CIRLOCX + RANDIST*COS(RANANG)
CONPTY(I,J,K)=CIRLOCY + RANDIST*SIN(RANANG)
XPINF(I,J,K)=CONPTX(I,J,K)
XOINF(I,J,K)=CONPTX(I,J,K)
50  YPINF(I,J,K)=CONPTY(I,J,K)
YOINF(I,J,K)=CONPTY(I,J,K)
A=X(MTARGET) - CONPTX(I,J,K)
B=Y(MTARGET) - CONPTY(I,J,K)
DIST=SQRT(A*A + B*B)
COSANG(I,J,K)=A/DIST
SINANG(I,J,K)=B/DIST
55  30 CONTINUE
IF(NCNPT(I,J).EQ. 0) GO TO 5
CON1(I,J)=CON2
60  5 NCONPT(I,J)=NCON2
1 RETURN
END

```

```

1      SUBROUTINE SPREAD(I,PROX,DISTAL)
COMMON/DATA1/NUMSOR,VAR(3),NT,NUMSOR1,SLOPE,DISTMAX
COMMON/DATA2/NUMTAR(4),ISOURCE(4),ITARGET(4,4)
5      COMMON/DATA3/A(4),Y(4),SPRRAD(4),NDEATH(4)
COMMON/DATA4/IN,T0,NEBIT(4),INOTINF(4)
COMMON/DATA5/DBHINIT(4),DBH(4),IDEAD(4)
COMMON/DATA9/NCONPT(4,4)
COMMON/DATA15/SORTARG(4,4)
10     COMMON/DATA18/NPTINF(4,4,12)
COMMON/DATA19/COSANG(4,4,12)
COMMON/DATA20/SINANG(4,4,12)
COMMON/DATA21/XPINF(4,4,12)
COMMON/DATA22/XDINF(4,4,12)
COMMON/DATA23/YPINF(4,4,12)
15     COMMON/DATA24/YDINF(4,4,12)
COMMON/DATA25/MAX(4,4,12)
INTEGER SORTARG
ALPHA=SLOPE*.50/5729.58
NSOURCE=ISOURCE(I)
20     IF(IDEAD(NSOURCE).EQ.1) GO TO 4
IF(NEBIT(NSOURCE).GT.NT) GO TO 2
IF(NEBIT(NSOURCE).LT.NT) GO TO 3
IF(NEBIT(NSOURCE).EQ.NT) SPRRAD(I)=0.0
3      SPRRAD(I)=SPRRAD(I) + DISTAL*COS(ALPHA)
25     IF(ISOURCE(I).EQ.1) GO TO 11
NUM=NUMTAR(1)
DO 20 J=1,NUM
NTARGET=ITARGET(1,J)
IF(NSOURCE.EQ.NTARGET) GO TO 1
30     CONTINUE
1      LL=NCONPT(1,J)
DO 30 JJ=1,LL
IF(NPTINF(1,J,JJ).NE.1) GO TO 30
XPINC=PROX*(COSANG(1,J,JJ))
35     XPINF(1,J,JJ)=XPINF(1,J,JJ) + XPINC
IF(MAX(1,J,JJ).EQ.1) GO TO 12
XDINC=-DISTAL*COSANG(1,J,JJ)
XDINF(1,J,JJ)=XDINF(1,J,JJ) + XDINC
YPINC=PROX*(SINANG(1,J,JJ))*COS(ALPHA)
40     YPINF(1,J,JJ)=YPINF(1,J,JJ) + YPINC
IF(MAX(1,J,JJ).EQ.1) GO TO 30
YDINC=-DISTAL*(SINANG(1,J,JJ))*COS(ALPHA)
YDINF(1,J,JJ)=YDINF(1,J,JJ) + YDINC
A=X(NSOURCE) - XDINF(1,J,JJ)
45     B=Y(NSOURCE) - YDINF(1,J,JJ)
DIST=SQRT(A*A + B*B)
IF(DIST.LT.DISTMAX) GO TO 30
MAX(1,J,JJ)=1
30     CONTINUE
50     GO TO 11
4      IF(DBH(NSOURCE).LT.5.0) GO TO 3
IF(DBH(NSOURCE).GE.5.0 .AND. DBH(NSOURCE).LT.10.0) GO TO 7
IF(DBH(NSOURCE).GE.10.0 .AND. DBH(NSOURCE).LT.20.0) GO TO 6
55     IF(DBH(NSOURCE).GE.20.0 .AND. DBH(NSOURCE).LT.40.0) GO TO 5
A=9.60
B=0.0022
GO TO 9
6      A=8.09
B=0.0033
GO TO 9
60     GO TO 9
7      A=8.84
B=0.0048
GO TO 9
65     GO TO 9
7      A=10.46
B=0.0067
GO TO 9
8      A=12.48
B=0.0167
9      NPERIOD=NT - NDEATH(I)
SPRINC=A*EXP(-B*NPERIOD)*COS(ALPHA)
SPRRAD(I)=SPRRAD(I) - SPRINC
IF(SPRRAD(I).LE.0.0) CALL REMRES(I)
70     RETURN
END

```

```

1      SUBROUTINE INFECT(I, NOUT, PROPIF, PROX, DISTAL)
COMMON/DATA1/NUMSOR, VAR(5), NT, NUMSOR1, SLOPE, DISTMAX
COMMON/DATA2/NUMTAR(4), ISOURCE(4), ITARGET(4,4)
5      COMMON/DATA3/X(4), Y(4), SPRRAD(4), NDEATH(4)
COMMON/DATA4/INIT0, NEBIT(4), INOTINF(4)
COMMON/DATA5/DBHINIT(4), DBH(4), IDEAD(4)
COMMON/DATA9/NCONPT(4,4)
COMMON/DATA13/CONPTX(4,4,12)
COMMON/DATA14/CONPTY(4,4,12)
10     COMMON/DATA15/SORTARG(4,4)
COMMON/DATA18/NPTINF(4,4,12)
COMMON/DATA19/COSANG(4,4,12)
COMMON/DATA20/SINANG(4,4,12)
COMMON/DATA21/XPINF(4,4,12)
COMMON/DATA22/XDINF(4,4,12)
COMMON/DATA23/YPINF(4,4,12)
COMMON/DATA24/YDINF(4,4,12)
DIMENSION PROPIF(50,4,4)
INTEGER SORTARG
20     ALPHA=SLOPE*43.0/5729.58
NSOURCE = ISOURCE(I)
NTAR=NUMTAR(I)
DO 50 J=1,NTAR
M=NCONPT(I,J)
25     IF(M.EQ.0) GO TO 50
NTARGET=ITARGET(I,J)
IF(NEBIT(NSOURCE).GT. NT) GO TO 2
DO 10 K=1,M
IF(NPTINF(I,J,K).EQ.1) GO TO 10
30     A=CONPTX(I,J,K) - X(NSOURCE)
B=CONPTY(I,J,K) - Y(NSOURCE)
DIST=SQRT(A*A + B*B)
IF(DIST.GT. SPRRAD(I)) GO TO 10
NPTINF(I,J,K)=1
35     A=CONPTX(I,J,K) - X(NTARGET)
B=CONPTY(I,J,K) - Y(NTARGET)
RIDIST=SQRT(A*A + B*B)
NRIT=NT + IFIX(RIDIST/(PROX*COS(ALPHA)) + 0.5)
40     IF(SORTARG(I,J).EQ.0) GO TO 1
IF(NRIT.LT. NEBIT(NTARGET)) NEBIT(NTARGET)=NRIT
GO TO 10
1     SORTARG(I,J)=1
IF(NEBIT(NTARGET).EQ.0) NEBIT(NTARGET)=NRIT
45     IF(NRIT.LT. NEBIT(NTARGET)) NEBIT(NTARGET)=NRIT
IF(NTARGET.NE.3) GO TO 5
IF(NOUT.EQ.1) GO TO 10
PROPIF(NT)=PROPIF(NT) + 1
NOUT=1
8     CALL ADDSOR(NTARGET)
50     CONTINUE
10     IF(IDEAD(NSOURCE).EQ.1) GO TO 6
IF(ISOURCE(I).EQ.1) GO TO 5
2     NN=NCONPT(I,1)
55     IF(NN.EQ.0) GO TO 50
NUM=NUMTAR(1)
DO 60 K=1,NUM
IF(NSOURCE.EQ. ITARGET(I,K)) GO TO 4
60     CONTINUE
4     N=NCONPT(I,K)
60     DO 30 LL=1,N
IF(NPTINF(I,K,LL).EQ.0) GO TO 30
DO 40 LLL=1,NN
IF(NPTINF(I,1,LLL).EQ.1) GO TO 40
65     A=XPINF(I,K,LL) - CONPTX(I,1,LLL)
B=YPINF(I,K,LL) - CONPTY(I,1,LLL)
DISTA=A*A + B*B
C=XDINF(I,K,LL) - CONPTX(I,1,LLL)
D=YDINF(I,K,LL) - CONPTY(I,1,LLL)
DISTB=C*C + D*D
70     E=XPINF(I,K,LL) - XDINF(I,K,LL)
F=YPINF(I,K,LL) - YDINF(I,K,LL)
DISTC=E*E + F*F
COSBETA=(DISTA + DISTC + DISTB)/(2.0*SQRT(DISTA*DISTC))
BETA=ACOS(COSBETA)
75     G=SQRT(DISTA)*SIN(BETA)
IF(DISTA.GT. 900.0 .AND. DISTB.GT. 900.0 .AND. G.GT. 30
1.0) GO TO 40

```



```

      NPTINF(I,J,LL)=1
      A=CONPTX(I,J,LLL) - X(NTARGET)
      B=CONPTY(I,J,LLL) - Y(NTARGET)
      RIDIST=SQRT(A*A + B*B)
      NRIT=NT + IFIX(RIDIST/(PRCX*COS(ALPHA)) + 0.5)
      IF(SORTARG(I,J).EQ.0) GO TO 7
      IF(NRIT.LT. NEBIT(NTARGET)) NEBIT(NTARGET)=NRIT
85      GO TO 40
      7      SORTARG(I,J)=1
      IF(NEBIT(NTARGET).EQ.0) NEBIT(NTARGET)=NRIT
      IF(NRIT.LT. NEBIT(NTARGET)) NEBIT(NTARGET)=NRIT
      IF(NOUT.EQ.1) GO TO 40
      PROFINF(NT)=PROFINF(NT) + 1.0
90      NOUT=1
      40      CONTINUE
      30      CONTINUE
      50      CONTINUE
95      6      RETURN
      END

```

```

1      SUBROUTINE ADDSOR(NTARGET)
      COMMON/DATA1/NUMSOR,VAR(5),NT,NUMSOR1,SLOPE,DISTMAX
      COMMON/DATA2/NUMTAR(1),ISOURCE(4),ITARGET(4,4)
      IF(NTARGET.EQ.3) GO TO 1
5      NUMSOR1=NUMSOR1 + 1
      ISOURCE(NUMSOR1)=NTARGET
1      RETURN
      END

```

```

1      SUBROUTINE DBHINC(DIAM,NAGE)
      COMMON/DATA1/NUMSOR,VAR(5),NT,NUMSOR1,SLOPE,DISTMAX
      COMMON/DATA4/INIT0,NEBIT(4),INOTINF(4)
      COMMON/DATA5/DBHINIT(4),DBH(4),IDEAD(4)
5      DIMENSION CIAM(91)
      DO 10 I=1,4
      IF(INOTINF(I).EQ.1) GO TO 10
      IF(IDEAD(I).EQ.1) GO TO 10
      DBH(I)=DIAM(NAGE+NT-20)
10     CONTINUE
      RETURN
      END

```

```

1      SUBROUTINE PLOTA(CUMCP,NEND)
      DIMENSION CUMCP(50),ICAR(2),DATA(50,1)
      DATA ICAR/1NA,1WX/
      DO 10 I=1,50
5      DATA(I,1)=CUMCP(I)
10     CONTINUE
      CALL PLOTP(DATA,NEND,1,50,ICAR)
      RETURN
      END

```

```

1      SUBROUTINE PLOTS(CUMCCP,DENSITY,KEND)
      DIMENSION CUMCCP(50),DENSITY(50),ICAR(3),DATA(50,2)
      DATA ICAR/1NC,1MO,1WX/
      DO 10 I=1,50
5      DATA(I,1)=CUMCCP(I)
      DATA(I,2)=DENSITY(I)
10     CONTINUE
      CALL PLOTP(DATA,KEND,2,50,ICAR)
      RETURN
      END
10

```

***** RUN 1 *****
 FIXED DISCRIM. VARIABLE LIST

NAME	VALUE
SLOPE	45.00
GRAVEL	2500.00
SOLOEP	80.00

SLOPE	45.00	
TREE SPACING	300.00	
SEED NUMBER FOR SUBROUTINES PICKCON AND CONTACT		.120*09
PROXIMAL SPREAD RATE	30.00	
DISTAL SPREAD RATE	30.00	
INITIAL TREE AGE	20	

CUMULATIVE DISTRIBUTION OF INITIAL INFECTION BY YEAR

1	.0200
2	.0200
3	.0800
4	.0800
5	.1400
6	.2200
7	.2200
8	.2400
9	.2600
10	.2600
11	.2800
12	.2800
13	.3200
14	.4000
15	.5600
16	.7600
17	.8400
18	.9000
19	.9200
20	.9800
21	1.0000

THERE WERE 50.00 OCCURRENCES OF CONTACT

CUM. DISTR. AND DENSITY OF EARLIEST TIME TO SOLE INFECTION

TIME	CDF	DENSITY
10	.0200	.0200
11	.0400	.0200
13	.1000	.0600
14	.1600	.0600
15	.2200	.0600
17	.2600	.0400
19	.2800	.0200
20	.3000	.0200
21	.6200	.3200
22	.7800	.1600
23	.8400	.1000
24	.9000	.0200
25	.9400	.0400
26	1.0000	.0600

DECILE TABLE FOR EARLIEST TIME TO SOLE INFECTION

1	10
2	13
3	15
4	16
5	17
6	18
7	19
8	20
9	21
10	22
11	24
	26

MEAN TIME TO EARLIEST SOLE INFECTION 19.92
STANDARD DEVIATION 4.04

FREQUENCY TABLE		
FROM	TO	NO. OCCURRENCES
3.76	7.80	8
7.80	11.84	22
11.84	15.88	29
15.88	19.92	30
19.92	23.96	30
23.96	28.00	6
28.00	32.04	6
32.04	36.08	0

APPENDIX F

Data for inter-tree root contact analyses

plot #	tree pair	DBH1 (cm)	DBH2 (cm)	slope distance (cm)	relative slope angle (degrees)	soil depth (cm)	slope (percent)	No. of contacts				Total
								1's	2's	3's	4's	
1	1 - 6	26.0	23.5	360.50	70.16	125.0	46.0					0
1	1 - 8	26.0	20.0	193.02	44.07	125.0	46.0	2	1	1		4
1	1 - 11	26.0	20.7	250.35	73.33	125.0	46.0					0
1	6 - 8	23.5	20.0	207.51	86.03	125.0	46.0					0
1	6 - 11	23.5	20.7	579.43	84.98	125.0	46.0					0
1	8 - 11	20.0	20.7	376.44	80.04	125.0	46.0					0
2	1 - 2	25.4	21.4	271.19	7.72	130.0	60.0	1				1
3	1 - 7	31.7	27.5	238.61	25.01	100.0	45.0	4	9		1	14
6	1 - 7	30.8	34.5	286.51	35.20	140.0	44.0	3				3
6	1 - 12	30.8	27.9	276.87	82.36	140.0	44.0	1				1
6	7 - 12	34.5	27.9	230.10	32.42	140.0	44.0	7	4	1	2	14
7	1 - 3	45.0	54.0	478.51	90.00	85.0	45.0	1	2		1	4
8	1 - 8	37.0	33.0	252.41	74.56	120.0	45.0					0
8	1 - 4	37.0	45.0	268.79	85.99	120.0	45.0	3	1			4
8	4 - 8	45.0	33.0	507.86	84.61	120.0	45.0					0
9	1 - 7	40.5	50.4	610.02	84.60	140.0	52.0	8				8
10	1 - 6	38.6	35.2	281.30	83.98	90.0	41.0	7	2	2		11
10	1 - 8	38.6	35.2	656.22	47.86	90.0	41.0					0
10	1 - 9	38.6	25.5	354.68	27.79	90.0	41.0					0
10	1 - 10	38.6	30.3	548.55	23.77	90.0	41.0	5				5
10	6 - 8	35.2	35.2	516.30	22.14	90.0	41.0					0
10	6 - 9	35.2	25.5	359.69	21.20	90.0	41.0				1	1
10	6 - 10	35.2	30.3	531.07	8.35	90.0	41.0	6				6
10	8 - 9	35.2	25.5	340.84	67.92	90.0	41.0	1				1
10	8 - 10	35.2	30.3	259.45	78.72	90.0	41.0	3		1		4
10	9 - 10	25.5	30.3	195.98	16.49	90.0	41.0	11	2			13

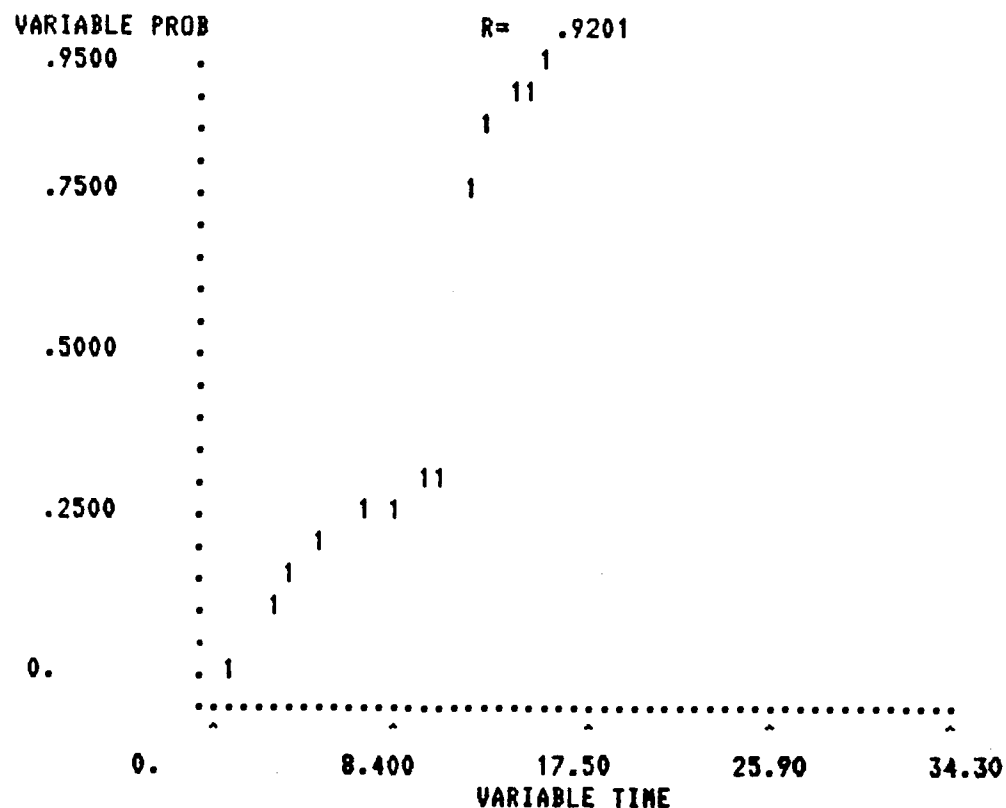
plot #	tree pair	DBH1 (cm)	DBH2 (cm)	slope distance (cm)	relative slope angle (degrees)	soil depth (cm)	slope (percent)	No. of contacts				Total
								1's	2's	3's	4's	
11	1 - 4	30.5	31.0	332.41	18.76	105.0	40.0	2				2
11	1 - 6	30.5	32.7	250.86	44.85	105.0	40.0	4	1			5
11	4 - 6	31.0	32.7	149.23	29.42	105.0	40.0	7	4		4	15
12	1 - 4	29.4	23.0	130.00	87.99	80.0	44.0	5	2	1		8
12	1 - 10	29.4	21.8	390.00	85.37	80.0	44.0	1	1			2
12	1 - 11	29.4	9.7	250.97	86.60	80.0	44.0	5	2	1		8
12	4 - 10	23.0	21.8	519.35	87.03	80.0	44.0					0
12	4 - 11	23.0	9.7	380.55	87.08	80.0	44.0					0
12	10 - 11	21.8	9.7	148.17	71.60	80.0	44.0	3	1			4
13	1 - 2	24.9	23.7	132.85	46.85	110.0	35.0	2	2	1	1	6
13	1 - 4	24.9	25.0	263.37	69.93	110.0	35.0					0
13	1 - 11	24.9	27.1	300.01	72.56	110.0	35.0	3		2	3	8
13	1 - 12	24.9	15.2	250.80	53.26	110.0	35.0					0
13	1 - 13	24.9	12.6	172.63	43.22	110.0	35.0		1			1
13	2 - 4	23.7	25.0	157.55	87.39	110.0	35.0	8	2	2		12
13	2 - 11	23.7	27.1	415.22	65.29	110.0	35.0					0
13	2 - 12	23.7	15.2	298.00	76.81	110.0	35.0					0
13	2 - 13	23.7	12.6	209.96	78.42	110.0	35.0					0
13	11 - 11	25.0	27.1	561.35	71.34	110.0	35.0					0
13	11 - 12	25.0	15.2	449.17	82.27	110.0	35.0					0
13	11 - 13	25.0	12.6	362.50	84.51	110.0	35.0					0
13	11 - 12	27.1	15.2	255.12	19.73	110.0	35.0	12	2			14
13	11 - 13	27.1	12.6	274.56	38.45	110.0	35.0	3				3
13	12 - 13	15.2	12.6	88.32	72.99	110.0	35.0					0

APPENDIX G

Simulation Output from Program SIMROT2

PLOT OF SIMULATION RUN 1
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 300.0
 initial DBH 21.59
 effective rooting depth 80.0

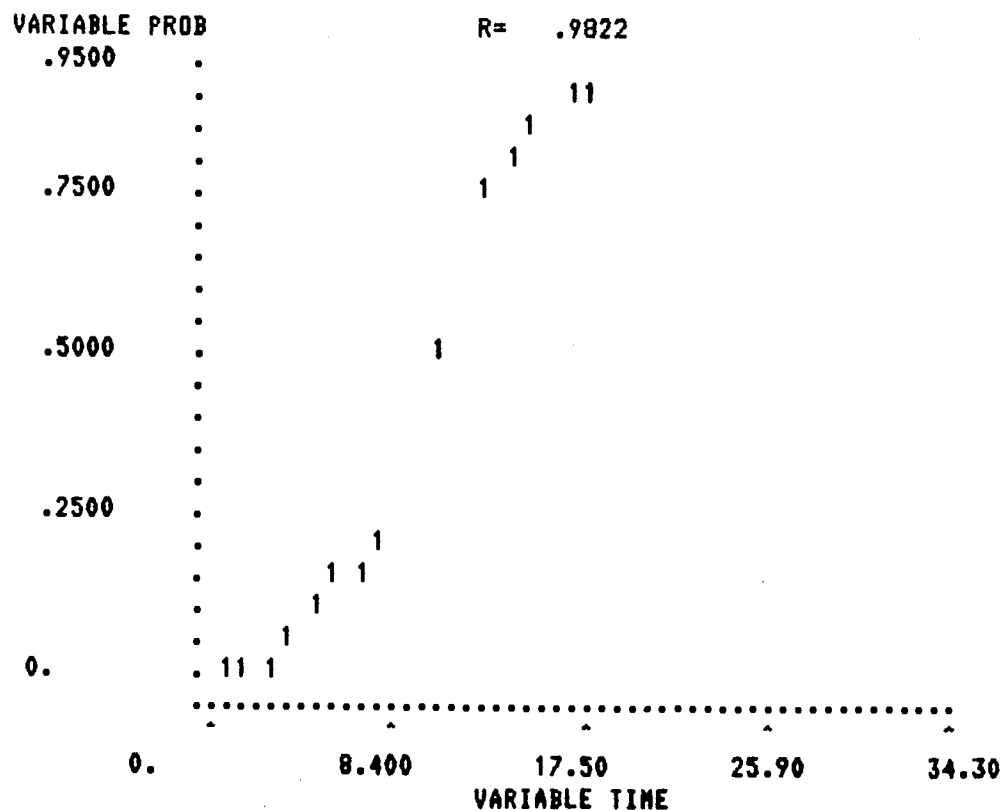


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
10	.0200	.0200
11	.0400	.0200
13	.1000	.0600
14	.1600	.0600
15	.2200	.0600
17	.2600	.0400
19	.2800	.0200
20	.3000	.0200
21	.6200	.3200
22	.7800	.1600
23	.8800	.1000
24	.9000	.0200
25	.9400	.0400
26	1.0000	.0600

PLOT OF SIMULATION RUN 2
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 300.0
 initial DBH 21.59
 effective rooting depth 100.0

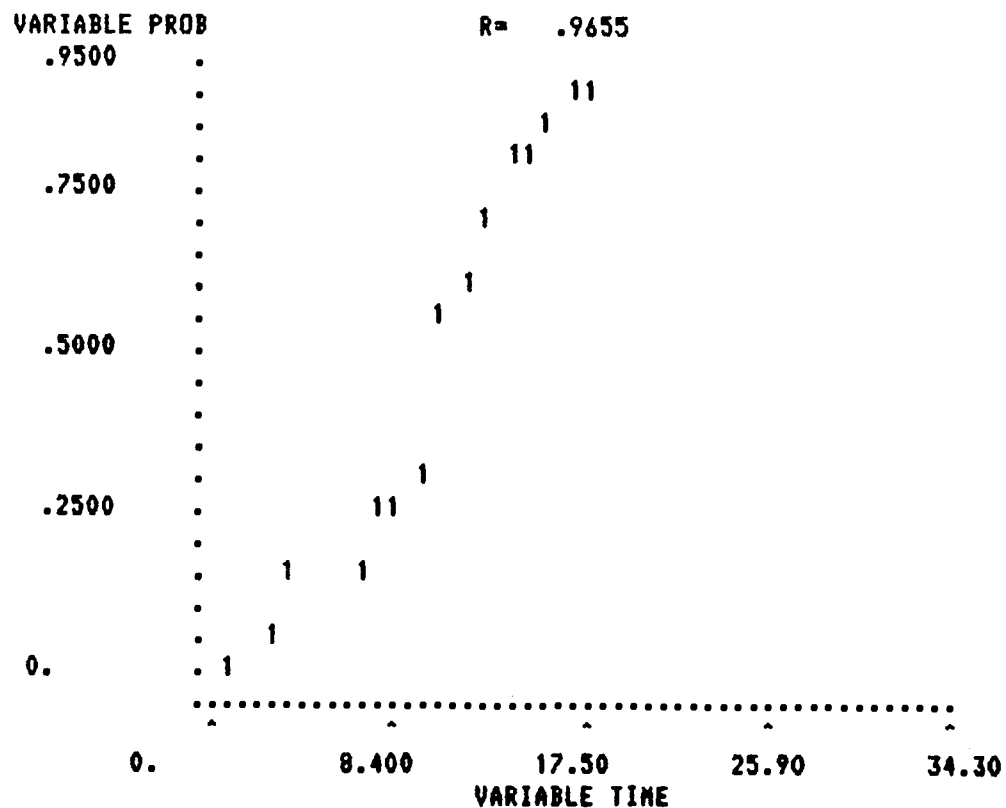


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
12	.0200	.0200
13	.0400	.0200
14	.0600	.0200
15	.1200	.0600
16	.1600	.0400
17	.1200	.0200
18	.2400	.0600
21	.5400	.3100
22		.1700
23	.7600	.0600
24	.8200	.0600
25	.8600	.0400
27	.9000	.0400
28	.9400	.0400

? SCATTER,1,(0.0,35.0),2,(0.0,0.0)
 PLOT OF SIMULATION RUN 3
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 300.0
 initial DBH 21.59
 effective rooting depth 120.0



Cumulative Distribution and Density of
Earliest Time to Bole Infection

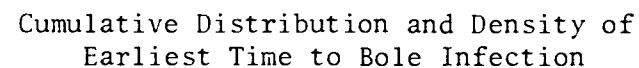
Time	CDF	Density
11	.0400	.0400
13	.0800	.0400
14	.1600	.0800
17	.1800	.0200
18	.2600	.0800
19	.2800	.0200
20	.3000	.0200
21	.5600	.0700
22	.6400	.0800
23	.7200	.0800
24	.8000	.0800
25	.8200	.0200
26	.8800	.0600
27	.9000	.0200
28	.9400	.0400

```

PLOT OF SIMULATION RUN 4
? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
LOWER BOUND OF X= 0.
UPPER BOUND OF X= 35.0000
LOWER BOUND OF Y= 0.
UPPER BOUND OF Y= 1.00000

```

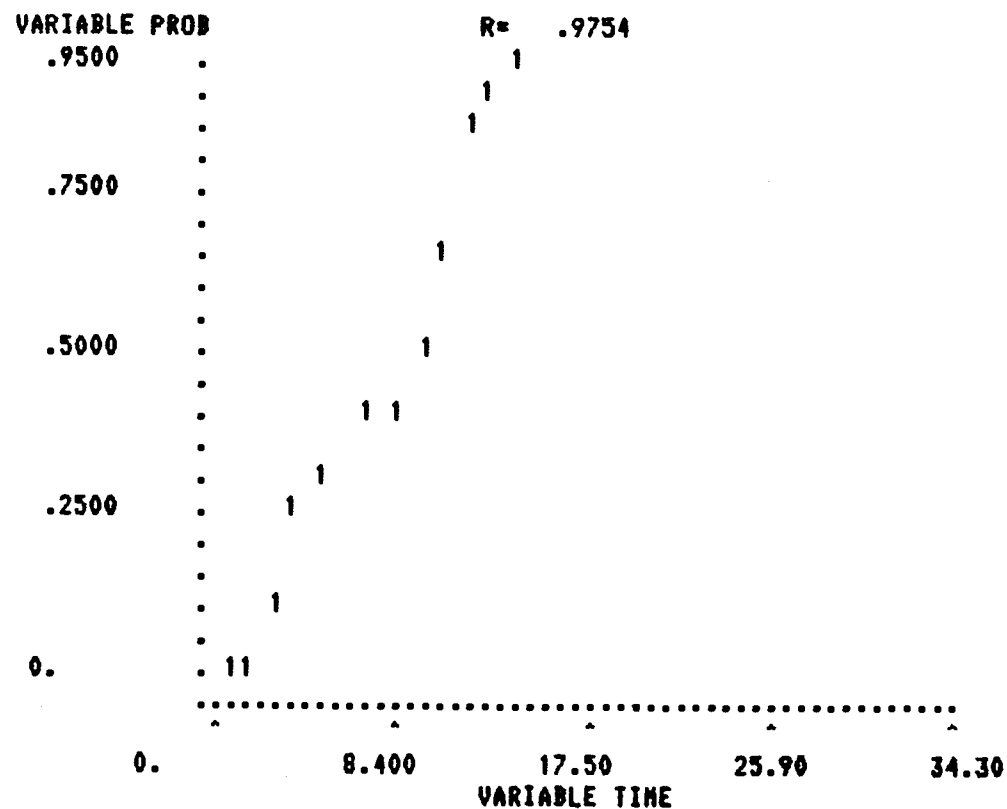
inter-tree distance	300.0
initial DBH	32.36
effective rooting depth	80.0



Time	CDF	Density
11	.0400	.0400
12	.1000	.0600
13	.2400	.1400
14	.3600	.1200
15	.4000	.0400
16	.4600	.0600
17	.5600	.1000
18	.6200	.0600
19	.6400	.0200
20	.6800	.0400
21	.8800	.2000
22	.9400	.0600
23	1.0000	.0600

PLOT OF SIMULATION RUN 5
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 300.0
 initial DBH 32.36
 effective rooting depth 100.0

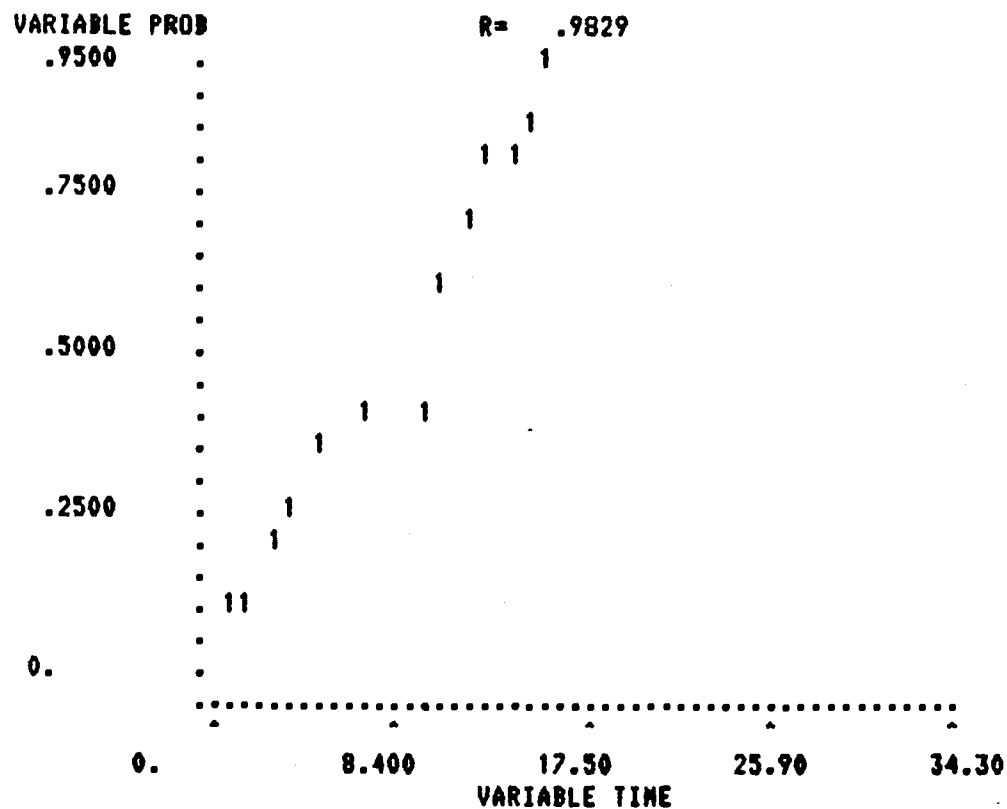


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
11	.0200	.0200
12	.0400	.0200
13	.1200	.0800
14	.2600	.1400
15	.3400	.0800
17	.4000	.0600
19	.4400	.0400
20	.5000	.0600
21	.6800	.1800
22	.8600	.1800
23	.9400	.0800
24	.9800	.0400

PLOT OF SIMULATION RUN 6
 ? SCATTER,1,(0.0,35.0),2,(0.0,1,0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 300.0
 initial DBH 32.36
 effective rooting depth 120.0

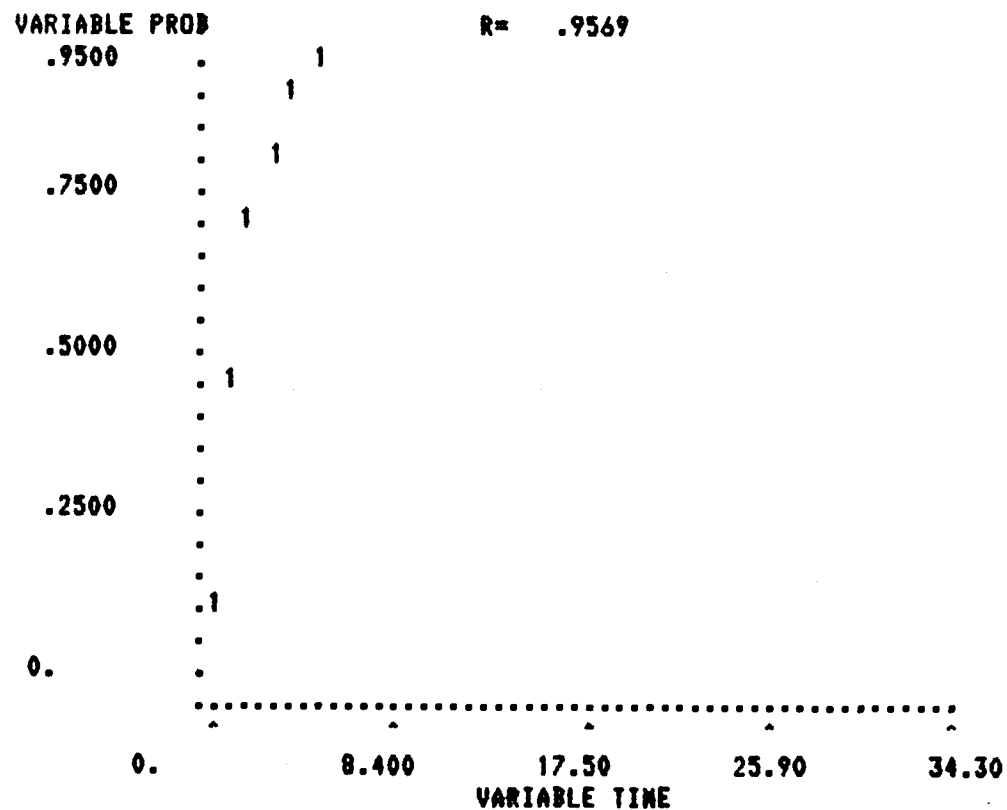


Cumulative Distribution and Density of
Earliest Time to Bole Infection

Time	CDF	Density
10	.1000	.0200
11	.	.0800
12	.1400	.0400
13	.2400	.1000
14	.2800	.0400
15	.3600	.0800
17	.4200	.0600
20	.4400	.0200
21	.6000	.1600
22	.7400	.1400
23	.8200	.0800
24	.8400	.0200
25	.8800	.0400
26	.9600	.0800

PLOT OF SIMULATION RUN 7
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 300.0
 initial DBH 46.23
 effective rooting depth 80.0

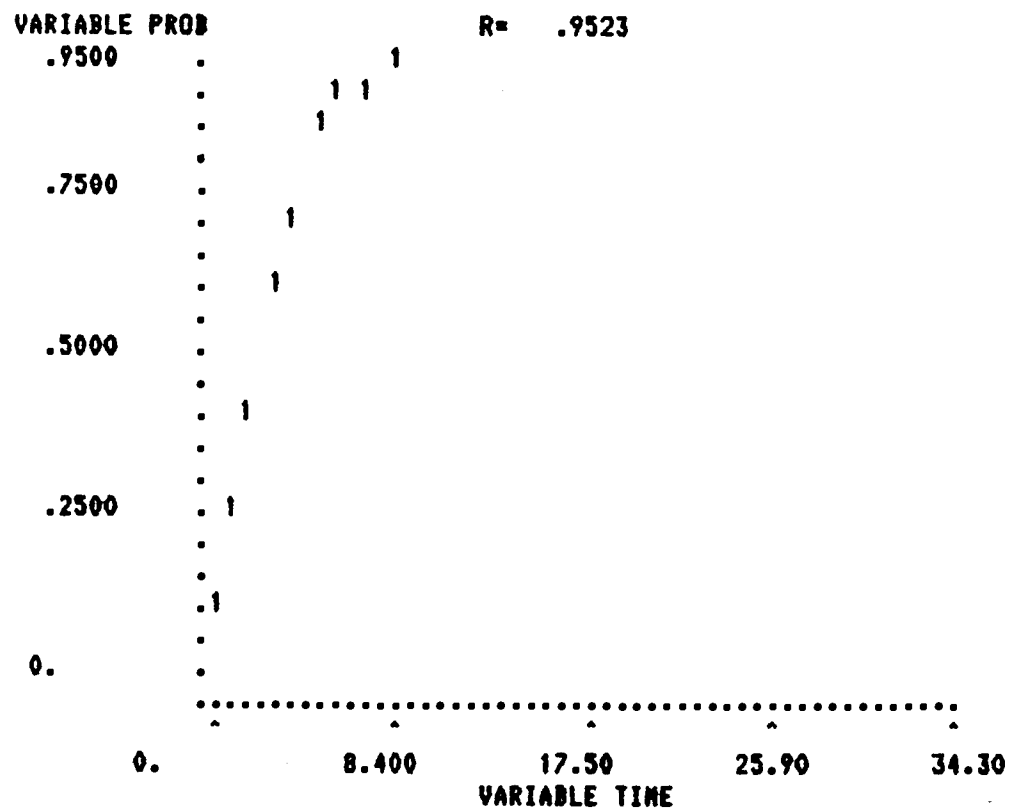


Cumulative Distribution and Density of
Earliest Time to Bole Infection

Time	CDF	Density
10	.1200	.1200
11	.4600	.3400
12	.7000	.2400
13	.8400	.1400
14	.9400	.1000
15	1.0000	.0600

PLOT OF SIMULATION RUN 8
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 300.0
 initial DBH 46.23
 effective rooting depth 100.0

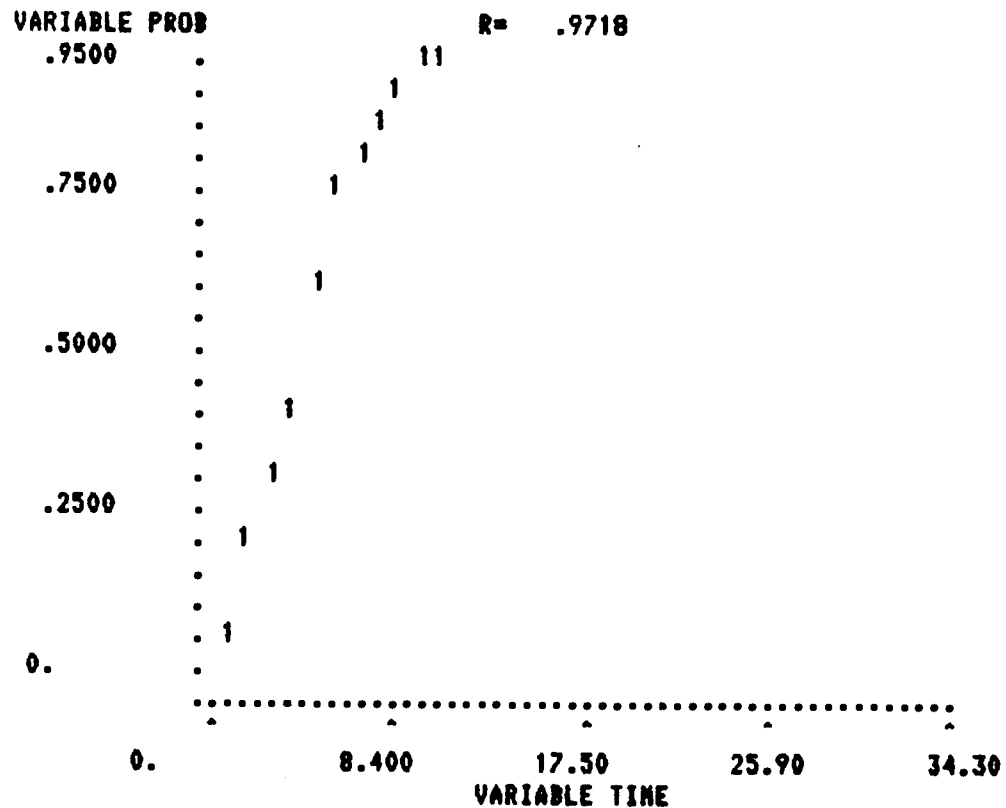


Cumulative Distribution and Density of
Earliest Time to Bole Infection

Time	CDF	Density
9	.0200	.0200
10	.1400	.1200
11	.2800	.1400
12	.4200	.1400
13	.6200	.2000
14	.7400	.1200
15	.8800	.1400
16	.9000	.0200
17	.9400	.0400
19	1.0000	.0600

PLOT OF SIMULATION RUN 9
 ? SCATTER,1,(0.0,35.0),2,(0.0,1,0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 300.0
 initial DBH 46.23
 effective rooting depth 120.0

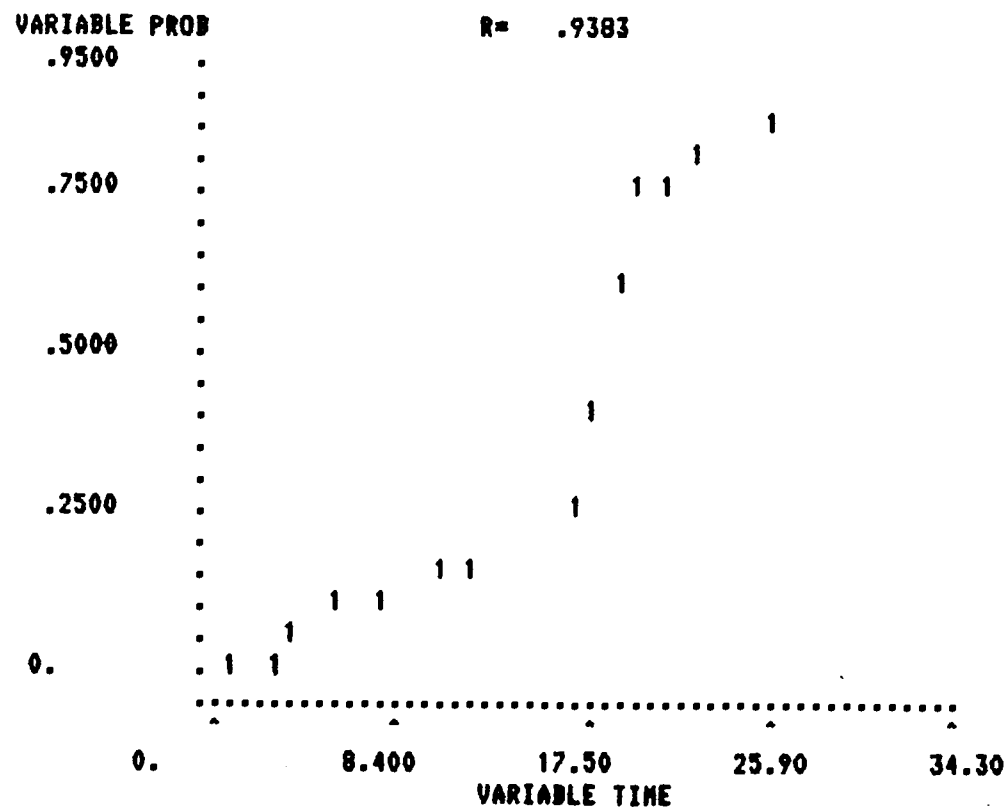


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
11	.0800	.0800
12	.2400	.1600
13	.3200	.0800
14	.4400	.1200
15	.6200	.1800
16	.7800	.1600
17	.8000	.0200
18	.8800	.0800
19	.9400	.0600
20	.9600	.0200
21	1.0000	.0400

PLOT OF SIMULATION RUN 10
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 400.0
 initial DBH 21.59
 effective rooting depth 80.0

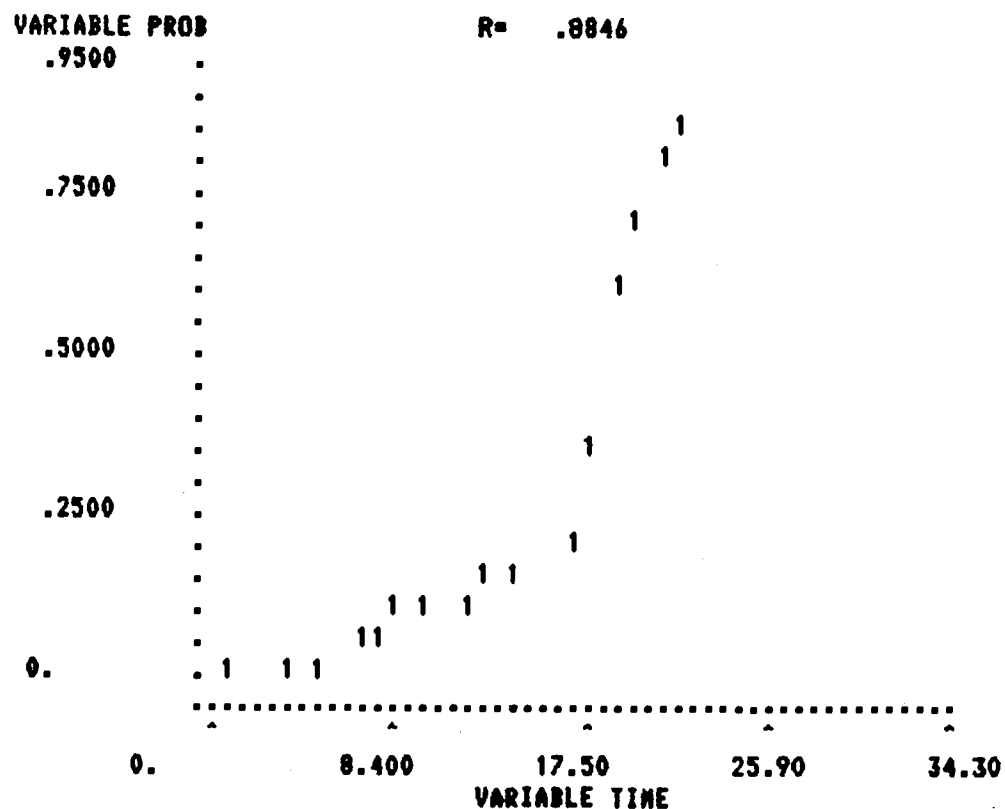


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
13	.0200	.0200
14	.0800	.0600
16	.1000	.0200
18	.1200	.0200
21	.1600	.0400
22	.1800	.0200
27	.2800	.1000
28	.4000	.1200
29	.6200	.2200
30	.7600	.1400
31	.7800	.0200
33	.8200	.0400
36	.8600	.0400

PLOT OF SIMULATION RUN 11
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 400.0
 initial DBH 21.59
 effective rooting depth 100.0

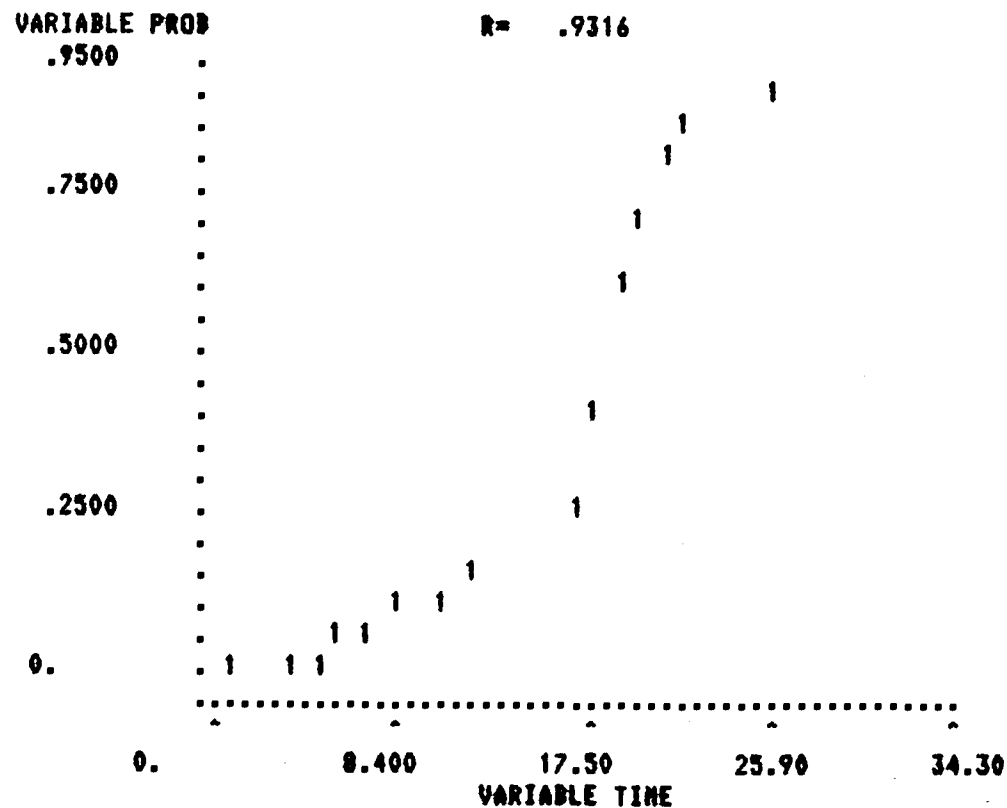


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
14	.0200	.0200
15	.0400	.0200
17	.0600	.0200
18	.0800	.0200
19	.1000	.0200
20	.1200	.0200
22	.1400	.0200
23	.1600	.0200
24	.1800	.0200
27	.2000	.0200
28	.3800	.1800
29	.6400	.2600
30	.7200	.0800
31	.8000	.0800
32	.8600	.0600

? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 PLOT OF SIMULATION RUN 12
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 400.0
 initial DBH 21.59
 effective rooting depth 120.0

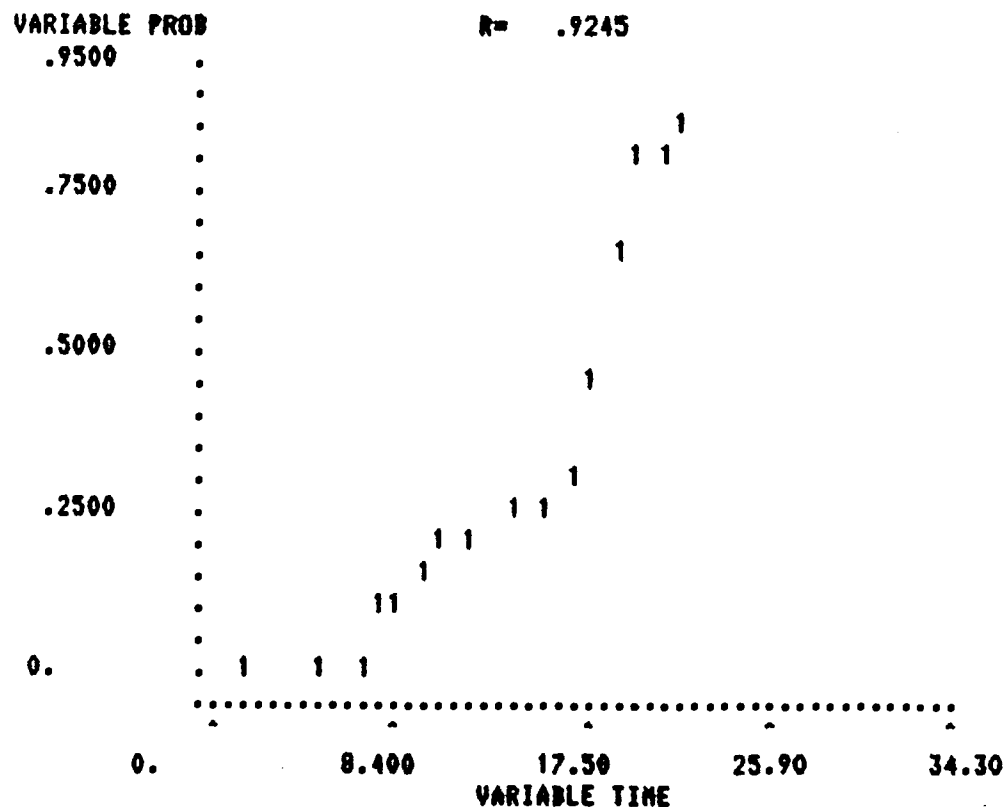


Cumulative Distribution and Density of Earliest Time to Bole Infection

Time	CDF	Density
14	.0200	.0200
15	.0400	.0200
16	.0600	.0200
17	.0800	.0200
19	.1000	.0200
21	.1200	.0200
22	.1600	.0400
27	.2600	.1000
28	.4000	.1400
29	.6400	.2400
30	.7400	.1000
31	.8400	.1000
32	.8800	.0400
36	.9000	.0200

? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 PLOT OF SIMULATION RUN 13
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 400.0
 initial DBH 32.36
 effective rooting depth 80.0

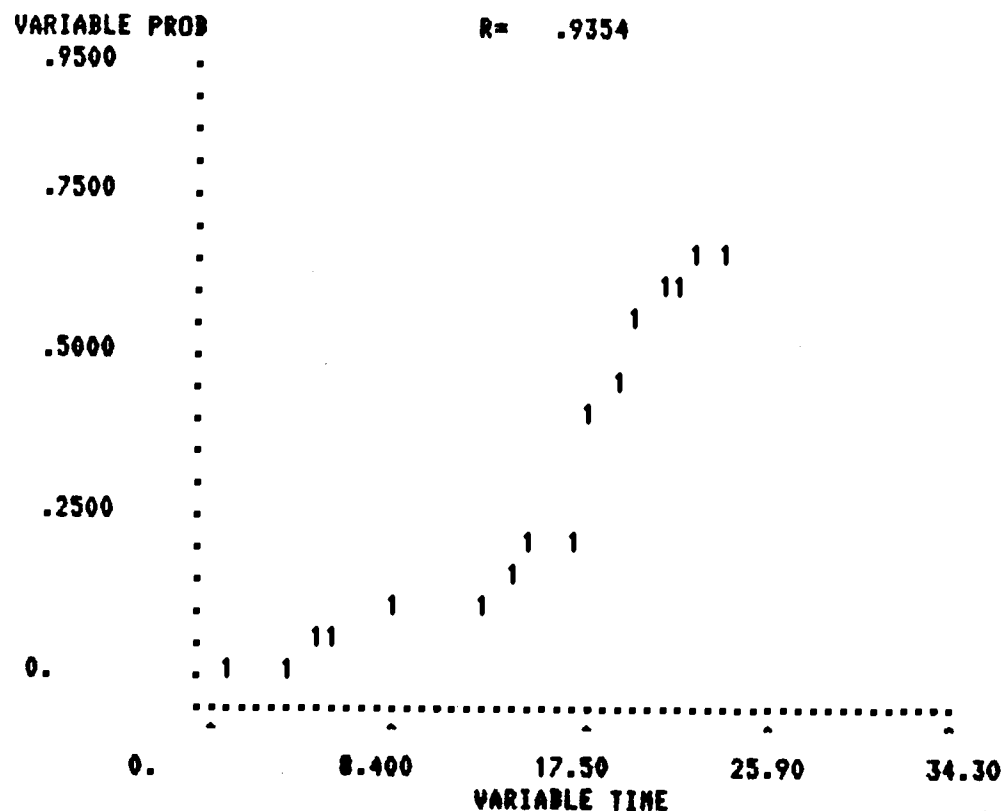


Cumulative Distribution and Density of Earliest Time to Bole Infection

Time	CDF	Density
15	.0200	.0200
17	.0400	.0200
18	.1200	.0800
19	.1400	.0200
20	.1800	.0400
21	.2000	.0200
22	.2200	.0200
24	.2600	.0400
26	.2800	.0200
27	.3200	.0400
28	.4800	.1600
29	.6600	.1800
30	.8000	.1400
31	.8400	.0400
32	.8800	.0400
34	.9000	.0200

PLOT OF SIMULATION RUN 14
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 400.0
 initial DBH 32.36
 effective rooting depth 100.0

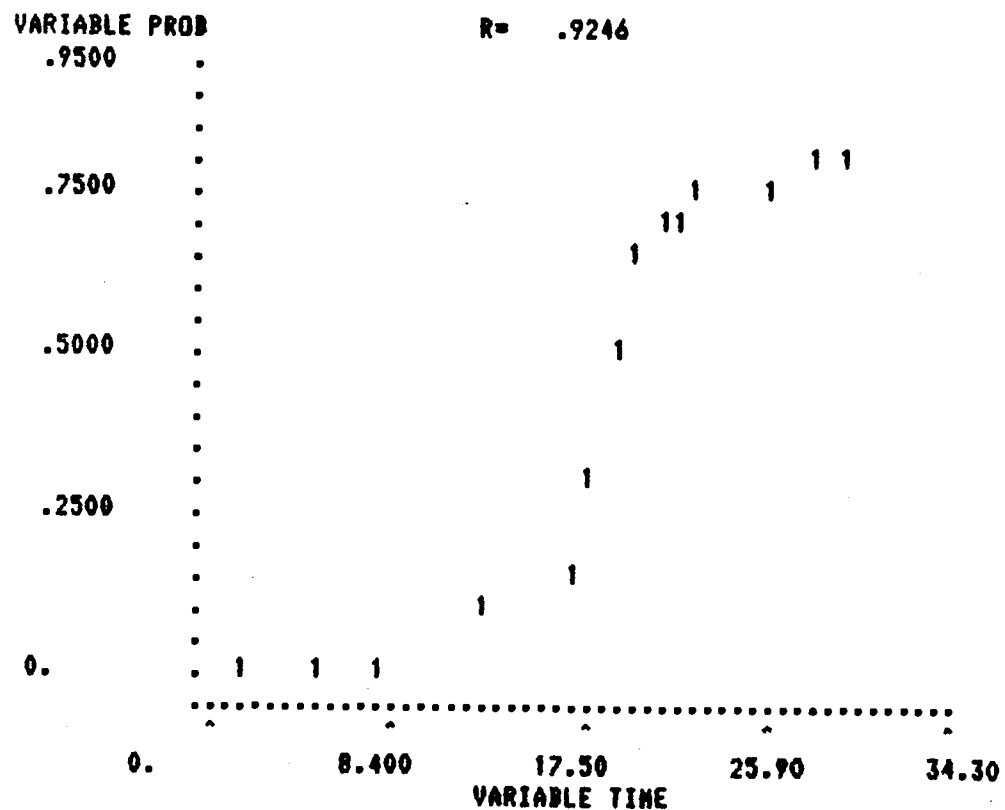


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
14	.0200	.0200
15	.0600	.0400
16	.0800	.0200
19	.1000	.0200
23	.1400	.0400
24	.1800	.0400
25	.2200	.0400
27	.2400	.0200
28	.4000	.1600
29	.4800	.0800
30	.5800	.1000
31	.6200	.0400
32	.6400	.0200
33	.6600	.0200
34	.6800	.0200
36	.7400	.0600

PLOT OF SIMULATION RUN 15
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 400.0
 initial DBH 32.36
 effective rooting depth 120.0

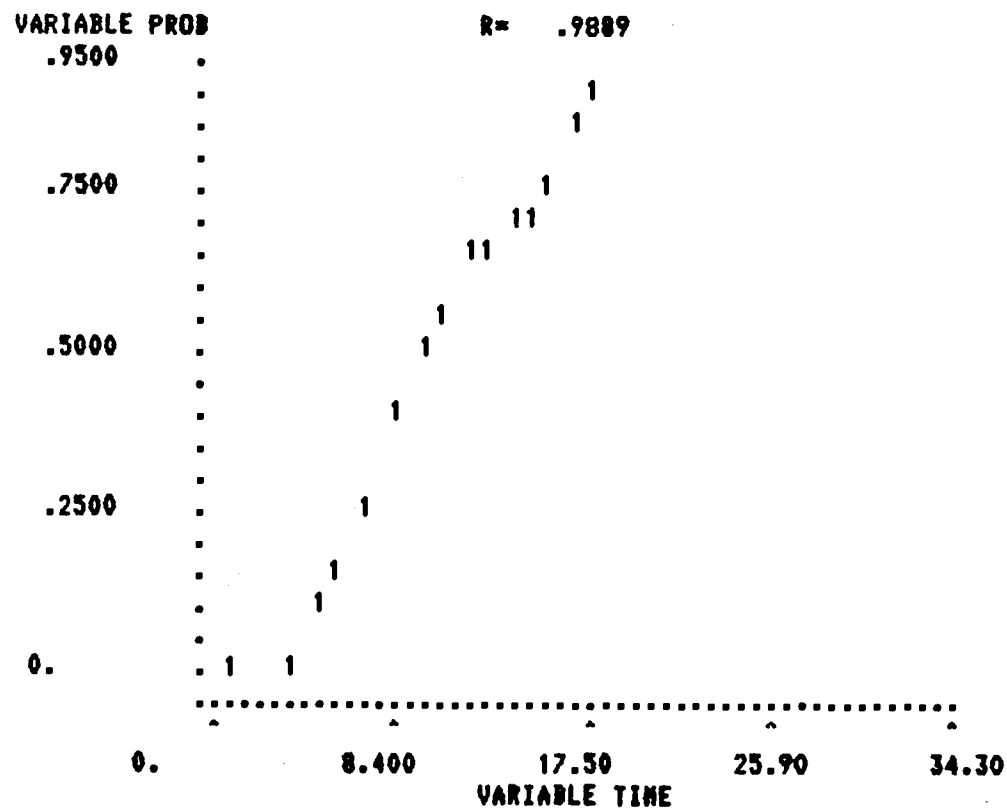


Cumulative Distribution and Density of
Earliest Time to Bole Infection

Time	CDF	Density
15	.0200	.0200
18	.0400	.0200
23	.1000	.0600
27	.1600	.0600
28	.3400	.1800
29	.5200	.1800
30	.6600	.1400
31	.7000	.0400
32	.7400	.0400
33	.7600	.0200
36	.7800	.0200
38	.8000	.0200
40	.8200	.0200

PLOT OF SIMULATION RUN 16
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 400.0
 initial DBH 46.23
 effective rooting depth 80.0

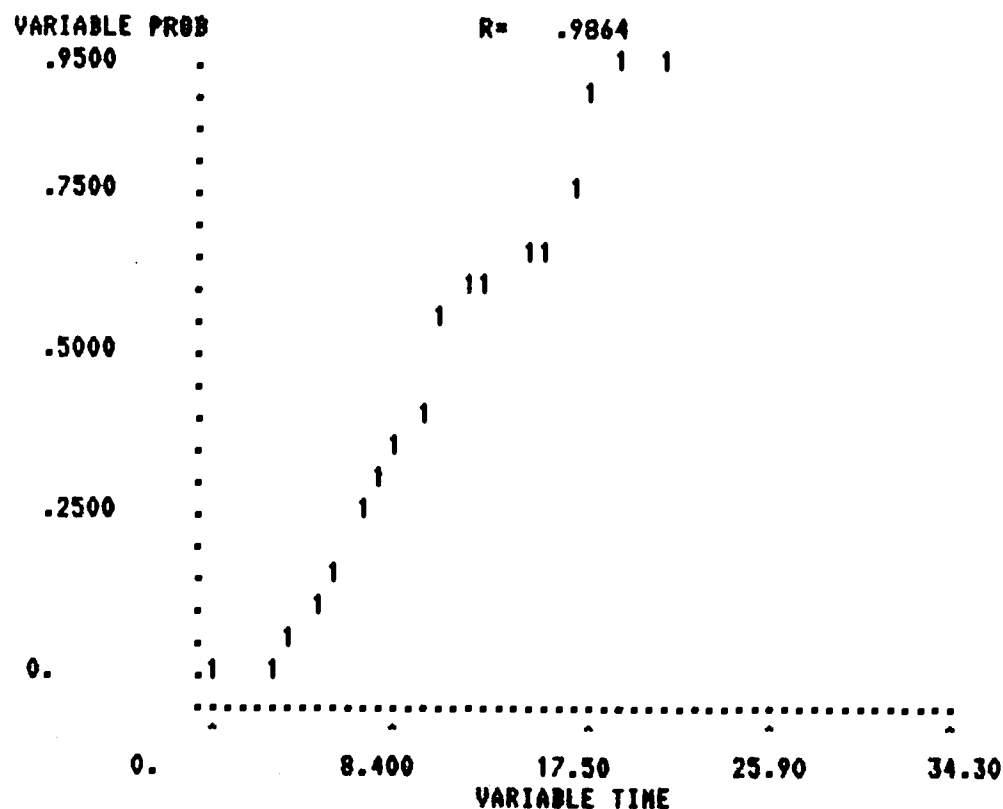


Cumulative Distribution and Density of
Earliest Time to Bole Infection

Time	CDF	Density
14	.0400	.0400
15	.1200	.0800
16	.1600	.0400
17	.2600	.1000
18	.3200	.0600
19	.4000	.0800
20	.5000	.1000
21	.5600	.0600
22	.6600	.1000
23	.6800	.0200
24	.7000	.0200
25	.7200	.0200
26	.7800	.0600
27	.8600	.0800
28	.9400	.0800
29	1.0000	.0600

PLOT OF SIMULATION RUN 17
 ? SCATTER,1,(0.0,35.0),2,(0.0,1,0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 400.0
 initial DBH 46.23
 effective rooting depth 100.0

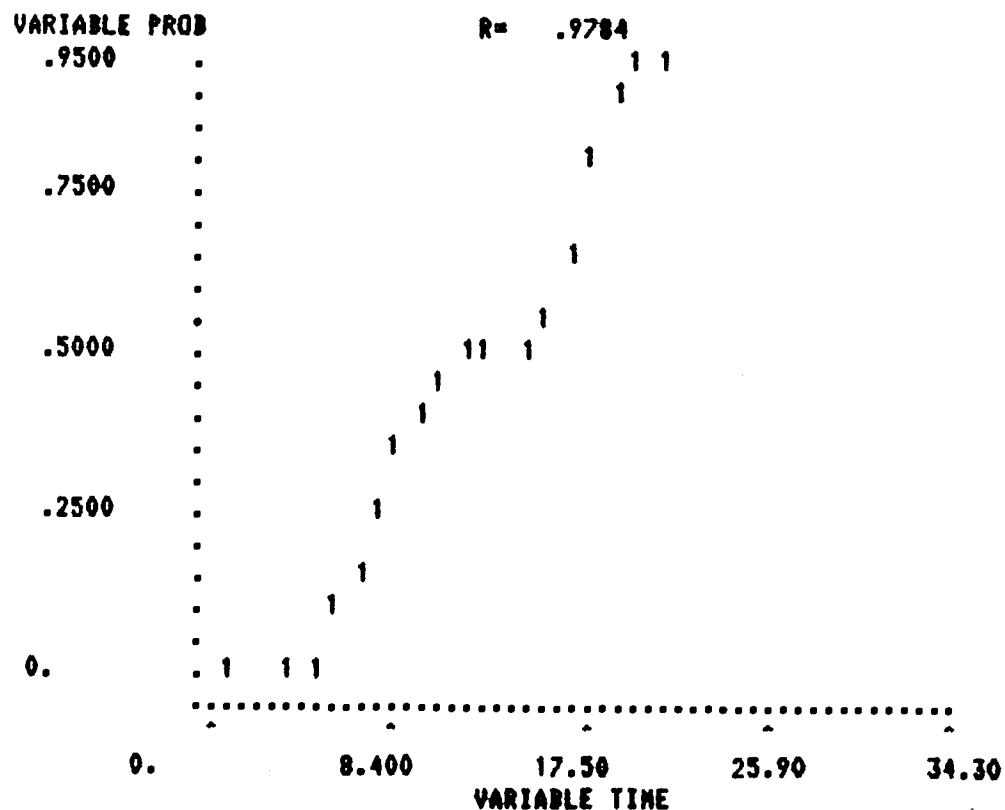


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
13	.0200	.0200
14	.0600	.0400
15	.1000	.0400
16	.1600	.0600
17	.2600	.1000
18	.3400	.0800
19	.3800	.0400
20	.4400	.0600
21	.5600	.1200
22	.6000	.0400
23	.6400	.0400
25	.6600	.0200
26	.6800	.0200
27	.7600	.0800
28	.9000	.1400
29	.9800	.0800
31	1.0000	.0200

PLOT OF SIMULATION RUN 18
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 400.0
 initial DBH 46.23
 effective rooting depth 120.0

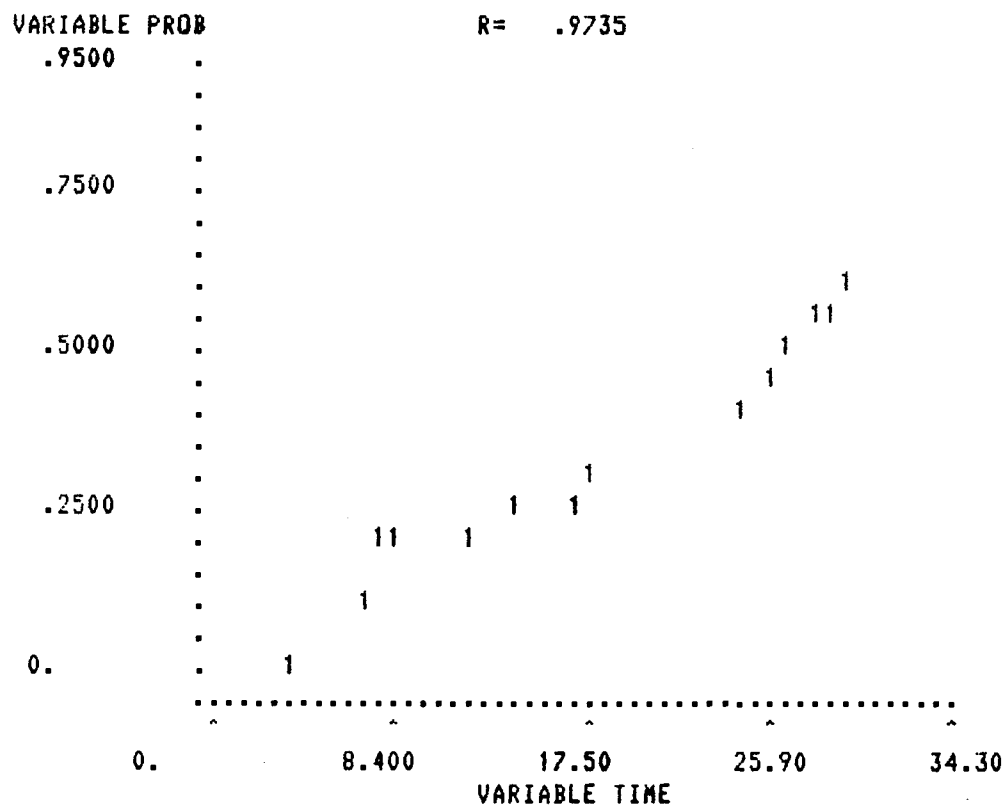


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
14	.0200	.0200
15	.0400	.0200
16	.1000	.0600
17	.1600	.0600
18	.2600	.1000
19	.3600	.1000
20	.4200	.0600
21	.4600	.0400
22	.5000	.0400
23	.5200	.0200
25	.5400	.0200
26	.5600	.0200
27	.6600	.1000
28	.8000	.1400
29	.9400	.1400
30	.9800	.0400
31	1.0000	.0200

PLOT OF SIMULATION RUN19
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 500.0
 initial DBH 21.59
 effective rooting depth 80.0

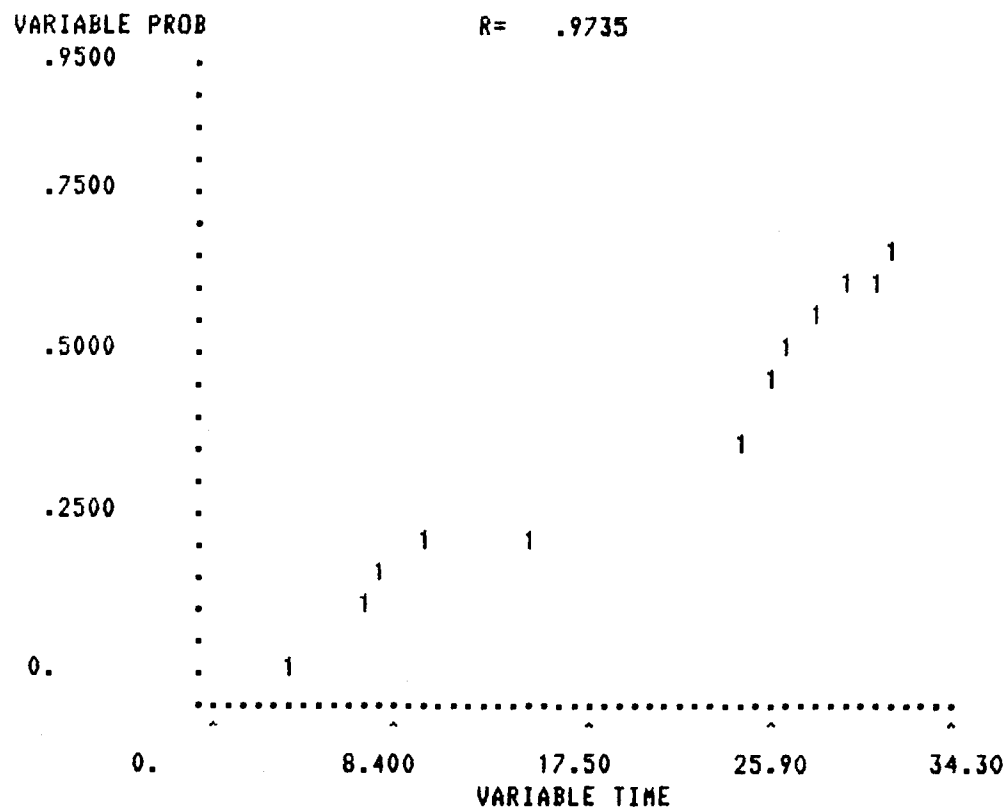


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
17	.1000	.1000
18	.2000	.1000
19	.2200	.0200
22	.2400	.0200
24	.2600	.0200
27	.2800	.0200
28	.3000	.0200
35	.4000	.1000
36	.4800	.0800
37	.5000	.0200
38	.5600	.0600
39	.5800	.0200
40	.6200	.0400

PLOT OF SIMULATION RUN 20
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 500.0
 initial DBH 21.59
 effective rooting depth 100.0

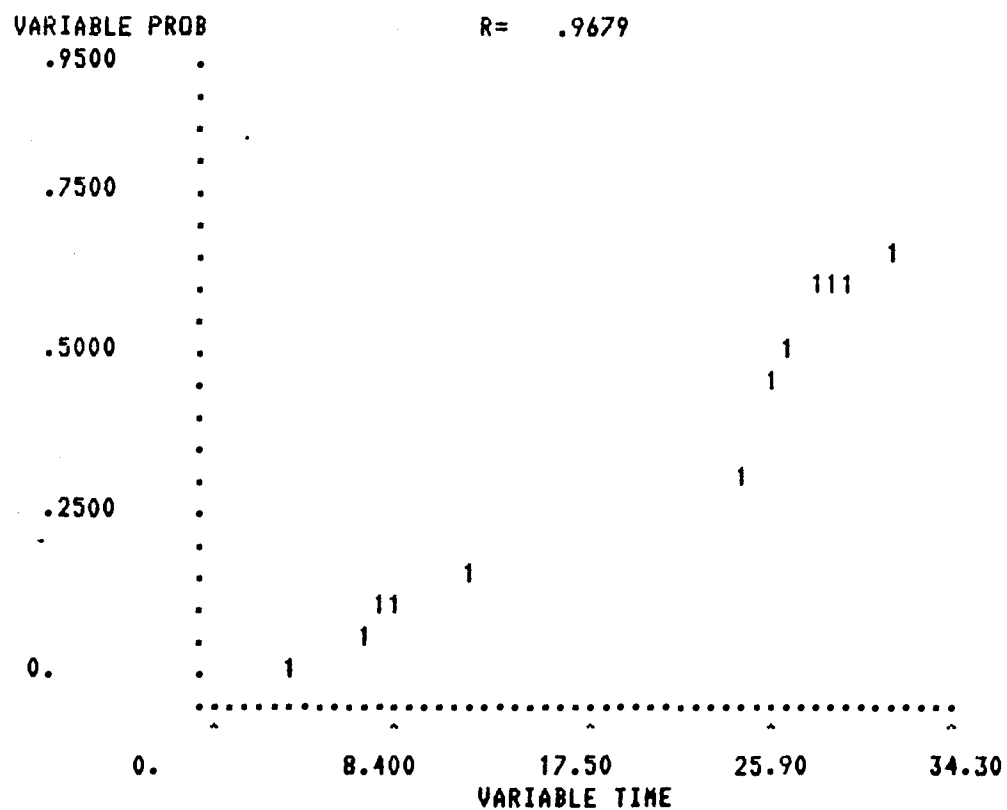


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
17	.1400	.1400
18	.1800	.0400
20	.2000	.0200
25	.2200	.0200
35	.3600	.1400
36	.4600	.1000
37	.5400	.0800
38	.5800	.0400
40	.6000	.0200
41	.6200	.0200
42	.6600	.0400

PLOT OF SIMULATION RUN 21
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 500.0
 initial DBH 21.59
 effective rooting depth 120.0

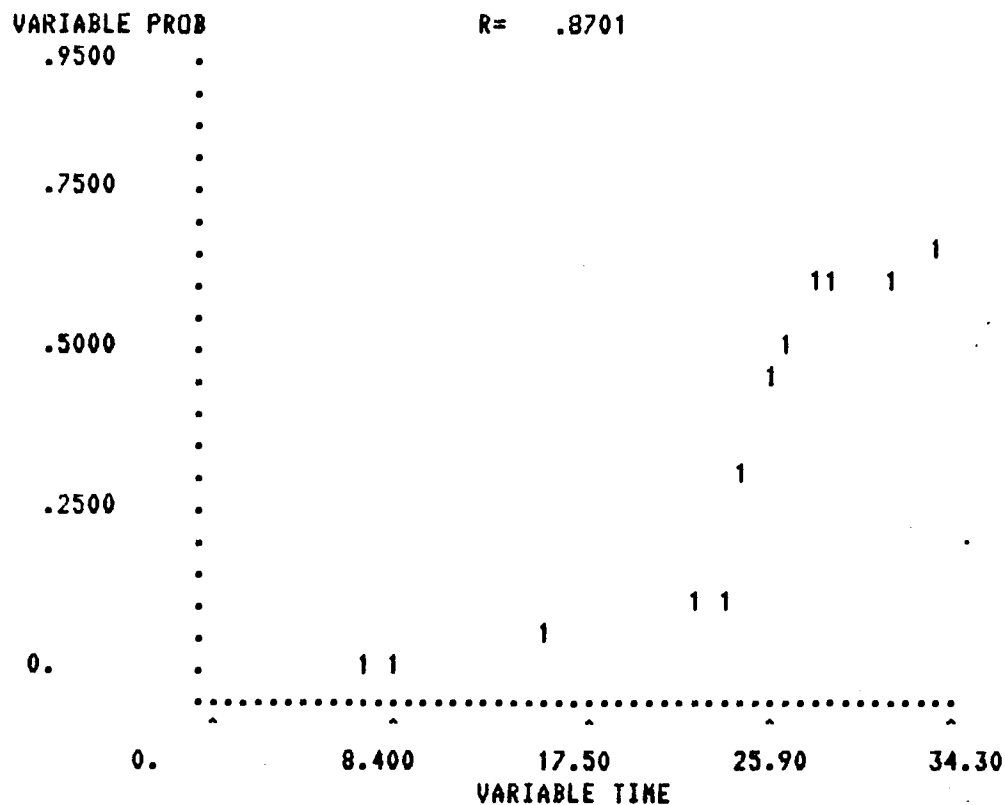


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
17	.0600	.0600
18	.1200	.0600
19	.1400	.0200
22	.1600	.0200
35	.3000	.1400
36	.4600	.1600
37	.5200	.0600
38	.6000	.0800
39	.6200	.0200
40	.6400	.0200
42	.6800	.0400

PLOT OF SIMULATION RUN 22
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 500.0
 initial DBH 32.36
 effective rooting depth 80.0

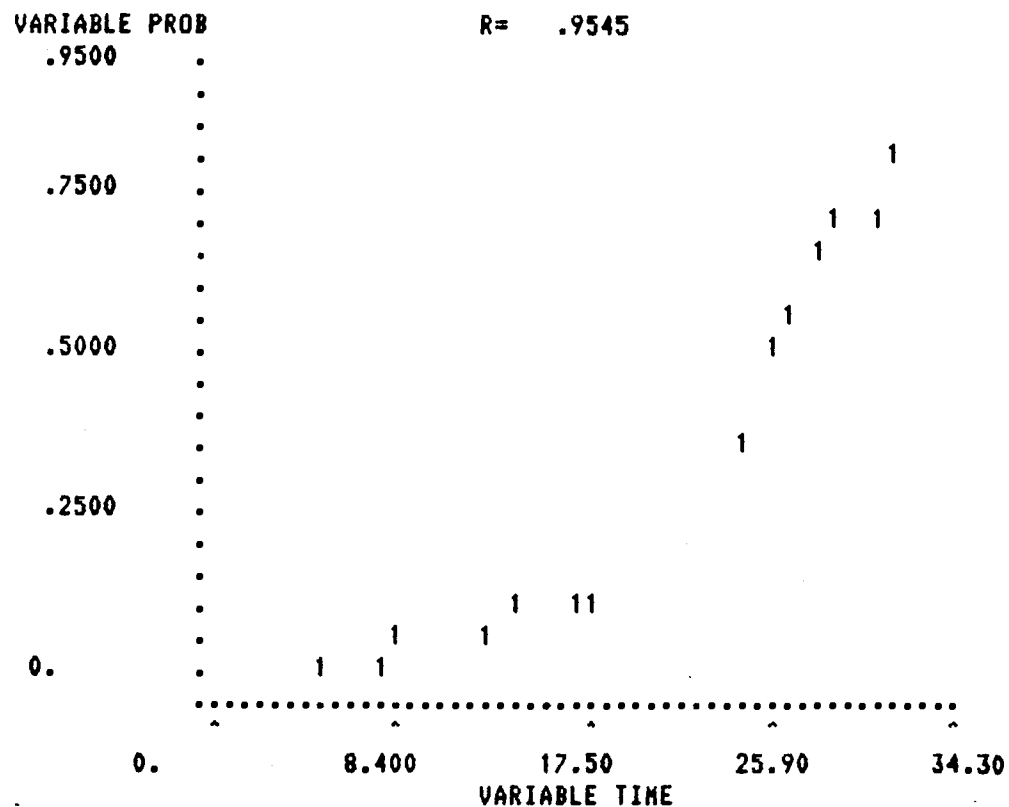


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
19	.0400	.0400
26	.0600	.0200
33	.1000	.0400
34	.1200	.0200
35	.3200	.2000
36	.4600	.1400
37	.5400	.0800
38	.6000	.0600
39	.6200	.0200
42	.6400	.0200
44	.6600	.0200

PLOT OF SIMULATION RUN 23
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 500.0
 initial DBH 32.36
 effective rooting depth 100.0

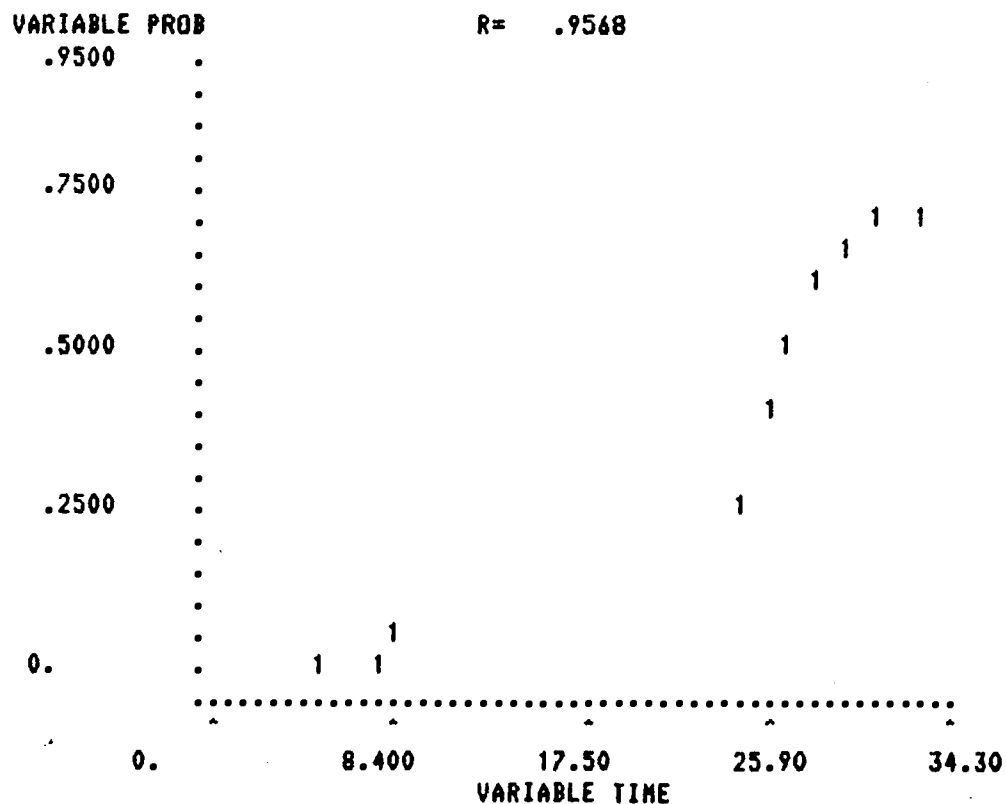


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
18	.0200	.0200
19	.0600	.0400
23	.0800	.0200
24	.1000	.0200
27	.1200	.0200
28	.1400	.0200
35	.3600	.2200
36	.5000	.1400
37	.5600	.0600
38	.6800	.1200
39	.7000	.0200
41	.7400	.0400
42	.8000	.0600

PLOT OF SIMULATION RUN 24
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 500.0
 initial DBH 32.36
 effective rooting depth 120.0

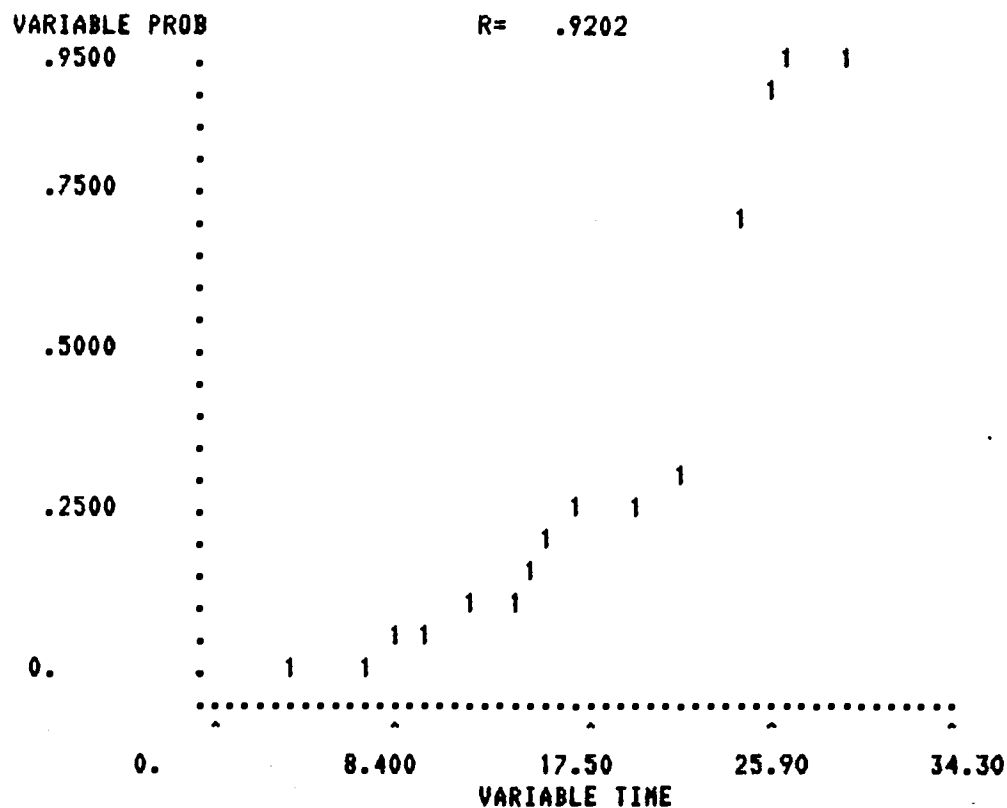


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
18	.0200	.0200
19	.0600	.0400
35	.2800	.2200
36	.4200	.1400
37	.5200	.1000
38	.6400	.1200
40	.6800	.0400
41	.7000	.0200
43	.7200	.0200

PLOT OF SIMULATION RUN 25
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 500.0
 initial DBH 46.23
 effective rooting depth 80.0

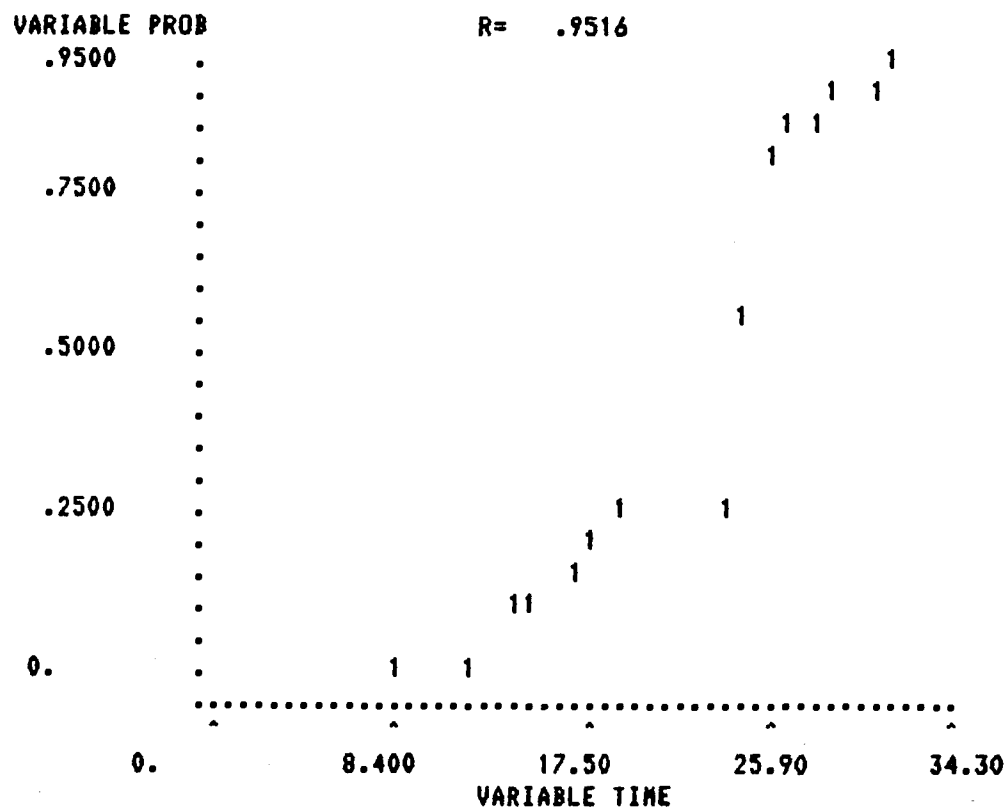


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
17	.0200	.0200
19	.0600	.0400
20	.0800	.0200
22	.1000	.0200
24	.1200	.0200
25	.1800	.0600
26	.2200	.0400
27	.2600	.0400
30	.2800	.0200
32	.3000	.0200
35	.7400	.4400
36	.9200	.1800
37	.9800	.0600
40	1.0000	.0200

PLOT OF SIMULATION RUN 26
 ? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 500.0
 initial DBH 46.23
 effective rooting depth 100.0

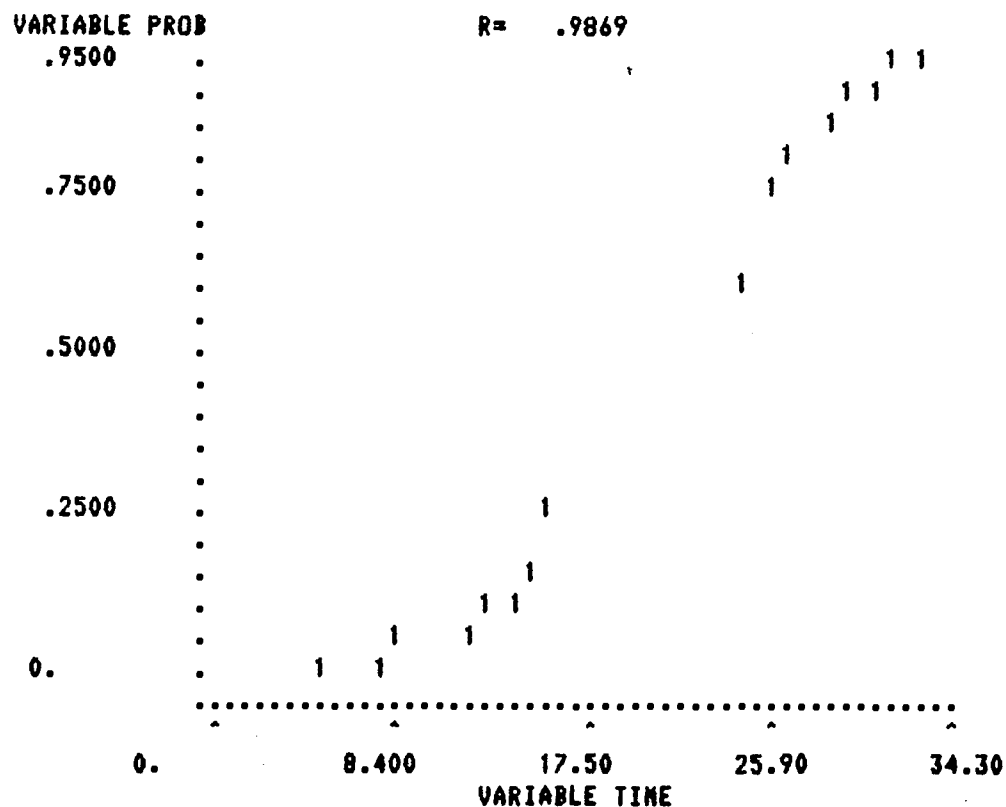


Cumulative Distribution and Density of
 Earliest Time to Bole Infection

Time	CDF	Density
22	.0400	.0400
24	.1200	.0800
25	.1400	.0200
27	.1800	.0400
28	.2000	.0200
29	.2600	.0600
34	.2800	.0200
35	.5600	.2800
36	.8000	.2400
37	.8600	.0600
38	.8800	.0200
39	.9200	.0400
41	.9400	.0200
42	1.0000	.0600

? SCATTER,1,(0.0,35.0),2,(0.0,1.0)
 PLOT OF SIMULATION RUN 27
 LOWER BOUND OF X= 0.
 UPPER BOUND OF X= 35.0000
 LOWER BOUND OF Y= 0.
 UPPER BOUND OF Y= 1.00000

INITIAL CONDITIONS:
 inter-tree distance 500.0
 initial DBH 46.23
 effective rooting depth 120.0



Cumulative Distribution and Density of
Earliest Time to Bole Function

Time	CDF	Density
18	.0400	.0400
19	.0600	.0200
22	.0800	.0200
23	.1200	.0400
24	.1400	.0200
25	.1800	.0400
26	.2800	.1000
35	.6400	.3600
36	.7600	.1200
37	.8400	.0800
39	.8800	.0400
40	.9200	.0400
41	.9400	.0200
42	.9600	.0200
43	.9800	.0200