PINOGRAM

A Pine Growth Area Model

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Proefschrift
ter verkrijging van de graad van
doctor in de landbouw- en milieuwetenschappen,
op gezag van de rector magnificus,
dr. H.C. van der Plas,
in het openbaar te verdedigen
op dinsdag 12 mei 1992
des namiddags te vier uur in de Aula
van de Landbouwuniversiteit te Wageningen.

1. De door de EG gehanteerde procedure om vele instellingen een projectvoorstel te laten schrijven, waarbij er bij voorbaat slechts enkele voorstellen gehonoreerd zullen worden, levert een enorme verspilling van tijd en geld.

2. Een gecompliceerd langdurig proces kan slechts succesvol onderzocht worden indien het wordt opgesplitst in deelprocessen, waarvan de samenhang duidelijk is weergegeven in een lange termijnplan voor onderzoek aan dit proces.

3. Het uitvoeren van een lange termijn plan als bovengenoemd dient zo min mogelijk afhankelijk te zijn van personen.

4. De kwaliteit van een universitaire vakgroep mag niet afhankelijk gesteld worden van het aantal door de betreffende vakgroep afgeleverde afgestudeerden resp. gepromoveerden.

5. Het komt het onderzoek niet ten goede als ervaren onderzoeksmedewerkers te snel worden vervangen door onervaren onderzoeksmedewerkers, zoals nu, na het invoeren van het AIO-stelsel, de tendens is.

6. Het creëren van nieuwe begrippen maakt meer stellingen mogelijk.

7. De indeling van groeifactoren in factoren die de groei fundamenteel beinvloeden ("normale groei") en factoren die de groei "toevallig" beïnvloeden is van essentieel belang voor groeimodellen (dit proefschrift).

8. De schatting van de hoogte van een boom met behulp van slechts de diameter (Loetsch, Zöhrer and Haller, 1973) is in zijn algemeenheid zeer onnauwkeurig en in principe onjuist.

9. Indien de kroonbreedte / boomhoogte verhouding van een boom voortvloeit uit de standruimte van deze boom, geeft deze verhouding een eenvoudige en doeltreffende maat voor de kans op sterfte van deze boom (dit proefschrift).

10. De bosbouwinstellingen in Nederland vertonen sterke overeenkomsten met bomen groeiend in dichte stand op een arme groeiplaats.

11. Geboortebeperking als middel om luchtvervuiling, broeikaseffect en bedreiging van het voortbestaan van soorten en natuurgebieden in de toekomst te verminderen, krijgt op het niveau van de landelijke politiek vaak te weinig aandacht.

12. De belangrijkste stelling is de aanstelling.

Woord vooraf

De voormalige vakgroep Bosteelt en Bosoecologie, welke nu is opgegaan in de vakgroep Bosbouw, stelde zich onder meer ten doel de kennis over groei en dynamiek van individuele bomen uit te breiden en toegankelijker te maken. Oldeman, Gremmen en Goudzwaard (1985) gaven een voorzet hiertoe in de vorm van teeltdiagrammen. Mijn opdracht in 1987 was het ontwikkelen van teeltdiagrammen afhankelijk van groeiplaats, herkomst en behandeling voor groveden.

Aangezien er in principe oneindig veel teeltdiagrammen gemaakt konden worden, heb ik in eerste instantie gezocht naar de invloed die leeftijd, groeiplaats, herkomst en behandelingswijze konden hebben op het boomuiterlijk. Al snel bleek dat invloeden van herkomst en groeiplaats op de groei van bomen niet eenvoudig uit elkaar te houden waren. Ir. C.P. van Goor heeft mij toen gewezen op een oude herkomstproef in Kootwijk (hfdst. 2.3), waarin de invloed van de herkomst op de groei van bomen duidelijk was te zien. Van deze herkomstproef waren een aantal belangrijke meetgegevens bekend (e.g. van Soest 1952). Deze meetgegevens heb ik gebruikt om een indruk te krijgen van de relaties tussen verschillende boomdimensies en opstandsdichtheid en de invloed van de herkomst hierop. Renaat van Rompaey wees mij op de mogelijkheid het spreadsheet programma LOTUS 123 te gebruiken voor deze correlatieberekeningen, wat mijn interesse voor het gebruik van computers heeft aangewakkerd. De gevonden correlaties moedigden aan om de invloed van de standruimte op een individuele boom nader te onderzoeken aan de hand van veldopnames. Bij de veldopnames werd ik vaak geholpen door Dela Boeijink, Leo Goudzwaard en Albert Zweers en tijdelijk door de stagaires Maria Della Chiesa, Zoltàn Mihàlyi en Kari Tuomela.

Na analyse van de verzamelde data bleken er goede correlaties te bestaan tussen verschillende boomdimensies, standruimte en leeftijd van de bomen. Om de effecten van de standruimte op de boomdimensies zichtbaar te maken besloot ik een grafisch simulatiemodel te ontwikkelen. De eerste versie was twee dimensionaal (alleen profieldiagram) en werd gemaakt in LOTUS 123. Jan Oudkerk heeft mij toen echter attent gemaakt op de mogelijkheden en de snelheid van de programmeertaal "C". Bovendien heeft hij me de beginselen van de taal bijgebracht en heeft hij mij ook later in raad en daad bijgestaan bij het ontwikkelen van het programma.

Bij het schrijven van het proefschrift werd ik vooral bijgestaan door prof. R.A.A. Oldeman, Pieter Schmidt, Jelle Hiemstra, Henk Koop, Hans Jansen en dr.ir. A.R.P. Janse. Mrs. Burrough-Boenish heeft het proefschrift op engels gecorrigeerd.

Bovengenoemde personen hebben rechtstreeks bijgedragen aan de tot stand koming van dit proefschrift en hebben daarvoor mijn hartelijke dank. Mijn beide paranimfen Jelle Hiemstra en Luc Koks wil ik vooral bedanken voor hun morele steun. Tenslotte bedank ik allen die hebben bijgedragen aan een prettige werksfeer en mij steeds hebben gestimuleerd bij het ontwikkelen van het model en het schrijven van dit proefschrift.

The PINOGRAM computer program is available on diskette at the Department of Forestry, WAU, the Netherlands. The price is $ 25.-.

CONTENTS

SYMBOLS

$\bar{a}$	mean *normal growth area vector (m)
$\bar{A}$	mean distance between stems (m)
A	distance between *sample tree and neighbouring tree (m)
a_act[k]	*actual growth area vector in one of sixteen directions (m)
a_max[i]	*maximum growth area vector in the direction of neighbour i, also *a_max[nr][i]*
a_max[k]	*maximum growth area vector in one of sixteen directions (m)
a_pot[i]	*potential growth area vector in the direction of neighbour i, also *a_pot[nr][i]*
a_pot[k]	*potential growth area vector in one of sixteen directions (m)
angle[i]	angle between the vector in direction of neighbour i and the 'North'(rad)
area	*normal growth area (m^2)
a[i]	*normal growth area vector in the direction of neighbour i (m)
C	competition constant ()
c.v.	coefficient of variation (%)
canopy_closure	sum of crown projection areas divided by the *transect area (%)
cl	crown length (m)
$\overline{cl}$	mean crown length of observed trees (m)
$\overline{cl}_{pre}$	predicted mean crown length (m)
$\overline{cw}$	mean crown width (m)
cw	crown width in one direction (m)
$\bar{d}$	mean stem diameter on breast height (cm)
dbh	stem diameter on breast height (cm)
dbranch	mean branch diameter in the lower part of the crown of a tree (cm)
d_g	diameter derived from mean basal area per tree (cm)
d_{gpre}	predicted diameter d_g (cm)
dist_transect[k]	distance from *sample tree to *transect border in direction $k*\pi/8$ (m)
$\bar{f}$	mean form factor ()
f	form factor of a tree $v/(g*h)$ ()
f_g	form factor derived from $V/(G*\bar{h})$ ()
f_{gpre}	predicted form factor f_g ()
g	basal area of a tree (m^2)
G	basal area ($m^2.ha^{-1}$)
$\bar{h}$	mean height of trees (m/ha)
h_{dom}	*dominant height of trees (m)
h_g	height of a tree of which dbh = dg (m)
i	range number of a neighbouring tree ()
k	fixed direction number (1-16; 17 is equal to one) ()
l	tree length (m)
n	number of *sample trees ()
N	number of stems per ha (ha^{-1})
nr	range number of *sample tree ()
r_max	*maximum distance of influence of a tree (m)
R^2	correlation ()
Random	a random value ()
r[i]	distance between *sample tree and *S[i]* (m)

SYMBOLS (continued)

S_{tree}	*S value for a tree (m)
Smax	maximum given *S value (m)
Smin	minimum given *S value (m)
S[i]	intersection of perpendiculars of vector *a[i]* and vector *a[i+1]* ()
t	age (year)
tree_xco	x coordinate of stem of tree (m)
tree_yco	y coordinate of stem of tree (m)
u	eccentricity in a normal distribution ()
v	stem volume of a tree (m^3)
V	volume of stems per ha ($m^3.ha^{-1}$)
V_{pre}	predicted volume V (m^3)
xco[k]	x coordinate of crown projection limit in direction $k*\pi/8$ (m)
x[i]	angle between vector *a[nr][i]* and vector *r[i]* (rad)
yco[k]	y coordinate of crown projection limit in direction $k*\pi/8$ (m)
y[i]	angle between vector *a[nr][i+1]* and vector *r[i]* (rad)
z[i]	angle between vector *a[nr][i]* and vector *a[nr][i+1]* (rad)

1 INTRODUCTION

1.1 Problem analysis

Views on forest and forestry have changed in recent years in the Netherlands as a result of an increasing demand for nature and recreation, and because of growing environmental problems (air pollution, global warming) and the declining forest area in the world. This has led to a change in the government's forest policy (Anonymus 1985, 1986, 1990). This new policy is intended to achieve a more natural-looking forest (uneven aged, mixed, native species), and forest management that is linked to natural processes and which, while cheaper, has more benefits. The long-term National Forest Plan (Anonymus 1986) intends to classify Dutch forest into forest domains, each of which will have a specific *target type of forest[1]. The target type of forest that is assigned to a forest domain depends upon the site's suitability for tree species, the present-day composition of the forest domain, and silvicultural and financial constraints.

As described in the long-term National Forest Plan (Anonymus 1986) the concept of a "target type of forest" suggests that a more or less static tree species composition and *forest architecture can be realized and maintained. Since forest, site and society change over time, a forest can never maintain all characteristics of its target type.

After a target type of forest has been chosen (Firet et al. 1985, Anonymus 1986, Paasman 1988), the question arises how and within what period it can be realized. In other words: how, by means of human interference, can natural processes be manipulated to help to achieve the target type of forest (see also Buiting 1989). This manipulation demands sound knowledge about the *autoecology and *synecology of trees; that is, knowledge about prerequisites for establishment and growth potential of a tree under influence of different abiotic and biotic factors such as soil, climate, forest architecture, community and disturbances.

In mixed forests an infinite number of *forest situations are possible. A forest situation is defined here as a snapshot of an area of forest with all its properties, comparable with the *phenotype of an individual (see section 2.2). Each forest situation has its own effects on the growth potential of trees. It is impossible to predict *growth of trees exactly for all these forest situations. So we need to restrict our investigations to those species, sites and site factors that are the most important for forestry. The long term National Forest Plan does give species combinations in the target types of forest and relates these target types of forest to site history. This is a first restriction to the number of potential combinations

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[1] A term preceded by an asterisk indicates that it can be found in the glossary.

of species and sites that could be investigated, but there are still many potential combinations left.

Nowadays computers can be used to calculate relations found between tree characteristics and factors influencing tree growth. Sometimes the relations found are similar for different tree species or different sites, but the order of magnitude may vary. Using interactive *models to simulate these relations may help to reduce the numbers of combinations of tree compositions and sites that have to be investigated to predict *growth for a wide range of possible combinations (cf. the model PINOGRAM; see section 1.3).

Since 1985 the Department of Silviculture and Forest Ecology at Wageningen Agricultural University has been studying the *growth and development of individual trees of three species: Douglas fir (*Pseudotsuga menziesii* Mirbel), beech (*Fagus sylvatica* spp.) and Scots pine (*Pinus sylvestris* L.). The research described in this book aimed to develop silvicultural information diagrams (= "teeltdiagram" cf. Oldeman et al. 1985a) for Scots pine, for different sites, provenances and treatments (tree history). These diagrams give information on characteristics such as tree architecture, crown form and crown dimensions, stem form, stem diameter and stem volume, and the likelihood and consequences of flowering and fructification, disease and damage at different developmental stages of a tree representative for a stand.

In principle, an infinite number of silvicultural information diagrams is possible (Oldeman 1985b p.199). Therefore the influence of age, site, provenance and treatment on the *phenotype of a tree has to be determined in order to be able to develop silvicultural information diagrams. If these relations are known, a silvicultural information diagram can be obtained by developing an interactive *model, in which data on age, site, provenance and treatment can be entered by the user. The model should depend on tree history and age, and therefore it was decided to develop a *growth model.

1.2 Growth models

Many *growth models have been developed at different spatial and temporal scales. The factors steering growth models also differ. A distinction is made between mathematical models (cf. Carvalho Oliveira 1980, Faber 1983, McFadden and Oliver 1988, Barreto 1988abc, Koop 1989, Delisle 1989), physiological models (cf. De Wit 1978, Bormann and Likens 1979, Goudriaan 1979, Hari et al. 1985, Mohren 1987) and architectural models (cf. Edelin 1977, Kellomäki and Oker-Blom 1983, Aono and Kunii 1984, Ross et al. 1986, Kuuluvainen et al. 1988, De Reffye et al. 1989, Roloff 1989, Oldeman 1990). The distinction between a physiological model, a mathematical model or an architectural model is not always very clear in the case of "growth and development models". However, a certain model may mainly deal with physiology or *architecture or a mathematical artefact such as density or *growing space.

Physiological models

Physiological models are often called *explanatory models, because a process is defined by its underlying subprocesses. One of the important parameters for *growth in these models is the primary production (De Wit 1978, Bormann and Likens 1979, Goudriaan 1982, Hari et al. 1985, Mohren 1987). "Primary production in plant canopies is defined as the accumulation of dry matter resulting from assimilation of carbon dioxide by green plants, in which solar radiation is used as the basic source of energy to drive the biochemical processes" (Newbould ex Mohren 1987 p.10). Mohren (1987 p.11) postulates that "ecophysiological aspects of primary production in plant canopies can be grouped into:

- absorption of photosynthetically active radiation by the foliage;
- uptake of carbon dioxide by assimilation through the stomata;
- loss of water vapour to the atmosphere through the open stomata, compensated for by root uptake of soil moisture, and subsequent transport to the foliage;
- maintenance of the living biological structure, thereby consuming assimilation products;
- distribution of the assimilates available for growth over the plant organs, and conversion of assimilation products into structural dry matter, together with incorporation of nutrients in the organic matter;
- nutrient uptake by roots."

Each of the above aspects has been shown to control or influence primary production (Mohren 1987).

If all the underlying processes that influence the primary production are known and can be calculated in a model, this model will be very important for making *growth predictions. But probably not all the underlying processes and their *interactions, that define the primary production of a section of forest can be expressed in numbers. Nevertheless it is often possible to explain a large part of the main process by some of the underlying processes (Mohren 1987).

The more complex a process becomes (the more explanatory variables are involved), the more underlying processes must be computed; these are usually difficult to measure, to calculate and to keep constant.

Many variables are in fact estimates with a mean and a standard deviation, such as the mean day temperature, or the water supply per ha, etc. (cf. Kellomäki and Hari 1980, Kellomäki and Kanninen 1980). A major process is thus explained by its underlying subprocesses, but these are not always very exactly determined. This means a large risk of error accumulation.

The profit of models depends upon their aim. If we wish to ascertain changes in the growth potential of an area of forest as influenced by nitrogen immission, physiological models may be quite useful.

One example of a physiological model is the one developed by Bormann and Likens (1979). This model gives the expected development over a period of several centuries of the northern hardwood ecosystem in the U.S. after clear cutting on the basis of changes in total ecosystem biomass and using a "nutrient flux and cycling model" and the "small watershed technique".

A disadvantage of physiological models is that primary production per hectare cannot very easily be measured by a forest manager; The resources of a research institute are generally needed to do this. Another disadvantage is that *growth predictions by means of pure physiological models reveal little about forest- and/or *tree architecture.

Architectural models

Oldeman (1990) defines architecture as a spatio-temporal *structure linked to a well-defined hierarchical level. Architectural models are principally useful because they describe the structure and relationship of a *forest situation.

Architectural models are not growth models in a strict sense (see section 2.2). Oldeman (1990 p.22) writes: "Architectural models are represented graphically. The great lines can be seen by the trained eye, and a few selected measurements go a long way in establishing or denying the truth of such models. For the same reason they also provide an easy way of communication with practical users, such as silviculturists or forest officers, a communication that depends on the blending and reciprocal translation of empirical and theoretical knowledge".

As the architectural model attains a higher hierarchical level (silvatic-mosaic > eco-unit > organism > organ) computations of all used data become more and more difficult. Separation into hierarchical levels and modelling within these levels is therefore very important (Oldeman 1990, Leersnijder and Boeijink 1990). Research and models, however, do not always move on one level. One step in modelling on a level between "organ" and "organism" has been made by De Reffye et al. (1989), who developed a model to simulate all tree architectural models (Hallé and Oldeman 1970, Edelin 1977, Hallé et al. 1978, Oldeman 1990) and their *reiterations. This model moves between the levels "organ" and "organism", because its output relates to whole tree architecture (level: organism) as well as to the architecture of different organs (level: organ). Differences in branch development are defined by random choices: - whether an internodium will grow; - the angle with the preceding axis, etc. De Reffye et al. (1989) used a probability function for the functioning of the meristems within an imitated environment and within the limits of the architectural model. So the growth of an internodium is not determined by real environmental factors, but at random within the range of possible values, based on many observations.

Aono and Kunii (1984) developed a similar model, using the Lindenmayer system. Important parameters in this model are left and right branching angle, contraction ratios of branch lengths and diameters, divergence angle and growth rate. By using attraction and inhibition points certain environmental factors (level: *eco-unit) influencing tree growth can be simulated. This brings us to a level between "organism" and "eco-unit". Computers are still too weak (not enough memory or too slow) or too expensive for the forestry sector to build in *interactions between all meristems (level: organ) and environment (level: eco-unit). Besides, it is questionable whether such complex models give the information that justifies their expense.

*Transect analysis has been improved in order to clarify the development of forest architecture (level "eco-unit") (Van Dort et al. 1979, Koop 1981, Oldeman et al. 1983, Leersnijder and Boeijink 1990). To date, a transect has been represented by a crown map, a profile diagram and some added numerical data. These transects are often very suitable for reconstructing previous forest development, but they still have little value for predicting future developments.

For transect studies Koop (1989) developed a computer model (SILVI-STAR) that shows these actual transects in a three-dimensional, but more abstract, form. On the basis of stand architecture and the stumps still present, this model can reconstruct the past to some extent by means of regression. Because *competition between trees is derived from diameter increment, no information can be given about crowns that have been grown asymmetrically. Therefore, competition between trees is not taken into account sufficiently in the reconstruction. Because of the enormous quantity of information it supplies, this model is especially useful for *monitoring forest systems. It can also compute irradiation intensity at different places within a stand and can thereby link up with the more physiological models.

Combined physiological and architectural models

In Finland models using *architecture and physiological processes have been developed (Kellomäki et al. 1980, Kellomäki and Hari 1980, Hari et al. 1985, Kellomäki 1986). This was preceded by many tree measurements at different levels ("organ", "organism" and "eco-unit"). Yet these models too are not able to predict changes of individual tree forms under influence of environmental factors at "*eco-unit" level.

Mathematical models

Mathematical ***growth** models describe the variation in time of a phenomenon in a *system (or some derivation from it) at an established hierarchical level and dependent upon certain factors. To do this, measured and weighted variables are compared and subjected to regression analysis (which assumes that the variable of interest is dependent upon one or more mutual independent variables). Then the best fitting statistical regression line is chosen. An equation can be derived from this line: its validity is restricted to the range in which the variables are measured.

Examples of mathematical growth models ("eco-unit" level) include *yield tables, which reveal the mean wood production, mean diameter and mean height of a closed even-aged *pure stand at certain age. Yield tables generally do not explain competitive relations between trees. Also they do not give any information on *forest architecture and they do not give yield data of open stands. However, the *growth area model developed by Faber (Faber 1983, 1986) enables *social position and the increment of height, diameter and volume to be calculated (see also section 3.2.2).

Hara (1988) gives an overview of models that describe "dynamics of size structure in plant populations" ("organism" and "eco-unit" level). He distinguishes "spatial models that require information about the position of each plant in a space, and non spatial models that do not require such information. The spatial models are further divided into distance models and domain models. Directly or indirectly, these dynamic models take into account *interactions between neighbouring plants (neighbourhood effects). In distance models, the *growth of the subject plant is determined as a function of the distances from the neighbours, the sizes, number and angular dispersion of the neighbouring plants" (Hara 1988 p.130).

In domain models each plant in a space has a circular domain, called the "zone of influence (ZOI)", correlated with its size. A plant whose ZOI overlaps with those of its neighbours has a growth rate derived from the potential growth rate according to the overlapped area of ZOIs. In nonspatial models plant sizes are assumed to be randomly distributed over a space at each growing stage, and any sub-space has the same size distribution pattern. Thus the averaged neighbourhood effects are considered (Hara 1988).

Combined physiological and mathematical models

Examples of combined physiological and mathematical *growth models are those of the JABOWA family (Botkin in West et al. 1981 p.39): "Briefly the assumptions used in the JABOWA model include the following. An individual tree of each species has an optimal or maximal growth curve, specific to that species and relating growth rate to size. This rate of growth is directly proportional to the amount of photosynthates that can be produced by the leaf tissue of the tree, and is inversely proportional to the amount of photosynthates required for the sustenance of existing nonphotosynthetic tissue. The rest of the photosynthate, according to simple algebraic formulation, goes into the production of new vegetative tissue.

"This optimal growth is decreased by suboptimal conditions of light, temperature, water, or any factor that a user of the model might want to add. The response to light is a monotonic curve, with an additional influence from temperature. Leaf weight is calculated from diameter.

"Each species has certain intrinsic population or life history characteristics, including rates of birth, growth, and death. *Pioneer species produce abundant and widely scattered seeds, grow quickly, and live a short time. Species of old-age forests are characterized by the production of fewer seeds, which germinate in less abundance, and which grow more slowly but live a longer time. With regard to inter- and intraspecific *competition, the primary assumption is that trees compete primarily for light, although some species grow much better in bright light than others, and the ones that grow well in bright light grow poorly in dim light."

The JABOWA models give a general insight into the potential development of an *eco-unit, but certainly are not yet able to predict proportions of individual trees with enough precision. *Growth predictions are the best here on a level between eco-unit and *silvatic-mosaic.

Clearly much work has been done trying to predict growth at different hierarchical levels responding to a different problem. It seems to be a good idea to develop hierarchical models that will fill in the gaps in the models discussed above and will connect the various *growth models with their different hierarchical levels.

1.3 The PINOGRAM growth model

Because a silvicultural information diagram should give the changes in time of the *phenotype of a tree, the model should link the levels of "organism" and *"eco-unit". The phenotype of a tree depends upon its "*normal growth" and also upon favourable and stress factors. "Normal growth" is defined by the genetic characteristics of a tree, by a more or less constant site quality and climate during its lifetime and by *competition for light, water and nutrients. Stress factors may be diseases and plagues, environmental pollution and damage by, for example, temporary climate extremes. Favourable factors may be fertilization, improved soil water supply, immigration of mycorrhizal fungi, etc.

The models present in the current literature are either related to another hierarchical level, or do not deal with crown growth or with the *growing space of individual trees and the *structure of the *eco-unit. Therefore none of them are really appropriate for creating a silvicultural information diagram for the different circumstances required. This is why a new model is needed.

Because crown proportions and stem proportions of individual trees are essential in silvicultural information diagrams the model needs information about *stand architecture more than physiological information. This does not mean that physiological information is less important. Changes in the height growth of trees can probably be better explained with the help of physiological models. In the model presented here the height growth is a black box and other tree characteristics are more or less derived from this height growth. If a physiological mathematical model can be developed in future to predict height growth better in relation to site, genetic traits, micro-climate and atmospheric conditions, that model could probably easily be combined with the PINOGRAM model presented here.

PINOGRAM stands for PINe GRowth Area Model. Its growth predictions are restricted to the "*normal growth". *Competition is understood as competition for qualified space and constraints are not defined (e.g. available light, water or nutrients). One of the most important ways of influencing the growth of a tree is to give it more space by felling neighbouring trees. The model does indeed show large similarities with the "spatial" models and, according to Hara's overview (Hara 1988), can be classified as a "distance model".

PINOGRAM predicts the proportions of each individual tree within an even aged stand at a continuously changing degree of *interaction with neighbours at any given age. Tree coordinates, tree height and crown length and crown width in several directions are calculated and drawn. The prediction of proportions of individual trees in even aged stands may offer a helpful framework for similar predictions for trees in uneven aged- and mixed stands, as described in several *target types of forest (Anonymus 1986).

PINOGRAM does not use data on tree architecture as used in the models of Aono and Kunii (1984), De Reffye et al. (1989), Roloff (1989) or Kunii and Enomoto (1991) and it also does not use data on *silvatic-mosaic (see for example Kessell 1979, who uses the concept, not the term, however). In PINOGRAM the attainable height of a tree is randomly determined within a range entered by the user and can be considered as a result of *interaction between genetic tree characteristics and site properties (see sections 2.2.2, 2.2.3 and 4.6), whereas height growth is calculated with the help of a function that describes the mean height growth of Scots pine in the Netherlands (see section 4.7).

Beneath some architectural data the model also computes classical yield data per ha and per tree, and in this way it is closely related to the many models dealing with these yield data (see section 4.17 and 4.20).

To cope with the multitude of *forest situations already appearing in very simple ecosystems, the model has been made interactive; the user can choose and input site, treatment, age, etc. can be chosen and entered by the user (see sections 4.5, 4.21, 4.23). Chapter 6 describes examples of treatments and the results obtained when using PINOGRAM on Scots pine (*Pinus sylvestris* L.) in pure even-aged stands in the Veluwe area in the Netherlands.

2 BASIC CONCEPTS USED IN THE PINOGRAM MODEL

2.1 Introduction

Section 2.2 gives some background information on *growth of Scots pine and the main factors that influence this growth. In section 2.3 data of an old provenance trial in Kootwijk (Province of Gelderland, the Netherlands) were used in order to test the predictability of the influence of provenance and stem density on mean tree dimensions.

2.2 Growth of Scots pine

2.2.1 Introduction

*Growth may be understood as a process which is steered by growth factors inherent in a certain starting *situation and driving it towards a new situation after some time. The starting situation may be understood as a *system at a certain hierarchical level, built up from subsystems at a lower hierarchical level.

Growth factors such as light, water, chemicals and warmth (Fanta 1985) may affect systems of any hierarchical level more or less directly. In order to explain the correspondence between a system and its steering growth factors, it is often more practical to classify growth factors according to hierarchical levels too, e.g. the factor light at "cell level" could be expressed in Joules per mm^2 per minute and at "organ level" it could be expressed in Joules per cm^2 per day, etc. Oldeman's Rules of Scale (1990 p.560) show that: "If, within a pair of interacting living systems, one system has n times the size or mass of the other, *interaction will occur most probably between the smallest living system and that subsystem of the largest one which is closest to n^{-1} of the size or mass of that largest system". In the same way one could classify growth factors according to the area on which they bring to bear direct influence and according to the duration of that influence. So, determining the influence of light on tree height increment per second is spurious, as is determining the influence of global warming on the growth of a single tree branch.

The higher the hierarchical level of the system, the less exactly the influence of different growth factors can be determined. One may use averages for larger areas or time intervals, adapted to the system's hierarchical level as explained above. One may also use a combination of growth factors as one new aggregated growth factor (super growth factor).

The PINOGRAM model acts on a level between organism and *eco-unit, because the output is expressed in dimensions compatible with eco-units as well as with organisms. The corresponding super growth factors used at this level are:

- *genotype (potential within-tree growth factor) (see section 2.2.2);
- site (potential outside-tree growth factor) (see section 2.2.3);
- *growing space (growth-limiting factor) (see section 2.2.4);

Each of these factors is principally built from a set of underlying factors or subfactors and their *interactions. The subfactors were not relevant in the research described here and they have therefore been left as if they were a black box.

The starting situation is explained by:

- age (years) (see section 2.2.5);
- *phenotype of the trees (architecture) (see section 2.2.6);

These are dimensions (time, space), not biological factors, for the description of the starting situation. However, as seen from a mathematical viewpoint these variables define a certain growth, so they indeed are *mathematical factors.

2.2.2 The genetic traits of a tree.

In the science of genetics two definitions, describing traits of a tree, are important: *genotype and *phenotype. The genotype of an individual describes the complete set of inherited genes, whereas the phenotype represents all aspects of morphology, physiology, behaviour and ecological relations (Suzuki et al. 1989). Trees with identical characteristics do not necessarily belong to the same genotype and trees with different characteristics may in principle belong to the same genotype.

In natural populations a phenotypically continuous distribution is found for many characteristics (e.g. height growth, seed production). This is partly caused by genetic differences within the population and partly by different environmental factors. However, what part of the phenotypical variation is genetically defined and what part is caused by the environment is very difficult to compute and can only be computed when the genotype is known and the mean phenotypical variation between genotypes is smaller than the variation between individuals within that genotype.

The exact genotype of Scots pine in the Netherlands is almost never known at a level below "species". However, sometimes the origin of the seed, the provenance, is known. Here, a provenance is defined as a population of trees within one species, sharing some similar traits, resulting from a lasting selection of that species within one geographic zone. Suzuki et al.(1989) mention "familiality" in this context: traits are "familial" if all members of one family share them (note: this is not a taxonomic family). The same more or less applies to a provenance: traits are provenance traits if all the trees of a species of one defined climatic zone share them. Hence, provenance traits are not by definition heritable. It is possible that trees of different provenances will show similar characteristics, if they are in the same environment.

Within one population the quantitative frequency of specific genotypes can be changed by recombination, immigration of genes and new mutations (Suzuki et al., 1989). Thus a provenance is not static.

In the Netherlands Scots pine shows a large variation of provenances. As early as the 16th century Scots pine seed was imported from abroad (Buis 1985, Tutein Nolthenius 1891, Fanta 1983, Wolterson 1972, Huisman 1983). At the end of the last century and at the beginning of this century large-scale afforestation with Scots pine began, mainly to anchor drifting sand, to use degraded sites, to create employment and to satisfy demand for pit props.

Seed of unknown provenance and genetically undesired quality has often been used for this afforestation (Huisman 1983, Kriek 1983). Since 1926 more control has been exerted on the provenance of seeds and young plants of Scots pine, first by the "Vereniging Waarborg Herkomst Groveden" (the Vereniging W.H.G) and since 1942 by the "Nederlandse Algemene Keuringsdienst voor Boomkwekerijgewassen" (N.A.K.B.). In 1960 a large selection and sampling programme was started. The first Dutch seed orchard "Grubbenvorst", was established in 1965, the second, "Voorsterbos", in 1972 (Van 't Leven 1979, Kriek 1983).

In the meantime, it was confirmed from separate provenance experiments that foreign provenances grow less well in the Netherlands than Dutch provenances (van Vloten 1927, Van Soest 1952, Kriek and Bikker 1973, Kriek 1983). Moreover, provenances from the North-West of the Netherlands appeared to grow better than those from elsewhere in the country, because of their greater resistance to *Lophodermium seditiosum* (Squillace et al. 1975, Van 't Leven 1979). However, most Dutch provenances originated from stock introduced one or more generations earlier. There was probably a fast selection for resistance to *Lophodermium seditiosum*, because the more humid maritime climate increased the chance of injury from this pathogen (Wiersma 1985).

Generally, provenances from Southern and Eastern Europe are more sensitive to *Lophodermium seditiosum*, and provenances from Northern and Western Europe grow more slowly (Van Soest 1952, Kriek 1983). The sensitivity to daylength and temperature of provenances of different latitudes is probably important here. It is well-known that the further north and the higher the altitude at which plants grow, the better they are adapted to low temperatures and long days, and the further south plants grow, the better they are selected for strong growth, resulting in taller and more branched trees (Wiersma 1985, Mayer 1984).

At the moment, the Scots pine population in the Netherlands still largely consists of poorly to badly adapted provenances. Much seed has been used from pines that were sown by wind, or from selected low-branched trees of unknown origin (Jansen and Van Broekhuizen 1952, Heybroek 1974). The use of these wind sown pines and border trees was indeed advised by Hesselink (1922). Moreover, seeds and plants were imported until the seventies (Van 't Leven 1979), because these seeds and plants were cheaper (Kriek 1983). Since the seventies, natural regeneration has become increasingly common (Fanta 1982). According to Fanta (1983), the natural regeneration of maladjusted provenances makes it unlikely that the Scots pine domain in the Netherlands will improve rapidly. However, most stands of Scots pine in the Netherlands are of unknown provenance. Sometimes old stands seem to have a bad provenance according to their *phenotype (very thick branches, many *reiterations, slow growth, etc.), but show a much better phenotype in the second generation (Prins and Kuper 1989).

Differences in increment between provenances may be crucial. In an experience with Scots pine provenances Van Soest (1952) found that some provenances had an average height growth 60 to 30% below others, mainly because of provenance differences (see section 2.3).

From the above it can be concluded that the Scots pine population in the Netherlands still includes much variation caused by different provenances. A given provenance can indicate probable growth characteristics, but we can never accurately predict the growth potential of individual trees. In his summary Hagner (1970) posits that variation in growth between trees within a stand is generally so large that a natural population can never be seen as completely adapted to any site, because there will always be some trees that are not adjusted genetically. One could also say that a natural population is optimally adapted to its site if there is enough genetic variation to ensure that there will always be individuals that survive or use temporary extremes in site conditions.

The provenance concept thus has less relevance for predicting the *growth of individual trees than for predicting the mean growth of a stand. However, it does indicate the most likely maximum and minimum growth and perhaps even the distribution within these limits. Statistical research on the relation between growth and provenance (cf. Hagner 1970) is very time consuming. Furthermore, very many combinations of provenances with different climate, site and age are possible (Oldeman et al. 1985a). A combined provenance-site classification may offer a solution.

2.2.3 Site

Researchers have for a long time been trying to find relations between site and growth potential (e.g. Cajander 1909, Rubner 1929, Schelling 1960, Van der Werf 1968, Schmidt 1969, Jansen 1972, Bannink et al. 1973, Van Goor et al. 1974, Van Lynden 1977, Kessell 1979, Fanta 1982, Fanta 1985, Firet 1986, Paasman 1988, Kapsenberg 1990). In the original conception, site was defined as the place where a plant, a tree or a forest grows, and having characteristics like water supply, fertility or surrounding organisms, that make it more or less suitable for plant growth.

The relations between different soil properties and growth of Scots pine stands are given briefly in Table 1 (after Van den Burg et al. 1983 and Mayer 1984).

TABLE 1 Soil properties in relation to growth potential of Scots pine (compiled from data from Van den Burg et al. (1983) and Mayer (1984)).

		growth potential (1)	Remarks
Mean spring groundwater level	< 25 cm -ground level	——	
	25-50 cm -ground level	—	
	> 50 cm -ground level	+	
Soil water supply (2)	< 50 mm	——	
	50-80 mm	—	
	> 100 mm	+	
N-total (3)	< 0.02 %	——	N-total is only important for soils poor in organic matter.
	0.02-0.06 %	—	
	> 0.06 %	+	
N-organic (4)	< 1.5 %	——	
	1.5-1.9 %	—	
	> 1.9 %	+	
P-total (5)	< 10 mg / 100g	——	On moist soils Scots pine needs less phosphorus.
	10-20 mg / 100g	—	
	> 20 mg / 100g	+	
pH_{kcl}	< 3	——	At pH > 5 more likelihood of crooked stems and thick branches, lime-induced chlorosis and infection by *Heterobasidion annosum*
	3-4	—	
	4-5	+	
	> 5	+	

(1) —— = *poor growth* ($I_{0-50} < 4.2$ *m*^{3} *per ha per year)*
— = *moderate growth* ($4.2 < I_{0-50} < 6.6$ *m*^{3} *per ha per year)*
\+ = *good growth* ($I_{0-50} > 6.6$ *m*^{3} *per ha per year)*
(I_{0-50} *= mean annual increment per ha from age = 0 year until age = 50 years)*

(2) The soil water supply is the amount of water that can be supplied to plant roots in a growth season of 150 days and in a very dry year.

(3) N-total is the percentage of nitrogen in the layer 0-25 cm below ground level.

(4) N-organic is the percentage of nitrogen of the organic matter in the layer 0-25 cm below ground level.

(5) P-total is the amount of phosphorus expressed in mg P_2O_5 *per 100 gram soil.*

Sites have often been classified by analysing the vegetation (cf. Cajander 1909, Clements 1916, Ilvessalo 1920, Du Rietz 1921, Braun Blanquet 1928/1951/1964, Tüxen and Diemont 1937, Becking 1951, Whittaker 1953, Kalela 1954, Scamoni 1954, Doïng 1962, Van der Werf 1968, Westhoff and Den Held 1969, Bannink et al. 1973, Koop 1981). The main point here is that site characteristics are reflected in the species composition of the vegetation. Mapping the vegetation thus gives information about the influence of environmental factors in the mapped area. This in its turn should reflect growth potential in that area.

In many site classifications for the Dutch forests only the undergrowth is considered. This is because most Dutch forests consist of exotic species and provenances, which are considered to be poor indicators of site potentials (Fanta 1985). The spontaneous undergrowth gives a much better indication, providing soil disturbance is minor (Fanta 1985, Kapsenberg 1990). Van der Werf describes two detailed "undergrowth classifications" for the Veluwe in the province of Gelderland, the Netherlands (Van der Werf 1968, Van der Werf in ten Houte de Lange 1977). He found a good correlation between types of undergrowth and tree growth (Van der Werf 1968, cf. Jansen 1972) and also between undergrowth types and phases of succession and regression (Van der Werf in ten Houte de Lange 1977).

Another detailed "undergrowth classification" for the Netherlands was described by Bannink, Leys and Zonneveld (1973). Here, "undergrowth types" are built up from a combination of sociological groups of species. A good correlation was found between "undergrowth types" and the nutrients available for trees. Differences in soil water supply were not always indicated by the undergrowth. Therefore, as well as an undergrowth map site classification needs a soil map, in which groundwater fluctuation, soil water supply and drainage are included (cf. Schütz and Van Tol 1982).

In addition to site classifications using vegetation, many site classifications in the Netherlands have used soil types, form and percentage of humus, groundwater fluctuations, pH, parent material and, recently, forest history and previous land use (Schelling 1960, Wallesch 1963, Van der Werf 1968, Van Goor et al. 1974, Van Lynden 1977, Van den Burg et al. 1983, Anonymus 1986).

In order to understand site characteristics, all these classification methods should be compared. The scheme drawn up by Fanta (1985; our Fig. 1) is a good guideline for this. Fanta (1985) describes a forest site as a complex of factors of the physical environment, establishing the existence, composition, development and growth of a forest. Once-off and occasional influences on the forest community (such as windthrow) are not included as site factors; neither is competition between trees in a stand. In this context Fanta (1985) distinguishes growth factors and site factors (Fig. 1). He defines them as follows:

- Primary growth factors for green plants are light, water and chemicals. The total amount and the availability in time of growth factors condition the

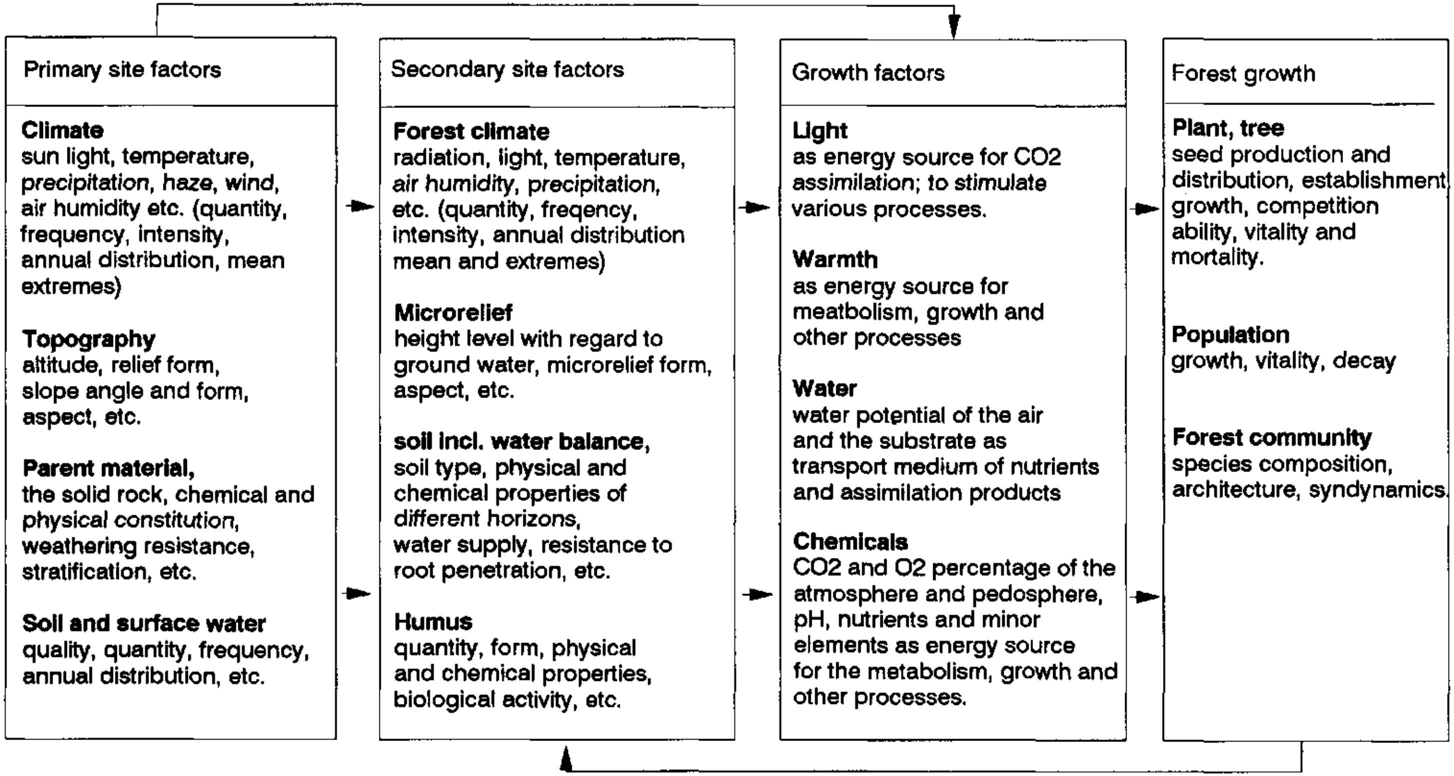


Fig. 1 Schematic diagram of relations among the primary and secondary site factors, growth factors and forest growth. The arrows show how site factors regulate the supply of growth factors to green plants and forest trees. The feedback indicates the influence of forest growth upon the secondary site factors (stabilizing interaction) (after Fanta (1985).

existence, growth and production of green plants and their competition with other plants and plant communities.

The arrows in Fig. 1 indicate how the supply of growth factors to plants and forest is regulated by site factors. The feedback gives the influence of the vegetation on secondary site factors (stabilizing interaction).

- Primary site factors are climate, topography and orography, parent material, groundwater and surface water. They are the causes of certain ecological characteristics of ecosystems. They are more or less constant and unlike secondary site factors do not belong to the ecosystem;
- Secondary site factors are forest climate, micro-relief, soil, humus and water management. These factors are not stable and arise from *interaction between biotic and abiotic components of the ecosystem. Secondary site factors are almost completely absent from young ecosystems, but have developed well in old forest ecosystems.

According to Fanta (1985) a site class is an assemblage of locations with the same combination of site factors, the same constitution of relations between site and forest and thus also with the same silvicultural potential. To be able to draw up and describe such a site classification requires much knowledge on forest ecology, geobotany, plant sociology, *forest architecture, soil science, climatology, geology and geomorphology, and history of forest and forestry. This knowledge is also required to be able to interpret the effects of site factors on the forest.

An almost infinite number of site classes can be distinguished within a classification based on so many characteristics. It is also important to know the aim of the classification. Thus, a classification that includes one or more (maybe sometimes even all) of the following aspects can be drawn up (Koop 1981, Fanta 1982):

- growth of tree species;
- vitality of tree species;
- likelihood of survival of tree species;
- production capacity of tree species;
- regeneration ecology of tree species;
- *architecture and development of a given forest community (Kuiper 1988);
- potential natural forest development related to composition, architecture and dynamics of the forest community;
- the risk of diseases, plagues, storm damage, etc.;
- carrying capacity of the area and its potential for recreation;
- the area's dependence on groundwater and surface water.

A site's suitability for the growth and production potential of tree species is often given with the help of the mean stem volume increment per ha at the age that this mean annual increment has peaked. For Scots pine this is generally at 50 years (Schütz and Van Tol 1982). This mean stem volume increment can be estimated from the dominant height and the age of a stand. The dominant height or top height is the average height of the hundred tallest trees per ha (Schütz and van Tol 1982). Jansen and Schmidt (1991) define top height as mentioned above and dominant height as the stand mean of the tallest tree per are (= 100m^2). In this book the former definition is used. The growth curve of trees of this dominant height appears to roughly reflect the site's suitability for that tree species: the more suitable the site is, the faster the growth. The *yield tables of Bastide and Faber (1972) are based on this principle. So, the height growth of trees is an important criterion for judging site suitability.

Old Scots pine trees often show a stagnation of height growth and a flat crown form (Mitscherlich 1970, Roloff 1989). This means that either the top of the tree bends and length growth continues, or top shoots repeatedly break off, building several *reiteration patterns and showing no clear height growth (Edelin 1977).

This crown flattening can be attributed to a defective water supply. When trees are healthy and have enough *growing space, branches can continue to grow laterally and diameter growth normally goes on (Van den Burg et al. 1983). Under certain circumstances it is possible that after initial flattening of the crown height growth is stimulated anew (Pretzsch 1985, 1987), for example by soil characteristics changing as a result of immission, fertilization or changing water management. Soil stratification can also have a large influence on height growth (for example when, as a tree grows older, its roots penetrate a deeper fertile layer). The expected course of height growth is thus rather uncertain, especially in older trees.

The maximum height that Scots pine reaches in the Netherlands is about 26 metres, dependent upon site and at an age of over 120 years. Heights of 23 to 26 metres occur only on the most fertile sites, but these are usually planted with more demanding coniferous and broad-leaved species (cf. Paasman 1984).

An example of a "combined" site classification, principally developed for predicting production potential and vitality of stands, is given by Schütz and Van Tol (1982). A very detailed combined site classification was developed (Firet et al. 1985) for use on *target types of forest (Anonymus 1986). A scale of 1:10 000 was proposed for this site classification.

At a level below the above-mentioned classification methods, in which a site class is seen as a homogeneous unit, come ordination methods for establishing gradients (Kessell 1979). In ordination, the sites and species are arranged along axes that represent hypothetical variables in such a way that these arrangements optimally (from a statistical viewpoint) summarize the species data (Jongman et al. 1987).

From the above we may conclude that it is not easy to develop site classifications in which each site class gives its own indication of the silvicultural prospects in connection with aspects as growth, vitality, likelihood of survival, production capacity etc. (see previous page). Primary site factors are usually easy to measure and often rather constant over large areas. Secondary site factors, however, can vary over very short distances and may be especially important in older forests. Moreover, secondary site factors usually change much faster than primary site factors.

Questions about production capacity of an area of forest are mostly related to at least several hectares. A site classification per m^2 or less for such an area is as useless as it is impossible. So secondary site factors will always be measured as averages for areas of at least several ares (scale of the stand 1:1000 to 1:5000).

However, a classification at this scale for the whole of the Netherlands is not manageable either. Perhaps in future a classification at a scale of 1:10 000 may be possible (cf. Firet et al. 1985). But, clearly, at this scale considerable differences in silvicultural potential might be found within each site class.

Furthermore, not all relations are known between site class as a combination of site factors and site potential respectively site constraints. Clearly, a site classification for the Netherlands will not fit the "eco-unit" level very well and will certainly not fit the "organism" level. Hence it is impossible to predict the course of height growth of individual trees on the basis of a site classification. But it might be possible to find a useful distribution function representing mean normal height growth and standard deviation of trees of a certain provenance per site class.

2.2.4 Growing space

Various researchers have studied the growing space of a tree; they include Wiedeman (1948), Faber (1971, 1983, 1986), Johansson (1986), Kellomäki (1986) and Mc Fadden and Oliver (1988). Mc Fadden and Oliver (1988 p.665) note that: "trees in even-aged stands first grow without competition from neighboring trees -"open growth". They expand in size at a rate governed by the site and their genetic makeup. As they expand they begin competing with neighbors for light, moisture, nutrients or other components of the "growing space" or "biological space" (Ross and Harper 1972). They often change their shape during competition - a "plastic response" (Harper 1977, Hutchings and Budd 1981)- as shade or root competition reduce the ability of certain limbs to grow and as the respiring tissue of each tree increases relative to its photosynthesizing tissue. The greater respiring tissue reduces the photosynthate allocation first to diameter growth, and then to height growth (Assmann 1970, Mitchell 1975). If all trees in a stand grow uniformly, they uniformly decline in diameter growth and then height growth until all photosynthesis is utilized for respiration (and needle and fine root replacement) and growth ceases."

Kellomäki and Kanninen (1980) found that in shaded conditions the growth of crown and stem characteristics was greater than expected on the basis of photosynthate supply. In the stem system this was especially apparent for height growth. Consequently, height growth was favoured at the expense of *radial growth in shaded conditions. Faber (1986) reports that only extremely low and extremely high stem numbers per ha, thus extremely large and extremely small growing spaces per tree, influence the height growth of a stand. According to Baker (1950 ex Hari et al. 1985) a larger height / diameter ratio arises from poor illumination.

The relation between mean growing space and mortality has also been described by several authors (Yoda et al. 1963, Harper 1977, White 1980, Carvalho Oliveira 1980, Valentine 1988, Barreto 1988a, McFadden and Oliver 1988, Hann and Wang 1990). Sometimes, probability of mortality is related to initial tree dimensions and mean tree dimensions per area (Miner et al. 1988, Hann and Wang 1990), sometimes probability of mortality is directly related to stem number per area (Yoda et al. 1963, Harper 1977, White 1980, Carvalho Oliveira 1980, Valentine 1988, Barreto 1988, Hann and Wang, 1990). The relation between density p and mean maximum biomass of a plant or tree w is described by these authors as "3/2 power law":

$$w = C_1 * p^{C_2} \tag{1}$$

in which c_1 is a constant dependent upon site and tree species, and in many case c_2 nears the value 3/2.

In conclusion it can be said that growing space defines the degree of *interaction between a tree and its neighbour. Here, interaction may be understood as competition for space. Hence, the size of the growing space can strongly influence tree growth: small growing spaces negatively affect diameter growth and very small growing spaces negatively influence height growth. A relatively small growing space per tree increases the likelihood of mechanical damage from branches of neighbouring trees.

According to Fanta's scheme (Fanta 1985 our Fig. 1) growing space is actually a secondary site factor.

2.2.5 Age

The height growth of Scots pine varies strongly with age. The mean cumulative height growth with age follows the usual S-shaped curve (sigmoid).

In the *innovation phase height growth is relatively slow, in the *aggradation phase it is fast, and in the *biostatic phase relative it is slow again (for phase definitions see Oldeman 1990). Contrary to Norway spruce (*Picea abies* L.) and giant fir (*Abies grandis* Lindl.), Scots pine does not tolerate a long-term suppression. It will quickly die when *suppressed, but Norway spruce and giant fir may ail for years but, after being released, may still achieve good *growth (Mayer 1984).

2.2.6 Phenotype

"*Growth" is often used to mean "increment", which means a net increase in biomass (Oldeman 1990). However, growth may also be used as a process, changing a specified original *situation into a new one within a specified time. In that case decay is also a form of growth, but in a negative sense (Oldeman 1978). Clearly, the condition of a tree, expressed in its *phenotype, has a large influence on how and how much a tree can grow.

Juvenile Scots pine trees grow according to Rauh's model (Hallé and Oldeman 1970, Edelin 1977). This means that the phenotype of Scots pine shows a more or less steady pattern (Fig. 2A,2B) and that only sizes differ. With increasing age diseases, injuries, drought, etc. bring about modifications to this model. For example, branches may bend in a strange way, die or break off and *reiterations may happen. For a detailed description of pests, diseases and injuries, see "Bosbescherming" (PUDOC 1982) and "Ziekten en plagen van de Nederlandse bossen" (Grijpma et al. 1988).

The crowns of trees that survive pests, diseases and injuries recover by reiteration. This means that when a top meristem dies one of the lateral meristems assumes the function of the top meristem, or when part of the crown breaks off other meristems try to compensate for the loss by forming a new crown part with the same architectural ground model. Then the crown no longer grows completely in accordance with its original model (Fig. 2C). A reiteration complex or a complex of crown parts arises, in which each of the crown parts conform wholly or partly to the architectural model (cf. Edelin 1977, Oldeman 1990). In general, as a tree ages, it becomes more damaged and the number of reiterations increase. This means that crown appearance at "organ-level" becomes less predictable with age.

Because these variations occur at a level which is too detailed for the present study, in the next chapters branch growth is generalized to crown width increment and crown length increment. Crown length and crown width appear to be fairly predictable ("organism" level).

2.3 A provenance trial in Kootwijk: a test case

As discussed in section 2.2.2, *growth is strongly dependent upon genetic factors and partly depends on provenance. To investigate the genetic influence on growth of Scots pine, a provenance trial in Kootwijk (Province of Gelderland, the Netherlands) was started in 1910 (Hesselink 1922, Van Vloten 1927, Van Soest

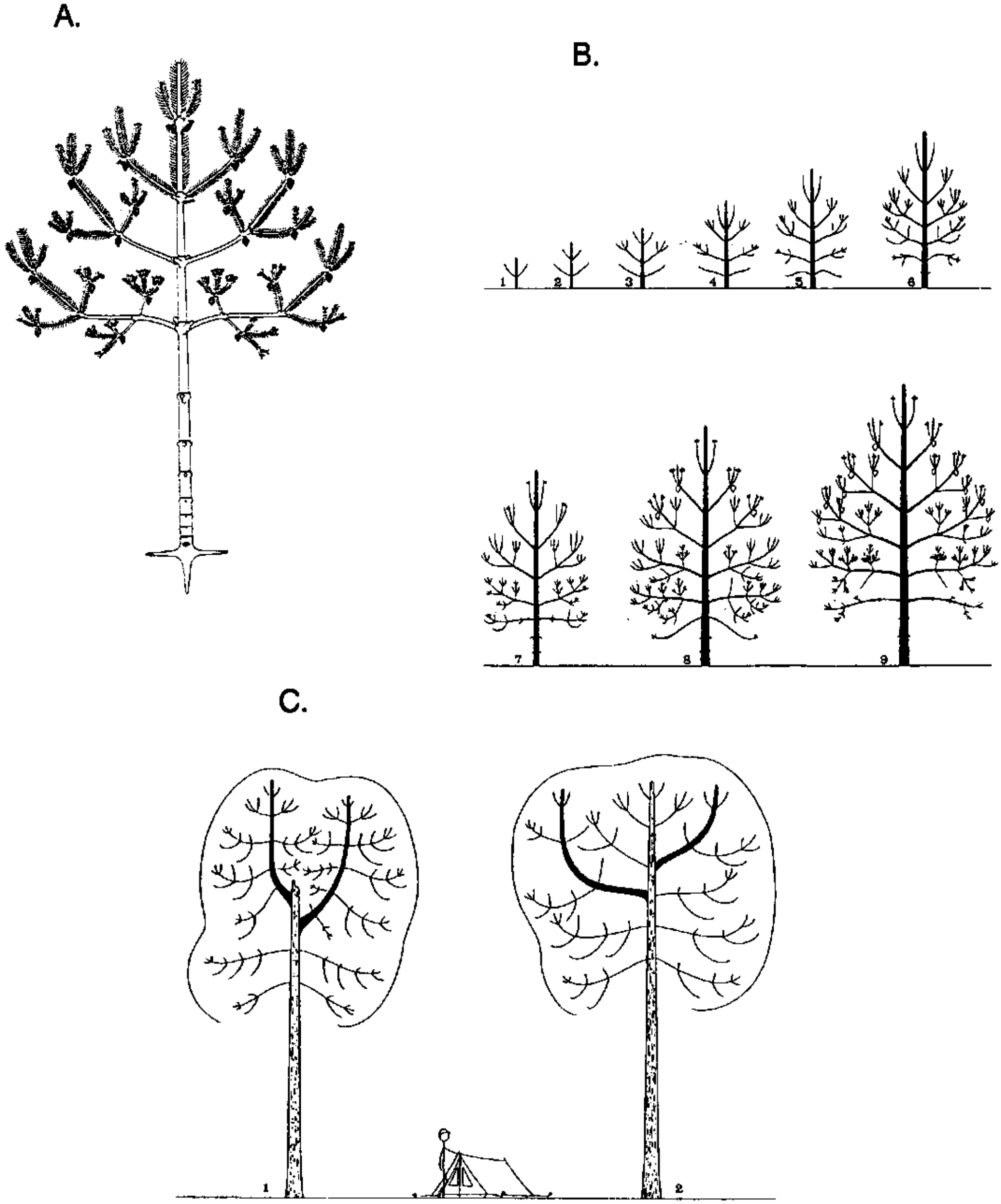


Fig. 2 A. Architectural model of Pinus sylvestris L. (Rauh's model).
B. Schematic design of the first 9 years of growth (flowering starts in year 8).
C. Reiteration can be traumatic (left) or, without injury, occur by branch dedifferentiation during crown expansion (right) (after Edelin 1977).

1952, Lucassen 1985). This trial was provided with material from different parts of Europe and is very important, because it is the only old experiment in the Netherlands. Other provenance trials in the Netehrlands date from 1963 onwards (see section 2.2.2).

The trial originally had three series, but only series I remained: series II was burnt and series III was too small. Table 2 shows the provenances used in series I.

TABLE 2 Summary of provenances of Scots pine used in series I of Kootwijk trial

In 1989 only the numbers 4, 5, 6, 7, 9, 11 and 14 has remained.
The other numbers were destroyed by storm in 1973.

1. Southern Germany
2. Western Hungary
3. Western Hungary
4. Eastern Prussia
5. Riga
6. Central Sweden
7. Hoenderloo (NL)
8. Belgian Kempen
9. Southern France
10. Northern Hungary
11. Scotland
12. Belgian Kempen
14. Northern Germany

In 1911 about 7500 one-year-old plants of each provenance were planted, except in the case of provenance 8 (Belgian Kempen) and provenance 11 (Scotland) (these were later discarded). This resulted in a density of about 20 000 plants per ha. This series was measured in 1911, 1916 and 1920 by Hesselink (1922), in 1926 by Van Vloten (1927) and in 1948 by Van Soest (1952). The data from van Soest are especially interesting, because they were gathered when the stands were more developed (Table 3 and 4). In table 3 it is striking that:

- provenance 7 (Hoenderloo) showed the fewest crown deficiencies; provenances 14 (Northern Germany), 5 (Riga), 4 (Eastern Prussia) and 9 (Southern France) did moderately well in this respect;
- provenance 5 (Riga) had a large proportion of straight stems, provenance 3 (Western Hungary), 6 (Central Sweden) and 7 (Hoenderloo) a moderate proportion and the other provenances just a few or none;
- the *phenotype of provenances 5 (Riga) and 7 (Hoenderloo) "looked better" than that of the other provenances.

Measured data that were used to analyse the relations between tree dimensions and stand density (or mean distance between stems $\bar{A}$) are given in table 4 (see also list of symbols at the back of this book).

TABLE 3 Data on the properties of stems and crowns of provenance series I of the Kootwijk trial on Scots pine in 1948/1949, each time for 50 trees. (Van Soest 1952)

$\bar{h}/dg$ = degree of slenderness
stem class 1 = straight stems
stem class 2 = intermediate stems
stem class 3 = crooked stems

Provenance	plot no	$\bar{h}/dg$	number of trees per stem class			number of trees with "many" branches	crown form			
			1	2	3		normal	flat	dead top	several tops
S Germany	1	82	-	1	49	3	30	5	4	1
W Hungary	2	73	-	-	50	6	19	12	7	15
W Hungary	3	83	2	5	43	1	25	3	3	12
E Prussia	4	73	1	1	48	3	38	1	6	5
Riga	5	97	18	8	24	7	39	-	2	9
C. Sweden	6	80	3	2	45	-	30	7	7	9
Hoenderloo	7	98	3	4	43	20	45	3	-	2
S France	9	70	-	-	50	2	37	6	3	4
N Hungary	10	76	1	1	48	4	30	7	3	1
Belg Kempen	12	92	-	2	48	2	26	10	7	9
N Germany	14	87	-	1	49	2	40	1	1	8

TABLE 4 Data on measurement of provenances of series 1 from the Kootwijk trial (Van Soest 1952)

$\bar{A}$ = mean distance between stems (m)
d_g = diameter derived from mean basal area per tree (cm)
f_g = form factor at d_g and $\bar{h}$
G = basal area (m^2/ha^{-1})
h_g = height at d_g (m)
$\bar{h}$ = mean height (m)
h_{dom} = dominant height (m)
$\overline{cl}$ = mean crown length (m)
N = number of stems (ha^{-1})
V = volume (m^3/ha^{-1}

stand	N	$\bar{A}$	$\bar{h}$	h_{dom}	h_g	d_g	G	f_g	V	$\overline{cl}$
1	2400	2.19	9.49	11.73	9.77	11.50	25.00	0.54	127.40	3.23
2	1980	2.41	7.44	11.45	8.04	11.10	19.30	0.52	75.30	3.42
3	3250	1.88	7.41	9.92	7.72	8.80	19.60	0.56	81.60	2.96
4	2000	2.40	8.37	10.49	8.35	11.10	19.20	0.52	83.20	4.02
5	3760	1.75	8.55	11.02	8.67	8.70	22.40	0.56	108.00	3.16
6	3620	1.79	5.90	8.80	6.64	8.40	20.30	0.61	72.90	2.54
7	2580	2.12	10.24	12.37	10.42	10.80	23.50	0.55	131.90	3.99
9	3060	1.94	5.92	8.30	6.15	8.40	16.90	0.61	61.10	2.72
10	1950	2.43	8.70	11.11	9.07	12.30	23.20	0.54	108.00	3.57
12	3210	1.90	8.39	10.42	8.54	9.00	20.50	0.60	103.70	2.52
14	2870	2.01	8.20	10.78	8.66	10.20	23.60	0.55	106.30	3.03

The symbols d_g, $\bar{h}$, f_g and $\bar{A}$ used in this table are defined as follows:

$$d_g \equiv \sqrt{\frac{1}{n} * \sum_{i=1}^{i=n} dbh[i]^2} \tag{2}$$

$$\bar{h} \equiv \frac{1}{n} * \sum_{i=1}^{i=n} h[i] \tag{3}$$

$$f_g \equiv \frac{n * \sum_{i=1}^{i=n} v[i]}{\sum_{i=1}^{i=n} h[i] * \sum_{i=1}^{i=n} g[i]} \tag{4}$$

$$\bar{A} \equiv \sqrt{\frac{10000}{0.5 * N * \sqrt{3}}} \tag{5}$$

in which
$h[i]$ = height of tree i (m)
n = number of sample trees
$dbh[i]$ = diameter at breast height of tree i (cm)
N = stem number per ha
$v[i]$ = volume of tree i (m^3)
$g[i]$ = basal area of tree i (m^2)

As explained in sections 2.2.3 and 2.2.4, there is a strong relation between tree dimensions and the site and growing space. So, for the study presented here the above data were used to compute non-linear regressions between diameter, crown length, volume and form factor as dependent variables, and the independent variables growing space (expressed by mean distance between stems) and site (expressed by tree height). Computations are done with the help of the "STATGRAPH" statistical package:

$$d_{gpre} = \bar{A}^{D1} * h_g^{D2} * D3 \tag{6}$$

$$\overline{cl}_{pre} = \bar{A}^{CL1} * \bar{h}^{CL2} * CL3 \tag{7}$$

$$V_{pre} = \bar{A}^{V1} * h_g^{V2} * V3 \tag{8}$$

$$f_{gpre} = \bar{A}^{F1} * \bar{h}^{F2} * F3 \tag{9}$$

The constants found are given in Table 5. These constants do not define intrinsic characteristics of trees, but empirically describe characteristics with the help of mean distance between stems and tree height.

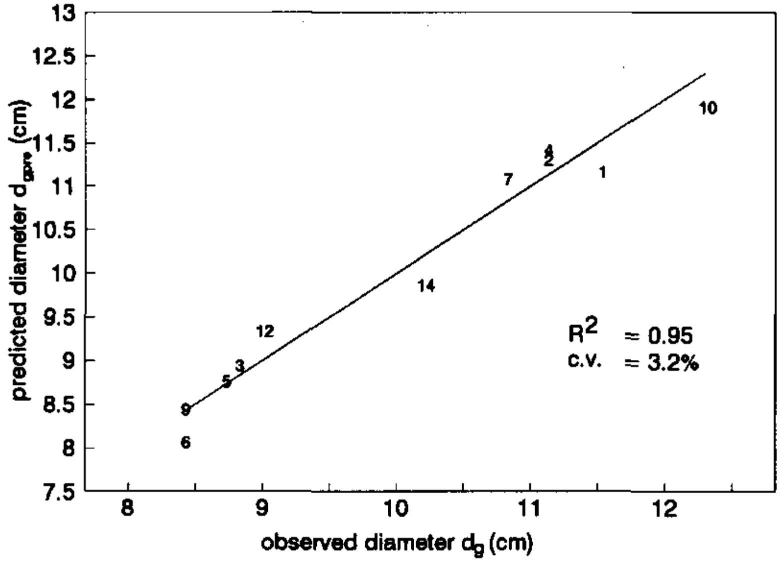


Fig. 3 Correlation between predicted and observed diameter (dg) of 11 provenances of Scots pine in the Kootwijk trial. The numbers indicate the stands (see Table 3; data after van Soest 1952).

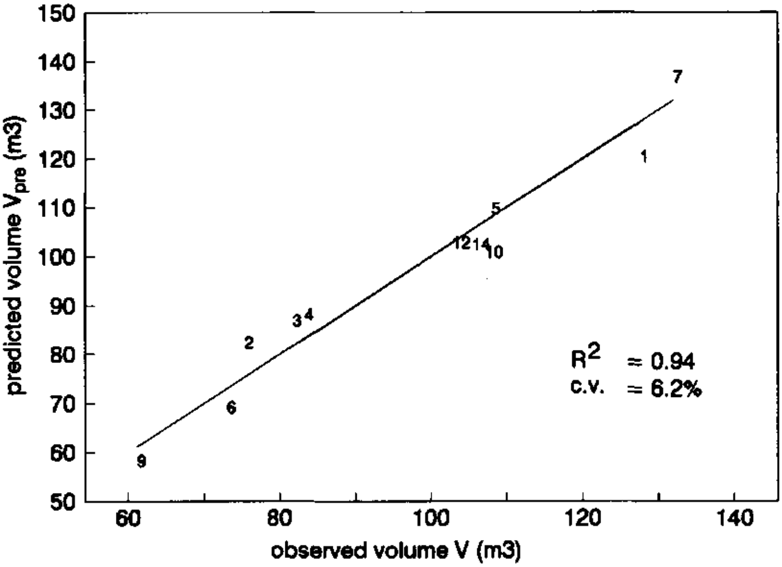


Fig. 4 Correlation between predicted and observed volume (V) of 11 provenances of Scots pine in the Kootwijk trial. The numbers indicate the stands (see Table 3; data after van Soest 1952).

TABLE 5 Constants found for equations (6), (7), (8) and (9) for diameter, crown length, volume and form factor

D1 = first constant for d_g = 0.885 (formula 6) etc.
c.v. = coefficient of variation
R^2_{adj} = R^2 adjusted for degrees of freedom

constants	1	2	3	c.v.	R^2_{adj}
D	0.885	0.372	2.386	3.2%	0.95
CL	0.758	0.440	0.735	9.8%	0.61
V	-0.488	1.696	3.707	6.2%	0.94
F	-0.317	-0.133	0.926	3.3%	0.69

The most interesting finding from the calculations described above is their relation to stands grown from seeds of different provenances. Despite the large variation in height of the different stands, it appeared that diameter, volume and, in some extend, form factor and crown length, can be estimated well from mean height and mean distance between stems.

The good correlation between diameter d_g and volume as dependent variables and height and mean distance between stems as independent variables (Figs. 3 and 4) can be frequently found in the literature (Wiedeman 1948, Grandjean and Stoffels 1955, Assmann 1961, Mitscherlich 1970, Faber 1971, Brünig en Schneider 1975, Carvalho Oliveira 1980, Faber 1983, Faber 1986, Abetz 1987, Mc Fadden and Oliver 1988).

Mean crown length is more difficult to predict solely from distances between stems and tree height (R^2_{adj} = 61%; Fig. 5). Management is important here. It is well-known that tree species such as Scots pine that prefer much illumination, will have a smaller crown length / height ratio in a narrow growing space as they grow taller (Stiell 1966, Mitscherlich 1970, Carvalho Oliveira 1980, Kellomäki and Nevelainen 1983, Abetz 1987, Ritchie and Hahn 1987). When a tree is released, its crown length is relatively short at that moment compared with its new growing space. After release, height growth continues without mortality in the lower part of the crown until competition with neighbours again becomes important and causes the lower branches to die. Crown length is difficult to measure exactly, especially when crowns are asymmetrical or when the lower branches are moribund.

The form factor f_g is "the form factor of the mean tree of the stand", which is the tree with the mean basal area (Eq. 9). This is in contrast to the mean form factor:

$$\bar{f} = \frac{1}{n} * \sum_{i=1}^{i=n} \frac{v_i}{g_i * h_i} \tag{10}$$

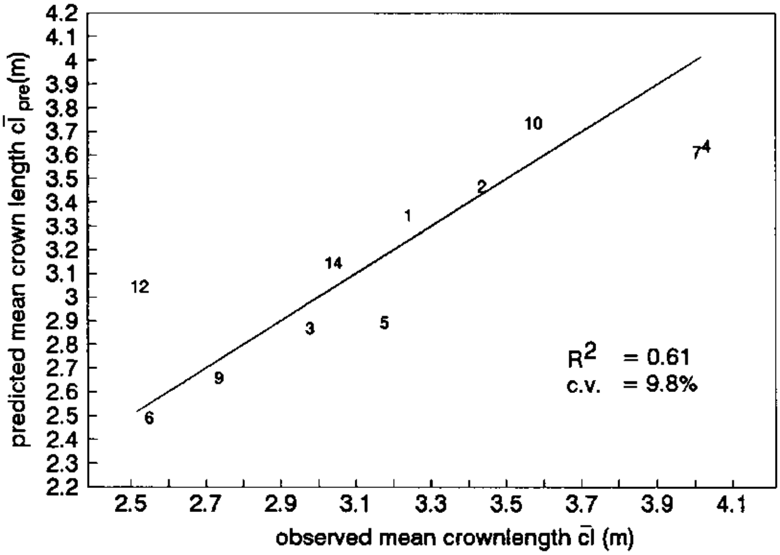


Fig. 5 Correlation between predicted and observed mean crown length ($\bar{cl}$) of 11 provenances of Scots pine in the Kootwijk trial. The numbers indicate the stands (see Table 3; data after van Soets, 1952).

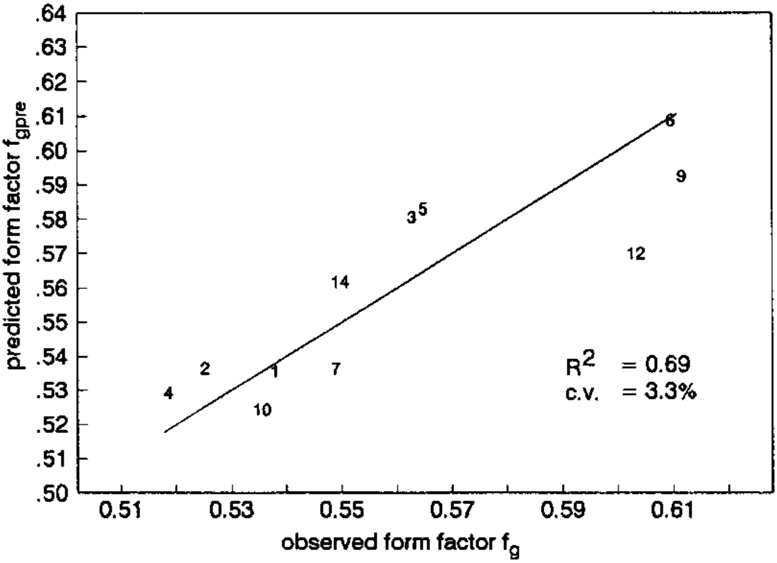


Fig. 6 Correlation between predicted and observed form factor (fg) of 11 provenances of Scots pine in the Kootwijk trial. The numbers indicate the stands (see Table 3; data after van Soets, 1952).

Unfortunately, there are no data on mean form factor for the trees in the Kootwijk trial. In general, thick trees have a smaller form factor than thin trees of the same height (cf. mass table of Dik 1984). The correlation between form factor and tree height and distances between stems is obvious, because diameter is also dependent upon height and distances between stems (Fig. 6). However, a better correlation can be found if form factor is related to diameter, height and crown length.

$$f_g = d_g^{F1} * \overline{h}^{F2} * \overline{cl}^{F3} * F4 \qquad (11)$$

F1, F2, F3 and F4 are respectively -0.195, -0.000, -0.194 and 1.093.

It appeared that especially diameter and crown length were important (R^2_{adj} = 0.78 and c.v. = 2.7%). This means that the stem diameter decreases relatively rapidly above the crown base.

The observed crown length of provenance 12 (Belgian Kempen) is very small compared to the predicted crown length (Fig. 5). This can be attributed to the relatively great homogeneity of the stand; the lower branches of the trees die to the same extent in all directions and so only a few asymmetrical crowns are present. In heterogeneous stands trees often have more space on one side than on the other, causing crowns to be lopsided. Since crown length is measured from the lowest living branch, asymmetrical crowns, by definition, have relatively deep crowns.

The correlations found strongly indicate that crown length, diameter and volume can largely be explained by height growth and changing *growing space, for example caused by forest management. Differences in provenance are mainly expressed by height growth and by factors such as resistance to diseases, yellow colouring in winter and crooked growth (cf. Kriek 1981).

Explanation of the correlations found

The *growth of a tree is mainly defined by its *genotype and by site factors such as available light, water and nutrients (see sections 2.2.2 and 2.2.3). *Competition for water and nutrients influences height growth and *radial growth. However, as long as the tree is not overgrown, competition for light has far more influence on the radial growth than on the height growth. Since height growth is favoured at the expense of radial growth in shaded conditions (see section 2.2.4) it is not surprising that radial growth correlates well with height growth (which depends on available light, water and nutrients) and *growing space. So, if height growth is not clearly correlated with growing space, then it may be hypothesized that height growth is mainly related to available water and nutrients and that radial growth can be derived from height growth and available amount of light.

3 COLLECTING AND PROCESSING DATA USED TO BUILD THE PINOGRAM MODEL

3.1 The field methodology used for this study

3.1.1 Introduction

Given the good correlations between mean diameter, volume per ha, mean crown length and form factor on the one hand and mean height and mean distance between stems on the other, in combination with the small coefficient of variation (Table 5), that was found with the help of van Soest's data (see section 2.3), it was decided to test these correlations on individual trees in even-aged *pure stands.

To be able to predict *growth of Scots pine, the dimensions an individual tree can attain within a certain period must be known. It is impracticable to *monitor the growth and dynamics of several hundreds of trees of different provenances, for many decades, on different sites, with different climates and at different *competition levels. Long series of data from trial stands are not always useful, because successive researchers tend to collect data for different reasons (cf. Hesselink 1922, Van Vloten 1927, Van Soest 1952). For example, in the past much data were collected in the Netherlands on tree diameter, mean tree height, *dominant tree height and stem number per ha, but measurements of crown form are patchy and incidental.

Since the present study had to be finished within three years, it was decided to investigate whether the dimensions of trees in a number of Scots pine stands of various age correlated significantly with their age, height and *growing space. A disadvantage of this method is that the exact history of each individual tree is not known (see section 3.2) and that site conditions and *genotypes are not uniform.

In order to investigate growth and dynamics of individual Scots pine trees, a field study was done. Choices made to carry out this field study are explained in next sections.

3.1.2 Choice of ages of the sample stands in the field study

Van Soest's data (Van Soest 1952) concerned trees of the same age (38 year). To check the validity of the correlations for trees of other ages the field study has to include a series of stands at different ages, so that different developmental phases such as *innovation phase, *aggradation phase and *biostatic phase are involved (cf. Oldeman 1990). Table 6 roughly indicates the phases Dutch stands of Scots pine represent.

TABLE 6 Developmental phases and estimated corresponding ages of *P.sylvestris* stands in the Netherlands

phase	age about
innovation phase	< 10 year
early aggradation phase	10 - 20 year
aggradation phase	20 - 30 year
late aggradation phase	30 - 40 year
early biostatic phase	40 - 60 year
biostatic phase	60 -100 year
late biostatic phase	> 100 year

Each of these phases was represented in the field study (see Table 7).

3.1.3 Choice of soil type for the field study

Scots pine can be found on very diverse soil types. Those soil types, on which Scots pine grows well (more than 6.6 m^3/ha.year), are increasingly being used for more productive tree species, such as larch (*Larix decidua* Mill. and *Larix kaempferi* Lamb.), Douglas-fir (*Pseudotsuga menziesii* Mirbel) and for broadleaved species as oak (*Quercus robur* L., *Quercus petraea* (Mattuschka) Lieblein) and beech (*Fagus sylvatica* L.) (cf. *Target types of forest in the long-term Forestry Plan).

The field study was restricted to less productive soils, namely humic podzols in fine sand, containing little, if any, loam. In retrospect this restriction was probably superfluous for the aim of this study. The great heterogeneity of humus percentage, loam percentage and texture of the humic podzols, varying every square metre, and the strongly changing production classes of the stands, varying between 4.5 and 7.1 m^3/ha.year ("boniteit" I-IV, according to the *yield table of Grandjean and Stoffels (1955)), demonstrated the small scale of this site classification, which is out of proportion to the larger scale of management of stands the PINOGRAM model was developed for.

3.1.4 Choice of provenance for the field study

Because the Scots pine population in the Netherlands includes many stands with unknown and mixed provenances and the *genotype generally differs per tree it was impossible to set up a field study for one specified provenance. So, the provenances in the field study presented here are unknown.

In the Netherlands it is unlikely that examples of all seven developmental phases could be found for one provenance. It is also impossible to *monitor the *growth of a tree during its whole life, although monitoring, of course, explains a tree's *phenotype better than equal-time observations on different trees of different ages do. This is because the histories of the trees are unknown at equal-time observations. Furthermore, the obeserved trees may have a different genotype and may have grown up under the influence of different site conditions.

3.1.5 Location of sample stands

The sample stands used for the field study were located in the Veluwe (Province of Gelderland, the Netherlands) in the forestry areas of Hoenderloo-Ugchelen, Kootwijk-Loobos, Het Loo (Hoog Soeren and Uddel) and De Sysselt (Table 7, Fig. 7).

TABLE 7 Data on stands used for the field study

Observations were done in 1988 and 1989

Forest district	stand no	age of the stand	year of germination	year of planting	sown/planted		initial soil cultivation	
					inter-row spacing	spacing in row		
Ugchelen	71c	8 years	1980	1983	15 dm	15 dm	plant holes	10-30 cm
Ugchelen	80c	13 years	1975	1978	20 dm	20 dm	plant holes	10-30 cm
Ugchelen	1c	13 years	1975	1975	sown	sown	unknown	
Hoog Soeren	?	20 years	1969	?	? dm	? dm	unknown	
Uddel (Loo)	17q	24 years	1964	1964	sown	sown	unknown	
Hoenderloo	85a	24 years	1964	1966	8 dm	10 dm	complete	10-30 cm
Kootwijk	165a	36 years	1952	1952	sown	sown	complete	10-30 cm
Hoenderloo	70b	36 years	1952	1954	10 dm	8 dm	complete	10-30 cm
Hoenderloo	44e	51 years	1937	1937	8 dm	8 dm	unknown	
Uddel (Loo)	83	78 years	1911	?	? dm	? dm	unknown	
Ugchelen	81b	80 years	1908	1980	20 dm	20 dm	plant holes	10-30 cm
Hoenderloo	68b	104 years	1885	1887	? dm	? dm	unknown	
Sysselt	9b	111 years	?	1878	? dm	? dm	unknown	

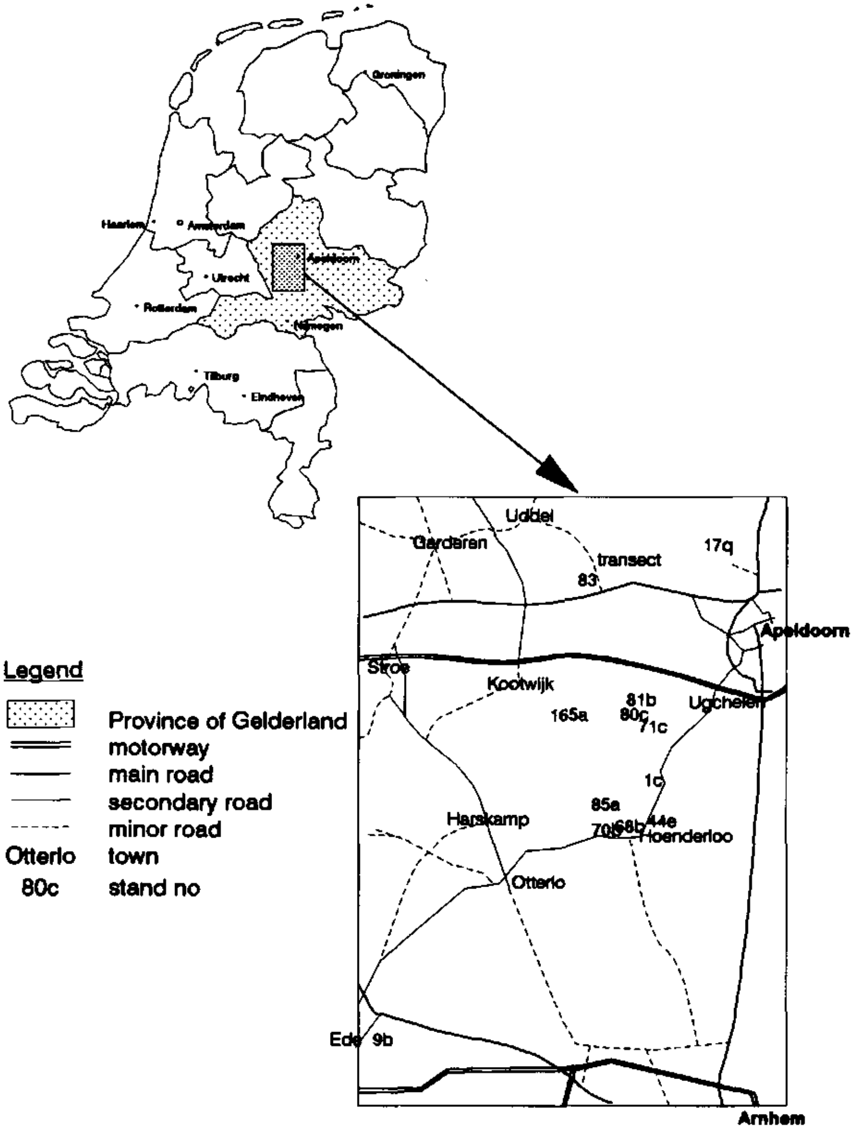


Fig. 7 Locations of the sampled stands of Scots pine in the Veluwe (Province of Gelderland, the Netherlands). For stand numbers: see table 7.

3.1.6 Choice of sample trees

In 1988 the stands in Ugchelen (71c, 80c, 1c, 81b), in Uddel (17q), in Hoenderloo (85a, 70b, 44e, 68b) and in Kootwijk (165a) were sampled. In these stands 8 to 12 representative trees were selected on the basis of the following criteria (see Table B1):

- trees with diameters corresponding to the mean basal area per ha (average tree in the stand; Dutch: opstandsmiddenboom);
- trees selected for the final stand (future tree; Dutch: toekomstboom);
- "variant" trees.

Average trees in the stand have not necessarily grown in a similar way. Some trees may initially have had a relatively fast diameter growth until this was hampered by *interaction with neighboring trees. Other trees may have had a relatively poor diameter growth from the outset, but have never been hampered by *competition. Hence, trees with different life histories may have the same diameter at the moment of measuring.

Trees selected for the final stand are trees assessed as being very likely to meet certain demands relating to the quality and stability of the final stand . According to Schütz and Van Tol (1982 p.175 translated from Dutch) this means:

"- selected trees should be stable or should become stable within a short time; this means they have a well-developed crown and by preference a good h/dbh-ratio (<70 for conifers), which is certainly for most conifers an important selection criterion;

- selected trees should be able to deliver good stem wood (so stems should be straight, with branches as fine as possible and free of injuries. For the most broad-leaved tree species this is the most important selection criterion);
- selected trees should be vital and should have a dense and full crown."

Generally, these selected trees have a diameter larger than the average. The advantage of choosing the "tree types" as mentioned above as representative trees is their standardized definition.

"Variant trees" were sampled to assess the validity of the correlations found between tree dimensions and age, height and growing space (see section 3.2). "Variant trees" included trees with unusually large or very small diameters, or trees with a strongly bent top.

To make it easier to statistically analyse the data per growth phase and per stand, data were gathered from four trees of each of the first two "tree types" and from two, three or four "variant" trees per stand.

As will be discussed in section 3.2, there were many disadvantages involved in using the criteria of "average trees of the stand", "future trees" and "variant" trees. Below, it will be explained how multiple correlations were calculated between tree dimensions such as crown length, crown width and diameter as dependent variables and the tree's height, age and *growing space as independent

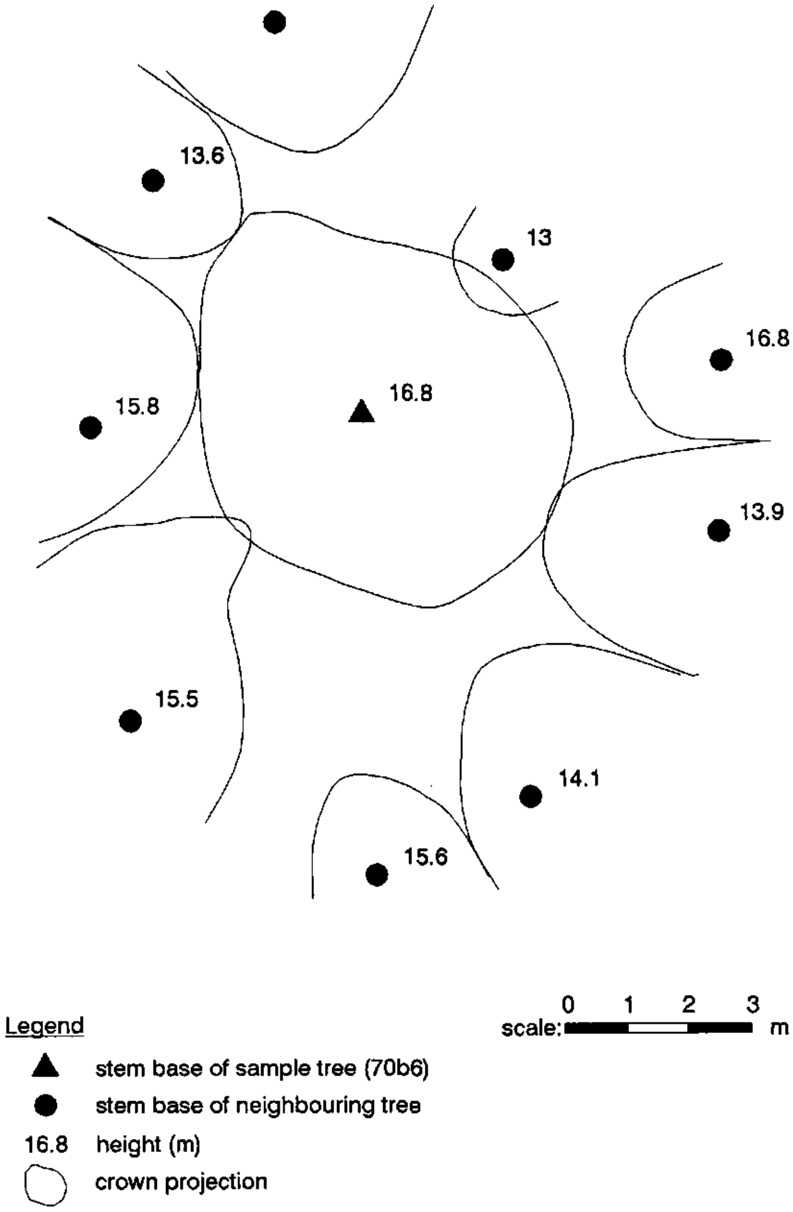


Fig. 8 Crown projection map of tree number 6 in plot 70b (Hoenderlo)

variables. Crooked and leaning trees, crowns deformed by diseases, broken branches, etc. and also released trees (calculated growing space had not yet been used up by the tree) cause poor correlations.

In summer 1989 the stands in de Sysselt (9b), Uddel (83) and a *transect in Hoog Soeren were sampled. The transect in Hoog Soeren had an area of 10 * 40 m^2, in which all 32 trees were sampled. The trees in plots 9b and 83 were chosen according to new criteria, namely:

- a straight stem;
- a crown touched by neighbouring crowns on all sides;
- undamaged trees, thus no broken tops or broken out crown parts (see section 2.2.6).

Of course, it was very difficult to find trees in older stands, that met these criteria. Trees that best fulfilled the criteria were selected.

3.1.7 Data collected from standing trees

Data on the following were collected from each of the 158 *sample trees (see also Table B1):

- height;
- diameter at breast height;
- crown length; being the distance from the top of the tree to the lowest living branch;
- crown projection (Fig. 8); from which mean crown width is derived;
- distance to and between relevant neighbouring trees; relevant neighbouring trees are those trees, that probably influence the sample tree (see section 3.2),
- height of neighbouring trees;
- diameter of neighbouring trees;
- places where neighbouring crowns touch the sample tree's crown;

As well the trees were photographed (Fig. 9) using a shift lens (Minolta; shift CA Rokkor; 35mm / f2.8). It appeared to be impossible to photograph trees without distortion. However, distortion with this lens is less than with a standard lens or a wide-angle lens.

3.1.8 Data collected from felled trees

Thirty eight trees were felled so that form factor and volume could be estimated and to investigate the branch growth of trees per stand. The following data were collected:

- *stem length;
- diameter at 0.3, 1.3, 3.3, 5.3, 7.3, etc. metres from tree base;

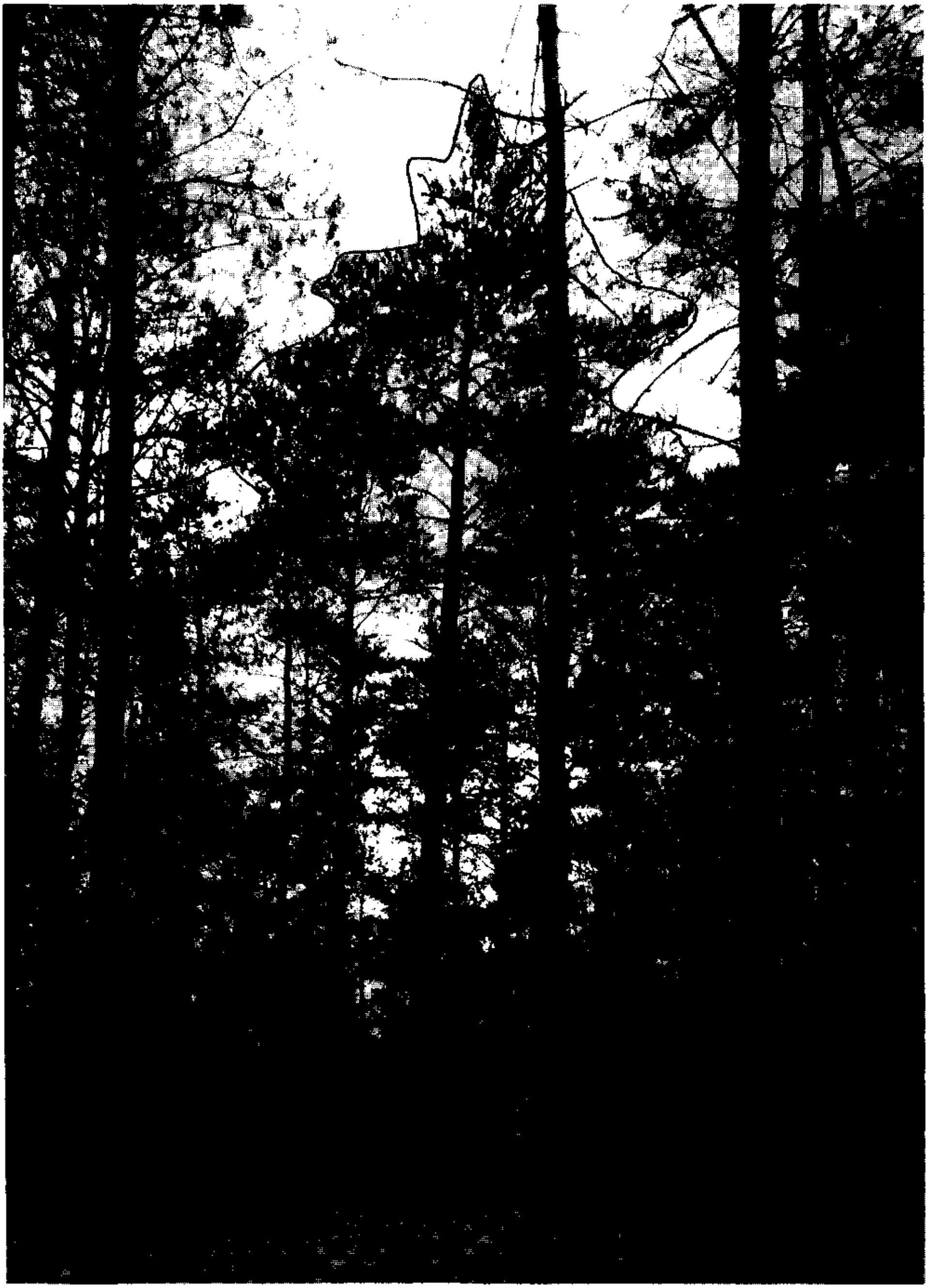


Fig. 9 *Pinus sylvestris L.* Hoenderlo, September 1988, photograph by R.P. Leersnijder. The contour line around the crown shows the crown form of tree number 6 in plot 70b.

- top shoot increment over the five years preceding the measurement.

In addition, whenever possible, three of the largest branches of one whorl were measured at heights of one-quarter, a half and three-quarters of the crown length from the crown base. The following were recorded:
- number of branches per whorl;
- branch length;
- branch diameter at 5 cm from the base of the branch;
- length of the foliated part of the branch;
- width of the foliated part of the branch;
- shoot lengths of the main axis and the observed first order branches over the last five years;
- number of cones;
- degree of needle loss caused by flowering;
- average number of living needle years;
- number of recognizable *reiterations (Oldeman 1990) of the main axis. This is the number of times a lateral axis takes over the function of the main axis.

These data were collected to provide information on the growth of trees at "organism" and "organ" level and are a minor significance for the *growth model described here. In a later study these data may be used for modelling the growth of individual trees at a level between "organ" and "organism" (see section 5.3). In this book, data on branch diameter and form factor are used most (Table B2).

3.2 The analysis of the data

3.2.1 Introduction

The tree's *growing space must be determined so that various correlations can be computed. The equations found by these correlation computations are important for predicting *growth (see also list of symbols at the back of this book).

3.2.2 Computation of growing space: growth area

Various authors have computed *growing space. They include Brown (1965), Jack (1967), Schulz (1968), Prodan (1968), Weihe (1978) and Faber (1983). Generally, the *growth area of a tree has been delimited by the perpendiculars of the lines between the *sample tree and its neighbours, resulting in a polygon. The distance from the sample tree to the perpendiculars is often determined with the aid of tree dimensions. Several authors use diameter in the following equation for computing growth area (e.g. Carvalho Oliveira, 1980):

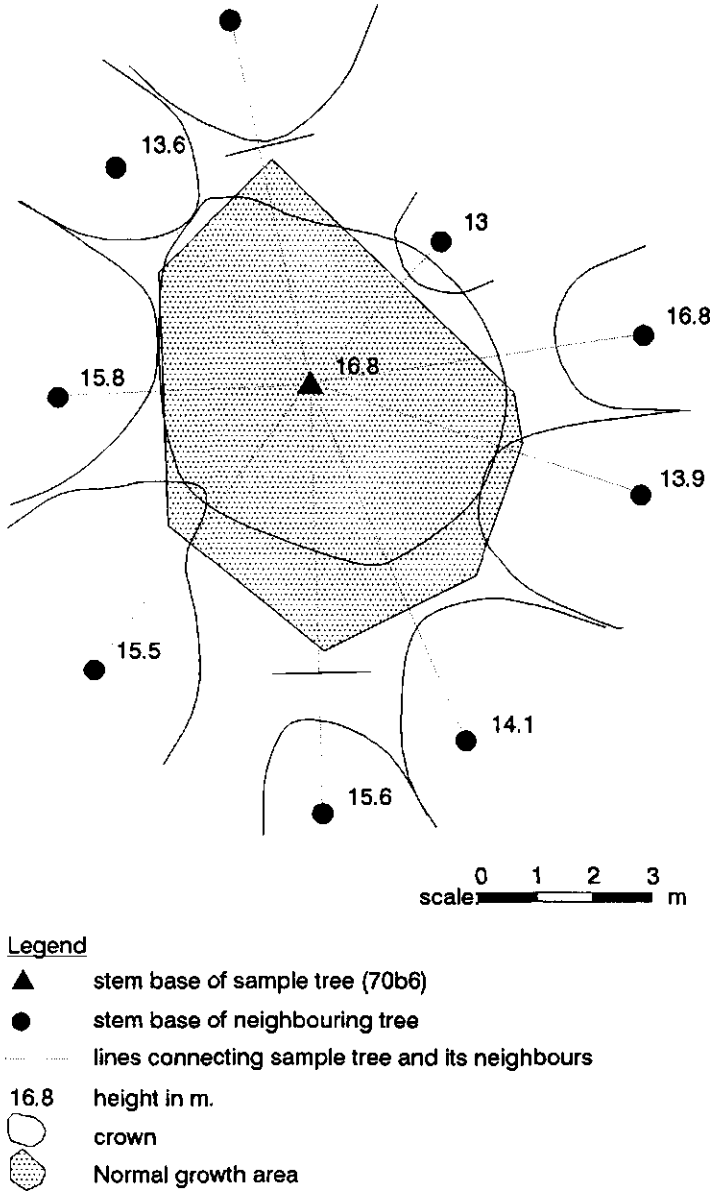


Fig. 10 The normal growth area as defined for tree number 6 in plot 70b (Hoenderlo).

$$a[nr][i] = \frac{dbh[nr]}{dbh[nr] + dbh[i]} * A[nr][i] \tag{12}$$

in which
a[nr][i] = growth area vector between sample tree and neighbouring tree (m)
dbh = diameter on breast height (cm)
nr = number of sample tree
i = number of neighboring tree
A[nr][i] = distance between sample tree and neighboring tree (m)

In the rest of this book *a[nr][i]* is called the ***normal growth area vector**.

If a sample tree and a neighbouring tree have the same diameter, then *a[nr][i]* = ½*A[nr][i]*. For every neighbour, a perpendicular is drawn on the line connecting the sample tree *nr* and the neighbouring tree *i* at a distance *a[nr][i]*. The area enclosed by the perpendiculars is, by definition, the normal growth area (Fig. 10). There are various mathematical methods for finding the numerical value of this area (Jack 1967, Schulz 1968, Prodan 1968).

To estimate the growth area Faber (1983) used a grid with pixels of one square decimetre and superimposed this on a *transect. Each pixel is assigned to the tree with the greatest factor of influence *U*, using the equation:

$$U = \frac{v^C}{A^2} \tag{13}$$

in which:
v = stem volume in dm^3
A = distance from pixel to tree (m)
U = factor of influence
C = empirical constant of competition

The *growth area is calculated by counting the pixels assigned per tree.

The advantage of this method is that the growth area of a large tree next to a small tree may extend further than the distance between both stems *A[nr][i]* and is not established by the rigid perpendiculars of the polygon method.

A disadvantage, however, is that large trees in stands with many gaps are assigned far too many pixels. Furthermore the entire area is divided among the different trees in Faber's model, whereas when perpendiculars are used, small areas are often not assigned to any tree because they generally do not intersect in the same point (Fig. 24: space excluded by the model).

A disadvantage of diameter-dependent growth area computations is that this growth area can only be used to predict the growth of individual trees within closed stands, because the basal area increment per ha is predicted on the basis of *dominant height increment (Faber 1983). This basal area increment per ha has to be divided among the trees, in proportion to their growth area. This can be done in closed stands, but in more open stands the following problems appear:

- the basal area increment per ha will be smaller than may be expected from the height growth;
- adjacent to large gaps in the canopy a tree may not completely use its large growth area calculated.

In this case, the basal area increment of a tree can not be predicted with the help of the above model and thus its growth area and volume can not be predicted.

This problem does not arise when the growth area of a tree can be determined from that tree's height and the height of its neighbours. This means that height growth is the only "black box" for growth predictions and can be assumed to depend directly upon the *interaction between site characteristics and a tree's genetic traits.

In this book, *growth area is determined by polygons. **The *growth area vector *a[nr][i]*, however, is not computed with the help of diameters, but with the help of heights:**

$$a[nr][i] = \frac{h[nr]^{C}}{h[nr]^{C} + h[i]^{C}} * A[nr][i] \tag{14}$$

in which

h[nr] = height of sample tree (m)
h[i] = height of neighbouring tree (m)
nr = sample tree number
i = number of neighbouring tree
A[nr][i] = distance between sample tree and neighbouring tree (m)
C = *competition constant

The empirical constant C has been added to the above equation to improve the expression of *competition between trees caused by differences in height. Faber (1983) used a similar measure of competition when determining the influence factor *U* (see preceding page). Later (section 3.2.3) the *growth area will be calculated for different values of C.

To compute the growth area all relevant neighbours are numbered clockwise.

The known factors are:

h[nr] = height of sample tree (m)
h[i] = height of neighbouring tree *i* (m)
h[i+1] = height of neighbouring tree *i+1* (m)
A[nr][i] = distance between sample tree and neighbour *i* (m)
A[i][i+1] = distance between neighbour *i* and neighbour *i+1* (m)
C = *competition constant (see section 3.2.3)

The unknown factors are:

a[nr][i] = normal growth area vector in the direction of neighbour *i* (m)
a[nr][i+1] = normal growth area vector in the direction of neighbour *i+1*(m)
S[i] = intersection of perpendiculars of vector *a[nr][i]* and vector *a[nr][i+1]*
r[i] = distance between sample tree and *S[i]* (m)
x[i] = angle between vector *a[nr][i]* and vector *r[i]* (rad)
y[i] = angle between vector *a[nr][i+1]* and vector *r[i]* (rad)
z[i] = angle between vector *a[nr][i]* and vector *a[nr][i+1]* (rad)

The normal growth area vectors *a[nr][i]* and *a[nr][i+1]* are calculated with the help of equation 14. The other unknown factors are calculated as follows:

$$\cos(z[i]) = \frac{A[nr][i]^2 + A[nr][i+1]^2 - A[i][i+1]^2}{2A[nr][i] * A[i][i+1]} \tag{15}$$

$$\cos(x[i]) = a[nr][i]/r[i] \quad \rightarrow \quad x[i] = \arccos(a[nr][i]/r[i]) \tag{16}$$

$$\cos(y[i]) = a[nr][i+1]/r[i] \quad \rightarrow \quad y[i] = \arccos(a[nr][i+1]/r[i]) \tag{17}$$

$$\cos(z[i]) = \cos(x[i]+y[i]) = \cos(x[i])\cos(y[i]) - \sin(x[i])\sin(y[i]) =$$

$$= \frac{a[nr][i] * a[nr][i+1] - \sqrt{(r[i]^2 - a[nr][i]^2)(r[i]^2 - a[nr][i+1]^2)}}{r[i]^2} \quad \Rightarrow \tag{18}$$

$$r[i]^2 = \frac{a[nr][i]^2 + a[nr][i+1]^2 - 2a[nr][i] * a[nr][i+1]\cos(z[i])}{\sin^2(z[i])} \tag{19}$$

If *x* and *y* are defined as being larger than zero, the following states may be distinguished to compute the part of the growth area *area[i]* that is defined by the sample tree and two neighbours (Fig. 11):

$$\textit{if } z[i] = x[i] + y[i] \quad \rightarrow \quad \textit{Area}[i] = \frac{1}{2}a[nr][i]^2\tan(x[i]) + \frac{1}{2}a[nr][i+1]^2\tan(y[i]) \tag{20}$$

$$\textit{if } z[i] = x[i] - y[i] \quad \rightarrow \quad \begin{array}{l} \textit{Area}[i] = \frac{1}{2}a[nr][i]^2\tan(z[i]) \\ \textit{Remaining area}[i] = -\frac{1}{2}r[i]^2\sin^2(y[i])\tan(z[i]) \end{array} \tag{21}$$

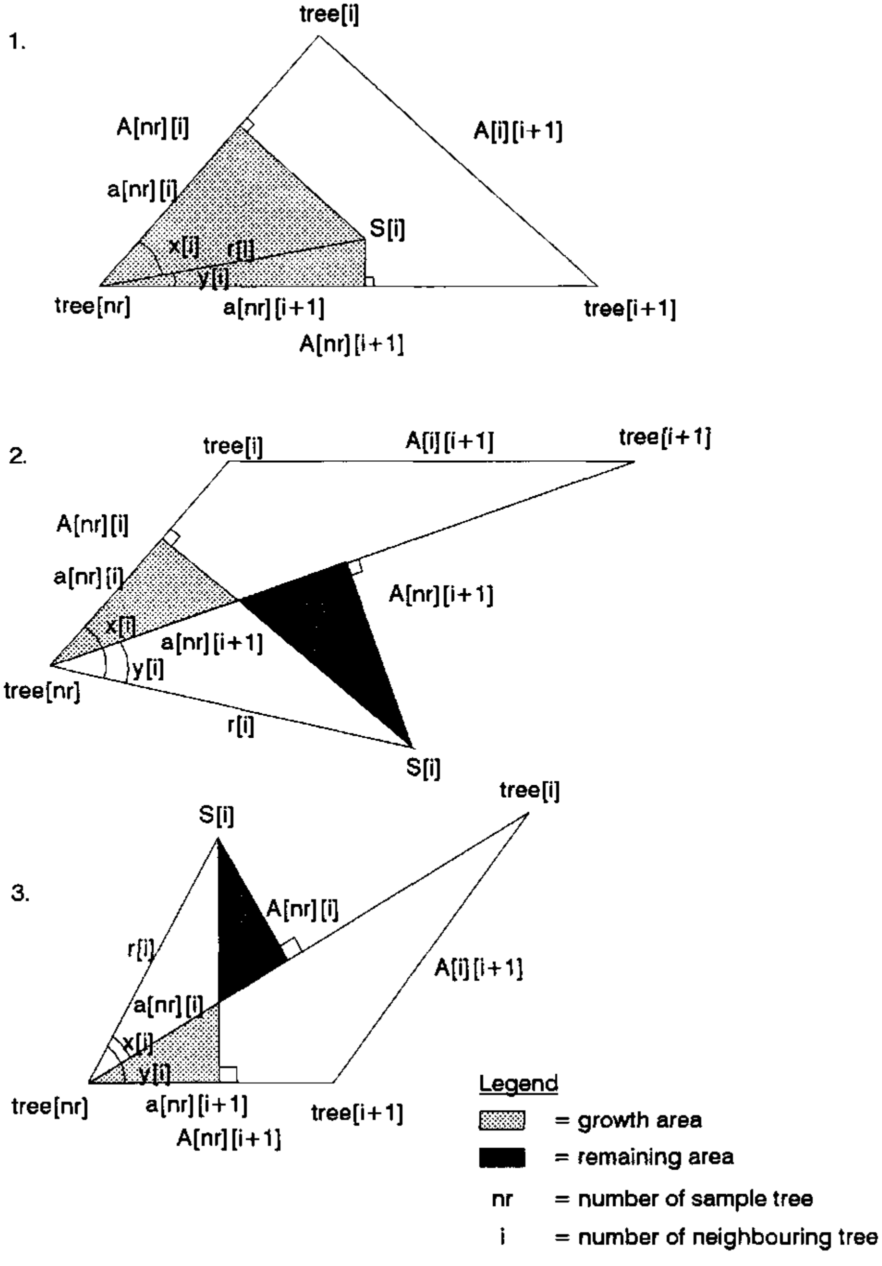


Fig. 11 Determination of the growth area included by a sample tree and two neighbours. Three possibilities are distinguished:
1. z[i] = x[i] + y[i]
2. z[i] = x[i] - y[i]
3. z[i] = y[i] - x[i]
(for explanation of symbols, see text)

$$\text{if } z[i] = y[i] - x[i] \rightarrow \begin{array}{l} Area[i] = \frac{1}{2}a[nr][i+1]^2\tan(z[i]) \\ Remaining\ area[i] = \frac{1}{2}r[i]^2\sin^2(x[i])\tan(z[i]) \end{array} \tag{22}$$

$$\text{if } z[i] > \pi \rightarrow Area[i] \text{ cannot be calculated.} \tag{23}$$

The remaining area in equation 21 and in Fig. 11.2 is the area to be subtracted from the area formed by sample tree *nr*, neighbour *i+1* and neighbour *i+2*. By analogy with equation 21, the remaining area in equation 22 is the area to be subtracted from the area formed by sample tree *nr* and its neighbour *i-1* and neighbour *i*. The total *growth area of a sample tree is defined by the sum of the parts of the area.

However, there is still a problem when establishing the growth area. In the field it is sometimes difficult to see which trees do influence the sample tree and which trees do not. In Figs 10 and 12 it is easy to see which neighbours have no influence. The growth area can be calculated with the "STAND" computer program (Appendix A) that automatically excludes the neighbours that have no influence on the sample tree. This exclusion of neighbouring trees is defined by two conditions (see also section 4.13 and Fig. 12):

$$r[i-1] > r[i] \quad and \quad z[i-1] = x[i-1] - y[i-1] \tag{24}$$

$$r[i+1] > r[i] \quad and \quad z[i+1] = y[i+1] - x[i+1] \tag{25}$$

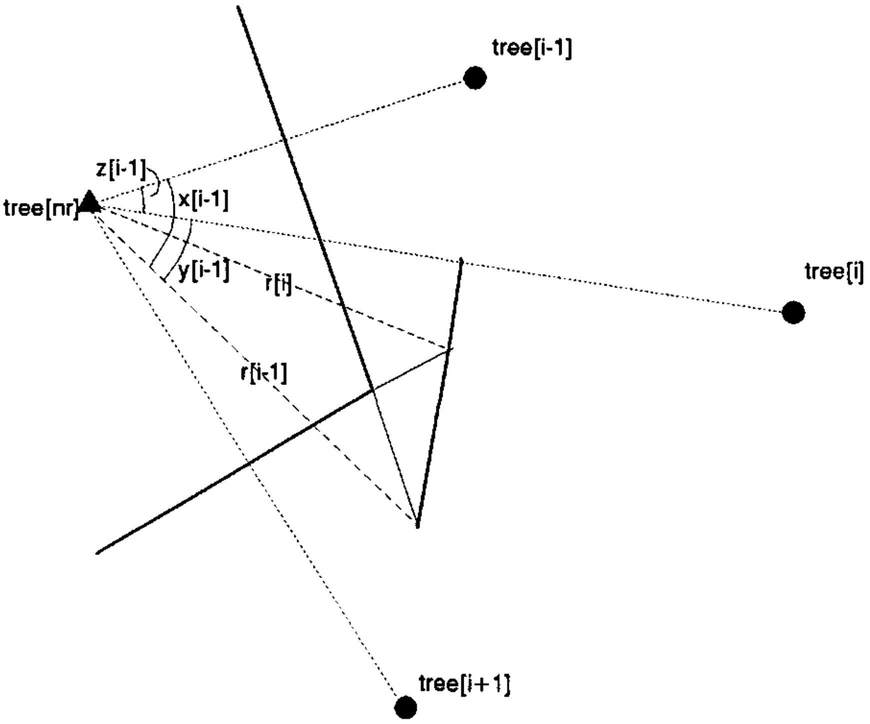
z[i] is the angle, constructed by the sample tree, neighbour *i* and neighbour *i+1*, *z[i+1]* is constructed by the sample tree, neighbour *i+1* and neighbour *i+2*, etc.

When a tree appears to have no influence on the sample tree, distance *A[i][i+1]* between the previous neighbour and the next neighbour is calculated according to the equation:

$$A[i][i+1]^2 = A[nr][i]^2 + A[nr][i+1]^2 - 2A[nr][i]*A[nr][i+1]*\cos(z[i]+z[i+1]) \tag{26}$$

The computer program removes data on trees that have no influence and calculates new distances between consecutive neighbours *A[i][i+1]* and the total growth area. The mean normal growth area vector $\bar{a}$ is calculated as follows:

$$\bar{a} = \sqrt{\frac{growth\ area}{\pi}} \tag{27}$$



Legend

▲	stem base of sample tree
●	stem base of neighbouring tree
———	perpendiculars on the normal growth area vectors
···········	lines connecting sample tree and its neighbours
- - - - - - -	line from sample tree to the intersection of consecutive perpendiculars

Fig. 12 Eliminating trees that do not influence the growth area of the sample tree
tree[i] will be eliminated if r[i-1] > r[i] and z[i-1] = x[i-1] - y[i-1]
(or if r[i+1] > r[i] and z[i+1] = y[i+1] - x[i+1])
x[i-1] = angle between vector to tree[i-1] and vector r[i-1]
y[i-1] = angle between vector to tree[i] and vector r[i-1]

3.2.3 Correlations

The previous section described the method used to calculate the *normal growth area of a tree. The next step is to find the *competition constant C, that gives the best results when calculating correlations. Because different values of C result in different values for the mean *normal growth area vector $\bar{a}$, which is one of the independent factors in the non-linear regressions calculated, in which values for C ranged from 1 to 6. The stem diameter and the mean crown width as well as the crown length were found to correlate with the age, height and mean normal growth area vector.

The mean crown width was directly computed from crown projection with the help of equation 28.

$$\overline{cw} = 2 * \sqrt{\frac{crown\ projection}{\pi}} \tag{28}$$

in which $\overline{cw}$ = mean crown width (m)

Non-linear regressions were computed with the help of the "STATGRAPH" statistical package (STATGRAPHICS 1986). Table 8 gives the results for different values of *competition constant C.

TABLE 8 Correlations and coefficients of variation found for different values of constant C.

		constant C					$a[nr][i] = \frac{h[nr]^C}{h[nr]^C + h[i]^C} * A[nr][i]$
		2.00	3.00	4.00	5.00	6.00	$\bar{a}$ = see p.3.2.2
diameter	R²	0.95	0.95	0.95	0.96	0.96	$dbh = t^{D1}.h^{D2}.\bar{a}^{D3}.D4$
	c.v.	18%	17%	17%	17%	18%	
crown length	R²	0.69	0.72	0.73	0.74	0.72	$cl = t^{CL1}.h^{CL2}.\bar{a}^{CL3}.CL4$
	c.v.	21%	20%	20%	20%	25%	
crown width	R²	0.84	0.84	0.84	0.84	0.83	$\overline{cw} = t^{CW1}.h^{CW2}.\bar{a}^{CW3}.CW4$
	c.v.	20%	19%	20%	20%	24%	

Table 8 indicates that at different values of *competition constant C the correlations and coefficient of variation do not differ greatly. It was decided to assign a value of 4 to C. Derived equations are:

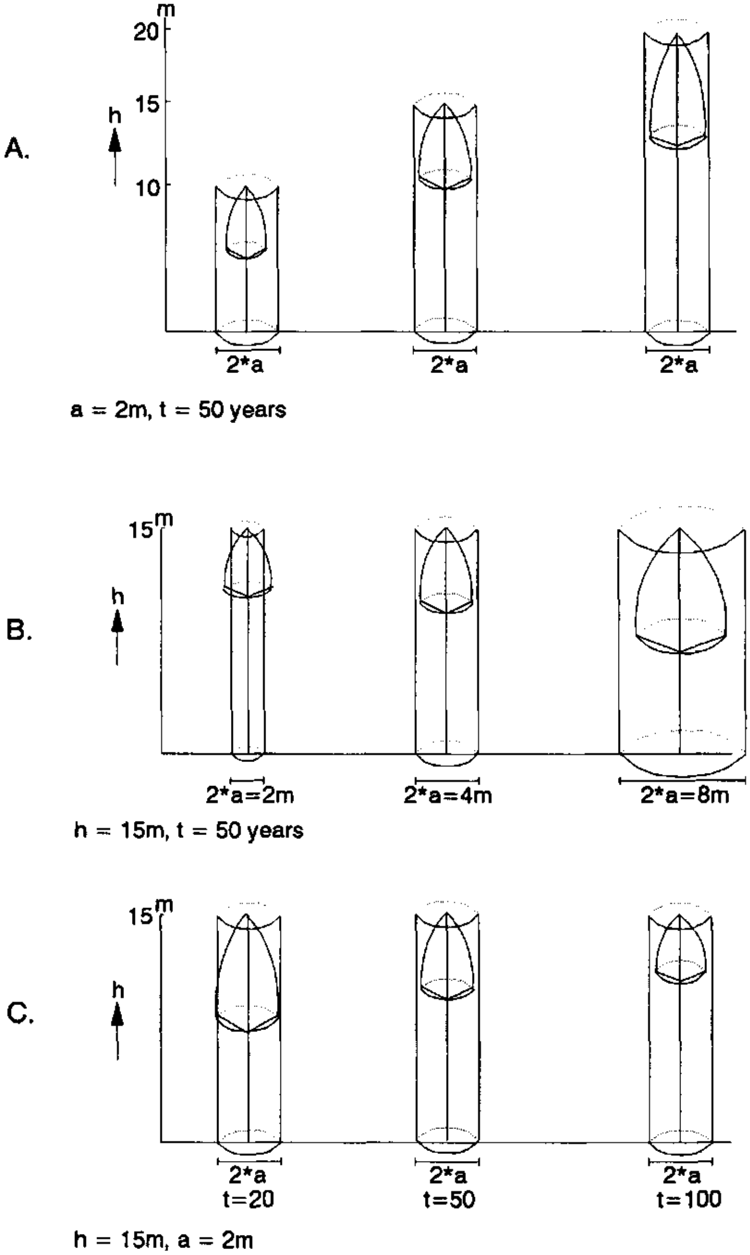


Fig. 13 Crown dimensions calculated according to equations 30 and 31 for A. different height (h), B. different growth area (a) and C. different time (t).

$$dbh = t^{D1} * h^{D2} * \bar{a}^{D3} * D4 \tag{29}$$

$$cl = t^{CL1} * h^{CL2} * \bar{a}^{CL3} * CL4 \tag{30}$$

$$\overline{cw} = t^{CW1} * h^{CW2} * \bar{a}^{CW3} * CW4 \tag{31}$$

The values of the constants found for these equations are given in Table 9. **Note that constants are given in capital letters and the variables in lower case.**

TABLE 9 Constants found for equations (29), (30) and (31) for diameter, crown length and crown width.

D1 = first constant for *dbh* = 0.14240 (see equation 29) etc.

constant	1	2	3	4
D	0.14240	0.63577	0.43714	1.58379
CL	-0.31238	0.45056	0.52910	3.87783
CW	-0.07894	0.16220	0.70191	2.02684

In Table B1 of appendix B relevant tree data are given. Table B3 of appendix B shows the correlations and coefficients of variation found per stand. Fig. 13 gives some examples of the influence of a tree's age, height and mean *normal growth area vector on its crown dimensions according to the equations (30) and (31).

One of the reasons for relatively large coefficients of variation may be the use of leaning trees, trees with deformed crowns and released trees (especially in older stands) (see section 3.1.6). In the following sections errors causing poor correlations and high coefficients of variation will be treated (see also Fig. 14).

3.2.4 Crown length

Fig. 15 shows the relation between measured and calculated crown length. Though the coefficient of variation is only 20% some trees deviate much more from the calculated value. Old trees are particularly likely to deviate considerably. The reasons for these deviations may be summarized as follows (Fig. 14):

- Crown length is the length from the top of the tree to the lowest living branch. This branch could be a solitary branch, while the crown proper starts higher. The vitality of this branch might be linked to the local light climate. A crown may also be strongly asymmetrical, because the tree experiences more *competition for light on one side than on another. So it is possible that a tree is unable to exploit a large *growth area on one side, whereas it experiences

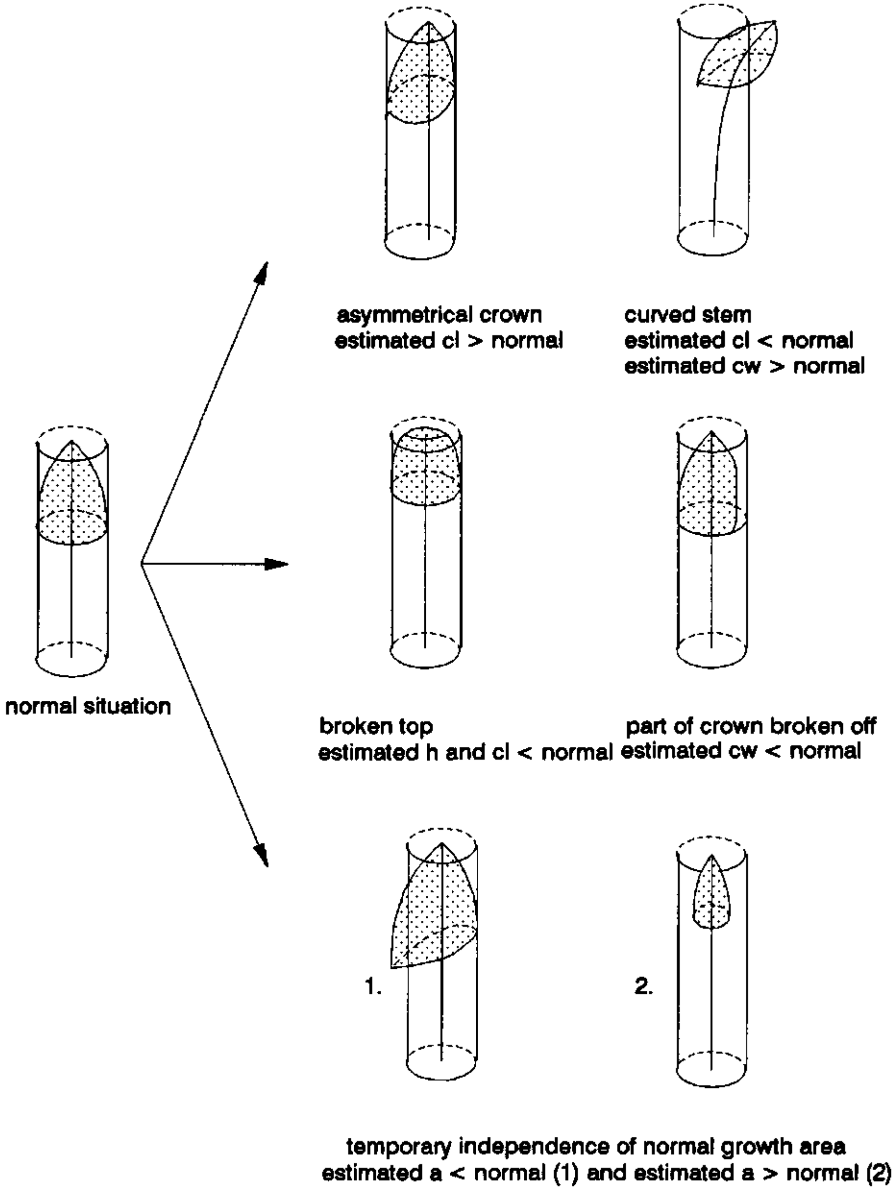


Fig. 14 Samples of errors in field data. The situations described above result in a poor correlation between dependent variables such as crown length, crown width or diameter, and independent variables such as height and growth area. Here, the normal situation means that dependent variables are well predicted by the equations.

a strong competition from one or more neighbours on other sides. This could be a very important cause of the deviations found.

- After a tree has been released, there is temporarily no competition for space with its neighbours. The crown can grow out freely until the available space is again restricted by neighbouring trees. Old trees take a very long time to fill the gaps created after release. If these gaps are still open, the correlation with the growth area is minor. In other words: crown length may be shorter than could be expected on the grounds of the normal growth area.
- Tree height and crown base above a height of eight metres were measured with a Blume-Leisz meter. Hence, deviations of 5 to 10% as a result of measuring errors cannot be excluded.
- Differences in *genotype of trees may result in a different need for light of the various trees. This affects the speed at which branches that do not receive enough light may die. These branches generally remain in the lower and inner crown part, so their dying also affects the crown length.

3.2.5 Crown width

Crown width also shows considerable deviations (Fig. 16). Relatively large errors may appear when the vertical crown projection is measured, because there was no tool available that could measure the crown projection more accurately than a measuring tape and a pair of eyes. (The measuring tape was connected to the stem and to the observer, who was consecutively standing below the different crown periphery points in order to measure the distances to the stem.) Furthermore, it is often unclear whether a small branch, that stretches out of the crown, should be taken into account.

The possible error resulting from releasing a tree, mentioned in section 3.2.4, and the possibility of influence from genetic traits and site characteristics also apply for the calculation of crown width. Furthermore, some leaning trees have a relatively large mean crown width, whereas some others have relatively small crowns, because branches or crown parts have broken off or died (Fig. 16).

3.2.6 Stem diameter

Stem diameter shows the best correlation with its age, height and *normal growth area vector (Fig. 17). Here too an error may arise if the tree has been released and the influence of genetic traits and site characteristics mentioned in the last two sections may also be significant. Diameters are relatively simple to measure, so errors of measuring may not be very large.

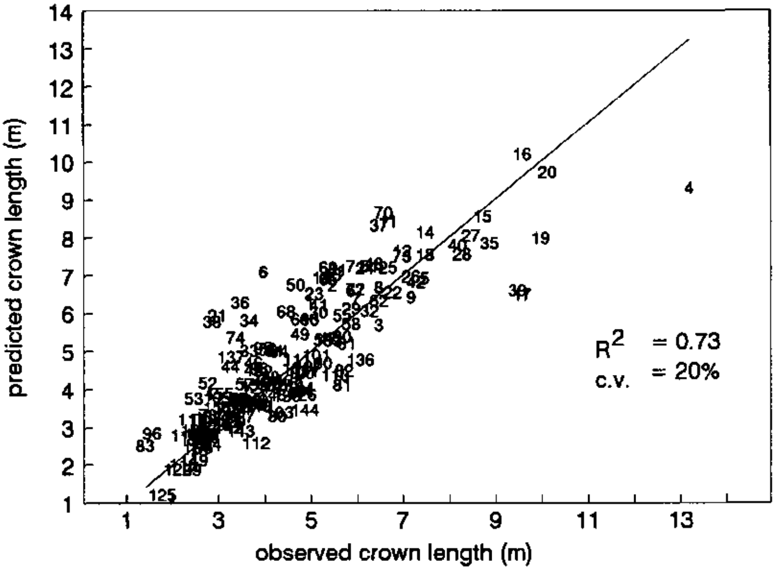


Fig. 15 Correlation between predicted and observed crown length of 158 sampled trees of Scots pine

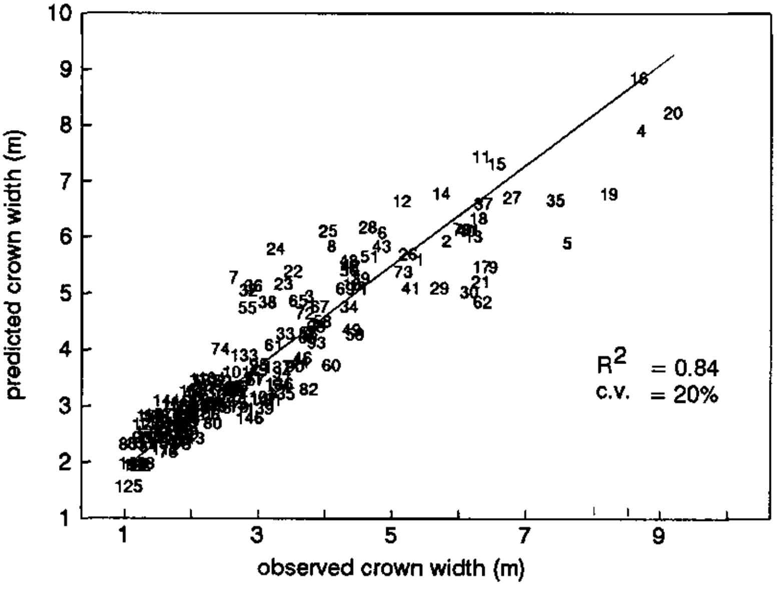


Fig. 16 Correlation between predicted and observed crown width of 158 sampled trees of Scots pine

3.2.7 Age

It can be assumed that the ages of the trees in the field survey are well documented in stand tables, and therefore any deviations in determining the tree dimensions will be minor. This was confirmed by counting the annual rings of the stems of the felled trees (section 3.2.12).

3.2.8 Height

Deviations occurred most frequently in taller trees, because of the measuring inaccuracies of the Blume-Leisz meter. Tree height is not always the same as tree length. Because of curving and *reiteration, a tree may be much longer than it is tall.

3.2.9 Growth area

*Calculating the growth area according to the method proposed has the disadvantage that the growth area of a large tree next to a small tree may extend further than the distance between both stems. Hence, in the model crowns will not easily expand over another tree. Some trees that are much larger or smaller than their neighbours, may have a growth potential that is insufficiently explained by the normal growth area. Released trees show a poor relation between tree dimensions and normal growth area.

3.2.10 Form factor

As mentioned in section 3.1.8, 38 *sample trees were felled. The data from these trees on stem diameter at different heights, were used to determine the form factor of a tree (appendix B: Table B2). The form factor was found to correlate with the tree length *l*, crown length *cl* and stem diameter *dbh* (Fig. 18).

$$f = l^{F1} * cl^{F2} * dbh^{F3} * F4 \tag{32}$$

The matching constants are given in Table 10

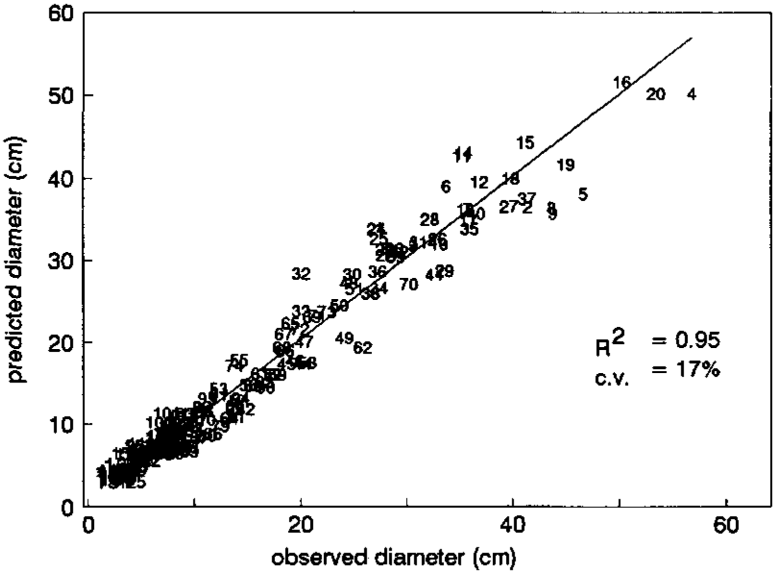


Fig. 17 Correlation between predicted and observed diameter of 158 sampled trees of Scots pine

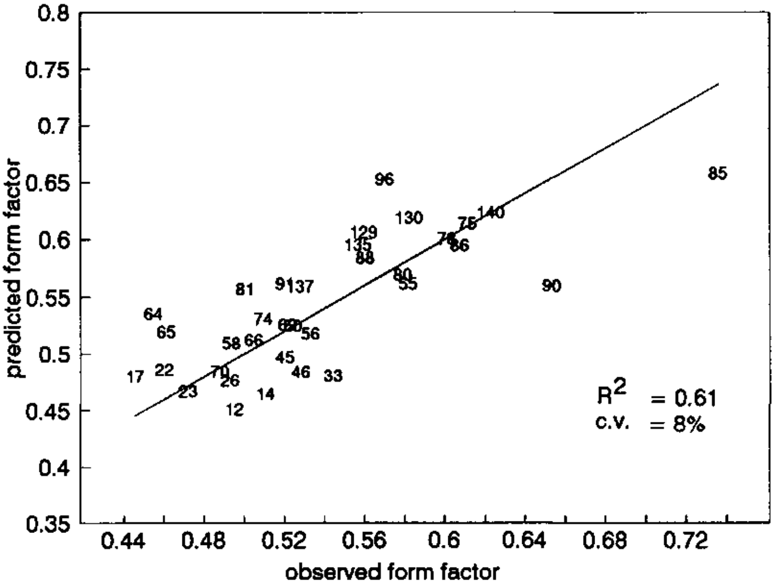


Fig. 18 Correlation between predicted and observed form factor of 38 sampled trees of Scots pine

TABLE 10 Constants found for equation 32 for form factor

constant	1	2	3	4	R^2	c.v.
F	0.01737	0.17124	-0.28462	0.86393	0.61	8%

thus F1 = 0.01737

Although the standard deviation is rather small, the correlation is not very good. The constants F1, F2 and F3 of Table 10 indicate that crown length and diameter better explain the form factor of a tree than the tree length does (see also section 2.3).

3.2.11 Branch diameter

Branch diameters five centimetres from the stem were measured on the felled trees. The branches measured were about one quarter, a half and three quarters along the crown length, starting from crown base. It was intended to measure the three thickest branches of one whorl at these three levels. This was no problem in the case of young trees, but many old trees often had less than three branches per whorl. Branch diameters of the lowest branches of the crown generally do not differ very much from those a quarter of a crown length higher. Sometimes the lowest branches were even smaller.

Mean branch diameter in the lower part of the crown was expected to show a good correlation with tree length l crown length cl and mean crown width $\overline{cw}$.

$$dbranch = l^{\mathrm{DB1}} * cl^{\mathrm{DB2}} * \overline{cw}^{\mathrm{DB3}} * \mathrm{DB4} \tag{33}$$

Table 11 shows the result of correlation:

TABLE 11 Constants found for equation 33 for the branch diameter in the lowest part of the crown

constant	1	2	3	4	R^2	c.v.
DB	0.06079	0.70171	0.51039	0.46735	0.77	20%

thus DB1 = 0.06079

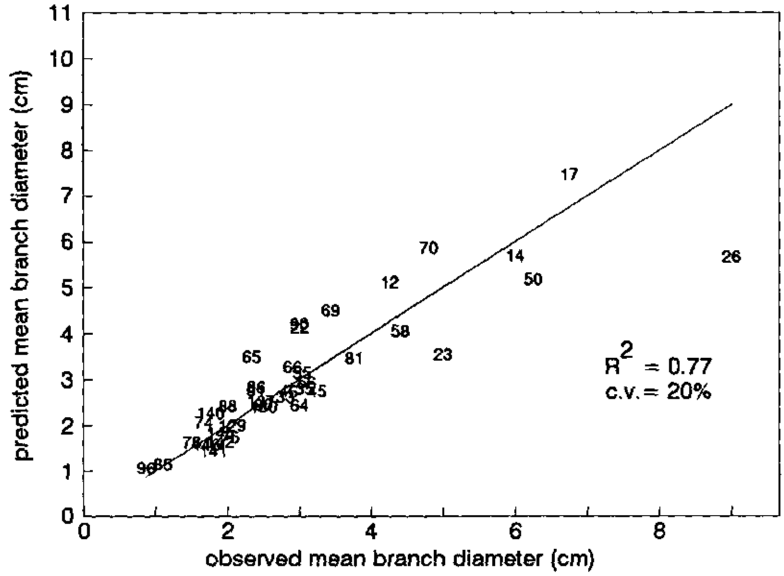


Fig. 19 Correlation between predicted and observed mean branch diameter in the lower part of the crown of 38 sampled trees of Scots pine.

The correlation and coefficient of variation (Fig. 19) were sufficiently good to justify using equation 33 in a predictive model. The deviations might be caused by strongly reiterated or rather broad branches. Hence, the correlation with crown width may be spurious.

If only one branch was present per whorl, this also causes a distortion, because that branch had grown in one direction only and hence branch length and branch diameter may not have shown a good correlation with mean crown width. Branch diameter was incorporated in the model, because it is a quality characteristic of the stem to be harvested. Large branch diameters low down on the stem deliver bad quality.

3.2.12 Other correlations

As well as mean branch diameter in the lower part of the crown, multiple correlations and coefficients of variation were also calculated for mean branch length, mean branch diameter, mean length and mean width of the foliated part of the branches at different heights in the crown (see section 3.1.8). Branch diameter and branch length were found to be correlated with tree length, crown length and crown width, and the mean length and width of the foliated part of the branches were found to be correlated with branch length and branch diameter (Table 12).

As expected, branch length in the lower part of the crown correlated well with tree length, crown length and mean crown width and had a small coefficient of variation. In the middle and upper part of the crown, the correlation was considerably smaller and the coefficient of variation considerably larger.

The mean length of the foliated part of the branch also correlated well with branch length and branch diameter and had a small coefficient of variation. The largest coefficient of variation was found for the mean width of the foliated part of the branch though the correlation was not poor. This is probably because no measured data were available on the space that a branch may occupy (called the 'growing space of the branch, analogous to the growing space of a tree).

Finally, the mean basal area increment at different stem heights (Fig. 20) was compared with the mean increment of the topshoot in the five years preceding the measurements (Table 13). The results are poor (very large coefficients of variation). An important reason for this may be that only the top shoot was involved in these calculations, instead of all living shoots. This will not be discussed any further.

TABLE 12 Correlations and coefficients of variation for different dimensions of branches

bottom of crown	R^2	c.v.	equation
branch length	0.83	20%	$l\_branch=l^{\mathrm{LB1}}*cl^{\mathrm{LB2}}*\overline{cw}^{\mathrm{LB3}}*\mathrm{LB4}$
branch diameter	0.85	22%	$d\_branch=l^{\mathrm{DB1}}*cl^{\mathrm{DB2}}*\overline{cw}^{\mathrm{DB3}}*\mathrm{DB4}$
mean width of the foliated part of the branch	0.79	27%	$cw\_branch=l\_branch^{\mathrm{CWB1}}*d\_branch^{\mathrm{CWB2}}*\mathrm{CWB3}$
mean length of the foliated part of the branch	0.87	17%	$cl\_branch=l\_branch^{\mathrm{CLB1}}*d\_branch^{\mathrm{CLB2}}*\mathrm{CLB3}$

middle of crown	R^2	c.v.	equation
branch length	0.56	24%	$l\_branch=l^{\mathrm{LB5}}*cl^{\mathrm{LB6}}*\overline{cw}^{\mathrm{LB7}}*\mathrm{LB8}$
branch diameter	0.73	28%	$d\_branch=l^{\mathrm{DB5}}*cl^{\mathrm{DB6}}*\overline{cw}^{\mathrm{DB7}}*\mathrm{DB8}$
mean width of the foliated part of the branch	0.56	37%	$cw\_branch=l\_branch^{\mathrm{CWB4}}*d\_branch^{\mathrm{CWB5}}*\mathrm{CWB6}$
mean length of the foliated part of the branch	0.91	10%	$cl\_branch=l\_branch^{\mathrm{CLB4}}*d\_branch^{\mathrm{CLB5}}*\mathrm{CLB6}$

top of crown	R^2	c.v.	equation
branch length	0.72	28%	$l\_branch=l^{\mathrm{LB9}}*cl^{\mathrm{LB10}}*\overline{cw}^{\mathrm{LB11}}*\mathrm{LB12}$
branch diameter	0.62	34%	$d\_branch=l^{\mathrm{DB9}}*cl^{\mathrm{DB10}}*\overline{cw}^{\mathrm{DB11}}*\mathrm{DB12}$
mean width of the foliated part of the branch	0.77	41%	$cw\_branch=l\_branch^{\mathrm{CWB7}}*d\_branch^{\mathrm{CWB8}}*\mathrm{CWB9}$
mean length of the foliated part of the branch	0.88	18%	$cl\_branch=l\_branch^{\mathrm{CLB7}}*d\_branch^{\mathrm{CLB8}}*\mathrm{CLB9}$

TABLE 13 Basal area increment dependent upon top shoot increment

	R^2	c.v.
basal area increment at 1.3 m.	0.77	50%
basal area increment at 0.5 * tree height	0.51	72%
basal area increment at 0.75 * tree height	0.59	55%

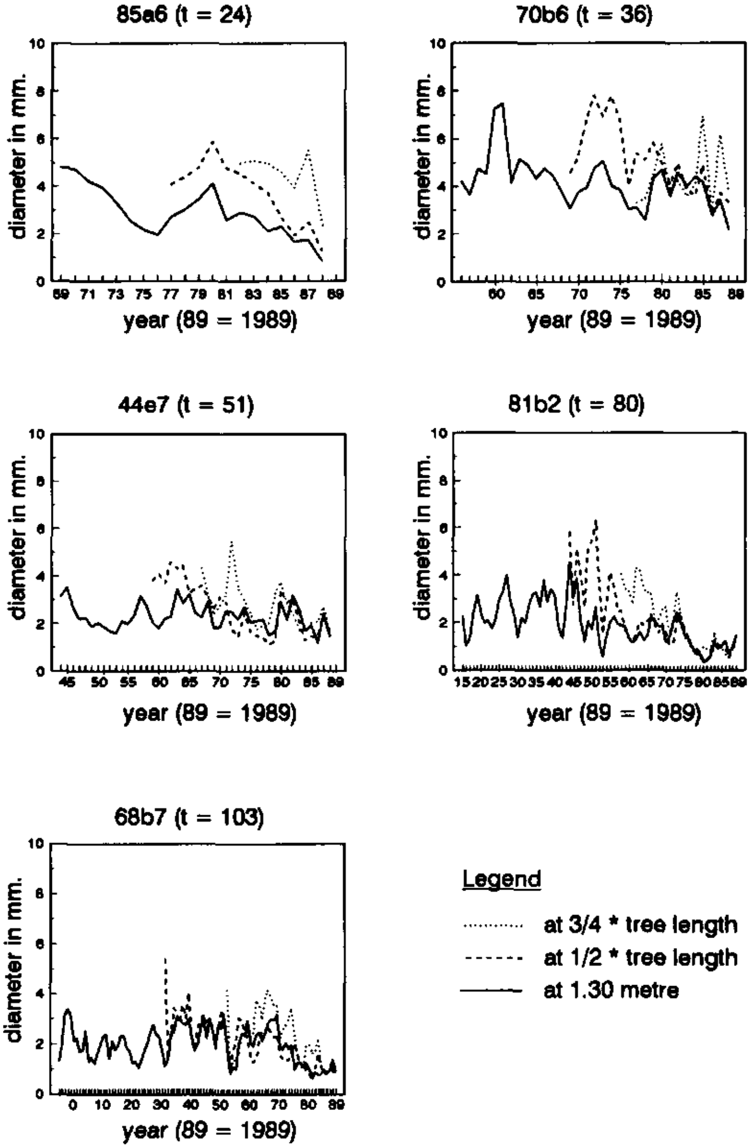


Fig. 20 Annual ring widths of stems of trees of different ages and at different distances from the tree base for five sample trees.

4 THE PINOGRAM SIMULATION MODEL

4.1 Introduction

This chapter discusses how the computer simulation program was constructed with the help of the growth equations derived from the field study (chapter 3). The programming language C will not be discussed in detail; readers are referred to the various handbooks of Microsoft Corporation (Microsoft Quick C 1984-1989). However, some of the concepts of this language need to be explained and this is done briefly in section 4.2. Figure 21 is a flow diagram of the main *structure of the PINOGRAM (= PINe GRowth Area Model) computer simulation program. Each section is preceded by the file names of the program code discussed in that section.

4.2 Declaring the variables, structures and functions

(FILES: SIM.H, TEXT.H, PINOGRAM.C).

Before a C-program can run, all constants used need to be defined and the global variables and *functions used need to be declared. Global variables are variables that are active anywhere in the program. Since there are hundreds of global variables, they have to be arranged properly. This is done by putting them in arrays and *structures. An array is used to assign a range number to a range of variables that have similar characteristics. For example, the array *release[i]* assigns the range number *i* to the variable *release*.

When a thousand trees are involved, *i* can have a value between 1 and 1000. Text is also kept in an array. For example, *text[i]* is a character of text in array *text*. In turn, variables and arrays of variables may be arranged in structures. The structure *tree*, for instance, contains data about tree number, the x and y coordinates, *S value, height, diameter, branch diameter, *growth area, *maximum distance of influence, form factor, volume and probable age at death. Finally, range numbers may be given to structures, thus creating an array of structures. In this way the structure *tree[127]* contains the above data for the 127th tree. We find in *tree[127].h* the height of tree 127.

The program is divided into various *functions, also called *subroutines. The subroutines used also have to be declared in advance. The *initiation phase in figure 21, for example, uses the subroutines opening(), set_mode(), screencolour(), fonts(), mouse_use(), scaling(), randomsys() and various standard C-functions. In the following sections the range numbers of variables will be enclosed by square brackets. Variables and arrays will be written in italics,

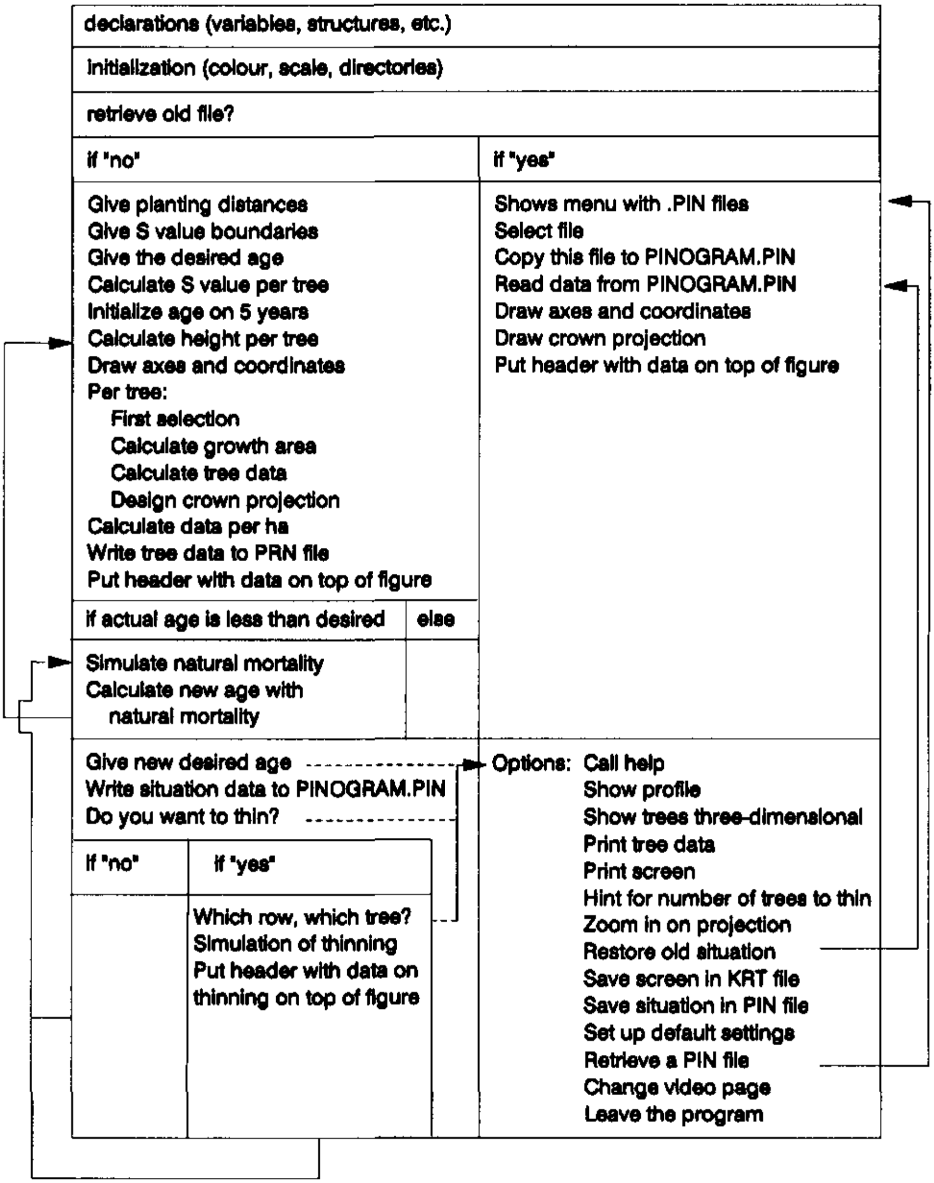


Fig. 21 Flow diagram of main functions of the PINOGRAM computer program.

*functions (=subroutines) are followed by () and structure characteristics are given after a full stop. File names and constants are written in capitals.

Various equations will be discussed in the following sections. In principle the same names for variables as used in these equations are used in the C source files. However, in the C source files it was necessary to group various variables in structures, for example: the height of a *sample tree *h[nr]* is written as *tree[nr].h* in the C source file and its crown width in a particular direction *cw[i]* is written as *crwi[nr].cw[i]*. The symbol *nr* is a Dutch abbreviation for number (see also the list of **symbols** at the back of this book). The subscript $_b$ and $_e$ behind a variable mean the value of the variable at the beginning and the end of a period.

4.3 Initiation

(FILES: OPEN.C, SETUP.C, SCREEN.C, MOUSE.C)
At *initiation the control checks the following:

- Graphical video mode. Options are: Video Graphics Array (VGA), Enhanced Graphics Adapter (EGA), Colour Graphics Adapter (CGA) and Hercules Graphics Chart (HGC);
- Avaialable memory (conventional Read and Access Memory). The program needs at least 550 kbytes to work properly;
- Existence of text font files with extension FON;
- Availability of a mouse;
- Existence of the file PINOGRAM.INI. This file contains data on default growth constants, screen presentation and default drives and directories, where user files are saved (files with extension PIN, PRN, KRT or SHW; see sections 4.23.1, 4.25.6, 4.25.7). This file can be created with the PGSETUP.EXE program;
- Existence of the given default drives and directories.

After these checks, colours are defined in accordance with the video configuration and the horizontal and vertical scaling factors are calculated for the screen presentation. The screen will then display:

```
                    PINOGRAM

     GROWTH SIMULATION PROGRAM FOR SCOTS PINE


                by Peter Leersnijder
               Department of forestry
                  WAU Wageningen


         Copyright (c) all rights reserved


                             Hit any key to continue
```

Next, the control looks to see if it is possible to create a file called PG?.PRN. A PRN file is an ASCI file with data on thinning per tree and per ha (see section 4.23.1). The question mark gives the command line argument. Here, this is a number given on the command line when starting up the program, for example:

```
a:>PINOGRAM 2
```

The number 2 gives the random range that is used to assign an *S value to a tree (see section 4.5). The S value of a tree S_{tree} is equal to its height at infinite age. In fact, it gives the starting point in a cyclic random range with numbers. If no number is given, then the starting point in the random range is dependent upon the time the program is started. By giving the program a number when starting up, a *situation that has been created can be reproduced.

4.4 Retrieving a situation

(FILE: OPEN.C)
The next step is to look for files with extension PIN in the default directory. These files were created by the user. A PIN file contains all the information necessary to reproduce a *forest situation that has been created before and to calculate a new situation after several years from the original situation.

If PIN files are found, the program asks whether it should retrieve an old situation or not. If the answer is "yes", a menu will appear, from which a PIN file may be selected. The selected file will be copied to a work file, called

PINOGRAM.PIN. The data required will be read, the crown projection of each individual will be drawn and a header giving stand data will be inserted. A new age may be given and a thinning may be executed (see section 4.23).

4.5 Starting up a new situation

(FILE: INITPAR.C)
To create a new *situation, the program asks for planting distance within and between rows and also for the height the smallest (*Smin*) and the largest (*Smax*) mature tree is likely to reach (see section 4.6 and 4.7); finally it asks for the age at which one want to view the forest:

Initial variables (meter, year)	
Give planting distance within a row	1.5
Give planting distance between rows	1.5
What is the maximum height of the smallest mature tree? (8-30)	14
What is the maximum height of the largest mature tree? (smallest-35)	24
Give the age at which you want to view the forest	■

Smin and *Smax* are the limiting values for the heights trees may reach at infinite age. With the above data the program is ready to compute the first situation when trees are five years old.

4.6 Calculating the S value of the trees from a normal distribution

(FILE: S_VALUE.C)
In the model is assumed that the *S values of the trees S_{tree} at the age of five years are still randomly distributed over the trees. For each tree an S_{tree} is chosen from a range of numbers with values between *Smin* and *Smax* according to a normal distribution at a confidence level of 0.95.

$$S_{tree} = \textit{mean } S_{tree} \textit{ value} + \textit{deviation} \quad (m) \tag{34}$$

The mean S value is:

$$\frac{Smax + Smin}{2} \quad (m) \tag{35}$$

A function giving a random number from a normal distribution is: (Dannenbring and Starr 1981):

$$\sum_{1}^{12} Random - 6 \tag{36}$$

Here, *Random* is a number between 0 and 1, in which every value has the same chance (for random range, see section 4.3). The deviation is computed as follows:

$$\frac{(\sum_{1}^{12} Random - 6) * (Smax - Smin)}{u * 2} \quad (m) \tag{37}$$

In a normal distribution eccentricity *u* has a value of 1.96 at a confidence level of 95%. Now the S value per tree S_{tree} will be:

$$S_{tree} = \frac{Smax + Smin}{2} + \frac{(\sum_{1}^{12} Random - 6) * (Smax - Smin)}{1.96 * 2} \quad (m) \tag{38}$$

As the stand ages it becomes more likely that tree height will follow a skew distribution increases, because of the non-random death of smaller trees as a result of *competition from larger neighbouring trees. Assmann (1961) was one of the authors who found that height of Scots pines in even-aged pure stands has an L-shaped distribution (see also Hara 1988). This phenomenon is probably clearest when the shortest trees are thinned (*low thinning).

4.7 Computing tree height

(FILE: S_VALUE.C)

As has been described in section 2 it is difficult to predict height growth (h_e/h_b). But mean cumulative height growth normally follows an S-curve. The Chapman-

Richards equation is often used to describe the mean cumulative height growth of *dominant trees (Van de Burg et al. 1983):

$$hdom = S * (1 - \exp(-\mathrm{H1} * t))^{\mathrm{H2}} \tag{39}$$

in which
$hdom$ = *dominant height (m)
S = site index (m)
t = age (year)
H1,H2 = height constants

Van de Burg et al. (1983) adapted the *yield tables of Grandjean and Stoffels (1955) to the Chapman-Richards equation. The derived height constants for Scots pine in Dutch circumstances were computed as: H1 = 0.0248 and H2 = 1.04749. Site index S is the *dominant height that a stand may reach at infinite age (Schütz and Van Tol 1982). Then the equation for height growth will be:

$$hdom_e = hdom_b * \left(\frac{1 - \exp(-\mathrm{H1} * t_e)}{1 - \exp(-\mathrm{H1} * t_b)} \right)^{\mathrm{H2}} \tag{40}$$

in which
t_b = age at the beginning of a period (m)
t_e = age at the end of a period (m)
$hdom_b$ = dominant height at t_b (m)
$hdom_e$ = dominant height at t_e (m)

One may question whether equation (40) may be applied to height growth of individual trees. This would mean that all trees in a stand grow similar, which is expressed by equations (39) and (40), but that only their *S values (= S_{tree}) differ. This probably applies reasonably well to *dominant trees, but not to *suppressed trees. Kellomäki and Hari (1980) report that, when calculated per needle biomass unit, the height growth, *radial growth, needle growth, and other growth constants were the greatest in suppressed trees. The suppressed trees thus appear to be more efficient in using the resources available for *growth than the trees in other classes. Suppressed Scots pines, however, do not survive very long because the species is very light-demanding. Therefore, for the time being, a growth equation per tree class has been abandoned. In practice the *social position of a tree is also influenced by damage of the main axis resulting from diseases, pests, fracture, etc.

4.8 Transect limits and tree coordinates

(FILE: GRAPH.C)
A *transect of 20 x 50 metres is used. The minimum possible planting distance within a row and between rows is one metres. This results in a maximum of one thousand trees per transect (= 10000 trees per ha).

A maximum of 640 kbytes of memory can be used in the DOS operating system. DOS (versions 3 and 4) itself needs about 60 kbytes, which means that only 580 kbytes are available for application programs.

Since the computer must retain many data per tree (210 bytes memory) and the remainder of the program needs another 350 kbytes, it remains impossible to work efficiently with more than thousand trees, while only 640 kbytes are available. However, if necessary, the program could be rewritten so that extended or expanded memory can be used (DOS handbooks and IBM handbooks).

Trees are placed in a triangular spacing. If the given distance between and within rows is 1.5 metres, there are 33 trees within a row and 13 between rows. The total number of trees is then 13 * 33 = 429 trees per 0.1 ha.

4.9 Primary selection

(FILE: SCAN.C)
The neighbouring trees that influence the *sample tree are identified in three steps. *Primary selection selects those trees that might have influence on the sample tree. With other words trees that certainly have no influence are rejected. *Secondary selection selects those trees from the primary selection that influence the *maximum growth area of the sample tree (see section 4.12). The *tertiary selection selects those trees from the secondary selection that influence the *actual growth area of the sample tree (see section 4.16).

It would be simple to skip the primary selection and to select all trees as neighbours that potentially influence the sample tree, but with one thousand trees almost a million secondary selection computations should be made. Secondary selection computations are very time consuming. Therefore attempts were made to find a primary selection method.

In the initial phase, trees are five years old and still very small. The degree to which the trees interact will also be minor and it will be sufficient to select primarily those trees that remain within a distance of twice the planting distance from the sample tree.

In later phases it is necessary to calculate the *maximum distance of influence. The maximum distance of influence is the distance from the stem of the sample tree up to the furthest corner of its *maximum growth area (see section 4.12 and 4.14). Figure 22 shows the growth area and maximum distance of influence for a sample tree and several neighbouring trees. If the maximum distance of influence of the sample tree and that of a neighbouring tree is more than the

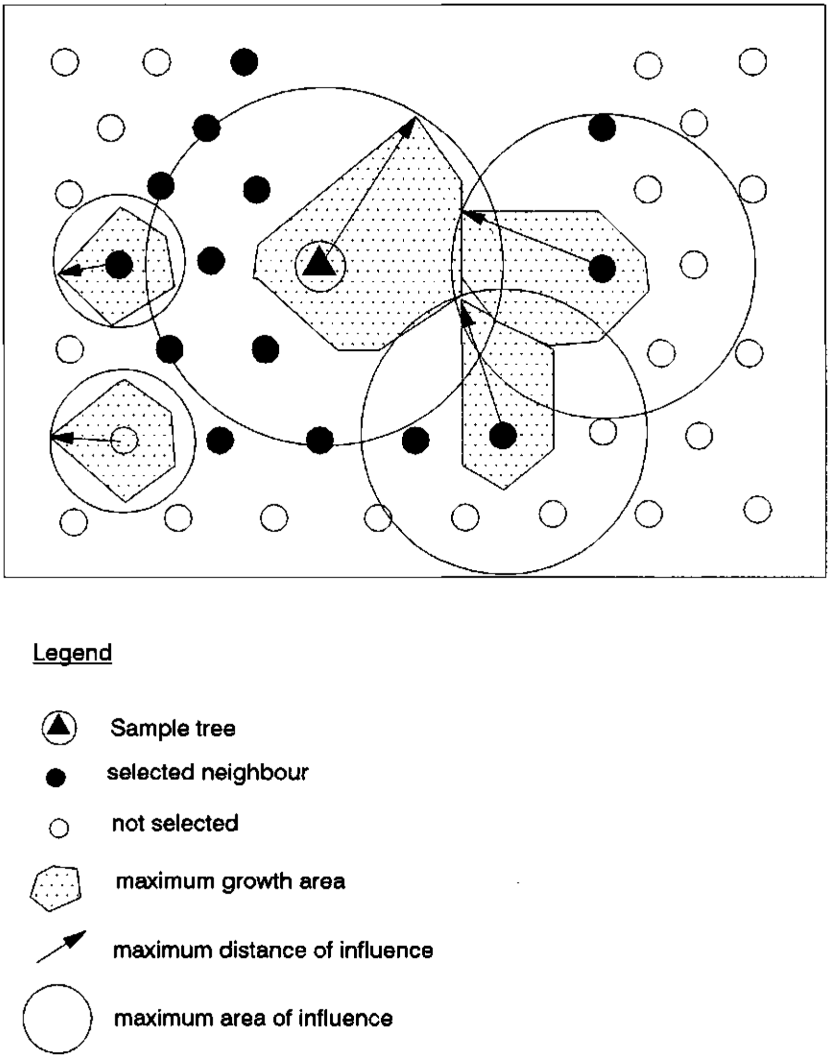


Fig. 22 Primary selection. Neighbouring trees with a maximum area of influence overlapping the maximum area of influence of the sample tree are selected first.

distance between the stems (circles overlap), then this neighbour will be designated as a potential neighbour with influence. Next, after each secondary selection (section 4.13), a table of selected neighbouring trees is created. These selected neighbours will always be selected primarily in subsequent *cycles, in spite of their distance of influence.

4.10 Vectors to neighbouring trees and angle of reference.

(FILE: SCAN.C)
For each *sample tree the distance $A[i]$ to its potential neighbours of influence and also the angle between the vector in the direction of the neighbouring tree and the "North" are calculated.

The "North direction" has an angle of zero degrees and is used as *angle of reference (Fig. 23). If the angle between vectors in the direction of two consecutive neighbours is equal to zero, in other words, if $\mathit{angle}[i+1] - \mathit{angle}[i]$ is smaller than 0.01 or more than -0.01, then the tree the furthest distance from the sample tree will be rejected from the selection. This occasionally creates an error if the tree furthest from the sample tree is much taller and the distance from the sample tree to the furthest tree differs little from that to the closer tree. In that case the relevant growth area vector from the sample tree in that direction is given too high a value.

4.11 Normal growth area

(FILE: GROW.C, GROWH.C)
The *normal growth area has a polygon structure (see section 3.2.2). At a distance a from *sample tree nr a perpendicular is drawn from the vector in the direction of neighbour i. The following applies (identical to equation 14):

$$a[nr][i] = \frac{h[nr]^{C}}{h[nr]^{C} + h[i]^{C}} * A[nr][i] \qquad (41)$$

in which
$a[nr][i]$ = normal growth vector of sample tree nr in the direction of a neighbouring tree i (m)
$h[nr]$ = height of sample tree nr (m)
$h[i]$ = height of neighbouring tree i (m)
C = *competition constant
$A[nr][i]$ = distance from sample tree nr to neighbouring tree i (m)

The normal growth area is included by these perpendiculars (Fig. 24). If the growth area is drawn for several neighbouring trees, small areas that cannot be

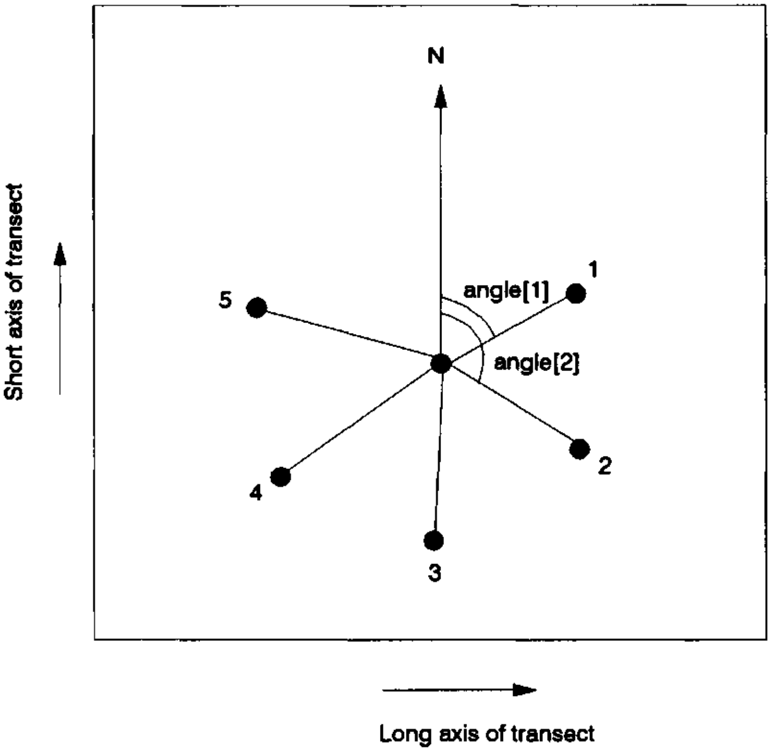


Fig. 23 Spatial distribution of sample trees and neighbouring trees and the angle between directions of neighbouring trees and the "North".

1,2,etc. = neighbouring trees
angle[1],angle[2],etc.= angle between direction of neighbouring tree and "North"
N = North

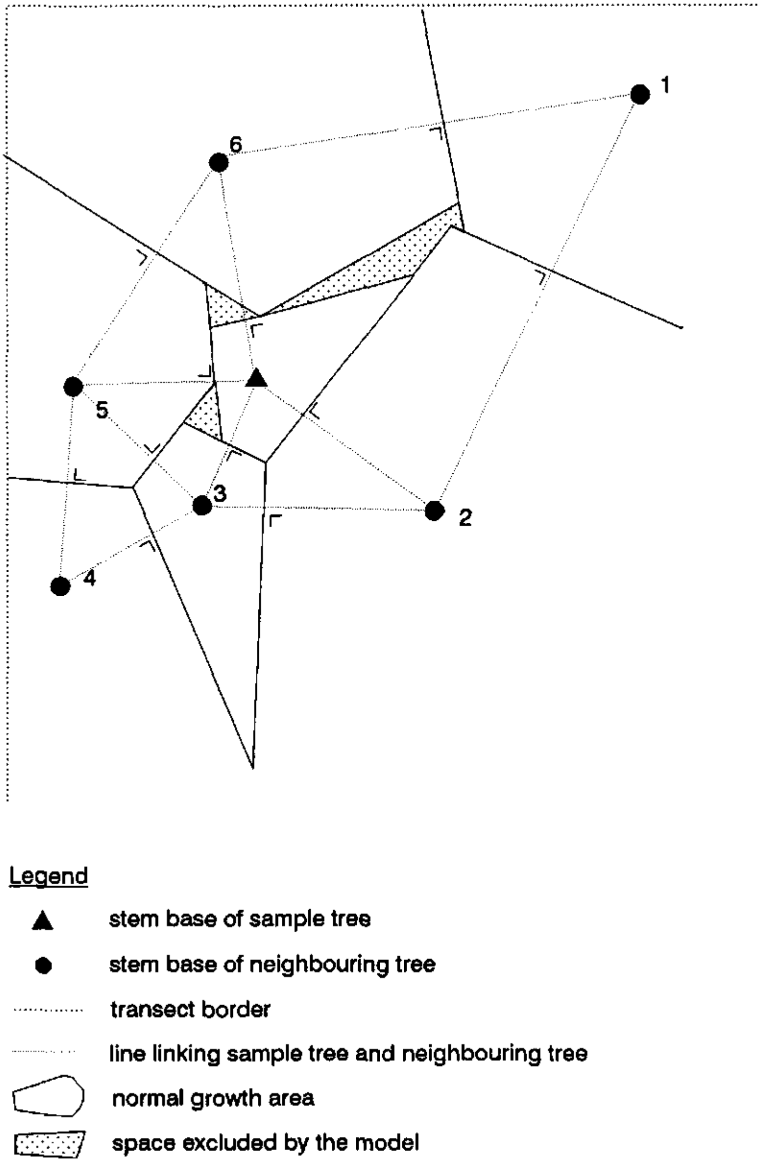


Fig. 24 Design of the normal growth area. The position of the perpendicular is dependent upon heights of sample tree and neighbouring tree. Perpendiculars enclose the normal growth area

assigned to any tree (= space excluded by the model) may arise. These unused areas could be assigned proportionally to the various surrounding trees (Weihe 1978), but this requires too much computing time compared to the added value it gives (see section 3.2). Besides, these unused areas only play a role if a tree is competing with its neighbours (see section 4.16).

The normal growth area is thus the polygon, directly derived from the height of the sample tree, the height of the neighbouring trees and the distances between the stem of the sample tree and the stems of the neighbouring trees.

4.12 Potential and maximum growth areas

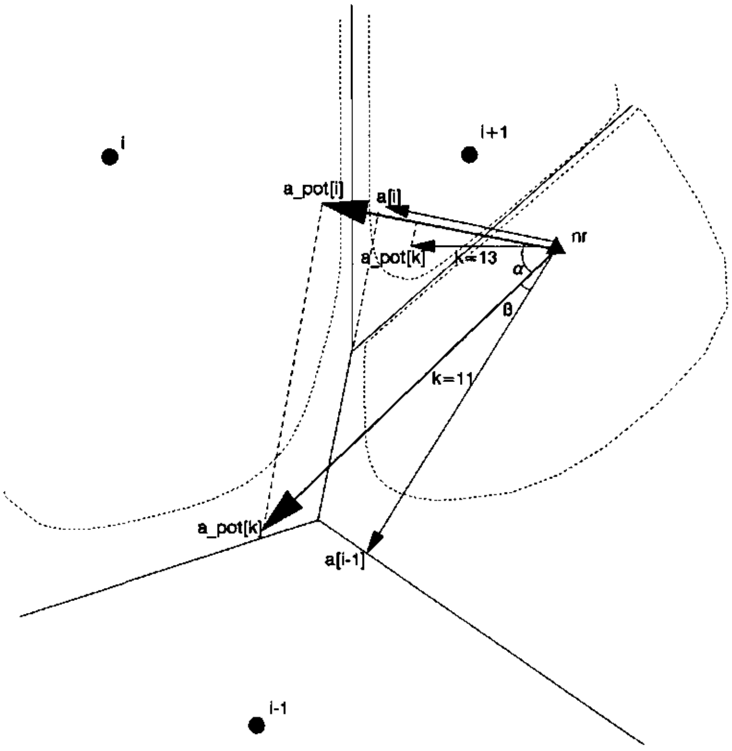
(FILE: GROW.C, GROWH.C)
The model assumes that if a tree is planted, it will occupy a certain (normal) growth area. Also, if a tree is cut or dies, the released space will be divided between the surrounding trees. However, in these cases it is impossible for trees to occupy their *normal growth area immediately. The amount of space a tree can use within a certain time limit can be calculated using the equation for crown length increment:

$$cl_e = cl_b * \left(\frac{t_e}{t_b}\right)^{CL1} * \left(\frac{h_e}{h_b}\right)^{CL2} * \left(\frac{a_e}{a_b}\right)^{CL3} \tag{42}$$

in which
cl_e = crown length at the end of a period (m),
cl_b = crown length at the beginning of a period (m),
t_e = age at the end of a period (year),
t_b = age at the beginning of a period (year),
h_e = height at the end of a period (m),
h_b = height at the beginning of a period (m),
a_e = normal growth area vector at the end of a period (m),
a_b = normal growth area vector at the beginning of a period (m).
CL1, CL2 and CL3 are crown length constants.

When a tree is released, the crown length can never increase more than the tree height, since Scots pine rarely produces epicormic shoots and the lowest branches do not die because of *competition for space with neighbouring trees. So the following applies:

$$cl_e = cl_b + h_e - h_b \tag{43}$$



<u>legend</u>

▲ stem basis of sample tree

● stem basis of neighbouring tree

——— normal growth area

·········· crown projection

- - - - - help lines

Fig. 25 Reconstruction of potential growth area vector a_pot[i] derived from the maximum a_pot[k]. In this example k varies between 11 and 14. Only the a_pot[k] for k=11 and k=13 was drawn here.
For explanation of calculation of a_pot[i], see text.

From both equations (42) and (43) the *potential growth area vector follows:

$$a\_pot = a_b * \left(\frac{cl_b + h_e - h_b}{cl_b} \right)^{\frac{1}{cl3}} * \left(\frac{t_e}{t_b} \right)^{-\frac{cl1}{cl3}} * \left(\frac{h_e}{h_b} \right)^{-\frac{cl2}{cl3}} \tag{44}$$

In this way, the potential growth area vector *a_pot[i]* in the direction of the tree's neighbour *i* can be determined with the help of the former crown length in the direction of neighbour *i*.

As will be explained in section 4.15 and 4.16, in every *cycle the crown length is calculated in sixteen directions. The angle between each consecutive direction is $\pi/8$. To determine the former crown length $cl[i]_b$ in the direction of the neighbouring tree, the crown lengths $cl[k]_b$ in which *k* provides next conditions (*k* is an integer variable between 1 and 16) may be taken:

- angle *k**PI/8 is larger than *angle[i-1]* and smaller than *angle[i+1]*;
- angle *k**PI/8 lies between *angle[i]* - $\pi/2$ and *angle[i]* + $\pi/2$.

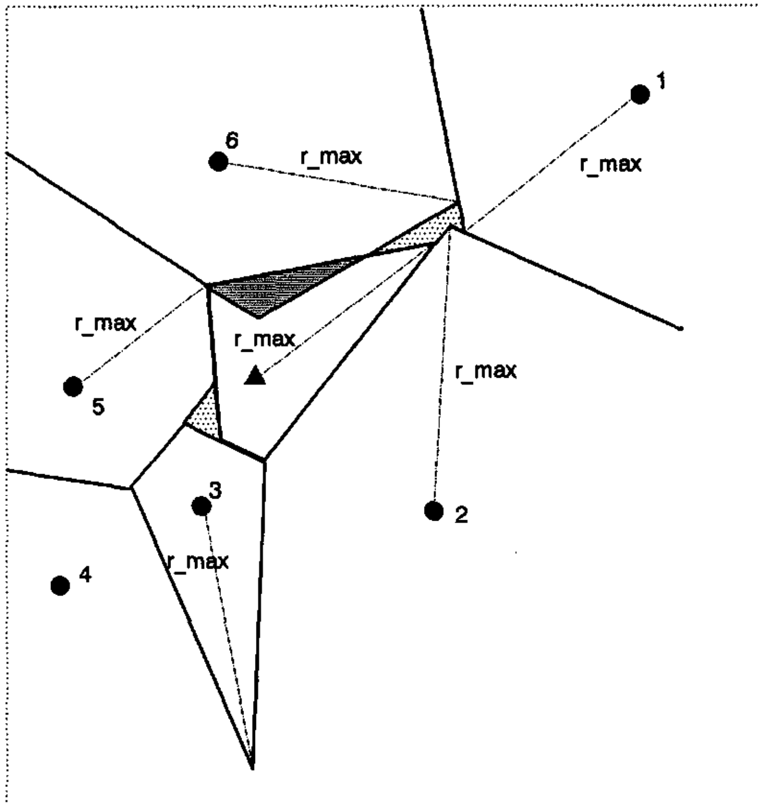
If i is equal to 1, then i-1 becomes equal to max and if i is equal to max then i+1 becomes equal to 1, in which max is the number of selected trees. Further, Angle[max+1] will become angle[1]+2π and angle[max+2] will become angle[2]+2π.

The *potential growth area vector *a_pot[k]* is calculated for each *k* that fulfils the above conditions. From this *a_pot[i]* is derived (Fig. 25):

$$a\_pot[i] = a\_pot[k] * \cos(\alpha) \tag{45}$$

in which α is angle between $k*\pi/8$ and *angle[i]* (rad).

The *maximum growth area vector is determined by the minimum of the largest *potential growth area vector *a_pot[i]* derived and the *normal growth area vector *a[i]*. However, a problem arises if a tree is cut; the released space is immediately divided among the surrounding trees, in proportion to their heights. This results in small trees gaining hardly any extra *growing space and large trees gaining a large part of the released space. However, the larger trees are not always able to use the assigned extra space as fast as the smaller trees. This means that the smaller trees have as much of the extra growing space at their disposal as the larger trees still cannot use. The maximum growth area vector *a_max* may be calculated as follows (Fig. 26):



Legend

▲	stem base of sample tree
●	stem base of neighbouring tree
········	transect border
--------	r_max = maximum distance of influence
⬭	maximum growth area
░	space excluded by the model
▓	overlap of maximum growth areas

Fig. 26 Design of the maximum growth area. Neighbour 6 cannot yet use its normal growth area completely. In this example the unused space (overlap of maximum growth areas) can be used by the sample tree. For calculation method see text.

```
if
    $a\_pot[nr][i] > a[nr][i]$
and
    $a\_pot[i][nr] < A[nr][i] - a[nr][i]$                                    (46)
then
    $a\_max[nr][i] = \min(a\_pot[nr][i], A[nr][i] - a\_pot[i][nr])$
else
    $a\_max[nr][i] = a[nr][i]$
```

In this equation *a_pot[nr][i]*, *a[nr][i]* and *a_max[nr][i]* are respectively the potential, normal and maximum growth area vectors of the sample tree *nr* in the direction of neighbour *i* and *a_pot[i][nr]* is the potential growth area vector of neighbour *i* in the direction of the sample tree *nr*. The distance between stems *A[nr][i]* is the distance between sample tree *nr* and neighbour *i*.

The maximum growth area vectors thus are derived from the normal and the potential growth area vectors of the sample tree and its neighbours. They can be larger or smaller than the normal growth area vectors and smaller than or equal to the potential growth area vectors.

4.13 Secondary selection

(FILE: GROW.C, GROWH.C)
The angle between *angle[i+1]* and *angle[i]*, formed by the vectors in the directions of two consecutive neighbouring trees, may be calculated with the help of tree coordinates. The distance *r* to the intersection of perpendiculars of these vectors is calculated as follows:

$$r^2 = \frac{a\_\mathrm{max}[i]^2 + a\_\mathrm{max}[i+1]^2 - 2 * a\_\mathrm{max}[i] * a\_\mathrm{max}[i+1] * \cos(z)}{\sin^2(z)} \qquad (47)$$

in which $z = angle[i+1] - angle[i]$ (rad)

Angle x is formed by the vector in the direction of *tree[i]* and the direction of r, and angle y is formed by the vector in the direction of *tree[i+1]* and the direction of r (see section 3.2.2).

In principle, there are three possibilities (Fig. 11):

1. $z = x + y$
2. $z = x - y$
3. $z = -x + y$

Whether a tree has influence on the *sample tree is illustrated by figure 12. For calculations, see section 3.2.2: equations 14 to 27. If a tree has no influence this tree is not selected for further calculations on the *maximum and *actual growth areas.

4.14 Maximum distance of influence, tertiary selection and border trees

(FILE GROW.C, GROWH.C)
After *secondary selection it will be possible to determine the *maximum distance of influence *r_max* (section 4.9 and Fig. 26).

If the *potential growth area vector of the *sample tree in the direction of a neighbour *a_pot[i]* is smaller than the *normal growth area vector *a[i]*, this neighbour has no influence on the sample tree. But the existence of this neighbour indicates that a sample tree is not a *border tree. A sample tree is a border tree if the angle between two consecutive neighbours is larger than 180°. The angle at which the border starts and at which it stops is recorded per border tree. In section 4.15 it will be explained how growth area vectors are calculated for border trees.

Only the neighbours that influence the sample tree are used (= *tertiary selection) to determine the *maximum growth area vectors in sixteen directions (see next section).

4.15 Determining maximum growth area vectors in sixteen directions.

(FILE GROW.C, GROWH.C)
Data on growth and shrink in all directions of a growth area cannot be stored in the computers memory; therefore it was decided to use sixteen fixed directions (North, North-North-East, North-East, etc.). The newly arisen *maximum growth area is drawn by connecting the ends of the vectors in these sixteen directions. This growth area is usually slightly smaller than its original (Fig. 27). It would be more accurate if more directions were calculated, but this was not possible given the computer's memory capacity.

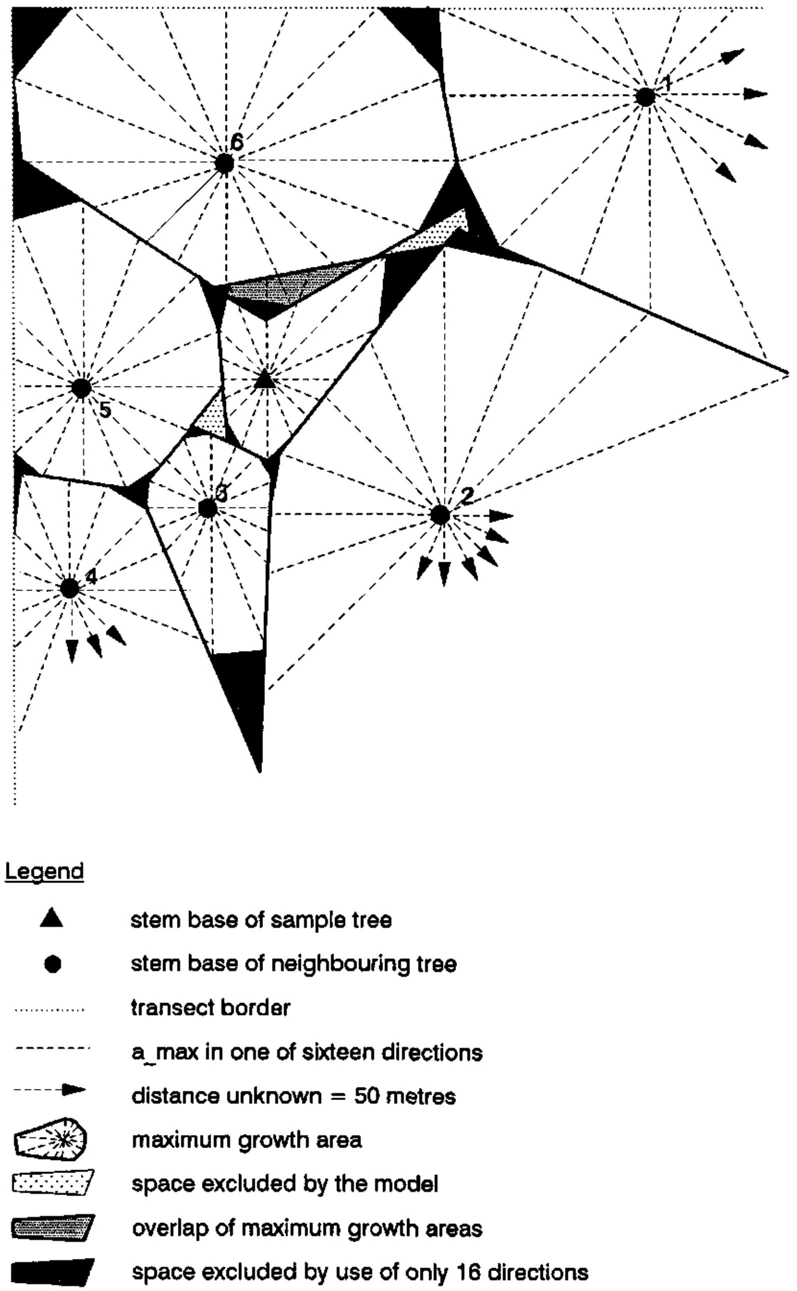


Fig. 27 Design of vectors of the maximum growth area in sixteen directions. Some space is excluded by the use of only these sixteen directions to determine the maximum growth area.

The procedure to calculate maximum growth area vectors in the sixteen directions was as follows. In each of the sixteen directions one of the perpendiculars, including the original maximum growth area is intersected. The perpendicular that is intersected gives the neighbour *i*, which influences the *sample tree in that direction. If *k* is a variable with a value between 1 and 16, then the *maximum growth area vector in one of the sixteen directions can be calculated as follows:

$$a\_\mathrm{max}[k] = \frac{a\_\mathrm{max}[i]}{\cos(angle[i] - k * \frac{\Pi}{8})} \tag{48}$$

in which *angle[i]* is the angle between the direction of *neighbour[i]* and the "North" and *a_max[i]* is the maximum growth area vector in the direction of the neighbour.

The value of $k * \pi/8$ should be within the range *angle[i]* - $\pi/2$ up to *angle[i]* + $\pi/2$. If not, the same calculation is done for the next *i*. If a certain *k* cannot be assigned to any *i*, then the denominator in the above equation is less than or equal to zero. If the sample tree *tree[nr]* is not a *border tree, then *a_max[k]* is temporarily given an extreme high value, because in this case a tree behaves like a border tree. However, it is not a border tree, because one may expect that in future it will again be influenced from all sides. Only when the *actual growth area is calculated (section 4.16) is *a_max[k]* recalculated and brought back to substantial proportions.

If the sample tree is a border tree and $k * \pi / 8$ lies in the domain between the starting and ending angles of the border, then, to indicate that it is a real border tree, *a_max[k]* will be multiplied by minus one. So a negative value for *a_max[k]* means that no *maximum growth area vector can be calculated in that direction and the sample tree will never be influenced from all sides.

4.16 Determining actual growth area vectors in sixteen directions.

(FILE GROW.C, GROWH.C)

In order to calculate data per ha one should ensure that the growth area of a tree cannot cover a domain outside the *transect. In other words, if the distance from a tree in the direction $k * \pi / 8$ to the transect border (= *dist_transect[k]*) is less than *a_max[k]* then *a_max[k]* will be assigned the value of *dist_transect[k]*. Thus:

$$a\_\mathrm{max}[k] = minimum(a\_\mathrm{max}[k], dist\_transect[k]) \tag{49}$$

In order to calculate the *actual growth area vector, the *maximum growth area vector *a_max[k]* is again compared to the *potential growth area vector in that direction. It could be indeed possible for the distance to a corner of the *maximum growth area to exceed the extend of the potential growth area vector in that direction. Besides, in directions without any influence of neighbours an extreme high value has been assigned to *a_max[k]* (see section 4.15). Therefore the equation from section 4.11 is used again:

$$a\_pot[k] = a\_act_b[k] * \left(\frac{cl_b + h_e - h_b}{cl_b}\right)^{\frac{1}{\alpha_3}} * \left(\frac{t_e}{t_b}\right)^{-\frac{\alpha_1}{\alpha_3}} * \left(\frac{h_e}{h_b}\right)^{-\frac{\alpha_2}{\alpha_3}} \qquad (50)$$

The *actual growth area vector in direction $k * \pi / 8$ is (Fig. 28):

$$a\_act[k] = minimum(a\_\mathrm{max}[k],\ a\_pot[k]) \qquad (51)$$

The above calculations are not executed if *a_max[k]* has a negative value (*border trees). The diameters of border trees are very important for calculating basal area and volume per ha. Therefore, growth areas of the border trees have to be estimated. For this purpose the average of all positive values of the growth area incremental factor ($a\_act[k]_e/a\_act[k]_b$) is calculated and those values of $a\_act[k]_e$ that are negative are multiplied by the result, providing the new values $a\_act[k]_e$ are not smaller than the old values $a\_act[k]_b$ (calculated in a preceding *cycle). The resulting value for $a\_act[k]_e$ may not exceed *dist_transect[k]*. Written in equations:

if

$$a\_\mathrm{max}[k] > 0$$

then

$$a\_mean\_factor = \frac{sum\ of\ positive\ values\ of\ \frac{a\_act_e[k]}{a\_act_b[k]}}{number\ of\ positive\ values\ of\ a\_act_e[k]} \qquad (52)$$

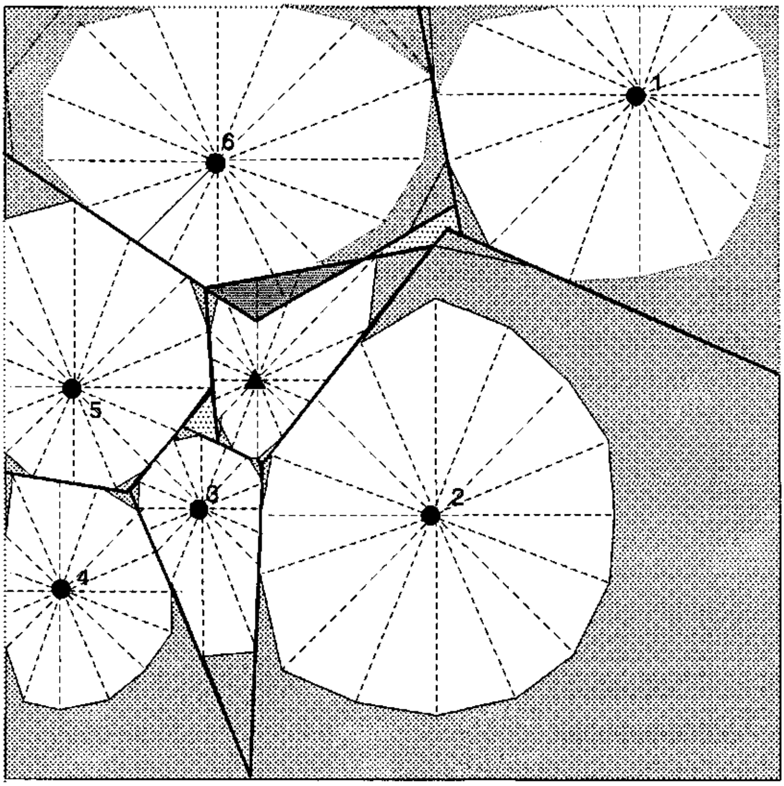
if

$$a\_\mathrm{max}[k] < 0$$

then

$$a\_act_e[k] = -minimum(dist\_transect[k],\ a\_mean\_factor * -a\_\mathrm{max}[k]) \qquad (53)$$

The above equation does not apply to the initial *situation (when $a\_act[k]_b$ is still equal to zero). In that case:



Legend

▲	stem base of sample tree
●	stem base of neighbouring tree
···········	transect border
- - - - - - -	a_act in one of sixteen directions
⬠	actual growth area
⬭	maximum growth area
░	space excluded by the model
▬	overlap of maximum growth areas (here: part of the actual growth area of the sample tree)
▒	space actually not used

Fig. 28 Design of the actual growth area vectors in sixteen directions. The actual growth area is only a part of the maximum growth area, because a tree will take some time to occupy the maximum growth area.

$$a\_mean\_factor = \frac{sum\ of\ positive\ values\ of\ a\_act_e[k]}{number\ of\ positive\ values\ of\ a\_act_e[k]} \tag{54}$$

if

$a_{max}[k] < 0$ (55)

then

$a\_act_e[k] = -minimum(dist\_transect[k],\ a\_mean\_factor)$

4.17 Calculation of tree data

(FILE: CALCTREE.C)
Once all the *actual growth area vectors are known, it is simple to calculate the corresponding tree data with the help of the growth equations of section 3.2.3. Crown length and crown width are calculated in sixteen directions.

In the initial phase (see equations 30 and 31):

$$cl[k] = cl^{CL1} * h^{CL2} * a\_act[k]^{CL3} * \mathrm{CL4} \tag{56}$$

$$cw[k] = 0.5 * t^{CW1} * h^{CW2} * a\_act[k]^{CW3} * \mathrm{CW4} \tag{57}$$

In *subsequent phases:

$$cl[k]_e = cl[k]_b * \left(\frac{t_e}{t_b}\right)^{CL1} * \left(\frac{h_e}{h_b}\right)^{CL2} * \left(\frac{a\_act[k]_e}{a\_act[k]_b}\right)^{CL3} \tag{58}$$

$$cw[k]_e = cw[k]_b * \left(\frac{t_e}{t_b}\right)^{CW1} * \left(\frac{h_e}{h_b}\right)^{CW2} * \left(\frac{a\_act[k]_e}{a\_act[k]_b}\right)^{CW3} \tag{59}$$

CW1, CW2, CW3, CW4 are crown width constants,
CL1, CL2, CL3, CL4 are crown length constants,
k is a direction while $1 <= k <= 16$.

If the actual growth area vector *a_act[k]* has a negative value, the crown width becomes zero, so that finally no crown will be drawn in this direction. Next, all negative actual growth area vectors are multiplied by minus one, so that all values become positive again.

In order to calculate diameter *dbh*, the actual growth area *area* is calculated from the sixteen actual growth area vectors:

$$area = \sum_{k=1}^{k=16} (0.5 * a\_act[k] * a\_act[k+1] * \sin(\tfrac{\pi}{8})) \tag{60}$$

From this it follows that the mean actual growth area vector $\overline{a\_act}$ is:

$$\overline{a\_act} = \sqrt{\frac{area}{\pi}} \tag{61}$$

In the initial phase it holds that (see equation 29):

$$dbh[k] = t^{\mathrm{D1}} * h^{\mathrm{D2}} * a\_act[k]^{\mathrm{D3}} * \mathrm{D4} \tag{62}$$

In subsequent phases:

$$dbh_e = dbh_b * \left(\frac{t_e}{t_b}\right)^{\mathrm{D1}} * \left(\frac{h_e}{h_b}\right)^{\mathrm{D2}} * \left(\frac{\overline{a\_act[k]}_e}{\overline{a\_act[k]}_b}\right)^{\mathrm{D3}} \tag{63}$$

D1, D2, D3, D4 are diameter constants.

In order to determine the mean branch diameter *d_branch* in the lower part of the tree's crown (see equation 33), its mean crown width $\overline{cw}$ and maximum crown length *cl_max* must be calculated. As in the case of growth area, crown surface is calculated from parts of the area from which mean crown width $\overline{cw}$ can be derived.

$$d\_branch = h^{\mathrm{DB1}} * \overline{cw}^{\mathrm{DB2}} * cl\_\max^{\mathrm{DB3}} * \mathrm{DB4} \tag{64}$$

DB1, DB2, DB3, DB4 are branch diameter constants.

For the form factor it holds that (see equation 32):

$$f = h^{F1} * cl\_\max^{F2} * dbh^{F3} * F4 \tag{65}$$

F1, F2, F3, F4 are form factor constants.

and for the volume v expressed in dm^3:

$$v = \frac{f * h * \pi * dbh^2}{40} \tag{66}$$

*Canopy closure is determined by dividing the sum of all crown surfaces by the area of the *transect. The equation is:

$$Canopy\_closure = \frac{\sum_{i=1}^{i=n} \left(\sum_{k=1}^{k=16} \left(0.5 * cw[i][k] * cw[i][k+1] * \sin(\frac{\pi}{8}) \right) \right)}{1000} \tag{67}$$

in which n = total number of trees in transect

4.18 Estimating age at which natural mortality occurs

(FILE: CALCTREE.C)
If no *thinnings are executed, then at a certain moment the model may create a very unnatural *situation, for example of 5000 trees per ha with a mean height of 20 metres. The crowns of the remaining trees are then extremely small. So, the relation between the size of a tree and its minimum *growth area needed to survive should be known. Unfortunately, I did not have any data for estimating this relation accurately. In order to estimate the minimum growth area of a tree the "3/2 power law" (Yoda et al. 1963) could be used:

$$\bar{v} = C_1 * N^{C2} \tag{68}$$

If $\bar{v}$ is the mean maximum volume of a tree per ha of a stand at certain age, then N is the maximum number of trees per ha. Rewritten for the mean *growth area vector, it holds that:

$$\bar{v} = C_1 * \left(\frac{10000}{2 * \sqrt{3} * \overline{a}^2} \right)^{C_2} \tag{69}$$

In this equation C_2 is about -3/2. However, the range in which C_1 and C_2 may vary (White 1981, Harper 1977) is too large to be able to calculate with acceptable accuracy the likelihood of individual trees dying. Furthermore, it is very difficult to estimate with acceptable accuracy the potential maximum volume of a stand.

The maximum tree height / crown width ratio at which a tree is still alive, henceforth called M (= mortality constant), reflects the competition a tree may endure. A high h/cw ratio arises from strong competitive pressure. My field experiments revealed that mean crown width of Scots pine on the Veluwe (Province of Gelderland, the Netherlands) was seldom less than one-sixth of the tree's height. To simulate mortality it seemed to be acceptable to use this value for the minimum crown width for the time being. Of course in reality the exact moment of death does not depend solely upon mean crown width.

According to this premise the time at which a tree dies may be calculated using the equation for crown width increment:

$$cw_e = cw_b * \left(\frac{t_e}{t_b}\right)^{\mathrm{CW1}} * \left(\frac{h_e}{h_b}\right)^{\mathrm{CW2}} * \left(\frac{a\_act_e}{a\_act_b}\right)^{\mathrm{CW3}} \tag{70}$$

Since height is a function of age, this equation can be rewritten as:

$$cw_e = cw_b * \left(\frac{t_e}{t_b}\right)^{\mathrm{CW1}} * \left(\frac{1-\exp(-\mathrm{H1}*t_e)}{1-\exp(-\mathrm{H1}*t_b)}\right)^{\mathrm{CW2}*\mathrm{H2}} * \left(\frac{a\_act_e}{a\_act_b}\right)^{\mathrm{CW3}} \tag{71}$$

The variable to resolve in equations (70) and (71) is t_e. Because the mortality constant deals with the mean crown width, the crown width in sixteen directions must be calculated at certain t_e. If a help variable is defined as:

$$help = \left(\frac{t_e}{t_b}\right)^{\mathrm{CW1}} * \left(\frac{1-\exp(-\mathrm{H1}*t_e)}{1-\exp(-\mathrm{H1}*t_b)}\right)^{\mathrm{CW2}*\mathrm{H2}} \tag{72}$$

then mean crown width may be calculated using the equation:

$$\overline{cw_e} = 2*\sqrt{\frac{\sum_{i=1}^{i=16} cw[k]_b*\left(\frac{a\_act[k]_e}{a\_act[k]_b}\right)^{\mathrm{CW3}} *cw[k+1]_b*\left(\frac{a\_act[k+1]_e}{a\_act[k+1]_b}\right)^{\mathrm{CW3}} *help^2}{16}} \tag{73}$$

in which $a\_act[17] = a\_act[1]$ and $cw[17] = cw[1]$

Because *border trees have negative values for their crown widths in some of the sixteen directions, only those directions known to have a positive crown width are involved in the equations (72) and (73).

By systematically testing different values for t_e, the age at which mean crown width is equal to $1/M$ times tree height is approached.

A major difficulty with this calculation is that the *actual growth area vector at t_e ($a\_act[k]_e$) is not known exactly. In most cases, however, $a\_act[k]_e$ will approach the *normal growth area vector *a[k]*. The normal growth area is indeed the growth area a tree occupies when it is influenced by neighbours from all sides. Generally this is the case when a tree has too small a crown because of competition. However, a tree at time t_e may have more space in one or more directions than the calculated normal growth area. Too much computer time is required to calculate $a\_act[k]_e$ exactly. A way of overcoming this will be discussed in section 4.21.

4.19 Drawing tree crowns

It is easy to draw tree crowns in the *transect, because crown widths are known in sixteen directions. So, a tree crown consists of sixteen corners connected by straight lines. If the *actual growth area vector *a_act[k]* is negative (= *border tree), then crown width will become zero in that direction and thus it will not be drawn. Since the model does not take crooked or leaning trees into account, the base of the stem always lies within the crown projection.

4.20 Calculation of data per ha

(FILE: DAHA.C)

Since the PINOGRAM model simulates growth of trees within a *transect of 0.1 ha, the number of stems per ha is ten times the number of stems in the transect. The mean basal area and the mean volume per tree are simple to calculate, and enable basal area *G* and volume *V* per ha to be calculated too.

$$G = \sum_{nr=1}^{nr=number} dbh[nr]^2 * \frac{\pi}{40000} * 10 \; m^2/ha \tag{74}$$

$$V = \sum_{nr=1}^{nr=number} f[nr] * dbh[nr]^2 * h[nr] * \frac{\pi}{40000} * 10 \; m^3/ha \tag{75}$$

4.21 Starting a new cycle

(FILE: CALCYEAR.C)
After calculating the data per ha, a header will be placed giving data on: planting distances; Smax, Smin; age, maximum, minimum and mean diameters, mean and *dominant heights; number of stems per ha; basal area per ha; volume per ha; and *canopy closure.

As mentioned earlier, the first *situation is given at an age of five years. If the given age was five years, then the question: "At what age do you want to see the stand?" appears on the screen. After the new age has been entered, the question: "Do you want to cut some trees?" (see section 4.23) appears.

If the given age at which one wants to see the forest is more than five years, (for example, it is 10 years), then, before calculating the new situation at the age of ten years, the program first calculates whether some trees have died (see section 4.18) and then searches to ascertain whether more trees will die in the next five years. This can be done because age of mortality has been estimated for every tree. This estimated age of mortality is not very exact and a tree might die sooner, therefore the new age *year* is calculated as follows:

```
$oldyear = year$
if
    $first\_mortality - oldyear > 1$
then                                                        (76)
    $year = \frac{(first\_mortality + oldyear)}{2} + 1$
else
    $year = oldyear + 1$
```

In the first step the variable *oldyear* will become the value of the present age *year*. Next the mean of the age at which the first tree would die *first_mortality* and the present age *oldyear* is calculated. The new age *year* will now become the value of this average, but is at least one year more than *oldyear*.
Next, the new age *year* is compared to the given age *endyear*. If the given age is less than the new age just calculated, then the new age will become the value of the given age.

$$year = minimum(year, endyear) \tag{77}$$

Next, the new situation is calculated and drawn.

*It sometimes happens that the *normal growth area of a tree at present is less than the *actual growth area at the calculated age of mortality. In some cases this results in many consecutive calculations of situations with intervals of one year without any trees dying.*

4.22 Saving a situation

(FILE: RETRIEVE.C)
When a new age has been entered the computer creates a temporary file, called PINOGRAM.PIN. This file contains all relevant information necessary to rebuild a *situation. This is useful, because:

- As long as no new age is given, the most recently saved situation may be retrieved;
- The file PINOGRAM.PIN may be copied to a file with a user-defined name with extension PIN. In this way any situation my be saved on disk and retrieved again at will. So different silvicultural systems with the same initial situation may be tested.

4.23 Thinnings

4.23.1 Introduction

(FILE: THINMETH.C)
After entering a new age at which he wants to see the *transect, the user will be asked whether he wants to cut some trees. If he does wish to thin, a menu with three options appears (see section 4.23.2, 4.22.3 and 4.22.4):

1 = *automatic low thinning;
2 = *automatic high thinning;
3 = *manual thinning.

Thinning occurs by removing a *structure from an array of structures, for example, if *i* is the number of the tree to be cut then *tree[i]* will be removed from computer memory by replacing the contents of structure *tree[i]* by the contents of structure *tree[i+1]* and the contents of *tree[i+1]* by that of *tree[i+2]*, etc.

Per tree those neighbouring trees that influence the *sample tree are kept in a structure *neighbour*. The variable *neighbour[2].nr[3]* gives the third neighbour of the second tree. After cutting this third neighbour, *neighbour[2].nr[3]* becomes *neighbour[2].nr[4]*, etc.

If a neighbour is removed, then the (normal) *growth area of the sample tree also changes and hence so does the *maximum distance of influence *r_max*. With the help of the remaining neighbours a new *r_max* will be calculated. If this is not possible because so many neighbours have been removed that the angle between these vectors from the sample tree to two consecutive neighbours is more than 180°, then *r_max* becomes 55 metres, which is about the longest possible distance within the transect. At the next, *primary selection *r_max* will be treated as follows:

$$\begin{array}{l} \textbf{\textit{if}} \\ \quad r\_\mathbf{max}[i] \geq 7 \textbf{\textit{ and }} r\_\mathbf{max}[nr] > 5 \\ \textbf{\textit{then}} \\ \quad r\_\mathbf{max}[i] = 50 \textbf{\textit{ and }} r\_\mathbf{max}[nr] = 5 \end{array} \tag{78}$$

$$\begin{array}{l} \textbf{\textit{if}} \\ \quad r\_\mathbf{max}[i] \geq 7 \textbf{\textit{ and }} r\_\mathbf{max}[nr] \leq 5 \\ \textbf{\textit{then}} \\ \quad r\_\mathbf{max}[i] = 7 \end{array} \tag{79}$$

So, in the first case the neighbour is always involved in the selection (scan distance = 55 metres), in the second case it is sometimes involved (scan distance ≤ 12 metres). This extra calculation may produce a reasonable improvement in speed, because not every tree is selected at primary selection.

After thinning, the number of stems, basal area and volume per ha are calculated; the data on thinning per ha are found by subtracting these new values from the old values. Data of thinning per tree are written in the file PG?.PRN (see section 4.3 and 4.25.7).

4.23.2 Automatic low thinning

(FILE: THINMETH.C)
*Low thinning anticipates natural thinning of a stand through *competition, by working upward from *overtopped to *dominant trees. Munns (1950) recognizes five intensities of cutting: grade A-light, grade B-moderate, grade C-heavy, Grade D-very heavy and accretion thinning (see glossary: low thinning).

In the PINOGRAM model trees will never be overtopped. Here, a low thinning is identical to thinning of the smallest trees. When the user chooses for automatic low thinning, the program asks for the volume of wood to be harvested. Next, all trees are sorted according to ascending volume. Trees are selected from the smallest tree until the required volume has been reached. A disadvantage of automatic low thinning is that in some cases somewhat larger open areas may arise than are desirable.

4.23.3 Automatic high thinning

(FILE: THINMETH.C)
*High thinning mainly involves trees in the upper crown classes: *codominant and *dominant trees that are competing strongly with the most promising individuals of these classes are removed. Cutting in the lower crown classes is directed towards removing trees that will die and be wasted before the next cutting and is done only if such trees have a positive net conversion value (Munns 1950).

In the PINOGRAM model the user can choose automatic high thinning. The program then asks for the volume of wood to be harvested. The user is also asked to enter the demanded maximum ratio of tree height / crown length. As default, the mean ratio of tree height / crown length is given. The trees are then sorted according to descending heights. Next the program searches for the neighbours that influence the first (and thus highest) tree. The normal growth area vector* and matching crown length in the direction of these neighbours are calculated. Indeed, the normal growth area vector of a tree in the direction of a neighbour is the same as the *actual growth area vector in that direction when this tree is competing with its neighbour.

If the largest ratio of tree height / crown length is more than the given value, the neighbour responsible for this small crown length will be selected for removal. The same procedure is applied to the next highest tree, and so on. If the neighbour with the largest influence on the *sample tree is taller than the sample tree, this neighbour will not be selected.

In this way all trees that are eligible to be released are released from only one side, starting at the highest tree, until the given volume is reached. If the given volume is still not reached, the procedure is repeated and trees will be released from two sides, etc.

A disadvantage of automatic high thinning as in the case of automatic low thinning is that in some cases somewhat larger open areas arise than are desirable, especially at higher age. When a large tree is removed because it competes with a still larger tree, a gap in the canopy arises, which may not close easily or may even remain open.

4.23.4 Manual thinning

(FILE: THINMETH.C)
If a *manual thinning has been chosen and the user has a mouse at his disposal, then he may use the mouse to indicate which trees have to be removed (Fig. 29). On the screen he can see how many trees per ha have been assigned for removal, together with the basal area and volume of thinning per ha.

If the user has no mouse, he may use the cursor keys to indicate the trees to be removed. Figure 29 shows the options for thinning.

4.24 Natural mortality

(FILE: NAT.C)
If the desired new age is given and a thinning has been accomplished, the program looks for trees with a mean crown width less than or equal to 1/M times tree height (M = mortality factor, see section 4.18). Mean crown width is calculated with the help of the equation:

$$\overline{cw} = 2 * \sqrt{\frac{\sum_{k=1}^{k=16} cw[k] * cw[k+1]}{16}} \qquad (80)$$

in which $cw[17] = cw[1]$

If some of the crown widths in one of the sixteen directions are equal to 0 (in the case of *border trees), only positive values for crown widths are involved in the equation. The same method as used for thinning (see section 4.23) applies for the removal of trees and for the calculations of the *maximum distance of influence *r_max* and data on natural mortality per ha

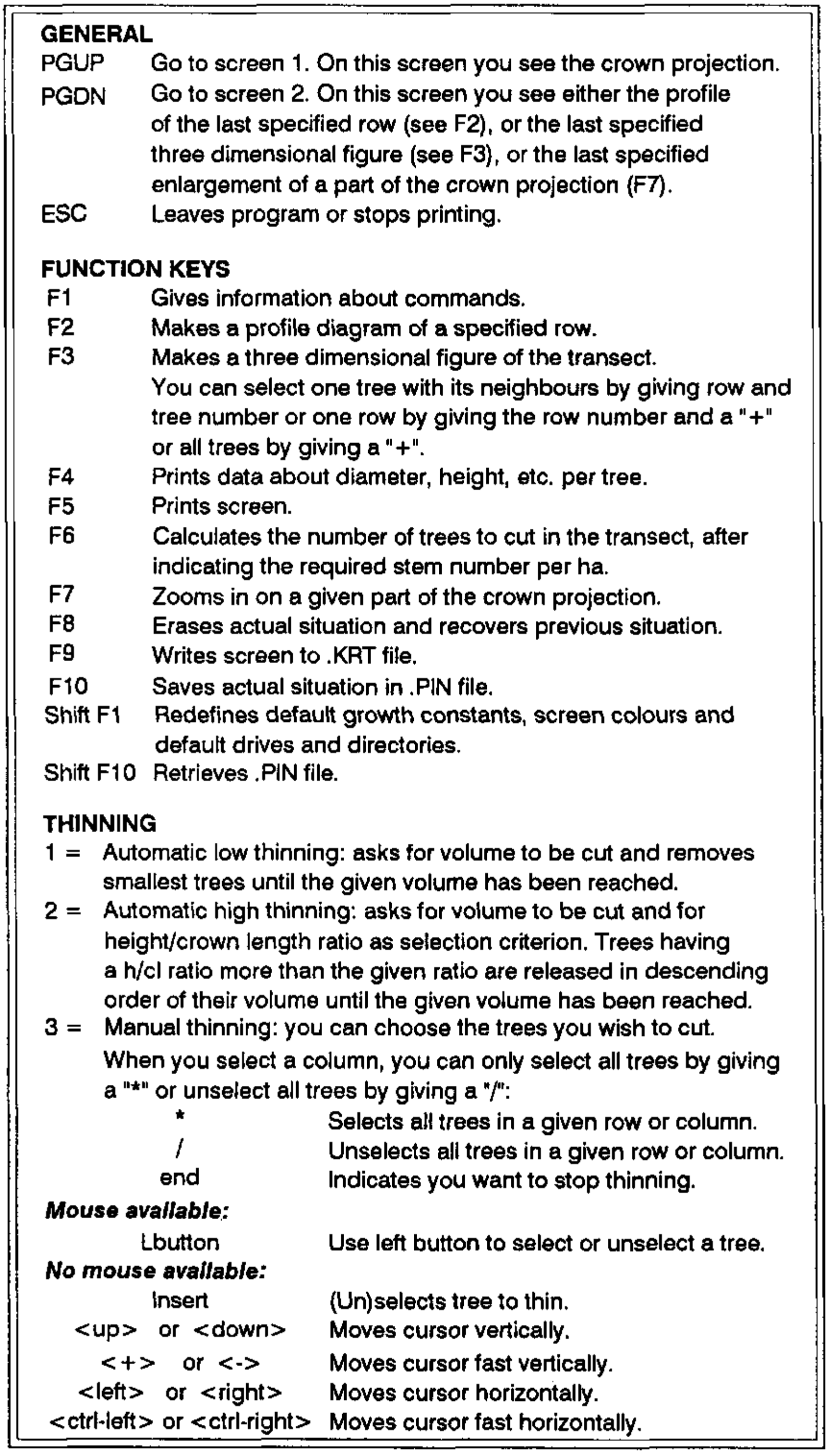
4.25 Options

4.25.1 Introduction

(FILE: INP.C)
When the program asks the user to give the new age or asks him whether he wants to thin or not, several options are at his disposal.

4.25.2 Helpscreen

(FILE: HELP.C)
One of the options is to call up a help screen. This discusses the possible options and keys that activate these options. Figure 29 summarizes the possible function keys and their use.



GENERAL

PGUP	Go to screen 1. On this screen you see the crown projection.
PGDN	Go to screen 2. On this screen you see either the profile of the last specified row (see F2), or the last specified three dimensional figure (see F3), or the last specified enlargement of a part of the crown projection (F7).
ESC	Leaves program or stops printing.

FUNCTION KEYS

F1	Gives information about commands.
F2	Makes a profile diagram of a specified row.
F3	Makes a three dimensional figure of the transect. You can select one tree with its neighbours by giving row and tree number or one row by giving the row number and a "+" or all trees by giving a "+".
F4	Prints data about diameter, height, etc. per tree.
F5	Prints screen.
F6	Calculates the number of trees to cut in the transect, after indicating the required stem number per ha.
F7	Zooms in on a given part of the crown projection.
F8	Erases actual situation and recovers previous situation.
F9	Writes screen to .KRT file.
F10	Saves actual situation in .PIN file.
Shift F1	Redefines default growth constants, screen colours and default drives and directories.
Shift F10	Retrieves .PIN file.

THINNING

1 = Automatic low thinning: asks for volume to be cut and removes smallest trees until the given volume has been reached.

2 = Automatic high thinning: asks for volume to be cut and for height/crown length ratio as selection criterion. Trees having a h/cl ratio more than the given ratio are released in descending order of their volume until the given volume has been reached.

3 = Manual thinning: you can choose the trees you wish to cut. When you select a column, you can only select all trees by giving a "*" or unselect all trees by giving a "/":

*	Selects all trees in a given row or column.
/	Unselects all trees in a given row or column.
end	Indicates you want to stop thinning.

Mouse available:

Lbutton	Use left button to select or unselect a tree.

No mouse available:

Insert	(Un)selects tree to thin.
<up> or <down>	Moves cursor vertically.
<+> or <->	Moves cursor fast vertically.
<left> or <right>	Moves cursor horizontally.
<ctrl-left> or <ctrl-right>	Moves cursor fast horizontally.

Fig. 29 Help screen at PINOGRAM.EXE.

4.25.3 Profile diagram, three dimensional diagram and zooming

(FILES: PROF.C, DIM.C, ZOOM.C)
If a computer is linked to an EGA, VGA or HGC video adapter, the user can use two video pages. Both video pages can be recalled in turn using the keys PGUP and PGDN . The first page is always used for the design of the crown projection. The second video page may be called up by the user to show (see Fig. 30: A, B and C):

- a profile diagram of one or more rows of the *transect,
- a three dimensional design of:
  - * one or more trees with their competing neighbours or
  - * one or more rows of trees, or
  - * all trees
- a close up design of a part of the crown projection (zooming).

The shape of the curves in the crowns of the profile diagram and the three-dimensional diagram are arbitrary.

In the three-dimensional figure coordinates of tree crowns are drawn assuming an angle of incidence of 45°. The sixteen crown coordinates *xco[k]* and *yco[k]* are calculated as follows:

$$xco[k] = \frac{1}{2}\sqrt{2} * tree\_yco + tree\_xco + cw[k] * \cos(k * \frac{\pi}{8}) \qquad (81)$$

$$yco[k] = \frac{1}{2}\sqrt{2} * (height - cl[k] + (tree\_yco + cw[k] * \sin(-j * \frac{\pi}{8})) \qquad (82)$$

The value of *j* in here is dependent upon *k* as follows:

TABLE 14 Relation between *j* and *k* in equation 81 and 82

k	*j*	*k*	*j*	*k*	*j*	*k*	*j*
1	-2.0	5	0.0	9	6.0	13	8.0
2	-1.5	6	1.5	10	6.5	14	9.5
3	-1.0	7	3.0	11	7.0	15	11.0
4	-0.5	8	4.5	12	7.5	16	12.5

4.25.4 The hint option

(FILE: DAHA.C)
Before the user starts to indicate which trees to thin he may ask for a hint about the number of trees to be removed. For example when there are 2364 trees per ha and one wants to keep about 1500 trees per ha after thinning, "Hint" says that (2364-1500)/10 = 86 trees have to be removed from the *transect.

4.25.5 Print actions

(FILE: PRINT.C)
There are options to print out the screen contents as well as tree data and data per ha. An example is given in figures 30-40 and table 15.

TABLE 15 Tree data and data per ha: example of output to printer (key F4)

row = row number
nr = tree in row
S = S_value (m)
h = height (m)
dbh = diameter at breast height (cm)
dbranch = branch diameter in the lower crown part (cm)
f = form factor
v = stem volume (dm^2)

Age: 10 years   Distance in row: 1.5 m.   Row distance: 1.5 m.

	Remaining stand	Thinning	Natural mortality
Number of stems per ha	4290	0	0
Basal area per ha	6.8 m^2	0.0 m^2	0.0 m^2
Volume per ha	18.2 m^3	0.0 m^3	0.0 m^3

row	*no*	*S*	*h*	*dbh*	*dbranch*	*f*	*v*
1	1	14.6	3.0	2.5	0.9	0.79	1
1	2	21.2	4.3	5.3	2.0	0.71	6
1	3	19.4	3.9	4.6	1.7	0.73	4
1	4	17.8	3.6	4.0	1.5	0.74	3
1	5	18.9	3.9	4.4	1.6	0.73	4
1	6	21.2	4.3	5.3	2.0	0.71	6
1	7	18.3	3.7	3.8	1.3	0.75	3
1	8	21.1	4.3	4.8	1.7	0.72	5
1	9	21.3	4.3	5.1	1.9	0.72	6
1	10	20.7	4.2	5.1	2.0	0.72	6

etc.

When printing the screen contents, the quality of the printout depends on the screen's resolution. In VGA and EGA screens the resolution is 640 * 350 pixels, in HGC it is 720 * 348 pixels and in CGA (which cannot use a second video page) it is 640 * 200 pixels. So a screen dump from a Hercules screen gives the best result and from a screen dump from a CGA the worst. Only a simple matrix printer can be used (for example, STAR-LC10).

4.25.6 Installation of growth constants, colours and default drives and directories

(FILES: SETUP.C, SCREEN.C)
The function key Shift-F1 is used to change default settings for growth constants, screen colours and default drives and directories for PRN, PIN and KRT files.
Growth constants are:

- H1 and H2 from equation 39;
- C from table 8;
- CL1 - CL4 from table 9;
- CW1 - CW4 from table 9;
- D1 - D4 from table 9;
- F1 - F4 from table 10;
- DB1 - DB4 from table 11;
- M - from section 4.18.

It is justifiable to change these constants only if further research reveals that adaptation is necessary (see also section 4.26). Other tree species may show growth dynamics similar to Scots pine, although with different values for the constants. In that case the PINOGRAM model can be used for these other species by changing the growth constants according to the values found for these species.

Screen colours, such as background colour, text colour and tree colour, may be changed at will if the user has a VGA or an EGA adapter at his disposal. With the EGA adaptor one may choose out of 64 colours, consisting of 4 blue, 4 green and 4 red tints. With the VGA adapter one may use 64 blue, 64 green and 64 red tints.

4.25.7 File actions

(FILES: XPIN.C, PRINT.C, READ.C, CRSHOW.C, SHOW.C)
As has been explained in section 4.4 a *situation is temporarily saved in a file PINOGRAM.PIN. This situation may be redrawn or copied to a PIN file with a name defined by the user. In this way a complete range of PIN files may be created, each containing values to create a different situation (such as a different age, or a different thinning regime or a different starting situation).

A menu of these PIN files may be called up when starting up the program or with the Shift F10 function key. From this menu a PIN file may be selected, and the once created situation, thus retrieved, can be investigated out further. The crown projection of this situation is shown on video page one.

The XPIN.EXE program enables important data per tree to be read from a given PIN file and written to an ASCI file. These data consist of initial values (see section 4.5), tree number *nr*, x and y coordinates *xco* and *yco*, *S value S_{tree}, height *h*, age *t*, diameter at breast height *dbh*, mean largest branch diameter *dbranch*, form factor *f*, volume *v*, *actual growth area vector in sixteen directions *a_act[k]*, crown length in sixteen directions *cl[k]*, crown width in sixteen directions *cw[k]* and the tree number of different neighbours per tree *neighbour.nr[i]*. The user must define the name of this ASCI file.

The screen contents may be written to a file with extension KRT, as well as to the printer. The READ.EXE program is able to read this file and to display it on the screen again. Here too it applies that function key F5 is used to have the screen contents printed by a simple matrix printer. It is also possible to read a second KRT file on video page two. The PGUP and PGDN keys enable the user to switch between video pages. This makes it easy to see differences between both figures.

The CRSHOW.EXE program creates a file with extension SHW. This program shows a menu with KRT files and asks the user to choose from these files in the order that he wishes to see these figures displayed. The SHOW.EXE program shows KRT files one by one at a certain given time interval.

A disadvantage of the method used to write screen contents to a file is that KRT files created with the help of a certain graphics adapter (for example HGC), cannot be displayed using one of the other adapters (for example CGA, EGA, VGA) and vice versa.

4.25.8 Leaving the program

(FILE: INP.C, PRINT.C)

The user presses ESC key to leave the program. Before the program is closed the user will be asked if he wants to save the last *situation. If so, the user must give the situation a name; the situation is then saved in a PIN file of the same name (see section 4.4).

4.26 Changing the values of the constants

The parameters in the equations for calculating crown length, crown width, diameter, form factor and branch diameter were estimated with the help of mathematical correlations, resulting in mean values with standard deviation. These mean values were used as growth constants in the model (= "standard approach"). But what are the consequences for tree forms and yield data per ha if the values of these parameters vary freely within their confidence limits (= "alternative approach") ?

In the model, values of the parameters could be randomly determined repeatedly within their confidence limits analoguous to the calculation of the *S value of a tree (section 4.6). For example, consider the equation for crown width. The crown width of a tree is calculated several times during the tree's lifetime in sixteen directions. Hence, the values obtained for the resulting crown projection area using either the "alternative approach" or the "standard approach" are more similar than the different crown radii calculated using both approaches. When the "alternative approach" is used to calculate a *forest situation for many successive ages, it becomes increasingly likely that the final crown forms of the older trees will also gradually correspond more to those found according to the "standard" approach.

The "alternative approach" also affects how quickly the h/cw ratio attains the critical mortality constant of 6 (see section 4.18). A tree's death influences its neighbours. If the pattern of mortality changes in the *transect, this also affects the transect *architecture and hence the yields per ha. The magnitude of these effects depends on the:

- number of trees in the transect;
- distance between neighbouring trees;
- number of trees that die sooner or later than according to the "standard approach";
- stand age at which trees die sooner or later than according to the "standard approach";
- time interval between the different moments of death calculated according to both methods.

A major disadvantage of the use of random values for the different constants is that the output of the model is very difficult to interpret. In other words, it is not easy to interpret the influences of thinning, planting distances or *heterogeneity on the development of trees in the transect (see section 6), which is the main purpose of the model. Therefore, it was decided to maintain the "standard approach".

Non-random change of values of the estimated constants (e.g. for a sensitivity test) does, of course, also influence tree architecture, transect architecture and yields per ha. Its influence on tree architecture may be directly calculated using the equations from section 4.17. Influence on transect architecture again depends on the above-mentioned characteristics. However, it does not seem very worthwhile to do another sensitivity test, because such a test is implicit in the assessment that the best values are estimated with the help of the data set used. As soon as a larger or better data set (see sections 3.1.6, 3.2, 5.2 and 5.3) is available, the constants can be adapted to improve the model in the way described earlier (see section 4.25.6).

5 DISCUSSION AND CONCLUSIONS

5.1 Potential applications of the PINOGRAM model

The PINOGRAM growth simulating program enables the *growth of individual trees within a stand to be visualized. Different silvicultural systems can be simulated, to discover their effects on stand growth. The graphical design makes this insight very communicable and useful (e.g. for teaching).

One of the ways the model can be used is to simulate the influence of stand *heterogeneity on stand development (see chapter 6). Heterogeneity may be caused by great variation in site characteristics and *genotypes. In more heterogeneous stands the natural mortality of trees, which is caused by *competition for space with neighbouring trees, is more dispersed through time than when the stands are more *homogeneous and all trees are similarly competitive. The model easily indicates the time at which *cleaning will become urgent and the probable time that the first commercial thinning, which depends on planting distances and the thinning regime, should be done. Stand heterogeneity can be depicted in a three dimensional drawing of the *transect. Diversity in crown forms and diameters as well as data on mean branch diameter in the lower part of the tree's crown are good indicators of assortment classes and the potential timber quality.

Another advantage of the model is its potential for simulating any thinning method that does not deal with stem and/or branch quality (such as crooked stems versus straight ones or dense crowns versus open crowns). This means that *weight and timing of thinning can be simulated, and so can the consequences of removing trees selected by the user. This is especially useful when searching for an optimum method of thinning that depends on the aim of management (e.g. minimizing costs, maximizing proceeds or yield, durability, or maximizing the likelihood for establishment of a certain flora, fauna and *architecture; cf. Oldeman 1991).

Planting distances, stand age and thinning regime result in a certain stand structure, which in combination with data on h/d ratio, cl/h ratio and cw/h ratio are useful input for risk analysis. For example, if risk trees (i.e. trees with a high h/d ratio, low cl/h ratio and low cw/h ratio) are found scattered all over the stand, the total risk is much smaller than if these trees are clustered.

*Severe thinnings and mortality cause gaps in the canopy. The model can calculate growth of trees next to these gaps and also the growth of more or less solitary trees. This is in contrast with many models that are based on closed stands (Faber 1983, Mohren 1987, Barreto 1988abc). Another advantage is that PINOGRAM will show whether a tree will fill a gap and to what extent.

Because the stem and crown coordinates of all trees in the transect are known, in principle the light climate on the forest floor may be predicted (cf. the model of Koop 1989). Light climate is one of the main conditions of controlling regeneration.

5.2 The model's drawbacks

Like all models, the present model has its drawbacks, some of which could be removed by further research.

The equations for growth given in the model cannot simply be used for real trees. The normal growth area of a tree, as measured in the field is often not the same as the *actual growth area the tree is really using at that moment. The actual growth area can be calculated with the help of the crown widths measured in sixteen directions, but generally the matching crown lengths and diameters calculated differ from the measured ones, because these tree dimensions are not 100% correlated with age, height and actual growth area.

The age distribution of the observed trees is skew; it contains more data on trees in juvenile phases than in older phases. This means that the data set used for calibrating the model is not normally distributed. This may be realistic, because young trees always outnumber old trees, but it is statistically unsound. However, it is uncertain whether measuring relatively more older trees gives a better base for the model, because as trees age they are more likely to diverge from "*normal growth". This larger divergence is caused by the accumulation of effects resulting from extreme weather conditions, pests, diseases, etc.

In the model, the height growth of trees is more or less a black box. Every tree grows according to the same equation (39) with the same constants H1 and H2, that are based on the mean height growth of many stands in the Netherlands (Van den Burg et al. 1983). Only the *S value S_{tree} that determines the absolute growth of a tree differs per tree. If the effect of factors influencing height growth of individual trees can be computed better, the model will be improved.

PINOGRAM calculates a *forest situation for a rather restricted area ($20*50$ m^2). However, the user may increase the number of these areas (*transects) and take the average of the results per ha. As computers improve it will become possible, if necessary, to involve larger areas or more trees per area unit in the simulation. To cope with the vast amount of information per screen area, it should be possible to show the required subareas on the screen in turn. One method is to show the complete area in a more schematized way with the option of being able to zoom in on a given subarea in order to look at it in more detail.

At the moment the model is unable to show *architecture of trees in detail. Simulation of the crown form is restricted to crown length and crown width in sixteen directions. This may cause large differences between the model's output and the reality, especially for older stands. In older stands the top of a tree's crown often breaks off or dries up under the influence of climatic factors such as storms, snow or drought. Generally this is followed by *reiteration. The very shallow but wide crowns that can often be found in the field but which are not accounted for in the model can be explained by this repeated breaking off and reiteration. The effects of genetic differences, diseases and abnormalities are probably also important.

In the model, trees will only die naturally if their cw/h ratio is less than 1/M (M = mortality constant = 6); so the simulation of natural mortality is rather simple. External influences such as *interaction with the forest climate, understory, fauna or air pollution are not directly accounted for in the model.

As yet, no data on trees that have matured unrestricted in space have been processed in the model. So it is not clear whether the growth equations may be used for trees next to large gaps in the canopy.

The model has only been calibrated using data from Scots pine on the Veluwe. It does not yet contain information about tree architecture, stem form, flowering and consequences of damage, diseases, climatic changes, environmental pollution and exposure to different climatic conditions in different compass directions.

The demands made on computer hardware and software increase as the program becomes more complex. At the moment the program works reasonably fast when a 286 processor is used together with a coprocessor. However, a 486 processor works ten times faster.

Most people will probably soon be using a 286 processor (instead of the 86 or 88 processor) or better. To use the potential of the much better 386 or 486 processor in combination with the new OS2 (= OPERATING SYSTEM 2) operating system instead of DOS, the program will have to be partly rewritten. The advantage is that the speed of the program will increase markedly and so will the potential for new applications.

5.3 Possibilities of extending the model

The range of observations used to define the growth equations is restricted to a part of the Veluwe in the Netherlands, so in principle the model is only valid for this area. New ranges of observations should be used to validate and possibly improve and generalize the model. Trees with strongly asymmetrical crowns or that are crooked and severely damaged should not be used anymore in the descriptive data set that is used to calculate crown length, crown width and diameter with the help of regression (see chapter 3.1.6). Instead, the consequences of damage to trees in relation to tree growth should be better studied and digitized.

It would be very interesting to apply the same growth rules to tree species other than Scots pine. Then next step may be to develop models predicting the growth of individual trees in mixed stands. However, if there are big differences in growth and dynamics between two species, then it will be important to know the light climate for trees in the lower story and its influence on those trees. The same applies when trees are of different ages. The length of the growth area vectors probably not only depends on tree height but also upon age, light reduction and the interaction between species. The following equation may apply:

$$a[nr][i] = \mathrm{f}(h[nr],t[nr],PLR[nr],sp[nr],h[i],t[i],PLR[i],sp[i]) * A[nr][i] \tag{83}$$

in which
f(h[nr],t[nr],PLR[nr],sp[nr],h[i],t[i],PLR[nr],sp[i]) being a function of height, age, photosynthetic light ratio (Kellomäki et al. 1980) and species of sample tree nr and neighbour tree i.

If equation (83) above does apply, the model will answer many questions important in forestry practice. Questions such as: "When will young Douglas-firs compete so vigorously with old Scots pines that it will be necessary to release these Scots pines to keep them alive?" and "How long can a given species mixture be reasonably maintained at given planting distances?" can be answered more precisely than at present.

The model could also be extended to provide a clearer explanation of possible height growth of individual trees. The model uses a "normally distributed" range of S values to simulate variation in genetic traits and site characteristics. Every tree has a chance of 0.95 of its S value S_{tree} being within the range of the given minimum and maximum S values. The development of a site classification giving a mean S value distribution for various tree species would enhance the practical value of the model presented here. However, every tree in the model shows the same relative height growth according to the Chapman-Richards equation (Van den Burg et al. 1983). In reality, height growth fluctuates more or less around this "mean height growth", but may also strongly change as a result of changing environmental factors. Social position, pests and diseases, environmental pollution and climatic changes may cause deviations in the mean height growth of individual trees. If the influence of these environmental factors on height growth could be computed the model might improve our understanding of survival and mortality of species and individuals under changing environmental conditions.

It would be relatively straightforward to link this model with other models, such as the light simulation model developed by Koop (1989) and the architectural model developed by De Reffye et al. (1979, 1989) or by Aono and Kunii (1984). With the help of the light simulation model the growth of individual trees in the lower story could be assessed, providing the relation between height growth and light intensity is known. And with the help of the architectural model the abstract tree forms can be depicted more realistically, giving a better insight in possible changes of tree forms that depend on factors derived from stand density, tree age and site. An example of a model that gives a rather detailed depiction of stand growth was developed by Kunii and Enomoto (1991). This is an interacting tree model that visualizes forest formation processes by algorithmic computer animation. Theirs is a kind of domain model (see chapter 1.2) that is combined with a model simulating tree architecture (Aono and Kunii 1984).

6 EXAMPLES OF SIMULATION USING PINOGRAM

6.1 Introduction

In this chapter some examples of simulations with the help of the PINOGRAM program are discussed. This chapter has been written to illustrate the potential applications of simulations. Four aspects have been focused on because of their primary importance for silvicultural management:

1. Method of thinning,
2. Initial number of stems per area,
3. *Homogeneity versus *heterogeneity of a stand,
4. *Weight of thinning.

6.2 Example 1: Method of thinning

6.2.1 Initial situation.

In the example we proceeded from command line argument 2 (see section 4.3), a within row spacing of 1.5 metres and a between-row spacing of 1.5 meter. The *S values ranged between 14 and 24 metres. In the first 20 years no thinning was done.

Figure 30A and 31A show crown maps at ages 10 years and 20 years. It is evident that the crowns overlap. At the age of 10 years there are still a few small gaps in the canopy, but these have practically disappeared by the age of 20 years. The calculated *canopy closure increases from 108% to 118% in this period.

Figure 30B, 31B and 30C, 31C represent a profile diagram and a three-dimensional design of trees in row number 7. The coefficient of variation of mean tree height in this example is 13% and that of mean crown length is 18%. The coefficient of variation of mean tree height in stands younger than 25 years lies between 10 and 18 percent according to table B1 and the coefficient of variation of mean crown length is between 17 and 36 percent. Thus the height and crown form distributions produced by the model are indeed realistic. The mean h/dbh-ratio at the age of 20 years is 96 with a coefficient of variation of 10% and a maximum of 136.

Mortality starts at the age of 17 years. It can clearly be seen how trees prune each other. In the profile diagram tree numbers 9, 16 and 20 are so small compared with their neighbours that it may be expected that they would have been overtopped by their neighbours in reality. In the model it appears that these trees die within a period of 1-6 years. Furthermore tree number 4 in row 7 disappears within 2 years, because of strong *competition with its neighbours in rows 6 and 8.

A mean height of 7.1 metres means a "boniteit II-III" (i.e. relative production class or site class) according to the *yield tables of Grandjean and Stoffels (1955) and bonität II according to the yield tables of Wiedemann (1943) and "Het Bosschap" (1990). The basal area and volume found were less than are given by the tables of Grandjean and Stoffels (1955) and Wiedeman (1943), but more than are given by the tables of "Het Bosschap" (1990). The volume classes are more or less normally distributed with the modal shifted somewhat to the left.

6.2.2 Thinning

Four stand treatments are discussed below to ascertain the effects of a method of thinning on *stand architecture and yield. The treatments are: natural mortality, *low thinning, *high thinning and *manual thinning.

Natural mortality (Figs 35 and 39)
In the example of natural mortality no thinnings have been performed. Here it is conspicuous that the basal area reaches a value of about 35 m^2 at the age of 35 years, and then appears to stay more or less constant. This means that the volume per ha keeps increasing, as long as height growth continues, which is indeed shown by the example.

The *canopy closure initially rises to 120% at the age of 20-30 years. Then it steadily decreases to 60% at the age of 120 years. This is because after the age of 30 years there is much more natural mortality.

On average the h/dbh ratio is 98 at the age of 30 years and 94 at the age of 40 years with coefficients of variation of 7% and 6% respectively, and maxima of 120 and 105 respectively. Oldeman (1974, 1990) describes an h/d ratio (d = diameter above the beginning of the root system) of 100 as a reference line (i.e. not a regression line or average line for all trees) to broad-leaved tropical rain-forest trees that grow conform their architectural model. After a stand has reached its maximum basal area, *interactions between trees decrease with the stand's aging. In other words, when a large tree dies, the remaining trees are not able anymore to use the entire space released, so they do not compete for space anymore and the mean h/dbh ratio decreases.

Low thinning, high thinning and manual thinning (Figs 32, 33, 34, 36 ,37, 38)
In the example of *manual thinning I removed tree at my own discretion bearing in mind three criteria:

- relatively large gaps in the canopy should be avoided;

- large trees must be released in time, so that crown forms arise as symmetrically as possible (cf. *high thinning);
- the smallest trees are removed.

In the example of *high thinning at the ages of 20 and 25 years a *low thinning was done first (see Table B5). After the age of 30 years an example was worked out for high thinning only and one for low thinning only. The aimed *intensity of thinning is the same in all three examples, so this intensity is approximately equal. Data on individual standing trees were saved in PIN files in steps of 10 years; data on thinned trees can be found in PG2.PRN.

The mean annual increment at the age of 50 years (= $\bar{i}_{50}$) in the examples of low thinning, high thinning and manual thinning appears to be respectively 7.17, 7.02 and 7.11 m^3 per ha per year. Compared with the *yield tables of Grandjean and Stoffels (1955) and Wiedemann (1943), the h/dbh ratios of the trees at about the same number of stems per ha are somewhat smaller, but are somewhat larger compared with the yield table of "Het Bosschap" (1990).

As expected, values of tree dimensions (such as diameter, crown width, crown length and tree height) in the example with high thinning show a wider range than in the examples with low thinning and natural mortality. After manual thinning this range is narrower than after high thinning, but it is larger than after low thinning. After high thinning and manual thinning the crowns of the largest trees generally tend to be more symmetrical than after low thinning, which benefits the timber quality. However, the assortment resulting from low thinning is more homogeneous in diameter than that produced by high thinning and manual thinning. Tables B4, B5 and B6 show the mean diameter and coefficient of variation of the thinned wood after low thinning, high thinning and manual thinning. The smaller variation in diameter at low thinning is striking. Compared with high thinning and manual thinning, low thinning causes the mean diameter of the thinned wood to be smaller at the beginning of the *rotation and larger at the end.

For all three examples with thinning the mean diameter increment from the age of 110 to 120 years is about 18 mm per tree and varies from 8 mm to 34 mm per tree. In the example without thinning the mean diameter increment is about 8 mm and varies from 3 mm to 15 mm.

The *canopy closure is a slightly less in low thinning than in high thinning. Canopy closure is the greatest at manual thinning. In the examples canopy closure diminishes from 120% at the age of 20 years (still unthinned) to less than 40% at the age of 120 years. This clearly shows how much irradiation increases within the stand with increasing age.

Because the volume and the diameter per tree of the thinnings and the clear-cutting have been calculated, it might be possible to calculate gross proceeds per ha as far as prices per assortment can be estimated. Since prices per assortment can never be accurately estimated within the next hundred years, the results of these calculations are of value only as an indication of what is the best silvicultural system at hypothetical price levels in different scenarios. Tables B4, B5 and B6 give the gross proceeds from the above discussed thinning systems, expressed in guilders per ha at different rates of interest. In our example, the prices of the assortments have been taken from the Long Term National Forest Plan (Anonymus 1986). **However, these prices are very inaccurate assessments and the results of the tables are merely intended to demonstrate what can be done with the simulation results.** In the examples given there is no big difference between the gross revenue of the low thinning and the high thinning. Manual thinning gives a somewhat better revenue, probably because of a more homogeneous closed canopy, so that the total area available is used better. The results depend greatly on the interest rate.

6.3 Example 2: Initial number of stems per ha

A large number of stems per ha also means high costs for planting material and plantation. A silvicultural system was simulated in order to determine the effect of a high initial number of stems per ha on the yield, starting with 10 000 trees per ha. Just as in the preceding sections the command line argument in this example is 2 (see section 4.3) and the given range of *S values lies between 14 and 24 metres. However, the within- and between-row spacings were set at one metre. No thinning was done in the first 20 years but then a *low thinning was done. Figure 40A shows the crown map at 20 years and figure 40B shows the profile diagram.

If no thinning is performed, the basal area appears already to reach its maximum value, which is about 35 m^2/ha, at the age of 25 years. Mortality starts as early as 11 years of age. The *canopy closure increases to 150% at the age of 15-20 years. At the age of 30 years this has already diminished to 118%. The mean h/dbh-ratio at the age of 20 years is 112, with a coefficient of variation of ca 8% and a maximum of ca 135. This reconfirms that many initial stems per area enlarges the chance of high h/dbh ratios and hence the likelihood of the stand being unstable.

If thinning is done, a much greater volume of trees is thinned than in the examples in the preceding section. This higher production lasts until the total volume per ha has fallen to the same level as that of the examples in the preceding section (Table B7), which is at the age of about 50 years in this example.

Thus, a greater initial number of stems per area tends to give a higher gross production and a better selection potential. However, because of its greater density it is more difficult to penetrate such a stand (see Fig. 40A, 40B), so that it is not always easy to use the better selection potential and secondly the costs of logging are generally higher.

6.4 Example 3: Stand homogeneity

Selection, breeding and soil management cause stands to become more *homogeneous. Because of the high costs of *cleaning the tendency is to postpone cleaning and thinning until a commercial assortment can be delivered. However, homogeneous stands would inhibit the necessary self-thinning, so that the required assortment will be achieved relatively late and the mean h/dbh ratios may increase to an extent that there is a high risk of storm damage.

In this example command line argument 2 was used again (see section 4.3), but the *S values were within a range of 18 to 24 metres in order to estimate the influence of homogeneity. The inter-row and within-row spacing were set at 24 metres. There was no thinning in the first 20 years.

Natural mortality appears for the first time at the age of 25 years. The maximum standing volume is reached sooner than in the more *heterogeneous stand discussed in section 6.2. Because natural mortality starts relatively late, more trees die at the age of 25-40 years, but occasionally a clump of trees dies at the same time, creating relatively large gaps in the canopy. These gaps are usually not too large so that trees usually manage to fill them after a certain time.
The higher average of *S values causes yield to be higher (Table B8), a larger maximum basal area and also a larger maximum *canopy closure. The mean diameter of the thinned trees is larger than in the example of section 6.2, because of the somewhat larger mean S value. The negative influence of the later self-thinning in this example on the mean diameter of the thinned trees is outweighed by the positive influence of the higher S values.
The mean h/dbh ratio is 96 at the age of 20 years and 101 at the age of 30 years with coefficients of variation of 5% and 4% respectively and maxima of 115 and 113 respectively.

6.5 Example 4: Weight of thinning

More *severe thinning boosts the increase in the *growth area per tree, causing trees to develop larger radial dimensions. This example simulates the influence of a more severe thinning than in section 6.2. Assuming the same *situation as in section 6.2, a low thinning was repeated.

From table B9 it appears that this more severe thinning of Scots pine will not be compensated for by a greater volume increment, but results in less standing volume per ha and finally in a lower yield. This more severe thinning may be effective if the aim is to produce heavy timber relatively fast and the smaller production of stem wood is of less importance or the interest rate is rather high.

Of course, this more severe thinning also results in less *canopy closure, which means that more light can reach the forest floor at an earlier stage and that eventually the undergrowth present is more likely to survive. It also means that another *eco-unit *architecture will be created with other trees, plants and animals, opening up other possibilities for use. From the ages 65 until 120 years no more thinning is done anymore in this example. Canopy closure is 37% at the age of 70 years and 46% at the age of 120 years. Dependent upon the site, one may consider underplanting with Douglas-fir or beech at the age of 65 years. However this cannot yet be simulated with this model.

```
                              Data per ha
                              ___________

Row distance: 1.5   S_min  : 14.0   Max. diam:  6.8   Stemnumber/ha:  4290
Dist. in row: 1.5   S_max  : 24.0   Min. diam:  2.1   Basal area/ha:   7.7
Age         :  10   H_mean :  3.9   Mean diam:  4.8   Volume/ha    :  19.7
                    H_dom  :  6.0                     Canopy clos. : 108.1%
```

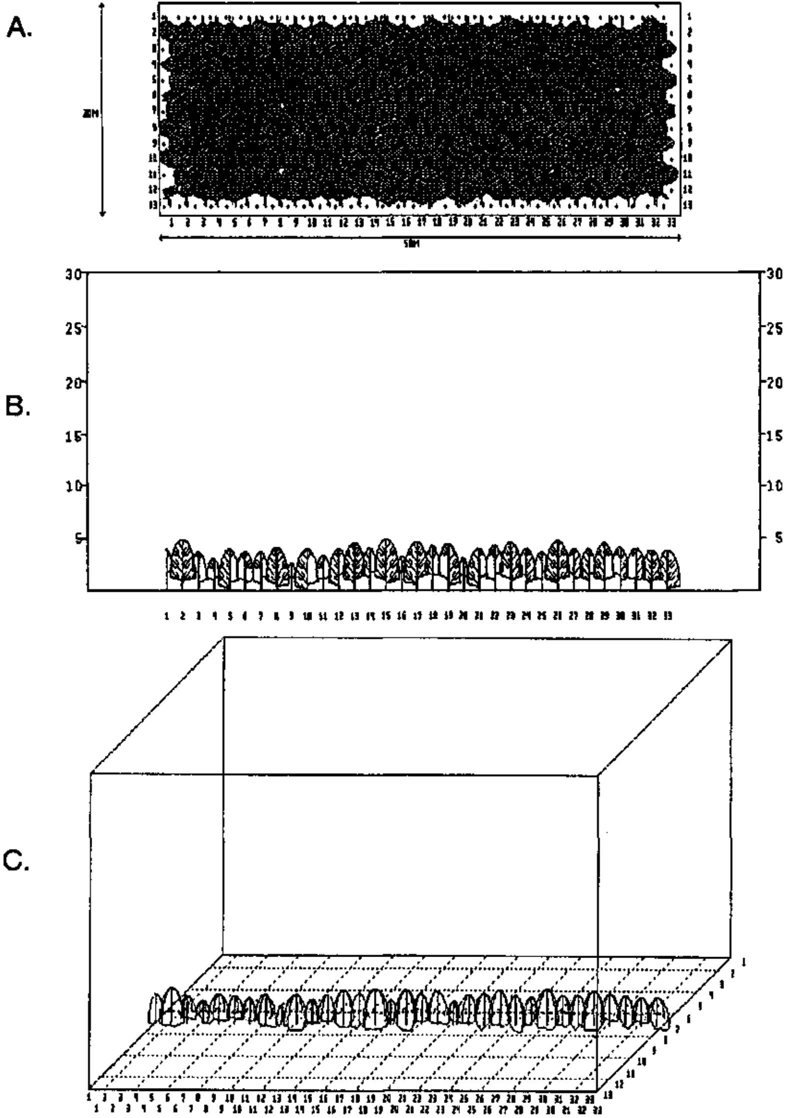
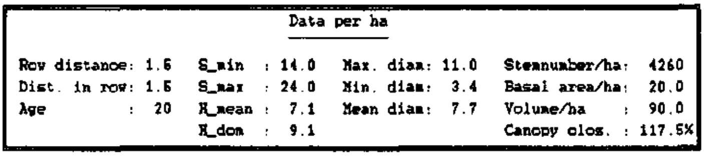


Fig. 30 Simulation of 10-year-old stand of Scots pine without thinning.
A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of row 7; vertical axis: tree height; horizontal axis: tree no. in row. C. Three-dimensional display of row 7; axes: see A.



```
                              Data per ha
                              ───────────
Row distance: 1.6   S_min  : 14.0   Max. diam: 11.0   Stemnumber/ha:  4260
Dist. in row: 1.5   S_max  : 24.0   Min. diam:  3.4   Basal area/ha:  20.0
Age         :  20   H_mean :  7.1   Mean diam:  7.7   Volume/ha    :  90.0
                    H_dom  :  9.1                     Canopy clos. : 117.5%
```

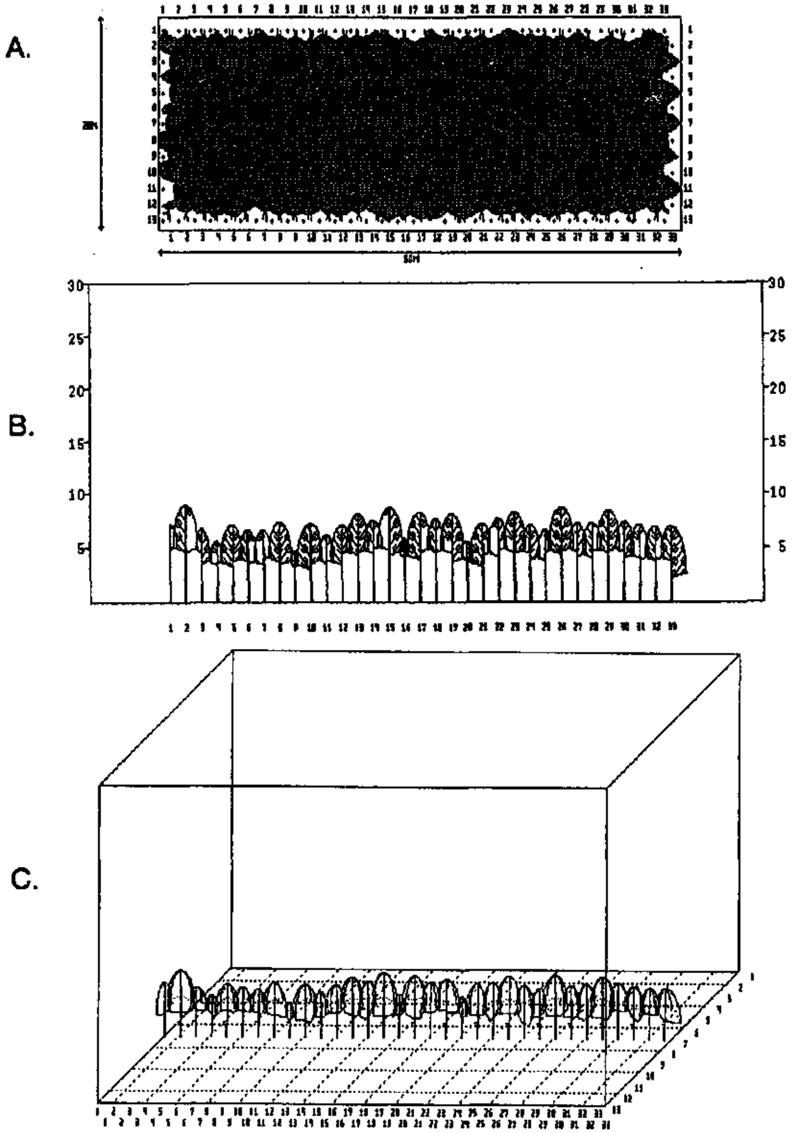
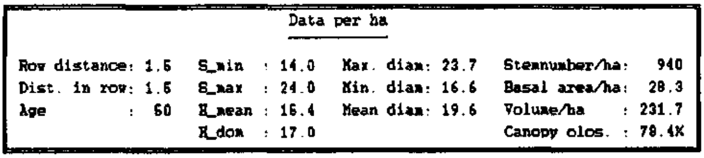


Fig. 31 Simulation of 20-year-old stand of Scots pine without thinning. A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of row 7; vertical axis: tree height; horizontal axis: tree no. in row. C. Three-dimensional display of row 7; axes: see A.



```
                              Data per ha

Row distance: 1.5   S_min  : 14.0   Max. diam: 23.7   Stemnumber/ha:    940
Dist. in row: 1.5   S_max  : 24.0   Min. diam: 16.6   Basal area/ha:   28.3
Age         :  50   H_mean : 16.4   Mean diam: 19.6   Volume/ha    :  231.7
                    H_dom  : 17.0                     Canopy clos. :  78.4%
```

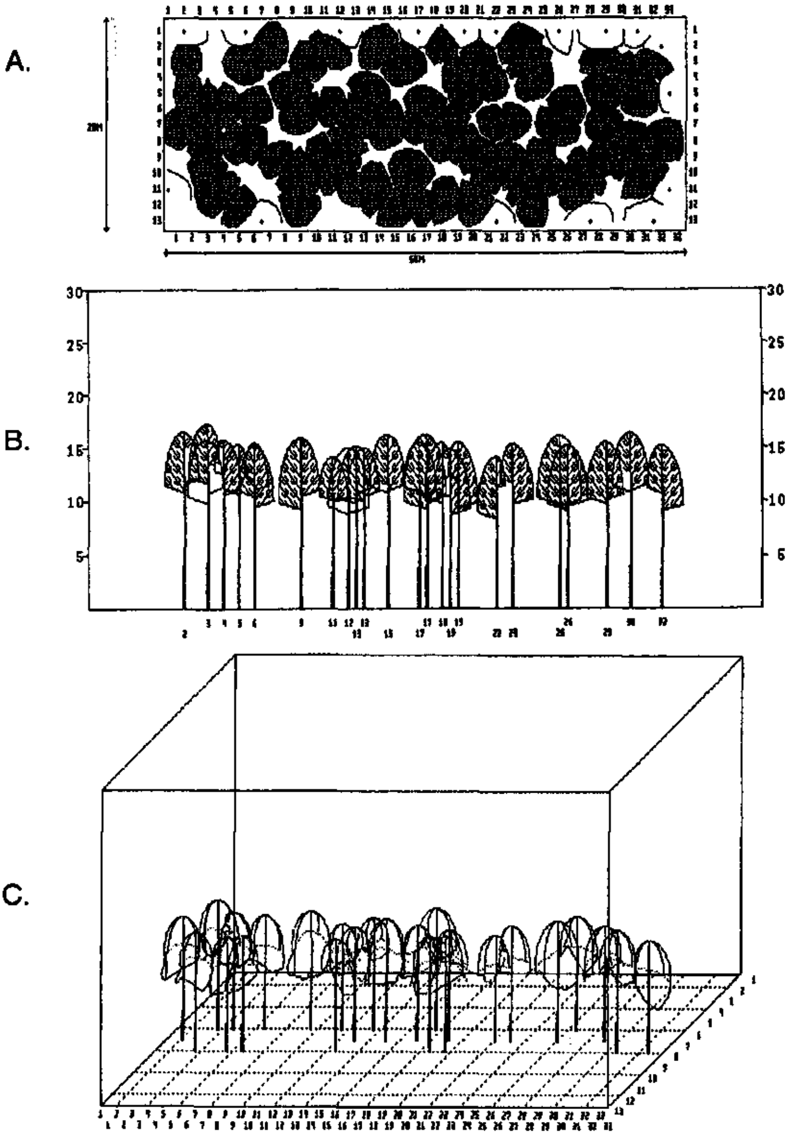
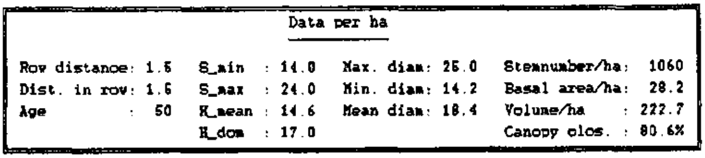


Fig. 32 Simulation of 50-year-old stand of Scots pine with low thinning.
A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of rows 6,7,8; vertical axis: tree height; horizontal axis: tree no. in row. C. *Three-dimensional display of rows 6,7,8; axes; see A.*



```
                              Data per ha
                              ───────────
Row distance: 1.5   S_min  : 14.0   Max. diam: 25.0   Stemnumber/ha:  1060
Dist. in row: 1.5   S_max  : 24.0   Min. diam: 14.2   Basal area/ha:  28.2
Age         :  50   H_mean : 14.6   Mean diam: 18.4   Volume/ha    : 222.7
                    H_dom  : 17.0                     Canopy clos. : 80.6%
```

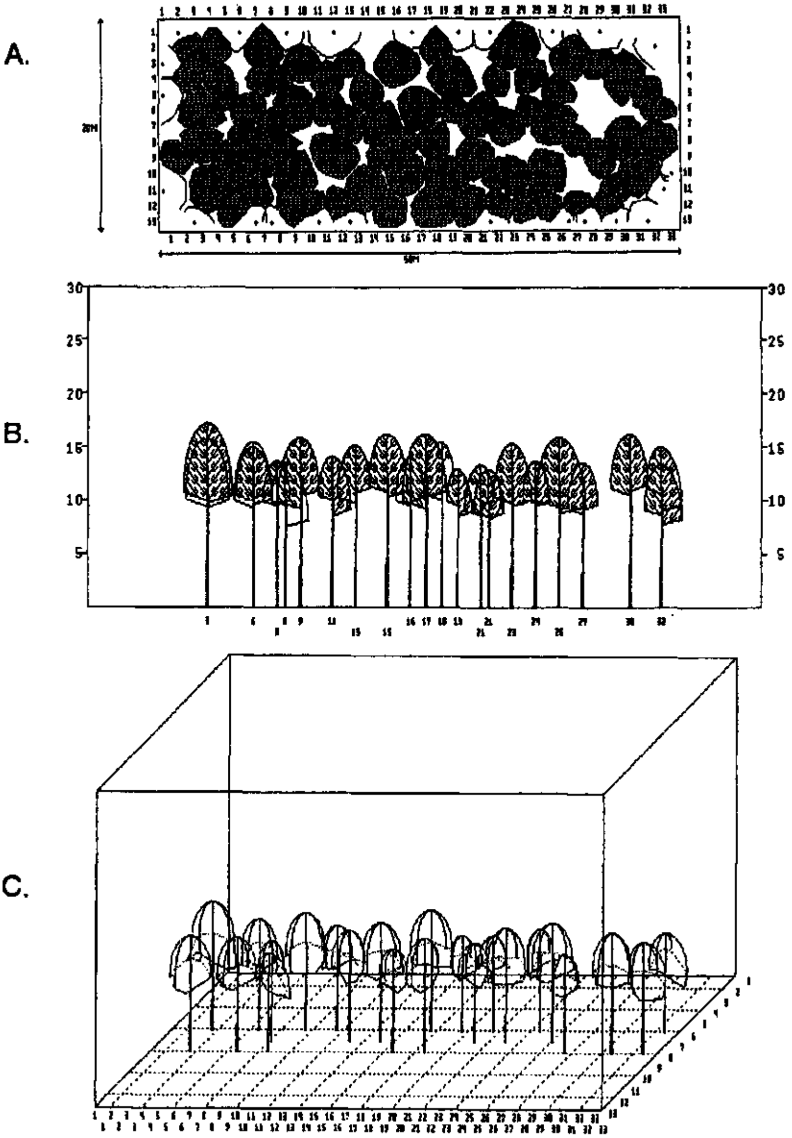
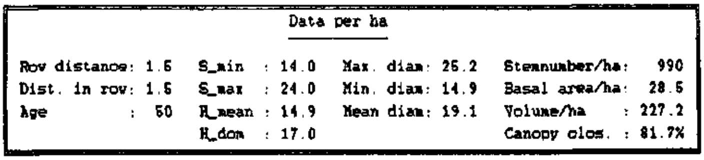


Fig. 33 Simulation of 50-year-old stand of Scots pine with high thinning.
A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of rows 6,7,8; vertical axis: tree height; horizontal axis: tree no. in row. C. Three-dimensional display of rows 6,7,8; axes: see A.



```
                          Data per ha

Row distance: 1.5   S_min  : 14.0   Max. diam: 25.2   Stemnumber/ha:   990
Dist. in row: 1.5   S_max  : 24.0   Min. diam: 14.9   Basal area/ha:  28.5
Age         :  50   H_mean : 14.9   Mean diam: 19.1   Volume/ha    : 227.2
                    H_dom  : 17.0                     Canopy clos. : 81.7%
```

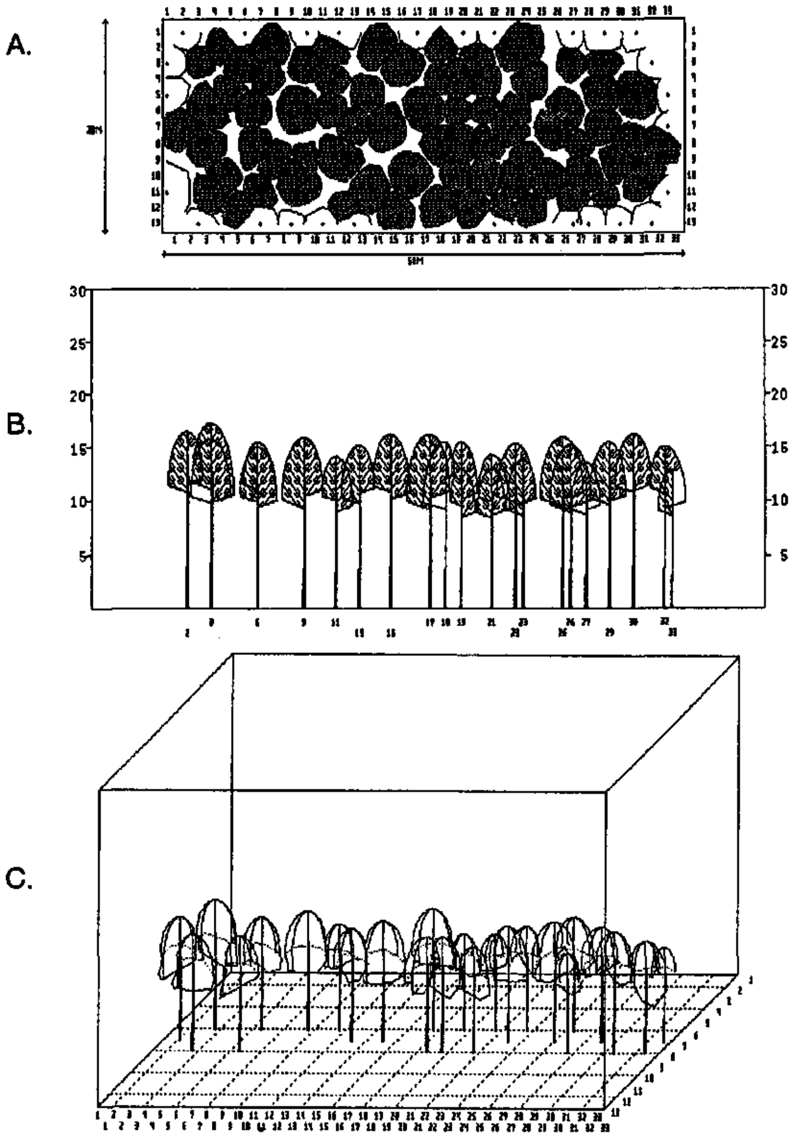


Fig. 34 Simulation of 50-year-old stand of Scots pine with manual thinning. A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of rows 6,7,8; vertical axis: tree height; horizontal axis: tree no. in row. C. Three-dimensional display of rows 6,7,8; axes: see A.

```
                          Data per ha
                          ___________

Row distance: 1.5   S_min  : 14.0   Max. diam: 22.7   Stemnumber/ha:   1690
Dist. in row: 1.5   S_max  : 24.0   Min. diam: 12.9   Basal area/ha:   34.8
Age         :  50   H_mean : 14.5   Mean diam: 16.7   Volume/ha     : 273.1
                    H_dom  : 16.9                     Canopy clos.  : 89.1%
```

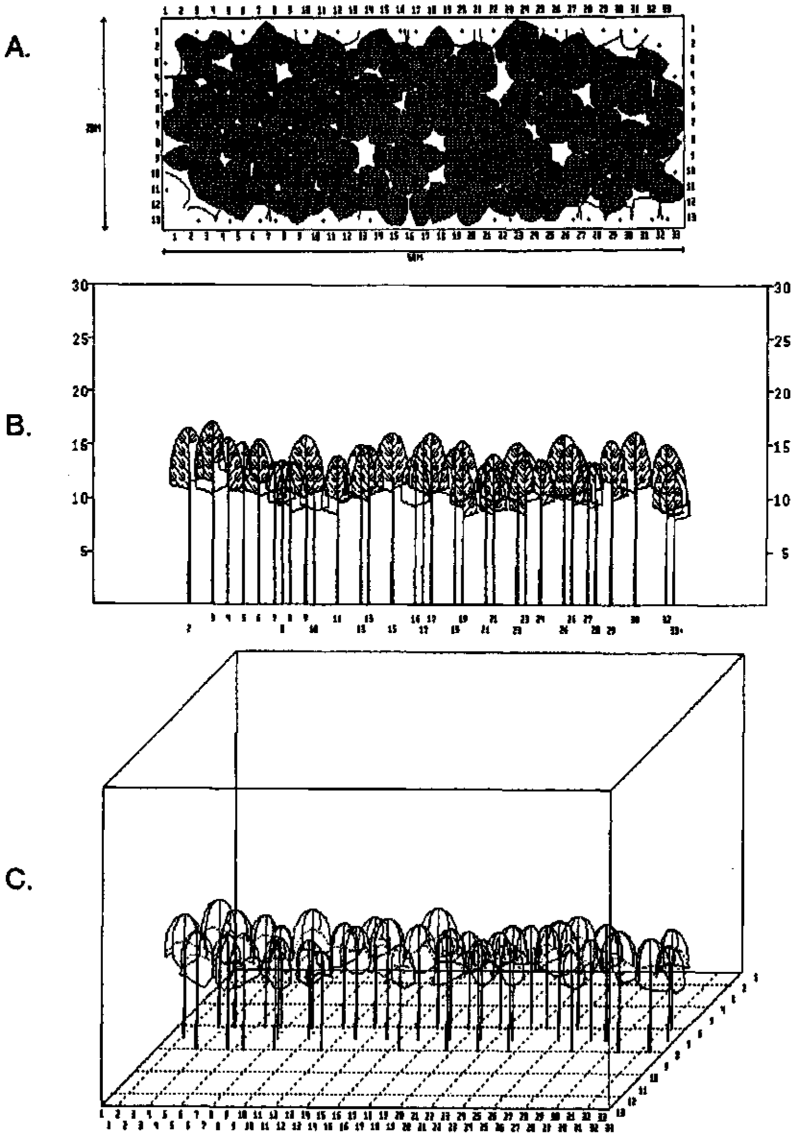


Fig. 35 Simulation of 50-year-old stand of Scots pine without thinning.
A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of rows 6,7,8; vertical axis: tree height; horizontal axis: tree no. in row. C. Three-dimensional display of rows 6,7,8; axes: see A.

```
                              Data per ha
                              ───────────
Row distance: 1.5   S_min  : 14.0   Max. diam: 37.8   Stemnumber/ha:   270
Dist. in row: 1.5   S_max  : 24.0   Min. diam: 30.4   Basal area/ha:  23.6
Age         : 100   H_mean : 21.2   Mean diam: 33.3   Volume/ha    : 234.6
                    H_dom  : 22.1                     Canopy clos. : 46.1%
```

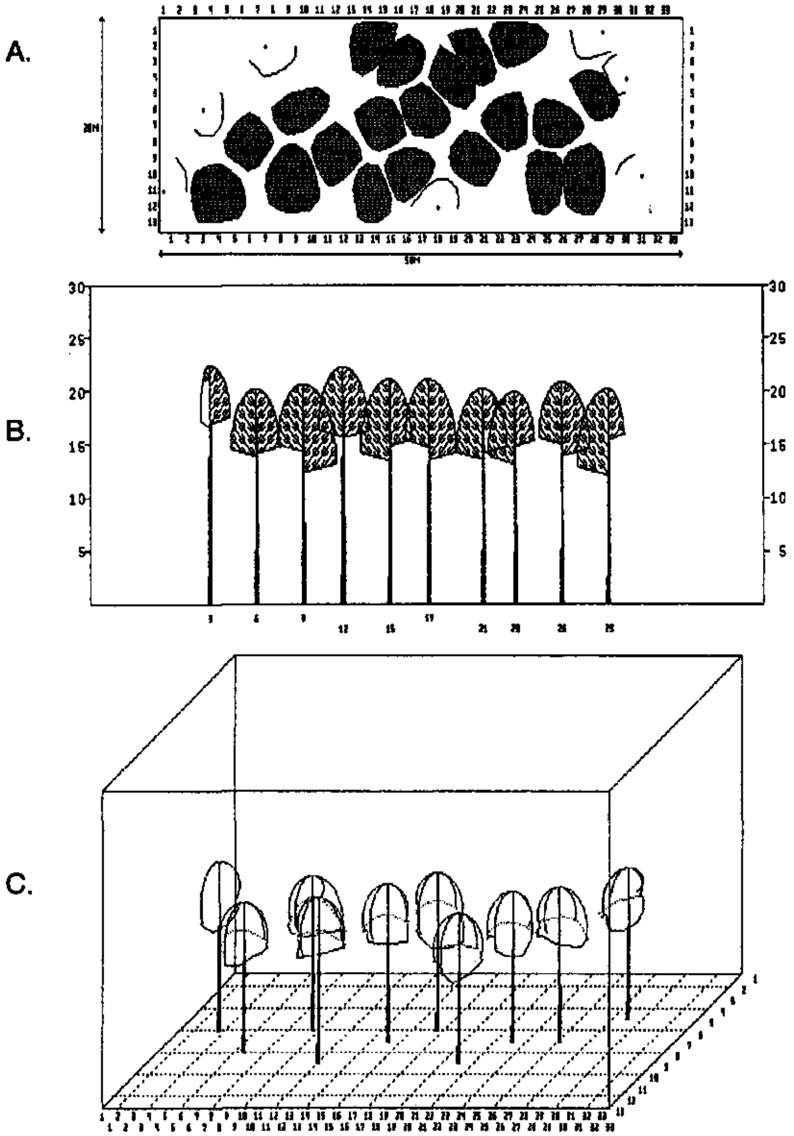
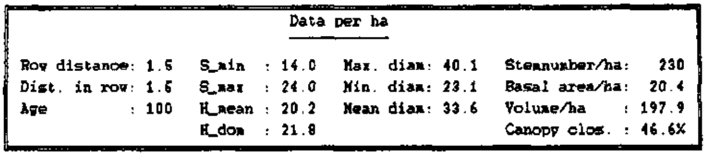


Fig. 36 Simulation of 100-year-old stand of Scots pine with low thinning.
A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of rows 5,6,7,8,9; vertical axis: tree height; horizontal axis: tree no. in row. C. Three-dimensional display of rows 5,6,7,8,9; axes: see A.



```
                              Data per ha

Row distance: 1.5   S_min  : 14.0   Max. diam: 40.1   Stemnumber/ha:   230
Dist. in row: 1.5   S_max  : 24.0   Min. diam: 23.1   Basal area/ha:  20.4
Age         : 100   H_mean : 20.2   Mean diam: 33.6   Volume/ha    : 197.9
                    H_dom  : 21.8                     Canopy clos. : 46.6%
```

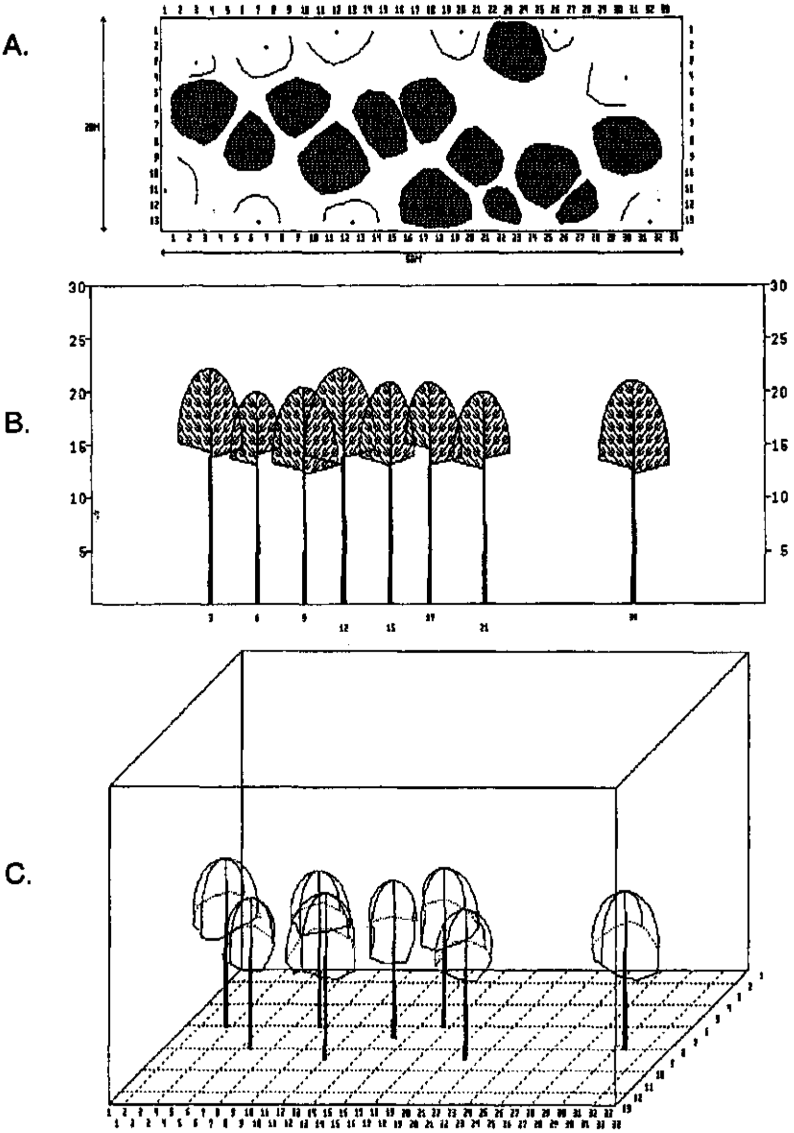


Fig. 37 Simulation of 100-year-old stand of Scots pine with high thinning. A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of rows 5,6,7,8,9; vertical axis: tree height; horizontal axis: tree no. in row. C. Three-dimensional display of rows 5,6,7,8,9; axes: see A.

```
                          Data per ha

Row distance: 1.6   S_min  : 14.0   Max. diam: 39.1   Stemnumber/ha:   270
Dist. in row: 1.6   S_max  : 24.0   Min. diam: 26.3   Basal area/ha:  24.4
Age         : 100   H_mean : 20.9   Mean diam: 33.9   Volume/ha     : 239.8
                    H_dom  : 22.0                     Canopy clos.  : 63.8%
```

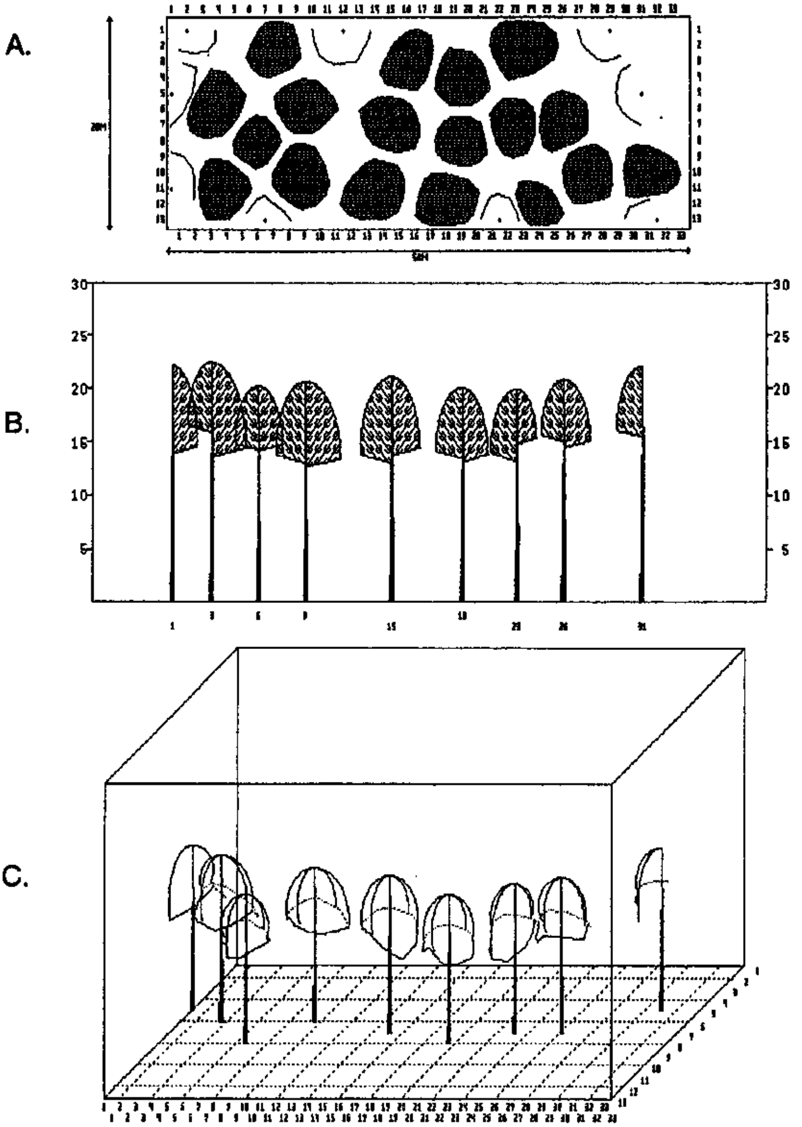
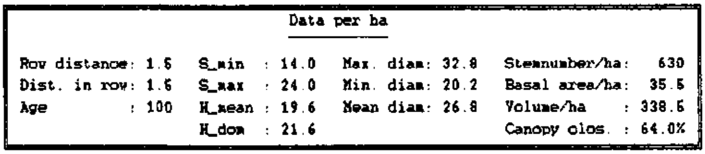


Fig. 38 Simulation of 100-year-old stand of Scots pine with manual thinning. A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of rows 5,6,7,8,9; vertical axis: tree height; horizontal axis: tree no. in row. C. Three-dimensional display of rows 5,6,7,8,9; axes: see A.



```
                              Data per ha

Row distance: 1.6   S_min  : 14.0   Max. diam: 32.8   Stemnumber/ha:   630
Dist. in row: 1.6   S_max  : 24.0   Min. diam: 20.2   Basal area/ha:  35.5
Age         : 100   H_mean : 19.6   Mean diam: 26.8   Volume/ha    : 338.5
                    H_dom  : 21.6                     Canopy clos. : 64.0%
```

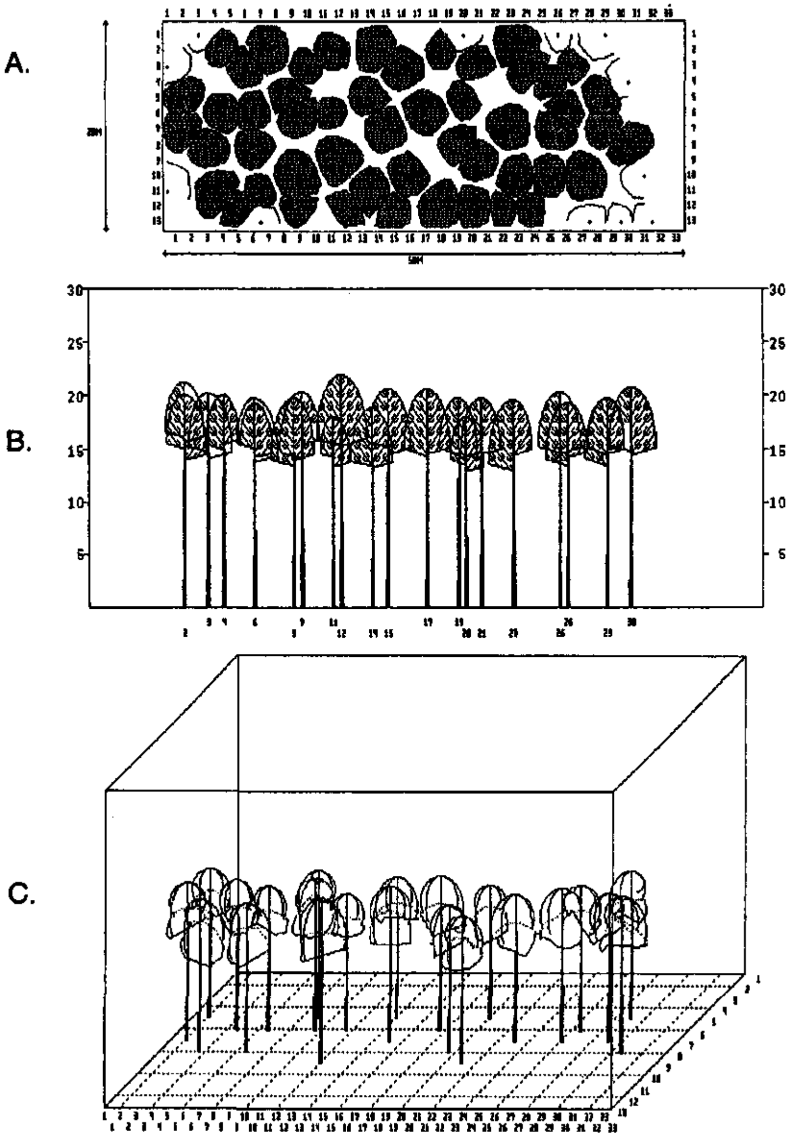
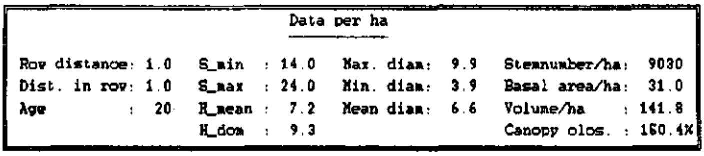
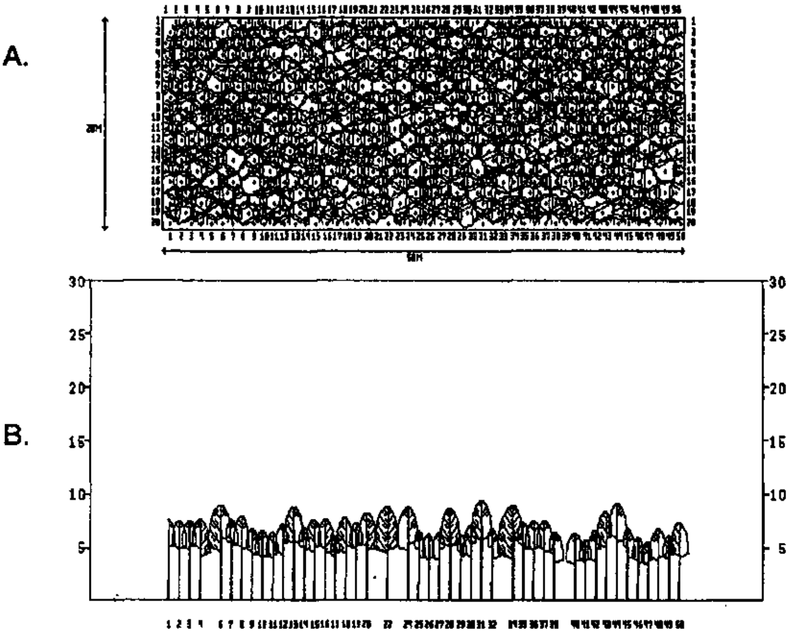
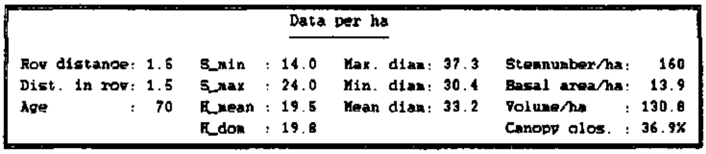


Fig. 39 Simulation of 100-year-old stand of Scots pine without thinning.
A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of rows 5,6,7,8,9; vertical axis: tree height; horizontal axis: tree no. in row. C. Three-dimensional display of rows 5,6,7,8,9; axes: see A.



```
                              Data per ha
                              -----------
Row distance: 1.0   S_min  : 14.0   Max. diam:  9.9   Stemnumber/ha:  9030
Dist. in row: 1.0   S_max  : 24.0   Min. diam:  3.9   Basal area/ha:  31.0
Age         :  20   H_mean :  7.2   Mean diam:  6.6   Volume/ha    : 141.8
                    H_dom  :  9.3                     Canopy clos. : 160.4%
```





```
                              Data per ha
                              -----------
Row distance: 1.6   S_min  : 14.0   Max. diam: 37.3   Stemnumber/ha:   160
Dist. in row: 1.5   S_max  : 24.0   Min. diam: 30.4   Basal area/ha:  13.9
Age         :  70   H_mean : 19.5   Mean diam: 33.2   Volume/ha    : 130.8
                    H_dom  : 19.8                     Canopy clos. :  36.9%
```

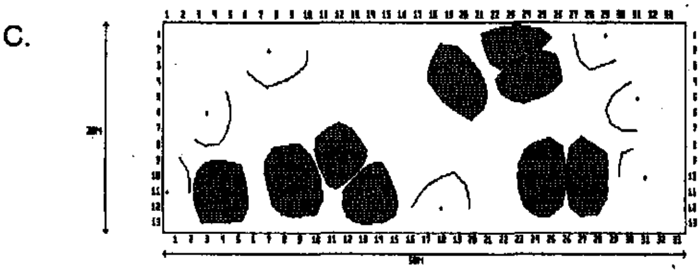


Fig. 40 Simulation of 20-year-old stand of Scots pine without thinning and initial stem number = 10000/ha. A. Crown projection; vertical axis: row number; horizontal axis: tree no. in row. B. Profile diagram of row 7; vertical axis: tree height; horizontal axis: tree no. in row. C. Simulation of crown projection of 70-year-old stand of Scots pine with severe low thinning and an initial stem number of 4290/ha; axes: see A.

APPENDIX

A The STAND program

The STAND computer program has been written in C language. It calculates the *normal growth area of a *sample tree. The input consists:

- the distances between the sample tree and the probable neighbouring trees that could influence the normal growth area (see section 3.2 and Fig 10),
- the distance between consecutive neighbours,
- the height of the sample tree and its neighbours
- the *competition constant.

Data are input from an input file or by typing the input data into the STAND program. Using an input file makes it possible to calculate the normal growth area of many different sample trees at the same time.

The program excludes trees that have no influence on the sample tree, calculates the normal growth area, the mean *normal growth area vector (see section 3.2.2) and calculates the error in measuring data by taking the sum of the angles *z[i]*, dividing it by 2π and reducing the result by 1:

$$angle\_error = \left(\frac{\sum_{i=1}^{i=max} z[i]}{2 * \Pi} - 1\right) * 100\% \qquad (84)$$

The output to the screen is a table and a graph of the results. The output to a file consists of the sample plot number (stand number and tree number), the normal growth area, the mean normal growth area vector and the errors in measuring data per sample tree.

B Tables

TABLE B1 Tree data

t = tree age

h = tree height

$\bar{a}$ = mean normal growth area vector

dbh = diameter at breast height

cl = crown length

$\overline{cw}$ = mean crown width

h/dbh = ratio of height/diameter

$\overline{cw}/h$ = ratio of mean crown width/tree height

stand	*tree*	*number*	*t*	*h*	$\bar{a}$	*dbh*	*cl*	$\overline{cw}$	*h/dbh*	$h/\overline{cw}$
9b	1	1	111	19.50	3.20	27.8	5.0	5.44	0.70	4.46
	2	2	111	20.50	3.51	41.7	5.5	5.83	0.49	2.75
	3	3	111	20.70	2.54	31.0	6.5	3.77	0.67	7.03
	4	4	111	25.20	5.40	57.0	13.2	8.74	0.44	3.95
	5	5	111	22.50	3.40	46.9	7.5	7.63	0.48	7.13
	6	6	111	22.50	3.57	34.1	4.0	4.87	0.66	4.94
	7	7	111	24.00	2.76	36.1	6.0	2.65	0.66	3.92
	8	8	111	21.00	3.38	44.0	6.5	4.11	0.48	3.96
	9	9	111	22.20	2.99	44.1	7.2	6.53	0.50	5.05
	10	10	111	19.50	2.79	33.4	5.0	4.41	0.58	4.01
68b	1	11	103	20.70	5.07	35.5	6.7	6.34	0.58	3.26
	2	12	103	21.00	4.18	37.2	7.0	5.16	0.56	4.07
	3	13	103	20.40	3.56	35.9	5.3	6.23	0.57	3.27
	4	14	103	23.90	4.20	35.7	7.5	5.75	0.67	4.16
	5	15	103	22.75	4.82	41.5	8.8	6.57	0.55	3.46
	6	16	103	23.50	6.52	50.5	9.6	8.69	0.47	2.70
	7	17	103	21.70	2.98	36.2	9.6	6.35	0.60	3.42
	8	18	103	22.80	3.79	40.1	7.5	6.31	0.57	3.62
	9	19	103	22.50	4.27	45.3	10.0	8.26	0.50	2.73
	10	20	103	24.50	5.75	53.7	10.2	9.20	0.46	2.66
	11	21	103	19.10	2.82	28.3	3.0	6.35	0.67	3.01
81b	1	22	80	19.10	2.91	28.4	6.8	3.54	0.67	5.40
	2	23	80	21.30	2.63	29.3	5.1	3.39	0.73	6.28
	3	24	80	20.80	3.23	27.6	6.2	3.28	0.75	6.34
	4	25	80	18.10	3.65	27.8	6.7	4.07	0.65	4.45
	5	26	80	19.80	3.17	33.3	7.2	5.26	0.59	3.76
	6	27	80	19.60	4.20	40.0	8.5	6.81	0.49	2.88
	7	28	80	20.20	3.63	32.6	8.3	4.66	0.62	4.34
	8	29	80	18.40	2.65	34.0	5.9	5.74	0.54	3.21
	9	30	80	18.20	2.60	25.3	5.2	6.17	0.72	2.95
	10	31	80	17.50	3.70	31.5	5.6	6.18	0.56	2.83
	11	32	80	18.20	2.62	20.5	6.3	2.86	0.89	6.35
	12	33	80	16.70	1.98	20.5	3.7	3.42	0.81	4.88

TABLE B1 Tree data (continued)

stand	*tree*	*number*	*t*	*h*	$\bar{a}$	*dbh*	*cl*	$\overline{cw}$	*h/dbh*	$h/\overline{cw}$
83	1	34	75	18.00	2.35	27.8	3.7	4.37	0.65	3.31
	2	35	75	17.50	4.24	36.3	8.9	7.46	0.48	3.00
	3	36	75	18.50	2.66	27.7	3.5	2.94	0.67	4.90
	4	37	75	21.50	3.97	41.7	6.5	6.39	0.52	2.46
	5	38	75	16.80	2.46	27.0	2.9	3.16	0.62	2.20
	6	39	75	20.00	2.74	29.4	9.5	4.55	0.68	4.11
	7	40	75	21.70	3.49	36.9	8.2	6.13	0.59	8.18
	8	41	75	18.20	2.64	33.0	5.2	5.30	0.55	4.43
	9	42	75	19.50	2.97	29.7	7.3	4.39	0.66	2.98
	10	43	75	18.00	3.36	28.8	5.5	4.86	0.63	4.08
44e	1	44	51	13.10	1.58	20.6	3.3	3.64	0.64	3.60
	2	45	51	14.00	1.44	19.1	3.8	3.03	0.73	4.63
	3	46	51	13.30	1.63	19.9	3.8	3.68	0.67	3.61
	4	47	51	14.40	1.93	20.8	5.4	3.76	0.69	3.83
	5	48	51	17.10	3.01	25.0	6.4	4.37	0.68	3.91
	6	49	51	14.55	2.00	24.6	4.8	4.42	0.59	3.29
	7	50	51	14.70	2.95	24.1	4.7	4.38	0.61	3.36
	8	51	51	16.00	3.13	25.5	6.3	4.68	0.63	3.42
	9	52	51	13.30	1.30	17.8	2.8	2.48	0.75	5.35
	10	53	51	11.80	1.19	12.8	2.5	2.08	0.92	5.68
165a	1	54	36	9.30	1.30	14.3	4.9	3.36	0.65	2.77
	2	55	36	11.10	2.40	14.7	5.7	2.86	0.76	3.88
	3	56	36	9.10	2.10	15.6	4.1	3.77	0.58	2.42
	4	57	36	9.80	1.36	14.6	3.6	2.98	0.67	3.29
	5	58	36	11.60	2.16	21.1	5.9	3.97	0.55	2.92
	6	59	36	10.70	2.00	18.3	5.3	4.46	0.58	2.40
	7	60	36	11.30	1.52	16.0	5.3	4.12	0.71	2.75
	8	61	36	11.60	1.80	16.7	5.8	3.25	0.69	3.57
	9	62	36	12.60	2.43	26.3	6.5	6.37	0.48	1.98
	10	63	36	8.90	1.18	9.6	3.5	2.55	0.93	3.50
	11	64	36	8.60	1.09	13.8	3.6	2.36	0.62	3.65
70b	1	65	36	16.30	2.30	19.5	5.4	3.61	0.84	4.51
	2	66	36	15.00	1.80	19.0	4.8	3.76	0.79	3.99
	3	67	36	15.00	2.26	18.9	6.0	3.94	0.79	3.81
	4	68	36	14.50	1.98	18.7	4.5	3.88	0.78	3.74
	5	69	36	16.30	2.49	21.5	5.4	4.32	0.76	3.77
	6	70	36	16.80	3.43	30.6	6.6	6.06	0.55	2.77
	7	71	36	16.50	2.48	22.0	6.0	4.52	0.75	3.65
	8	72	36	16.50	2.11	20.4	6.0	3.71	0.81	4.44
	9	73	36	15.80	2.77	22.9	7.0	5.19	0.69	3.04
	10	74	36	13.30	1.69	14.3	3.4	2.46	0.93	5.42

TABLE B1 Tree data (continued)

stand	*tree*	*number*	*t*	*h*	$\bar{a}$	*dbh*	*cl*	$\overline{cw}$	*h/dbh*	$h/\overline{cw}$
17q	1	75	24	8.10	0.76	8.0	3.4	1.66	1.01	4.88
	2	76	24	7.10	0.50	7.6	2.6	1.69	0.93	4.21
	3	77	24	8.20	0.80	7.7	3.2	1.61	1.06	5.10
	4	78	24	8.35	0.81	7.8	2.8	1.88	1.07	4.43
	5	79	24	8.80	0.98	13.0	3.5	2.74	0.68	3.21
	6	80	24	8.30	0.80	11.7	4.3	2.34	0.71	3.55
	7	81	24	10.00	1.04	14.4	5.7	3.24	0.69	3.09
	8	82	24	10.50	1.17	15.3	5.8	3.78	0.69	2.78
	9	83	24	6.65	0.59	5.2	1.5	1.08	1.28	6.14
	10	84	24	7.40	0.55	7.1	2.9	1.37	1.04	5.39
	11	85	24	8.00	0.57	5.0	2.6	1.21	1.60	6.63
85a	1	86	24	10.70	1.18	11.2	3.9	2.68	0.96	3.99
	2	87	24	9.50	0.99	10.8	4.8	2.32	0.88	4.09
	3	88	24	10.90	1.06	11.4	4.2	2.03	0.96	5.38
	4	89	24	10.40	0.85	10.5	3.5	1.88	0.99	5.53
	5	90	24	12.70	1.40	17.2	5.7	3.56	0.74	3.56
	6	91	24	12.30	1.26	12.8	4.3	2.95	0.96	4.17
	7	92	24	10.80	1.14	14.3	4.0	2.65	0.76	4.07
	8	93	24	11.70	1.75	17.1	5.0	3.89	0.68	3.01
	9	94	24	11.10	1.37	14.8	4.4	3.37	0.75	3.29
	10	95	24	10.50	1.48	11.7	4.0	3.03	0.90	3.47
	11	96	24	7.80	0.64	4.9	1.6	1.28	1.59	6.09
*transect	1	97	20	8.55	1.23	8.8	4.8	2.77	0.97	3.09
	2	98	20	5.39	0.61	5.2	2.7	1.88	1.04	2.87
	3	99	20	5.20	0.38	5.2	2.5	1.22	1.00	4.25
	4	100	20	8.30	1.26	7.2	4.8	2.27	1.15	3.66
	5	101	20	9.02	1.41	7.9	5.2	2.69	1.14	3.35
	6	102	20	8.45	1.11	8.4	4.1	2.48	1.01	3.41
	7	103	20	8.59	0.74	7.3	4.3	1.90	1.18	4.51
	8	104	20	8.67	1.01	8.7	4.8	2.33	1.00	3.72
	9	105	20	7.90	0.97	8.2	3.0	1.90	0.96	4.16
	10	106	20	7.90	0.89	7.3	3.8	2.25	1.08	3.52
	11	107	20	9.70	1.18	9.3	5.0	2.20	1.04	4.42
	12	108	20	9.07	0.84	7.9	3.5	1.48	1.15	6.11
	13	109	20	7.64	0.68	6.9	2.9	1.93	1.11	3.97
	14	110	20	9.80	1.06	11.2	5.6	2.95	0.88	3.32
	15	111	20	9.42	1.30	9.6	4.7	2.20	0.98	4.29
	16	112	20	7.20	0.52	4.4	3.8	1.63	1.64	4.42
	17	113	20	8.16	0.85	7.2	3.9	1.66	1.13	4.91
	18	114	20	7.23	0.80	5.5	3.0	1.43	1.31	5.05
	19	115	20	6.62	0.64	5.9	2.3	1.78	1.12	3.71
	20	116	20	7.70	0.86	7.2	3.2	1.93	1.07	3.99

TABLE B1 Tree data (continued)

stand	*tree*	*number*	*t*	*h*	$\bar{a}$	*dbh*	*cl*	$\overline{cw}$	*h/dbh*	$h/\overline{cw}$
*transect	21	117	20	7.12	0.78	7.6	2.5	1.81	0.94	3.94
	22	118	20	5.84	0.39	4.8	2.3	1.27	1.22	4.61
	23	119	20	6.29	0.64	5.5	2.5	1.83	1.14	3.44
	24	120	20	6.95	0.78	7.2	3.3	1.70	0.97	4.08
	25	121	20	6.70	0.65	6.4	2.6	1.45	1.05	4.61
	26	122	20	5.28	0.38	4.1	2.2	1.20	1.29	4.41
	27	123	20	6.90	0.63	6.3	2.7	1.70	1.10	4.07
	28	124	20	8.08	1.09	9.7	3.8	2.21	0.83	3.66
	29	125	20	4.56	0.19	4.6	1.8	1.08	0.99	4.21
	30	126	20	8.40	0.96	9.1	4.8	2.08	0.92	4.04
	31	127	20	7.36	0.79	7.1	3.5	1.34	1.04	5.48
	32	128	20	6.42	0.72	5.7	2.5	1.39	1.13	4.63
80c	1	129	13	5.00	1.07	8.2	3.7	1.90	0.61	2.63
	2	130	13	5.60	1.04	8.6	4.5	2.16	0.65	2.60
	3	131	13	5.80	1.36	8.0	4.9	2.23	0.73	2.60
	4	132	13	5.35	1.24	8.2	4.2	2.66	0.65	2.01
	5	133	13	6.40	1.69	10.0	5.4	2.81	0.64	2.28
	6	134	13	5.80	1.39	8.6	4.7	2.32	0.67	2.50
	7	135	13	5.50	1.20	9.4	3.8	3.36	0.59	1.64
	8	136	13	7.30	1.25	11.8	6.1	3.33	0.62	2.19
	9	137	13	5.80	1.56	10.5	3.3	3.30	0.55	1.76
	10	138	13	5.35	1.30	8.8	4.6	2.58	0.61	2.08
	11	139	13	5.40	1.01	9.6	3.7	3.05	0.56	1.77
	12	140	13	5.25	1.04	7.5	3.8	2.35	0.70	2.23
1c	1	141	13	4.25	1.17	5.5	4.0	1.65	0.77	2.58
	2	142	13	5.60	0.65	6.0	3.3	1.41	0.93	3.96
	3	143	13	5.35	0.64	5.1	3.5	2.02	1.05	2.65
	4	144	13	5.60	0.86	5.8	4.9	1.94	0.97	2.88
	5	145	13	6.95	1.01	9.5	4.5	2.64	0.73	2.64
	6	146	13	6.20	0.86	8.8	3.7	2.89	0.70	2.14
	7	147	13	6.20	1.09	9.8	4.3	3.10	0.63	2.00
	8	148	13	6.05	0.99	7.8	4.2	2.41	0.78	2.51
	9	149	13	4.85	0.39	2.9	2.5	1.14	1.67	4.24
	10	150	13	5.50	0.91	4.0	3.3	1.41	1.38	3.89
71c	1	151	8	2.55	0.66	2.9	2.6	1.61	0.88	1.58
	2	152	8	2.70	1.03	3.1	2.7	2.00	0.87	1.35
	3	153	8	2.70	0.90	3.2	2.7	1.83	0.84	1.48
	4	154	8	2.65	0.84	3.0	2.7	1.66	0.88	1.60
	5	155	8	3.05	1.34	3.7	3.1	2.04	0.82	1.50
	6	156	8	3.00	1.14	3.8	3.0	1.77	0.79	1.69
	7	157	8	2.90	1.01	4.2	2.8	1.52	0.69	1.91
	8	158	8	2.75	0.76	3.3	2.8	1.68	0.83	1.64

TABLE B2 Some data on cut trees

v = volume
f = form factor
l = tree length
cl = crown length
dbh = diameter at breast height
dbranch = mean branch diameter at 3/4 of crown length from top of tree and at 5 cm from stem.

stand	*tree*	*nr*	*v*	*f*	*l*	*cl*	*d*	*dbranch*
68b	2	12	1253.13	0.50	22.30	7.00	38.00	4.3
	4	14	1258.28	0.51	24.20	7.50	36.00	6.0
	7	17	1185.01	0.45	22.60	10.30	38.70	6.8
81b	1	22	634.49	0.46	21.30	6.80	28.70	3.0
	2	23	734.35	0.47	22.60	5.60	29.60	5.0
	5	26	971.90	0.49	21.70	8.00	34.00	9.0
	12	33	319.97	0.54	17.80	3.70	20.50	2.8
44e	2	45	242.04	0.52	14.80	4.40	20.00	3.3
	3	46	234.08	0.53	14.10	3.80	20.00	2.9
	7	50	372.11	0.52	15.30	8.30	24.30	6.3
165a	2	55	114.18	0.58	11.10	5.70	15.00	3.0
	3	56	107.35	0.53	9.30	4.30	16.60	3.1
	5	58	241.92	0.49	12.10	6.40	22.70	4.4
	11	64	81.80	0.46	9.65	4.60	15.40	3.0
70b	1	65	224.61	0.46	16.30	5.40	19.50	2.3
	2	66	214.77	0.50	15.00	4.80	19.00	2.9
	5	69	334.36	0.52	17.65	6.75	21.50	3.4
	6	70	659.41	0.49	17.90	7.70	31.00	4.8
	10	74	99.23	0.51	13.60	3.40	13.50	1.7
17q	1	75	26.46	0.61	8.00	3.70	8.30	2.0
	4	78	26.00	0.60	8.60	3.05	8.00	1.5
	6	80	61.49	0.58	8.65	4.70	12.50	2.5
	7	81	101.13	0.50	10.30	6.00	15.80	3.8
	11	85	12.51	0.74	8.00	2.55	5.20	1.1
85a	1	86	75.11	0.61	11.90	5.10	11.50	2.4
	3	88	75.74	0.56	11.75	5.00	12.10	2.0
	5	90	228.31	0.65	14.20	7.20	17.70	3.0
	6	91	89.78	0.52	12.60	4.55	13.20	2.4
	11	96	9.04	0.57	8.40	2.20	4.90	0.9

TABLE B2 Some data on cut trees (continued)

stand	*tree*	*nr*	*v*	*f*	*l*	*cl*	*d*	*dbranch*
80c	1	129	20.84	0.56	5.60	4.25	9.20	2.1
	2	130	25.19	0.58	6.10	5.00	9.50	2.5
	7	135	28.21	0.56	6.20	4.50	10.20	3.0
	9	137	36.33	0.53	6.40	3.90	11.70	2.5
	12	140	20.86	0.62	5.90	4.35	8.50	1.8
71c	5	155	8.82	0.80	3.90	3.70	6.00	1.9
	6	156	7.49	1.06	3.60	3.30	5.00	1.7
	1	151	4.86	1.10	3.20	3.10	4.20	1.8
	2	152	6.05	1.19	3.50	3.20	4.30	1.9

TABLE B3 R^2 and c.v. of *dbh*. $\overline{cw}$ and *cl* in relation to *t*, *h* and $\bar{a}$ per stand

		dbh	*cl*	$\overline{cw}$
9b	R^2	58%	47%	55%
	c.v.	17%	30%	31%
68b	R^2	78%	67%	37%
	c.v.	10%	26%	17%
81b	R^2	59%	71%	30%
	c.v.	15%	14%	32%
83	R^2	77%	55%	64%
	c.v.	8%	37%	22%
44e	R^2	79%	90%	77%
	c.v.	11%	13%	16%
165a	R^2	66%	84%	54%
	c.v.	18%	11%	24%
70b	R^2	89%	78%	83%
	c.v.	7%	12%	12%
17q	R^2	73%	84%	82%
	c.v.	25%	19%	21%
85a	R^2	88%	76%	95%
	c.v.	14%	20%	9%
transect	R^2	77%	79%	69%
	c.v.	13%	15%	16%
80c	R^2	58%	60%	25%
	c.v.	10%	14%	20%
1c	R^2	80%	73%	71%
	c.v.	22%	12%	23%
71c	R^2	80%	96%	61%
	c.v.	7%	1%	8%

TABLE B4 Data on low thinning per ha

'Rotation = 120 years
Initial number of trees per ha = 4290
Range of 'S values: 14-24 metres

age (year)	volume of thinning (m^3)	$\bar{d}$ (cm)	c.v.	Returns at rate of interest *i* (guilders)				
				i=0%	*i*=1%	*i*=2%	*i*=3%	*i*=4%
20	19.9	6.1	15.0	199	163	134	110	91
25	14.9	8.8	2.6	149	116	91	71	56
30	19.5	10.6	2.7	548	407	303	226	169
35	24.6	12.2	2.2	932	658	466	331	236
40	23.9	13.9	2.6	1043	701	472	320	217
45	24.1	15.6	2.9	1251	800	513	331	214
50	23.5	17.2	1.8	1411	858	524	322	198
55	22.6	18.8	2.1	1357	785	457	267	157
60	25.0	20.4	1.9	1792	987	546	304	170
65	23.1	22.5	2.3	1733	907	478	254	135
70	23.1	23.3	1.1	1729	861	432	218	111
75	21.9	24.7	2.1	2080	986	471	227	110
80	20.0	25.9	2.5	1997	901	410	188	87
85	22.6	28.1	1.0	2261	970	420	183	81
90	38.2	29.0	1.7	3822	1561	643	267	112
100	37.1	31.1	1.8	3714	1373	513	193	74
110	34.6	33.5	1.0	3457	1157	391	134	46
120	205.5	37.6	5.9	22787	6904	2117	656	206
total	624			52261	21095	9381	4602	2470
mean	5.2			435	175	78	38	20

TABLE B5 Data on high thinning per ha

*Rotation = 120 years
Initial number of trees per ha = 4290
Range of *S values: 14-24 metres

age (year)	volume of thinning (m^3)	$\bar{d}$ (cm)	c.v.	Returns at rate of interest *i* (guilders)				
				$i=0\%$	$i=1\%$	$i=2\%$	$i=3\%$	$i=4\%$
20	19.9	6.1	15.0	199	163	134	110	91
25	14.9	8.8	2.6	149	116	91	71	56
30	19.6	12.3	9.9	766	569	423	316	236
35	25.0	12.7	6.3	986	696	493	350	250
40	24.2	13.6	9.6	1046	702	474	321	218
45	24.9	17.1	13.6	1476	943	606	390	253
50	24.2	18.1	7.1	1478	898	549	337	208
55	24.3	19.4	9.9	1642	950	553	323	190
60	24.2	18.6	11.0	1550	853	472	263	147
65	24.8	24.1	11.4	2209	1157	610	323	173
70	23.0	21.5	18.4	1793	894	448	227	115
75	23.1	22.0	14.4	1817	862	412	198	96
80	21.8	24.5	19.0	1970	888	404	185	85
85	22.0	27.2	15.5	2121	910	394	172	76
90	31.9	25.4	18.1	2886	1179	486	202	85
100	39.8	29.6	20.9	4082	1509	563	212	81
110	39.9	32.7	13.3	3985	1334	451	154	53
120	156.7	40.2	12.3	19014	5761	1766	548	172
total	584			49169	20385	9328	4703	2584
mean	4.9			410	170	78	39	22

TABLE B6 Data on manual thinning per ha

*Rotation = 120 years
Initial number of trees per ha = 4290
Range of *S values: 14-24 metres

age (year)	volume of thinning (m^3)	$\bar{d}$ (cm)	c.v.	Returns at rate of interest i (guilders)				
				$i=0\%$	$i=1\%$	$i=2\%$	$i=3\%$	$i=4\%$
20	19.9	6.2	16.2	199	163	134	110	91
25	15.1	8.8	10.6	175	137	107	84	66
30	19.7	10.8	10.3	559	415	309	230	172
35	24.8	12.2	14.5	991	700	496	352	251
40	24.4	13.1	8.1	1027	690	465	315	214
45	24.3	15.0	7.4	1245	796	511	329	213
50	24.4	17.1	8.1	1429	869	531	326	201
55	24.7	18.2	8.5	1496	866	503	294	173
60	23.3	19.1	9.4	1539	847	469	261	146
65	25.0	21.3	10.9	1879	984	519	275	147
70	22.6	21.9	8.1	1734	864	434	219	111
75	23.8	25.7	7.5	2285	1083	517	249	121
80	22.9	27.9	4.9	2288	1032	469	215	99
85	23.4	25.9	9.0	2162	928	402	175	77
90	36.4	26.5	12.4	3557	1453	598	249	104
100	38.4	29.0	9.8	3841	1420	530	200	76
110	38.4	35.6	8.1	4377	1465	496	169	59
120	206.1	38.9	8.0	24779	7508	2302	714	224
total	638			55562	22218	9791	4768	2546
mean	5.3			463	185	82	40	21

TABLE B7 Data on low thinning per ha

*Rotation = 120 years
Initial number of trees per ha = 10000
Range of *S values: 14-24 metres

age (year)	volume of thinning (m^3)	$\bar{d}$ (cm)	c.v.	Returns at rate of interest i (guilders)				
				$i=0\%$	$i=1\%$	$i=2\%$	$i=3\%$	$i=4\%$
20	39.9	5.5	10.5	399	327	268	221	182
25	39.7	7.9	4.3	397	310	242	190	149
30	39.6	10.2	3.2	897	665	495	369	276
35	39.3	12.1	3.1	1449	1023	725	515	367
40	39.6	14.3	2.4	1890	1269	856	579	394
45	38.5	16.3	2.4	2202	1407	903	582	377
50	22.9	18.0	2.3	1376	837	511	314	194
55	22.7	19.5	1.9	1402	811	472	276	162
60	24.1	21.2	1.1	1805	994	550	306	172
65	21.7	22.4	1.9	1628	852	449	238	127
70	25.0	24.1	1.4	2186	1089	547	276	140
75	23.8	25.6	1.3	2377	1127	538	259	125
80	21.3	26.4	2.2	2125	959	436	200	92
85	23.4	27.9	1.6	2337	1003	434	189	83
90	38.8	28.9	3.0	3881	1585	653	271	114
100	38.2	30.9	1.2	3820	1412	527	199	76
110	36.6	33.8	2.0	3659	1225	414	142	49
120	196.0	37.5	4.6	22099	6696	2053	637	200
total	731			55929	23591	11074	5764	3279
mean	6.1			466	197	92	48	27

TABLE B8 Data on low thinning per ha

Rotation = 120 years
Initial number of trees per ha = 4290
Range of S values: 18-24 metres

age (year)	volume of thinning (m^3)	$\bar{d}$ (cm)	c.v.	Returns at rate of interest *i* (guilders)				
				i=0%	*i*=1%	*i*=2%	*i*=3%	*i*=4%
20	29.9	7.3	7.6	299	245	201	165	136
25	25.0	9.7	2.3	257	200	157	123	96
30	24.8	11.6	2.1	725	538	400	299	224
35	29.1	13.3	2.0	1165	822	582	414	295
40	29.5	14.9	2.0	1474	990	667	452	307
45	29.0	16.8	2.0	1738	1110	713	459	297
50	29.9	18.3	1.5	1792	1089	666	409	252
55	28.0	19.7	2.0	1721	996	579	339	199
60	28.7	21.5	1.8	2151	1184	656	365	204
65	29.7	22.9	1.5	2230	1168	616	326	174
70	29.6	24.4	1.0	2854	1422	714	360	183
75	28.9	25.6	2.1	2886	1368	654	314	152
80	27.8	27.5	1.3	2778	1253	570	261	121
85	24.3	28.7	1.9	2432	1044	452	197	87
90	34.0	29.8	1.5	3396	1387	571	237	100
100	32.4	32.4	0.6	3236	1196	447	168	64
110	37.3	34.0	2.0	3730	1248	422	144	50
120	204.6	39.0	4.5	25034	7585	2325	721	226
total	702			59896	24847	11391	5755	3168
mean	5.9			499	207	95	48	26

TABLE B9 Data on low thinning per ha

*Rotation = 120 years
Initial number of trees per ha = 4290
Range of *S values: 14-24 metres

age (year)	volume of thinning (m^3)	$\bar{d}$ (cm)	c.v.	Returns at rate of interest *i* (guilders)				
				$i=0\%$	$i=1\%$	$i=2\%$	$i=3\%$	$i=4\%$
20	25.0	6.3	15.5	250	205	168	138	114
25	29.9	9.4	4.1	312	243	190	149	117
30	29.9	11.8	3.7	980	727	541	404	302
35	29.9	14.4	3.3	1437	1014	719	511	364
40	29.3	16.8	3.8	1725	1159	781	529	359
45	27.8	19.5	2.5	1737	1110	713	459	297
50	27.0	21.7	3.3	2028	1233	753	463	285
55	28.3	24.6	1.3	2825	1634	951	556	327
60	19.9	27.0	1.5	1987	1094	606	337	189
65	24.3	29.0	1.1	2427	1271	670	355	190
120	229.7	42.0	8.9	28154	8530	2615	811	254
total	501			43862	18221	8707	4712	2799
mean	4.2			366	152	73	39	23

GLOSSARY

Actual growth area vector:

A vector of the *actual growth area in one of sixteen fixed directions.

Actual growth area:

The *growth area that is really used by a tree at a given moment.

Aggradation phase:

Here: A phase in *eco-unit development, starting as soon as the canopy closes and ending when the trees generally can no longer close gaps that have arisen in the canopy.

Angle of reference:

The angle between the vector in the direction of the neighbouring tree and the "North".

Architecture:

Spatio-temporal *structure linked to a well-defined hierarchical level (Oldeman 1990).

Autoecology:

Ecology of one population in a central role, and the rest of the ecosystem as its environment (Oldeman 1990).

Automatic thinning:

In PINOGRAM program: the program points out which trees have to be removed.

Biostatic phase:

A phase in *eco-unit development, succeeding the *aggradation phase. The biostatic phase ends when the woody biomass in the *eco-unit decreases steadily (cf. Oldeman 1990).

Border trees:

Trees flanking the *transect border. No *normal growth area can be calculated for border trees, because there are no neighbouring trees within a sector of 180°.

Canopy closure:

Here: Sum of crown projection areas divided by the *transect area (%)

Cleaning:

An operation in a young stand in which the trees have a *dbh* less than 4 inches: (a) to free small trees as in plantations from weeds, vines or sod-forming grasses, and (b) to provide better growing conditions by liberating crop trees from other individuals of similar age but of less desirable species or form which are overtopping or likely to overtop them (Munns 1950).

Codominant tree:

Tree with crown forming the general level of the crown cover and receiving full light from above, but comparatively little from the sides; usually with medium-sized crowns more or less crowded on the sides (Munns 1950).

Competition :

(1) Striving to be the first in obtaining the usable amounts of light, water and nutrients when provision of several or one of these is limited. In the PINOGRAM model: competition for qualified space; constraints are not defined:

(2) The kind of *interaction in which one of the competing living systems profits from the decay of the other.

Competition constant:

An empirical constant used as a weight in calculations of *growth area vectors in order better to express *competition between trees that is caused by the trees being of different height.

Crown class:

Any class (e.g. *dominant, *codominant, *intermediate, *suppressed) into which the trees forming a crop or stand may be divided on the basis of both their crown position and crown development relative to the crowns of adjacent trees and the general canopy (Ford-Robertson 1971).

Cycle:

The set of computations the PINOGRAM program does between the moment a new age at which the user wants to see a *forest situation is specified and the moment that the program shows this new *situation.

Descriptive model:

A model that gives only the properties of a *system as seen from the outside (Oldeman 1990).

Dominant height:

The dominant height or top height is the average height of the hundred tallest trees per ha (Schütz and van Tol 1982). Jansen and Schmidt (1991) define top height as mentioned above and dominant height as the stand mean of the tallest tree per are (= $100m^2$).

Dominant tree:

A tree whose crown extending above the general level of the crown cover and receives full light from above and partly from the sides; larger than the average trees in the stand, and with its crown well-developed, but possibly somewhat crowded on the sides (Munns 1950).

Eco-unit:

Every surface of ground on which at any moment in time a vegetation has begun to develop, and whose architecture*, eco-physiological functioning and species composition are ordained by one set of trees until the end (Oldeman 1990).

Explanatory model:

A model that represents a *system at least in terms of its subsystems (Oldeman 1990).

Forest architecture:

The visible, morphological, expression of a forest, created by the *architecture and pattern of the occurring organisms.

Forest situation:

A snapshot of a forest or part of a forest with all its properties, comparable to the *phenotype of an individual

Frequency of thinning:

Thinning periodicity, where the thinning interval may be either regular or iiregular (Ford-Robertson 1971).

Function (see subroutine).

Genotype:

The genotype of an individual describes the complete set of inherited genes (Suzuki et al. 1989).

Growing space:

The space available to a tree, i.e. the space in which a tree is more competitive than its neighbours.

Growth:

1. The process of growing or developing; a) gradual development towards maturity; b) formation and development. 2.a) degree of increase in size, weight, power, etc.; b) the full extent of such increase (Neufeldt and Guralnik, 1988).

Growth area:

The calculated *growing space.

Growth area vector:

The distance from stem of a tree to the border of its *growth area in a certain direction.

Growth model:

A model that describes the variation in time of a variable of a *system (or some derivation from it) at an established hierarchical level and dependent upon certain factors.

Heterogeneous stand:

Here: Stand with large differences in tree height.

High thinning = thinning from above:

Mainly involves trees in the upper crown classes: *codominant and *dominant trees that are competing strongly with the most promising individuals of these classes are removed. Cutting in the lower crown classes is directed t^Iwards removing trees that will die and be wasted before the next cutting and is done only if such trees have a positive net conversion value (Munns 1950, Ford-Robertson 1971).

Homogeneous stand:

Here: Stand with small differences in tree height.

Initiation:

Here: the phase in which the program "PINOGRAM" is started up until the moment that the dimensions of all trees at five years of age have been calculated and drawn.

Innovation phase:

The phase in *eco-unit development that starts after the *zero event and ends as soon as the canopy closes (cf. Oldeman, 1990).

Intensity of thinning:

A measure of the combined *frequency and *weight of thinnings, in terms of the volume removed during any succession of thinnings (Ford-Robertson 1971).

Interaction:

Mutual influence. There are different kinds of interaction, e.g. *competition, parasitism, commensalism, synergism.

Intermediate tree:

Tree shorter than the *dominant and *codominant trees, but with its crown either below or extending into the crown cover formed by dominant and codominant trees, receiving a little direct light from above, but none from the sides; usually with a small crown considerably crowded on the sides (Munns 1950).

Low thinning:

Anticipates natural thinning of a stand through competition, by working upward from *overtopped to *dominant trees, in five recognized intensities of cutting, as follows: *Grade A-light*. Removes the poorest overtopped trees. *Grade B-moderate*. Removes all overtopped trees and the poorer *intermediate trees. *Grade C-heavy*. Removes all overtopped and intermediate trees and often a few *codominant trees. *Grade D-very heavy*. Removes all overtopped and intermediate trees and many to most of the codominant trees. *Accretion thinning*. A cutting heavier than the D grade, removing all the codominant and a few dominant trees to obtain exceptionally rapid diameter growth on reserved trees (Munns 1950).

Here: Thinning of the smallest trees.

Manual thinning:

In program PINOGRAM: the user points out which trees have to be removed.

Mathematical factors:

Any of two or more quantities which form a product, when multiplied together (Neufeldt and Guralnik, 1988).

Maximum growth area:

The *growth area included by the perpendiculars of the *maximum growth area vectors.

Maximum growth area vector:

The maximum growth area vectors are derived from the *normal and the *potential growth area vectors of the *sample tree and its neighbours. They can be larger or smaller than the *normal growth area vectors and smaller than or equal to the *potential growth area vectors (for calculations: see section 4.12).

Maximum distance of influence:

The distance from the stem of the *sample tree until the furthest corner of its *maximum growth area (see section 4.9, 4.12 and 4.14)

Model:

A theory concerning a limited *system which is a piece of reality that we delimit and distinguish within the whole of reality, and which is explained in terms of the subsystems it contains (Oldeman 1990).

Monitoring:

Here: regularly checking how a forest (or elements of it) are changing or progressing over a period of time.

Normal (tree) growth:

Here: Growth defined by the genetic characteristics of a tree, by a more or less constant site quality and climate during its lifetime and by *competition for light, water and nutrients.

Normal growth area:

The *growth area included by the perpendiculars of the *normal growth area vectors.

Normal growth area vector:

The distance from the stem to the border of the *normal growth area in the direction of a neighbouring tree, derived from the height of the *sample tree, from the height of its neighbour and from the distance between the *sample tree and the neighbour.

Overtopped tree:

Tree with crown entirely below the general level of the crown cover receiving no direct light either from above or from the sides (Munns 1950).

Phenotype:

The phenotype of an individual represents all aspects of morphology, physiology, behaviour and ecological relations (Suzuki et al. 1989). An organism as observed, i.e. as judged by its visually perceptible characters resulting from the interaction of its *genotype with the environment (Ford-Robertson 1971).

Pioneer species:

A species capable of invading bare areas often in large numbers and over a considerable area, and of persisting until displaced as forest succession proceeds (Munns 1950, cf. Ford-Robertson 1971).

Potential growth area vector:

The *potential growth area vectors are derived from the potential crown length increment without *competition in the given direction. They can be larger or smaller than the *normal growth area vectors (for calculations: see section 4.12).

Primary selection:

Those trees that might influence the *maximum growth area of the *sample tree are primarily selected. In other words, trees that certainly have no influence are not selected (for calculations see section 4.9).

Pure stand:

Stand of trees of the same species.

Radial growth:

Horizontal expansion and contraction of a tree expressed in diameter increment and increment or decrease of crown width and crown length.

Reiteration:

Development of shoots outside the normal expression of the architectural model of a tree, as a specialized environmental response (Hallé et al. 1978).

Rotation:

The planned number of years between the formation or regeneration of a stand or crop and its final cutting at a specified stage of maturity (Ford-Robertson 1971).

S value:

The *dominant height a stand can reach at infinite age (Schütz and van Tol 1982). Here: the height a tree can reach at infinite age.

Sample tree:

The tree that is being focused on.

Secondary selection:

Selection of neighbouring trees that influence the *maximum growth area of the *sample tree (see section 4.13).

Severe thinning:

A large number of trees are felled at about the same time.

Silvatic-mosaic:

Every forest area that is situated in one continuous volume and subjected to the same regime of climate and soil, which shows the same complex of silvigenetic dynamics, resulting in an *eco-unit composition that oscillates around a specific state and determining the *architecture and ecological functioning as long as the resource regime remains unchanged (Oldeman 1990).

Situation (see forest situation).

Social position:

Position of trees in relation to that of its neighbours (see crown class).

Stand architecture:

The visible, morphological, expression of a stand, created by the phenotype and arrangement of the component organisms.

Stem length:

The length of the main axis from the bottom to the top of a tree.

Structure (1):

Includes all data in time and space that are derived from *models, not directly from living *systems (Oldeman 1990).

Structure (2):
Arrangement of arrays and variables in C programming language (cf. Microsoft C 1984-1989).

Subroutine:
Part of a program with a defined input and output of variables, which improves the organization of the program.

Subsequent phase:
Here: the phase after the *initiation in which the "PINOGRAM" program calculates and draws the dimensions of trees at the given age.

Suppressed trees:
Trees that are relatively short because of strong *competition from taller neighbours (also see overtopped tree).

Synecology:
Ecology of the *interaction between several different populations (Oldeman 1990).

System
Arrangement of units that function together.

Target type of forest:
A forest type with a species composition, production, *rotation, *architecture, fauna and management, defined as a result of political decisions.

Tertiary selection:
Selection of neighbouring trees that really compete with the *sample tree. If the *potential growth area vector of the *sample tree in the direction of a neighbour is equal to or larger than the *normal growth area vector, then this neighbour will be selected.

Thinning:
*Automatic thinning, *manual thinning, *high thinning, *low thinning, *frequency of thinning, *intensity of thinning, *severe thinning, *weight of thinning.

Top height (see dominant height).

Transect:
A traject through part of a forest represented on a map or as a profile diagram of stems and crowns of trees. It may also contain much more data, for example on shrubs, herbs, dead wood etc.

Tree architecture:
The visible, morphological, expression of the genetic blueprint of organic tree growth and development (Hallé et al. 1978)

Weight of thinning:
The number of trees per area that are felled at the same time.

Yield table:

A table showing for one or more species the growth pattern of a managed even-aged stand, derived from measurements at regular intervals covering its useful life; it includes mean diameter (generally *dbh*) and height, number of stems, and standing volume per unit area, and may further include e.g. volume of thinnings, main crop or total-volume, current annual increment and mean annual increment, main crop basal area, and other data (Ford-Robertson 1971).

Zero event:

The factor that causes forest development locally to start anew (like fire, wind, water, pests, and harvests that cause gaps or clearings).

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INDEX

SUMMARY

Ideas about forest and forestry in the Netherlands have changed in recent years, partly because nature and recreation are in greater demand, partly because of growing environmental problems (air pollution, global warming) and partly because of the decrease in forest area worldwide. This has led to a change in the government's forest policy (Anonymus 1985, 1986, 1990). The current aim is to achieve a more natural-looking forest (uneven aged, mixed, native species) and to have forest management linked to natural processes and which, while cheaper, has more benefits.

As a result of this shift in policy, forestry is expected to change significantly. In the first place, silvicultural practices in Dutch forests will be aimed at achieving a more continuous forest. Clear-cutting and large plantations will be replaced by silvicultural systems in which the cutting and regeneration processes are extended over several decades and in which mixing of species plays an important role. The management of such uneven-aged and mixed forests will have to be based much more on knowledge of the behaviour of the individual tree and its *interaction with the biotic and abiotic environment than is currently the case in even-aged and pure forests.

To be able to achieve the desired changes in composition, functions and management of the Dutch forests successfully, it will be necessary to make use of the natural dynamics and developmental processes of forests. However, our current knowledge of these is certainly not complete, or is not appropriate to the Dutch *situations or has not yet been translated in silvicultural strategy. There is a clear need to find out more about forest dynamics under specific Dutch circumstances.

Forest dynamics may be studied with the help of the *autoecology and *synecology of the different forest components. Because trees are the main components establishing forest architecture, it seems rational to start by investigating the autoecology and synecology of trees. The research presented here was directed at the Scots pine (*Pinus sylvestris L.*), the most common tree species in the Netherlands. It aimed at developing silvicultural information diagrams for Scots pine for different sites, provenances and treatment (tree and stand history). Silvicultural information diagrams should give information on characteristics such as *tree architecture, crown form and -dimensions, stem form, stem diameter and stem volume, and the likelihood of flowering and fructification, disease and damage and their consequences.

In principle an infinite number of silvicultural information diagrams is possible; therefore, it is necessary to determine the influence of age, site, provenance and treatment on the *phenotype of a tree to fulfil the above aim. If these relations are

known, the above aim can be achieved by developing an interactive model, in which the user can input age, site, provenance and treatment. Because the model should be dependent upon tree history and age, it was decided to develop a *growth model.

Growth models may be classified according to the hierarchical levels of their output; for instance the levels "organ", "organism", "*eco-unit" and silvatic-mosaic as defined by Oldeman (1990). Growth models rarely involve more than two levels. Growth may be understood as a process which is steered by growth factors inherent in a certain starting *situation and driving it towards a new situation over time. The starting situation may be understood as a *system of a certain hierarchical level, built up from subsystems of a lower hierarchical level. Growth models on a level between "organ" and "organism" have been developed by Aono and Kunii (1984), De Reffye et al. (1989) and others. Models such as those in the "JABOWA-family" (Botkin in West et al. 1981) mainly involve the levels "eco-unit" and "silvatic-mosaic". "Spatial models" (Hara 1988) are usually at the "organism" and "eco-unit" level.

As well as being classified according to the hierarchical levels mentioned, growth models may also be classified as physiological models, architectural models and mathematical models. This classification roughly indicates the method used to describe or declare the *situations or processes the model is dealing with. Physiological models are based on physiological processes; a process is described as the result of interacting underlying processes (see De Wit 1965, Borman and Likens 1979, Hari et al. 1985, Mohren 1987). Architectural models are based on the structural appearance of a *system, in which the appearance of a system (e.g. *silvatic-mosaic, *eco-unit, organism) is defined by the pattern and appearance of the subsystems (respectively eco-units, organisms, organs). Examples of these are the models developed by Aono and Kunii (1984), De Reffye et al. (1989), Koop (1989) and others. Mathematical growth models describe the changes in the appearance of a system over time and in relation to factors that probably influence these changes. Generally, correlations and not causal relations are used to find growth equations. The "spatial" and "nonspatial" models (see Hara 1988) can be classified as mathematical models.

Because a silvicultural information diagram should demonstrate the temporal changes of the *phenotype of a tree, the model should involve both the levels between "organism" and "eco-unit". The phenotype of a tree depends upon its "*normal growth" and also upon favourable and stress factors. "Normal growth" is defined by the genetic characteristics of a tree, by a more or less constant site quality and climate during its lifetime and by *competition for light, water and nutrients. Stress factors may be diseases and plagues, environmental pollution and damage by, for example, temporary climate extremes. Favourable factors may be fertilization, changing soil water supply, immigration of mycorrhiza, etc.

The model presented here has been restricted to "normal growth". Competition is understood as competition for qualified space and constraints are not defined (e.g. available light, water or nutrients). One of the most important ways of influencing tree growth is to provide more space by cutting neighbouring trees. The model does indeed show large similarities with "spatial" models.

The models present in the current literature are either related to another hierarchical level, or do not deal with crown growth or with the *growing space of individual trees and the architecture of the *eco-unit. Therefore none of them are really appropriate for creating a silvicultural information diagram for the different circumstances required. This is why a new model is needed.

Using information from the literature and data from an old provenance trial in Kootwijk (Province of Gelderland, the Netherlands), the influence of genetic traits, site, growing space, age and phenotype on the growth of trees was studied. It was found that the height growth of trees is mainly defined by *genotype, site characteristics and climate and that *radial growth is mainly defined by height growth and growing space. It still seems impossible to precisely predict the height growth of an individual tree during its life time. But it is probably possible to forecast the mean height growth and standard deviation for a tree of a certain provenance and on certain site.

In order to calculate the influence of the *growing space on the radial growth of trees a field study was done, in which diameter, crown length, crown width, tree height, volume, age and *normal growth area of 158 trees divided over 13 stands were measured once. The normal growth area is defined as the area in which a tree has more competitive power than its neighbours. It is calculated with the help of the distances from the *sample tree to its neighbouring trees, the distances between the consecutive neighbours and the heights of all these trees. Non-linear regression was used to correlate crown length, mean crown width and stem diameter with tree height, age and mean *growth area vector. The resulting correlations were sufficiently good to enable growth equations to be derived.

A good non-linear correlation, based on 38 felled trees, was also found between form factor on the one side and tree length, crown length and diameter on the other side. In the resulting regression equation the crown length defines the form factor better than tree length does. A reasonably good non-linear correlation was also found between mean branch diameter in the lower part of the crown and tree length, crown length and mean crown width.

The derived growth equations were used to develop a growth simulation program, called "PINOGRAM". This program, written in "Microsoft C", visualizes the growth of individual trees in relation to the *competition they experience.

In the PINOGRAM program growth is simulated in a *transect of 50 * 20 metres. The user first enters the planting distance within a row and between rows. He must also enter a minimum and maximum *S value. These values are defined as respectively the minimum and maximum heights that a tree of a certain provenance on a certain site can reach at infinite age. In *homogeneous stands the minimum and maximum S value do not differ greatly, in contrast with *heterogeneous stands. The program then assigns to each tree an S value S_{tree} according to a normal distribution and a confidence interval of 95% between minimum and maximum S values. Finally, the user must enter the age at which he wants to see the transect.

The program calculates the height of each tree (called: sample tree) at the given age according to the Chapman-Richards function. Using the heights of a sample tree and its neighbours and the distances between these trees, the *normal growth area vectors between the sample tree and its neighbours are calculated first. Next the extent to which the trees can use these normal growth area vectors is calculated. This depends upon the possible crown length increment in the direction of the neighbour within the given time interval and without *competition (= *potential growth area vector). The normal growth area vectors and the potential growth area vectors of the sample tree and its neighbours are used to calculate the *maximum growth area that the sample tree can occupy (= maximum growth area vector). The perpendiculars of the maximum growth area vectors include the maximum growth area. Within this maximum growth area, new *maximum growth area vectors are calculated in sixteen compass points (N, NNE, NE, ENE, E, etc.). In order to find the growth area actually occupied (= *actual growth area), the potential growth area vectors in these sixteen directions are also calculated. The *actual growth area vectors are derived from the minimum of the maximum growth area vectors and the potential growth area vectors.

The actual growth area vectors are used to calculate the diameter, the crown length and crown width in sixteen directions. Next, form factor, volume and mean branch diameter (in the lower part of the crown) can be computed per tree and finally also the yield data per ha and the *canopy closure are computed. Now all the necessary data for drawing a crown map, a profile diagram or a three-dimensional picture of the transect are available.

After one *situation has been computed and the crown map has been drawn, a new age can be entered and the user can request some trees to be felled. He can choose between *manual thinning (the user points out which trees have to be removed) and *automatic thinning (the user indicates whether a low thinning or a *high thinning has to be carried out and how many m^3 have to be removed. At high thinning the user can indicate the critical h/cl ratio, at which a neighbouring tree should be removed). Natural mortality of a tree occurs when the tree height divided by the mean crown width of a tree exceeds six (= mortality factor M). The trees selected to be thinned are removed and now the heights and *growth areas of the remaining trees are calculated at the new age, from which the new tree dimensions are then derived.

The program displays information about stem number per ha, stem distribution, crown length and crown width, crown asymmetry, canopy closure and tree height by means of a crown map, profile diagrams and three-dimensional drawings. Underneath it displays a table showing data on the tree height, stem diameter, form factor, mean branch diameter in the lower part of the crown for individual trees, plus data on stem number per ha, basal area per ha and volume per ha of the remaining stand and of thinnings. Note that growth performance according to the equations as used in the model results in a mean expected growth for an individual tree at a given thinning regime.

This growth simulating program enables the growth of individual trees within a stand to be depicted graphically. Different silvicultural systems can be applied, to study their effects on stand growth. The graphical design makes this insight very communicable and useful (for instance, for teaching). And the results can be used in further modelling (for example, in a model of stand structure and light, or of cost and benefit, or of silvicultural system and timber quality).

The growth equations used in the model cannot be used directly on real trees. The *normal growth area of a tree, as measured in the field, often differs from the *actual growth area the tree is using at that moment. The actual growth area can be calculated using the crown widths measured in sixteen directions, but generally the matching crown lengths and diameters calculated differ from the measured ones, because these tree dimensions are not 100% correlated with age, height and actual growth area.

The model has only been tested for Scots pine on the Veluwe. It does not yet give information about *tree architecture, stem form, flowering and consequences of damage, diseases, climatic changes and environmental pollution. In its present form it also cannot yet be applied to mixed and uneven-aged stands. There is scope for improvement; fruitful avenues of future research are suggested in section 5.3.

SAMENVATTING

De visie op bos en bosbouw in Nederland is de laatste jaren onder andere als gevolg van de toenemende behoefte aan natuur en recreatie, de groeiende milieuproblemen (luchtvervuiling, broeikaseffect) en de afname van het bosareaal op wereldschaal sterk veranderd. Dit heeft geleid tot een gewijzigd regeringsbeleid ten aanzien van het bos (Anonymus 1985, 1986, 1990). Gestreefd wordt naar een meer natuurlijk bosbeeld (ongelijkjarig, gemengd, inheemse soorten), een beheer wat aansluit bij de natuurlijke processen, beperking van de kosten van dat beheer en verhoging van de opbrengsten. Voor de bosbouw zal dit tot een aantal ingrijpende veranderingen leiden.

In de eerste plaats zullen teeltingrepen in het Nederlandse bos in de toekomst veel meer dan in het verleden tot een continu bosbeeld moeten leiden. Ingrepen zoals leegkap en vlaktegewijze, kunstmatige verjonging zullen in belangrijke mate vervangen worden door teeltsystemen waarbij het kap- en verjongingsproces zich over tientallen jaren uitstrekt en waarbij gestreefd wordt naar meer gemengde bossen. Het beheer van zulke naar soort en leeftijd gemengde bossen zal zich veel meer moeten baseren op de kennis van het gedrag van de individuele boom en zijn interactie met het biotisch en abiotisch milieu, dan tot nog toe bij het gelijksoortig en gelijkjarig leegkapbos het geval was.

Om de hierboven genoemde veranderingen in beheer, samenstelling en functies van het Nederlandse bos met succes te kunnen doorvoeren is het nodig om aan te sluiten bij de (al dan niet natuurlijke) ontwikkelingsprocessen in bossen. De hiervoor beschikbare bosoecologische kennis is echter verre van volledig en deels niet van toepassing op de Nederlandse situatie of nog niet teeltkundig geïnterpreteerd. Om deze redenen is meer inzicht in de bosontwikkelingsprocessen onder specifiek Nederlandse omstandigheden dringend gewenst.

Bosontwikkelingsprocessen kunnen worden bestudeerd aan de hand van de autoecologie en synecologie van de verschillende boscomponenten. Aangezien de bomen de belangrijkste componenten zijn die de bosstructuur bepalen, ligt het voor de hand het onderzoek in eerste instantie hierop te richten. Het hier gepresenteerde onderzoek richt zich op de groveden (*Pinus sylvestris L.*), welke in Nederland de meest voorkomende boomsoort is. Het doel van dit onderzoek is het ontwikkelen van teeltdiagrammen voor grove den, afhankelijk van groeiplaats, herkomst en behandeling (boom- en opstandsgeschiedenis), waarbij deze teeltdiagrammen afhankelijk van de leeftijd van de boom informatie moeten verschaffen over onder andere boomarchitectuur, kroonvorm en -afmetingen, stamvorm, -diameter en -volume, kans op en gevolg van bloei en zaaddracht, ziektes en beschadigingen.

Omdat er in principe een oneindig aantal teeltdiagrammen mogelijk is, is het, wil men aan bovenstaande doelstelling beantwoorden, noodzakelijk de invloed van leeftijd, groeiplaats, herkomst en behandelingswijze op het fenotype van een boom te kwantificeren. Als deze relaties bekend zijn, kan aan bovenstaand doel worden beantwoord door een interactief model te ontwikkelen, waarbij leeftijd, groeiplaats, herkomst en behandelingswijze kunnen worden opgegeven door de gebruiker. Omdat het model afhankelijk wordt gesteld van boomgeschiedenis (behandelingswijze) en leeftijd is gekozen voor het ontwikkelen van een groeimodel.

Groeimodellen kunnen worden ingedeeld volgens de hierarchische niveaus van hun output. Oldeman (1990) geeft een indeling in de niveaus "organ", "organism", "*eco-unit" en "*silvatic-mosaic". Groeimodellen hebben doorgaans betrekking op twee niveaus. Onder groei wordt het proces verstaan waarbij groeifactoren een zekere beginsituatie zodanig sturen, dat na verloop van tijd een nieuwe situatie ontstaat. Onder de beginsituatie wordt een systeem verstaan van een zeker hierarchisch niveau dat is opgbouwd uit subsystemen van een lager hierarchisch niveau.

Groeimodellen op het niveau van "organ" en "organism" zijn ontwikkeld door onder andere De Reffye et al.(1989) en Aono and Kunii (1984). De modellen van onder andere de "JABOWA-family" (Botkin in West et al. 1981) liggen vooral op het niveau "eco-unit" en "silvatic-mosaic". Modellen op het niveau van "organism" en "eco-unit" vinden we vooral terug in de spatial and non-spatial models (Hara 1988).

Behalve naar hierarchisch niveau kunnen groeimodellen ook worden ingedeeld in fysiologische modellen, architectuurmodellen en mathematische modellen. Deze indeling geeft ruwweg de gebruikte methode aan om die situaties en processen te beschrijven en verklaren waar het model aan gerelateerd is.

Fysiologische modellen gaan uit van fysiologische processen, waarbij een proces wordt verklaard door samenwerking van subprocessen (vgl. onder andere De Wit 1965, Borman and Likens 1979, Hari et al. 1985, Mohren 1987).

Architectuurmodellen gaan uit van verschijningsvormen, waarbij een verschijningsvorm van een systeem (*silvatic-mosaic, *eco-unit, organism) wordt bepaald door de rangschikking en de verschijningsvorm van de subsystemen (eco-units, organisms, organs). Voorbeelden hiervan zijn de modellen van onder andere Aono and Kunii (1984), De Reffye et al. (1989) en Koop (1989).

De mathematische groeimodellen beschrijven de verandering van een verschijningsvorm van een systeem in de tijd in relatie tot factoren, waarvan verwacht mag worden dat deze invloed hebben op deze verandering. Er wordt doorgaans gewerkt met correlaties en minder met bewezen causale verbanden. Hieronder vallen onder andere de "spatial" en "nonspatial" models (zie Hara 1988).

Omdat een teeltdiagram de verandering in de tijd van het fenotype van een boom moet weergeven moet het gewenste model zich begeven tussen de niveaus "organism" en "*eco-unit". Het fenotype van een boom is enerzijds afhankelijk van zijn "*normale groei" en anderzijds door verstorende en begunstigende factoren. De "normale groei" wordt bepaald door de genetische eigenschappen van de boom, door een min of meer constante bodemkwaliteit en klimaat tijdens zijn leven en door concurrentie. Verstorende factoren kunnen bestaan uit ziektes en plagen, milieuverontreiniging en beschadigingen door bijvoorbeeld tijdelijke klimaatsextremen. Begunstigende factoren kunnen bestaan uit bemesting, veranderingen in beschikbaar bodemvocht, immigratie van mycorrhyza, etc.

Het hier gepresenteerde model zal zich beperken tot de "normale groei". Concurrentie is hier opgevat als concurrentie met buurbomen om ruimte, waarbij in het midden wordt gelaten of het gaat om concurrentie om licht, concurrentie om water of concurrentie om voedingsstoffen. Immers één van de belangrijkste vormen van beïnvloeding van groei van een boom is het geven van ruimte door het wegnemen van dichtbijstaande buurbomen. Het gevraagde model vertoont dan ook sterke overeenkomsten met de "spatial models".

De in de literatuur gevonden modellen spelen zich echter of af op een ander hierarchisch niveau, of zij houden geen rekening met kroongroei of zij houden geen rekening met de groeiruimte van een individuele boom en de structuur van de *eco-unit, zodat ze geen van allen echt geschikt zijn om een teeltdiagram onder de gestelde omstandigheden te vervaardigen. Daarom was een nieuw model nodig.

Aan de hand van een literatuuronderzoek en berekeningen aan een oude herkomstproef in Kootwijk is de invloed van genetische eigenschappen, de groeiplaats, de groeiruimte, de leeftijd en het fenotype op de groei van bomen onderzocht. Hieruit bleek dat de hoogtegroei van bomen voornamelijk bepaald wordt door genetische eigenschappen, bodemeigenschappen en klimaat en dat de radiale groei voornamelijk wordt bepaald door de hoogtegroei en de groeiruimte. Een precieze voorspelling van de hoogtegroei van een enkele boom gedurende zijn leven blijkt vooralsnog onmogelijk. Wel is het waarschijnlijk mogelijk een gemiddelde hoogtegroei met standaardafwijking voor een boom van een bepaalde herkomst en bij een bepaald groeiplaatstype aan te geven.

Om de invloed van de groeiruimte op de radiale groei van bomen te berekenen, is een veldproef uitgevoerd. Hierbij zijn in verschillende bosgebieden diameter, kroonlengte, kroonbreedte, boomhoogte, volume, leeftijd en *normale standruimte van 158 bomen gemeten. De normale standruimte is de oppervlakte, waar een boom meer concurrentiekracht bezit dan zijn buurbomen en wordt berekend aan de hand van de afstand van de proefboom tot de buurbomen, de afstanden tussen opeenvolgende buurbomen en de hoogtes van proefboom en buurbomen. Met behulp van niet-lineaire correlatie zijn achtereenvolgens kroonlengte, kroonbreedte en stamdiameter gecorreleerd met boomhoogte, leeftijd en standruimte. De correlaties bleken goed genoeg om groeiformules af te leiden.

Aan de hand van 38 gevelde bomen is onder andere een goede niet-lineaire correlatie gevonden tussen het vormgetal enerzijds en de boomlengte, kroonlengte en diameter anderzijds. Hierbij beschrijft de kroonlengte het vormgetal beter dan de boomlengte. Ook is een redelijke niet-lineaire correlatie gevonden tussen de gemiddelde takdiameter onder in de kroon enerzijds en de boomlengte, kroonlengte en kroonbreedte anderzijds.

Met behulp van de groeiformules is een groeisimulatieprogramma ontwikkeld, dat de groei van individuele bomen in hun onderlinge concurrentie visualiseert. Het programma is geschreven in Microsoft C.

Groei wordt gesimuleerd in een *transect van 50 * 20 meter. Men geeft op wat de plantafstand is binnen een rij en tussen rijen. Daarnaast moet men een minimum en maximum S-waarde opgeven. De S-waarde is hier de hoogte die een boom met een zekere herkomst of genetische eigenschappen op een zekere groeiplaats maximaal kan bereiken. Bij *homogene opstanden verschillen minimum en maximum S-waarde niet zo sterk, i.t.t. *heterogene opstanden. Het programma deelt vervolgens aan elke boom een S_waarde toe volgens een normale verdeling en een betrouwbaarheidsinterval van 95% tussen maximum en minimum S-waarde. Tenslotte geeft men de leeftijd waarbij men het transect wil zien.

Het programma berekent de hoogte van elke boom (= proefboom) bij de opgegeven leeftijd volgens de Chapman-Richards functie. Afhankelijk van de hoogte van een "proefboom" en die van zijn buurbomen en de afstanden tussen deze bomen worden eerst de *normale standruimtevectoren tussen proefboom en buurbomen uitgerekend. Vervolgens wordt berekend in hoeverre de bomen deze normale standruimte in gegeven richting kunnen benutten. Dit is afhankelijk van de mogelijke kroonlengtebijgroei binnen de gegeven tijdsinterval, wanneer een boom niet beconcurreerd wordt (= potentiële standruimtevector). Afhankelijk van de normale- en de *potentiële standruimtevectoren van de proefboom en die van zijn buurbomen wordt berekend welke standruimte een boom ter plekke maximaal kan innemen (= maximum standruimtevector). De loodlijnen van de maximum standruimtevectoren sluiten de maximum groeiruimte in. Binnen de zo ontstane "maximum standruimte" wordt in zestien windrichtingen (N, NNO, NO, ONO O etc.) de afstand van stam tot de rand van de maximum standruimte bepaald. Om de werkelijk ingenomen standruimtevectoren te bepalen die de werkelijk ingenomen oppervlakte aangeven (= actuele standruimte) worden de potentiële standruimtevectoren in deze zestien richtingen berekend. De actuele standruimtevectoren worden berekend door het minimum te nemen van de maximum- en de potentiële standruimtevectoren.

Met behulp van de actuele standruimtevectoren kunnen de diameter en de kroonlengtes en kroonbreedtes in de zestien richtingen berekend worden. Daarna kunnen vormgetal, volume en de gemiddeld grootste takdiameter onder in de kroon per boom worden bepaald en tenslotte ook opbrengstgegevens per ha en de kronensluiting. Daarmee zijn alle gegevens aanwezig om een plattegrond, een profieldiagram of een driedimensionale tekening van het transect te laten zien.

Nadat bovenstaande per boom is uitgerekend voor de opgegeven leeftijd kan men aangeven dat er gedund moet worden. De dunning geschiedt door het aanwijzen van de te dunnen bomen door de gebruiker of automatisch, waarbij de gebruiker aangeeft of het een hoogdunning dan wel een laagdunning betreft en hoeveel m^3 er gekapt moet worden. Bij de hoogdunning kan men bovendien de gewenste critische h/cl-grens opgeven, waarbij een buurboom gekapt moet worden. Natuurlijke sterfte treedt op als de hoogte gedeeld door de gemiddelde kroonbreedte van een boom groter is dan 6 (= mortality factor M). De te dunnen bomen worden vervolgens verwijderd en de hoogtes en standruimtes van de resterende bomen worden berekend bij de nieuwe leeftijd, waaruit de nieuwe boomafmetingen worden afgeleid.

Er wordt informatie verschaft over stamtal per ha, stamtalverdeling, kroonlengte en kroonbreedte, kroonasymmetrie en boomhoogte d.m.v. een kroonprojectietekening, profieltekeningen en driedimensionale tekeningen. Daarnaast wordt een tabel gemaakt met per boom gegevens over hoogte, diameter, vormgetal, gemiddeld dikste tak onder in de kroon en volume, alsmede gegevens over stamtal per ha, grondvlak per ha en volume per ha van zowel de blijvende opstand als van de dunningen. Men moet echter wel bedenken dat de weergave van de groei met behulp van de in het model gebruikte formules resulteren in een gemiddelde verwachte groei voor een individuele boom bij een gegeven dunningsregime.

Aan de hand van dit groeisimulatieprogramma kan men de groei van individuele bomen binnen een opstand, afhankelijk van het teeltsysteem, grafisch weergeven, met als doel inzicht te krijgen in dit teeltsysteem en dit inzicht overdraagbaar te maken. Bovendien kunnen de resultaten een handvat bieden voor verdere modellering (bijvoorbeeld structuur-lichtmodel, kosten-batenmodel, teeltsysteem-houtkwaliteitmodel).

De hier gegeven groeiformules kunnen niet zomaar gebruikt worden voor reële (in het veld gemeten) bomen. De normale standruimte van een boom, zoals die in het veld wordt gemeten, is vaak ongelijk aan de actuele standruimte die de boom op dat moment werkelijk gebruikt. Het is mogelijk de actuele standruimte te berekenen met behulp van de gemeten kroonbreedtes in zestien richtingen., maar in het algemeen zijn de bijbehorende berekende waardes voor de kroonlengte en diameter niet gelijk aan de gemeten waardes, omdat deze boomafmetingen niet 100% gecorreleerd zijn aan leeftijd, hoogte en actuele groeiruimte.

Het model is alleen getest voor grove den op de Veluwe en het geeft nog geen informatie over boomarchitectuur, stamvorm, bloei en mogelijke gevolgen van beschadigingen, ziektes en milieuverontreiniging. In zijn huidige vorm kan het ook nog niet worden gebruikt voor gemengde en ongelijkjarige bossen. Er is echter uitzicht op verdere vooruitgang. Richtlijnen voor toekomstig onderzoek zijn gegeven in hoofdstuk 5.3.

Curriculum Vitae

Peter Leersnijder werd geboren op 3 januari 1959 te Heemstede. In 1977 behaalde hij het Gymnasium-ß diploma aan het Coornhert-Lyceum in Haarlem. In dat zelfde jaar begon hij zijn studie Bosbouw aan de toenmalige Landbouwhogeschool te Wageningen. In 1982 ging hij samen met Luc Koks zes maanden op stage in Schweinsberg (provincie Hessen, Duitsland). Deze stage stond in het kader van de "Naturgemäße Waldwirtschaft". Samen met Luc Koks schreef hij twee doctoraalscripties: het eerste betrof een onderzoek naar de mogelijkheden voor omvorming van grootschalig naar kleinschalig bosbeheer in Nederland; het tweede betrof een onderzoek naar de bosontwikkeling in een voormalig middenbos in het Gerendal (provincie Zuid-Limburg, Nederland). In 1985 voltooide hij zijn ingenieursopleiding. Het doctoraalexamen omvatte de volgende vakken: De houtteelt gematigde luchtstreken; de boshuishoudkunde; de regionale bodemkunde; de vegetatiekunde en plantenoecologie. In 1986 is hij te werk gesteld als pro-Deo werker bij de vakgroep Bosteelt en Bosoecologie. Het werk bestond uit een inventarisatie van bodem, vegetatie en houtvoorraad van het landgoed van de Stichting Oranje Nassau's Oord en het maken van een ontwikkelingsplan hiervoor. Sinds maart 1987 werkte hij bij de toenmalige vakgroep Bosteelt en Bosoecologie (de tegenwoordige vakgroep Bosbouw) als assistent in opleiding aan dit proefschrift. Van mei 1991 tot maart 1992 werkte hij deeltijd samen met Jelle Hiemstra op dezelfde vakgroep aan het project "Bosontwikkeling" en aan het opstellen van een projectvoorstel voor de EG: "New Forests on old farm lands".