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Intensification of growth and yield studies in previously logged forest

The ITTO permanent sample plots in Papua New Guinea : Progress in growth model development 1997

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Executive summary

There are 72 ITTO-sponsored permanent plots in Papua New Guinea, of which 66 have been remeasured at least once over a minimum 2-year interval. This report describes progress towards the development of a growth model based on this data that will inform forest management regarding issues of sustainability and projected yield.

The report documents 8 programs developed in FoxPro to extract data for the analysis of the plots. These cover cross-checking successive measurements; analysis of basal area and tree numbers by size classes; summaries of basal area increment, mortality and recruitment; lists of most abundant species for plots, and rectangular plot-species matrices for botanical association analysis; species summary statistics to facilitate the formation of species groups for modelling purposes; diameter increment summaries for species or species groups, classified by factors such as crown position, crown quality, tree defect, tree diameter, competing basal area; mortality summaries, similarly classified; and recruitment lists.

These programs are now being used to develop growth functions for the integrated model, which is being called PINFORM (PNG/ITTO Natural Forest Model). Two aspects of this modelling work are reported in more detail. These concern the formation of species groups, and development of a growth index for plot basal area increment projection.

Species groups are formed using an ordination of mean diameter increment on the 90% cumulative diameter in a logarithmic space. An Excel workbook is described that carries out all aspects of the analysis, using the outputs from the PSP database. These groups tend to relate functionally similar species: Small, slow growing trees in the understorey, ephemeral pioneers, medium and large timber trees, slow growing smaller or larger dense hardwoods. In all, 21 groups are derived, indicated by the codes A-X. 78% of all trees, and 36% of species, fall into 7 main groups, denoted by the letters A-G. A table is given of the group characteristics and principle species. These groups do not replace the economic species groups, but are used together with them in the PINFORM model.

Species associations among the plots were analysed using reciprocal averaging. Only the principal axis of variation could be studied, due to lack of suitable software. This shows that there is a principle gradient between plots which tend to have species such as *Planchonella*, *Hopea* and *Vatica* as co-dominant with *Syzygium*, at one end of the scale, to plots on which *Pimeliidendron*, *Celtis*, *Ficus*, and *Pometia* are common. However, there are no marked discontinuities, and

species such as *Syzygium*, *Myristica*, *Dysoxylum*, *Cryptocarya*, *Canarium*, and *Horsfieldia* occur commonly throughout the range. This gives confidence that the plots, though widely distributed over lowland PNG, represent a consistent forest type, albeit with gradients of species distribution.

An explanatory model for stand basal area increment was developed. This was based on mean diameter increment for species, plot stocking, in trees/ha, and a growth index for different provinces. It was found that plots in East Sepik and Madang were the most productive, and those in Morobe and the Southern Highlands the least, with a range from +25% to -20% of the mean increment, which was close to 0.5 m²/ha/yr. This is approximately 3 m³/ha/yr in volume, although much of this will not be commercial, and natural mortality must also be deducted. The increment growth model accounted for 77% of the observed variation between plots.

During the increment model development, a variety of complex functions were tested for their performance, incorporating factors such as crown position, crown quality or competing basal area. These proved to be less precise and more biased than the simple model finally adopted, whose equations are detailed in the report.

The programme of work planned for the first quarter of 1998 is reviewed. This will see the completion and testing of the PINFORM model. It is intended to spend some time at Forest Authority headquarters demonstrating the model and adapting it to practical planning purposes.

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Objectives This report covers activities undertaken by the consultant during 1997 under ITTO project PD162/91. This work has involved two trips of one month each to the Papua New Guinea Forest Research Institute. These trips were undertaken in July and November 1997 respectively. The objective of this work has been to further the analysis of the data gathered from permanent sample plots established in logged-over natural forest in PNG. This analysis is directed at developing a growth model that can be used in a flexible way for silvicultural and management planning. This in turn will lead to a review of general policies within the PNG Forest Authority with regard to felling cycles and minimum felling diameter limits. The model will indicate likely levels of yield in regrowth forests, and consequently inform strategic planning within the forest sector.

Secondary but very important objectives are to provide training in PSP data handling and analysis, and to provide a permanent and user-friendly suite of PSP data analysis programs. This combination of skills and computer programs can enable the Forest Research Institute to maintain and update the model as further PSP data is acquired.

Work programme

Under the project, a total of five months has been allowed for consultancy on PSP data analysis, growth modelling, and related training. This has been split over 1997 and 1998 in approximately equal periods. The 1997 work has been undertaken during July and November under separate trips by the author. An interim report was prepared for the July period, which included a review of the data, and development of most of the analysis programs.

The present report gives a user's guide to those programs, and provides details of the analyses which have been undertaken so far. These include:

- The species grouping method used to develop growth models.
- Species distribution and site variation between the plots.
- Characteristics of diameter increment with respect to tree diameter, crown position, crown quality, and tree basal area.
- Testing diameter increment functions for a growth model.

It also describes the growth modelling strategy that will be adopted, and the further steps required to complete and test the model during the first quarter of 1998.

Overview

The data analysis package for the ITTO plots comprises eight Fox-Pro modules, accessible through a common interface program called ANALYSIS. It can be started from Windows by clicking an icon which has been set up for this purpose¹. It can also be started from the PERSYST program by clicking on the button labelled *data analysis*.

The following sections detail the programs, their input and outputs, and the options available for their execution. The programs are designed to output DBF files which can be imported into Excel or statistical packages for further analysis. These output files are all named commencing with a tilde (~), to indicate that *they are temporary files which may be deleted* when disk space is at a premium.

On the ITTO computers at FRI, the PERSYST system is in a directory called C:\PSPS. The analysis suite of programs is in a sub-directory C:\PSPS\ANALYSIS. The output files produced are also placed in this directory.

XCHEK cross-checking program

The cross-checking program is designed bring together the various measurement files for a PSP and check them for consistency. The program is also designed to facilitate error correction, which is rather slow and difficult using PERSYST.

When the program start, four options can be set before running the check:

- *The plots to be processed* may be entered as a complete plot code (eg. OOMSI01) or as a wild-card designation, such as OOMSI*. In the latter form, all plot codes which match the wild card will be included in the output report.
- *The species to be included* can be entered as a wild card designation. By default this is *, indicating any species code will be included. For example, ANI* would include ANI, ANI THU, ANI CHI, ANI POL, etc.
- *The output file name can be specified*. By default this is called ~MERGE.
- *If the re-process option box is marked*, then the existing merge file will be activated without carrying out any processing.

The Run button re-builds the merge file from the original PSP data files, carrying out checks on successive measurements. If the *re-process* option has been selected, the existing merge file is activated directly. It is then possible to view or print all or selected

¹ On the ITTO project computers, the icon properties are set to execute the command FOXPROW C:\PSPS\ANALYSIS\ANALYSIS. The working directory is C:\PSPS\ANALYSIS.

portions of the merge file, together with any associated error messages. The selection screen allows plots and quadrats to be selected using wildcard characters. By default, all quadrats are selected (using *), with the same plot designator as was used to create the ~MERGE file.

The **view** button displays the printed report using the FoxPro report viewer. The **print** button will send the report directly to the printer. Note that the printed reports can be very long. Even a single plot may require 30-50 pages. All data for all measurements of a plot are listed, with the successive measurements for each tree shown adjacent, and observations or error messages in the right hand column. It is therefore recommended when printing a plot that it is limited to a particular quadrat that needs detailed examination. Most checks and error correction can be done on screen without printing.

The **edit** button provides the most useful facility for routine corrections. The data is displayed as a FoxPro *browse* screen, with the successive measurements for each tree in sequence, and error messages in the right-hand column. Corrections made to this screen will be posted back to the original PSP data files if the following 2-step sequence is followed to exit the screen:

- Use **ctrl-W** to exit. If **esc** is used, any updates will not be saved to the original files, although they will be retained in the ~MERGE file and can be saved later.
- When the program prompts *Update the original PSP files with corrections?*, press **Y**.

Corrections which involve the addition or deletion of tree records at particular measurements cannot be done directly from XCHECK, but must be done from PERSYST.

The **summary** button gives a quick summary showing the types of errors and the numbers of trees affected. This is useful for a quick check on the data from a plot.

BADIS stand structure tables

The BADIS program tabulates basal area and tree numbers by 20-cm diameter classes for each measurement of all PSPs. The data are arranged with the successive measurements for each plot adjacent. A report format prints this out directly in a neat and intelligible format. The output file, called ~BADIS, can also be imported into Excel or other packages to produce graphs.

The program requires no inputs from the user. On execution it prompts **~BADIS file exists. Re-build?** Pressing **Y** causes the plot data files to be re-processed. Otherwise the existing output file

from a previous run of the program is opened directly for browsing or printing in report format.

BANAL stand dynamic analysis

The BANAL program provides information about total and dominant basal area and tree numbers at the initial measurement. It shows changes over time in basal area and numbers due to growth, recruitment, and losses. It also gives the percentage error in basal area increment due to odd measurements¹. It operates in the same way as BADIS, in that it requires no user parameters except a confirmation of whether or not to re-build the output file ~BANAL if it already exists.

SPABUN species abundance by plots

The SPABUN program is designed to provide outputs that can be used for ordination or cluster analysis of the PSPs according to species abundance. There are several options which appear when the program starts up. Under method, one of three alternatives can be selected:

1. *List the most common species.* This format is the only one which can be output in a report. A selected number of the most common species are listed for each plot, with N/ha, the selected abundance index, cumulative abundance, species name and family.
2. *List abundances by plots and species groups.* This produces a rectangular matrix with plots as rows, and species groups as columns. Each element contains the group abundance. This type of data is suitable for plot ordination using the species groups.
3. *List abundances by plots for an indicator species list.* A list of species can be set up which are considered to be indicative of forest types. This option will produce a rectangular matrix of abundances by plots (rows) and indicator species (columns).

The indicator species list can be edited by clicking the box labelled ***View/edit indicator species list***. This is a browse table to which new rows can be added with the ctrl-N key. Existing rows can be deleted with the mouse by clicking the left-hand edge of the row. When a species code is entered in the list, the corresponding name will be looked up automatically. An error message is given if the code does not correspond to a species.

¹These include recruit trees over 30 cm and trees shrinking more than 1 cm or growing over 5 cm per year.

Neither of the two rectangular matrix formats (options 2 or 3) can be printed as a report; both are designed to be imported into a statistical package with ordination or cluster analysis facilities.

The abundance index can be selected as either tree numbers as a percent of the total stocking, or basal area %.

The output file produced will default to the name ~SPABUN, but an alternative name can be given if required. An Excel workbook called SPABUN.XLS exists which will process format 1 files as described on page 12.

SPPORD species statistics for grouping

The SPPORD program is designed to provide a list of all species which occur on the plots together with key statistics that can be used to form species groups. The species codes, economic group, botanical and family name are given. The total number of trees, tree numbers by 20 cm diameter classes, and the number of plots on which the species is present are calculated. Mean increment with standard error are shown, and the 90% quantile of the diameter distribution (D_{90}).

The output file is called ~SPPORD. If it exists when the program is run, the user will be asked if it is to be re-built. Press **Y** to reconstruct the file from the current PSP data and species list file SPECLIST.DBF.

The program provides for a printed report which lists species and their summary statistics. This can be sorted according to three options: By species code, by economic value, or by frequency of occurrence.

The principle analysis undertaken with this file is via the Excel workbook SPPORD.XLS. This provides the facilities for creating or modifying the species groups.

TREEINC diameter increment analysis

The TREEINC program provides facilities for calculating diameter increments and forming classified summaries against different variables. When the program is started, an option screen appears as shown in Figure 1.

Under Species Grouping it is possible to select either individual species summaries, or summaries by the growth model groups¹.

¹The model groups are determined by the MODEL field in the SPECLIST.DBF file that will be found in the PERSYST directory (normally C:\PSPS).

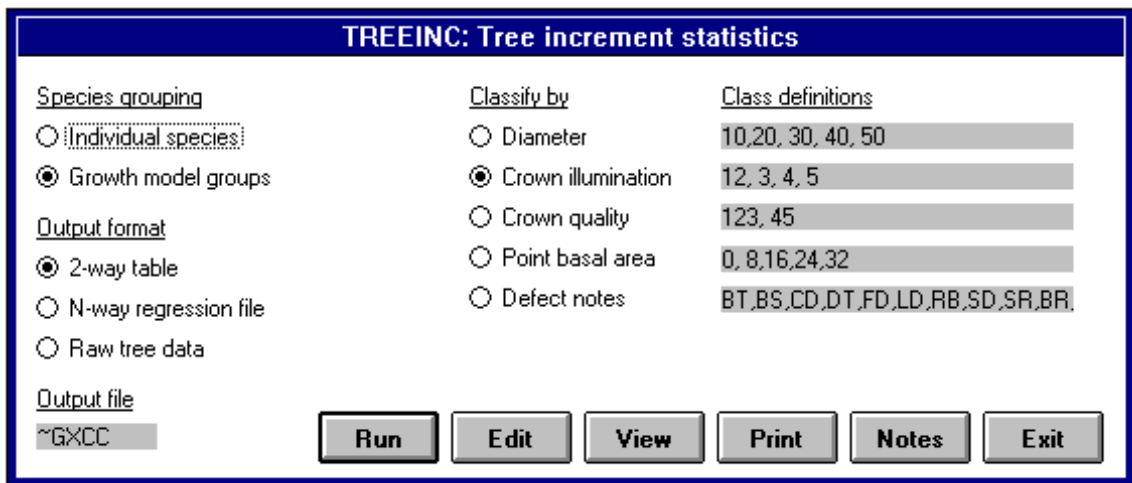


Figure 1 Options screen for TREEINC program

Three output formats can be selected:

- *2-way table*. This provides a printable report which summarises species or species groups classified by one of the selected factors under the Classify by list.
- *N-way regression file*. For each species or species groups, mean increment can be summarised for a combination of several of the factors in the Classify by list. This type of output can be viewed as a browse screen with the **Edit** button, but cannot be printed as a report. The main objective of this option is to provide a data file suitable for analysis of factors affecting increment using graphical methods, multiple regression or general linear modelling. When this option is selected, the Classify by list is changed to a series of check boxes, any combination of which can be selected to include the factor in the output. The list is also extended to include stratum code¹ as a possible factor for classification.
- *Raw tree data*. This allows individual tree increments to be output, together with a variety of other data for each tree that is useful. This includes tree diameter, crown diameter, crown point and total height, crown position and quality. These output files can be used for allometric studies such as height-diameter, or crown-tree diameter regressions, as well as increment studies. When this option is selected, the right-hand portion of the screen changes as shown in Figure 2. With this, the raw data output can be limited to a species group, a genus code, species code, or data may be output for all species. The latter will generate a large file (currently about 17,000 records).

¹Stratum code is determined by the STRATUM field in the file PSP_LIST.DBF, which should be found in the PERSYST directory.

Figure 2 Special options when extracting raw data with TREEINC

<u>Extract by</u>	<u>Group, genus or species code</u>
<input type="radio"/> Species group	ANI THU
<input type="radio"/> Genus code	
<input checked="" type="radio"/> Species code	
<input type="radio"/> All species	

For the *2-way* and *N-way* tables, the classes used are determined by the lists given under Class definitions (see Figure 1). The class definitions are constructed as follows:

- *Diameter and Point basal area*: The entries given are numeric values which determine the lower bound of each class.
- *Crown illumination and quality*: Each class is defined by a list of crown codes.
- *Defect notes*: There are always two classes, *defective* and *non-defective*, indicated by **True** or **False** in the output data files. The trees to be classified as defective are indicated by a list of codes. If a tree has any of these codes in the TCCODES field of the plot data file at the first measurement, it will be classed as defective.

It should be noted that for *2-way tables*, printed reports can only be produced if there are 5 or fewer classes. If more classes are defined, then the output file will be produced correctly, but it cannot be printed as a report. It must be exported to *Excel* or a similar program for formatting and presentation.

MORTAL mortality rate analysis

The MORTAL program operates in a very similar way to TREEINC, except that there is no concept of raw data output. For classes of diameter, crown position, crown quality, competing basal area or defective/non-defective, the annual mortality rate (AMR) for a species or species group can be produced as a *2-way* or *N-way* table.

RELIFT program for recruitment lists

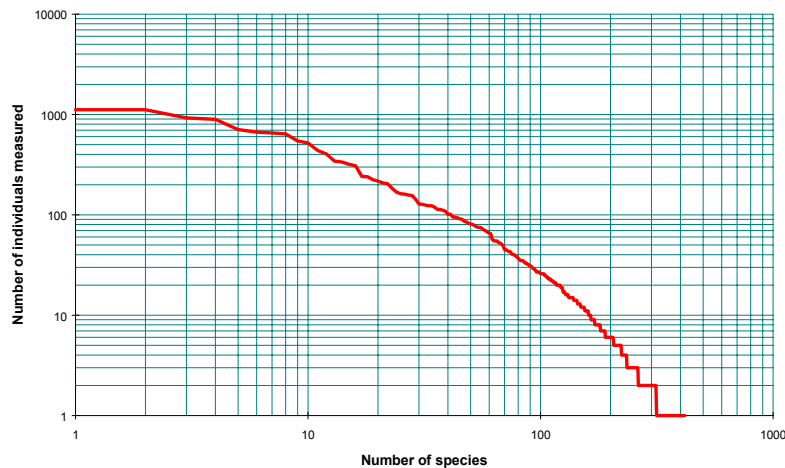
The RELIFT program summarises the trees which occur as recruits in a database table called ~RELIFT. For each plot, the species code, number of recruits per ha, and estimated diameter increment are calculated. The estimated diameter increment is the size of the recruit when observed, less 10 cm (the minimum diameter for measurement on the PSPs), divided by the measurement interval.

Species grouping for growth modelling

The need for species grouping

There are some 417¹ species and genera recognised on the 66 re-measured PSPs. Of these, as Figure 3 below shows, only some 40 species have 100 or more individuals sampled on the plots. Some 300 species have less than 30 individuals measured, and about 100 species are represented by only 1 or 2 trees each.

Figure 3 Sampling intensity for different numbers of species



Some grouping of the species is therefore necessary in order to estimate growth parameters and provide a manageable number of species groups for growth modelling. The purpose of such grouping is to bring together sufficient observations from species with similar growth habits to allow reasonable estimates of increment and mortality rates.

These groups, referred to as *growth model groups* do not replace commercial groupings, which are still required to summarize forest growing stock and yield for planning purposes.

A robust method for forming groups

The method adopted here is one which the author has refined for several growth models in Latin America (eg. Alder, 1995). A 2-dimensional ordination is made of mean increment against typical species size for mature trees. Typical size is indicated by the 90% point on the cumulative diameter distribution where there are 10 or more observations, or by the largest diameter for a species with fewer than 10 trees. The essential logic is the correlation that necessarily exists between typical size and mortality rate for a species. Hence this ordination gives an orthogonal presentation of the two main components of net growth for a species.

¹Many trees are identified only down to the generic level. A more precise botanical classification would considerably increase the number of species encountered.

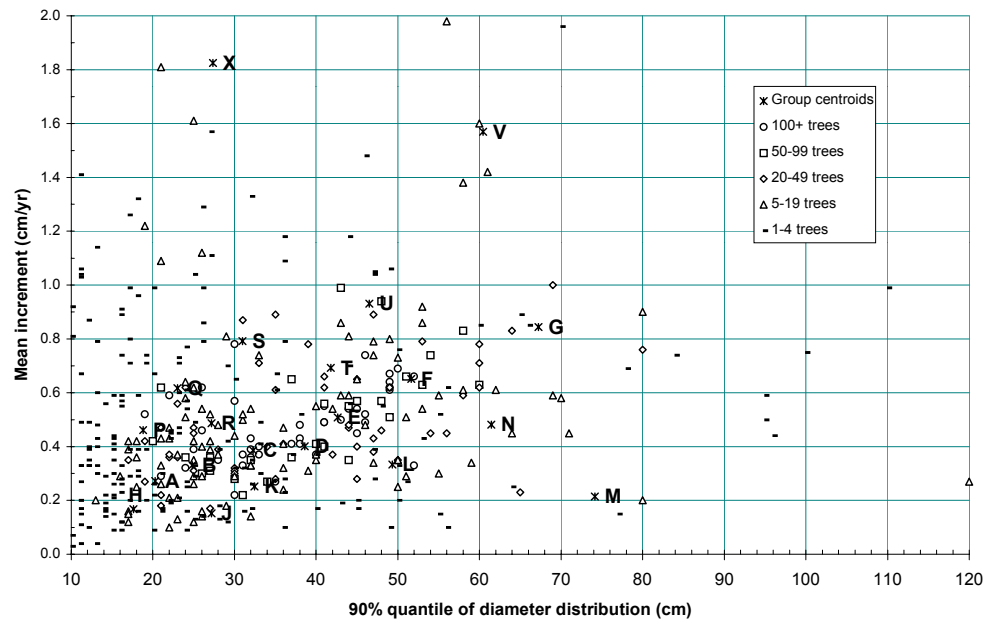


Figure 4 Data used to group species into growth models

The SPPORD program (see page 5) produces a data file which contains the mean increment and 90% diameter for each species. The results of plotting these two statistics against each other is shown in Figure 4.

The formation of groups is a semi-manual process¹. Group centroids are placed on the graph and moved to convenient locations near to common species that cover the range of variation. This is done with an Excel workbook (SPPORD.XLS), which allows the centroids to be moved using the mouse.

A Visual Basic macro² is then executed which calculates the groups nearest to the centroid in a logarithmic ordination space. When all species have been considered, revised centroid values are written onto a worksheet. These can be used to replace the original values, and the process repeated two or three times until the centroids do not change.

Group characteristics and species

The final groupings are shown in Figure 5. There are 21 models, each designated by an alphabetic letter A-X (I,O and W are not used). The models A-G represent the *main series* of species, corresponding to 78% of the data and 36% of the species. The *slow growing* series H-M comprise 8% of the data, although 26% of species, whilst the fast growing species constitute 12% of the data, and 38% of species. The fast growing series includes many typical

¹Use of automatic clustering via *k-means* within packages such as SYSTAT or STATISTICA does not give good results, in author's experience, as these packages do not properly allow for the weighting of points.

²The macro *MakeGroups* will be found on sheet *Macros* of the workbook SPPORD.XLS.

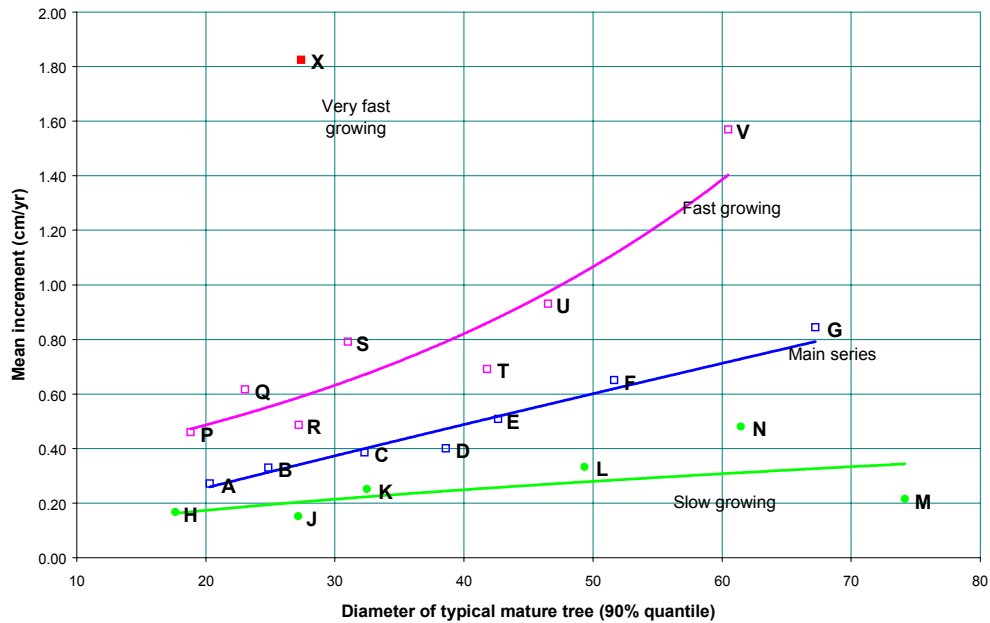


Figure 5 Mean increment and typical size of growth model groups

pioneer and ephemeral trees, whilst the larger slow growing species tend to be shade tolerant, with dense, heavy timber.

Table 1 lists the typical diameter, mean increment, and typical species for each model group. The principal species, shown in bold, is the commonest species in the group in each case. The remaining species are those which are also common within the group. The 90% diameter and mean increment in each case is a weighted mean for the group. The total number of species within each group is shown. It will be seen that the smallest diameter groups (A, H, and P) comprise the largest number of species (107 species). Many of these are represented by one or a few observations.

Use of growth models in data summaries

The model codes are copied back from the SPPORD workbook into the main species list file SPECLIST, where they are stored in the field called MODEL. This field is accessed by the various summarization programs in the ANALYSIS package, as has been discussed. It is relatively simple to update or amend the groupings as new data is received.

Table 1 Growth model group characteristics and typical species

Growth model	Diam <90%	Mean Dinc	No. trees	No. spp.	Principal species	Other common species
A	20.3	0.27	338	29	Timonius	<i>Mammea, Cleistanthus</i>
B	24.8	0.33	1899	22	Myristica	<i>Polyalthia, Medusanthera, Pouteria luzonensis</i>
C	32.3	0.39	2784	20	Horsfieldia	<i>Garcinia, Aglaia, Barringtonia, Chisochiton</i>
D	38.6	0.40	3509	16	Syzygium	<i>Canarium, Planchonella, Dysoxylum</i>
E	42.7	0.51	3778	27	Cryptocarya	<i>Pimeleodendron, Ficus, Calophyllum, Litsea, Celtis</i>
F	51.6	0.65	2091	23	Pometia pinnata	<i>Terminalia, Dillenia, Euodia, Homalium, Sloanea, Intsia</i>
G	67.2	0.84	219	13	Nothofagus	<i>Spondias, Camptosperma, Vitex</i>
H	17.6	0.17	139	35	Zygodynum	<i>Aralia, Ryparosa, Fagraea, Psychotria</i>
J	27.2	0.15	133	21	Cnesmocarpon	<i>Mallotus, Oreocallis</i>
K	32.5	0.25	775	16	Maniltoa	<i>Diospyros, Kibara, Carallia, Parastemon</i>
L	49.3	0.33	325	17	Vatica rassak	<i>Ilex, Gmelina, Schizomeria</i>
M	74.2	0.21	46	8	Alstonia	<i>Decussocarpus</i>
N	61.5	0.48	119	11	Teijsmanniodendron	<i>Neonauclea, Pterygota</i>
P	18.8	0.46	354	43	Gnetum gnemon	<i>Dendrocnide, Melanolepsis</i>
Q	23.0	0.62	576	29	Macaranga	<i>Ziziphus</i>
R	27.2	0.49	596	18	Microcos	<i>Prunus</i>
S	31.0	0.79	218	15	Elaeocarpus	<i>Alphitonia, Neubergia, Duabanga</i>
T	41.8	0.69	412	12	Anisoptera thurifera	<i>Cerbera, Galbulimima, Cananga</i>
U	46.5	0.93	238	15	Anthocephalus	<i>Artocarpus, Tristiropsis</i>
V	60.5	1.57	41	7	Hernandia	<i>Albizia, Ailanthus, Octomeles</i>
X	27.4	1.82	86	20	Trichospermum	<i>Actinodaphne, Lithocarpus, Acacia mangium, Trema</i>

Species distribution and site variation

The ITTO plots are widely distributed throughout PNG, and considerable variation in site and species association can be expected. The SPABUN program was developed to explore species distributions between plots, and to provide files for various types of association and ordination analysis (see page 4).

Reciprocal sorting of species and plots

It was found that a conventional ordination or clustering using common species was difficult with available statistical packages. A simple algorithm was therefore written in Visual Basic to perform a reciprocal sorting of plots and species (Hall & Swaine, 1976). This brings together species that tend to occur on a similar range of plots, and plots which have a similar distribution of species. The analysis was carried out using an Excel workbook, SPABUN.XLS, which contains the following worksheets:

- **Database** This is a copy of the file ~SPABUN.DBF output by the FoxPro analysis program SPABUN. It is created using mode 1 described on page 4, which gives a list of the most common species for each plot.
- **Genera** This is a list of genera codes, obtained by stripping off the first three characters of the species code.
- **Program** This contains the Visual Basic macros used to produce the output matrix. This is discussed further below.
- **Matrix** This is the output, as shown in Figure 6 overleaf.

The Visual Basic programs consist of two main programs which can be executed from the Excel **Tools/Macro** menu, and two sub-routines, which should not be executed directly. The main programs are:

- **FormMatrix**. This should be executed first. It reads the data from the Database sheet and forms the initial matrix, which is then sorted via the *BiSort* and *RippleSort* subroutines.
- **CodeShade**. This shades the cells in the matrix according to their abundances for a clearer presentation. It can be run after the sorted matrix has been produced.

A constant called PMIN is set at the top of the program sheet. This gives the minimum number of plots on which a species must occur in order to be included in the matrix.

Figure 6 shows the results when the plots and species are sorted on a presence-absence basis. Relative abundance is not taken into account.

Three types of simplification have been imposed to reduce the number of species in the matrix to a manageable level for presentation and discussion purposes:

- Only genera are considered. This is also appropriate as many identifications are not made to the species level.
- Genera which do not occur on 3 or more plots are excluded.
- Only genera which fall into the top ten most abundant species list for some one plot are included.

In Figure 6, the density of shading indicates the relative abundance by basal area. *Black* squares have more than 10% of the plot as the designated genus. *Darker grey* squares have 5-10%, and *light grey* indicates 1-5%.

Species associations and gradients

It can be seen from the figure that certain genera are common throughout the range of plots, including *Syzygium*, *Myristica*, *Dysoxylum*, *Cryptocarya*, *Canarium*, and *Horsfieldia*¹.

Another group of common species is represented by *Terminalia*, *Pimeli dendron*, *Vitex*, *Celtis*, *Pometia* and *Ficus*. However, there is a recognisable gradient between the occurrence of these species and that of the first group, and they are distinctively absent from those plots on which *Syzygium* is most common.

Planchonella tends to occur more commonly on a restricted range where *Pometia* is absent or rare and *Syzygium* is common. *Hopea* and *Flindersia* are also dominant elements on some plots at this end of the gradient.

As can be expected, *Nothofagus* occurs predominantly on the highland plots. These plots tend to share the high levels of *Planchonella*, *Syzygium* and *Cryptocarya* with those lowland plots which are characterised by the absence of the *Pimeli dendron-Celtis-Pometia* complex.

Plots dominated by *Vatica* occur at the same end of the gradient as *Hopea* and *Planchonella*. *Anisoptera* dominated forest, on the other hand, tends towards the middle part of the principal gradient.

It is apparent that the right-hand end of the gradient in Figure 6 is more characteristic of plots in New Britain, New Ireland, Madang and Sepik. The extreme left-hand end are the Southern Highland plots, whilst the other mainland plots of Morobe, Oro and the low-

¹For the examples cited, the genus code in Figure 6 is the first three letters of the name. However, for *Pometia*, it is shown as PO. This is due to lack of space for the letter M in the column.

lands of Papua constitute the predominantly *Pometia* poor plots. This can be explored objectively by calculating a score for each plot based on the species ordination, and plotting province mean scores, but the consultant has not had time to do that as yet.

A principal observation from this analysis is that although there are many plots characterised by locally dominant species, there do not appear to be major discontinuities. Most common species are widely represented, and it is reasonable to treat all the plots as a single data set for analysing growth functions.

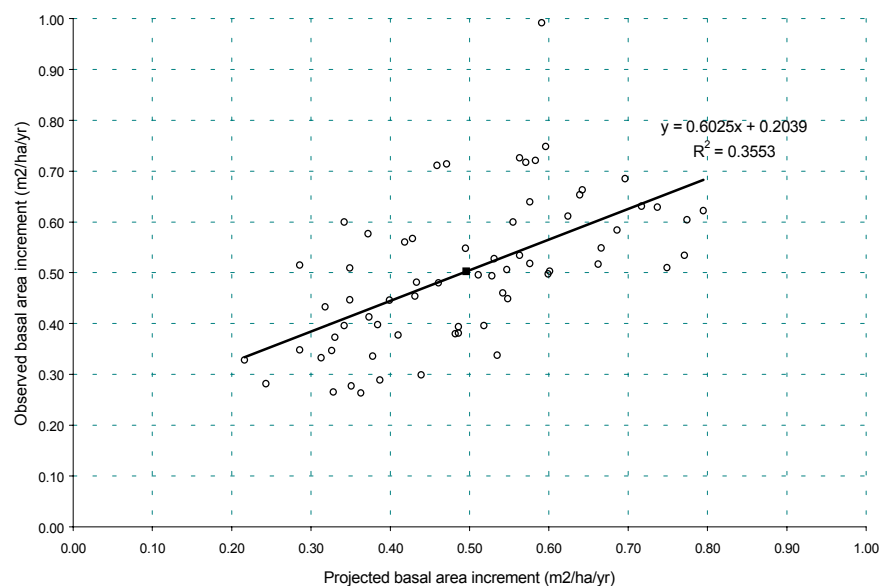
Species abundance as a factor in basal area increment

Table 1 provides mean increments for each species. By calculating the expected basal area increment of a plot using this mean increment and the number of trees of each species group on a plot, it is possible to see how much variation in increment is accounted for by the differences between species associations.

Figure 7 shows how the results can be presented. It plots the observed BAI (y axis) against the projected BAI (x axis). The latter is based on an estimate of increment using only the growth model mean increments in Table 1, without respect to tree size, crown position or any other factor.

For a linear regression, the plot of Y_{obs} on Y_{pred} has the same R^2 as the regression, a slope of 1 (unity), and an intercept of zero (0). These are mathematical identities. For this model, there is a slope of 0.603, indicating a lack of fit in the model which can be explained by some other factor. The model accounts for 36% of the variation in basal area increment.

Figure 7 Variation in basal area increment accounted for by species composition



In other words, simply considering mean increments of species and their abundances accounts for 36% of the variation in basal area increment between plots.

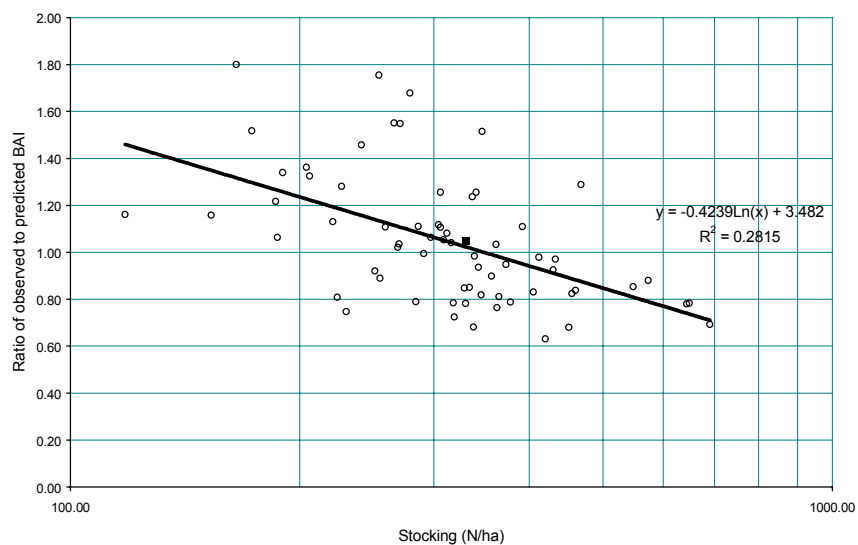
Stand density as an additional factor

Various tests were made to account for as much residual variation as possible from Figure 7. Models were examined which used crown position and crown quality to estimate increment of trees, or which related tree basal area increment to tree BA¹. It was found that these complex models did not usefully improve the results obtained. The best reduction in variation was achieved by fitting the ratio of observed to projected values from Figure 7 to the logarithm of stocking, as shown in Figure 8. Applying this ratio in combination with the mean increment model gave an R² between observed and predicted values of 45%, with negligible lack of fit.

A growth index for site variation

The ratio of observed to predicted values from this combined model were used to estimate a growth index by provinces. The mean ratio for each province was calculated, and then again used in a combined model which now accounted for mean increments by species, the effect of stocking on growth, and the effects of site at the province level. The resulting predictive model for basal area increment is shown in Figure 9. This accounts for 77% of the total variation in basal area increment, which is exceptionally high compared with models that the author has developed in the past, where an R² of 20% to 30% would be more typical. The complete system of equations may be defined symbolically in the three steps described below:

Figure 8 Residual stand increment explained by stocking



¹ This type of function is used in the CAFOGROM model described in Alder, 1995, page 168. The various test programs will be found in the ANALYSIS directory as programs MODLTST1, MODLTST2, etc.

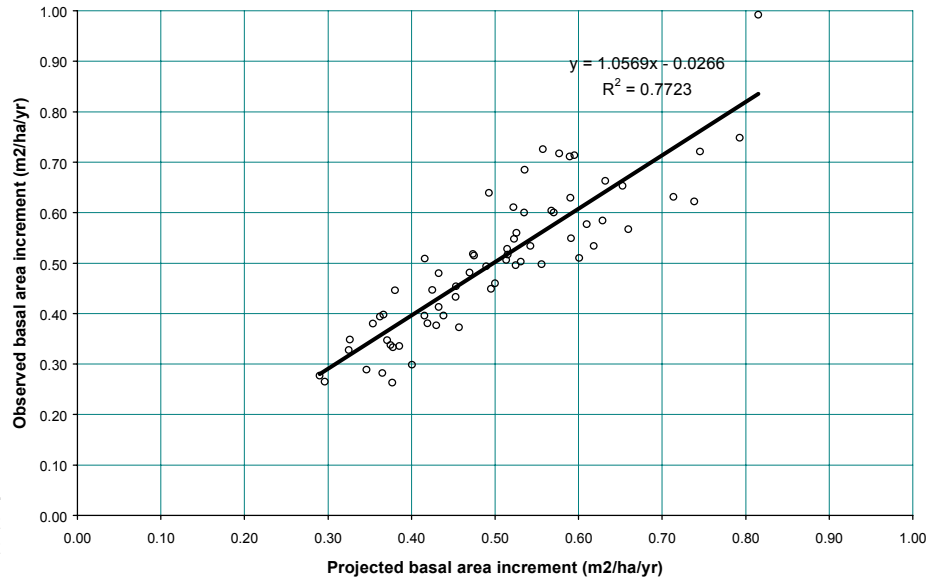


Figure 9 Combined species-stocking-site model for plot basal area increment

- Firstly, an estimate of basal area increment is derived using mean tree increments for species groups:

$$\Delta G_1 = 2.k \sum d_i . \Delta d_m \quad \{\text{eqn. 1}\}$$

where:

- ΔG_1 is the first estimate of basal area increment for the plot, in $\text{m}^2/\text{ha}/\text{yr}$.
- k is the constant 0.00007854.
- d_i is the diameter in cm of the i 'th tree on the plot.
- Δd_m is the mean diameter increment for species group m , being the species group of the i 'th tree.

- This first estimate of basal area increment is then adjusted for the effect of stocking with the equation:

$$\Delta G_2 = \Delta G_1 . [\alpha + \beta . \ln(N)] \quad \{\text{eqn. 2}\}$$

where:

- ΔG_2 is the second estimate of basal area increment, adjusted for stocking, in $\text{m}^2/\text{ha}/\text{yr}$.
- α, β are the regression coefficients 3.482 and -0.4239 respectively (see Figure 8).
- N is the stocking of the plot, in trees/ha.

- This second estimate is then adjusted further for site variation at the province level, to give the final estimate, with:

$$\Delta G_3 = \Delta G_2 . S_p \quad \{\text{eqn. 3}\}$$

where:

- ΔG_3 is the final estimate of basal area increment, adjusted for site, in $m^2/ha/yr$.
- S_p is the growth index for province p where the plot is located, taken from Table 2 below.

Figure 9 compares, on the x -axis, the predicted basal area increment ΔG_3 from the above system of equations with the measured basal area increment on the plots (y -axis). It shows that the overall R^2 of the predictive system is 77%. The slope and intercept are close to one and zero, respectively, and the equation is unbiased, passing through the observed mean increment of $0.5 m^2/ha/yr$.

Table 2 gives the growth index values, in the column labelled **Site**, for each stratum, as identified in the stratum field of the PSP_LIST table of the PSP database. These strata in fact correspond to provinces at the present time. However, it would be relatively easy to re-define the strata in future if key environmental variables that influence the growth index can be determined.

Table 2 Growth indices for different PSP strata

Province	Stratum	Site
East Sepik	SPKE	1.47
Gulf	GULF	1.26
Madang	MAD	1.26
New Ireland	NI	1.16
Central	CEN	1.13
Oro	ORO	1.03
East New Britain	ENB	1.00
Western	WEST	0.99
West Sepik	SPKW	0.92
Manus	MAN	0.90
West New Britain	WNB	0.90
Milne Bay	BAY	0.86
Southern Highlands	SH	0.83
Morobe	MOR	0.76

Further strategy for model development

General strategy The growth model based on the ITTO plots will be completed during the first quarter of 1998. The author has developed several models over the past three years which provide a basis in terms of experience and computer code for rapid completion of the work once the basic growth functions have been established. The following are the key features for the proposed model:

- It will be called PINFORM, as an acronym for **P**apua New Guinea/**I**TT**O** Natural **F**orest **M**odel.
- It will be written in Visual Basic for Excel. An existing model for Quintana Roo, Mexico, called MOSQIRO, will be adapted as the basis of the model (Alder, 1997b).
- PINFORM will be a stand model, able to project the characteristics of single stands over time, accept options for different felling and treatment regimes, different commercial groupings, and starting from a basis of conventional inventory data.
- Like its predecessor models, PINFORM will use a cohort modeling strategy, with growth functions for increment, mortality, recruitment and felling damage.

Diameter increment functions The equations described on page 17 provide a basis for diameter increment estimation that accommodates stand density and site effects, and is unbiased with respect to basal area calculation at the stand level. However, further testing of the completed version of PINFORM may show that this simple system of equations does not maintain a reasonable stand structure between diameter classes. In this case, some additional elaboration of the diameter increment model may be needed.

Mortality functions The programs required for the analysis of mortality have been completed, but at the moment about one-third of the plots require editing using XCHEK to insert the proper codes for dead trees. It is a common weakness of PSP procedures on many projects that insufficient attention is given to mortality identification and coding, and the same applies to the ITTO plots in PNG. However, the author anticipates that these questions will be resolved before his next visit in January 1998.

The final development of unbiased mortality functions will follow a similar logic to that for the increment models described on page 17. Mortality at the plot level will be explained by a combination of species mean rates, density and damage related effects.

Recruitment

Recruitment modelling requires first that aggregate levels of in-growth are determined that are as unbiased as possible and can be related to historical disturbances. Secondly, this total recruitment needs to be partitioned into a reasonable list of species that takes account of current stand composition, and the propensity for pioneers to come in after heavy disturbance.

Integrated testing The complete model will be tested at several levels:

- By short run tests with each PSP to ensure that the net growth of the stands is predicted as accurately as possible, considering the combined effects of increment, mortality and recruitment.
- By testing the model over long periods and under extreme treatments in order to ensure that its behaviour is reasonable, in the light of knowledge of tropical forest behaviour. It should for example, show a density limited maximum basal area of around 35 m²/ha. The Q-ratios of successive diameter classes should respect patterns normally observed, with a gradual reduction in Q-ratio over time to a stable state after disturbance. Maximum tree sizes should remain within the limits appropriate for the species. Heavy fellings should induce the normal successional processes between pioneer and shade tolerant species.

Application to forest management It is proposed to spend time as necessary at the Forest Authority headquarters in Port Moresby adapting PINFORM to the needs of forest management and providing training in its use. It is envisaged that the model could be used routinely for management planning, as is being done with the SIRENA model in Costa Rica (Alder, 1996, 1997c).

Conclusions

The various data analysis programs that are documented in this report provide information from the ITTO plots in a form suitable for growth model development. A number of Excel workbooks have been developed that use the output files from these programs for further statistical analysis and presentation. Two of these, SPPORD.XLS and SPABUN.XLS are discussed in some detail. Training has also been given to counterpart staff on the use of these programs.

The sample plot database has been extended and corrected since the consultant's previous visit in July 1997. Ten additional plots have been remeasured, bringing the total to 66, and about 40 plots have been checked and cleaned using the XCHEK program. Of particular importance in this respect is the insertion of codes to properly mark dead trees. Until this is completed, development of mortality functions will be delayed.

A method of species grouping to form consistent groups for growth modelling has been elaborated. There are 21 groups covering a range of combinations of mean increment and typical mature tree diameter. The latter is equated to the 90% point of the cumulative diameter distribution. The groups are represented by single letter codes from A-X¹. The data analysis programs allow detailed statistics on increment or mortality to be derived either for individual species or for species groups (see Figure 5, page 10). These growth model groups are intended to be used in conjunction with commercial groups, and do not replace them.

An analysis of species associations on the plots has been made. This shows that there is a principle gradient between plots which tend to have species such as *Planchonella*, *Hopea* and *Vatica* as co-dominant with *Syzygium*, at one end of the scale, to plots on which *Pimeliidendron*, *Celtis*, *Ficus*, and *Pometia* are common. However, there are no marked discontinuities, and species such as *Syzygium*, *Myristica*, *Dysoxylum*, *Cryptocarya*, *Canarium*, and *Horsfieldia* occur commonly throughout the range.

Site variation has also been analysed in terms of a growth index applicable at the province level. An increment function has been developed incorporating mean species increment, stocking on the plots (trees/ha), and growth index for the province. This function accounts for 77% of the observed variation in plot basal area increment on the plots.

¹ The letters I, O and W are not used in the present classification.

High growth indexes, about 25% above the mean, occur in East Sepik, Madang, and Gulf provinces. Lower productivity is seen West Sepik, Manus, West New Britain and Milne Bay. The lowest productivities (about 20% below average) occur in Morobe and the Southern Highlands (Table 2, page 18).

This increment model for species-site-density effects requires further testing for long term projections within the context of an integrated model. For short-term projections and as an indicator of productivity it appears to be unbiased and relatively accurate by the standards of natural forest modelling.

In the first quarter of 1998, the work on the model development will be completed, and efforts will be made to integrate it into the management planning process of the PNG Forest Authority. The further steps that remain involve the development of unbiased aggregate mortality and recruitment functions, and methods for their application at the tree level. These will parallel the increment function that has been developed to date. The integrated model will then be tested over a range of conditions to ensure that it is unbiased in the short run, and behaves in a reasonable and expected fashion for long-term projections.

Within the ITTO project unit at the Forest Research Institute, the priority is for the completion of error checking on the data, especially for dead trees and for recruits. Both of these latter can be confused with missing entries. Mortality in particular is sensitive to small levels of data error, and requires scrupulous examination of each instance where no explicit code for a dead tree has been given.

In the longer run, the data analysis programs that have been developed allow a large amount of new information to be extracted from the existing database. A start should be made on developing a series of research articles which can be published both locally, in the journal of the Forestry Association of PNG, *Klinkii*, and internationally in journals such as the Commonwealth Forestry Review.

Denis Alder
Lae, 4 December, 1997

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