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EXECUTIVE SUMMARY

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The 300 Index stand-level growth model has proved able to reliably predict radiata pine growth over a wide range of site types and silvicultural regimes. However in many circumstances, distance-independent individual tree growth models are preferred over stand-level models. These models have the advantage of retaining measurement information of individual trees allowing for more accurate estimation of log products. This report describes a distance-independent individual tree growth model which is compatible with the 300 Index stand-level model. The model relates relative growth rate of an individual tree (i.e., the growth rate of the tree divided by the mean growth rate) to relative size of the tree (i.e., the size of the individual tree divided by the mean size). Absolute growth rate of the mean tree is driven by the stand-level 300 Index model. The model has been developed using radiata pine growth data covering a wide range of stockings and site types. Relative individual tree basal area growth rate is shown to be a linear function of relative individual tree basal area, with the slope of the relationship increasing with stand basal area. A similar but weaker relationship is shown to exist for individual tree height. A method of predicting the surviving trees per hectare represented by each tree in the list while retaining compatibility with the 300 Index mortality function, is also described. The individual-tree model based on these relationships is shown to perform very well against the model dataset and against independent data, proving that the approach is conceptually sound. Further development of the model is underway, and will include the facility to thin or prune individual trees in the list. A tested and validated version of the model will be available by mid-2008.

INTRODUCTION

Growth and yield models are important components in long term planning of forest inventory. By improving the performance of growth models, quantitative estimates of future forest resources can be made more precisely. Models are used for a number of purposes including regime evaluation, silvicultural scheduling, harvest planning, forest valuation, log stumpage sales, and in general for both long-term and short-term decision making.

Stand-level growth models are widely used in New Zealand for evaluating regimes, for silvicultural scheduling, and for making long-term yield predictions. There are various models available for radiata pine in systems such as STANDPAK, the Radiata Pine Calculator, YTGEN, and FORECASTER. The 300 Index growth model (Kimberley et al., 2005) is the latest stand-level model, and validation has confirmed it to perform well at a national level and shown that it reliably predicts growth for different silvicultural regimes, including the influence of stocking, pruning and thinning (Kimberley & Knowles, 2005; Kimberley & Dean, 2006).

The 300 Index Model has various advantages over previous generations of models used for radiata pine in New Zealand. In particular, the discontinuity between ‘earlier’ and ‘later’ growth models associated with many current growth modelling systems is removed. The model also introduces the concept that productivity indices of both MAI volume (300 Index) and top height at a reference age (Site Index) are required. It also largely avoids the complexity associated with the use of regional models, although the most recent version of the 300 Index Model does recognise that minor regional differences in growth patterns can exist, and introduces regional parameters to account for them.

Another common use of growth models is to use data from forest inventories for projecting future yield to assist with short-term and medium-term planning. Generally, this requires the prediction of yields for different log types or products. However, stand-level models such as the 300 Index model can only predict a limited number of stand-level attributes, such as total stem volume, stocking, basal area (*BA*), and mean top height (*MTH*). To use these models for detailed prediction of log products, generalised tree size distribution functions are used. These are derived from the stand-level variables rather than being generated directly from the inventory data. Inventory projection using stand-level models therefore results in considerable underutilisation of the information contained in the inventory.

Therefore, for inventory projection, distance-independent individual tree growth models are generally preferred over stand-level models. These models use a list of trees obtained from an inventory as the starting point for projecting future yield. The advantage of tree list projection is that information on the distribution of individual tree sizes is retained. Furthermore, quality attributes for each tree obtained in the inventory, such as measures of stem straightness and form, pruned height, branch size, and internode length can be carried through to the projected tree list. The detailed information on individual tree size and quality attributes in the projected tree list can then be used to accurately predict yields of different log types, hence providing better estimates of stand value. The need for such detailed information has led to the development of a series of distance-independent individual tree models for radiata pine by the Growth Modelling Cooperative (Gordon & Shula, 1999; Shula, 1997a; Shula, 1997b; Shula, 1997c; Lundgren & Gordon, 1997).

Although these individual tree models provide good short-term predictions, it is less certain that their long-term predictions are as reliable as those of stand-level models such as the 300 Index Model, particularly as site productivity is only predicted by Site Index. The 300 Index Model has proved to be very robust in its ability to predict the influence of site and stocking on overall yield over long-term prediction intervals, especially when they incorporate silvicultural operations. It seems a desirable goal, therefore, to combine this stand-level model robustness into an individual tree inventory projection framework.

A model incorporating individual tree projections integrated into a stand-level model for Douglas-fir in North America was developed by Goulding (1972). This report describes how this approach was used to develop an individual tree model for radiata pine which retains consistency with the 300 Index Model. This early version of the model is intended to demonstrate whether the modelling approach is conceptually sound. Ultimately, more complex forms of the model will be developed which are more sensitive to variations in stand-level conditions.

GENERAL FORM OF MODEL

The model described in this report uses as input a list of trees. For each tree in the list, there is a tree identifier, the number of trees per hectare represented by the tree, the diameter at breast height (*DBH*), and tree height. Height may be measured for all trees or for a sub-sample chosen to cover the *DBH* range. Additional data associated with each tree may include quality variables such as pruned height, stem form, branching, etc. In the model described in this report, these quality variables are not used in projecting the tree size data, but they are available to be used when assessing quality and value of the projected trees.

The individual tree model described in this report also requires standard 300 Index Model inputs. These are all stand-level variables and include age and stocking at the time of measurement. By combining the tree list data with stocking, the 300 Index stand-level variables, basal area (*BA*), and mean top height (*MTH*) can be calculated using standard methods. The 300 Index model also requires historic stocking, thinning and pruning history data. The model described in this report projects the tree list forward from the age of measurement to some future specified age. This early version of the model has deliberately been kept fairly simple, and no test of its ability to predict thinning or pruning operations is included in this report. The effects of earlier silviculture on tree size will be implicitly contained in the tree list itself, and in the stand-level predictions which the individual tree model is constrained to follow. Future versions of the model will include the facility to thin or prune trees in the list. This will be possible using the form of model described in this report but will require additional tree selection procedures. The current individual tree model is also not responsive to between-tree differences in crown length, fertilisation or tree breeding.

The mortality function in the 300 Index Model predicts mortality at the stand level, and the tree list model must provide some means of assigning this to the tree list. There are two approaches that could be used. In the stochastic modelling approach which was taken by Goulding (1972), trees in the list are selected to survive or not using a random number generator. Stochastic models have some advantages, especially in complex situations. Also, the variation between repeated runs can give some indication of prediction uncertainty. However, most users find it disconcerting when duplicate runs produce slightly different predictions, and this can cause practical difficulties. An alternative approach is to retain all trees in the list, but to predict a survival probability for each tree. These probabilities can be converted into the number of stems per hectare represented by each tree in the projected list, and can be used as weights when calculating stand means of log products. This latter method was adopted in this study.

The requirements of the model are therefore: to project forward to the specified age each individual tree *DBH* or *BA*; to project each tree height; and to calculate the number of stems per hectare represented by each tree in the list at the specified age. These projected heights, diameters, and stems/ha must be consistent with the stand-level *BA*, *MTH* and Stocking predicted by the 300 Index Model.

The form of the individual tree model adopted in this study is based on a Douglas-fir model developed by C. Goulding (1972). In this model it is assumed that during a given growth increment, the growth rate of an individual tree relative to the mean tree is related to the size of that tree relative to the mean tree size. This form of model is therefore concerned with relative growth rates. The absolute growth rate of the mean tree is driven by the stand-level model.

The structure of the model is as follows. It is assumed that growth is to be predicted over the time interval $\Delta T = T_2 - T_1$. The stand level model provides predictions of the change in stocking over the prediction interval ($\Delta N = N_2 - N_1$), the change in mean tree *BA* ($\Delta B = B_2 - B_1$), and the change in mean tree height ($\Delta H = H_2 - H_1$). If the *BA* of the i^{th} tree at the start of the interval is B_{1i} then the relative *BA* of this tree at the start of the interval is defined as:

[1] $RB_{1i} = B_{1i}/B_1$

Similarly, relative *BA* growth rate for the i^{th} tree is defined as:

[2] $\Delta RB_i = \Delta B_i/\Delta B$

In its most general form, the model assumes that the relative growth rate is related by some function to the relative initial size, and optionally to one or more stand-level parameters α_1, β_1,…, etc., i.e.,

[3] $\Delta RB_i = f(RB_{1i}, \alpha_1, \beta_1, \ldots)$

The stand-level parameters could include, e.g., stocking, age, mean *BA*, etc. The function $f()$ may be a simple linear function or a more complex nonlinear function. For example, the simplest form of the model is:

[4] $\Delta RB_i = (1 - b) + b \times RB_{1i}$

This model assumes that relative growth rate in *BA* is linearly related to relative *BA*, and that the relationship does not alter with any stand-level condition. Note that the intercept parameter for this model must equal $1 - b$ because, by definition relative *BA* and relative *BA* growth rate, both have a mean of one.

More complex versions of Model [4] may be used. For example, it may be more realistic to assume that the relationship between relative growth rate and relative size is nonlinear (e.g., by adding a quadratic term to [4]). More importantly, it is likely that relative growth rate is affected by stand-level conditions. One way of introducing additional stand-level information into the model is to make the slope parameter b a function of relevant stand-level variables.

Stand-level competition is one of the conditions likely to affect the relationship. It is well established, for example, that smaller trees become increasingly suppressed with increasing competition. This suggests that the slope parameter *b* should increase with competition. Therefore, some measure of stand-level competition is a good candidate for inclusion in the model. Such variables could include stand-level *BA*, or the Stand Density Index (*SDI*) developed for use in the 300 Index Mortality function (Kimberley, 2007b).

To apply the linear model (Equation [4]), it is necessary to obtain estimates for the coefficient *b* from the model dataset. The parameter *b* can be estimated by fitting a regression model to the relative *BA* and *BA* increments. However, for this approach to be successful, it is essential that all trees are correctly identified at each measurement, and that there are no measurement errors. It would be unwise to assume that this is always the case with Permanent Sample Plot (PSP) data. A more robust approach is to estimate *b* indirectly from the coefficients of variation (CVs) of the distributions. If the CVs of individual tree *BA* at the start and end of each measurement interval are CV_1 and CV_2 respectively, and their ratio is $R = CV_2/CV_1$, then it can be shown that:

[5] $$b = \left(R \times \overline{B}_2 - \overline{B}_1\right) / \left(\overline{B}_2 - \overline{B}_1\right)$$

where $\overline{B}_1$ and $\overline{B}_2$ are respectively the mean tree *BA* at the beginning and end of the interval. As will be shown later, the relationship between ΔRB_i and RB_{1i} was found to be linear for the model dataset, meaning that Model [4] was appropriate. Therefore the above robust estimation approach for estimating *b*, was used in this study. The CV ratios *R* were calculated for each stocking in each trial for each measurement increment and converted into estimates of *b* using Equation [5]. Regression models for predicting *b* from various stand-level variables were then tested.

The above model development for individual tree *BA* can just as readily be applied to individual tree height, although it is likely that the equation for predicting relative height growth will be less dependent on stand-level competition, because tree height is known to be far less influenced by competition than *BA*.

The other requirement for the model is to predict survival probability, P_i, for each tree in the list over the prediction interval. Survival probabilities must be consistent with the stand-level model predictions, i.e., effectively,

[6] $$\Sigma P_i = 1 - \Delta N / N_1$$

Within the bounds of this constraint, probabilities may be varied as functions of stand-level and or tree-level variables. The most likely candidates for variables that affect relative survival are those concerned with relative tree size, as it is known that smaller more suppressed trees have a lower survival probability than larger trees. Therefore, survival is likely to be a function of some measure of relative tree size such as:

[7] $$RS_i = D^2H_i / \text{mean}(D^2H).$$

MODEL DATASET

A series of 19 final crop stocking trials was selected from Scion's PSP system (Pilaar and Dunlop, 1990) to develop the individual tree equations (Table 1). The data was simplified into increments of approximately five years, meaning that only selected ages were required from each trial. Measurements corresponding approximately to ages 10, 15, 20, and 25 years were used. The Model Dataset consisted of a total of 19,180 measurements from 5,249 trees in 333 plots from the 19 trials across New Zealand. Data was checked, and obvious anomalies removed prior to analysis.

Table 1. Summary of stocking trials used as the Model Dataset.

Trial code	300 Index (m^3/ha/yr)	Site Index (m)	Stocking treatments	Ages used to develop model
AK 465/ 0	29.6	31.8	100, 200, 400	10, 15, 20, 25
AK 1025/ 1	23.3	28.0	50, 100, 200, 400	8, 14, 20, 24
AK 1025/ 2	21.8	24.5	50, 100, 200, 400, 600	10, 15, 19, 25
AK 1025/ 3	22.0	26.8	50, 100, 200, 400, 600	10, 16, 20, 26
AK 1056/ 0	16.2	26.2	100, 200, 400, 600	11, 15, 21, 27
CY 588/ 1	23.6	26.9	50, 100, 200, 400, 600	10, 14, 18, 26
CY 588/ 2	17.4	17.9	50, 100, 200, 400	11, 17, 21, 25
CY 588/ 3	26.0	24.6	50, 100, 200, 400	10, 16, 20, 26
CY 588/ 4	22.7	24.0	50, 100, 200, 400	9, 14, 20, 24
CY 597/ 0	13.6	21.4	100, 200, 400, 600	11, 15, 19, 24
NN 525/ 1	24.6	23.9	50, 100, 200, 400, 600	10, 15, 19, 25
NN 525/ 4	29.7	25.5	50, 100, 200, 400, 600	9, 14, 20, 24
NN 529/ 1	22.3	28.4	100, 200, 400, 600	11, 15, 19, 24
RO 382/ 1	31.9	30.1	50, 100, 200, 400	10, 15, 20, 25
RO 589/ 2	24.0	28.3	100, 200, 400	10, 15, 20, 25
RO 2067/ 1	33.7	36.8	50, 100, 200, 400, 600	10, 15, 19, 25
RO 2098/ 0	27.7	31.1	100, 200, 400, 600	11, 15, 19, 24
SD 474/0	23.6	22.6	100, 200, 400	10, 15, 20, 26
SD 680/ 1	21.4	15.9	50, 100, 200, 400	10, 15, 19, 25

MODEL COMPONENTS

Basal Area Model

Individual tree *BA* model equations were derived from the Model Dataset with the data simplified into increments of approximately five years. Individual tree *BA* and mean *BA* per plot were obtained for each selected measurement. For each increment, relative *BA* and relative *BA* growth were calculated for each tree. Stand-level parameters such as *BA*, *MTH*, stocking and *SDI* were also calculated for each plot measurement. When implemented, the model will not be invariant to step length and it was necessary to take account of this when fitting the model to the data. For example, because the data used to develop the model had step lengths of approximately five years, if the independent variables such relative *BA* and the stand-level parameters were calculated at the beginning of each increment, the model would only be correct if implemented with a step length of five years. However, as the model will be implemented with a very short step length of less than one month, the appropriate procedure was to calculate these variables at the midpoint of each increment (i.e., using the mean of the start and end of the interval).

Relative *BA* growth was plotted against relative *BA* for data pooled across all trials and split into several classes on the basis of stand *BA*. The relationship was generally close to linear (e.g., Fig. 1). A minor exception to the linear relationship was that at high levels of competition, some smaller suppressed trees showed negligible *BA* growth forming a small 'tail' at the base of the relationship (Fig. 2). The linearity of the relationship is illustrated in Fig. 3 which shows that cubic spline functions fitted to each class are close to straight lines. Fig. 3 also shows that the slope parameter *b* increases with competition. As the *BA* increases in a stand, the slope becomes steeper implying that the spread of the *BA* distribution increases.

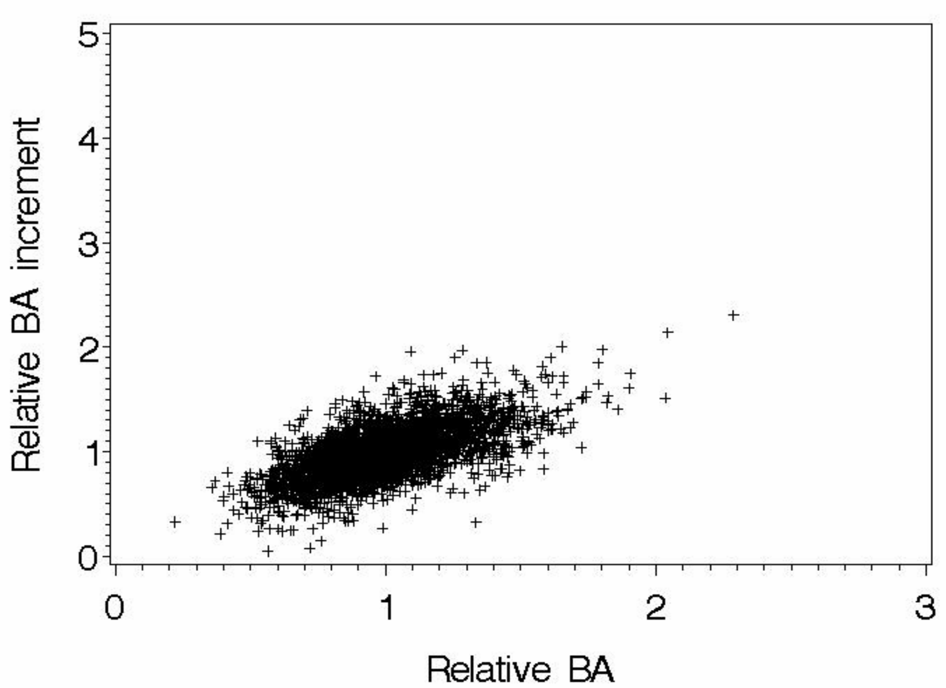

Fig. 1. Relative *BA* growth versus relative *BA* for data pooled across all trials for stand BA less than 13.6 m^2/ha.

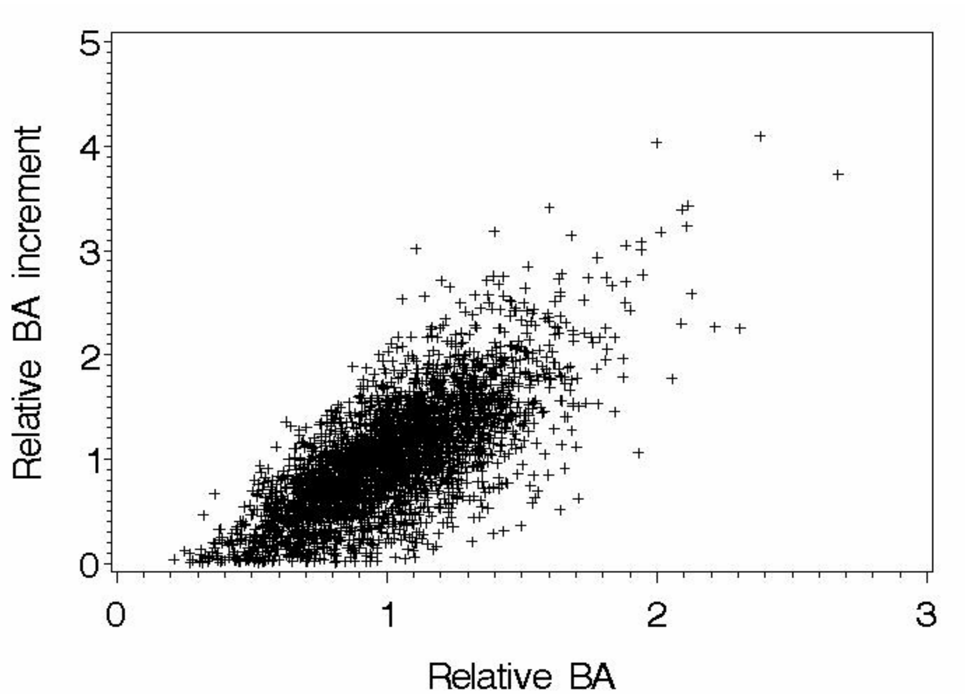

Fig. 2. Relative *BA* growth versus relative *BA* for data pooled across all trials for stand BA greater than 36.5 m^2/ha.

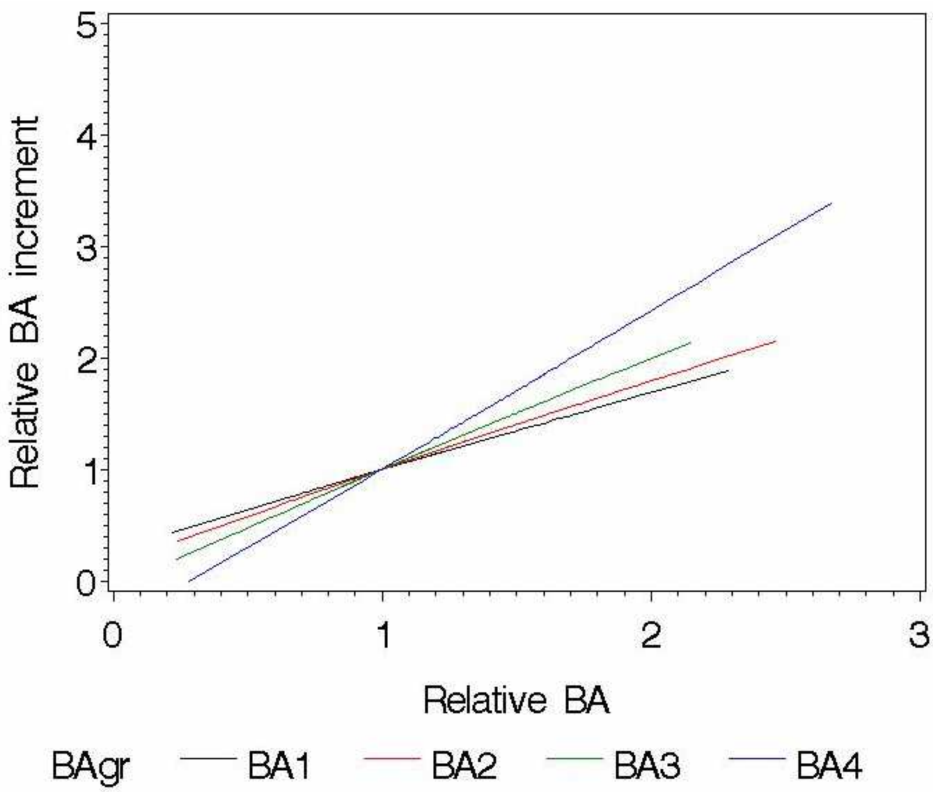

Fig. 3. Relative *BA* growth versus relative *BA* for data pooled across all trials and split into the following four BA classes: <13.6, 13.6-23.2, 23.2-36.5, >36.5 m^2/ha. For each class, a smoothing cubic spline function has been fitted to illustrate the general relationship.

Equation [5] was used to estimate *b* for each measurement increment and various stand parameters were tested for predicting *b*. Stand *BA* was found to perform better than any other parameter including *SDI*, age, stocking and *MTH*. Once *BA* was included in the model, neither stocking nor *MTH* gave any further improvement in fit. Although adding age to the model gave a small but significant improvement in model fit, for this first generation version of the model, it was decided for simplicity to use a function of *BA* only. During future development of the model using broader model datasets it will be determined whether more complex multi-variable equations give improved performance. The relationship between *b* and *BA* was found to be linear:

$$[8] \quad b = 0.7116 + 0.01524 \times BA$$

where *BA* is the stand basal area in m^2/ha. The model for predicting relative *BA* increment is therefore given by Equation [4] with *b* calculated using Equation [8].

Height Model

Because of the cost and difficulty of obtaining accurate tree height measurements, often only a sub-sample is measured for height. Therefore, when the tree list model is used in practice, a method of estimating missing tree heights is required, and will in fact be the first step in processing the data. In the test version of the model developed in this study, the procedure of Deadman and Goulding (1979) was used. This involves fitting a linear regression model to the trees measured for height and diameter using a linearised form of the standard height/diameter model used in New Zealand, i.e.,

[9] $(H - 1.4)^{-2.5} = a + b / DBH$

Heights are estimated using this function for the unmeasured trees. However, although this is a practical solution to estimating missing height data and in most case will give acceptable results, it will distort the distribution of heights in the projected tree list. For example, the variance of heights obtained in this manner will generally be less than the true variance. Because of this, only measured trees were used when developing and testing the height model equations in this study.

The slope parameter b for relative height growth showed much less response to competition than did relative BA. However, there was a small but significant increase in b with increasing BA as shown by the following linear function:

[11] $b = 0.4390 + 0.01226 \times BA$

Survival Probability Model
Trees were classified into groups based on relative tree size RS, and mean survival probability calculated for each group. Survival probability was lower in the smaller RS classes representing the smaller trees in a stand (Fig. 4). The following nonlinear regression function was fitted to this data:

[11] $P_i = 1 - 0.00539 \times RS_i^{-1.68}$

To apply this relationship to the tree list, the survival probabilities must be scaled so that the sum of the individual tree survivals agrees with the stand-level predicted mortality, i.e.,

[12] $P_i = (N_2 / N_1) \times (1 - RS_i^{-1.47}) / \Sigma (1 - RS_i^{-1.47})$

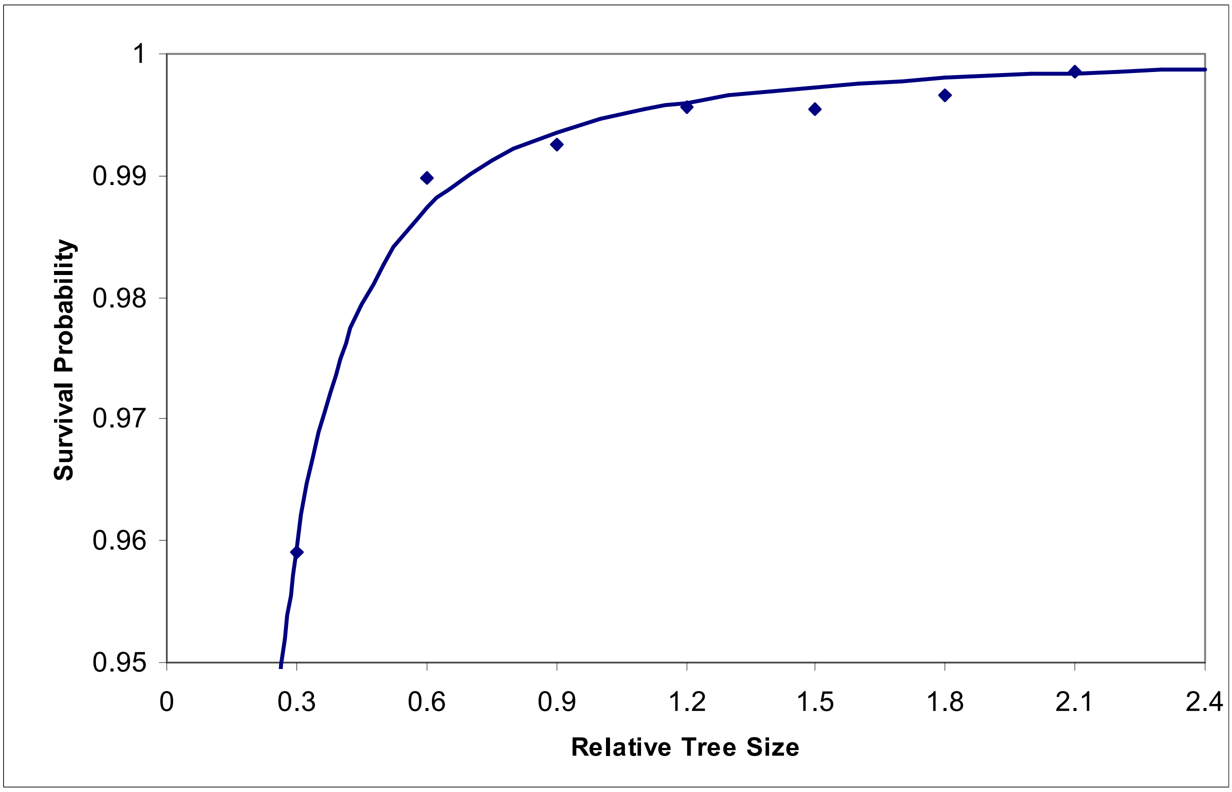

Fig. 4. Mean survival probability versus relative tree size with the fitted prediction Equation [11].

Conversion between individual tree and stand-level parameters

To maintain compatibility between the stand-level and individual tree model components, it is necessary to convert between the stand-level parameters (Stocking, *BA*, and *MTH*) and individual tree height and *DBH* values. For example, at the beginning of each model run, the starting values required by the stand-level model must be derived from the tree list. Secondly, during the prediction process, the individual tree heights and diameters must be scaled to agree with the stand level parameter predictions. Conversions to and from stand-level *BA* and Stocking and the individual tree *DBH* values are trivial. However, the stand-level National Height Model used in the 300 Index Modelling system predicts tree height using *MTH*, a measure of the height of the dominant trees in the stand, while the individual tree model predicts heights of individual trees. From the tree list, mean tree height can readily be obtained, but *MTH* is not immediately available. Therefore, a method of converting from mean height to *MTH* and vice versa is required. In the model described in this report, the following standard equations derived from PSP data are used, with *N* the stocking in stems/ha:

$$H_{mean} = MTH \times (1 - 0.07 \times (1 - \mathrm{Exp}(-0.00399 \times (N - 100))))$$

[13]

$$MTH = H_{mean} / (1 - 0.07 \times (1 - \mathrm{Exp}(-0.00399 * (N - 100)))))$$

Combined Model

Combining Equations [4], [8], [10], and [12] produces a model for relative growth and survival of individual radiata pine trees. Relative *BA* and height growth predicted by Equations [4], [8] and [10] are converted into actual growth using the 300 Index stand-level model. In practice, simple multiplication of relative growth rates by the predicted mean growth rates will lead to slight errors for two reasons. Firstly, because the slope parameter *b* can be greater than one under high levels of competition, Equation [4] can produce negative growth increments for small suppressed trees. Even though in practice suppressed trees can actually shrink slightly in the year or so before death, it seems preferable at this stage to reset any predicted negative increments to zero. Secondly, when calculating mean *BA* and height, they must be weighted using the survival probabilities P_i. Because of this, predicted *BA* growth is obtained by multiplying relative *BA* growth (from Equation [4]) by the ratio of the stand-level *BA* growth (predicted using the 300 Index Model) to the weighted mean relative *BA* growth. A similar process is used to scale the predicted heights.

This model has been incorporated into a test version of the stand-level 300 Index Model using Visual Basic for Applications (VBA). This test version of the 300 Index Tree List Model can be run in batch mode against tree list data extracted from the Scion PSP system. Its performance is summarised in the following section.

PERFORMANCE OF THE MODEL

The performance of the model against the model dataset was tested by examining the distributions of actual diameters and heights and comparing them with predictions generated from measurements taken at earlier ages. Fig. 5 shows actual diameter distributions at age 25 years for three stockings in three trials, and compares them with distributions projected from age 15 year tree lists. All trees were pooled across replications for each stocking in each trial. In all three trials, the distributions of the projected diameters closely match those of actual diameters for all stockings. In Fig. 6, plots of actual and predicted height versus *DBH* at age 25 years are compared for the same data. There is a good match between actual and predicted *DBH*/height distributions.

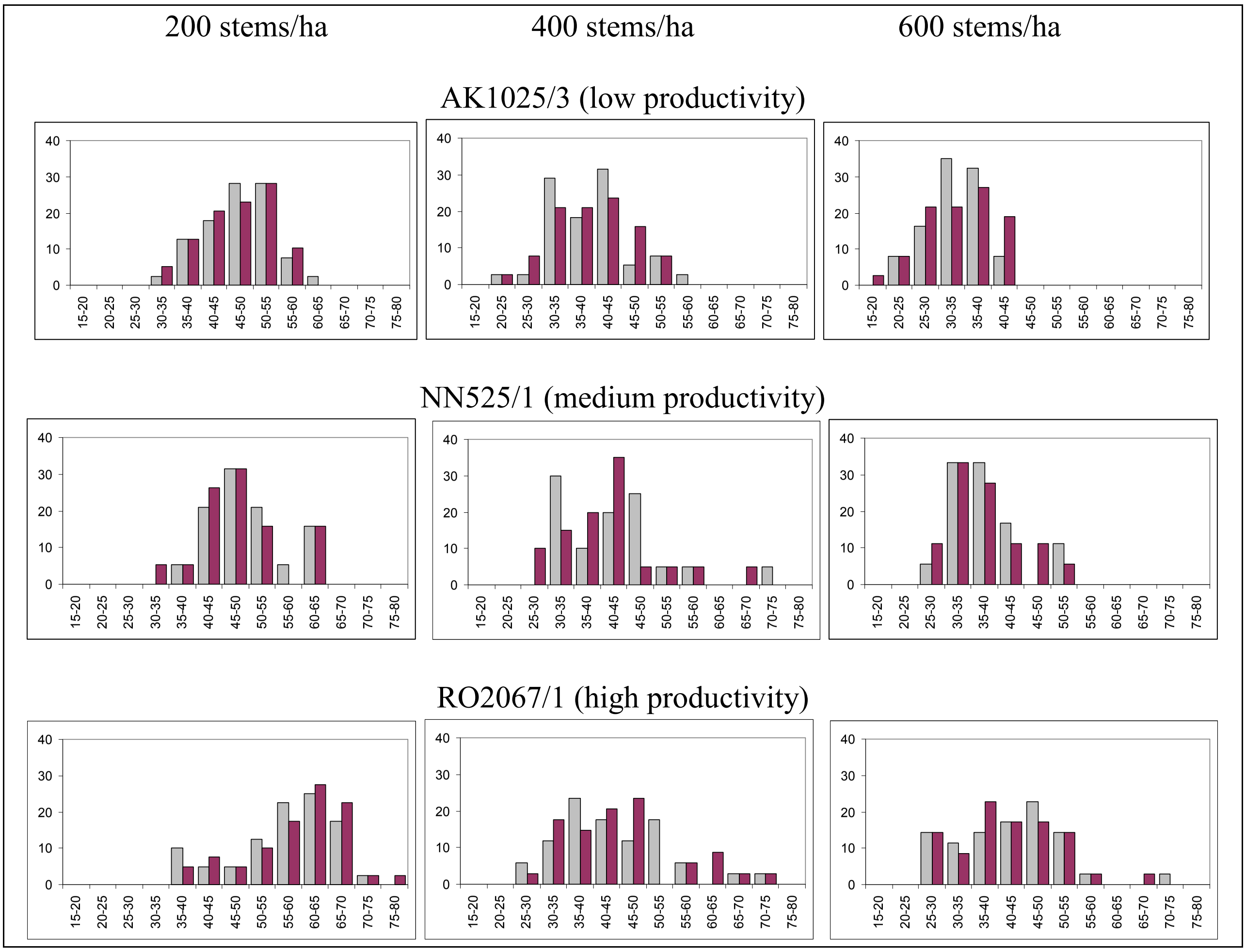

Fig. 5. Distributions of actual (light bars) and predicted (dark bars) *DBH* at age 25 years for 3 stockings (200, 400 and 600 stems/ha) in 3 trials. Predictions are projected from age 15 year measurements.

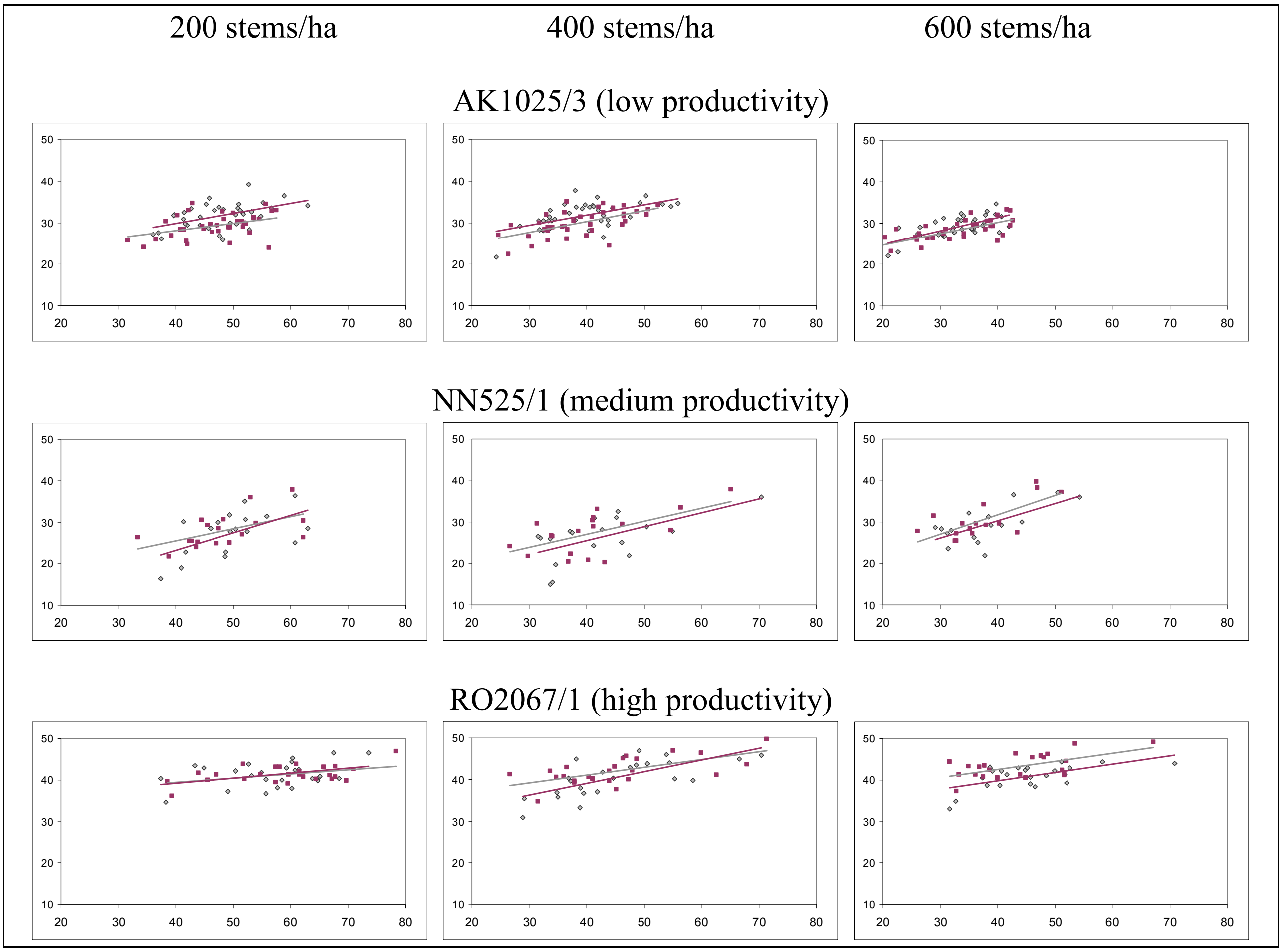

Fig. 6. Actual (light points) and predicted (dark points) height (vertical axis) versus *DBH* (horizontal axis) at age 25 years for 3 stockings (200, 400 and 600 stems/ha) in 3 trials. Predictions are projected from age 15 year measurements.

The interquartile range (i.e., the distance between the 25th and 75th percentile) was calculated for each stocking in each trial for *DBH* at ages 10, 15, 20 and 25 years, and for predicted *DBH* projected from earlier ages. This is summarised in Table 2 which shows the interquartile range averaged across all trials for each stocking, and across all stockings. Table 3 shows a similar analysis of the range between the 10th and 90th percentiles. Both tables show close agreement between actual and predicted *DBH* ranges. The mean interquartile range at age 25 years across all stockings and trials is 9.3 cm, which compares well with predictions from age 10, 15 and 20 years of 9.2, 9.3, and 9.1 cm. Similarly, the mean range between the 10th and 90th percentiles at age 25 years of 18.1 cm compares well with the predictions from age 10, 15 and 20 years of 17.3, 18.3, and 17.9 cm. These tables show subtle trends in the way the *DBH* range responds to stocking. At age 15 years, the range in actual *DBH* is lowest at 400 stems/ha, and is higher at both lower and higher stockings. By age 25 years, inter-tree competition has caused the range to be greatest at the highest stocking, and lowest at the lowest stocking. These trends are reflected in the *DBH* predictions.

Table 2. Interquartile range (cm) of actual and predicted *DBH* distributions averaged across trials for each stocking and overall. Interquartlile ranges are given at ages 15, 20 and 25 years, and predictions projecting from measurements at ages 10, 15 and 20 years.

	Age 15		Age 20			Age 25			
Stocking	Act.	Pred. from age 10	Act.	Pred. from age 10	Pred. from age 15	Act.	Pred. from age 10	Pred. from age 15	Pred. from age 20
50	6.5	5.5	7.2	6.6	7.9	8.2	7.7	9.1	8.3
100	5.9	5.5	7.2	6.9	7.6	8.8	8.3	9.2	8.7
200	5.8	5.5	6.9	7.1	7.5	9.1	8.9	9.5	8.7
400	5.4	6.1	7.7	8.2	7.2	10.2	10.3	9.1	9.8
600	6.3	7.1	8.0	9.1	7.9	10.4	11.4	9.9	10.0
Overall	5.9	5.8	7.3	7.5	7.6	9.3	9.2	9.3	9.1

Table 3. Range from the 10th to 90th percentile (cm) of actual and predicted *DBH* distributions averaged across trials for each stocking and overall. Ranges are given at ages 15, 20 and 25 years, and predictions projecting from measurements at ages 10, 15 and 20 years.

	Age 15		Age 20			Age 25			
Stocking	Act.	Pred. from age 10	Act.	Pred. from age 10	Pred. from age 15	Act.	Pred. from age 10	Pred. from age 15	Pred. from age 20
50	12.2	10.3	15.8	12.4	14.8	18.5	14.4	17.2	18.5
100	11.3	9.9	14.4	12.3	14.2	18.5	14.9	17.2	17.5
200	11.1	10.3	13.8	13.4	14.4	17.1	16.8	18.2	17.4
400	11.3	11.7	14.1	15.5	14.9	17.7	19.7	19.0	17.9
600	11.6	13.4	15.2	17.3	15.1	19.3	21.5	18.9	19.1
Overall	11.4	10.9	14.5	14.0	14.6	18.1	17.3	18.1	17.9

Tables 4 and 5 show the interquartile and 10th to 90th percentile ranges for actual and predicted heights. The mean interquartile ranges for predicted heights at age 25 years from measurements at age 10, 15 and 20 years are 3.4, 3.6, and 3.9 metres respectively, which compare well with the actual mean interquartile range of 3.5 metres. The model also correctly predicts a slight increase in height variation with increasing stocking.

Table 4. Interquartile range of actual and predicted height distributions averaged across trials for each stocking and overall. Interquartlile ranges are given at ages 15, 20 and 25 years, and predictions projecting from measurements at ages 10, 15 and 20 years.

	Age 15		Age 20			Age 25			
Stocking	Act.	Pred. from age 10	Act.	Pred. from age 10	Pred. from age 15	Act.	Pred. from age 10	Pred. from age 15	Pred. from age 20
50	2.2	2.1	2.9	2.4	2.6	3.5	2.7	2.9	3.3
100	2.6	2.3	3.1	2.8	3.0	3.3	3.2	3.5	3.7
200	2.4	2.1	3.3	2.5	2.9	3.4	3.0	3.4	4.0
400	2.4	2.4	3.1	3.0	3.0	3.7	3.7	3.7	3.8
600	2.7	3.2	4.0	4.0	3.6	4.2	5.0	4.5	5.1
Overall	2.5	2.4	3.2	2.9	3.0	3.5	3.4	3.6	3.9

Table 5. Range from the 10th to 90th percentile of actual and predicted height distributions averaged across trials for each stocking and overall. Ranges are given at ages 15, 20 and 25 years, and predictions projecting from measurements at ages 10, 15 and 20 years.

	Age 15		Age 20			Age 25			
Stocking	Act.	Pred. from age 10	Act.	Pred. from age 10	Pred. from age 15	Act.	Pred. from age 10	Pred. from age 15	Pred. from age 20
50	4.8	4.2	6.0	4.8	5.6	6.9	5.4	6.4	6.8
100	4.7	4.2	5.7	5.0	5.5	6.3	5.7	6.4	6.6
200	4.6	4.4	6.0	5.3	5.5	6.5	6.3	6.6	7.2
400	4.7	4.8	6.0	6.0	5.8	6.8	7.3	7.1	7.4
600	5.1	5.6	7.0	7.1	6.4	7.8	8.8	8.1	9.0
Overall	4.7	4.6	6.1	5.5	5.7	6.8	6.6	6.8	7.3

In Figs. 7-10, the 10th, 25th, 50th (median), 75th and 90th percentiles are shown for actual and predicted age 25 year *DBH* in each trial for various projection ages and stockings. The median *DBH* is generally predicted well especially for projection ages 15 and 20 years. Projections from age 10 years, mostly made immediately following thinning are somewhat less precise. The close agreement between actual and predicted median *DBH* confirms that the stand-level 300 Index Model performs well for these trials. The other percentiles also match well for actual and predicted *DBH* distributions. These Figures show that the model performs equally well on high and low productivity sites.

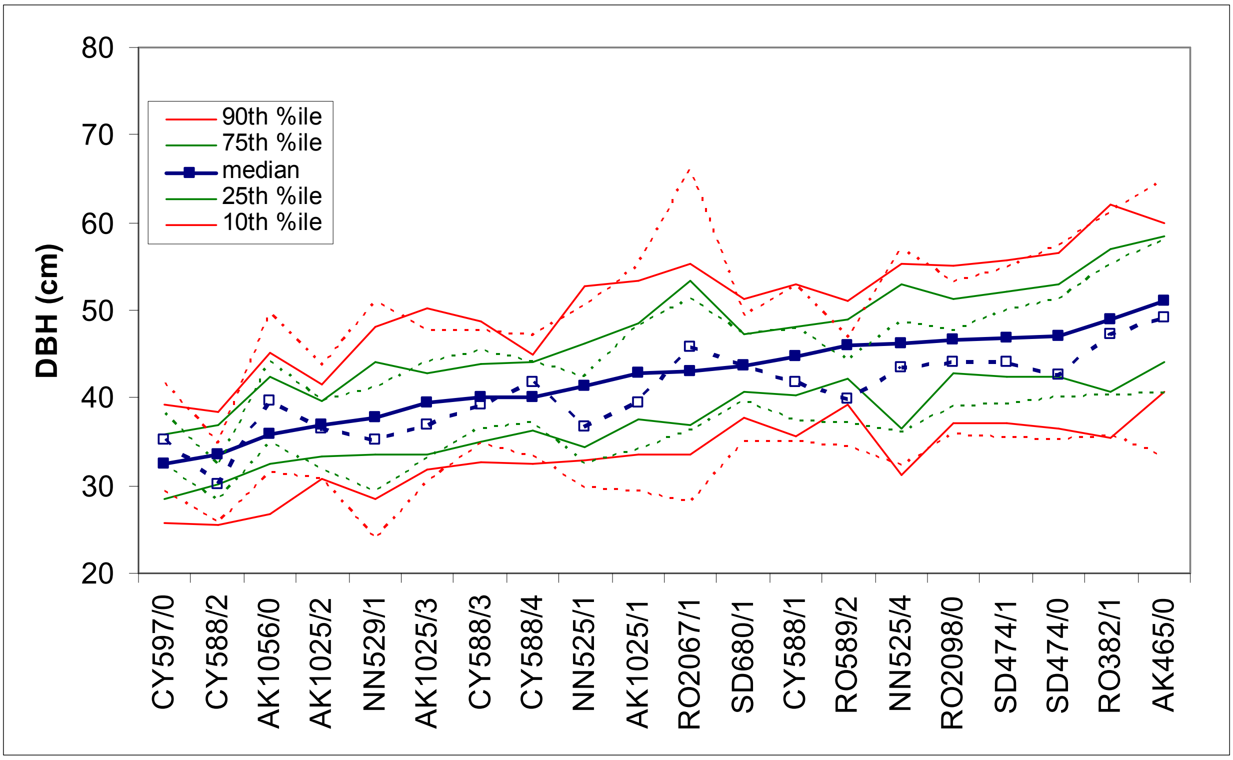

Fig. 7. Percentiles of distributions of actual (solid lines) and predicted (dashed lines) *DBH* at age 25 years for the 400 stems/ha treatment in each trial. Predictions are projections from age 10 year measurements. Trials are ordered in ascending productivity.

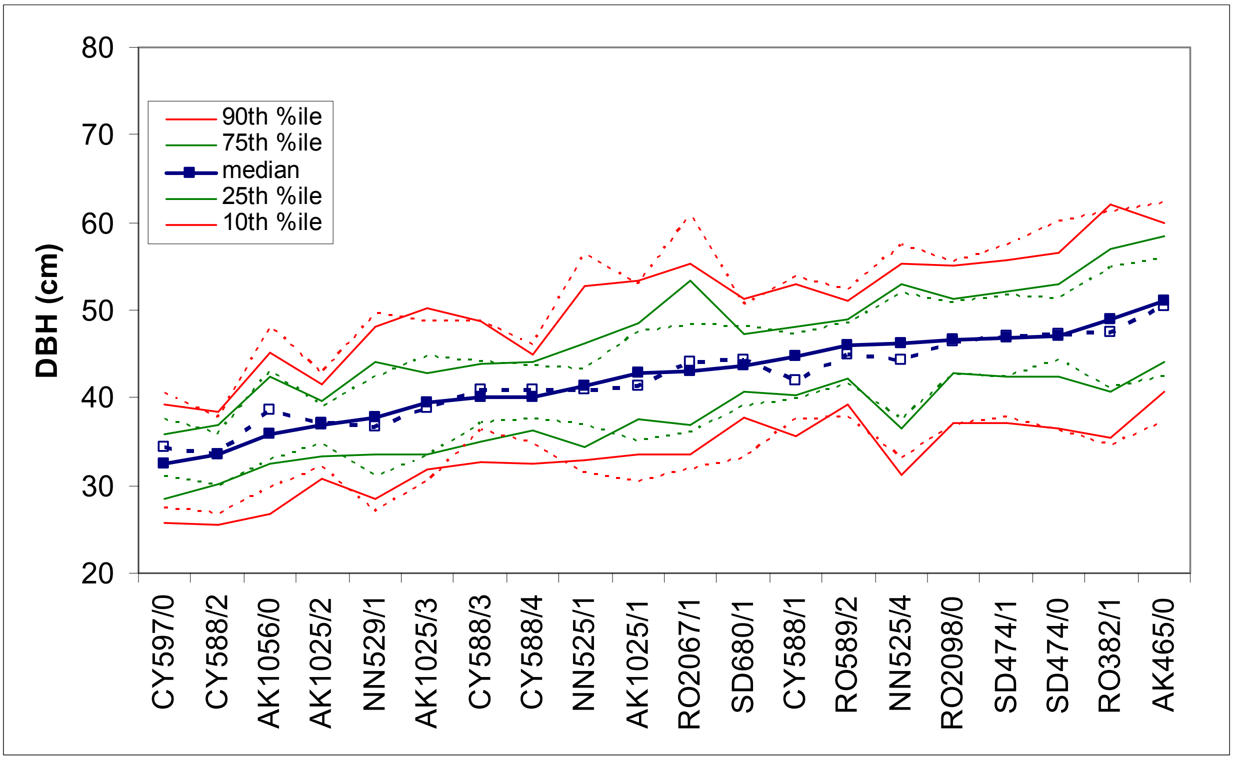

Fig. 8. Percentiles of distributions of actual (solid lines) and predicted (dashed lines) *DBH* at age 25 years for the 400 stems/ha treatment in each trial. Predictions are projections from age 15 year measurements. Trials are ordered in ascending productivity.

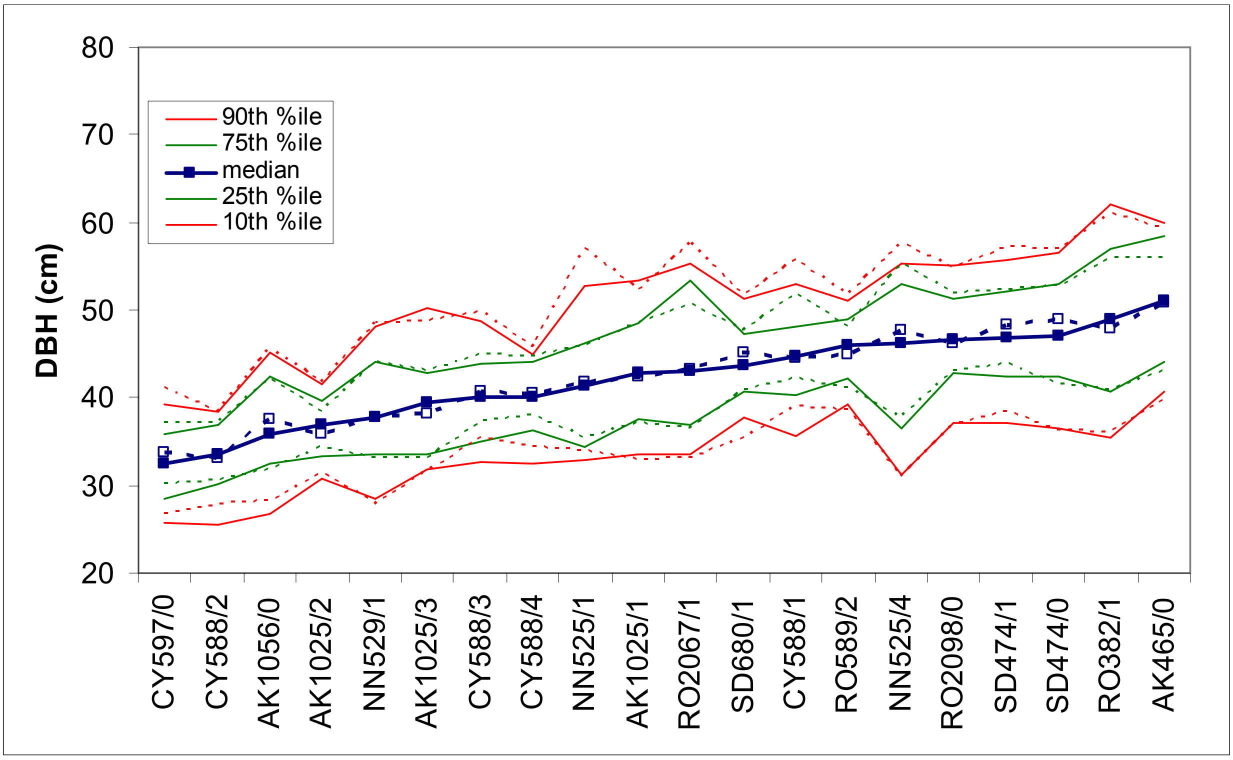

Fig. 9. Percentiles of distributions of actual (solid lines) and predicted (dashed lines) *DBH* at age 25 years for the 400 stems/ha treatment in each trial. Predictions are projections from age 20 year measurements. Trials are ordered in ascending productivity.

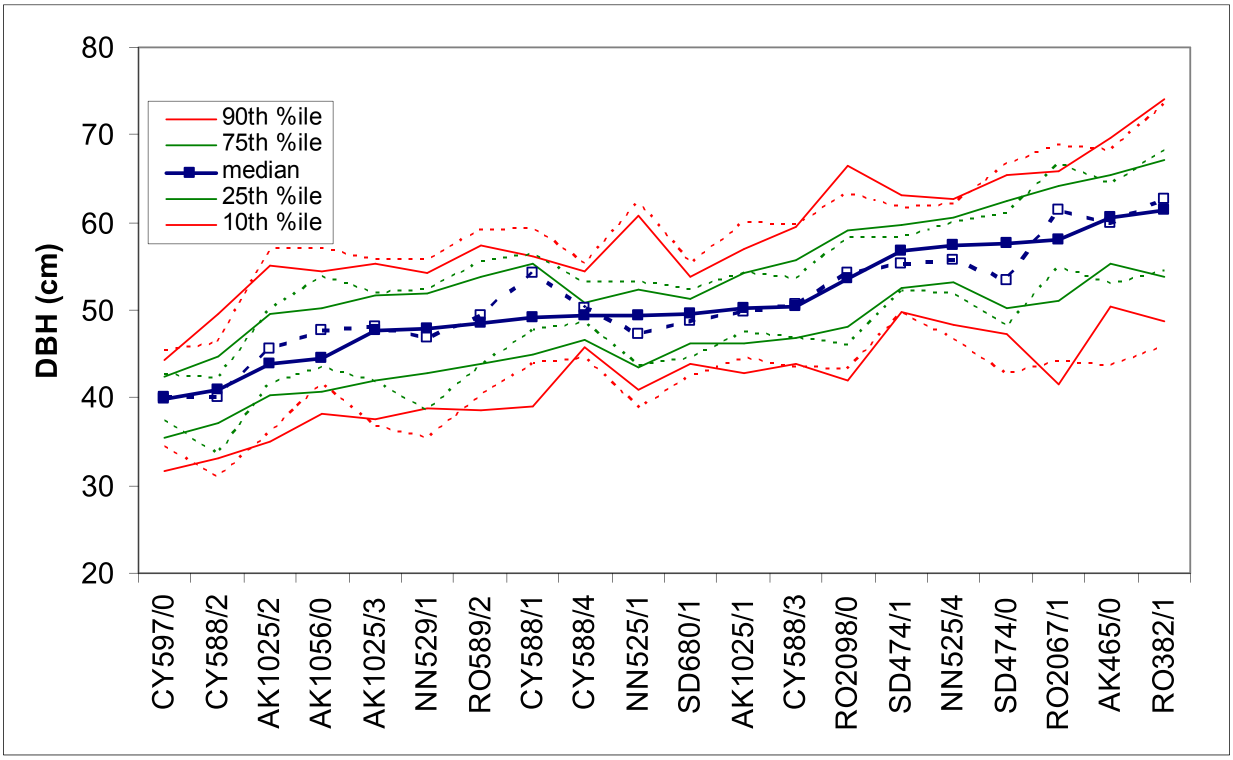

Fig. 10. Percentiles of distributions of actual (solid lines) and predicted (dashed lines) *DBH* at age 25 years for the 200 stems/ha treatment in each trial. Predictions are projections from age 15 year measurements. Trials are ordered in ascending productivity.

In Figs. 11-13, the 10th, 25th, 50th (median), 75th and 90th percentiles of the actual and predicted age 25 year height averaged across all stockings in each trial for various projection ages. These Figures show that the model performs equally well for both high and low site indices.

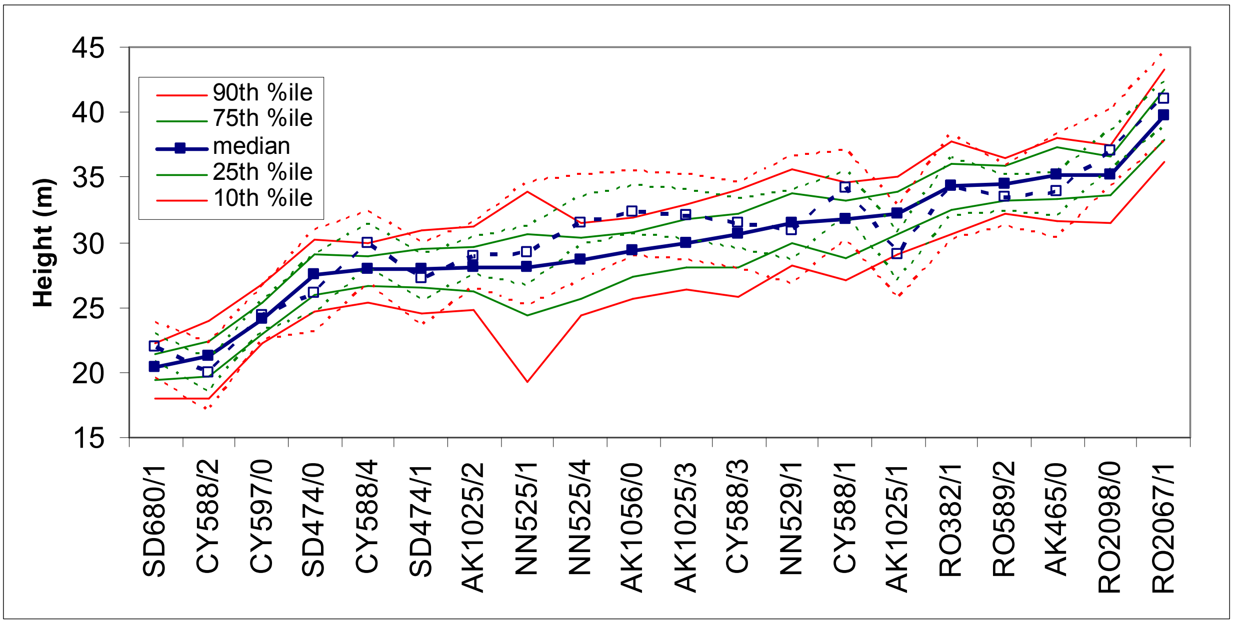

Fig. 11. Percentiles of distributions of actual (solid lines) and predicted (dashed lines) height at age 25 in each trial. Predictions are projections from age 10 year measurements. Trials are ordered in ascending productivity.

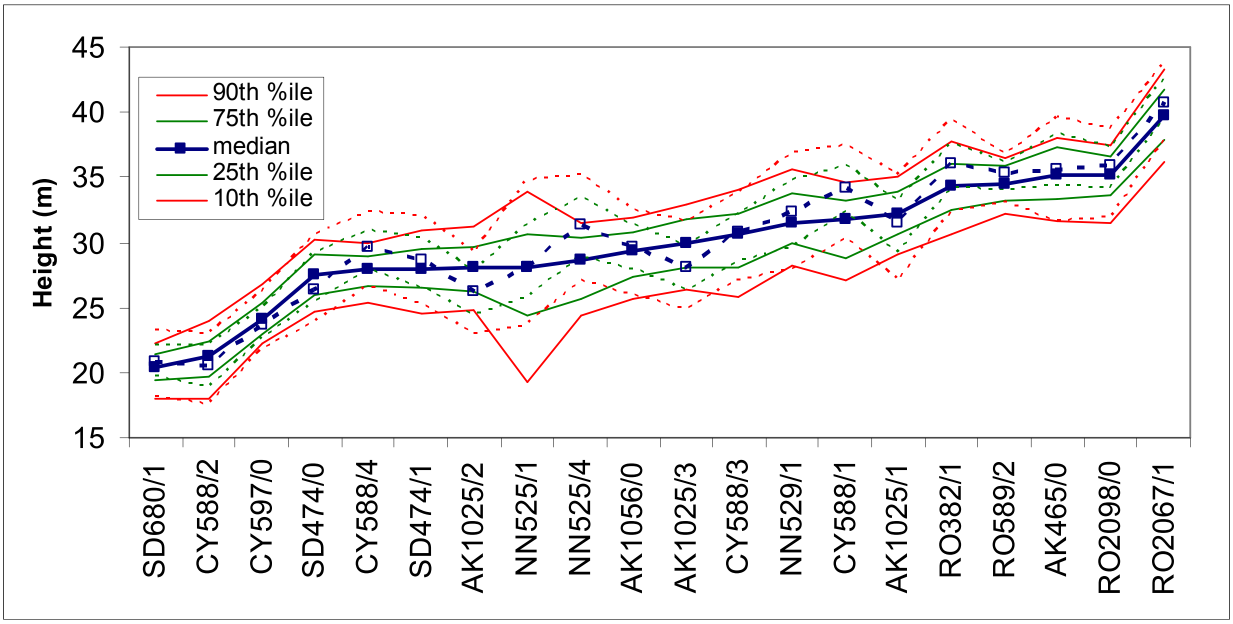

Fig. 12. Percentiles of distributions of actual (solid lines) and predicted (dashed lines) height at age 25 in each trial. Predictions are projections from age 15 year measurements. Trials are ordered in ascending productivity.

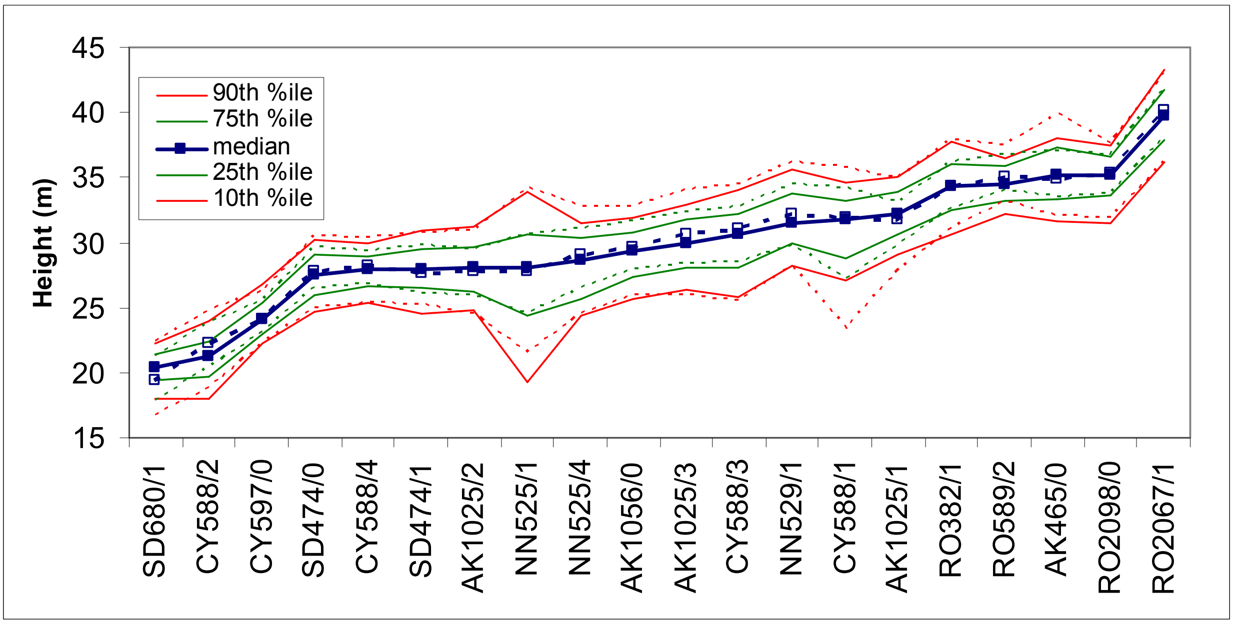

Fig. 13. Percentiles of distributions of actual (solid lines) and predicted (dashed lines) height at age 25 in each trial. Predictions are projections from age 20 year measurements. Trials are ordered in ascending productivity.

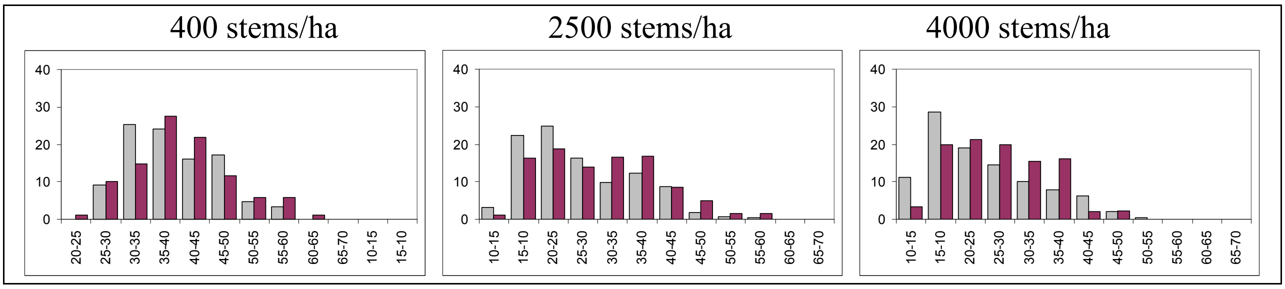

Fig. 14. Distributions of actual (light bars) and predicted (dark bars) *DBH* at age 25 years for 3 stockings (400, 2500 and 4000 stems/ha) in RO955. Predictions are projected from age 15 year measurements.

The above tests of performance are against the model dataset which covers a wide range of site types and stockings. However, ongoing and future validation will test the model against independent data, and combinations of site and silviculture not included in the model dataset. As is usual in the development of an empirical model, it is almost certain that the model will go through several iterations of development as a result of such validation. Weaknesses in the model are most likely to be exposed for extreme input conditions. For example, it could be expected that that the model would be most severely tested when simulating extremely highly stocked stands, especially as no such stands were included in the model dataset.

As a first stage in validating the model against independent data, it was therefore tested using a trial in Tarawera Forest, RO955, which contains two extremely highly stocked unthinned treatments (5,000 and 2,500 stems/ha) in addition to a thinned treatment (400 stems/ha). The performance of the model in predicting *DBH* at age 25 years from an age 15 year measurement for these three stockings is shown in Fig. 14. Overall performance was good, especially for the 400 stem/ha treatment, but the proportion of small suppressed stems was under-predicted for the most highly stocked treatment. This partly reflects the fact that the 300 Index stand-level model has a tendency to over-predict mean BA at stockings over 2,500 stems/ha as noted in Kimberley (2007a). Although model performance at such high stockings is of largely academic interest, we believe it is important that the model should behave well over a wider matrix of site and stand conditions than are generally encountered to improve the overall robustness of the model and give confidence in its performance even at more normal settings. Therefore, some attention to performance at high stockings will be included in the ongoing development of the model.

FUTURE WORK

This report describes a preliminary version of a distance-independent individual tree growth model compatible with the 300 Index stand-level model. We believe that the performance of the model proves that the approach adopted to develop this model is conceptually sound. However, the model requires further development before it is implemented in software packages such as FORECASTER or YTGEN. This includes:

1. Extending the model dataset (e.g., ages less than 10 years and greater than 30 years, very high stockings, late thinned stands)
2. Incorporating the facility to prune or thin trees in the list – this will require the model to respond to differences in crown lengths of individual trees
3. Providing a formal validation of the model

4. Developing methods for running the model when there is incomplete historical data
5. Predicting individual tree starting values when only stand-level parameters are available
6. Adding fertilisation and genetics

Work on the first three of the above tasks is underway. It is intended that the initial version of the model will released for use by June 2008.

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