Pilot Study for Internal Stem Modelling:
Evaluation of Relationships between Crown, Ring Area and Basic Density

D. Pont

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EXECUTIVE SUMMARY

A pilot study, to develop a data collection strategy for rotation age trials, was carried out in abandoned plots from Experiment FR172/3. Crown structure and wood property data were collected from 7 visually straight trees and 5 visually bent trees.

Data from the straight trees were used to test an extension to TreeBLOSSIM which predicts stem growth ring area and wood density, varying with ring from the pith and height up the stem, from crown structure. These 7 trees represented seedlots with a range of internode length, wood density and GF values.

Crown structure was assessed in terms of foliage mass and average distance to foliage on 7 or 8 sample branches selected from each tree to cover the range of branch age and diameter. Stem ring area and basic density was measured by Silviscan analysis of 2 or 3 radial strips cut from discs taken at 4 or 5 levels up the stem of each tree. Models estimating ring area and density from crown structure were then evaluated.

The ring area model makes good predictions of stem ring area (R-square 0.91) although it might need more development to predict stem form better at the base of the tree. The model for basic density is not as accurate as the ring area model although the use of crown/stem relationships still shows promise. A satisfactory fit (R-square 0.74) was obtained only by fitting the model to each tree. This is possibly a result of the wide range of seedlots represented in the data set.

Additional data sets are required to analyse the effects of varying sites, silvicultural treatments and genotypes on internal stem structure.

Pilot Study for Internal Stem Modelling:
Evaluation of Relationships between Crown, Ring Area and Basic Density

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BACKGROUND

Data from an NZ Forest Research Institute Ltd project comprising detailed measurements of crown architecture and wood properties from internodal discs was used to develop a prototype model relating annual ring area increment and basic density with the mass and location of foliage within the crown (Pont 2003). As a result of the new SGMC research theme (Internal Stem Modelling) and the associated strategy (SGMC Report 114) a pilot study was carried out in experiment FR172/3, Kaingaroa to develop methodology for future sampling and to provide data to test the prototype model of Pont (2003). SGMC Report 126 covers the data collection methods, and SGMC Report 127 summarises the data and makes recommendations for future sampling. This report covers use of crown and stem wood properties data to evaluate the prototype model of Pont (2003).

MATERIALS

A total of 12 trees were destructively measured in experiment FR172/3, this study uses data from the 7 trees classified as "straight", representing 4 of the 5 seedlots sampled (refer to SGMC reports 126 and 127 for additional information). Table 1 lists the basic features of the trees covered by this report.

Table 1. Sample trees classified as "straight" from experiment FR 172/3.

Seedlot	PlotID	Plot/Tree Number	Unique Number	Tree DBH (mm)
Highly multinodal (GF27)	1	A16	116	388
Highly multinodal (GF27)	1	A24	124	385
High wood density (GF18)	3	C9	309	349
Low wood density (GF28)	4	D11	411	388
Low wood density (GF28)	4	D13	413	316
Gwavas seed orchard (GF14)	5	E16	516	318
Gwavas seed orchard (GF14)	5	E17	517	352

METHODS

Crown data

The prototype model (Pont 2003) was based on detailed measurement of growth unit lengths and foliage mass of entire branching structures cut from the stem for a number of branches selected to represent crown architecture. Such detailed measurements were not practical for the pilot study and a simplified measurement method was utilised. Seven or eight branches were selected from each tree to cover the range of live branch diameter and age. For each branch total mass and distance from basal end to centre of mass were measured with and without foliage. All branches on the stem were measured for diameter, and ring counts made below each cluster were used to assign ages to branches.

Stem data

Internodal discs were sampled at 4 or 5 levels along the stem for each of the straight trees. Two opposing radial strips were cut from all discs and on the lowest disc from each tree two additional radial strips were cut at right angles to the first two. This sampling strategy resulted in 10 to 14 radial strips from each tree, giving a total of 84 strips. The strips were measured using SilviScan, annual ring boundaries identified and a data set containing ring radii and ring average basic density produced.

RESULTS

The analysis consists of 3 main stages:

Branch foliage

Relating branch diameter growth with the amount and average distance to foliage

Crown development

Estimating foliage carried by each branch in the crown at each prior age of tree growth

Crown / Stem relationships

Relating stem wood properties for each growth ring and position on the stem with the foliage carried above that point on the stem at that age

BRANCH FOLIAGE

Distance to Branch Foliage

Branch average distance to foliage (D_{fb}) was calculated from the field branch measurements of mass and distance to centre of mass (CM), with and without foliage. The equation for a one-dimensional CM with two component masses, wood and foliage, is:

$$CM_{wf} = \frac{l_w m_w + l_f m_f}{m_w + m_f}$$ Equation 1

where:

CM_{wf}	centre of mass of the wood and foliage
l_w and l_f	distance to the centre of the mass of wood, and foliage, respectively.
m_w and m_f	mass of wood, and foliage, respectively.

Equation 1 is rearranged to obtain the average distance to foliage:

$$l_f = \frac{(CM_{wf}(m_w + m_f)) - (l_w m_w)}{m_f}$$ Equation 2

Substituting in symbols for the quantities measured and the unknown gives:

$$D_{fb} = \frac{d_1 w_1 - d_2 w_2}{w_1 - w_2}$$ Equation 3

where:

D_{fb}	is average distance to foliage for branch *b.*
d_1 and d_2	are CM of branch with and without foliage.
w_1 and w_2	are weight of branch with and without foliage.

D_{fb} was calculated for the 53 branches with complete foliage measurements from the 7 trees, and plotted against branch basal area (Figure 1). For any given branch basal area there is quite a spread of D_{fb} values but no trends were evident with plot or tree.

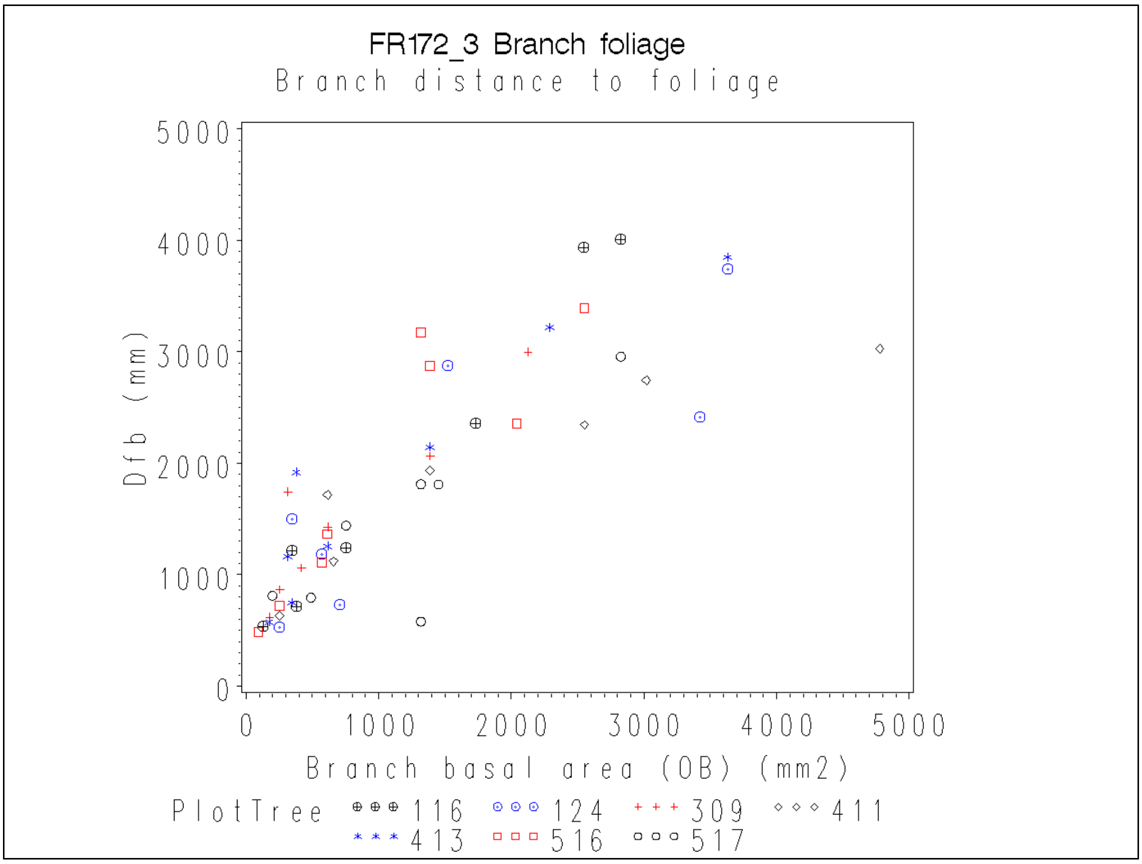


Figure 1. Average distance to foliage plotted against branch basal area.

The following model (Pont 2003) was fit in SAS using PROC NLIN:

$$D_{fb} = aG_b^c$$ Equation 4

where:

D_{fb}	is average distance to foliage (mm) for a given branch b
G_b	is basal area (mm^2) over bark for a given branch b
a and c	are model parameters

The SAS output is shown below. The estimates for the parameters a and c are 48.1 and 0.52 respectively.

Source	DF	Sum of Squares	Mean Square	F Value	Approx Pr > F
Regression	2	2.0766E8	1.0383E8	398.49	<.0001
Residual	51	13288304	260555		
Uncorrected Total	53	2.2095E8			
Corrected Total	52	57621087			

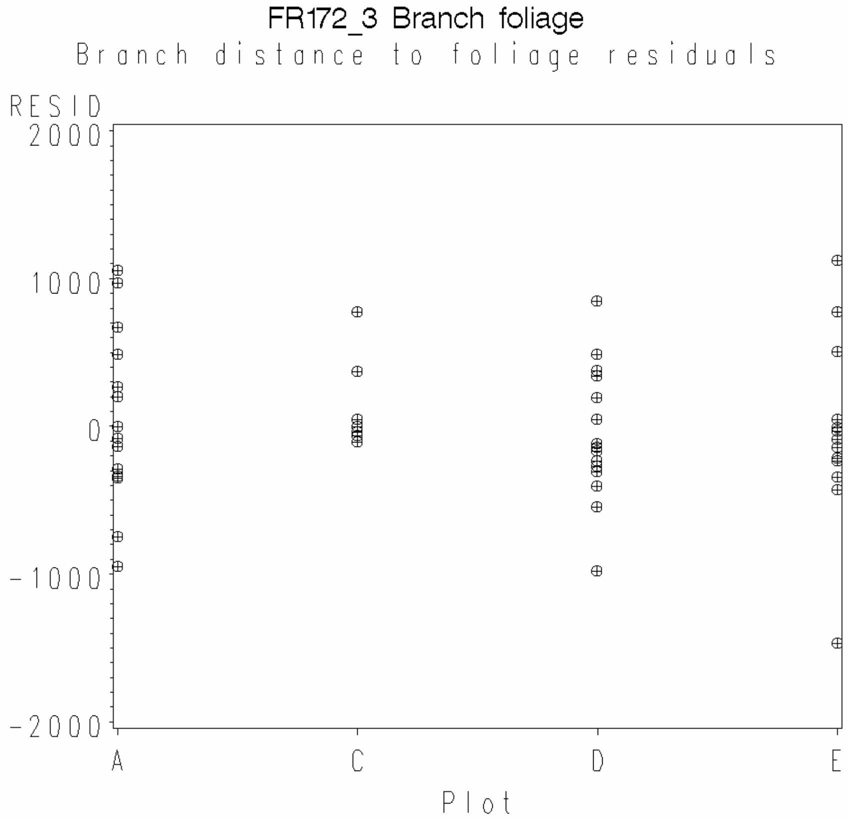
Parameter	Estimate	Approx Std Error	Approximate 95% Confidence Limits	
a	48.0744	16.8787	14.1891	81.9597
c	0.5220	0.0465	0.4287	0.6152

Figure 2b shows that the model fitted to the FR172/3 data set does not differ greatly from that of Pont (2003). The FR172/3 data set seemed to have a slightly better range of branch sizes, and it was decided to retain the newly fitted model for use in subsequent analysis.

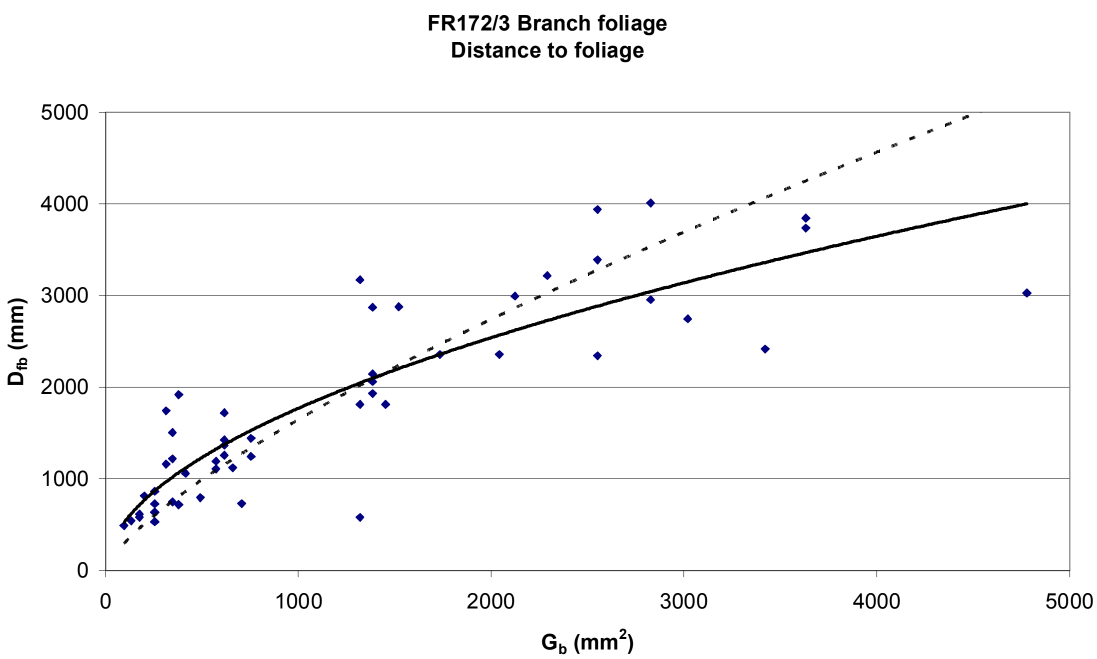
The R-square for the model was 0.77 and no strong trends were noted in residuals plotted against a number of variables including seedlot which is represented as Plot (see Table 1) in Figure 2a.

Branch Foliage Mass

Initial examination of branch foliage mass W_{fb} showed a slightly better relationship with branch basal area G_b (Figure 3b) than with branch basal area increment ΔG_b (Figure 3a), the latter used by Pont (2003). Examination of Figure 3a indicated that the relationship between W_{fb} and ΔG_b varied with branch age. Younger branches had higher basal area increment for a given amount of foliage than older branches, possibly due to higher consumption of assimilate (respiration) in the larger older branches. This assumption lead to formulation of a model relating branch foliage mass with basal area increment (growth) and branch basal area (maintenance), but the parameter for the basal area increment term was not significantly different from zero.

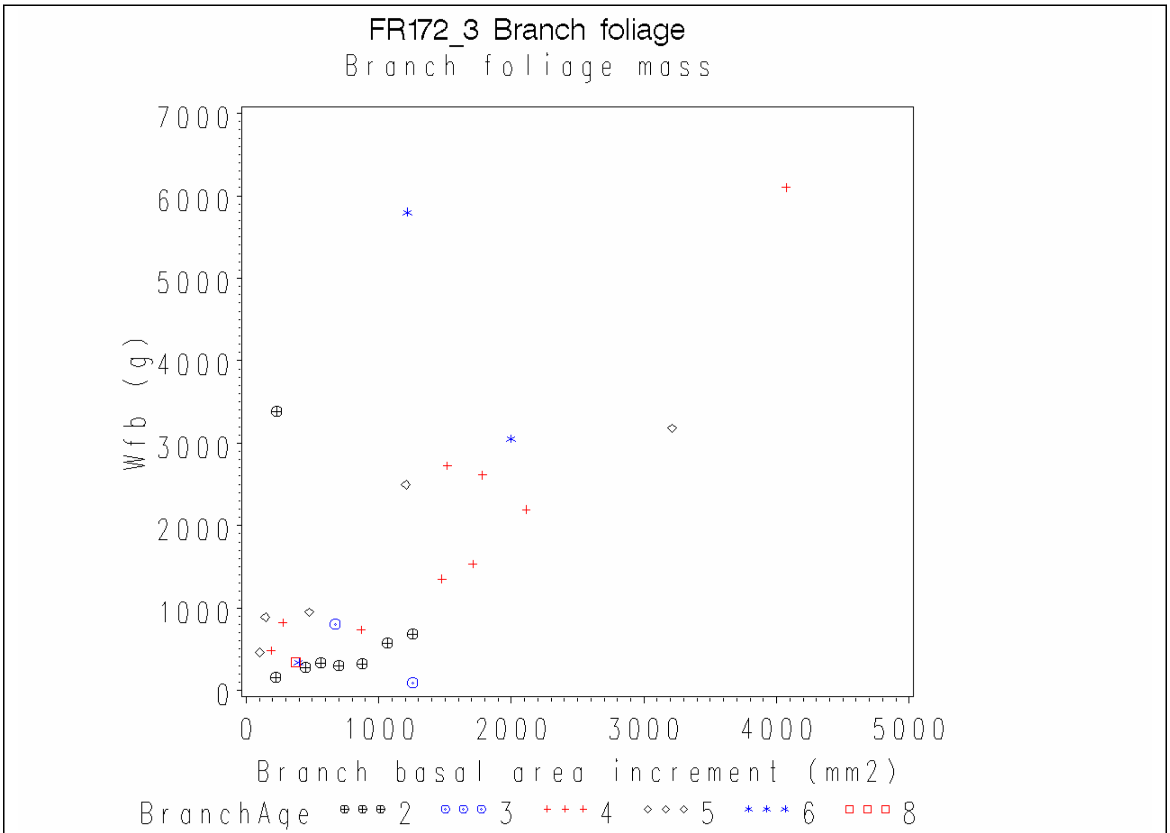


a. D_{fb} model residuals by Plot, each plot represents a seedlot.

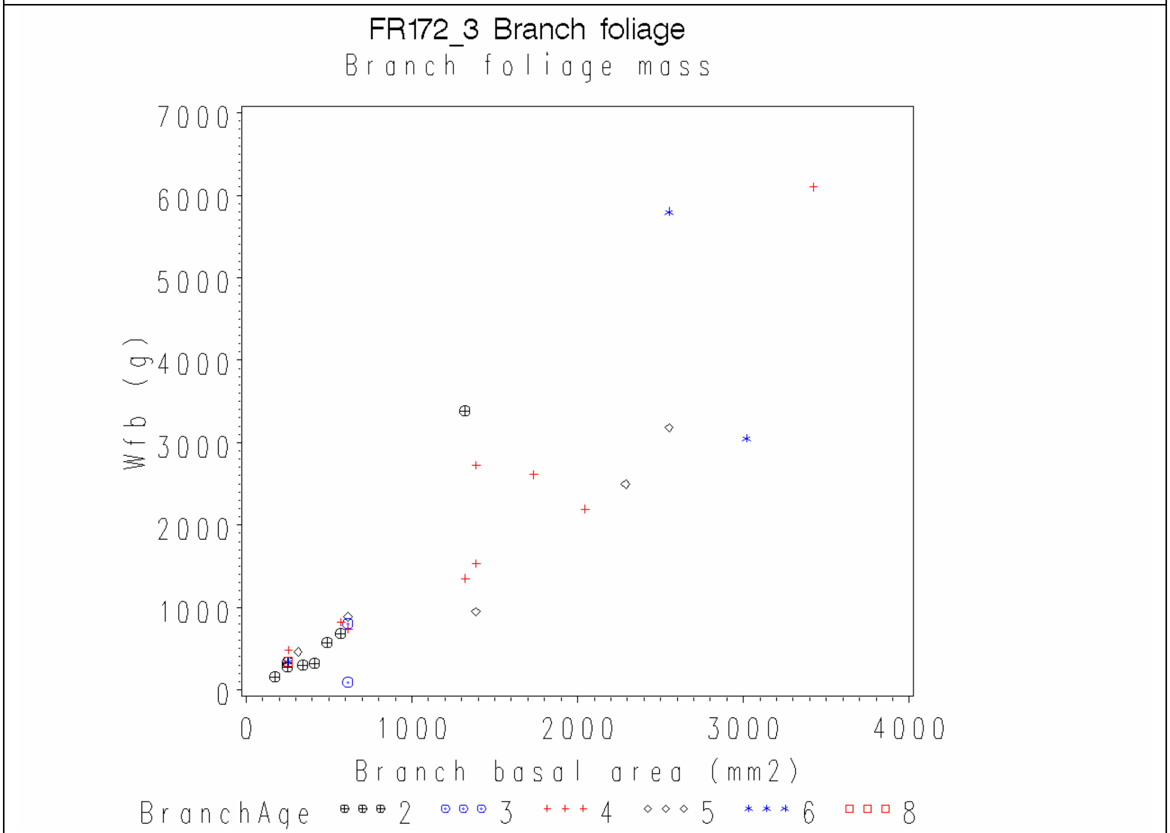


b. D_{fb} data set and models. Model by Pont (2003) in dashed line, model fitted to current data set in solid line.

Figure 2. Results for fit of D_{fb} model to FR172/3 data.



a.



b.

Figure 3. Branch foliage mass plotted against branch basal area increment and branch basal area.

The following simplified model was fit using SAS PROC NLIN:

$$W_{fb} = aG_b$$ Equation 5

where:
W_{fb} is weight of foliage (g) for branch b
G_b is basal area (mm^2) for branch b
a is the model parameter

The SAS output is shown below. The estimate for a is 1.44.

Source	DF	Sum of Squares	Mean Square	F Value	Approx Pr > F
Regression	1	1.224E8	1.224E8		
Residual	27	14236609	527282		
Uncorrected Total	28	1.3663E8			
Corrected Total	27	70628746			

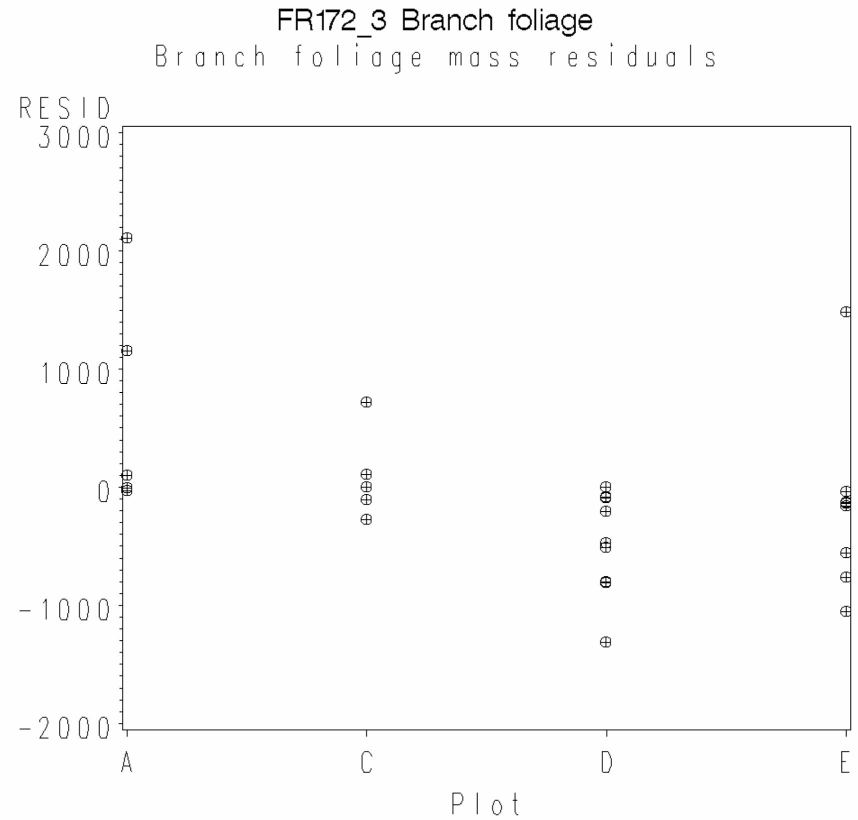
Parameter	Estimate	Approx Std Error	Approximate 95% Confidence Limits	
a	1.4443	0.0948	1.2498	1.6388

The R-square was 0.80, examination of residuals showed variation by plot (Figure 4a). Each plot represents a seedlot (see Table 1), indicating genotypic variation in the relationship. The above model was retained on the basis of a lack of data to derive separate relationships by plot. Figure 4b shows the data and the fitted regression line for the W_{fb} model (Equation 5).

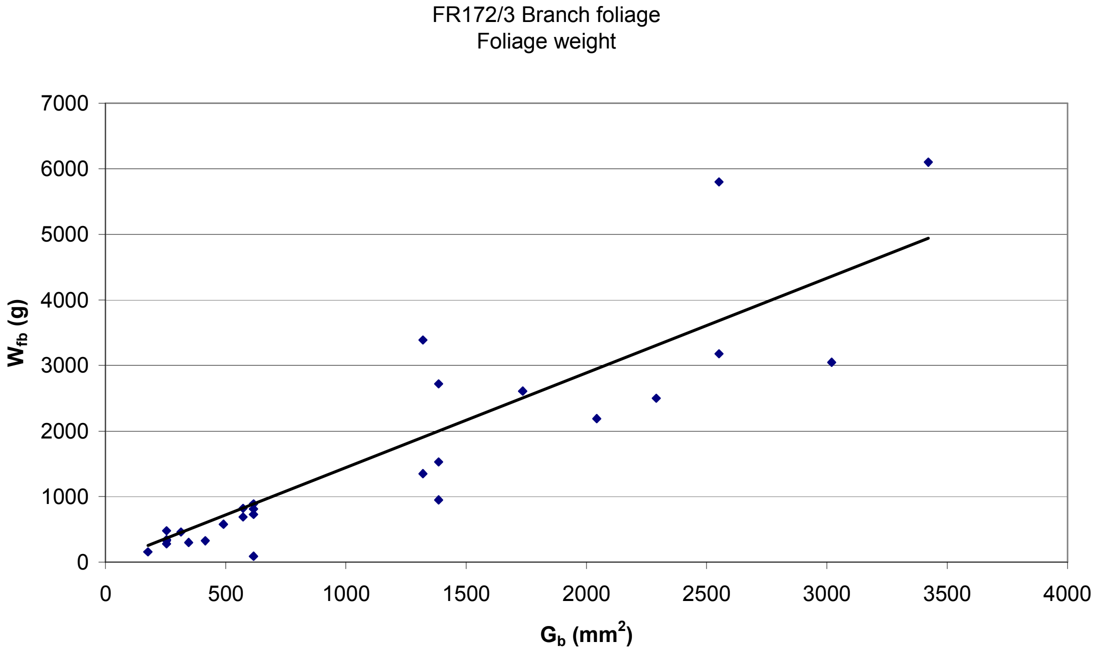
Initial calculations of crown development using the W_{fb} model based on branch basal area (Equation 5) appeared to grossly overestimate the amount of foliage carried in the crown. This resulted from the fact that branch basal area increases continuously to a maximum while the amount of foliage carried by a branch increases to a maximum and then declines to zero at branch mortality. These observations supported a model based on branch basal area increment (as in Pont 2003) and the following model was fit using SAS PROC NLIN:

$$W_{fb} = a\Delta G_b$$ Equation 6

where:
W_{fb} is weight of foliage (g) for branch b
ΔG_b is basal area increment (mm^2) for branch b
a is the model parameter



a. Model residuals by measurement plot.



b. W_{fb} model data set and fitted regression line (Equation 5).

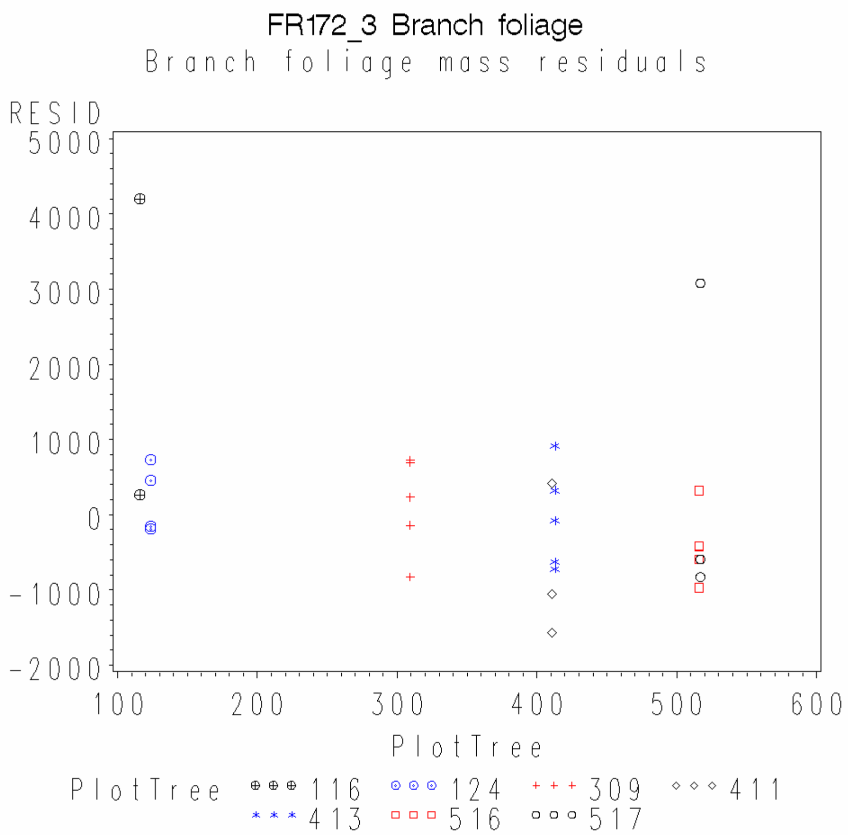
Figure 4. Model of branch foliage mass based on branch basal area (Equation 5).

The SAS output is shown below. The estimate for a is 5.3.

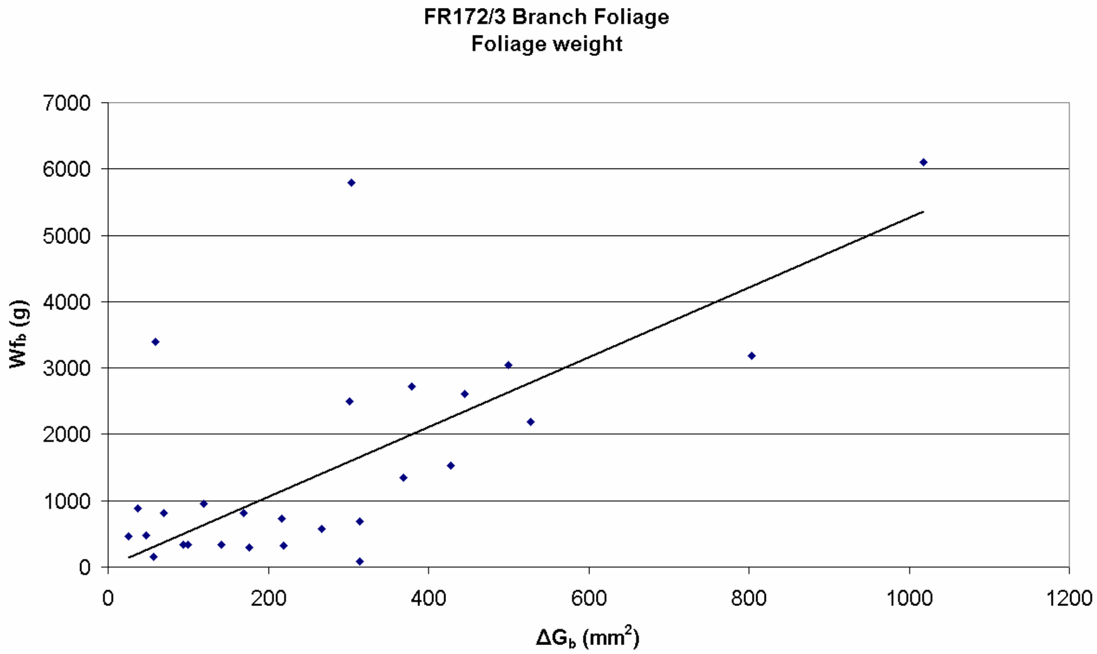
Source	DF	Sum of Squares	Mean Square	F Value	Approx Pr > F
Regression	1	98452121	98452121		
Residual	26	38103229	1465509		
Uncorrected Total	27	1.3656E8			
Corrected Total	26	68994457			

Parameter	Estimate	Approx Std Error	Approximate 95% Confidence Limits	
a	5.2697	0.6429	3.9482	6.5913

The R-square for the model was 0.45. Examination of residuals plotted against a number of variables showed two outliers and no noticeable trends (Figure 5a). The two outliers are also apparent in Figure 5b, having a relatively high amount of foliage mass for their branch basal area increment. It must be noted that the basal area increment is estimated from the measured branch diameter and age. The model given in Equation 6 has a poorer fit to the data than that given in Equation 5 but is selected on the basis that it is based on branch growth rather than branch size, thus providing a more realistic prediction of crown development. Equation 6 also agrees with the model form in Pont (2003). Figure 5b shows a line representing the fitted model overlayed on the data.



a. Model residuals by plot and tree.



b. W_{fb} model data set and fitted regression line (Equation 6).

Figure 5. Model of branch foliage mass based on branch basal area increment (Equation 6).

CROWN DEVELOPMENT

Branch Growth

Reconstruction of past branch diameters was carried out for all branches using the branch growth functions from TreeBLOSSIM for the Central North Island (SGMC Report No. 125). The first step was to estimate branch growth potential using the measured branch diameter and age (from the number of rings at the base of the cluster). The branch growth function is not easily rearranged to obtain growth potential given age and diameter so growth potential was solved using an iterative search process. Given the growth potential for a branch its diameter could then be estimated at any age.

The second step was to calculate the entire growth history for every branch, in terms of: year of growth and branch diameter. Using the relationships derived earlier the foliage mass and average distance to foliage could be estimated for every branch at any given year. Then for each tree the foliage mass W_{fi} and average distance to foliage D_{fi} could be calculated for a given year and position within the stem.

The final step was to produce a data set containing estimates of W_{fi} (total foliage mass above position *i*) and D_{fi} (average distance to foliage above position *i*) corresponding to the measures of ring area and basic density obtained from SilviScan analysis of radial strips (SGMC Report 127).

Note that a complete description of the crown foliage should include foliage growing at the top of the main stem. Insufficient data were available to make reliable estimates of this foliage component and as it is only a tiny portion of the total it was excluded from foliage calculations in this study.

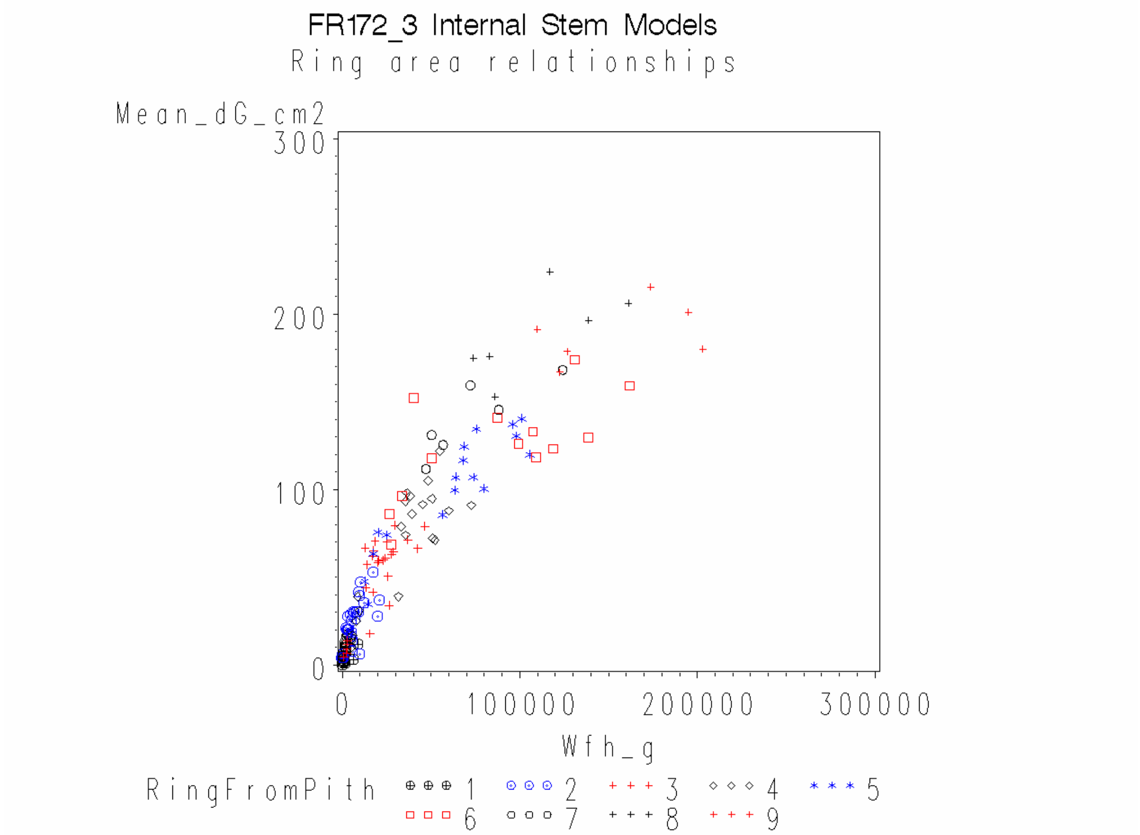
CROWN / STEM RELATIONSHIPS

Stem annual ring area increment was calculated from SilviScan ring radii. Annual ring area and basic density for each growth ring were averaged across multiple strip directions (2 or 4 strips) for each disc. Because of the pruning at the base of the trees it was not possible to estimate the foliage measures for the first few years of tree growth. This required exclusion of one or more inner rings from the lower disc positions, giving a set of stem data suitable for correlation with the foliage data (W_{fi} and D_{fi}) derived earlier.

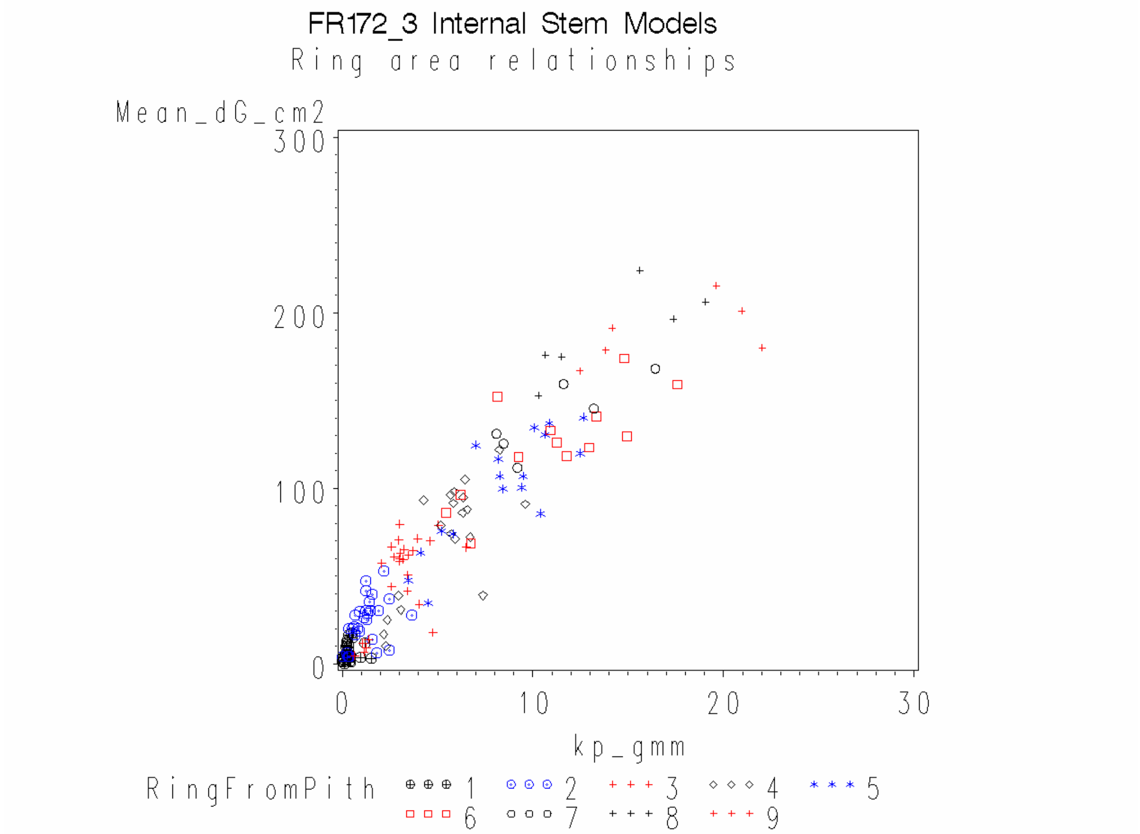
Initial analysis of ring area and basic density revealed that the final year of growth had lower ring area and density and it was excluded from the data set as being an incomplete growth ring. The trees were felled and measured in early March.

Stem ring area

Examination of Figure 6 shows a slightly curvilinear relationship between ring area and foliage mass (Figure 6a) and between ring area and $kp = \frac{W_f}{D_{fT}}$ (Figure 6b), supporting the use of the same model form used in Pont (2003).



a. Relationship between stem ring area (Mean_dG_cm2) and mass of foliage above (Wfh_g).



b. Relationship between stem ring area and $kp = \frac{W_f}{D_{fT}}$

Figure 6. Stem ring area plotted against foliage mass above the sample point.

The following model that will account for the observed curvilinearity was fit using SAS PROC NLIN:

$$\Delta G = \frac{aW_f^b}{D_{fT}^c} \qquad \text{Equation 7}$$

where:

ΔG is stem ring area (cm^2)

W_f is weight of foliage (kg) above a given position and at a given age

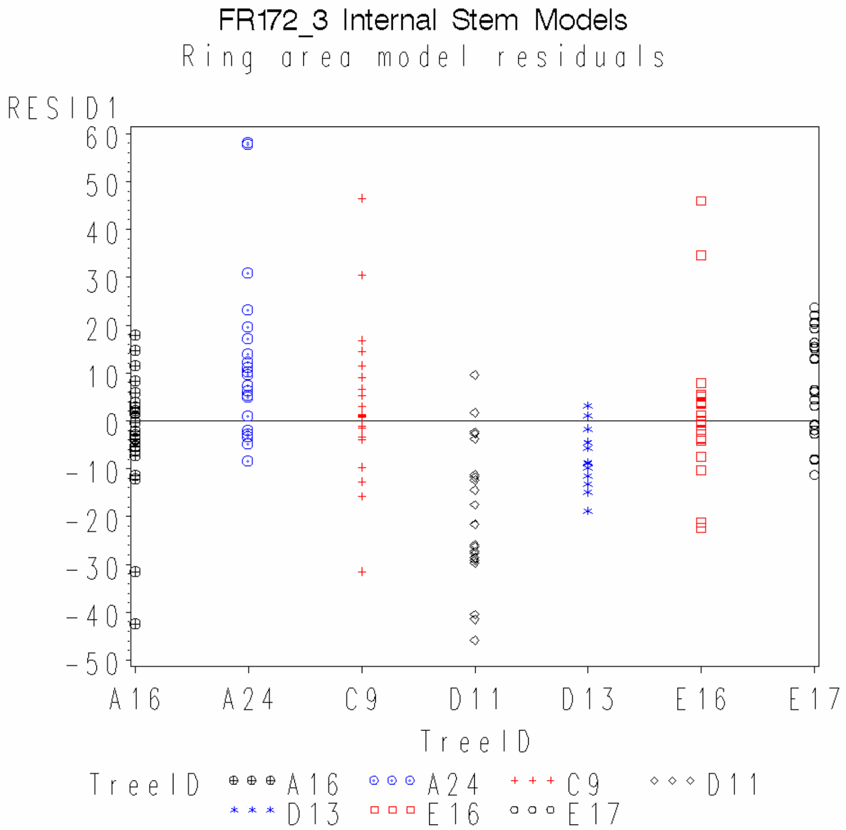
D_{fT} is average distance to foliage (m) at ground level and at a given age

a, b, c are the model parameters

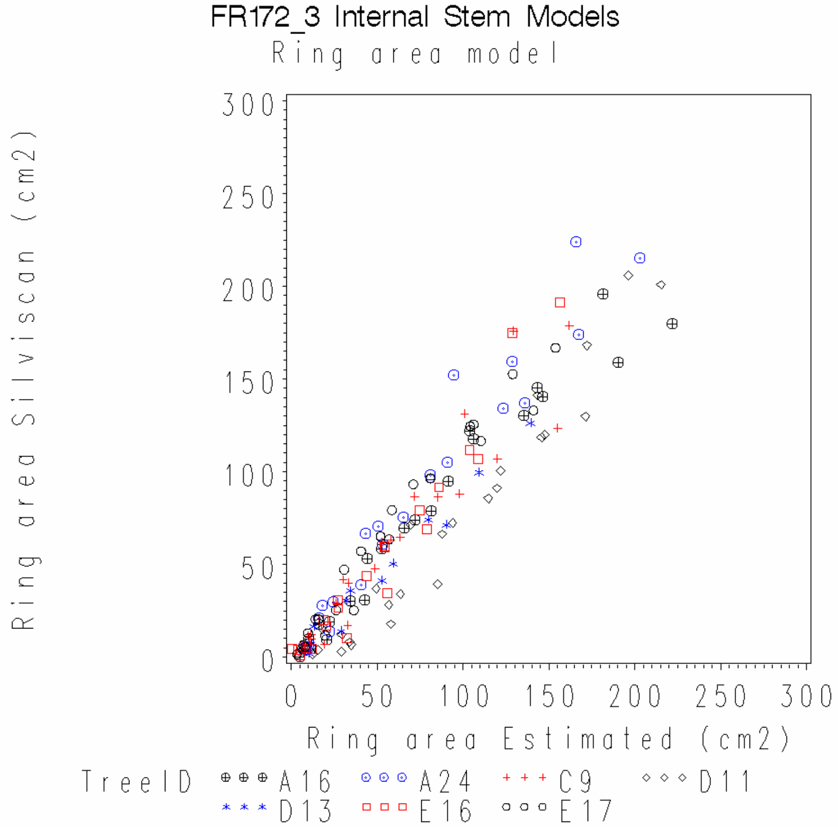
The SAS output is shown below. The estimates for the parameters a, b and c are 14.4, 0.68 and 0.39 respectively.

Source	DF	Sum of Squares	Mean Square	F Value	Approx Pr > F
Regression	3	1130864	376955	1241.52	<.0001
Residual	146	44329.2	303.6		
Uncorrected Total	149	1175193			
Corrected Total	148	502091			

Parameter	Estimate	Approx Std Error	Approximate 95% Confidence Limits	
a	14.4441	2.0499	10.3927	18.4954
b	0.6762	0.0325	0.6120	0.7404
c	0.3871	0.1033	0.1830	0.5912



a. Model residuals plotted against TreeID.



b. Measured stem ring area plotted against model estimates.

Figure 7. Stem ring area model.

The R-square for the model of stem ring area was 0.91. Examination of residuals showed association of errors with TreeID (see Figure 7a).

Fitting the model by tree improved the R-square to an average of 0.96, indicating that the relationship may vary by tree. At this early stage of investigation it was decided to retain the model fitted to all trees. Figure 7b shows measured stem ring area plotted against estimated ring area, showing the model predicts reasonably well. Close examination does reveal slight variation associated with individual trees.

A simpler model than that given in Equation 7, of the form proposed by Pont (2003) after a theoretical analysis of Presslers law, was also fit to the ring area data (Equation 8).

Equation 8

$$\Delta G = \frac{aW_f}{D_{fT}}$$

This model, effectively a linear fit to the variables plotted in Figure 6b, had a lower R-square of 0.86 and residual plots showed it did not model the relationship accurately.

Stem Ring Basic Density

Initial analysis of the basic density data showed the trees exhibited a range of different patterns of within stem variation. Figure 8 (a-g) presents the pith-to-bark series for each tree and examination of these figures shows that elevated density values often occur at the lowest disc level and near the pith. Excluding the lowest level the pith to bark series at different levels within a tree tend to be similar.

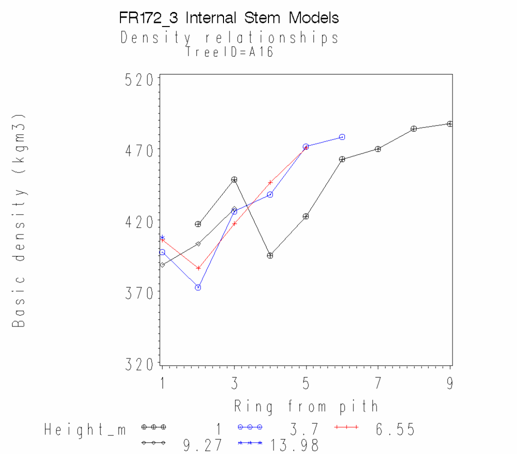
Initially a model of the form used by Pont (2003) was fit to the basic density data (Equation 9). This relates basic density to the ratio of the average distance to foliage above and the total foliage mass for the tree.

Equation 9

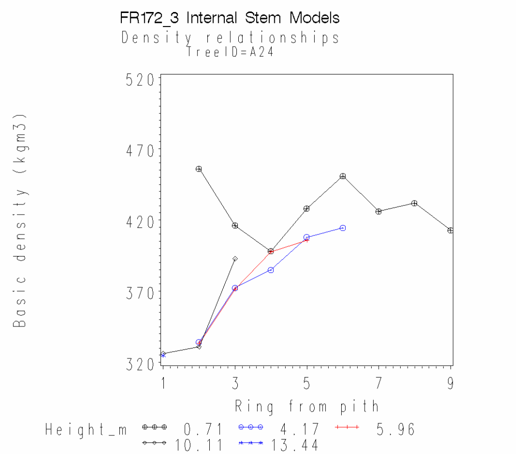
$$\rho = a\left(\frac{D_f}{W_{fT}}\right)^b$$

where:

ρ	is stem ring basic density (kgm^{-3})
D_f	is average distance to foliage (m) above a given position and at a given age
W_{fT}	is whole-tree foliage mass (kg) at a given age
a and b	are the model parameters



a. Tree A16



b. Tree A24

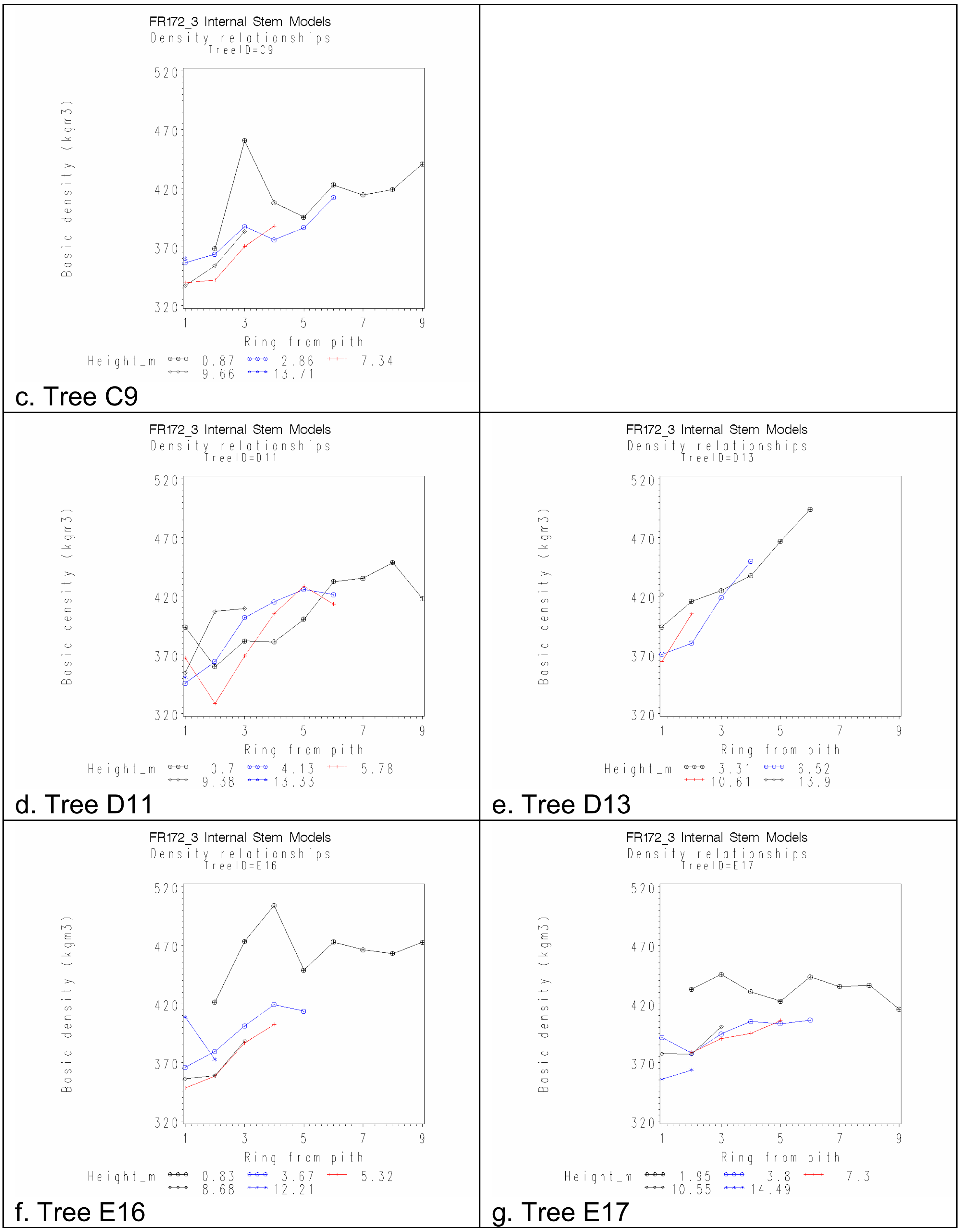


Figure 8. Pith to bark density profiles from SilviScan analysis of strips at different positions in the stem for each tree.

This model gave a very poor fit to the data for all trees. Residuals showed strong patterns associated with ring number from the pith and to a lesser degree with TreeID. Incorporating ring number from the pith into the model gave the following (Equation 10):

$$\rho = aR^c \left(\frac{D_f}{W_{fT}} \right)^b \qquad \text{Equation 10}$$

where:

ρ	is stem ring basic density (kgm^{-3})
D_f	is average distance to foliage (m) above a given position and at a given age
W_{fT}	is whole-tree foliage mass (kg) at a given age
R	is ring number from the pith
a, b, c	are the model parameters

The SAS output is shown below. The estimates for the parameters a, b and c are 383.7, 0.018 and 0.93 respectively.

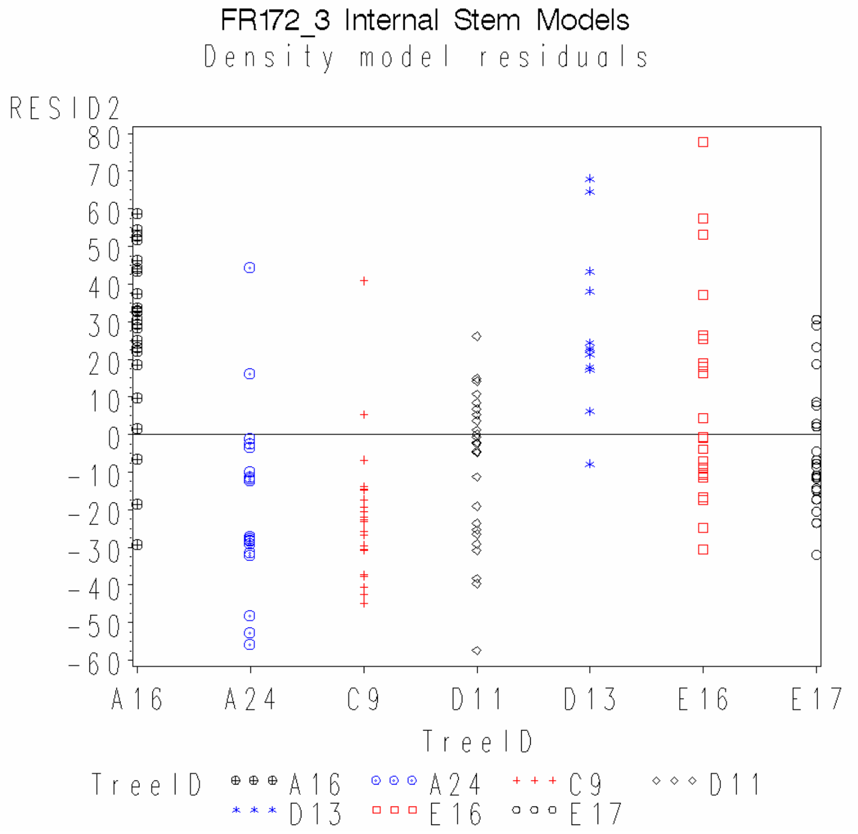
Source	DF	Sum of Squares	Mean Square	F Value	Approx Pr > F
Regression	3	24503404	8167801	10375.8	<.0001
Residual	146	114931	787.2		
Uncorrected Total	149	24618335			
Corrected Total	148	220803			

Parameter	Estimate	Approx Std Error	Approximate 95% Confidence Limits	
a	383.7	8.2232	367.4	399.9
b	0.0181	0.00589	0.00650	0.0298
c	0.0926	0.00886	0.0751	0.1101

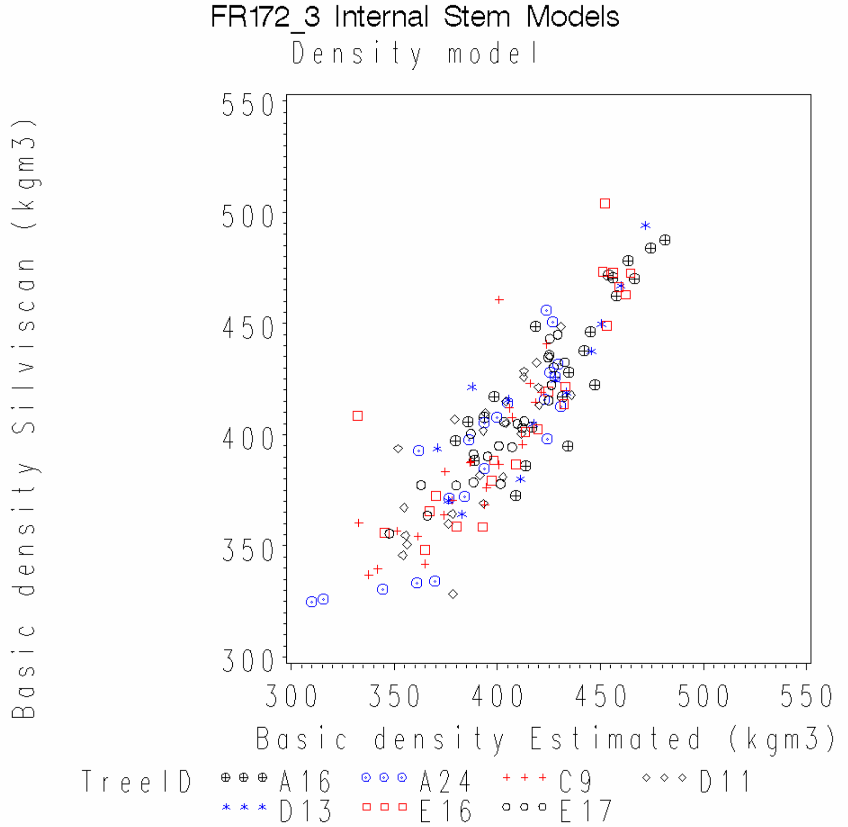
The R-square of the model including ring number was 0.48. Examination of the residuals showed a strong association with TreeID (Figure 9a).

Fitting Equation 10 by tree improved the R-square significantly to an average of 0.74 and examination of residuals plotted against available variables did not reveal any systematic trends. Plotting measured density against estimated (Figure 9b) shows there is some unexplained variation but the model predicts reasonably well over the range of this data set.

Figure 10 shows the results of the internal stem models fitted in this study applied to each tree. Measured size and age of each branch is used to reconstruct past crown growth. This allows use of crown metrics to estimate stem ring area and basic density at each internode in each year of growth. Variations in stem profile result from the different crown structures of each tree affecting stem area increment. The variations in basic density result from differences in crown structure and the fact that the density model parameters were fit to each tree, resulting in different patterns for each tree.



a. Residuals for Equation 10 (fitted to all trees) plotted against TreeID.



b. Measured basic density plotted against estimated values for Equation 10 fitted by tree.

Figure 9. Basic density model including ring number (Equation 10)

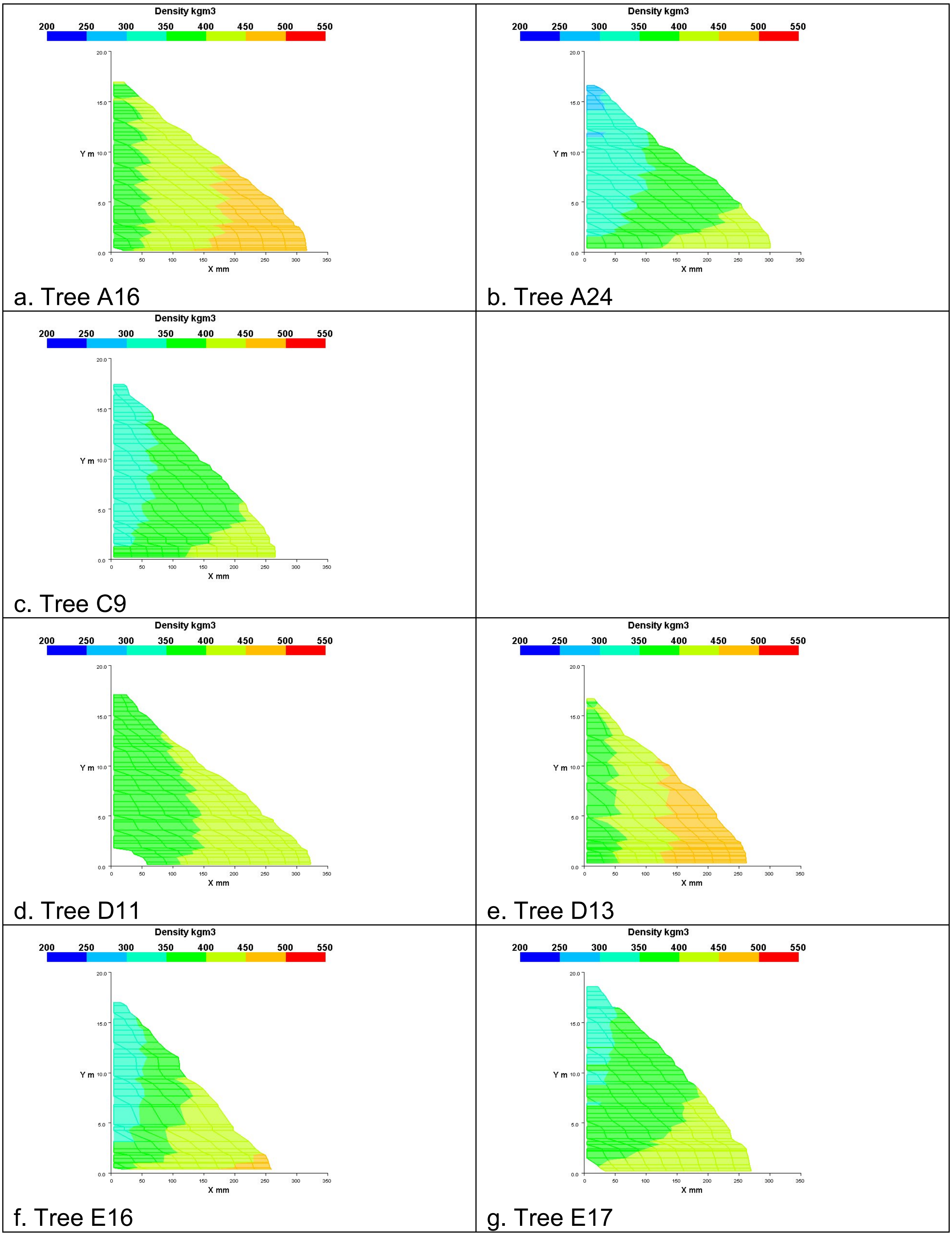


Figure 10. Diagrams representing predictions from ring area and basic density models (respectively: Equation 7 and Equation 10, the latter fitted by tree). Predicted ring area is reflected as the series of longitudinal stem profiles in each diagram. Predicted basic density is represented by a range of colours.

DISCUSSION

The amount of foliage per unit branch basal area increment (Equation 6) was higher (3.5 times) than found by Pont 2003. This might be due to site related differences in the amount of foliage. It also could be due to drying of foliage in the study by Pont (2003) in which some foliage masses were not measured until several days after felling.

Pruning at the base of the trees precluded estimation of crown structure for the first few years of tree growth. This prevented including the strong gradients present in ring area and density values in analysis of relationships with crown structure.

Photographs of the sample strips (SGMC Report 127, Appendix 1) showed that many strips contained visible compression wood. It is likely this has contributed to variability in the density and, to a lesser degree, ring area data.

Given that the ring area and basic density models of Pont (2003) were fitted to data from a single tree and it was expected that model parameters, and possibly model forms, would require revision. The same model forms have proved adequate and new parameters have been estimated for the FR172/3 data set.

Figure 10 shows the output of the models fitted for ring area and basic density, illustrating the models are capable of representing the varied internal stem patterns in the FR172/3 data set.

The ring area model makes good predictions of ring area although it might need more development to predict stem form better at the base of the tree. Difficulty in modelling the so-called "butt flare" is a well-known problem in classical stem form/taper research.

The model for basic density is not as accurate as the ring area model although the use of crown/stem relationships still shows promise. The current need to fit the model by tree probably reflects variation in internal stem structure of genetic origin, significant in this data set as trees were chosen to represent a wide range of breeding traits. Broader data sets are required to analyse the effects of varying sites, silvicultural treatments and genotypes on internal stem structure.

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