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Measurement and prediction of biomass and carbon content of *Pinus pinaster* trees in farm forestry plantations, south-western Australia

Peter Ritson[*], Stanley Sochacki

Department of Conservation and Land Management, Cooperative Research Centre for Greenhouse Accounting, Kensington 6153, WA, Australia

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Abstract

A total of 148 *Pinus pinaster* trees from 18 farm plantations in south-western Australia were destructively sampled to develop biomass and carbon mass prediction equations for inventory application. Sampling covered a range of ages (1–47-year-old), sizes (e.g. DBH 0–47 cm) and spacings (close- and open-spaced arrangements).

Equations were developed to predict biomass and carbon mass of whole-trees and tree components (stems, crowns, tops and roots) as functions of stem diameter (DBH), tree height (h) and height to crown base (h_c) or basal stem diameter (d_{10}) of small trees. One equation was sufficient to predict biomass (or carbon mass) of both close- and open-spaced trees as a function of DBH and h_c.

For developing prediction equations a weighted non-linear (WNL) model was always best if DBH was included in the predictor variables. Either a log-transformed allometric (LTA) model or the WNL model were best for predictions as a function of d_{10}, but a weighted combined variable (WCV) model was never best.

Root:shoot (R:S) ratio decreased with increasing tree size in both close- and open-spaced trees but was higher in open-spaced trees than close-spaced trees of the same size. From literature review, we conclude that increased partitioning of biomass to roots in open-spaced stands may be due to increased light availability or, more likely, more pronounced root thickening on open-spaced trees in response to greater mechanical stress from wind sway.

Keywords: *Pinus pinaster*; Biomass prediction; Carbon sequestration; Root:shoot ratio; Farm forestry

1. Introduction

In 1996, the Forest Products Commission of Western Australia (then Department of Conservation and Land Management) commenced a cropshare scheme with private landowners to increase planting of maritime pine (*Pinus pinaster*, Portuguese race) on farms in south-western Australia. The target area was the 400–600 mm per year rainfall zone. Planting has progressively increased each year with around 14,700 ha planted to 2001.

The *P. pinaster* plantations, like farm plantations of other species in higher rainfall areas, are multi-purpose. Besides timber products and diversification of farm income the objective is to deliver a range of environmental benefits. These include salinity

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[*] Corresponding author. Tel.: +61-8-9334-0316;
fax: +61-8-9334-0327.
E-mail address: peter@calm.wa.gov.au (P. Ritson).

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amelioration by reversing the rise of saline watertables (Schofield et al., 1989; State Salinity Council, 2000); reducing greenhouse effects by sequestering carbon dioxide from the atmosphere (Shea et al., 1998); reducing soil erosion and providing shelterbelts for farm pastures, crops and livestock; and reducing the leaching of fertilisers that pollute waterways.

One research program in the farm plantations aims to quantify potential greenhouse benefits from carbon sequestration (removal of carbon dioxide from the atmosphere) and biomass production (potential biofuel to replace some fossil fuel use). Studies include destructive sampling to develop biomass and carbon mass prediction equations for individual trees that could be applied in biomass/carbon inventory. Data from destructive sampling are also being used to develop stand-level models of biomass growth and carbon sequestration.

This paper describes studies to develop biomass and carbon mass prediction equations for individual *P. pinaster* trees in plantations established on cleared farmland. The ratio of below- to above-ground biomass (root:shoot (R:S) ratio) and factors that may affect R:S ratio in *P. pinaster* are also explored as, with knowledge of this ratio, root biomass can be predicted from the more easily assessed above-ground biomass.

2. Methods

2.1. Study sites

Study sites were farm plantings of *P. pinaster*, 1–47-year-old, within the general area of *P. pinaster* planting on farms (Fig. 1).

2.2. Sample tree selection

A total 148 sample trees for biomass and carbon determination were selected to represent the variables judged likely to affect tree biomass and carbon, i.e. tree age, stem diameter, tree height, site quality and planting layout. This was done using plots of 6–10 trees. Each plot was selected to be representative of the general stand condition and contain trees from the range of crown dominance classes (suppressed to dominant), thus providing coverage of stem diameter and tree height variation. The plots were selected to represent the range of tree age, site quality and belt or block planting arrangements (Table 1).

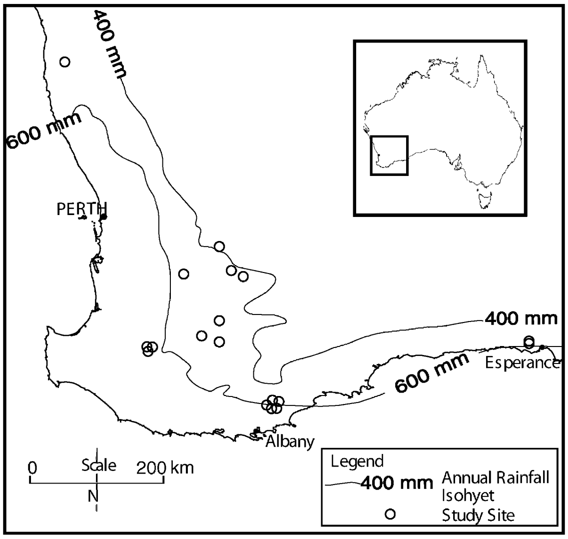

Fig. 1. Location of the study sites.

The plots were located in block plantings and belt plantings as both are common planting layouts for *P. pinaster* on farms in south-western Australia. The belts, typically 1–10 rows wide, may be planted as an isolated strip of trees (shelterbelts) or in parallel strips (alley farming).

Generally the plots of 6–10 trees were from a single row within a block or belt planting. This was done to minimise impact on the remaining stand, though some double-row plots (3 × 2 or 5 × 2 arrangements) were also sampled. However, most farmers were understandably reluctant to allow felling of plots of 6–10 trees in narrow shelterbelt plantings as this would compromise the valuable windbreak effect of the belt. Therefore, outside rows (R1) and the next row (R2) of block plantings were sampled to represent narrow belt plantings.

2.3. Destructive sampling and estimation of biomass

The above-ground portion of each sample tree was divided into components (Fig. 2) and the fresh weight of each component measured. With use of a bipod (anchor rope to tree) and block-and-tackle one person could comfortably weigh loads of up to 200 kg.

Table 1
Destructive sampling plots

Plot no.	Age (years)	No. of trees	Layout[a]	Thinned	Stocking (trees ha^{-1})[b]	DBH range (cm)	d_{10} range (cm)[c]	Height range (m)	h_c range (m)[d]	Category[e]	Soil[f]
1	1	10	B	No	1590	–	0.4–1.4	0.2–0.6	0.0–0.1	S	Sand
2	1	10	B	No	1800	–	0.3–1.2	0.2–0.4	0.0–0.2	S	Sand
3	1	10	B	No	1550	–	0.4–1.6	0.2–0.8	0.0–0.1	S	Sand (G0.5)
4	2	10	B	No	1310	1–4	5–7	1.5–2.3	0.0	S	Sand
5	2	10	B	No	1630	2–4	2–5	0.6–1.8	0.0	S	Sand (G0.25)
6	2	10	B	No	1510	2–5	2–5	0.8–1.8	0.0	S	Loamy sand
7	3	10	B	No	1270	3–6	3–6	1.2–2.3	0.0	S	Duplex (C1.7)
8	5	8	R1	No	1660	7–11	12–17	4.0–4.7	0.0	S&OS	Duplex (G1.1,C2.0)
9	5	8	R2	No	1570	7–11	11–17	4.4–5.1	0.0	S&CS	Duplex (G1.0, C2.0)
10	5	8	R3	No	1470	3–11	8–19	3.1–5.5	0.0	S&CS	Duplex (G1.1, C2.0)
11	13	6	B	No	1000	16–23	20–29	11–12	4–5	CS	Duplex (G0.8, C1.3, SP3.3)
12	14	6	B	No	920	17–23	20–31	12–14	5–6	CS	Sand
13	14	6	R1	No	850	22–40	31–52	12–15	0–7	OS	Duplex (G1.9, C2.4, SP4.5)
14	14	6	B	Yes	130	24–28	27–31	12–14	6–7	OS	Duplex (C0.8, G1.2)
15	15	7	B	No	980	11–30	19–39	6–14	1–5	CS	Sand
16	17	7	B	Yes	320	28–37	32–43	14–16	4–7	OS	Duplex (C0.8)
17	23	6	B	Yes	130	32–47	37–53	17–20	7–8	OS	Duplex (C2.1)
18	47	10	B	No	2200	12–30	16–34	12–19	9–13	CS	Duplex (C0.75)
Total		148									

[a] R1, R2 and R3: outside row, second and third row from plantation edge; B: block planting (R > 3).

[b] Stocking: $\geq$850 trees ha^{-1} in unthinned stands and $\leq$320 trees ha^{-1} in thinned stands.

[c] d_{10}: stem diameter at a height of 10 cm.

[d] h_c: height to crown base.

[e] S: small trees (DBH < 10 cm); CS: close-spaced trees (unthinned stands, except R1); OS: open-spaced (thinned stands or R1). Small and open-spaced trees defined to have DBH > 5 cm, i.e. some overlap with small trees.

[f] Soil profiles recorded from coring to approximately 6 m depth (>2-year-old trees) or from coring to excavation depth (1- and 2-year-old trees). Soil tended to be either deep sand (>6 m sand) or duplex sand over clay. Numbers in brackets indicate depth in metres to clay (C), ferruginous gravel layer (G) or silicious hardpan (SP).

Representative samples of each component (200–800 g) were taken at the time of bulk weighing and weighed in the field on a portable digital balance. These samples were oven-dried to constant weight at 70 °C to determine the proportion of dry matter (biomass) in each component.

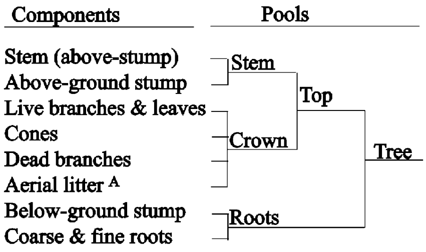

Fig. 2. Biomass components and pools. ^{A}Aerial litter mainly consisted of fallen leaves held up on branches and stem forks.

Root sampling procedures were similar to those applied to above-ground components except, as will be outlined, the root component was sampled in three steps using some novel methods.

2.4. *Sampling and estimation of root biomass*

Each sample tree was allocated an area (sub-plot), the boundaries being mid-way between the sample tree and adjoining trees. Root sampling to estimate root biomass in a sample tree sub-plot was then a three-step process (Fig. 3).

Step 1 (Excavation). The surface soil from around the stump and out to the sub-plot boundaries was excavated (tractor back-hoe or small excavator) and put through a coarse (25 or 50 mm) sieve. The sieve

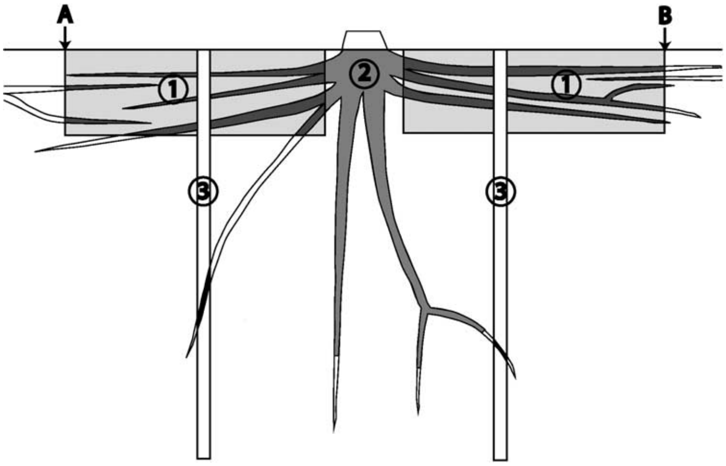

Fig. 3. Root sampling procedure. AB = sub-plot boundary. (1) Surface soil around stump excavated and most roots retrieved on coarse sieve. (2) Stump and attached deep roots pulled out. (3) Coarse-sieved soil returned to the pit and soil cores taken to estimate root biomass missed in Steps 1 and 2.

consisted of wire netting suspended on a 2 m × 1 m section of weld mesh (100 mm square grid) with supports to make a convenient field sieve table. Excavation depth was typically around 0.6–0.8 m, including all the zone of surface root proliferation. Most of the roots could be picked off the sieve table for weighing but some, generally smaller roots, would pass through.

Step 2 (Stump-pulling). Once the lateral roots from around the stump were cut the stump and attached tap roots were pulled out (chain to back-hoe bucket) for weighing. Some of the roots would break off towards their tips. Any soil on the stump and attached roots was removed by washing or brushing prior to weighing. Generally the same machine that was used to pull the stump out was used to weigh the stump (spring balance between the bucket and the stump).

Step 3 (Coring). The excavation pit was back-filled with the coarse-sieved soil, levelled and soil cores taken (Fig. 4) to assess roots missed in Steps 1 and 2. Where possible a soil auger (150 or 100 mm diameter barrel) with motor power head was used. In hard soils, a trailer-mounted drilling rig was used (hollow-auger system, 45 mm diameter core).

All core samples were put through a fine (2 mm) sieve to extract roots for weighing. Thus, coring sampled roots in the back-fill (generally small roots that passed through the coarse sieve) and deep roots. In some cases (1- and 2-year-old trees only) no coring was undertaken below the excavated pit as inspection of the soil in the pit base indicated no roots there. Otherwise coring proceeded to a depth where no roots were observed in 1 m length of soil sample. Minimum coring depth for sample trees >2-year-old was 2 m and the maximum 6 m.

All core samples from Step 3 were wet-sieved. Samples from clay soil required soaking for 12–24 h to disperse the soil prior to sieving.

In thinned stands a small proportion of roots recovered in Steps 2 and 3 was from fused stumps—root systems of trees felled up to 15 years previously and still living from root grafts with retained trees. These roots were retained in the samples.

Root samples from cores were dried (70 °C) and weighed for dry weight determination. However, as for above-ground biomass, taking representative samples

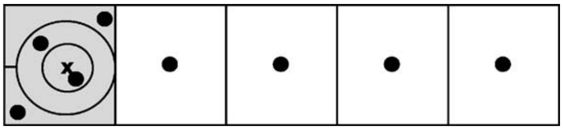

Fig. 4. Coring for volumetric soil/root samples. One core (●) located in each of four strata in the sub-plot (shaded rectangle) of a sample tree (×). If the sample tree was from an outside row (R1) additional strata were defined (light rectangles) out into to the paddock to the limit of lateral root extension.

of roots from Steps 1 and 2 was necessary. Scaling up from root mass in cores to estimated root mass from coring in a tree sub-plot was simply from the ratio of the area of the sub-plot to total cross-sectional area of cores in the sub-plot.

Steps 1 (surface soil excavation) and 2 (stump-pulling) were completed on all sample trees in a plot. However, as coring and sieving with 2 mm sieve is a laborious process (especially clayey or gravely soils), Step 3 (soil coring) was only done on two of the sample trees per plot. These trees were selected to represent one of the larger and one of the smaller trees in the plot. In rank order of size, the sample trees were trees 2 and 5 (six-tree plot), trees 2 and 7 (eight-tree plot) or trees 3 and 7 (10-tree plot).

The ratio of combined root mass from coring (Rc) to other biomass (OB) found in the two sub-plots subject to coring was assumed to apply to the other sub-plots. Thus, to estimate root mass from coring in the *i*th sub-plot

$$\mathrm{Rc}_i = \left(\frac{\mathrm{Rc}}{\mathrm{OB}}\right)\mathrm{OB}_i$$

Total root biomass in a plot (R) was then estimated as the sum of all estimates of root biomass on all sub-plots

$$R = \sum R_{ki}$$

where R_{ki} is estimate of root biomass from the *k*th step (Steps 1–3) on the *i*th sub-plot.

2.5. Allocation of root biomass to sample trees

Only roots retrieved by the stump-pulling step could be attributed directly to a sample tree. The origin of roots obtained in soil samples (excavation and coring steps) was not known. This is because, except for the youngest sample trees, some roots from each sample tree would have grown outside its sub-plot and, conversely, some roots from neighbouring trees would have grown in.

To estimate root biomass of sample trees we allocated the root biomass estimated from excavation and coring steps (Rec) within a plot amongst the sample trees in proportion to other biomass of each sample tree (OB_i) in the plot

$$\mathrm{Rec}_i = \left(\frac{\mathrm{Rec}}{\mathrm{OB}}\right)\mathrm{OB}_i$$

Finally, the estimate of root biomass of the *i*th tree in a plot was calculated as the sum of root biomass estimated from stump-pulling (Rs_i) and Rec_i

$$R_i = \mathrm{Rs}_i + \mathrm{Rec}_i$$

2.6. Carbon content of biomass

Representative sub-samples of all tree components were re-dried to constant weight at 70 °C and analysed for carbon content by the combustion furnace method (Rayment and Higginson, 1992; method 6B2).

2.7. Prediction equations

Biomass components were grouped into pools (Fig. 2) and both biomass and carbon mass prediction equations developed for each pool. Although ground-litter (fallen leaves and branches) and logging residues (above-ground slash, dead stumps and roots) were also measured, the results are not presented in this paper.

Categories recognised initially for development of prediction equations were outside row trees (R1), second row trees (R2) and internal trees (R3+), all from unthinned stands, plus trees from thinned stands (T). Also, data for each category were grouped into overlapping sets: group I with DBH < 10 cm and group II with DBH > 5 cm (Fig. 5). Candidate predictor variables for group I trees were stem diameter at a height of 10 cm (d_{10}) and tree height (h). For group II trees (DBH > 5 cm) candidate predictor variables were DBH, h and height to the crown base (h_c). The variable h_c was included to account for variation

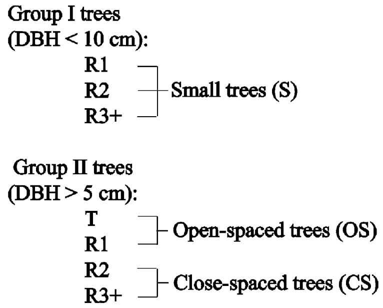

Fig. 5. Grouping of trees by DBH and row position/spacing categories for regression analysis. R1, R2 and R3+ = outside row, second row and internal trees, all from unthinned stands. T: Trees in thinned stands (all internal to block plantings).

in pruning height (range 0–6 m of pruning). Crown base was defined as the lowest part of the green crown, not including epicormic branches.

Dummy variable analysis (Hosmer and Lemeshow, 1989) was used to test for significant differences in the regression surfaces for different categories and categories combined where differences were not significant at $P = 0.05$ level. Fig. 5 shows grouping of categories for the whole-tree pool.

Categories were further grouped (S&CS, CS&OS) for individual pools if dummy variable analysis for a pool indicted no significant difference between categories. Thus, cases for development of biomass and carbon mass prediction equations were combinations of categories (S, CS, S&CS, OS and CS&OS) and biomass pools (stem, crown, top, roots and whole-tree). Regression analysis for each case was as follows.

Several alternative prediction models were compared as recommended by Clutter et al. (1983) and Parresol (1999)

combined variable :

$$Y = b_0 + b_1 d^2 + b_2 h + b_3 d^2 h - b_4 h_c d^2 + \varepsilon \qquad (1)$$

$$\text{non-linear}: \quad Y = b_0 + b_1 d^{b_2} h^{b_3} - b_4 h_c d^2 + \varepsilon \qquad (2)$$

$$\text{allometric}: \quad Y = b_1 d^{b_2} h^{b_3} (h - h_c)^{b_4} \varepsilon \qquad (3)$$

where d is the stem diameter (DBH or d_{10}), h the tree height, h_c the height to crown base, b_0, b_1, b_2, b_3 and b_4 the parameters to be estimated and ε the error term. The term $b_4 h_c d^2$, in Eqs. (1) and (2) was derived from the product of the relative height of pruning ($h_c h^{-1}$) and index of trees size ($d^2 h$), i.e. $b_4(h_c h^{-1})(d^2 h) = b_4 h_c d^2$, h conveniently cancelling out.

Eqs. (1) and (2) were fitted by weighted linear and weighted non-linear (WNL) regressions, respectively, weighting being necessary to satisfy the condition of constant variance (homoscedasticity) for regression analysis (Clutter et al., 1983). The weighted forms of these equations were

$$Yx^{-k} = (b_0 + b_1 d^2 + b_2 h + b_3 d^2 - b_4 h_c d^2 + \varepsilon) x^{-k} \qquad (4)$$

and

$$Yx^{-k} = (b_0 + b_1 d^{b_2} h^{b_3} - b_4 h_c d^2 + \varepsilon) x^{-k} \qquad (5)$$

where x^{-k} is a weighting factor, either d^{-k} or $(d^2 h)^{-k}$ depending on whether the model had d only or both d and h as predictor variables. The optimum value of k, to the nearest interval of 0.1, was selected on the basis of lowest Furnival index (FI) (Furnival, 1961; Bi and Hamilton, 1998).

Eq. (3) was log-transformed both to reduce heteroscedasticity and enable fitting by linear regression

$$\ln Y = \beta_1 + \beta_2 \ln d + \beta_3 \ln h + \beta_4 \ln (h - h_c) + \ln \varepsilon \qquad (6)$$

where the parameters in Eq. (3) are estimated as $b_1 = (e^{\beta_1}\mathrm{CF})$, $b_2 = \beta_2$; $b_3 = \beta_3$, $b_4 = \beta_4$. CF is a correction factor applied to correct the proportional bias in the estimate of Y introduced by the back-transformation. The correction factor was calculated as the ratio of the mean of sample values to the mean of back-transformed predicted values from the regression (Snowdon, 1991).

Backwards elimination was used to find a best model from each of Eqs (4)–(6). Thus, predictor variables were removed one at a time, first non-significant variables, then least significant variables if there was multi-collinearity ($R^2 > 0.9$) between remaining predictor variables.

Finally, a best model was selected from the best solutions to each of the alternative regression model (Eqs. (4)–(6)) based on the lowest FI. This index has the advantage that it is suitable for comparing regression models with different dependent variables; Yd^{-k}, $Y(d^2 h)^{-k}$ and $\ln Y$ in our examples. When the dependent variable is some function of Y, FI may be thought of as an average standard error transformed to units of Y (Furnival, 1961; Parresol, 1999).

A variety of goodness-of-fit statistics (Table 2) were calculated for each 'best model' as recommended by Schlaegel (1981) and Parresol (1999).

Table 2
Goodness-of-fit statistics presented for 'best models'

Coefficient of determination	$R^2 = 1 - \mathrm{RSS}/\mathrm{TSS}$	(7)
Fit index	$\mathrm{FI} = 1 - \mathrm{RSS}/\mathrm{TSS}$	(8)
Standard error of estimate	$S_e = ((\mathrm{RSS})/(n-p))^{0.5}$	(9)
Coefficient of variation	$\mathrm{CV} - (S_e/\bar{Y})100$	(10)

RSS, residual sum of squares ($\sum(Y - \hat{Y})$); TSS, total sum of squares ($\sum(Y - \bar{Y})$) either in weighted or transformed units (Eq. (7) or actual units (Eqs. (8)–(10)); n, number of samples; p, number of model parameters.

Table 3
Percentages of total root biomass retrieved by sampling method

Sampling method	Mean (%)	Range (%)
Surface soil sampling		
Coarse sieve	23	14–31
Fine sieve	13	10–18
Stump-pulling	42	22–53
Deep coring	22	10–51
Total	100	

Data for whole plots, block-planted and ≥5-year-old.

3. Results

3.1. Root sampling methods

Table 3 provides an indication of the proportions of the root biomass obtained by root sampling method. In mature block-planted *P. pinaster*, surface soil sampling typically yielded around 36% of the root biomass. This comprised roots obtained by coarse-sieving the soil (mean 23%) plus root biomass estimated by coring and fine-sieving the spoil from coarse-sieving (mean 13%). Most root biomass was obtained by the stump-pulling step (mean 42%). A substantial amount of roots were also obtained by the deep coring step (mean 22%, though the maximum recorded was 51% on one plot of 5-year-old trees).

3.2. Carbon content of biomass

A total of 61 samples were analysed, 44 from above-ground tree components and 17 from roots (Table 4). Analysis of variance indicated no significant difference between above-ground components ($P = 0.19$). The mean carbon content of all above-ground samples was 50.3%, not significantly different from 50.0% ($P = 0.26$). However, mean carbon content of roots at 48.1% was significantly different from 50.0% ($P = 0.001$). Therefore, the carbon content of biomass was taken as 50.0% for all above-ground components and 48.1% for all root material in subsequent carbon mass calculations.

Table 4
Carbon content of biomass components

Component	$C^{70\,^{\circ}C}$ (%)		
	n	Range	Mean
Aerial litter	3	50.8–53.1	52.0
Dead branches	5	48.9–52.6	50.2
Cones	6	48.3–52.6	50.1
Live branches and leaves	15	48.1–53.1	50.6
Stem	15	46.7–52.7	49.7
Roots	17	45.0–52.3	48.1

3.3. Biomass and carbon prediction

Best prediction equations with associated fit statistics are shown in Table 5. While biomass prediction equations are presented for all pools (stem, crown, top, roots and whole-tree), carbon prediction equations are only presented for whole-tree. However, carbon in other pools can easily be estimated by applying the appropriate carbon content percentage (50.0% for above-ground pools and 48.1% for roots).

In the case of crown, top and roots pools there were significant ($P < 0.05$) differences between the regression surfaces for close- and open-spaced trees. Hence, separate biomass prediction equations were required and are presented for close- and open-spaced trees, i.e. crown (Eqs. (12) and (13)); tops (Eqs. (15) and (16)); and roots (Eqs. (19) and (20)). However, there was no significant difference in the regression surfaces for biomass of whole-trees ($P > 0.05$). Hence data for close- and open-spaced trees were combined to calculate one biomass prediction equation (Eq. (25)). This was due to a compensating effect. For the same DBH (d) and h_c, close-spaced trees were predicted to have more top biomass but less root biomass than open-spaced trees. Similarly, only one carbon mass prediction equation was required for close- and open-spaced trees (Eq. (26)).

In general, stem diameter (d or d_{10}) was a better predictor variable for biomass than tree height (h). This is illustrated in the case of whole-tree biomass in Fig. 6. Tree height was only significant for predicting biomass in the case of stem biomass (Eq. (11)). However, height to crown base (h_c), in combination with stem diameter, was often a significant predictor variable (Eqs. (12), (13), (15), (19), (25) and (26)).

A variety of prediction equations for root biomass are presented. First root biomass is predicted as a function of d_{10} (Fig. 7; Eqs. (17) and (18)). This is to provide for root biomass estimation in post-logging

Table 5
Biomass and carbon prediction equations

Pool	Category[a]	Best prediction equation[b,c]	Regression model[d]	Weighting factor[e]	n	R^2	FI	S_e (kg)	CV (%)
Stem	CS&OS	$\mathrm{Bs} = 2.1 + 0.0140d^{2.168}h^{0.815}$	WNL	$(d^2h)^{-0.8}$	77	0.99	0.99	16.4	13
Crown	CS	$\mathrm{Bc} = 6.6 + 0.0252d^{2.672} - 0.015h_cd^2$	WNL	$d^{-1.8}$	44	0.94	0.87	13.9	38
Crown	OS	$\mathrm{Bc} = 11.2 + 0.00367d^{3.110} - 0.0069h_cd^2$	WNL	$d^{-1.4}$	33	0.97	0.96	26.5	19
Top	S	$\mathrm{Btp} = 1.078\mathrm{e}^{-3.183}(d_{10})^{2.336}$	LTA		87	0.99	0.95	1.8	39
Top	CS	$\mathrm{Btp} = 9.34 + 0.0389d^{2.709} - 0.0077h_cd^2$	WNL	$d^{-1.9}$	44	0.98	0.96	15.9	17
Top	OS	$\mathrm{Btp} = 12.7 + 0.0154d^{2.912}$	WNL	$d^{-1.7}$	33	0.99	0.98	44.7	13
Roots	S&CS	$\mathrm{Br} = 1.060\mathrm{e}^{-3.169}(d_{10})^{2.063}$	LTA		115	0.98	0.95	4.2	40
Roots	OS	$\mathrm{Br} = 0.00648(d_{10})^{2.803}$	WNL	$(d_{10})^{-2.5}$	33	0.97	0.93	37.1	24
Roots	CS	$\mathrm{Br} = 7.9 + 0.00582d^{2.892} - 0.0035h_cd^2$	WNL	d^{-1}	44	0.97	0.95	4.7	18
Roots	OS	$\mathrm{Br} = 8.9 + 0.00337d^{3.096}$	WNL	$d^{-1.7}$	33	0.97	0.97	27.6	18
Roots	S&CS	$\mathrm{Br} = 0.922\mathrm{e}^{-0.448}\mathrm{Btp}^{0.856}$	LTA		115	0.99	0.98	2.4	22
Roots	OS	$\mathrm{Br} = 0.714\mathrm{Btp}^{0.912}$	WNL	$\mathrm{Btp}^{-1.2}$	33	0.99	0.94	36.0	24
Tree	S	$\mathrm{Bt} = 1.060\mathrm{e}^{-2.482}(d_{10})^{2.235}$	LTA		87	0.98	0.96	2.4	33
Tree	S	$\mathrm{Ct} = 1.115\mathrm{e}^{-3.139}(d_{10})^{2.194}$	LTA		87	0.98	0.95	1.3	37
Tree	CS&OS	$\mathrm{Bt} = 20.1 + 0.0270d^{2.877} - 0.0079h_cd^2$	WNL	$d^{-1.7}$	77	0.99	0.99	42.9	15
Tree	CS&OS	$\mathrm{Ct} = 9.8 + 0.0138d^{2.868} - 0.0040h_cd^2$	WNL	$d^{-1.6}$	77	0.99	0.99	21.3	15

R^2 calculated in weighted or transformed units. Other goodness-of-fit statistics (FI, Se, CV) calculated on original biomass or carbon mass units. See Section 2 for details.

[a] Categories: small trees (S); close-spaced trees (CS); open-spaced trees (OS). There are no prediction equations for stem and crown of small trees as these components were not measured separately on small trees. Equations for two categories combined where there was no significant difference in the regression surfaces for those categories.

[b] Bs, Bc, Btp and Br indicate biomass of stem, crown, top and roots in kg; Ct = carbon mass of the whole-tree (top and roots) in kg; d_{10} and d = stem diameter over-bark in cm at heights of 10 cm and 130 cm (breast height); h = tree height in metres; h_c = height to crown base in m.

[c] LTA equations of the form $Y = b_1X^{b_2}$ expanded to $Y = \mathrm{CFe}^{b_1}X^{b_2}$ indicate the bias correction factor (CF).

[d] Best regression model for fitting parameters in prediction equation. Candidates were WCV (Eq. (4)), WNL (Eq. (5)) and LTA (Eq. (6)).

[e] Weighting factor if best fit by WNL. WCV never best and no weighting if LTA.

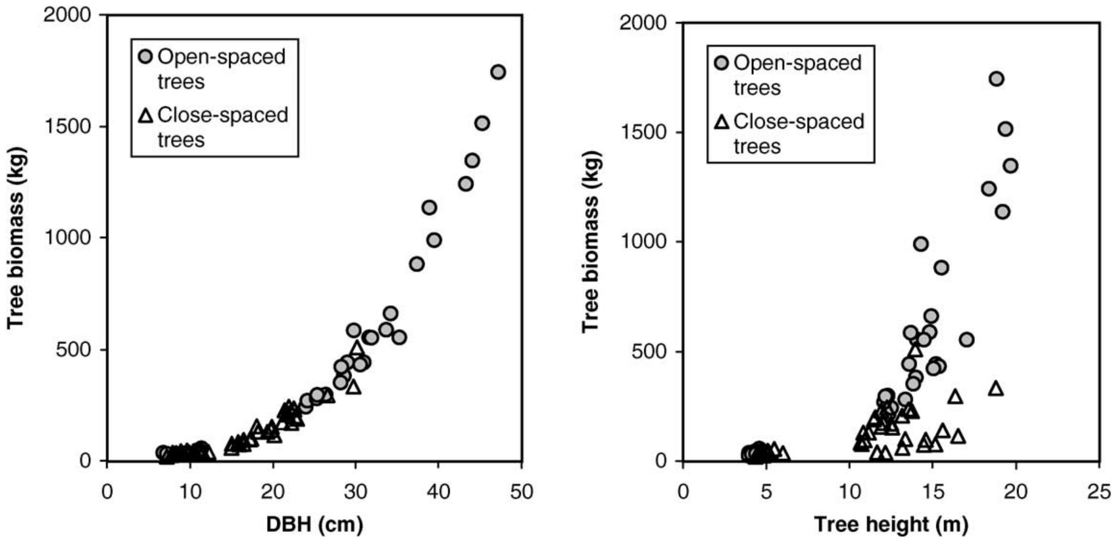

Fig. 6. Relationships between tree biomass and DBH and tree height.

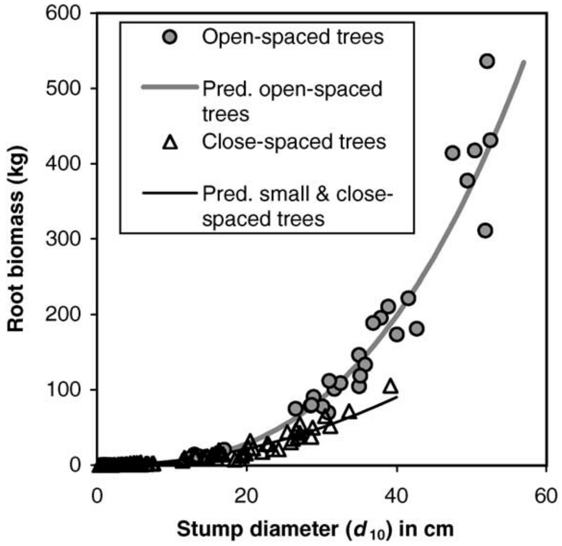

Fig. 7. Root biomass in relation to stump diameter in open-spaced and close-spaced trees.

inventory where only stump diameter of felled trees may be measured. Root biomass is also predicted as a function of DBH (Eqs. (19) and (20)) as this is a tree dimension that is easily and commonly measured on standing trees in timber or biomass inventory programs. Finally, root biomass is predicted as a function of top biomass (Eqs. (21) and (22) in Table 5). As will be discussed this is to provide for estimation of R:S ratios.

3.4. Root:shoot ratio

'R:S ratio' is used in this paper to indicate the ratio of root:top where 'top' is all live and dead biomass in and supported by the stem (material in or derived from shoots). Although the term top:root ratio appears in scientific literature, particularly in relation to trees (Smith, 1962; Komiyama et al., 2000), we use R:S ratio as this term is well established (Cripps, 1971; Reynolds and Thornley, 1982).

Dividing both sides of Eqs. (21) and (22) by Btp gives equations of the form

$$\mathrm{Br}(\mathrm{Btp})^{-1} = b_1\mathrm{Btp}^{b_2-1} \tag{27}$$

Substituting R:S for $\mathrm{Br}(\mathrm{Btp})^{-1}$ and inserting values of b_1 and b_2 from Eq. (21) into Eq. (1), the equation for small and close-spaced trees (S&CS) becomes

$$\mathrm{R{:}S} = 0.589\mathrm{Btp}^{-0.144} \tag{28}$$

Similarly, the equation for open-spaced trees becomes

$$\mathrm{R{:}S} = 0.714\mathrm{Btp}^{-0.088} \tag{29}$$

Predicted R:S ratios from Eqs. (28) and (29) are compared to actual R:S ratios of sample trees in Fig. 8. The fit for open-spaced trees was better than for CS&S trees. R:S ratio of S&CS trees with Btp < 50 kg was particularly variable. R:S ratio of larger (Btp > 50 kg) CS&S trees was less variable and clearly less than R:S ratio of open-spaced trees of similar top biomass.

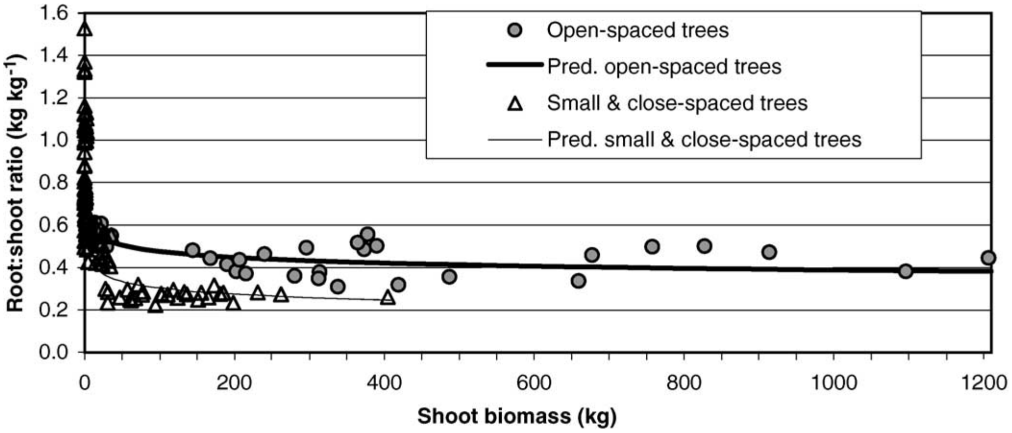

Fig. 8. Measured and predicted R:S ratios in open-spaced and close-spaced trees.

4. Discussion

4.1. Sampling methods

4.1.1. Above-ground biomass

The complete-harvest method for above-ground biomass determination was quick and simple compared to the effort required to estimate root biomass. With a bipod and block-and-tackle to weigh individual loads up to 200 kg, two people could complete the field sampling of above-ground components of a tree up to 2.5 t combined stem and crown weight in 2 h. After completing this study a digital load cell capable of weighing loads up to 2 t was tested. Used in combination with a back-hoe or other machine to hoist heavy loads, this makes above-ground sampling even more time-efficient.

Alternative methods for estimating crown and stem biomass, such as random branch sampling or importance sampling (Gregoire et al., 1995) involve sub-sampling. An advantage of the complete-harvest method is that, for fresh-weight determination at least, no sub-sampling errors are involved.

4.1.2. Root biomass

More time and effort was, of course, required to estimate root biomass. The two stage sieving process made the processing of bulk soil/root samples practical. A team of three people, including the back-hoe operator could process the soil area for an individual tree sub-plot (around 12 m^2, approximately 12 t of soil to 0.8 m depth) to obtain the fresh weights of roots from the coarse-sieving and stump-pulling steps in around 3–4 h. These steps typically yielded around 23 and 42% of root biomass (Table 3). Use of a 2 mm sieve only would have been impractical for the large soil volumes. Alternatively, use of a larger diameter sieve only would have resulted in more loss of small diameter roots through the sieve.

Core sampling from the surface soil (coarse-sieved spoil) and deep soil to estimate the remaining approximately 45% of root biomass was more time consuming. For a typical tree sub-plot, approximately 20 person-hours were required to obtain the core samples and another approximately 20 person-hours to sieve and clean the root samples for drying and weighing.

A problem with root sampling is that because of the extent to which tree roots from neighbouring trees in forest stands intermingle (Will, 1966; Wood and Bachelard, 1970), it is not possible to take soil/root samples and be sure of the origin of the roots. It is possible to excavate whole intact root systems (Watson and O'Loughlin, 1990; Mackie-Dawson and Atkinson, 1991) but this would be impractical for developing biomass prediction equations due to the large number of trees that must be sampled. The approach taken in this study of estimating root biomass in representative plots of trees and 'allocating' root biomass of uncertain origin to each tree in the plot in proportion to the biomass of known origin in those trees seems reasonable. There was no practical way of checking the assumption behind this approach. However, provided sample tree selection was unbiased, then the prediction equations developed will give an unbiased estimate of stand root biomass when applied in biomass inventory, i.e. overestimates for some trees would be counter-balanced by under-estimates for other trees.

4.2. Regression models

Of the candidate regression models the WNL model (Eq. (4)) was always best where DBH was a predictor variable (Eqs. (11)–(13), (15), (16), (19), (20), (25) and (26); Table 5). The superiority of the WNL model over the commonly applied log-transformed allometric (LTA) model (Eq. (6)) was not surprising. This is because back-transformation of the LTA model gives a model without any intercept (Eq. (3)), thus predicting zero biomass for a tree with zero DBH. However, trees 1.3 m tall ($\mathrm{DBH} = 0$) will have some biomass. Forcing the regression line through the origin, as the allometric model does, also has the effect of underestimating the biomass of trees with small DBH.

Other advantages of the weighted non-linear model are that, like the allometric model, compatibility with the homogeneity of variance assumption is possible but it is not necessary to correct for transformational bias (Crow and Laidly, 1980). The weighted combined variable (WCV) model also has these advantages and is popular for estimating the volumes or weights (Clutter et al., 1983; Deans et al., 1996; Bi and Hamilton, 1998) but, in this study WCV, was never best (Table 5).

With prediction based on d_{10}, rather than DBH, the LTA model proved best in four out of five cases

(Eqs. (14), (17), (23) and (24)), the WNL model being best in the other case (Eq. (18)). This indicates that where $d_{10} = 0$ (height 10 cm) biomass is so small that inclusion of an intercept term is unnecessary. A further indication of this is that, where weighted non-linear or WCV models were applied to estimated biomass as a function of d_{10}, the intercept was always not significant ($P > 0.05$).

Thus, the WNL model was best for biomass prediction as a function of DBH but where prediction as a function of d_{10} was necessary either the LTA model (with bias correction on back-transformation to actual units) or the WNL model were best.

That just one equation (Eq. (25)) was sufficient to predict biomass of both close- and open-spaced trees as a function of DBH and h_c was a fortunate result for carbon (or biomass) inventory application. In inventory, it would not be necessary to record whether a tree was close- or open-spaced to estimate tree biomass or carbon mass. However, to estimate biomass of components (crown, top or roots) it would be necessary to record whether a tree was close- or open-spaced to apply the appropriate prediction equation (Table 5).

The lack of usefulness of tree height (h), either as a sole predictor variable or in combination with stem diameter, was surprising. This is, however, convenient for ground-based inventory as h is difficult to measure from the ground, whereas stem diameter is comparatively easy to measure (DBH in particular and d_{10} to a lesser extent).

On the other hand, the lack of usefulness of h as a predictor variable is not convenient for inventory from remote sensing. Tree height can be measured in many remote sensing applications but stem diameter generally cannot. Crown cover may be useful for predicting biomass, particularly in areas of sparse tree or shrub cover. However, crown cover was not measured as a candidate predictor variable in this study as crown closure is reached early in plantation development. Following crown closure little or no further increase in crown cover is expected, negating the usefulness of crown cover for predicting further increases in biomass. That foliage biomass (related to crown cover) reaches a maximum with crown closure has been shown in other *Pinus* species, including *P. radiata* (Madgwick, 1994) and *P. sylvestris* (Usol'tsev and Vanclay, 1995). The same studies showed that stems, branches and roots continue to thicken after crown closure (monotonic increase with stand age).

Inclusion of height to crown base (h_c) as a predictor variable (Eqs. (12), (13), (15), (19), (25) and (26)) makes the prediction equations more versatile in that they take into account the effect of pruning. Thus, separate equations for pruned and unpruned trees were unnecessary. Interestingly h_c was a significant ($P < 0.05$) predictor variable for whole-tree, top and crown biomass even when analyses were confined to unpruned close- and open-spaced trees ($n = 58$).

Crown length (depth) has been used as a predictor variable for foliage and crown biomass (Madgwick, 1994). However, we did not find any references to h_c having been used in other studies. Use of h_c, which is equivalent to the difference between tree height and crown depth, has the advantage over crown depth measurement in that h_c is much easier to measure in ground-based inventory. If all trees in a measurement plot have been pruned to constant height or the natural crown base is at a constant level, it may not be necessary to measure h_c on all trees in the plot, one measurement applied to all trees in the plot may be sufficient.

4.3. Root:shoot ratio

The decline in R:S ratio with stand age and tree size, observed particularly in close-spaced trees and to a lesser extent in open-spaced trees (Fig. 8), is consistent with the other studies, e.g. in *P. pinaster* in France (Lemoine et al., 1986; Danjon et al., 1999), *P. radiata* in New Zealand (Beets and Pollock, 1987) and *Eucalyptus* species in northern Australia (Werner and Murphy, 2001).

However, the results also show a large difference in R:S ratio between close- and open-spaced *P. pinaster* trees of the same age or size. Open-spaced trees, which were either from outside rows or heavily thinned stands, had higher R:S ratios. In comparison, the few reported studies of the effect of spacing on R:S ratio in trees indicate a variable response.

Eastham and Rose (1990) report one study where R:S ratio increased with increasing spacing (decreasing stocking). They sampled 2.5-year-old *Eucalyptus grandis* afforestation in Qld., Australia and found that R:S ratio increased to 0.19, 0.32 and 0.77 in stockings of 2150, 304 and 88 trees ha^{-1}. Similarly, Puri et al.

(1994) sampled 9-year-old *Populus deltoides* afforestation in northern India and found that R:S ratio increased to 0.22, 0.33 and 0.75 at stockings of 2250, 531 and 208 trees ha^{-1}. These are large differences in R:S ratio though they are determined from limited sampling; one *E. grandis* and three *P. deltoides* trees only were sampled at each stocking density.

Beets and Pollock (1987) also predicted an increase in R:S ratio of *P. radiata* in New Zealand as a transient response to thinning. This was based on above-ground sampling at age 6 years (pre-thinning) and age 12 years (post-thinning), coring for fine roots and application of a general coarse root prediction equation to plot DBH data.

But other studies indicated R:S ratio was unaffected by spacing or that differences were too small to be statistically significant. One such study was of 33-year-old *Picea sitchensis* in Wales and UK. R:S ratios may have increased slightly from 0.27 at the highest stocking level (11,960 trees ha^{-1}) to 0.32 at lowest stocking level (640 trees ha^{-1}) but these differences were not significant at $P = 0.05$ (Fraser and Gardiner, 1967). Analysis of data in Usol'tsev and Vanclay (1995) for *P. sylvestris* on the dry steppe of Kazakhstan indicated almost identical R:S ratios at ages 20–50 years for plantations (4000–2000 trees ha^{-1}) compared to higher stocking native stands (16,000–6000 trees ha^{-1}). R:S ratios were around 0.5 at age 30 years and 0.37 at age 50 years. Atkinson et al. (1976) concluded that R:S ratio of 'golden delicious' apples in Kent, UK, were unaffected by spacing ranging from 111,000 to 1740 trees ha^{-1} when the trees were excavated 4.5 years after planting.

Just why there should be such variation in the effect of spacing on R:S ratio in tree plantations is not clear. One possibility is that, where no response of R:S ratio to spacing was established, this was because spacing was not increased sufficiently in the experimental treatments. But it is clear that, where a wide spacing treatment was included (stocking 320 trees ha^{-1} in our *P. pinaster* study and the *E. grandis* and *P. deltoides* studies) the effect of increasing spacing was to increase R:S ratio. Two possible explanations for this will be discussed: (1) that increased exposure to sunlight in open stands results in trees partitioning more to roots than foliage or other above-ground components; and (2) greater wind sway in open stands causes the roots to thicken more than stems and branches.

4.3.1. *Light effect*

Numerous experiments with tree seedlings and herbaceous plants have shown shading will decrease root growth more than shoot growth (decrease R:S ratio) but high levels of light increase R:S ratio (Brouwer, 1962; Ledig, 1983). The theory is that, if conditions limit photosynthesis as would occur with shading, photosynthate will be mostly used for crown growth, less for root growth. The converse tends to apply if water or nutrients (sourced by the roots) are limiting so that shoot growth is restricted more than root growth (increase in R:S ratio) (Brouwer, 1962; Thornley, 1971; Reynolds and Thornley, 1982; Ledig, 1983; Cannell, 1985).

The effect of increasing spacing, either through open planting layouts or thinning, would be to increase light availability. In particular, lower crowns would tend to be shaded on closed-spaced trees but receive full sunlight on open-spaced trees. Therefore, it is possible that the effect of increasing R:S ratio with increasing spacing in the *P. pinaster* trees was at least partly due to increased light availability. However, no reports of studies confirming or rejecting that increasing light increases partitioning to roots in mature trees were found. The R:S ratios of young apple trees in Western Australia (high light) were around double those of similar apple trees in England (comparatively low light) (Cripps, 1971; Cannell, 1985) but this effect may also have been due to confounding factors, such as higher water stress in Western Australia.

4.3.2. *Wind sway effect*

In classic experiments, mostly with *P. radiata* in the Australian Capital Territory, Jacobs (1939, 1954) showed that stems and roots thicken in response to wind sway. Such thickening was most pronounced at the bases of stems and roots where stress from wind is greatest. The effect was greater in heavily thinned stands (high wind exposure) than in a dense stand (less wind exposure) and could be reduced by staying trees to alleviate wind sway. That trees in open-spaced stands are subject to greater wind pressure than trees in close-spaced stands as evident from the susceptibility to wind-throw of trees remaining in stands after heavy thinning (Cremer et al., 1982).

Fayle (1976) described a similar experiment with *P. sylvestris* in Ontario. Thickening of basal roots and basal stem of stayed and free-standing trees were compared for 2 years before and after staying. Thickening was more pronounced in the free-standing trees and the effect was more pronounced in the basal roots than basal stems. However, the results may have been influenced by the removal of soil around the stem/root base of all trees (50 cm radius and 30 cm deep) that was not replaced.

The conclusion that roots thicken at the base in response to mechanical stress, notably wind sway is supported by several studies and reviews since Jacob's and Fayle's experiments (Wilson, 1964; Pritchett and Lyford, 1978; Fayle, 1980; Coutts, 1983; Crook and Ennos, 1996; Ennos and Pellerin, 2000). Cremer (1993) also concluded that extra thickening of proximal roots (taper) is a response to mechanical stresses of tree sway. He found that heartwood formation tends to be confined to the tapering proximal portions of roots and suggested it is formed as the innermost sapwood dies when in excess of the needs for conduction and storage.

Thus, the effect of thinning may be to increase the growth rate of all tree components (crown, stem and roots). However, based on our results with *P. pinaster* and the studies of wind sway, we hypothesise that the relative rate of increase is proximal roots $>$ lower stem $>$ upper stem. The hypothesis is supported by the fact that, for the same DBH, close-spaced *P. pinaster* trees had more top (shoot) biomass than open-spaced trees, the reverse applying to roots (Eqs. (12), (13), (19) and (20)).

5. Conclusions

The complete-harvest method for measuring biomass of above-ground tree components was a time-efficient and accurate sampling method. Root sampling was aided by a two-stage sieving process in which all surface soil was put through a coarse (25 or 50 mm) sieve then sub-samples of the spoil put through a fine (2 mm) sieve.

Biomass or carbon mass in trees with DBH > 5 cm can be reliably predicted as a function of DBH and either height to crown base (h_c) for whole-trees, crown and stem components or tree height (h) for the stem component. Biomass and carbon mass of small trees (DBH < 10 cm) or roots can be reliably predicted from basal stem diameter (d_{10}).

Average carbon content of root biomass is around 48.1% and of above-ground biomass components (stem, live branches and leaves, cones, dead branches and aerial litter) around 50.0%.

Of the three regression models compared, the WNL model was always best for prediction of biomass and carbon mass as a function of DBH and h_c. However, for prediction as a function of d_{10}, either the LTA model or the WNL model were best. A WCV model was never best.

The superiority of the WNL model over the LTA model for prediction from DBH was due to the provision for an intercept in the WNL model but not the LTA model. Logically, a regression model for tree biomass as a function of d_{10} should have an intercept term too. However, the biomass of trees 10 cm tall is so small it could be ignored (LTA model acceptable).

For the same DBH and h_c, close-spaced trees will have more crown and top biomass but less root biomass than open-spaced trees. This fortunate compensating effect meant that just one equation was sufficient for close- and open-spaced trees to predict biomass, or carbon mass, as a function of DBH and h_c. However, separate biomass prediction equations were required for close- and open-spaced trees for crown, tops or roots.

Two notable trends in R:S ratio were: (1) R:S decreased with increasing tree size; and (2) R:S was higher in open-spaced trees than close-spaced trees. Increased light availability in open-spaced stands may be a factor contributing to increased partitioning to roots in open-spaced trees. A more likely explanation is that open-spaced trees are subject to greater mechanical stress from wind sway and, while the response is a thickening throughout the tree (stem, branches and roots), the thickening is most pronounced in roots.

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