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Restore and sequester: estimating biomass in native Australian woodland ecosystems for their carbon-funded restoration

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Abstract. In the south-western region of Australia, allometric relationships between tree dimensional measurements and total tree biomass were developed for estimating carbon sequestered in native eucalypt woodlands. A total of 71 trees representing eight local native species from three genera were destructively sampled. Within this sample set, below ground measurements were included for 51 trees, enabling the development of allometric equations for total biomass applicable to small, medium, and large native trees. A diversity of tree dimensions were recorded and regressed against biomass, including stem diameter at 130 cm (DBH), stem diameter at ground level, stem diameter at 10 cm, stem diameter at 30 cm, total tree height, height of canopy break and mean canopy diameter. DBH was consistently highly correlated with above ground, below ground and total biomass. However, measurements of stem diameters at 0, 10 and 30 cm, and mean canopy diameter often displayed equivalent and at times greater correlation with tree biomass. Multi-species allometric equations were also developed, including 'Mallee growth form' and 'all-eucalypt' regressions. These equations were then applied to field inventory data collected from three locally dominant woodland types and eucalypt dominated environmental plantings to create robust relationships between biomass and stand basal area. This study contributes the predictive equations required to accurately quantify the carbon sequestered in native woodland ecosystems in the low rainfall region of south-western Australia.

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Introduction

The recognised biodiversity hotspot of south-western Australia (Mittermeier *et al*. 2005) has suffered significant levels of biodiversity loss as a result of large-scale land clearing and the on-going pressure from fragmentation of native habitats (Hobbs 1998). The removal of woody vegetation has also exacerbated the expansion of dryland salinity (Eberbach 2003) further endangering the conservation of biodiversity and associated ecological functions of the region (Cramer and Hobbs 2002). The re-establishment of woody vegetation on cleared lands is widely recognised as an effective strategy for ameliorating these negative environmental impacts (Harper *et al*. 2007; Radford and Bennett 2007). However, markets to fund large-scale conservation focussed on reforestation have been lacking.

The emerging market for carbon sequestration may provide a solution. Biosequestration through reforestation is widely recognised as an effective strategy for absorbing atmospheric carbon (IPCC 2003). To date, however, most large-scale reforestation projects have relied on non-native plantation trees harvested for timber products (Conte and Kotchen 2010) often in higher rainfall areas, and generally providing limited benefits to native biodiversity. Such permanent land-use change fails to restore the highly depleted (historically cleared) forest and woodland ecosystems, and the structural and functional attributes they provide (Flynn *et al*. 2009; Munro *et al*. 2009). The international carbon markets were estimated in 2007 to be worth US$64 billion (Capoor and Ambrosi 2008). This new market presents a significant opportunity to invest in the restoration of woodland ecosystems for both carbon sequestration, and the many additional services they provide (Bekessy and Wintle 2008; Freudenberger 2010). A significant barrier to attracting investment in this carbon market is the absence of credible, consistent and cost efficient methods for quantifying the carbon sequestered in restored native woodlands. In contrast, the simplicity of commercial plantation systems, and a history of growth measurement methods for timber production, have resulted in robust and widely accepted techniques for calculating that approach to carbon biosequestration.

The primary aim of this research was to develop allometric equations to predict tree biomass from tree dimensional measurements in order to improve the estimation of carbon sequestered and stored in the low rainfall Eucalypt woodlands of south-western Australia. This research also included a

collection of stand inventory measurements for use in estimating the carbon carrying capacity of native Eucalypt woodlands. Until now, there were few allometric equations for native 'non-timber' tree species located in low rainfall regions. This has delayed the accurate quantification of carbon carrying capacities for these woodland ecosystems and their potential to sequester carbon (Grierson *et al*. 2000; Berry *et al*. 2010). This information gap has also contributed to the delay in investments in reforestation projects that seek to restore native woodland ecosystems for carbon sequestration. This in turn has delayed the restoration of many of the ecological services provided by native vegetation including provision of biodiverse habitats, reduction of soil erosion, filtration of water, and abatement of dryland salinity. Such reforestation projects could substantially benefit the highly cleared and fragmented agricultural zone prevalent in the south-western region of Western Australia (Harper *et al*. 2007), while also protecting and buffering the remnant ecosystems within this biodiversity hotspot (Hopper 2009).

Materials and methods

To address this gap in carbon accounting capability, a carbon research program was initiated in south-western Australia through Greening Australia, a not-for-profit organisation working to re-establish and manage native vegetation. A total of 71 trees were harvested across five sites, made up of eight species that commonly occur in this region. Trees sampled ranged from small (DBH = 2.3 cm, height = 2.5 m) to large (DBH = 79.0 cm, height = 20.1 m), and represented three different genera. Field inventory data was collected from 83 plots across 25 sites of remnant native woodland ecosystems and 10 sites of environmental reforestation plantings, equating to a total of 6719 trees measured. This research also quantified biomass allocation to various plant structures, above and below ground.

Study area

The entire dataset was collected within the Fitz-Stirling operational area of the Gondwana Link (http://www.gondwanalink.org, accessed 3 October 2011), a conservation initiative spanning ~10 000 km^2. Six sites were selected for destructive sampling of total biomass across a partially cleared agricultural landscape located between the Stirling Ranges and Fitzgerald River National Parks in the south-west of Western Australia, north-east of the regional centre of Albany, Australia. The sites were selected based on having the required species, range of tree sizes, and landholder permission for destructive sampling of some trees. The climate of the region is Mediterranean, with an average annual rainfall of ~450 mm, 70% of which falls in the cooler months from April to October (Bureau of Meteorology 2010). The landscape hosts a diverse mix of vegetation types including tall closed Mallee (multi-stemmed eucalypts with swollen fire-resistant roots), mixed Mallee scrub, tall open woodland, and low closed forests. The soils of the region are old, highly weathered, and often nutrient poor. The patch-like distribution of these soils has given rise to a highly diverse flora with high levels of endemism (Hopper and Gioia 2004).

Species selection

Native trees species were selected for total biomass sampling which most consistently occupied the upper-storey structural stratum within the three main local vegetation associations 'Mallee', 'Moort' and 'Yate' woodlands (Boland *et al*. 2006). The species selected were also noted to occur in widely distributed populations with stand densities likely to make substantial contributions to the local carbon pool.

The following eight tree species were selected: *Eucalyptus occidentalis*, *E. platypus* subsp. *platypus*, *E. annulata*, *E. captiosa*, *E. falcata*, *E. flocktoniae*, *Acacia saligna* ('Tweed River' variant), and *Allocasuarina huegeliana*. These trees represent four different growth forms: a tall woodland form (*E. occidentalis*), a medium woodland form (*A. saligna*, and *Al. huegeliana*), a Mallee form (*E. falcata*, *E. captiosa*, *E. flocktoniae*, and *E. annulata*) and the marlock form (*E. platypus*). A marlock is a single-stemmed small tree with spreading branches that are densely leafy almost to the ground when growing in the open, yet forming a low closed canopy with little lateral branching when growing close together (Boland *et al*. 2006; Nicolle 2006). The marlock growth form demonstrated by *E. platypus*, lacks a lignotuber, and is the defining characteristic of the Moort vegetation association. As the Mallee-type vegetation associations are widespread across southern regions of Australia, the selection of multiple species within this growth form aimed to test the efficacy of a multi-species ('generic') allometric relationship.

Tree selection and measured dimensions

All trees destructively sampled followed the methods of Snowdon *et al*. (2002). Trees were subjectively selected from remnant woodland stands of unknown age. All selected trees appeared to be unaffected by forestry management such as pruning or stand thinning, however some may have benefited from proximity to agricultural systems and access to adjacent fertilised cropping areas. Selected trees had no major missing branches, obvious canopy decline, or advanced epicormic re-sprouting. Sampling occurred across a diverse range of landscape positions and soil types. For each species, trees were selected to provide a wide range of sizes, using DBH as a guide (Fig. 1). This broad sample of trees aimed to provide allometric equations suitable for the diversity of trees sizes and locations in both newly established environmental plantings and mature woodland ecosystems in this region of south-western Western Australia.

For each tree, dimensional variables for allometry (predictors) were recorded along with photos and GPS coordinates. Measured dimensions were: stem diameter at 130 cm (DBH), stem diameter at ground level (D_0), stem diameter at 10 cm above ground (D_{10}), stem diameter at 30 cm above ground (D_{30}), total tree height (H), height to canopy break (H_C), canopy width (C_W), and canopy length (C_L). C_W was measured directly perpendicular to C_L. All stem measurements were conducted over the bark.

For trees with more than one stem, the quadratic mean of all stem diameters was calculated to produce a single representative value (Snowdon *et al*. 2002). For Mallee species, all stem measurements were taken in relation to the lignotuber surface, as opposed to ground level. Heights for all trees were measured

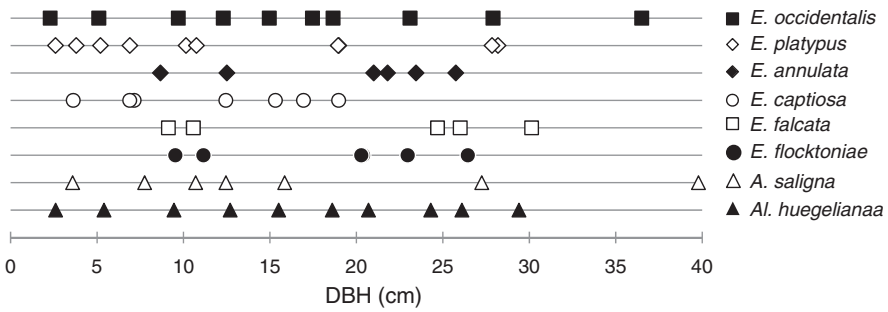

Fig. 1. Distribution of diameter at breast height (DBH) measurements for individual trees destructively sampled for total or above ground biomass.

using a clinometer, at a distance of 20 m from each individual. A diameter tape was used to record all stem diameter measurements. H_C was measured from ground level to the base of the live crown. Canopy diameter (C_D) was the calculated average value of C_W and C_L.

The full suite of dimensional measurements was not always possible for every tree or across all species. For example the fluted buttress-like lower trunk of *Al. huegeliana* made the D_0 measurement impractical. In addition, some stem diameter measurements were not able to be recorded due to irregularities in woody growth such as unusual branching or burl formations. This difficulty in obtaining the full suite of measurements is reflected in the variable sample size for each allometric equation listed in the result tables and appendices.

For species sampled with a Mallee growth form, that have multiple stems originating from a common lignotuber, an alternative approach to developing allometric relationships for above ground biomass was used. As described above, a whole of tree allometric equation for total biomass was always developed using the quadratic mean of all stem diameters (Snowdon *et al.* 2002). Results for these analyses are presented in Tables 1–6. However, in Appendix 1, allometric equations for above ground biomass of species from the Mallee growth form were developed using individual stems, rather than the quadratic mean of all stems. This was done because during collection of field inventory data from Mallee woodlands, it can be difficult to determine whether a collection of stems comes from a single lignotuber (one tree) or from multiple lignotubers, particularly in old remnants. We suggest that use of individual stem allometrics will provide a more precise estimate of above ground biomass when measuring species with a Mallee growth form. The use of quadratic means of multiple stem measurements introduces unnecessary errors due to the problem of distinguishing between individual trees. This uncertainty is removed for the analysis of total biomass since each lignotuber is excavated and individual trees and their stems can be determined with certainty. Further, in the context of carbon accounting, biomass per tree is less important than total biomass per unit area.

Partitioning of tree biomass

Prior to felling each tree, all coarse woody debris at ground level below and around the sampled tree was removed. Brittle deadwood material was first collected from the tree by hand. Felling was then executed sequentially starting with the branching locations first, and then working down to ground level. Woody biomass was partitioned into different representative material categories. The allocation of fresh weight biomass into specific size and material categories varied both between and among species, but the categories of leaves plus green shoots, dead wood plus bark, and small-, medium- and large branch size classes were consistent across all trees and species measured.

Partitioning of fresh biomass into selected size classes aimed to aggregate materials of similar water content. For large trees, the number of different categories increased. For example, in the largest tree sampled (*E. occidentalis*, DBH = 79.0 cm), 14 fresh weight categories were used to appropriately stratify the above ground biomass materials into representative size classes. In contrast, small trees (DBH < 10.0 cm) had as few as three partitioned size classes when sampling above ground fresh biomass. This approach enabled subtle differences in fresh biomass water content to be measured from one material category to another, improving the accuracy of the fresh weight to dry weight ratios used to calculate total dry biomass.

For all trees sampled, locations of chainsaw cuts were guided by the natural branching patterns. Cuts were made immediately following branching nodes, helping to manage and segregate branch thickness categories, often expressed in differences in the extent of core hardwood versus sapwood and their associated water content.

Once above ground biomass materials were partitioned into representative size classes, the total fresh weight biomass was measured using a platform balance (±0.05 kg for <25.0 kg, and ±0.25 kg for >25.0 kg). Immediately following this procedure, representative subsamples for each fresh weight size class was collected and weighed on a smaller compact balance (±0.1 g up to 3000 g). All fresh weight subsamples were greater than 300 g in mass. The subsamples were collected as follows: two to three representative leaf plus shoot 'units' were taken and bulked to form a single subsample for this category. For branches and main stems, several cross-sectional discs (4–10 cm in length) were cut at both the centres and ends of the branches and main stem to include any difference in water content across each measured unit. All subsamples were then dried to constant weight in a fan-forced oven at 70°C.

Below ground excavation of roots

Below ground biomass was determined for 51 of the 71 trees sampled, including all of the species sampled for above ground biomass, with the exception of *A. huegeliana.*

A mechanical excavator was used to remove all roots and soil located within a 1.5-m hemispherical radius from the centre of each tree base. This approach is likely to have underestimated the full extent of below ground biomass, as lateral roots were not pursued beyond the 1.5-m boundary. However, previous studies on below ground biomass for eucalypt trees have shown that up to 75% of coarse root material is located within a 1-m^2 area centred on the tree base (Resh *et al*. 2003). Where earth moving equipment was not available or needed, root excavation within this zone was carried out manually.

Excavated root materials were sieved and sorted into five size categories including fine (<10 mm), medium (10–30 mm), and large (30–60 mm) roots. In addition, the large subsurface tree bole (termed 'root crown' for this study), and the larger roots still attached to the root crown following excavation (termed 'large tap and lateral roots') were also measured separately. In the case of the Mallee tree forms, the root crown was defined as the lignotuber, with all other root categories remaining consistent with the other tree forms.

A sieve with 20-mm aperture was used to separate the root material from the soil medium. The root materials were sorted by visual assessment and allocated into their appropriate size categories. All soil was removed from root materials manually using metal tools and wire brushes. Total fresh weight biomass of each size class was measured. Subsampling protocols for determining dry biomass were the same as those described for above ground biomass.

Allometric relationships between tree dimensions and biomass

All tree dimensions (predictors) were tested individually for both species-specific and generic regressions. As the data demonstrated a level of heteroscedasticity, all variates were transformed to their natural logarithm (ln).

The following models were used for this study:

$$\ln(Biomass) = a + b\ln(\text{predictor}) \text{ (Model 1)}$$
$$\ln(Biomass) = a + b\ln(\text{predictor 1}) + c\ln(\text{predictor 2}) \text{ (Model 2)}$$

Due to natural logarithmic transformation of the data, and a need to back transform the resulting biomass values into real terms, a bias correction factor was applied using the ratio method of Snowdon *et al*. (2002). The correction factor is defined as the ratio of the arithmetic mean of the observed biomass values and the arithmetic mean of the back-transformed biomass predictions for a given regression. Once calculated for a regression, the bias correction factor was applied to all back-transformed values produced by the given regression to achieve a more accurate prediction of biomass.

For the transformed data, calculations of the error mean square (EMS), and the coefficient of determination of the transformed data (R^2) are reported. The EMS of the transformed data was calculated by dividing the sum of the squares (the difference between the observed and predicted values squared $[(o-p)^2]$, by the number of samples (n). The R^2 value was calculated by subtracting the ratio of the sum of the squares and the sum of the mean squares (the squared value of the observed transformed biomass value minus the average of all observed transformed biomass values), from a value of 1 following standard statistical procedures (Freedman *et al*. 2007).

For the back-transformed data, the coefficient of variation (CV), and the model efficiency (EF) values are reported. The CV is a percentage value calculated as the standard error divided by the mean of all observed biomass values. The standard error was calculated as the square root of the sum of the squares, divided by n subtracted by a value that represents the number of coefficients used in the regression. Consistent with the approach used in Paul *et al*. (2008), the EF was calculated by subtracting the ratio of the sum of the squares and the mean square values of the back-transformed bias corrected data, from a value of 1. The mean square value is defined as the squared value of the observed (non-transformed) biomass value minus the average of all observed (non-transformed) biomass values. All statistical analyses for single variable regressions were undertaken in Microsoft Excel (2007), while multi-variate analyses were undertaken in GENSTAT version 8.1 (VSN International, Hemel Hempstead, UK).

Stand inventory data

Inventory data for estimating the tree stand carbon pool were collected from 35 sites across the local landscape sampling a mix of environmental plantings (reforestation) of known age ($n = 10$), and mature remnant stands of the dominant ecosystems types of the region: Yate woodland ($n = 8$), mixed Mallee woodland ($n = 9$), and Moort woodland ($n = 8$). Environmental plantings were typically established on farms with a mixture of regionally native eucalypts and acacias. These plantings were generally small (less than 10 ha), and positioned beside cleared agricultural lands in belts 4–5 tree rows in width. Trees growing on the outer rows adjacent to cultivated fields were excluded from measurement.

Plots were randomly positioned within tree stands of representative composition and densities. Plot size was on average 200 m^2 however this increased at times to ensure a minimum of 20 trees were measured per sample plot area. Tree diameter measurements were recorded for all trees within each plot.

Calculation of total stand biomass

Using the newly developed allometric equations, field inventory data was converted to biomass. Biomass values were then converted from kilograms to tonnes per plot, and then scaled up to per-hectare values. A regression between stand basal area (SBA) and total biomass per hectare was also determined following Burrows *et al*. (2000) and Burrows *et al*. (2002).

Tree basal area (TBA, cm^2) was defined as:

$$\text{TBA} = \pi(\text{DBH}/200)^2$$

The units used for the DBH values entered in the TBA equation are centimetres.

SBA (m^2 ha^{-1}) was defined as:

$$\text{SBA} = \Sigma(\text{TBA of all trees in plot})\,(\text{plot area}^{-1})\,(10\,000)$$

The units for the plot area are m^2, while the equation is then multiplied by 10 000 to convert unit area measurement of the output values to hectares.

Results

Single variate allometric equations for biomass

A variety of easily measured tree dimensions were found to be well correlated for above ground, below ground, and total biomass. Full lists of all relationships developed from this study are provided in Appendices A, B, and C. Allometric equations for total biomass were developed for seven of the eight species sampled. We were unable to sample below ground biomass for *A. huegeliana.* These relationships are presented in Fig. 2, where each of the tree dimensions measured were regressed against total biomass for the sampled species. All stem diameter measurements were found to be highly correlated with total biomass, with the strongest relationships occurring using D_0, D_{30}, D_{10}, and DBH. The C_D was also highly correlated with total biomass. Height was not found to be well correlated for total biomass in this study. Table 1 reports the tree dimensional measurements that were highly correlated with total biomass for each individual tree species. Full results for total biomass analysis are provided in Appendix 2.

Predicting above and below ground biomass

Consistent with the findings for total biomass, a variety of easily measured tree dimensions were also found to be highly correlated with both above and below ground biomass (Appendices B and C). For estimating above and below ground biomass pools from a given stem measurement, DBH was found to have the most consistent correlation across all species analysed. For example, DBH was found to have the best correlation with above ground biomass for *E. platypus* ($R^2 = 0.977$), *E. captiosa* ($R^2 = 0.920$), *E. falcata* ($R^2 = 0.969$) and *A. saligna* ($R^2 = 0.996$). Conversely, other tree dimensions were also found to be just as well correlated or more closely correlated with above and below ground biomass. For above ground biomass, D_{30} was shown to have the highest correlation in three of the eight species modelled (*E. occidentalis*, $R^2 = 0.995$; *E. annulata*, $R^2 = 0.964$; *A. huegeliana*, $R^2 = 0.997$). Diameter measurements at D_{10} were also found to be highly correlated for above ground biomass (*E. falcata*, $R^2 = 0.953$; *E. platypus*, $R^2 = 0.977$; *E. captiosa*, $R^2 = 0.812$; *A. huegeliana*, $R^2 = 0.993$). Surprisingly C_D was also highly correlated with above ground biomass, especially for *E. occidentalis* ($R^2 = 0.988$) and *E. flocktoniae* ($R^2 = 0.993$). Of all tree dimensions measured, H was consistently the least correlated with above ground biomass for every species modelled.

Similarly, stem diameter measurements at D_0, D_{10}, and D_{30} were highly correlated with below ground biomass. The diameter measurement at D_{30} was shown to be highly correlated with below ground biomass, particularly for *E. occidentalis* ($R^2 = 0.996$) and *E. platypus* ($R^2 = 0.975$). DBH was the best correlate with below ground biomass for *E. falcata* ($R^2 = 0.968$) and *A. saligna* ($R^2 = 0.992$), while D_{10} had the highest correlation for *E. annulata*

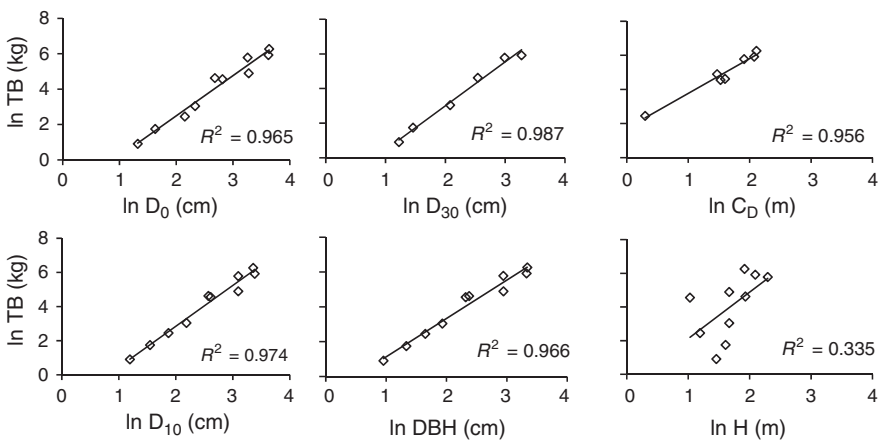

Fig. 2. Relationships between a full suite of ln-transformed tree dimensional measurements and the observed ln-transformed total dry biomass (kg) for *Eucalyptus platypus*.

Table 1. Allometric equations[A] between total biomass (TB, kg) and a variety of independent variables (predictors) at the individual species level
All tree dimensional units (P) are in centimetres, except for C_D, which is reported in metres. EMS is the error mean square of the transformed data. Bias is the ratio method reported in Snowdon *et al*. (2000). CV is the coefficient of variation reported for the back-transformed data. EF is a measure of the model efficiency

Species	*n*	R^2	Predictor	P range	*a* (s.e.)	*b* (s.e.)	EMS	Bias	CV	EF
E. occidentalis	10	0.999	LN D_{30}	2.9–41.0	−2.194 (0.094)	2.474 (0.034)	0.005	1.046	14.8	0.990
E. platypus	6	0.987	LN D_{30}	3.4–26.4	−2.076 (0.345)	2.541 (0.145)	0.047	0.944	52.6	0.850
E. annulata	5	0.997	LN D_{10}	8.9–28.9	−0.260 (0.177)	1.803 (0.059)	0.002	1.078	12.3	0.968
E. captiosa	7	0.965	LN D_{10}	6.0–21.4	−1.325 (0.487)	2.199 (0.188)	0.036	1.023	31.2	0.885
E. falcata	5	0.995	LN DBH	9.1–30.1	−0.030 (0.219)	1.852 (0.075)	0.004	0.997	13.3	0.973
E. flocktoniae	5	0.993	LN C_D	3.0–8.5	1.820 (0.179)	1.982 (0.094)	0.004	1.003	10.1	0.969
A. saligna	7	0.997	LN DBH	3.6–39.8	−1.624 (0.143)	2.254 (0.054)	0.008	0.985	9.5	0.997

[A]Model applied is: ln (TB) = *a* + *b*ln (predictor).

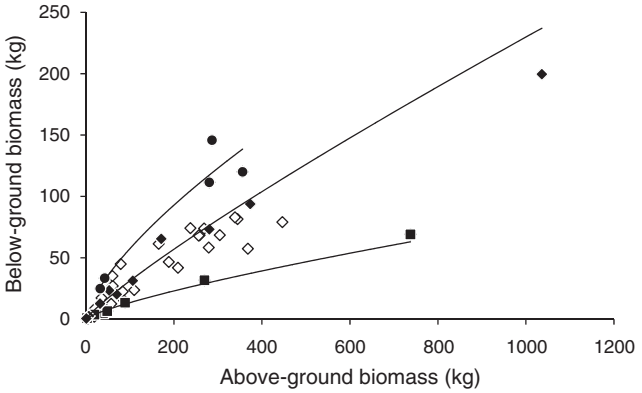

Fig. 3. Relationships between above ground biomass and below ground biomass. ● = *E. falcata* ($y = 2.37x^{0.69}$, $R^2 = 0.97$), ◆ = *E. occidentalis* ($y = 0.578x^{0.87}$, $R^2 = 0.99$), ■ = *A. saligna* ($y = 0.386x^{0.77}$, $R^2 = 0.99$), ◇ = other four species measured.

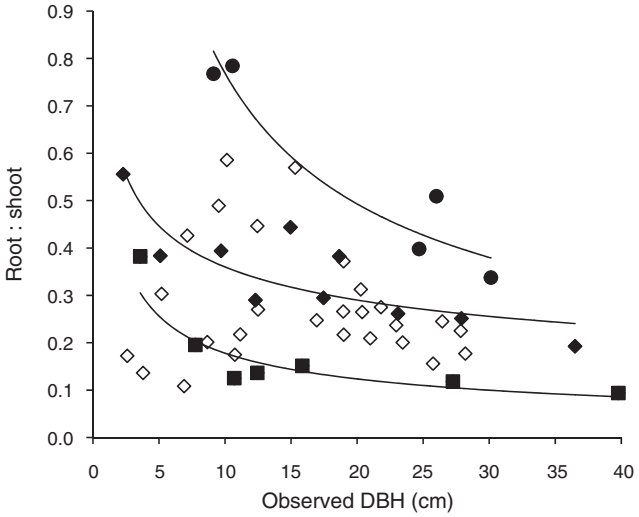

Fig. 4. Relationships between diameter at breast height and root to shoot ratios for: ● = *E. falcata* ($y = 3.37x^{-0.69}$, $R^2 = 0.89$), ◆ = *E. occidentalis* ($y = 0.74x^{-0.31}$, $R^2 = 0.68$), ■ = *A. saligna* ($y = 0.60x^{-0.53}$, $R^2 = 0.84$). ◇ = other four species measured.

($R^2 = 0.969$). C_D was generally well correlated with below ground biomass, and surprisingly provided the strongest correlation for both *E. captiosa* ($R^2 = 0.963$) and *E. flocktoniae* ($R^2 = 0.992$). In line with the results from above ground biomass, H was consistently the weakest correlate with below ground biomass.

Biomass partitioning

Biomass allocation between above and below ground biomass varied among the species (Fig. 3). *E. falcata*, a Mallee form with a large ligno-tuber, had a greater proportion of below ground biomass than other species, ranging from 78% for smaller trees (DBH = 10.6 cm) to 34% for large trees (DBH = 30.1 cm). This was in contrast to the fast-growing *A. saligna* where relatively low quantities of below ground biomass were observed, ranging from 38% for small trees (DBH = 3.6 cm) to 9% for large trees (DBH = 39.8 cm).

The ratio of below ground biomass to above ground biomass (root : shoot ratio) generally decreased as the overall size of the individual increased (Fig. 4). Smaller (younger) trees generally had a greater proportion of biomass below ground compared with larger (older) trees, which had increasing proportions of biomass above ground.

On average, approximately half (56%, s.e. ± 2.9) of total tree biomass (above and below ground) was found in live branches and main stems with the exception of *A. saligna* with ~71% (s.e. ± 2.5) of total biomass as live branches and main stem (Table 2). On average, only 17% (s.e. ± 1.3) of total biomass was found in leaves and shoots (fine green stems). Of particular interest is the fraction of total biomass with a high probability of being combusted during a wildfire event. This fraction was defined as the leaves and shoots plus bark and dead branches. This volatile fraction comprised on average 23% (s.e. ± 1.9) of total biomass across the seven species measured (Table 2).

Multivariate allometric equations for biomass

Several multivariate analyses were run to test the merits of using more than one tree dimension in regressions to estimate biomass. To test their usefulness for species-specific allometric relationships, H and C_D were added to DBH, and D_{30} regressions for total biomass. Mixed results were shown across the species modelled following the inclusion of a second variate. In all cases, the improvement in precision for the biomass estimates using two variates was minor given the already strong predictive strength generated from the models based on a single variate. While the inclusion of (H) as a second variate was not found to be statistically significant, C_D was shown to be a significant second predictor (*F*-prob. <0.001) to include with DBH or D_{30} measurements (Tables 3 and 4).

Table 2. The above ground partitioning of biomass as a fraction of total (above and below ground) biomass [mean fraction (±s.e.)]

	Mean fractions of total biomass			
Species	Leaves + shoots	Bark + dead branches	Live branches + stem	Volatile fraction[A]
E. occidentalis	0.183 (0.021)	0.024 (0.006)	0.543 (0.032)	0.207 (0.019)
E. platypus	0.164 (0.019)	0.071 (0.021)	0.581 (0.038)	0.235 (0.021)
E. annulata	0.216 (0.044)	0.084 (0.017)	0.545 (0.043)	0.300 (0.031)
E. captiosa	0.175 (0.008)	0.048 (0.002)	0.553 (0.008)	0.223 (0.006)
E. falcata	0.162 (0.026)	0.067 (0.017)	0.421 (0.041)	0.310 (0.089)
E. flocktoniae	0.171 (0.011)	0.036 (0.007)	0.540 (0.029)	0.207 (0.011)
A. saligna	0.095 (0.008)	0.058 (0.008)	0.706 (0.025)	0.154 (0.008)
Mean (±s.e.)	0.167 (0.013)	0.055 (0.007)	0.556 (0.029)	0.234 (0.019)

[A]Leaves + shoots + bark + dead branches.

Table 3. Species-specific ln-transformed allometric equations[A] for total biomass (TB, kg) and ln(DBH) and ln(C_D)
EMS is the error mean square of the transformed data. Bias is the ratio method reported in Snowdon *et al*. (2000). CV is the coefficient of variation reported for the back-transformed data. EF is a measure of the model efficiency

Species	*n*	R^2	*a* (s.e.)	*b* (s.e.)	*c* (s.e.)	EMS	Bias	CV	EF
E. occidentalis	10	0.992	−1.114 (0.387)	1.928 (0.309)	0.518 (0.372)	0.028	1.027	20.2	0.984
E. platypus	9	0.963	0.151 (0.465)	1.225 (0.331)	0.932 (0.302)	0.126	0.810	46.5	0.860
E. annulata	6	0.955	−0.92 (1.01)	2.324 (0.978)	−0.29 (1.20)	0.032	1.012	28.6	0.863
E. captiosa	7	0.983	0.372 (0.297)	1.254 (0.256)	0.766 (0.339)	0.017	0.998	28.0	0.926
E. falcata	5	0.996	0.032 (0.280)	1.726 (0.256)	0.191 (0.366)	0.003	0.995	14.7	0.979
E. flocktoniae	5	0.992	1.229 (0.888)	0.459 (0.672)	1.576 (0.603)	0.005	0.987	12.9	0.966
A. saligna	7	0.999	−1.880 (0.150)	2.633 (0.164)	−0.523 (0.220)	0.004	1.031	12.9	0.995

[A]Model applied is: ln (TB) = $a + b\ln(DBH) + c\ln(C_D)$.

Table 4. Species-specific ln-transformed allometric equations[A] for total biomass (TB, kg) and ln(D_{30}) and ln(C_D)
All abbreviations are consistent with those previously described

Species	*n*	R^2	*a* (s.e.)	*b* (s.e.)	*c* (s.e.)	EMS	Bias	CV	EF
E. occidentalis	10	0.999	−1.964 (0.166)	2.290 (0.118)	0.219 (0.135)	0.003	1.023	11.5	0.995
E. platypus	5	0.989	−1.66 (1.28)	2.286 (0.837)	0.198 (0.662)	0.047	0.937	58.9	0.855
E. annulata	6	0.990	−0.612 (0.372)	1.818 (0.291)	0.292 (0.376)	0.007	0.999	11.6	0.977
E. falcata	5	0.990	−0.891 (0.786)	1.511 (0.460)	1.088 (0.497)	0.009	1.009	19.8	0.961
E. flocktoniae	5	0.991	1.038 (0.799)	0.557 (0.554)	1.497 (0.492)	0.006	0.986	13.8	0.961
A. saligna	7	0.992	−2.147 (0.447)	2.251 (0.386)	0.157 (0.489)	0.022	1.072	40.6	0.952

[A]Model applied is: ln (TB) = $a + b\ln(D_{30}) + c\ln(C_D)$.

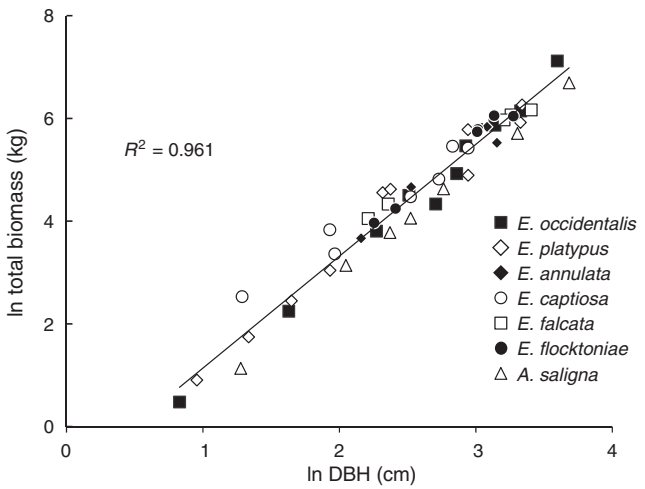

Fig. 5. Transformed relationship of total biomass and DBH ($y = 2.18x - 1.04$, $R^2 = 0.96$) for the seven tree species sampled for both above and below ground biomass.

Multi-species allometric equations

The relationship between DBH and total biomass was generally similar among all species (Fig. 5), though species as a factor in the multivariate analysis was significant (*F*-prob. <0.001). This statistical analysis indicated that *A. saligna* had a significantly different relationship to the eucalypts (*t* prob. <0.001). However, no statistical differences among the eucalypts were detected (*t* prob. >0.05). Hence, a range of 'generic' equations for only the eucalypt genus were developed for total biomass in order to provide more generalised and broadly applicable allometric equations (Tables 5 and 6).

The selected groups of generic relationships were defined as the 'Tall Mallee' growth form (*E. annulata*, *E. captiosa*, *E. falcata*, and *E. flocktoniae*) and the '*Eucalypts*' generic set defined as all the 'Tall Mallee' species plus *E. occidentalis* and *E. platypus*. For these 'generic' relationships, each of the stem diameter measurements (DBH, D_0, D_{10}, and D_{30}) was highly correlated with total biomass (Table 5).

Multivariate models were again developed to assess the merits of adding a second variate to these multi-species allometric equations. H and C_D were again tested in Model 2 (see Sect. 2.2.4), coupled with DBH and D_{30}. Consistent with the single species equations, the addition of H did not significantly improve the model (*F* prob. >0.1), whereas adding C_D as a second variate did significantly improve the models (*F* prob. <0.001) (Table 6).

Calculation of biomass for environmental plantings and mature remnant woodlands

A combination of species-specific and generic allometric equations, along with inventory data of stem diameters were used to develop a single relationship between total dry biomass and SBA combining the three main woodland ecosystem types (remnants) and environmental reforestation plantings (Fig. 6). A single relationship is reported because 'vegetation type' was not a significant variate in the model ($P = 0.29$). It should be noted this relationship only included the tree component of the carbon pool, thus did not include any contributions made by shrubs, herbaceous materials, or coarse woody debris. The individual woodland type biomass (*y*) to SBA (*x*) relationships were:

Table 5. Generic 'Tall Mallee' and 'Eucalypt Genera' allometric equations[A] for total biomass (kg) using DBH, D_0, D_{10}, D_{30}, H, and C_D
Each generic group is composed of species combinations (see Methods) to produce 'Tall Mallees' (4 species), and 'Eucalypt Genera' (6 species) regressions. Predictor ranges (P range) report non-transformed values in centimetres, except for H and C_D, which are reported in metres

Generic set	Predictor	P range	*n*	R^2	*a* (s.e.)	*b* (s.e.)	EMS	Bias	CV	EF
All species sampled of the 'Tall Mallee' growth form ($n=4$)[B]	LN DBH	3.6–30.1	24	0.969	−0.163 (0.202)	1.906 (0.073)	0.033	1.019	19.4	0.932
	LN D_0	11.2–36.3	17	0.933	−1.617 (0.479)	2.201 (0.152)	0.050	1.006	30.7	0.768
	LN D_{10}	6.0–32.7	22	0.972	−1.195 (0.236)	2.143 (0.082)	0.031	1.012	23.4	0.914
	LN D_{30}	9.1–31.3	19	0.958	−1.086 (0.326)	2.164 (0.109)	0.029	1.002	20.1	0.887
	LN H	2.5–9.0	24	0.681	1.140 (0.576)	2.265 (0.330)	0.336	1.109	51.1	0.529
	LN C_D	1.9–8.5	23	0.889	1.437 (0.287)	2.269 (0.175)	0.120	1.023	39.7	0.700
All species sampled of the 'Eucalypt Genera' ($n=6$)[C]	LN DBH	2.3–36.5	44	0.966	−0.936 (0.167)	2.162 (0.062)	0.075	1.010	31.6	0.911
	LN D_0	3.8–38.0	27	0.959	−2.061 (0.290)	2.320 (0.096)	0.082	0.991	36.3	0.790
	LN D_{10}	3.3–32.7	32	0.972	−1.636 (0.198)	2.290 (0.071)	0.053	0.997	28.3	0.898
	LN D_{30}	2.9–41.0	35	0.982	−1.902 (0.160)	2.423 (0.056)	0.042	0.986	21.6	0.952
	LN H	2.5–12.3	44	0.488	0.210 (0.722)	2.515 (0.398)	1.143	1.305	74.4	0.505
	LN C_D	0.9–10.0	42	0.914	1.558 (0.168)	2.236 (0.109)	0.196	1.047	45.3	0.806

[A]Model applied is: $\ln(TB) = a + b\ln(\text{predictor})$.
[B]'Tall Mallee': *E. annulata*, *E. captiosa*, *E. falcata*, and *E. flocktoniae*.
[C]'Eucalypt Genera': *E. occidentalis*, *E. platypus*, and all species of the 'Tall Mallee' growth form.

Table 6. Generic 'Tall Mallee' and 'Eucalypt Genera' allometric equations for predicting total tree biomass (TB, kg) from two independent variables
The model applied is: $\ln(TB) = a + b\ln(P_1) + c\ln(P_2)$, where P_1, and P_2 are represented by the first and second predictor variables listed below. All abbreviations and species lists are consistent with previous Tables

Generic set	P_1	P_2	*n*	R^2	*a* (s.e.)	*b* (s.e.)	*c* (s.e.)	EMS	Bias	CV	EF
'Tall Mallee'[A] growth form	ln(DBH)	ln(C_D)	23	0.982	0.120 (0.187)	1.449 (0.153)	0.611 (0.191)	0.019	1.011	16.6	0.950
	ln(D_{30})	ln(C_D)	18	0.972	0.619 (0.347)	1.651 (0.209)	0.619 (0.214)	0.019	1.001	16.2	0.923
'All Eucalypt' species[A]	ln(DBH)	ln(C_D)	42	0.981	−0.268 (0.178)	1.501 (0.130)	0.754 (0.139)	0.043	1.000	28.4	0.926
	ln(D_{30})	ln(C_D)	33	0.988	−1.278 (0.223)	1.939 (0.141)	0.496 (0.135)	0.029	0.990	17.1	0.969

[A]See Methods for definitions of 'Tall Mallee' and 'All Eucalypt' species.

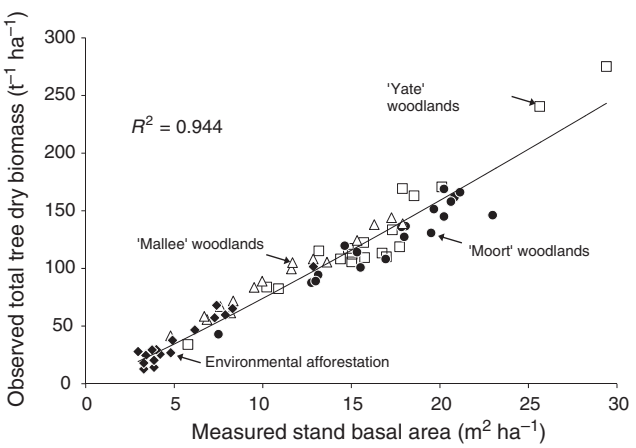

Fig. 6. Relationship between field measured stand basal area (SBA) and predicted total dry stand biomass ($y = 5.84x^{1.10}$, $R^2 = 0.94$) for three dominant Eucalypt woodland ecosystems ('Yate' – *E. occidentalis*, 'Moort' – *E. platypus*, and 'Mallee' – mixed Mallee Eucalypt species) and eucalypt-dominated environmental reforestation plantings measured in sites within the study area.

Moort ($y = 4.21x^{1.19}$, $R^2 = 0.94$), Mallee ($y = 9.28x^{0.96}$, $R^2 = 0.98$), and Yate ($y = 4.17x^{1.23}$, $R^2 = 0.94$), and for the environmental reforestation type plantings ($y = 4.51x^{1.25}$, $R^2 = 0.82$).

Discussion

Choice of stem dimensional measures for field inventory

Through the analysis of a broad suite of easily measured tree dimensions, the equations developed in this study demonstrate that allometry is consistent when observed across several different locations on a tree. Within the literature, a broad range of different tree measurements have been reported, and this has been noted as an obstacle in the comparative analysis of independently published results (Eamus *et al.* 2000; Keith *et al*. 2000; Snowdon *et al.* 2000). A full analysis of different tree dimensions, and their correlation to tree biomass, can help researchers and managers interpret and apply past and present works. The results demonstrate that stem diameter measurements from the ground level up to 1.3 m (DBH) generally have similar predictive utility, as long as tree bole development is not affected by fluting or other morphological irregularities.

Forest inventory data has historically been collected manually from commercial plantations. DBH is a sensible stem measurement in terms of both worker ergonomics and the dominance of single stems in plantations. As investments in carbon abatement projects for non-timber environmental reforestation projects increase, new approaches to measurement are likely to be required. For example, most species from arid and semi arid zones do not have a single stem form and often have excessive branching at 1.3 m. In these situations, access to D_0, D_{10}, or D_{30} allometric equations

can reduce the number of measurements from many multiple stems per tree to just one.

C_D was another useful measurement for predicting total biomass. For trees with relatively uniform canopy form, C_D was highly correlated with total tree biomass. Hence, remotely sensed measurement of C_D (e.g. digital aerial photography) may have potential as a low cost and accurate method for carbon accounting across large areas. This is of particular interest for spatially heterogeneous environments where stand biomass can vary greatly due to relatively small-scale changes in soil properties (e.g. slope, texture and depth). We suggest future studies on biomass allometry include canopy diameter measurements linked to remotely sensed data to further explore this potential.

Tree height had the weakest correlation with biomass for trees sampled in this study. These findings are in contrast to published results from other regions and other tree types (Burrows *et al*. 2000; Keith *et al*. 2000; Wang 2006; Werner and Murphy 2001). The utility of height as a predictor for biomass is likely to be associated with several environmental factors that govern tree stand growth responses, where natural cues such as shading due to high stocking densities result in competition for light and subsequent elongated growth. Relationship between crown geometry, shade tolerances, and height have been found to strongly correlate to tree biomass in mixed temperate hardwood forests from the south-east of the United States (Dietze *et al*. 2008). Regional biophysical variables such as rainfall, soil depth, fire interval, and genetic disposition are likely to influence tree stand development, natural rates of senescence, and resulting stand height. For the low rainfall, and nutrient poor soils found in this region of south-west Western Australia, height was not found to be a strong predictor for biomass.

Generalised allometry

There are over 800 species of *Eucalypts* and nearly 1000 *Acacias* found across Australia. All have potential to be included in carbon sequestration plantings; however published allometric equations for estimating biomass are available for just a few of them. The development of species-specific allometric equations for every *Eucalypt* and *Acacia* species is both impractical and inefficient. Like some previously published studies (Burrows *et al*. 2000; Williams *et al*. 2005; Wang 2006; Berry *et al*. 2010), we found that a generic or multi-species approach to estimating biomass is justified. The eight species used in the current study show a broadly consistent relationship between stem measurements and total biomass, even though these eight species were from three different genera and of markedly different growth forms. Consistent among the trees sampled for this study were the relatively uniform levels of high evaporation, low rainfall and nutrient-poor soils. Further research is needed to assess the influence of bioclimatic (e.g. regional) variation on the accuracy of generic (multi-species) allometric relationships across different tree species and variable growth forms.

The generic equations developed in this study are likely to have direct application to the measurement of carbon in low rainfall woodland ecosystems across the south-western region of Western Australia due to similar biophysical characteristics and dominant tree genera composition (Berry *et al.* 2010). While much interest has been made about the capacity of monocultures of Mallee species to sequester carbon, no known data has been published which quantifies the carbon carrying capacity of such plantations. Likewise no known data has been published which quantifies the carbon carrying capacity of mixed Mallee eucalypt woodlands that include a diversity of species. The allometric relationships presented in this study between SBA and total biomass for Eucalypt woodlands, along with the predictive tools required to produce them, provide managers and researchers some capacity to do so. Our methodological approach is also recommended for application in other regions where the restoration of native woodland systems is desired.

Biomass partitioning

There are few studies that report on the total above and below ground biomass for trees within natural woodland systems. Most available literature on allometric equations has traditionally focussed on above ground biomass. As a consequence, managers and researchers have been required to use estimations of below ground biomass values when attempting to calculate total biomass values for a given site. Our results have shown that different species demonstrate different levels of above and below ground biomass partitioning depending on species form, age, and specific life cycle growth strategies. For example, the large woodland tree, *E. occidentalis*, is an obligate seeder, which is fast growing and long lived (Nicolle 2006) and allocates a large proportion of total biomass to above ground mass (Fig. 3). In contrast, a species with quite a different life cycle and growth strategy is *E. falcata*, a long-lived slower-growing Mallee, which readily regenerates from its lignotuber following fire. Given its strategy of resprouting following disturbance, a Mallee tree requires significant investment in below ground biomass for storage of regenerative resources. The third species highlighted in Fig. 3 is *A. saligna*, a short-lived, fast-growing medium-sized woodland tree that is an obligate seeder often killed by fire. Given its smaller size and limited longevity, the apparent growth strategy for this species is to invest large resources into above ground biomass.

The different growth strategies demonstrated by the three species highlighted in Fig. 3, and their observed differences in biomass partitioning, illustrate how differences in carbon pool accumulation and storage in mixed woodland ecosystems occurs. We suggest that a diversity of tree species with varying life cycles and growth strategies should be included in carbon sequestration plantings, especially in climatically variable environments prone to droughts and wildfires. Previous assumptions that monocultures consistently sequester more carbon than diverse systems have been shown to be incorrect in both Australia rainforest systems (Kanowski and Catterall 2010) and Mediterranean forests (Vila *et al*. 2007). The inclusion of fast-growing species like *A. saligna* can provide initial and rapid sequestration of carbon for a site, as well as provide nitrogen fixation. However in the region, *Acacias* are relatively short lived (10–40 years) and therefore lack the capacity to make long-term contributions to the local carbon pool. Through the inclusion of long-lived *Eucalypt* tree species

such as Mallees, large proportions of biomass are stored below ground, minimising the risk of carbon loss following stochastic events like a high intensity wildfire. This strategy of using a diversity of functionally different trees for long-term biosequestration has been implemented by Greening Australia in south-western Western Australia (Jonson 2010).

We also argue that the perceived threat of fire to terrestrial biosequestration projects in the fire-prone ecosystems such as Australia may not be as great as considered. Through the use of locally adapted species, the potential 'volatile' component of tree biomass is relatively small. Based on our biomass partitioning results (Table 4), we predict that less than 25% of total biomass is likely to be lost during a hot fire. A large proportion of biomass will remain post-fire stored in the large branches, stems and roots. Given the investment in biosequestration projects to offset greenhouse gas emissions globally, additional research to quantify the specific changes to carbon pools following wildfire events is clearly needed across a full spectrum of woodland ecosystems worldwide.

Carbon-funded restoration

Our study fills a knowledge gap for accurately estimating the carbon sequestration capacity of native woodland ecosystems for the low rainfall region of south-western Australia. Our research greatly improves the capacity to develop regional-based growth models that accurately estimate carbon sequestration and storage in native woodlands. This has been identified as a key area in need of further development (Barrett *et al*. 2001; Dean *et al*. 2004; Richards and Brack 2004).

Ecologically focussed restoration of marginal agricultural landscapes in Australia and other continents have the potential to sequester substantial quantities of atmospheric carbon, while also ameliorating land degradation and biodiversity loss (Freudenberger 2010). With an estimated area of 11.6 M ha of Mallee woodlands cleared for agriculture, and 7.6 M ha of eucalypt open woodlands cleared in Western Australia alone (Cofinas and Creighton 2001), there is great scope for their restoration. In order to attract carbon investments and capture the environmental benefits achievable through large-scale ecological restoration of cleared lands, certainty in both yield forecasting and on-going carbon accounting is required. Central to this process is the development of robust measurement tools for the accurate calculation of carbon sequestered in species diverse plantings. The approach used in this study provides a comprehensive example of how new allometric equations can be developed using a diversity of tree measurements. These equations are important tools for estimating carbon sequestered in a diversity of native woodland trees. Already, these tools are being used to quantify carbon yield and successfully attract investment in the restoration of native woodland ecosystems in southern Australia (Berry *et al*. 2010; Jonson 2010).

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Appendix 1. Eight species-specific ln-transformed allometric equations for total biomass (TB, kg) predicted by DBH, D_0, D_{10}, D_{30}, H, and C_D
Model 1 is used: ln (TB) = a + $b$ln(predictor), with standard error values reported in parentheses. Predictor ranges (P range) report non-transformed values in centimetres, except for H and C_D, which are reported in metres. All abbreviations are consistent with those previously described. Dases indicate missing data

Species	Predictor	P range	n	R^2	a (s.e.)	b (s.e.)	EMS	Bias	CV	EF
E. occidentalis	LN DBH	2.3–36.5	10	0.989	−1.549 (0.241)	2.341 (0.089)	0.039	1.092	29.2	0.962
E. occidentalis	LN D_0	–	–	–	–	–	–	–	–	–
E. occidentalis	LN D_{10}	–	–	–	–	–	–	–	–	–
E. occidentalis	LN D_{30}	2.9–41.0	10	0.999	−2.194 (0.094)	2.474 (0.034)	0.005	1.046	14.8	0.990
E. occidentalis	LN H	2.5–12.3	10	0.909	−3.305 (0.895)	3.877 (0.434)	0.313	1.263	79.7	0.715
E. occidentalis	LN C_D	1.1–10.0	10	0.941	1.138 (0.336)	2.749 (0.243)	0.202	0.822	31.2	0.956
E. platypus	LN DBH	2.6–28.2	10	0.966	−1.073 (0.357)	2.203 (0.146)	0.107	0.955	43.2	0.875
E. platypus	LN D_0	3.8–38.0	10	0.965	−2.063 (0.425)	2.275 (0.153)	0.110	0.997	42.0	0.882
E. platypus	LN D_{10}	3.3–29.5	10	0.974	−1.944 (0.358)	2.393 (0.138)	0.081	1.013	42.6	0.879
E. platypus	LN D_{30}	3.4–26.4	6	0.987	−2.076 (0.345)	2.541 (0.145)	0.047	0.944	52.6	0.850
E. platypus	LN H	2.8–9.9	10	0.335	−0.643 (2.377)	2.764 (1.376)	2.091	1.795	97.5	0.364
E. platypus	LN C_D	0.9–8.3	9	0.956	1.791 (0.239)	1.993 (0.162)	0.148	1.086	26.4	0.947
E. annulata	LN DBH	8.7–25.7	6	0.955	0.751 (0.660)	2.095 (0.228)	0.032	1.005	24.8	0.863
E. annulata	LN D_0	11.2–36.3	5	0.982	−0.853 (0.471)	1.908 (0.148)	0.014	0.997	19.8	0.938
E. annulata	LN D_{10}	8.9–28.9	5	0.997	−0.260 (0.177)	1.803 (0.059)	0.002	1.078	12.3	0.968
E. annulata	LN D_{30}	9.1–27.0	6	0.989	−0.736 (0.318)	2.027 (0.106)	0.008	1.000	11.6	0.970
E. annulata	LN H	4.1–8.2	6	0.668	0.517 (1.689)	2.750 (0.969)	0.235	1.029	56.2	0.296
E. annulata	LN C_D	3.1–7.7	6	0.873	1.115 (0.806)	2.459 (0.470)	0.090	1.007	36.2	0.707
E. captiosa	LN DBH	3.6–19.0	7	0.960	0.188 (0.386)	1.764 (0.162)	0.041	1.038	26.2	0.919
E. captiosa	LN D_0	–	–	–	–	–	–	–	–	–
E. captiosa	LN D_{10}	6.0–21.4	7	0.965	−1.325 (0.487)	2.199 (0.188)	0.036	1.023	31.2	0.885
E. captiosa	LN D_{30}	–	–	–	–	–	–	–	–	–
E. captiosa	LN H	2.5–8.6	7	0.677	1.453 (0.907)	1.957 (0.604)	0.329	1.069	47.0	0.739
E. captiosa	LN C_D	1.9–6.4	7	0.876	1.361 (0.516)	2.234 (0.376)	0.127	1.049	32.7	0.874
E. falcata	LN DBH	9.1–30.1	5	0.995	−0.030 (0.219)	1.852 (0.075)	0.004	0.997	13.3	0.973
E. falcata	LN D_0	14.8–34.7	5	0.964	−3.182 (0.960)	2.713 (0.305)	0.031	0.989	36.2	0.804
E. falcata	LN D_{10}	12.7–32.7	5	0.967	−2.040 (0.788)	2.427 (0.258)	0.028	0.989	33.8	0.830
E. falcata	LN D_{30}	12.5–31.3	5	0.946	−1.824 (0.995)	2.396 (0.331)	0.047	0.990	36.9	0.797
E. falcata	LN H	3.6–8.6	5	0.888	0.950 (0.914)	2.557 (0.525)	0.096	0.998	51.7	0.600
E. falcata	LN C_D	3.1–7.4	5	0.898	1.367 (0.788)	2.520 (0.490)	0.088	1.007	54.4	0.558
E. flocktoniae	LN DBH	9.5–26.4	6	0.981	−1.108 (0.448)	2.251 (0.156)	0.014	0.995	22.2	0.899
E. flocktoniae	LN D_0	13.3–31.8	6	0.963	−1.720 (0.696)	2.249 (0.221)	0.028	1.006	24.7	0.875
E. flocktoniae	LN D_{10}	11.2–28.3	5	0.982	−1.274 (0.519)	2.170 (0.172)	0.015	1.010	22.9	0.924
E. flocktoniae	LN D_{30}	10.4–26.2	6	0.982	−1.065 (0.436)	2.174 (0.147)	0.013	1.004	17.8	0.935
E. flocktoniae	LN H	5.1–9.0	6	0.610	−2.039 (2.951)	3.712 (1.485)	0.289	1.103	57.2	0.326
E. flocktoniae	LN C_D	3.0–8.5	5	0.993	1.820 (0.179)	1.982 (0.094)	0.004	1.003	10.1	0.969
A. saligna	LN DBH	3.6–39.8	7	0.997	−1.624 (0.143)	2.254 (0.054)	0.008	0.985	9.5	0.997
A. saligna	LN D_0	4.6–15.3	3	0.991	−2.414 (0.537)	2.327 (0.225)	0.016	1.010	31.7	0.924
A. saligna	LN D_{10}	4.4–14.9	4	0.987	−2.236 (0.436)	2.299 (0.186)	0.017	0.998	26.6	0.916
A. saligna	LN D_{30}	4.1–39.0	7	0.992	−2.256 (0.267)	2.371 (0.096)	0.022	1.089	38.5	0.946
A. saligna	LN H	3.5–11.2	7	0.783	−4.048 (1.966)	4.156 (0.979)	0.602	1.453	69.9	0.822
A. saligna	LN C_D	2.1–9.5	6	0.971	1.119 (0.325)	2.380 (0.207)	0.042	1.096	10.1	0.996

Appendix 2. Eight species-specific ln-transformed allometric equations for above ground biomass (AGB, kg) predicted by DBH, D_0, D_{10}, D_{30}, H, and C_D
Model 1 is used: ln (AGB) = a + $b$ln(predictor), with standard error values reported in parentheses. Predictor ranges (P range) report non-transformed values in centimetres, except for H and C_D, which are reported in metres. All abbreviations are consistent with those previously described. Equations for the multi-stem Mallee species are for individual stems, not whole trees (*E. annulata*, *E. captiosa*, *E. falcata and E. flocktoniae*). Dashes indicate missing data

Species	Predictor	P range	*n*	*a* (s.e.)	*b* (s.e.)	R^2	EMS	Bias	CV	EF
E. occidentalis	LN DBH	2.2–79.0	14	−2.140 (0.189)	2.467 (0.061)	0.993	0.040	1.076	19.6	0.993
E. occidentalis	LN D_0	–	–	–	–	–	–	–	–	–
E. occidentalis	LN D_{10}	–	–	–	–	–	–	–	–	–
E. occidentalis	LN D_{30}	2.9–41.0	11	−2.194 (0.157)	2.463 (0.056)	0.995	0.014	1.068	18.4	0.995
E. occidentalis	LN H	2.4–20.1	14	−4.632 (0.721)	4.439 (0.319)	0.942	0.323	1.305	53.2	0.941
E. occidentalis	LN C_D	1.1–18.4	14	0.771 (0.242)	2.801 (0.138)	0.972	0.156	0.921	17.6	0.972
E. occidentalis	LN C_D	1.4–18.4	13	1.225 (0.156)	2.577 (0.086)	0.988	0.046	1.060	15.8	0.988
E. platypus	LN DBH	2.6–28.1	17	−1.203 (0.207)	2.161 (0.085)	0.977	0.057	0.983	34.6	0.977
E. platypus	LN D_0	3.7–38.0	17	−2.223 (0.349)	2.242 (0.126)	0.955	0.112	1.047	39.8	0.955
E. platypus	LN D_{10}	3.3–29.5	11	−2.057 (0.303)	2.358 (0.120)	0.977	0.069	1.032	45.0	0.977
E. platypus	LN D_{30}	3.4–26.8	13	−2.171 (0.339)	2.433 (0.137)	0.967	0.085	1.024	33.7	0.966
E. platypus	LN H	2.8–9.9	17	−1.092 (1.621)	2.980 (0.968)	0.387	1.520	1.589	101.6	0.387
E. platypus	LN C_D	0.7–8.2	16	1.497 (0.248)	2.059 (0.182)	0.902	0.254	1.128	38.8	0.902
E. annulata	LN DBH	5.8–21.0	16	−1.118 (0.363)	2.159 (0.150)	0.937	0.040	1.025	22.4	0.936
E. annulata	LN D_0	9.7–20.2	15	−3.623 (0.789)	2.829 (0.294)	0.877	0.060	1.033	32.3	0.877
E. annulata	LN D_{10}	7.8–18.4	15	−2.771 (0.516)	2.658 (0.203)	0.929	0.035	1.021	18.3	0.929
E. annulata	LN D_{30}	7.3–26.5	16	−1.863 (0.307)	2.385 (0.123)	0.964	0.022	0.963	34.5	0.964
E. annulata	LN H	4.1–8.2	6	0.270 (1.689)	2.779 (0.969)	0.673	0.235	1.031	57.4	0.673
E. annulata	LN C_D	4.1–8.2	6	0.886 (0.807)	2.478 (0.470)	0.874	0.090	1.010	36.8	0.874
E. captiosa	LN DBH	3.6–15.3	10	−0.811 (0.479)	2.012 (0.209)	0.920	0.056	1.027	39.5	0.920
E. captiosa	LN D_0	–	–	–	–	–	–	–	–	–
E. captiosa	LN D_{10}	6.0–18.4	10	−2.235 (1.021)	2.434 (0.414)	0.812	0.133	1.020	53.1	0.812
E. captiosa	LN D_{30}	10.5–14.4	5	−0.296 (3.435)	1.809 (1.382)	0.363	0.073	1.044	36.6	0.363
E. captiosa	LN H	2.5–8.6	7	0.324 (0.892)	2.414 (0.594)	0.768	0.318	1.020	50.9	0.768
E. captiosa	LN C_D	1.9–6.4	7	0.594 (0.773)	2.461 (0.565)	0.792	0.285	1.112	46.6	0.792
E. falcata	LN DBH	2.8–27.2	25	−1.183 (0.192)	2.159 (0.080)	0.969	0.053	1.026	34.4	0.969
E. falcata	LN D_0	4.0–25.3	19	−2.575 (0.358)	2.450 (0.138)	0.949	0.087	1.027	32.1	0.949
E. falcata	LN D_{10}	4.5–28.1	22	−2.342 (0.303)	2.446 (0.121)	0.953	0.077	0.981	37.6	0.953
E. falcata	LN D_{30}	3.3–31.0	24	−1.521 (0.336)	2.171 (0.134)	0.923	0.130	0.975	54.3	0.923
E. falcata	LN H	3.6–8.5	5	0.031 (1.103)	2.839 (0.633)	0.870	0.140	1.002	64.2	0.870
E. falcata	LN C_D	3.1–7.3	5	0.416 (0.823)	2.847 (0.513)	0.911	0.096	1.001	59.3	0.911
E. flocktoniae	LN DBH	4.5–22.2	14	1.330 (0.366)	2.275 (0.149)	0.951	0.034	0.937	33.7	0.954
E. flocktoniae	LN D_0	6.0–22.9	13	−2.868 (0.432)	2.590 (0.156)	0.962	0.029	1.026	15.8	0.961
E. flocktoniae	LN D_{10}	5.8–21.2	12	−2.788 (0.516)	2.653 (0.195)	0.949	0.040	1.017	20.5	0.949
E. flocktoniae	LN D_{30}	5.8–20.2	13	−2.715 (0.480)	2.711 (0.186)	0.951	0.037	0.991	20.9	0.951
E. flocktoniae	LN H	5.1–9.0	5	−2.289 (2.373)	3.798 (1.189)	0.773	0.166	1.019	58.0	0.773
E. flocktoniae	LN C_D	2.9–8.5	5	1.235 (0.195)	2.152 (0.102)	0.993	0.005	1.004	11.2	0.993
Ac. saligna	LN DBH	3.5–39.7	7	−2.010 (0.187)	2.341 (0.070)	0.996	0.013	0.970	8.7	0.996
Ac. saligna	LN D_0	4.6–15.3	3	−2.964 (0.434)	2.474 (0.182)	0.995	0.010	1.006	25.8	0.995
Ac. saligna	LN D_{10}	4.4–14.9	4	−2.768 (0.399)	2.444 (0.170)	0.990	0.014	0.991	22.8	0.990
Ac. saligna	LN D_{30}	4.1–39.0	7	−2.677 (0.255)	2.466 (0.091)	0.993	0.020	1.079	38.2	0.993
Ac. saligna	LN H	3.5–11.2	7	−4.603 (1.984)	4.355 (0.988)	0.795	0.613	1.455	68.4	0.795
Ac. saligna	LN C_D	1.8–9.5	7	−0.088 (0.592)	2.992 (0.402)	0.917	0.248	0.954	9.7	0.917
A. huegeliana	LN DBH	2.6–29.4	10	−1.647 (0.277)	2.277 (0.103)	0.984	0.045	1.070	21.9	0.984
A. huegeliana	LN D_0	–	–	–	–	–	–	–	–	–
A. huegeliana	LN D_{10}	3.6–43.8	10	−2.199 (0.195)	2.229 (0.065)	0.993	0.019	0.989	21.2	0.993
A. huegeliana	LN D_{30}	3.2–36.5	10	−2.115 (0.136)	2.314 (0.048)	0.997	0.010	1.009	9.5	0.997
A. huegeliana	LN H	3.25–7.5	10	−6.040 (1.293)	5.991 (0.743)	0.890	0.310	1.061	52.8	0.890
A. huegeliana	LN C_D	1.2–6.3	10	0.272 (0.270)	3.081 (0.192)	0.970	0.086	0.996	46.2	0.970

Appendix 3. Eight species-specific ln-transformed allometric equations for below ground biomass (BGB, kg) predicted by DBH, D_0, D_{10}, D_{30}, H, and C_D
Model 1 is used: ln (BGB) = $a + b$ln(predictor), with standard error values reported in parentheses. Predictor ranges (P range) report non-transformed values in centimetres, except for H and C_D, which are reported in metres. Dashes indicate missing data

Species	Predictor	P range	*n*	R^2	*a* (s.e.)	*b* (s.e.)	EMS	Bias	CV	EF
E. occidentalis	LN DBH	2.3–36.5	10	0.990	−2.354 (0.203)	2.110 (0.075)	0.028	1.019	18.7	0.997
E. occidentalis	LN D_0	–	–	–	–	–	–	–	–	–
E. occidentalis	LN D_{10}	–	–	–	–	–	–	–	–	–
E. occidentalis	LN D_{30}	2.9–41.0	10	0.996	−2.925 (0.132)	2.226 (0.047)	0.010	0.988	11.4	0.991
E. occidentalis	LN H	2.5–12.3	10	0.905	−3.915 (0.825)	3.484 (0.400)	0.266	1.154	56.2	0.791
E. occidentalis	LN C_D	1.1–10.0	10	0.923	0.100 (0.347)	2.451 (0.251)	0.215	0.828	47.3	0.852
E. platypus	LN DBH	2.6–28.2	10	0.912	−3.073 (0.617)	2.307 (0.253)	0.320	0.946	63.0	0.688
E. platypus	LN D_0	3.8–38.0	10	0.934	−4.188 (0.629)	2.412 (0.226)	0.240	0.970	59.8	0.719
E. platypus	LN D_{10}	3.3–29.5	10	0.932	−4.027 (0.623)	2.522 (0.240)	0.247	0.998	54.0	0.771
E. platypus	LN D_{30}	3.4–26.4	6	0.975	−4.481 (0.522)	2.755 (0.219)	0.108	1.010	69.8	0.767
E. platypus	LN H	2.8–9.9	10	0.215	−1.797 (2.776)	2.405 (1.608)	2.854	2.152	81.8	0.474
E. platypus	LN C_D	0.9–8.3	9	0.953	−0.032 (0.261)	2.101 (0.177)	0.178	1.024	27.8	0.929
E. annulata	LN DBH	8.7–25.7	6	0.885	−2.158 (1.035)	1.981 (0.357)	0.079	1.014	39.4	0.628
E. annulata	LN D_0	11.2–36.3	5	0.961	−2.422 (0.684)	1.856 (0.215)	0.029	0.994	15.2	0.960
E. annulata	LN D_{10}	8.9–28.9	5	0.969	−2.069 (0.569)	1.845 (0.189)	0.023	1.006	27.9	0.897
E. annulata	LN D_{30}	9.1–27.0	6	0.955	−2.260 (0.637)	1.955 (0.213)	0.031	1.000	19.9	0.905
E. annulata	LN H	4.1–8.2	6	0.620	−0.962 (1.774)	2.602 (1.018)	0.259	1.038	57.0	0.219
E. annulata	LN C_D	3.1–7.7	6	0.824	0.430 (0.931)	2.346 (0.542)	0.120	1.013	42.8	0.560
E. captiosa	LN DBH	3.6–19.0	7	0.841	0.189 (0.603)	1.299 (0.253)	0.101	1.037	21.5	0.907
E. captiosa	LN D_0	*	*	*	*	*	*	*	*	*
E. captiosa	LN D_{10}	6.0–21.4	7	0.904	−1.066 (0.632)	1.675 (0.245)	0.061	1.014	18.5	0.931
E. captiosa	LN D_{30}	*	*	*	*	*	*	*	*	*
E. captiosa	LN H	2.5–8.6	7	0.398	1.496 (0.975)	1.181 (0.649)	0.380	1.137	53.2	0.433
E. captiosa	LN C_D	1.9–6.4	7	0.963	0.794 (0.222)	1.843 (0.162)	0.024	0.996	12.1	0.971
E. falcata	LN DBH	9.1–30.1	5	0.968	0.091 (0.446)	1.437 (0.152)	0.017	1.005	25.3	0.878
E. falcata	LN D_0	14.8–34.7	5	0.917	−2.286 (1.141)	2.084 (0.362)	0.044	1.007	40.2	0.690
E. falcata	LN D_{10}	12.7–32.7	5	0.926	−1.425 (0.932)	1.869 (0.305)	0.039	1.006	37.9	0.725
E. falcata	LN D_{30}	12.5–31.3	5	0.914	−1.284 (0.990)	1.854 (0.329)	0.046	1.006	37.5	0.731
E. falcata	LN H	3.6–8.6	5	0.925	0.732 (0.587)	2.055 (0.337)	0.040	0.997	29.3	0.836
E. falcata	LN C_D	3.1–7.4	5	0.842	1.229 (0.771)	1.921 (0.480)	0.084	1.023	50.1	0.518
E. flocktoniae	LN DBH	9.5–26.4	6	0.914	−1.866 (0.873)	1.984 (0.304)	0.053	1.008	23.5	0.867
E. flocktoniae	LN D_0	13.3–31.8	6	0.965	−2.635 (0.616)	2.056 (0.196)	0.022	1.001	16.6	0.934
E. flocktoniae	LN D_{10}	11.2–28.3	5	0.949	−2.123 (0.789)	1.949 (0.262)	0.036	1.012	12.3	0.975
E. flocktoniae	LN D_{30}	10.4–26.2	6	0.961	−1.966 (0.588)	1.963 (0.199)	0.024	1.005	10.2	0.975
E. flocktoniae	LN H	5.1–9.0	6	0.477	−2.145 (3.119)	2.998 (1.569)	0.323	1.121	46.4	0.483
E. flocktoniae	LN C_D	3.00–8.5	5	0.992	1.194 (0.155)	1.544 (0.082)	0.003	1.000	8.8	0.967
A. saligna	LN DBH	3.6–39.8	7	0.992	−2.525 (0.198)	1.815 (0.074)	0.015	1.034	9.5	0.996
A. saligna	LN D_0	4.6–15.3	3	0.978	−2.557 (0.562)	1.576 (0.235)	0.018	1.011	31.8	0.902
A. saligna	LN D_{10}	4.4–14.9	4	0.963	−2.404 (0.506)	1.558 (0.216)	0.023	1.002	26.5	0.869
A. saligna	LN D_{30}	4.1–39.0	7	0.977	−3.010 (0.362)	1.900 (0.129)	0.041	1.106	32.4	0.950
A. saligna	LN H	3.5–11.2	7	0.735	−4.291 (1.751)	3.253 (0.873)	0.478	1.371	69.5	0.768
A. saligna	LN C_D	1.9–9.5	7	0.932	−1.066 (0.417)	2.343 (0.283)	0.123	1.013	9.1	0.996