

Tree biomass models for the entire production cycle of Quercus suber

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Introduction

Forest land has recently emerged as a strategy to achieve carbon neutrality, often through the afforestation and reforestation of production species (IPCC 2019, Pilli et al. 2022, Santos et al. 2022). However, the pace of climate change may ex-

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The demand for accurate biomass estimates is more pressing than ever. Cork oak (Quercus suber) presents particular challenges for biomass estimation due to variability among trees, even within the same stand. One issue is that small cork oak trees in the understory are often overlooked, leading to an underestimation of stand biomass. Characterising stand biomass is a significant concern for process-based modelling, as inaccuracies in observed values can result in further output uncertainty. Moreover, the production and management of cork oak are primarily focused on cork extraction, which alters several tree biomass components, particularly after the first debarking. This study provides a set of models for estimating cork oak biomass (total and per-tree component) across all stand layers. The models were developed using seemingly unrelated regression, ensuring additivity between biomass compartments. The separation of the cork oak life cycle reflects tree development and the production cycle of interest for managers, resulting in three sub-groups (juvenile trees, adult virgin trees, and debarked trees), along with four compartments (leaves, branches, stem, and aboveground). The juvenile model requires only total tree height, while the virgin model requires diameter at breast height and total tree height. No other tree variable was tested in the juvenile model, and only the number of first-order main branches was tested in the virgin model, but the associated parameter was not significantly different from zero. Two alternative models were developed for the debarked trees: a simple model that offers an alternative when only diameter under bark is available (predictive modelling efficiency, EF = 0.35 for branches and EF = 0.89 for total aboveground biomass); and a complex model that incorporates crown and stand variables, demonstrating better performance for branches and stem when parameters depend on the crown length and stand basal area, respectively (EF = 0.63 for branches and EF = 0.90 for total aboveground biomass). Our results underscore the need to consider crown and stand variables in the later stages of development.

Keywords: Cork Oak, Biomass, Empirical Models, Regeneration

ceed the tree growth rate, hindering the adaptation of forests to new climatic conditions (Kolström et al. 2011, Sharma et al. 2022). This context heightens the need for accurate and adequate characterisation of forest stand biomass, which is essential for several purposes related to climate change mitigation strategies, such as accounting for carbon sequestration (Ruiz-Peinado et al. 2017), estimating forest fuel stock (Calvo et al. 2023), and calibrating and validating process-based models (Mäkelä et al. 2000).

The Mediterranean region represents the largest productive area of cork oak forests (Tomé et al. 2020) and is also highly susceptible to drought and wildfires (Giorgi & Lionello 2008, Lindner et al. 2010, Spinoni et al. 2020). While drought is not the only factor negatively affecting cork oak growth (Braisier 1996, Costa et al. 2010), it is arguably the most significant (Piayda et al. 2014). Therefore, the need for reliable and up-to-date models that can quantify tree biomass *vis-a-vis* current mitigation strategies is imperative. The most common model used to estimate individual tree biomass, whether total or per tree component, is

the allometric model, which enables accurate estimates of stand biomass through aggregation (Parresol 1999). This modelling approach typically requires tree diameter at breast height (d) along with total tree height (h) and is developed for adult trees ($d \ge 7.5$ cm – Ter-Mikaelian & Korzukhin 1997, Zianis et al. 2005). Crown and/or stand variables are sometimes included to enhance model performance (António et al. 2007, Forrester et al. 2017). However, existing models do not address very young trees, which represent the next layer of stand development.

Young cork oak trees can be categorised into two groups, both presenting practical problems that contribute to their exclusion from biomass modelling. According to the Portuguese National Forest Inventory (NFI), young trees are classified as regeneration if h < 1.3 m and as smaller trees if $h \ge$ 1.3 m but d < 7.5 cm (ICNF 2019). This implies that for young trees classified as regeneration, it is impossible to obtain a measure of d at the standard height of 1.3 m. Additionally, it might be challenging or unfeasible for young trees classified as smaller trees to take d measurements be-

fore the tree reaches h = 2 to 3 m, as young trees often exhibit a very dense crown shape with more than one main branch. Smaller trees may ultimately not be of interest for management decisions regarding even-aged stands other than for pruning or thinning (Cañellas & Montero 2002, Pereira & Tomé 2004). Nevertheless, they are crucial for stand regeneration and for managing complex stands, such as uneven-aged or mixed-species forests. However, research focused on cork oak forest regeneration often tends to be qualitative (Mechergui et al. 2023) or primarily aimed at seedling mortality (Clark et al. 1999, Gómez-Aparicio et al. 2008), despite the pressing need for quantitative models.

Regional models to estimate cork oak biomass of adult trees from diameter under bark at breast height (du) and h were recently developed for the entire area of cork oak distribution (Jorge et al. 2023). However, to ensure compatibility among the various datasets used in that study, it was not possible to test some variables that might be relevant for cork oak biomass estimation, namely vertical debarking height (hdf), stem height (hs), stem bifurcation height (hbif), crown length (cl), number of first-order main branches (nbr), number of first-order main branches that have been debarked (nbru), number of trees, and basal area per hectare (N and G, respectively). Several other models (Paulo & Tomé 2006, 2010, 2014) exist, but all rely on du, a variable not easily measured in young non-debarked trees. The variable du can be directly measured only after the first debarking – a management operation regulated by legislation that can occur only when the tree circumference \geq 70 cm – or calculated if cork thickness is known, which is also challenging to measure. To the authors' knowledge, currently no model is available to estimate tree biomass in the younger layers of the stand. The first objective of this study is to provide allometric models to estimate cork oak tree biomass, both total and per tree component, applicable to the entire production cycle of cork oak, namely: (i) a model for young trees as a function of *h*; (ii) a model for virgin trees as a function of d and h; (iii) two models for debarked trees - a simple and a complex version – as a function of du only and du as well as h, respectively.

These models entail extensive sampling of tree biomass across a wide range of stand conditions and characteristics, achieved by integrating datasets from various projects. The second objective is to evaluate whether the performance of these models improves when additional tree/stand variables are included.

Materials and methods

Data for this study were obtained from the destructive sampling of 236 trees spanning a wide range of ages (7 to 106 years), with 59 trees classified as regeneration, 96 smaller trees, and 81 adult trees, following NFI standards. The field procedure for harvesting biomass is described elsewhere (Varela et al. 2000, Paulo & Tomé 2008). However, the dataset was used with different groupings from the NFI standards to enhance model fit and continuity by overlapping groups. The groupings (hereafter referred to as life stages) are illustrated in Fig. 1a, Fig. 1b, Fig. 1c, and Fig. 1d, considering tree development and the production cycle as follows: (i) Juvenile – trees with h <3 m (n = 204, comprising 59 trees that are regeneration, 96 smaller trees, and 49 adult un-debarked trees); (ii) Virgin - trees with d measured over the virgin cork (n = 151, consisting of 82 smaller and 69 adult un-debarked trees); (iii) Debarked - trees with du measured and debarked at least once (n = 22).

The debarked stage includes only 22 adult debarked trees, ten of which were selected from the adult virgin trees as they met the legal circumference for cork debarking. The debarking operation was simulated using equations to estimate cork biomass (Paulo & Tomé 2014). This approach was imposed by current legislation that prohibits the harvest of cork oak trees, complicating the sampling of adult trees.

The biomass was aggregated into four compartments common to all life stages: leaves (*wl*); branches with $d \le 7.5$ cm (*wbr*), stem (*ws*), including all branches with d > 7.5 cm, namely the main and secondary branches; and total aboveground biomass (*wa*). Branches and stem included some virgin cork biomass that was considered. Basic descriptive statistics of the tree variables are provided in Tab. 1.

Regarding stand characteristics, 31 of the largest adult trees were harvested across a wide range of stand densities (N = 39-304 trees ha⁻¹, G = 0.20 - 10.13 m² ha⁻¹) in four separate stands in central Portugal, the primary area of cork production. The remaining trees – the smallest – were harvested in the context of provenance trials across central and northwest Portugal in stands with a planting density between 540 and 556 trees ha⁻¹ (Varela et al. 2000).

The model fitting procedure was consistent across the three life stages, each associated with a specific equation form. It started with fitting individual allometric models for each compartment (C_{bio}) using ordinary least squares, and testing the significance of expressing the parameters as a function of tree and stand variables. The equation forms and variables can be described as follows (eqn. 1 to eqn. 3):

$$C_{bio} = a \cdot h^{c_0}$$

 $C_{bio} = a \cdot d^{(b_0 + b_1 n b r)} \cdot h^{(c_0 + c_1 n b r)}$

$$C_{bio} = a \cdot du^{(b_0 + b_1 z)} \cdot y^{(c_0 + c_1 z)}$$
(3)

where eqn. 1, eqn. 2, and eqn. 3 correspond to the juvenile, virgin, and debarked stages, respectively; *d* is the diameter at breast height, *du* is the diameter at breast height under bark, h is the total tree height, y represents tree variables related to height, and z includes other tree or stand variables, such as nbr, the number of first-order main branches. The coefficients b_0 , b_1 , c_0 and c_1 are part of the expression used for the allometric exponents and a is the allometric scalar.

Variables in the exponents of the allometric models associated with parameter estimates not significantly different from zero $(\alpha = 0.05)$ were discarded. The selected individual allometric models for each compartment were then simultaneously fitted as an additive system of equations, i.e., with total aboveground biomass equal to the sum of leaves, branches, and stem, using seemingly unrelated regression. The continuity between the equations for the tree life stages was verified graphically by comparing predicted and observed values. Eqn. 3 has two versions: complex, using all significant variables for the model, and simple, which employs just readily available variables.

Model evaluation was conducted using a leave-one-out cross-validation approach, extracting the so-called PRESS (predicted sum of squares of errors) residuals (Myers 1990) to calculate the following validation statistics: mean of PRESS residuals (mPRESS) for bias evaluation; mean of absolute PRESS residuals (maPRESS) and predictive modelling efficiency (EF) for precision evaluation (Myers 1990). Heteroscedasticity was visually assessed using plots of standardised residuals versus fitted values, and a weight function was applied when heteroscedasticity was not verified, following the methodology suggested by Parresol (2001). Normality was evaluated through visual assessment of QQ-plots of standardised weighted residuals.

Results

(1)

(2)

All coefficient estimates, corresponding standard errors, and significance levels can be found in Tab. 2. The juvenile stage model was fitted as a function of h, as it is the only available variable at that life stage. The final models for each biomass compartment of the juvenile stage are (eqn. 4 to eqn. 7):

$$wl = 0.380 h^{1.375}$$
 (4)

$$wbr = 0.401 h^{2.343}$$
 (5)

$$ws = 0.339 h^{2.539}$$
 (6)

$$wa = ws + wbr + wl \tag{7}$$

where eqn. 4, eqn. 5, eqn. 6, and eqn. 7 correspond to juvenile biomass of leaves (*wl*, kg), branches (*wbr*, kg), stem (*ws*, kg), and total aboveground (*wa*, kg), respectively; *h* is the total tree height. All coefficients in the juvenile stage related to *h* were significantly different from zero (p < 0.001 - Tab. 2).

In the virgin stage, both *d* and *h* are avail-



Fig. 1 - The four biomass compartments as a function of total tree height. Each panel represents one biomass compartment (kg) versus total tree height (m): (a) leaves, (b) branches, (c) stem, and (d) aboveground. The colours distinguish the data into the three life stages: juvenile (green dots), virgin (orange dots), and debarked (purple dots).

able. An additional tree variable (*nbr*) was tested in the branches and stem compartments, as it was the only common variable. It was tested by expressing the parameters b_1 and/or c_1 as a linear function of *nbr*, but these associated parameters were not significantly different from zero. The final models for each biomass compartment of the virgin stage are as follows (eqn. 8 to eqn. 11):

 $wl = 0.059 d^{1.216} \cdot h^{0.590}$ $wbr = 0.032 d^{1.864} \cdot h^{0.736}$

$$ws = 0.006 d^{2.651} \cdot h^{0.699}$$

$$wa = ws + wbr + wl$$

where eqn. 8, eqn. 9, eqn. 10, and eqn. 11 correspond to the virgin biomass of leaves (wl, kg), branches (wbr, kg), stem (ws, kg), and total aboveground (wa, kg), respectively; d is the diameter at breast height (cm) and h is the total tree height (m). All coefficients in the virgin stage related to d and h were significantly different from zero (p < 0.001, except for c_0 in the wl compartment, with a p > 0.01 – Tab. 2).

In developing the model for the debarked stage, a wider range of available tree variables was considered, and it was the only life stage where stand variables were tested. However, the debarked simple model was fitted as a function of du only, as the parameter associated with h was not significant. The final simple models for each biomass compartment of the debarked stage are as follows (eqn. 12 to eqn. 15):

 $wl = 0.313 \, du^{1.238}$

$$wbr = 0.395 du^{1.724}$$

(8)

(9)

(10)

(11)

$$ws = 0.049 \, du^{2.660}$$
 (14)

 $wa = ws + wbr + wl \tag{15}$

where eqn. 12, eqn. 13, eqn. 14, and eqn. 15 are the simple models for debarked biomass of leaves (*wl*, kg), branches (*wbr*, kg), stem (*ws*, kg), and total aboveground (*wa*, kg), respectively; *du* is the diameter under bark at breast height (cm).

The debarked complex model used all

Tab. 1 - Basic descriptive statistics of the tree variables. (*d*): diameter at breast height; (*du*): diameter at breast height under bark; (*h*): total height; (*cl*): crown length; (*wl*): leaf biomass; (*wbr*): branch biomass; (*ws*): stem biomass; (*wa*): aboveground biomass. Descriptive statistics – (n): number of trees; (Min): minimum; (Max): maximum; (SD): standard deviation.

(12)

(13)

Tree variable	n	Min	Median	Mean	Max	SD
<i>d</i> (cm)	163	3.80	7.45	11.52	63.25	11.18
du (cm)	31	6.90	20.95	24.28	58.75	14.41
<i>h</i> (m)	236	0.63	1.87	2.55	11.20	2.30
<i>cl</i> (m)	31	3.00	5.37	5.49	9.80	1.64
wl (kg)	236	0.19	0.73	2.99	51.28	7.69
wbr (kg)	236	0.06	1.44	16.22	496.34	56.42
ws (kg)	236	0.004	1.47	57.39	2655.50	267.98
wa (kg)	236	0.34	3.93	76.94	3078.68	324.24

Model	Comp.	а	bo	b ₁	C ₀	C 1
Juvenile	wl	0.380 ± 0.009 ***	-	-	1.375 ± 0.056 ***	-
	wbr	0.401 ± 0.031 ***	-	-	2.343 ± 0.118 ***	-
	ws	0.339 ± 0.015 ***	-	-	2.539 ± 0.071 ***	-
Virgin	wl	0.059 ± 0.017 ***	1.216 ± 0.210 ***	ns	0.590 ± 0.214 **	ns
	wbr	0.032 ± 0.007 ***	1.864 ± 0.153 ***	ns	0.736 ± 0.143 ***	ns
	ws	0.006 ± 0.001 ***	2.651 ± 0.109 ***	ns	0.699 ± 0.102 ***	ns
Debarked - simple	wl	0.313 ± 0.204	1.238 ± 0.176 ***	-	ns	-
	wbr	0.395 ± 0.259	1.724 ± 0.189 ***	-	ns	-
	WS	0.049 ± 0.020 *	2.660 ± 0.106 ***	-	ns	-
Debarked - complex	wl	0.223 ± 0.152	1.339 ± 0.189 ***	ns	ns	ns
	wbr	0.032 ± 0.014 *	1.771 ± 0.106 ***	ns	1.296 ± 0.151 ***	ns
	ws	0.010 ± 0.004 *	3.077 ± 0.109 ***	-0.008 ± 0.003 *	ns	ns

available variables. The final complex models for each biomass compartment of the debarked stage are as follows (eqn. 16 to eqn. 19):

$wl = 0.223 du^{1.339}$	(16)
$wbr = 0.032 du^{1.771} \cdot cl^{1.296}$	(17)
$ws = 0.010 du^{(3.077 - 0.008 G)}$	(18)
wa=ws+wbr+wl	(19)

where eqn. 16, eqn. 17, eqn. 18, and eqn. 19 are the complex models for debarked biomass of leaves (*wl*, kg), branches (*wbr*, kg), stem (*ws*, kg), and total aboveground (*wa*,

kg), respectively; du is the diameter under bark at breast height (cm), cl is the crown length (m), and G is the basal area (m²) per hectare. We found that *cl* was superior to *h* in the branches compartment (p < 0.001 -Tab. 2) and that expressing the exponent of du as a linear function of G originated a b₁ parameter estimate significantly different from zero (p < 0.05 - Tab. 2) in the stem compartment, which, in this case, did not include any height variable. The a coefficient in the debarked life stage was sometimes not significantly different from zero; however, the null hypothesis H_0 (parameter = 0) does not apply to this parameter, as it is a multiplicative term in the non-linear allometric equation. The issues

Tab. 3 - The biomass compartments (Comp.) – (wl): leaf biomass; (wbr): branch biomass; (ws): stem biomass; (wa): aboveground biomass. The performance metrics – (mPRESS): mean of PRESS residuals (kg); (maPRESS): mean of absolute PRESS residuals (kg); (EF): predictive modelling efficiency.

Model	Comp.	mPRESS	maPRESS	EF
	wl	0.00	0.32	0.43
Juvenile	wbr	0.02	0.78	0.49
	WS	-0.03	0.51	0.68
	wa	-0.01	1.19	0.70
	wl	0.23	0.89	0.74
	wbr	-0.31	2.13	0.93
virgin	ws	1.78	5.33	0.89
	wa	2.18	6.51	0.93
Debarked - simple	wl	1.17	7.19	0.63
	wbr	-7.64	60.05	0.35
	ws	-0.35	143.21	0.90
	wa	-4.50	178.37	0.89
	wl	0.66	7.47	0.61
Debarked - complex	wbr	-10.87	42.31	0.63
	WS	26.55	166.14	0.92
	wa	18.65	166	0.90

with the p-values of some parameters in non-linear regression are well discussed by Frost (2024) who recommends an analysis of the most appropriate null hypothesis for each parameter. Therefore, this was not considered a problem.

Tab. 3 shows the performance metrics of each model. The juvenile stage exhibits the lowest overall EF. The virgin stage's *wl* and *wbr* demonstrate reasonable modelling efficiency. Compartment *wl* indicates the lowest EF values, except when compared to *wbr* in the debarked simple model, where EF is 0.35. Additionally, the performance and continuity of the best overall models can also be visually evaluated from Fig. 2a, Fig. 2b, Fig. 2c, and Fig. 2d.

Discussion

Estimating cork oak biomass is challenging due to its complex architecture and the difficulty in separating compartments (Paulo et al. 2017). For instance, aggregating all aboveground biomass into one compartment does not provide sufficient separation for some biomass estimation purposes, such as their application in processbased models (Landsberg & Waring 1997). Further, the dimension of biomass values in each compartment can vary significantly. To address these issues, we organised the biomass into four compartments relevant for managers and other applications throughout the tree's production cycle: leaves, branches, stem (including branches with $d \ge 7.5$ cm and virgin cork), and aboveground, which is simply the sum of all other compartments.

The leaves compartment naturally exhibits higher variability (Andivia et al. 2018, Jorge et al. 2023), while the wood compartments are much more consistent. However, this is not true for branches, which suffer extensive changes, whether through pruning when the trees are young to produce a proper stem shape or when the



Fig. 2 - A visual representation of model performance. Each panel represents one biomass compartment (kg) of observed versus predicted biomass values: (a) leaves, (b) branches, (c) stem, and (d) aboveground. The colours distinguish the data into the three life stages: juvenile (green dots), virgin (orange dots), and debarked (purple dots). The predicted biomass values for each life stage were calculated with the final models that showed the best performance. The dashed line across the graphs serves as a guide for visually inspecting the model performance.

trees are older and develop a more complex canopy structure. This structural diversity in branches across all life stages possibly accounts for the variability in predictive performance values between models (EF of 0.49, 0.93, 0.35, and 0.63 for the juvenile, virgin, debarked simple, and complex models, respectively - Tab. 3). The high EF of the virgin stage is perhaps due to the homogeneity of branches, and indeed, virgin wbr has a relatively low standard deviation compared to other compartments (results not shown). However, the same cannot be said for the juvenile stage, despite juvenile wbr also exhibiting low standard deviation. This discrepancy is possibly due to *h*, being the only variable in the model and less correlated with biomass growth than d or du; however, it is one of the easiest variables to measure at this stage. Juvenile trees are not immediately exploited for cork production and are often overlooked or missed in inventories due to the increased requirements for biometric measurements or the limitations of sensors (Navarro et al. 2019). Having a comprehensive understanding of stand biomass will facilitate the management of cork oak woodlands (Simonson et al. 2014, Arosa et al. 2017), and this model enables biomass estimation from relatively simple measurements, even if the predictive performance is not optimal (with a maximum EF = 0.70 for above ground biomass – Tab. 3).

The model for trees in the debarked stage was divided into two - simple and complex - because we found that the complex model performed better overall (Tab. 3) but required two variables that may not be readily available. The complex model is defined as a function of du, h, cl, and G, which were the only tree and stand variables associated with parameters significantly different from zero. We found that cl improved the branches equation (EF = 0.35 and EF = 0.63 for the simple and complex models, respectively - Tab. 3), as verified by other authors (António et al. 2007, Zribi et al. 2016). The stand variables N and G were tested by expressing the parameters b_1 and/or c_1 as linear functions of those variables. We found that the estimates of those parameters were not significantly different from zero when associated with N, which aligns with similar research (Jorge et al. 2023). However, the estimates for both parameters differed significantly from zero when associated with G in the stem equation and further improved when associated with the du exponent. All biomass was harvested in relatively low-density stands (maximum observed N = 304). Since G is a better indicator of inter-tree competition than N – because it accounts for both stem number and tree girth - this may explain why this stand density measure performs better than N, as also found by Faias et al. (2019). To further assess the effects of N and G, having a broader sample of trees from stands concerning these variables would be ideal, particularly in the adult debarked trees, where the effects of inter-tree competition should be more pronounced. The simple model excludes all variables from the complex model except for du. We found the parameter associated with h neither significant as a replacement for cl in the wbr compartment nor as an additional multiplicative term in the ws compartment (p > 0.05, results not shown).

Regarding model continuity of the best overall models, there is overlap at the beginning and end of each stage transition (Fig. 2a, Fig. 2b, Fig. 2c, and Fig. 2d) that suggests acceptable continuity, particularly between the juvenile and virgin stages. The virgin model slightly underestimates leaf biomass for observed values \geq 10 kg. All other compartments exhibit more or less linear trends for the relationship between observed and predicted values, which is the ideal behaviour. While there are some limitations to these models regarding continuity, we believe that these limitations were mitigated by model design, for instance, by considering smaller virgin trees (h < 3 m) in fitting the juvenile model. This also ensured a large sample size in a model that relies solely on h. Nevertheless, it is important to indicate that some divergence in estimates may occur at the junction of juvenile and the virgin models or virgin and debarked models. We recommend that the model for juvenile trees should be employed when d has not been measured, while the model for virgin trees should be used when d with virgin cork is measured. The biomass for all other trees should be estimated using the models for debarked trees.

Conclusions

The effort to incorporate regeneration into modelling is relatively recent, though it has gained importance in the context of climate change. Young cork oak trees are often neglected and not accounted for in biomass estimates, preventing a comprehensive characterisation of the stand and thus, causing uncertainty in biomass estimates. We successfully developed a set of four model systems that can estimate cork oak biomass for each life stage of the production cycle - one model for juvenile trees, one for virgin trees, and two for the debarked stage. All models estimate total aboveground biomass by compartment (leaves, stem, and branches). The juvenile model requires total tree height, while the virgin model requires diameter at breast height and total tree height. Two models were developed for the debarked life stage - a simple and a complex model. The complex model requires diameter at breast height under bark, total height, crown length, and basal area, while the simple model uses only diameter at breast height under bark, reducing model requirements. Although continuity between each model equation could be improved, these models aim to enhance cork oak management by refining the applicability of empirical models.

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