



24 year after each coppicing than in subsequent years of the cycle. Our findings suggest  
25 that this feature of nature must be accommodated in the modelling procedure either  
26 through the model formulation (decreasing the parameter variability with the  
27 inclusion of age as a dummy predictor variable) or by selecting the sample  
28 according to the stage of development of the above-ground biomass (which will  
29 depend on the goals of the predictions). The minimum sample size proposed to  
30 construct a model capable of predicting biomass regardless of age in SRC was 50  
31 trees. Furthermore, the uncertainty was quantified in two models for total above-  
32 ground dry woody biomass, the first based only on the basal diameter and the other  
33 on the basal diameter along with the number of shoots per stool; the inclusion of  
34 the latter was advisable to increase the accuracy and reduce the mean deviation in  
35 biomass predictions at different ages.

36 **Keywords:** Poplar; allometric models; age-influence; mean deviation.

## 37 **1. Introduction**

38 In the near future, woody biomass from Short Rotation Coppice (SRC) plantations, could  
39 be an essential addition to the biomass supply from forests and related industries in the  
40 European biomass market (European Commission, 2014). The biomass produced in SRC  
41 is characterized by a precise location and a foreseeable yield, a pronounced temporality  
42 and likely yield according to the areas of cultivation. The quality of this type of biomass  
43 makes it suitable for use in the production of bioenergy through different processing  
44 methods, as well as to obtain multiple bioproducts (Zhang *et al.*, 2011). Therefore the  
45 production and use of this biomass should be viewed within the general framework of  
46 renewable energies, not only as an effective tool in the mitigation of the effects of climate  
47 change but also as a means to promote the development of the bioeconomy (European  
48 Commission, 2012). For the operational establishment of this type of plantation on a  
49 commercial scale, it is essential to maximize the benefits by combining economic  
50 viability with environmental sustainability. Species belonging to the *Salicaceae* family  
51 (*Populus* spp. and *Salix* spp.) have proved to be the most suitable for short rotation  
52 management in northern and southern Europe (Nassi O Di Nasso *et al.*, 2010; Verwijst *et*  
53 *al.*, 2013; Aust *et al.*, 2014) and there are many examples of commercial plantations  
54 aimed at energy production (Srirangan *et al.*, 2012).

55 Accurate tools for estimating standing biomass in SRC crops are an essential component  
56 for the most basic management decisions, such as determining the most appropriate  
57 rotation length, maximum volume production or the financial rotation, as well as to assess  
58 the amount of primary energy available at the end of the rotation or to estimate the  
59 nutritional balance.

60 Allometric models relating tree diameter or other easily measurable tree variables to any  
61 biomass component or total above-ground biomass are the most commonly used tool for

62 estimating biomass in forest inventories and ecological studies (Peichl and Arain, 2007;  
63 Shaiek *et al.*, 2011). These methods have also been used for estimation purposes in SRC  
64 (Verwijst *et al.*, 2013; Mosseler *et al.*, 2014; Verlinden *et al.*, 2015). Apart from the  
65 variety of models that can be used to assess specific relationships, we are confronted with  
66 a large number of factors which create uncertainty in allometric relationships (Verwijst  
67 *et al.*, 2013). We should distinguish between the factors that affect the biological  
68 relationship on one hand, such as i) species or genotypes, ii) the age of the shoot or iii)  
69 the coppicing rotation, and on the other hand factors affect the modelling of the  
70 relationship: iv) the fitting algorithms, v) the size of the sample used to fit the model or  
71 vi) the sample selection criteria as a function of the stage of development. Some of these  
72 factors may be considered as general to all forest monitoring conditions. It is hypothesized  
73 that factors ii), iii) and v) have an important effect on SRC because of the differences in  
74 the stages of development of above and below-ground biomass after resprouting.

75 The effect of species or genotypes within species on biomass allometry has been  
76 extensively studied (Ter-Mikaelian and Korzukhin, 1997; Bond-Lamberty *et al.*, 2002).  
77 When estimating the above-ground biomass of a forest, the use of species-specific models  
78 are preferred because there can be large differences between species in terms of tree  
79 architecture and specific gravity of the wood (Ketterings *et al.*, 2001). For poplar species  
80 and clones, successful generalizations have been developed, although deviations were  
81 found for certain tree components (Tuskan and Rensema, 1992).

82 The sample size must be large enough and distributed appropriately so that the fitted  
83 model accurately represents the underlying biological relationship (Hui and Jackson,  
84 2007; Zapata-Cuartas *et al.*, 2012; Sileshi, 2014), although even so, the sample selection  
85 criteria will influence the model setting (Zianis and Mencuccini, 2004). The decisions as  
86 regards the model fit, such as the fitting techniques (Zapata-Cuartas *et al.*, 2012; Ahmed

87 *et al.*, 2013) or the model formulation and the predictor variables (van Breugel *et al.*,  
88 2011; Tumwebaze *et al.*, 2013; Mosseler *et al.*, 2014), are an additional source of  
89 uncertainty (van Breugel *et al.*, 2011; Sileshi, 2014). Additionally, other factors such as  
90 site quality (Ketterings *et al.*, 2001), proportion of branches (Cannell, 1984), or damaging  
91 agents such as frost (Verwijst *et al.*, 1996), leaf rust (Tuskan and Rensema, 1992) or  
92 animal browsing (Verwijst and Telenius, 1999) may also affect the allometric  
93 relationship. Various other factors such as stand density are more controversial. Although  
94 a stand density effect is assumed in some studies (Peichl and Arain, 2007), others, such  
95 as Willebrand *et al.* (1993) or Di Matteo *et al.* (2012) report that the effect is only  
96 statistically significant at certain stages of development, while other studies have not  
97 found statistically significant effects of stand density on tree allometry (Adegbidi *et al.*,  
98 2001; Antonio *et al.*, 2007; Amichev *et al.*, 2010).

99 Age dependence of tree allometry is a specific issue which has been analyzed on several  
100 occasions (Saint-André *et al.*, 2005; Antonio *et al.*, 2007; Peichl and Arain, 2007). The  
101 relationship between the tree variables and the biomass yield may be modified by changes  
102 in the allocation of biomass to individual components over the life cycle of the tree (Sato  
103 and Madgwick, 1982). For this reason, the inclusion of stand age in a biomass model was  
104 found to contribute significantly to improving the quality of the fit of the model to the  
105 data, and different allometric biomass models may therefore be required depending on  
106 the development stage of the tree (Peichl and Arain, 2007). In coppice plantations,  
107 biomass allocation varies not only with the age but also with rotation, since below-ground  
108 biomass age for a given above-ground biomass age will not be the same in different  
109 rotations. Under such circumstances it is hypothesized that the effect of age on allometry  
110 is more pronounced than in single stem plantations.

111 The aim of this study was to improve the model development methodology for more  
112 robust biomass prediction. The main objective was to analyze the changes in allometry at  
113 stool level produced by: i) age and ii) coppicing rotation in an SRC system measured over  
114 two rotations. A second objective was to estimate the effect on parameter estimates,  
115 accuracy and mean deviation of: iii) the sample size, iv) sample selection criteria and v)  
116 model formulation. Finally, the improvement in the biomass estimation and robustness of  
117 the model by including other regressor variables together with basal diameter was  
118 evaluated.

## 119 **2. Material and methods**

### 120 **2.1. Trial site and experimental design**

121 The study site is located on the central plateau of Spain (latitude N 41° 28' 20.06'';  
122 longitude W 2° 32' 54.68'' and 827 m a.s.l.). The climate in this area is sub-Mediterranean  
123 with certain continental characteristics (mean annual temperature of 11.8 °C and average  
124 annual rainfall of 561 mm). The soil has a sandy clay loam texture with moderately basic  
125 pH (8.2) and organic matter content of about 2.5%. In the spring of 2005, a clonal trial  
126 was installed using six different genotypes. Five clones belong to the hybrid *Populus x*  
127 *canadensis* Moench ('A4A', 'A2A', 'I-214', '2000 Verde' and 'Luisa Avanzo') and the  
128 other was a native *Populus nigra* L. clone ('Lombardo Leonés'). The plantation had an  
129 initial density of 17,316 stools ha<sup>-1</sup>, established in twin rows, 3 m apart with a distance of  
130 0.5 m between single rows. A total of 1,019 unrooted cuttings of each clone were planted  
131 in adjacent pairs of rows, including six clones planting consecutively. Prior to planting,  
132 8-15-15 N-P-K fertilizer was applied. Weed control was carried out by applying  
133 Oxifluorfen at 4 l ha<sup>-1</sup> after planting and by mechanical weeding in midsummer. Irrigation  
134 was applied by surface irrigation from June to September. After the first vegetative period  
135 (winter of 2006), the plantation was cut-back in order to stimulate sprouting. Hence, after

136 resprouting, root age (R) was 2 and shoot age (S) was 1 year (R2S1). From then on, two  
137 rotations of three years were applied. Three random clusters per clone were randomly  
138 selected in the plantation each year for destructive biomass measurement. Each cluster  
139 included 16 contiguous trees per clone, surrounded by a buffer of two rows. The distance  
140 between the biomass sampling plots established in different years was at least 20 m.

## 141 **2.2. Variables measured**

142 In the first rotation (2006-2008) the number of shoots per stool ( $n$ ), the dominant shoot  
143 diameter at basal height ( $D_{10}$ , mm, considering the dominant shoot as the thickest shoot  
144 per stool and basal height as 10 cm) and the total height of the dominant shoot ( $H$ , cm)  
145 were recorded in 16 stools for each cluster and clone at the end of the growing season.  
146 Additionally, these stools were destructively sampled immediately, in order to quantify  
147 the biomass. The dry matter content was calculated for a subsample of one tree from the  
148 most frequent diameter class for each clone, which was oven dried at 100°C to constant  
149 weight. In the second rotation (2009-2011) the same evaluation procedure was followed,  
150 with the exception of the year 2010, when the shoots were measured but biomass data  
151 was not recorded. The stage of development is expressed in terms of their root and stem  
152 age, so R2S1 is the first year after coppicing, year 1 (2006), R3S2 is year 2 (2007), R4S3  
153 is year 3 (2008), R5S1 is year 4 (2009, the first year after coppicing in the second rotation)  
154 and the last one is R7S3, which is year 6 (2011). The complete biomass sampling size  
155 was then 16 trees x 3 clusters x 5 years x 6 clones.

## 156 **2.3. Statistical analysis**

157 Biomass models were fitted using a nonlinear least-squares procedure (*nls* procedure of  
158 the *R software program* (R Development Core Team, 2014)), to relate dry biomass yield  
159 ( $W_s$ ) to dominant shoot diameter at basal height ( $D_{10}$ ), height of the dominant shoot of the  
160 stool ( $H$ ) and number of shoots per stool ( $n$ ).

### 2.3.1. Evaluation of the effect of age and model formulation

To evaluate the effect of age and model formulation on parameter estimates, three different model formulations were considered: a) a general model for all years for each clone (hereinafter "general", equation 1), b) a different model for each clone and year (hereinafter "simple", equation 2), and c) a model with expanded parameters through dummy variables (with a common  $a$  parameter, hereinafter "dummy", equation 3).

$$W_{ik} = a \cdot X_{ik}^p + \varepsilon_{ik} \quad (1)$$

$$W_{ijk} = a \cdot X_{ijk}^p + \varepsilon_{ik} \quad (2)$$

$$W_{ijk} = a \cdot X_{ik}^{(p_1 \cdot I_1 + \dots + p_j \cdot I_j + \dots + p_6 \cdot I_6)} + \varepsilon_{ik} \quad (3)$$

where  $W$  is the dry biomass,  $X$  are the predictor variables,  $p$  are the parameters associated to each one of the predictor variables,  $I$  are the dummy variables for the levels of the factor "year" and  $\varepsilon$  is the additive residual term. Using  $i$  to index tree,  $j$  to index the levels of the factor "year" and  $k$  to index clone.

The aim of the parameter expansion is to take into consideration the time elapsed since the first coppicing, thus the dummy variables  $I_1$ ,  $I_2$ ,  $I_3$ ,  $I_4$  and  $I_6$  take the value 1 for each corresponding year for which biomass data are available ( $I_1$  corresponds to 2006 (R2S1);  $I_2$  to 2007 (R3S2),  $I_3$  to 2008 (R4S3),  $I_4$  to 2009 (R5S1) and  $I_6$  to 2011 (R7S3)) respectively, otherwise 0. Three variables were considered as predictive in the fitting process: basal diameter of the dominant shoot ( $D_{10}$ ), the height of the dominant shoot per stool ( $H$ ) and the number of shoots per stool ( $n$ ). All the fitted models are shown in table 1. Hereinafter the models will be denominated as the nomenclature expressed in table 1, the letters of the models indicate the predictor variables included in the model and capital letters indicate that the parameter associated with that predictor variable has been expanded through dummy variables.

182 Kruskal-Wallis non-parametric analysis of variance (ANOVA) was used to assess  
183 differences in parameter estimates to analyze their trends among model formulation, age  
184 and rotation. This test was selected due to the lack of homogeneity in the variances among  
185 groups (without assuming them to follow a normal distribution) and the presence of more  
186 than two groups. The null hypothesis is that groups present the same parameter estimates,  
187 so small *p-values* lead us to reject the null hypothesis that groups share the same  
188 allometric estimates, presenting significantly differences among the parameter estimates.

### 189 **2.3.2. Evaluation of the effect of sample size and sample selection**

190 Effect of sample size and sample selection were analyzed by considering the 'I-214'  
191 clone. This clone is a hybrid between *Populus deltoides* Marsh and *Populus nigra* L., and  
192 is a well-known clone which is widely planted in Mediterranean environments because  
193 of its largely consistent productivity across sites and large yield (Cruset and Voltas, 2009;  
194 Sixto *et al.*, 2014). The descriptive statistics from the information available for this clone  
195 are shown in table 2. As model *d* is the most commonly used for biomass estimation, the  
196 effect of sample selection and sample size was evaluated by considering only this model.  
197 Model *dn* was also considered to evaluate the improvement in the residual sum of squares  
198 by adding the number of shoots as a predictor variable.

#### 199 **2.3.2.1. Effect of sample size**

200 The full database of 186 trees for the 'I-214' clone was randomly split to evaluate the  
201 uncertainty in parameter estimate bounds for the sample size (*ss*) considered to fit the  
202 allometric models. In order to obtain a final random sample in which all the diameter  
203 classes were represented, the database was divided into 6 groups with 31 trees per group,  
204 based on diameter range. Models with the same sample intensity and which cover all the  
205 diameter classes presented in the total database were fitted (McRoberts *et al.*, 2015).  
206 Sample size was tested from 12 (2 trees per group) to 168 trees (28 trees per group). The

207 procedure was randomized 1000 times for each sample size to quantify the variance  
208 among estimates for different sample sizes.

209 A common fitting for the 186 trees was performed, obtaining confidence intervals for  
210 parameter estimates with a probability level of 99% (Venables and Ripley, 2002), in order  
211 to analyze the minimum sample size required to achieve that level of confidence. The  
212 estimated parameters in the bootstrap for different sample sizes were compared to that  
213 confidence interval, establishing the need to include the interquartile range (25<sup>th</sup>-75<sup>th</sup>  
214 percentile range) in that interval.

### 215 **2.3.2.2. Uncertainty bounds for the sample selection**

216 In order to evaluate the uncertainty in biomass estimates derived from the selection of  
217 standard trees at different ages and coppice rotations for destructive sampling, eight  
218 scenarios were defined. Bootstrapping was used to calculate the residuals using cross-  
219 validation techniques with the *statistical package R* (R Development Core Team, 2014).  
220 Each simulation was repeated 1000 times and data were randomly selected, making sure  
221 that the sample size was the same for each year. The proposed simulations were defined  
222 based on the subset of data chosen for sampling as described in table 3.

223 The estimation uncertainty is measured on the basis of the mean relative deviation or  
224 percentage error (PE, %), the mean residuals (*MRES*, g) to evaluate the mean deviation  
225 and the root mean square error (RMSE, g) to evaluate the accuracy, all of which relate to  
226 the validation data. To facilitate the interpretation of results, they were represented in  
227 box-plots.

$$PE (\%) = \frac{100}{x} \cdot \sum \left( \frac{y_i - \hat{y}_i}{y_i} \right) \quad (19)$$

$$MRES(g) = \frac{\sum(y_i - \hat{y}_i)}{x} \quad (20)$$

$$RMSE (g) = \sqrt{\frac{\sum(y_i - \hat{y}_i)^2}{x - p}} \quad (21)$$

228 where  $y_i$  is the observed value (g),  $\hat{y}_i$  is the estimated value (g),  $x$  is the number of  
 229 observations, and  $p$  is the number of parameters.

### 230 **2.3.3. Evaluation of the effect of predictor variables**

231 To analyze the improvement in the predictive ability of the models by adding another  
 232 variable to the model apart from  $D_{10}$ , the process explained in the previous section was  
 233 repeated. In this case, the improvement obtained by including the number of shoots in the  
 234 model is tested (model  $dn$ ). Only this variable was considered as it is hypothesized to  
 235 have a great degree of importance in biomass estimation in several rotations of coppice  
 236 plantations, as the values of  $n$  vary greatly for different rotations.

237 Analysis of variance (ANOVA) was performed, using the statistical package R (R  
 238 Development Core Team, 2014) to evaluate the effect of the inclusion of the number of  
 239 shoots as a predictor variable in the general model, through an F-test based on the extra  
 240 sum of squares.

## 241 **3. Results**

### 242 **3.1. Effect of the model formulation on the evolution of allometry**

243 The model formulation can consider either simple or dummy models. The same parameter  
 244 notation was used for all model formulations as follows:  $b$  is the exponent of  $D_{10}$ ,  $c$  is the  
 245 exponent of  $H$  and  $d$  is the exponent of  $n$ . The results of parameter estimates when simple  
 246 models are applied (a different model for each age and clone) with different combinations  
 247 of predictor variables are shown in figure 1, where the years are represented on the x-  
 248 axis, and the variability in the estimations of the parameters is represented on the y-axis,  
 249 and the graphics included in the upper right quadrant of each parameter are zooms of  
 250 specific regions of each parameter to allow a better interpretation. Overall, greater

251 variability is observed for the estimates of parameters  $b$  and  $c$  in models that include both  
252 predictor variables (basal diameter and height (model  $dh$ )) and even number of shoots  
253 (model  $dhn$ ), which is partly due to the strong correlation observed between  $D_{10}$  and  $H$   
254 (Pearson correlation coefficient = 0.92). It should also be noted that years 1 and 4 are those  
255 with the greatest variability in the estimates, revealing the important changes in stool  
256 allometry as a result of coppicing. Year 4 presents by far the greatest variability, showing  
257 a greater degree of instability in the estimates of parameters  $b$  and  $c$  when height is  
258 included as a predictor variable than when it is not included. For the harvesting years, the  
259 values tend to group, regardless of the variable included in the model.

260 The estimates of parameter  $b$  show a decreasing trend within each rotation, always with  
261 biologically meaningful, positive values, provided that height was not included as a  
262 predictor variable ( $p$ -value < 0.01 for both rotation). For the simple model which includes  
263 only height, parameter  $c$  has an increasing trend with age ( $p$ -value < 0.05). If diameter and  
264 height (and even number of shoots) are included as predictor variables, the parameter  $c$   
265 estimate has a clear decreasing trend with age ( $p$ -value < 0.01), maintaining positive  
266 values, thus showing a reduction in the relevance of height in explaining stool biomass.  
267 In parameter  $d$  (Figure 1), the variability decreases with time after coppicing for the first  
268 rotation ( $p$ -value < 0.05), while it remained stable within the second rotation ( $p$ -  
269 value > 0.50). The data do not show an overall trend for both rotations, but the values in  
270 the second rotation appear to be greater than those estimated for the first ( $p$ -value < 0.05).  
271 Within the first rotation, a decreasing trend with age is evident ( $p$ -value < 0.05).

272 Figure 2 shows the evolution of the  $b$  and  $c$  parameter estimates when dummy models are  
273 fitted. Overall, if we compare it with figure 1, it can be seen that the variability between  
274 different models is smaller in dummy models, revealing more robust parameter  
275 estimation. Greater variability in parameter  $b$  and  $c$  estimates is observed for the dummy

276 models that expand the parameter associated with height ( $DH$ ,  $DHn$  and  $DHN$ , figure 2  
277 bottom-left) ( $p\text{-value}<0.01$  for both parameters  $b$  and  $c$ ). Estimates of parameter  $b$  are  
278 much more stable for the dummy procedures than for the simple one (even for the  
279 harvesting years), as can be seen in figure 2 (top and centre-left) for the models  $D$ ,  $DhN$   
280 and  $Dhn$ , as a result of using a common parameter  $a$  for all years ( $p\text{-value}>0.50$ ).

281 The evolution of parameter  $c$  estimates for the dummy models  $H$ , which exclusively  
282 expand this parameter, shows clear stability of the values ( $p\text{-value}>0.50$ ), in contrast to  
283 the abovementioned increasing trend found for the simple model ( $p\text{-value}<0.05$ ). The  
284 simultaneous expansion of  $b$  and  $c$  parameters in model  $DH$ ,  $DHN$  and  $DHn$  produces a  
285 decreasing trend in parameter  $c$  estimates (Figure 2 right) ( $p\text{-value}<0.01$ ), whereas the  
286 inclusion of number of shoots in models  $DHN$  and  $DHn$ , also produces unrealistic  
287 negative estimates for some years.

### 288 **3.2. Effect of sample size on the model prediction ability for the 'I-214' clone**

289 Figure 3 shows the results of the parameter estimates for clone 'I-214', model  $d$  and the  
290 simple procedure of fitting. As expected, the variability of the parameter estimation  
291 decreases as the sample size increases (Figure 3). We calculated the minimum sample  
292 size necessary to assure that the interquartile range between the 25<sup>th</sup> and 75<sup>th</sup> percentile  
293 of the parameter  $b$  estimates was inside the 99% confidence interval derived from the  
294 fitting of the whole data set (parameter  $a$  from 0.01 to 0.31 and  $b$  from 2.36 to 3.19 (these  
295 values were the limits in the y-axis for the zooms in figure 3). This minimum size was  
296  $ss=48$  for parameter  $b$  and  $ss=36$  for parameter  $a$  when all years are considered together.

297 The development of an allometric model which includes basal diameter and the number  
298 of shoots per stool as predictor variables would require a similar sample size to obtain  
299 similar, stable estimations of the parameters. However, the RMSE and MRES values were  
300 greater, even when small sample sizes were used. Parameter  $a$  required more than 24,

301 parameter  $b$  36 and parameter  $d$  required 48 to obtain the same level of accuracy as a  
302 confidence interval of 99% in model  $dn$  for the whole data base (Figure 4) (parameter  $a$   
303 from 0.05 to 0.51,  $b$  from 2.01 to 2.58 and  $c$  from 0.4 to 0.61 (these values were the limits  
304 in the y-axis for the zooms in figure 4)). Estimates of parameter  $d$ , in samples of less than  
305 60, presented some negative values, which denotes a negative relationship between the  
306 number of shoots and biomass yield. In samples of more than 60 this parameter is  
307 stabilized, showing only positive values.

### 308 **3.3. Model uncertainty according to sample selection criteria for the 'I-214'** 309 **clone**

310 Figure 5 presents the results in terms of PE (%) derived from the eight sample selection  
311 alternatives simulated. Sampling by considering all the data, irrespective of crop age  
312 (Sim. 8), would produce good results when used to estimate biomass at any growth stage,  
313 with a general overestimation of 7%, but would result in an underestimation of  
314 approximately 50% for the first year after each coppicing. PE in Sim. 8 decreased  
315 gradually with increasing rotation years, reaching the smallest values in the harvesting  
316 years, and with the second rotation values being smaller than the first rotation. The option  
317 where sampling was focused on cutting years (Sim. 2) provided similar PE results to those  
318 of Sim. 8 although the sampling activity is more concentrated in time.

319 In cases where the rotations are sampled separately (Sim. 4, Sim. 5, Sim. 6 and Sim. 7),  
320 it is clear that significant mean deviations results when data from the second rotation  
321 (Sim. 5 and Sim. 7) are used to estimate first rotation biomass, particularly at harvest  
322 (R4S3, year 3) (Table 4). Sampling in the first rotation (Sim. 4 and Sim. 6) is a better way  
323 to achieve lower mean deviations at age R4S3 (year 3), but leads to positive mean  
324 deviations when applied to biomass estimation in the second rotation.

325 Sampling exclusively one-year-old shoots after coppicing (Sim. 3) presented the greatest  
326 mean deviation, hence is not recommended.

327 Although PE in Sim. 1, Sim. 2 and Sim. 8 was smaller (Figure 5), MRES for general  
328 models reached values of up to 1400 g per stool in the cutting years (Table 4), while the  
329 fittings for each rotation presented lower mean deviations both in general and in the  
330 cutting years (~ 50 g per stool in both rotations).

331 The RMSE at stool level (g) provides values of precision for the simulations analyzed.  
332 The accuracy of all models was low, the RMSE increasing over the years in all  
333 simulations. The specific simulations for each rotation were better but the RMSE values  
334 reached up to 1200 g per stool in the cutting year of the first rotation and up to 2500 g per  
335 stool in the second rotation (Table 4).

### 336 **3.4. The inclusion of the number of shoots per stool**

337 The inclusion of the number of shoots per stool in the biomass model for clone 'I-214',  
338 resulted in a significant improvement in the model  $d$  ( $p$ -value < 0.01). To quantify the  
339 increase in the predictive ability of model  $dn$  in comparison to  $d$ , the same analysis as that  
340 described in the previous sections was performed.

341 There was an improvement in the PE obtained, most notably at the end of the first rotation  
342 and in the second rotation (Figure 6). The year R5S1 (year 4) showed the best response  
343 to the inclusion of the number of shoots, with the PE decreasing in nearly all simulations.  
344 However, there were no differences in the PE between model  $d$  and model  $dn$  in year  
345 R2S1 (year 1). Moreover, in Sim. 1, for example, the general PE in model  $dn$  was more  
346 than double that obtained with model  $d$  (Figure 5). The best response to the inclusion of  
347 the number of shoots was observed in Sim. 2 and Sim. 8. No appreciable variations were  
348 detected in Sim. 4 and Sim. 6.

349 RMSE and MRES behaved very similarly to PE in the model  $dn$  (Table 4), improving  
350 general simulations (Sim. 1, Sim. 2 and Sim. 8) in relation to model  $d$ , while the behaviour  
351 in Sim. 4 and Sim. 6 was quite similar to model  $d$  although with greater mean deviation  
352 and lower accuracy.

## 353 **4. Discussion**

354 The variability in parameter estimations for individual tree biomass models can be a  
355 problem in forest modelling. However, the behaviour of the allometric parameters, as well  
356 as the interaction with the cutting regime in coppice stands has not been analyzed in the  
357 literature as far as we know. Bearing in mind that coppice crops present a different below-  
358 ground biomass age for a given above-ground biomass age in different rotations, some of  
359 these factors may have an important impact.

360 A significant effect of stand age on tree allometry has been identified in our study, with  
361 more effect in the first year after harvest. By using data from only one site we are isolating  
362 the site variability in parameter estimates. The hypothesis of the authors is that there is  
363 no interaction in the trends observed in the parameters' variability with site.

### 364 **4.1. Parameter estimate variability**

365 Most of the published biomass models assume a constant relationship between age and  
366 allometry (Ter-Mikaelian and Korzukhin, 1997; Bi *et al.*, 2004; Pérez-Cruzado *et al.*,  
367 2011). This implies a constant rate of relative growth of biomass and diameter regardless  
368 of age. However, a number of studies have reported a change in the allometric relationship  
369 at a given point within the valid application range of the models. Bond-Lamberty *et al.*  
370 (2002) observed a change in the allometry beginning when diameter at breast height is  $\sim 3$   
371 cm, suggesting different allometry for saplings than for mature trees. Some authors have  
372 addressed this problem by including age as a predictor variable in the models (Saint-  
373 André *et al.*, 2005; Shaiek *et al.*, 2011).

374 Our study shows that there is a clear relationship between the estimated value of each  
375 parameter and the stage of development of the stand (Figures 1 and 2), as previously  
376 reported by Saint-André *et al.* (2005) and Antonio *et al.* (2007). Thus, the application of  
377 allometric models leads to considerable systematic lack of fit in tree components biomass  
378 predictions (Peichl and Arain, 2007). This lack of fit was found to be greater in the case  
379 of the short rotation coppice plantations studied, as the development stages fall within the  
380 range where most of the parameter variation occurs.

381 The evolution of the parameter estimates with age showed greater variability in the first  
382 year after each coppicing than in the remaining years of the rotation. A general trend  
383 towards stabilization at the end of each rotation was also identified. This greater  
384 uncertainty in the estimation of the parameters at ages 1 and 4 (years following coppicing)  
385 may be due to the tree changes after coppicing. Such as for example, an extraordinary  
386 allocation of resources to the aerial part after resprouting or the fact that the proportion of  
387 free growth as opposed to predetermined growth (preformed leaves over-wintered in the  
388 bud) is greater after the coppicing, this proportion decreasing with age. According to our  
389 findings, the first year after each coppicing should be avoided for sampling in the biomass  
390 model construction process, unless these dimensional classes are of specific interest.

391 Other factors affecting parameter estimates are the predictor variables used in the model  
392 as well as the model formulation. The basic model proposed here uses the basal diameter  
393 as a predictor variable (model *d*), which is advisable for very young woody crops (Long  
394 *et al.*, 1981; Smith and Brand, 1983; Pitt and Bell, 2004). The inclusion of height in  
395 estimation models led to more variability in the parameters for each year, particularly in  
396 the first year after each coppicing. The use of height in simple models could nevertheless  
397 increase the accuracy of predictions without increasing parameter instability in the  
398 harvesting years.

399 The variability of parameter estimates decreased with the use of formulations that include  
400 age as a dummy variable (Figure 2). Although trends were similar for all model  
401 formulations, dummy formulations produced less variability because of the inclusion of  
402 a common  $a$  parameter, for all years. Therefore these models seem to be more robust and  
403 probably more suitable than the simple formulation to make consistent predictions for  
404 different years.

405 There are studies that support the use of a universal parameter  $b$ , without distinction  
406 between species, site or year, assigning for example a value of  $b=8/3$  according to the  
407 model proposed by West *et al.* (1999) (hereinafter, WBE model), which has been widely  
408 studied (Chambers *et al.*, 2001; Anfodillo *et al.*, 2006; Niklas, 2006). Nevertheless, it is  
409 generally accepted that there is substantial variation in parameter  $b$  from one species to  
410 another (Ter-Mikaelian and Korzukhin, 1997; Ketterings *et al.*, 2001), and even within  
411 the same species. Despite the fact that Zianis and Mencuccini (2004) propose an empirical  
412 value for parameter  $b$  ( $b=2.36$ ), they also state that the use of a universal value for the  
413 exponent should only provide a rough estimate of tree biomass. Although the scale for  
414 parameter  $b$  is between 2 and 3 (Zianis and Mencuccini, 2004), for small trees (diameter  
415 at breast height ( $dbh$ )  $<15$  cm) it is generally less than 2 (Duursma and Robinson, 2003).  
416 In juvenile stages, it was observed that the values of parameter  $b$  had greater variability,  
417 suggesting that the WBE model (West *et al.*, 1999) is only applicable in actively-growing  
418 plants (Pilli *et al.*, 2006). According to our findings, the value of the  $b$  parameter could  
419 be close to those observed by other authors, with some differences arising from the  
420 consideration of basal or breast height diameters.

421 Therefore, the acceptance of a constant value of  $b$  should be viewed as tentative, and  
422 applicable only for rough predictions of biomass (Zianis and Mencuccini, 2004). For  
423 more accurate predictions it is necessary to take into account differences in species, sites

424 and ages. In spite of this, some ecophysiological models, as the model 3PG (Physiological  
425 principles in predicting growth) (Landsberg and Waring, 1997), use a fixed value of the  
426 parameter  $b$  to predict the biomass from diameter or the other way round.

#### 427 **4.2. Sample size**

428 The requirement as regards sample size to obtain an adequate description of a population  
429 by means of an empirical model is still to be determined. Heterogeneity in empirical  
430 values of the allometric parameters can result from methodological artefacts including  
431 small sample size, the regression methods used and fitting of models to parts of a dataset  
432 (Sileshi, 2014). While some studies point to the need for at least 50 observations to obtain  
433 stable estimations of the parameter values (Coomes and Allen, 2009; Sileshi, 2014), other  
434 studies observe that the effect of uncertainty in model predictions can only be considered  
435 below the sampling uncertainty when sample size is greater than 100 trees (McRoberts  
436 and Westfall, 2014). The minimum sample size necessary to achieve stable parameter  
437 estimates under the conditions studied was evaluated in this paper. It was only evaluated  
438 for the one clone due to the minimum sample size is dependent of the genotype studied.  
439 For the clone 'I-214' it was concluded that as sample size increased, parameter variability  
440 decreased (Figure 3 and 4), as reported by other authors who have addressed the influence  
441 of this factor on a wide range of species (Zapata-Cuartas *et al.*, 2012). The parameters  $a$   
442 and  $b$  display great variability when the sample size is small. Therefore, a small sample  
443 size leads to a great deal of uncertainty in the exponent values. In our case, for the clone  
444 'I-214', a threshold of 48 stools for short rotation coppice plantations was also proposed  
445 as the minimum sample size necessary to reduce the variability of the parameters, at least  
446 in cases where all the stages of development were included in the model. These results  
447 highlight the conclusions drawn from the simulation of different sampling schemes, as a  
448 sample size of  $\sim 50$  was considered for all sampling options simulated.

### 4.3. Uncertainty analysis

449 Age and rotation play an important role in individual tree allometry in coppice stands.  
450 Large uncertainties, both in precision and accuracy, were observed in models fitted for  
451 conditions different to those for which they are applied, or when age or rotation was not  
452 considered in the model formulation. This suggests that the decision to prioritize different  
453 aspects of allometric model development depends on the specific research objectives (van  
454 Breugel *et al.*, 2011) and potential use of the final models. Under such conditions, the  
455 predictive ability of the model cannot be improved by increasing the sample size but  
456 rather by stratifying the development conditions.  
457 There are multiple disadvantages associated with using the PE criterion alone for  
458 analyzing the prediction uncertainty, such as values being extremely skewed when  
459 observed biomass values are close to zero (Sileshi, 2014), which can occur in the  
460 simulations that include data from the first year after each coppicing (Sim. 1, Sim. 3, Sim.  
461 6, Sim. 7 and Sim. 8); a heavier penalty on positive deviances than on negative deviances;  
462 and unrealistic mean values when negative and positive deviances offset each other  
463 (Sileshi, 2014). For these reasons, each simulation is evaluated using a global PE and a  
464 specific PE for each year (Figures 5 and 6). MRES and RMSE were also calculated to  
465 contrast the PE results (Table 4). The RMSE also gives a relatively high weight to large  
466 uncertainties due to the squaring of errors before they are averaged (Sileshi, 2014).  
467 Some studies have reported good predictive abilities of models (total aboveground,  
468 belowground or total tree biomass) that depend only on diameter for entire age sequences  
469 (Peichl and Arain, 2007), which in the present study was considered in the Sim. 8  
470 sampling option. However, our results show that this is not a good approach for coppice  
471 plantations, the inclusion of other predictor variables (such as the age or the number of  
472 shoots per stool) being advisable in these cases to achieve accurate biomass estimates.  
473

474 The use of development stage-specific models was found to be the option with the  
475 smallest mean deviation and greatest accuracy, as well as minimizing the sampling effort  
476 and associated costs. The latter option, however, limits the use of these models at different  
477 stages of development both within the same rotation and between different rotations. The  
478 above findings lead us to recommend the use of models with age as a predictor variable  
479 when the objective is to provide predictions for all dimensional stages, or age-specific  
480 models when the interest is focused on predictions at a specific development stage.

481 The fact that the accuracy of the specific fittings for the second rotation was not as good  
482 as for the first rotation may be due to the greater variability over successive rotations. The  
483 growth rate was greater during the second rotation, therefore the diameter variability was  
484 greater, although a larger number of rotations and clusters would be necessary to assess  
485 the precise evolution according to the rotations. If  $D_{10}$  alone is used as a predictor variable  
486 in the model, bearing in mind the possibility of greater diameters in successive rotations  
487 due to a more developed root system (depending on the rotation number, the site  
488 conditions and the genotype), skewed estimations are likely to occur when such  
489 variability is not taken into account. Under these circumstances it would be advisable to  
490 introduce other variables that are sensitive to these changes in the growth pattern.

491 Only data from the first rotation years were used to fit the model in Sim. 3, which would  
492 be a similar option to the small trees sampling scheme (SSS) proposed by Zianis and  
493 Mencuccini (2004). It was observed that the biomass values of the smallest trees strongly  
494 affected the values of the coefficients in the allometric relationship between biomass and  
495 diameter (Chave *et al.*, 2001; Pérez-Cruzado and Rodríguez-Soalleiro, 2011). According  
496 to our results, the use of this technique causes much larger uncertainties in the cutting  
497 year, which makes it inappropriate unless the interest is focused on prediction at these  
498 specific ages.

499 The use of the cutting year alone to fit the predictive model for each rotation would appear  
500 to be the most accurate and unbiased option for the predictive purpose with regard to  
501 biomass crops. Despite the fact that the smallest sample size for fitting the model was that  
502 used for simulations Sim. 4 and Sim. 5 (below the limit set for the sample size), the lack  
503 of data may be of less consequence given the more specific range of values. The use of a  
504 common fit for both rotations, using only the cutting years or all the stages of  
505 development gives poorer predictions for the cutting years but better results for all the  
506 years in general. Thus, the decision as to the best option depends on the final aim of the  
507 model, bearing in mind that each choice with regard to the construction of the model  
508 implies associated uncertainty that will affect the predictions.

509 The inclusion of the number of shoots per stool as a predictor variable improved the  
510 biomass models under the coppice conditions studied. The inclusion of this variable had  
511 a significant influence in terms of uncertainty reduction (Figure 6) and also reduced the  
512 sample size necessary to achieve the same level of accuracy (Figure 4), apart from the  
513 frequency of negative parameter predictions for the  $c$  parameter. The uncertainty  
514 decreased with the inclusion of the number of shoots per stool in common models (Sim.  
515 2 and Sim. 8), due to differences in  $n$  between the first and the second rotation. In Sim. 4,  
516 in which only the cutting year of the first rotation was used to fit the model, the inclusion  
517 of the number of shoots per stool did not improve the fitting neither in mean deviation or  
518 accuracy. However in Sim. 5 (second rotation), the inclusion of the number of shoot per  
519 stool in the model improves the accuracy but not the mean deviation in the cutting year.  
520 This fact is attributed to the greater number of shoots per stool in consecutive rotations  
521 with respect to the first rotation. Under such circumstances, there are several dominant  
522 shoots rather than a single dominant shoot, resulting in a larger biomass accumulation.

## 523 **5. Conclusions**

524 A greater variability in biomass prediction has been observed in an SRC plantation  
525 depending on the factors studied, such as the predictor variables used in the models, the  
526 model formulation, the sample size and even the sample selection criteria. There is a  
527 notable influence of age on allometry in the years after harvest. The implicit inclusion of  
528 age in the model as a dummy variable, expanding the exponent of diameter, reduces the  
529 variability in parameter estimations for each year and each rotation. However, the sample  
530 selection criteria may also reduce the influence of age in the model. It is evident that  
531 different options may be employed depending on the purpose of the model, so it is  
532 advisable to carefully consider the aim of the model in order to select the most appropriate  
533 time of sampling. If the final objective is to predict biomass at different ages in an SRC  
534 plantation, the inclusion of a specific variable such as the number of shoots per stool  
535 seems appropriate since it is easy to record, reduces the mean deviation and increases the  
536 accuracy. The minimum sample size to construct the model in this case is 50. However,  
537 if the final aim is to predict the biomass at the planned cutting year, only the use of cutting  
538 year data in the model construction will suffice. The greater degree of accuracy achieved  
539 by only collecting data from the cutting year means that the sample size required can be  
540 smaller and therefore the sampling activity can be more concentrated in time.

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549 **Conflict of interest statement**

550 None declared.

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1 **Figure 1.** Evolution of the exponential parameters of the simple models with age:  $b$   
2 parameter (left),  $c$  parameter (centre) and  $d$  parameter (right). The letters of the models  
3 indicate the predictor variables included in the model. Zooms are included in the upper  
4 right quadrant.

5 **Figure 2.** Evolution of the exponential parameters for the dummy models with age:  $b$   
6 parameter (left) and  $c$  parameter (right). The letters of the models indicate the predictor  
7 variables included in the model. Capital letters indicate that the parameter associated  
8 with that predictor variable has been expanded through dummy variables. Zooms are  
9 included in the upper right quadrant.

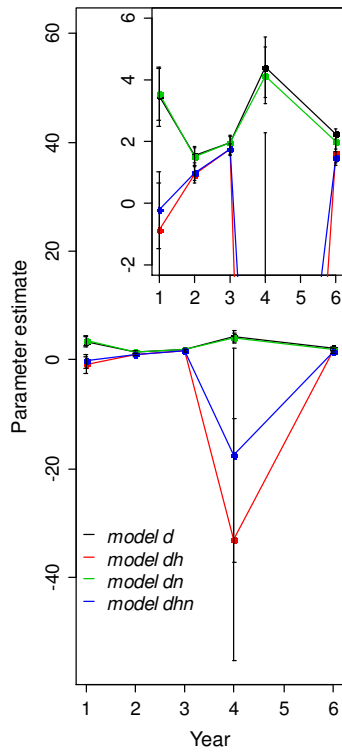
10 **Figure 3.** Uncertainty in parameter estimation for clone 'I-214' and model  $d$  for  
11 different sample size simulations: Parameter  $a$  (top-left), parameter  $b$  (top-right), RMSE  
12 (g) (bottom-left) and MRES (g) (bottom-right).

13 **Figure 4.** Evolution of the estimations of the parameters for clone 'I-214' and model  $dn$   
14 for different sample size simulations. Parameter  $a$  (top-left), parameter  $b$  (top-centre)  
15 and parameter  $d$  (top-right), RMSE (g) (bottom-left) and MRES (g) (bottom-right).

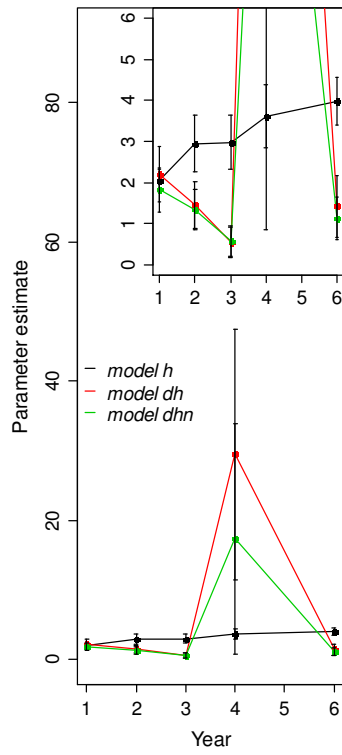
16 **Figure 5.** Percentage error (PE, %) at stool level for the clone 'I-214' in model  $d$  for  
17 each simulation (both in general (left) and by years (right)).

18 **Figure 6.** Percentage error (PE, %) at stool level for the clone 'I-214' in model  $dn$ , for  
19 each simulation (both in general (left) and by years (right)).

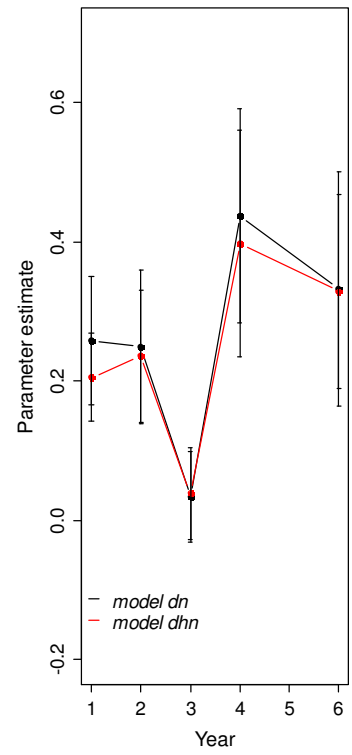
**b parameter**



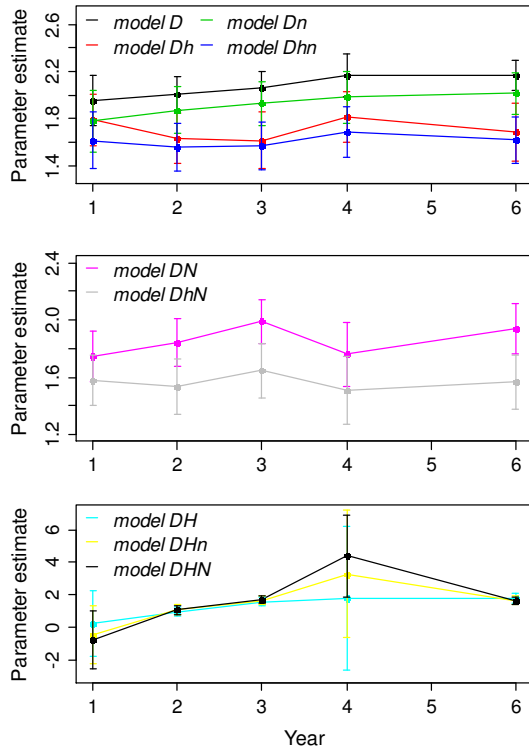
**c parameter**



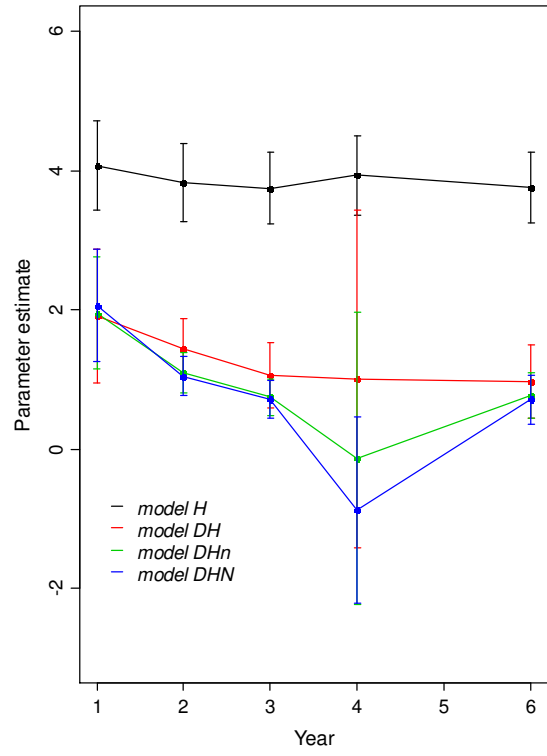
**d parameter**

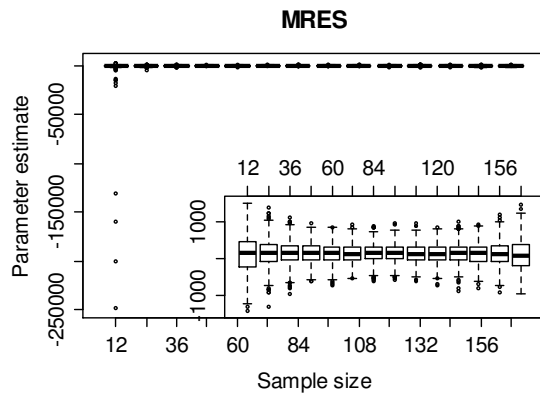
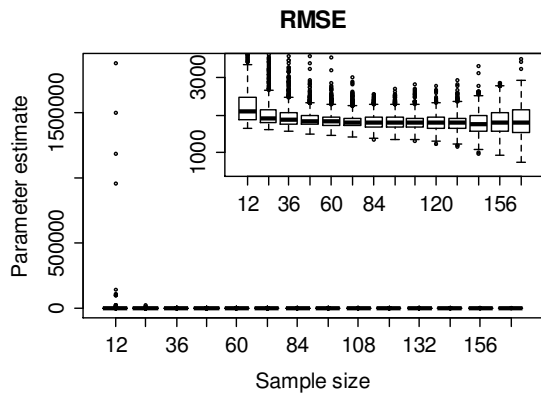
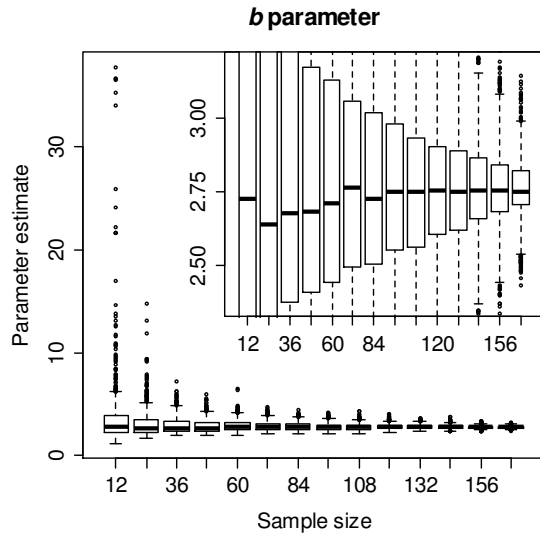
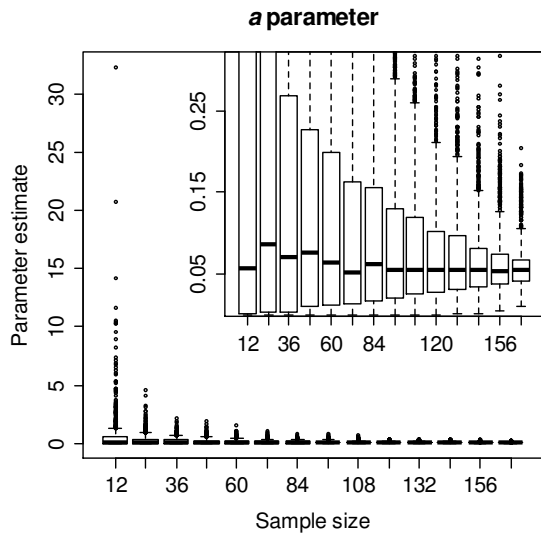


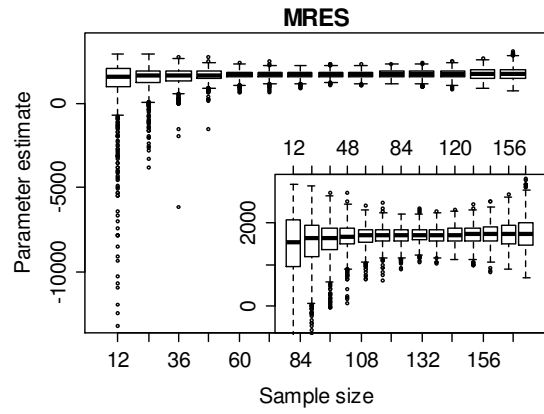
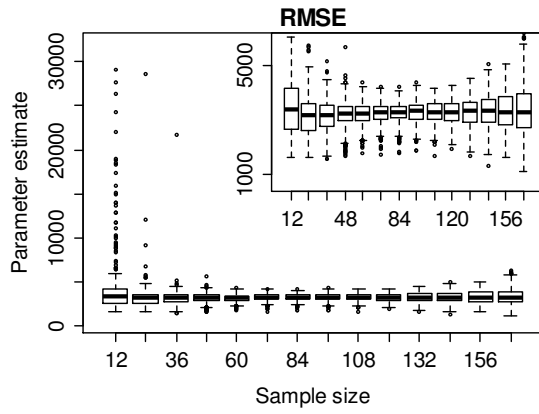
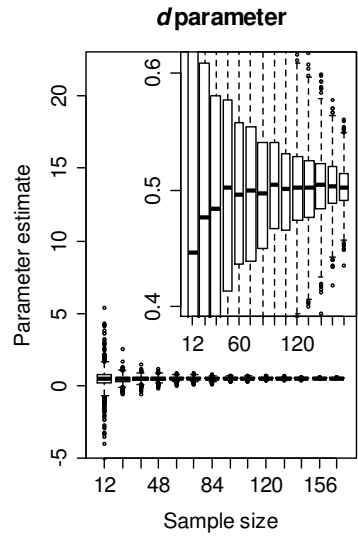
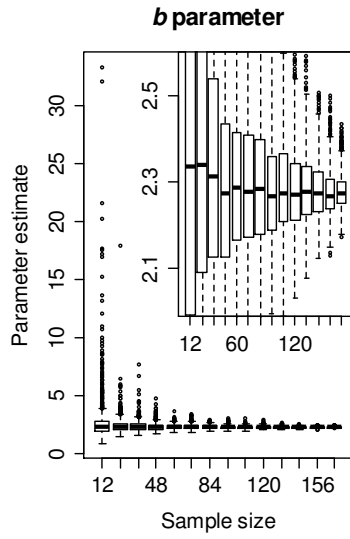
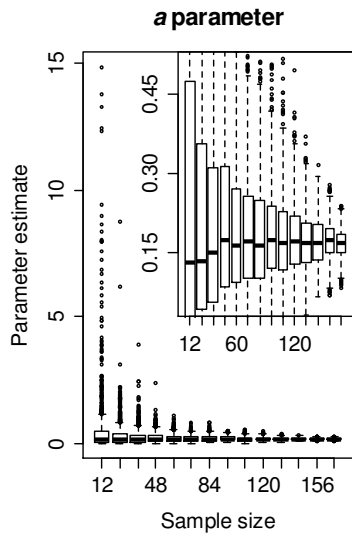
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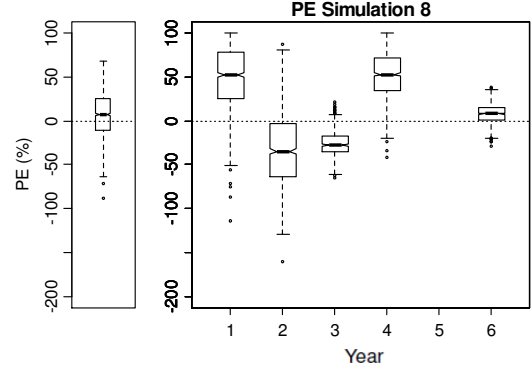
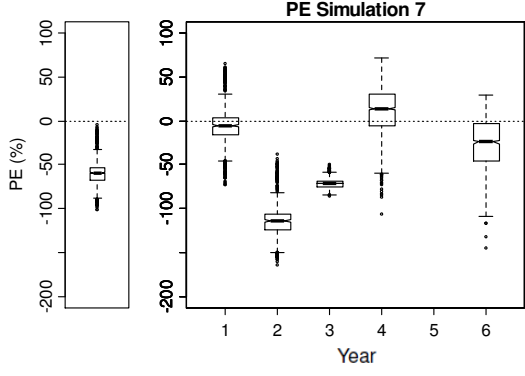
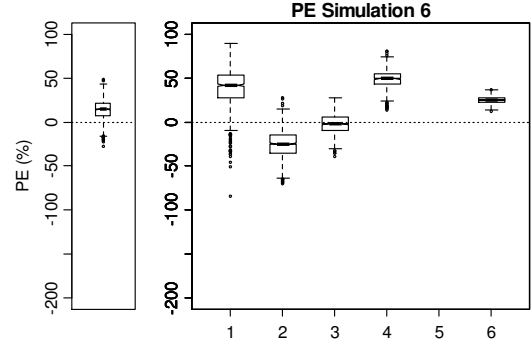
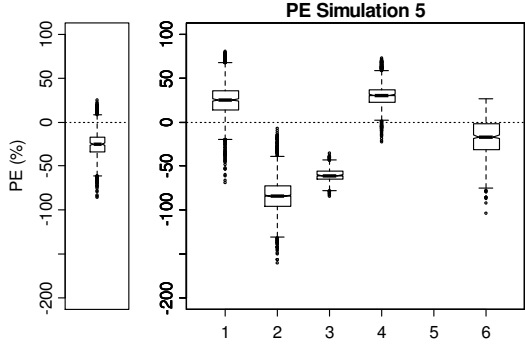
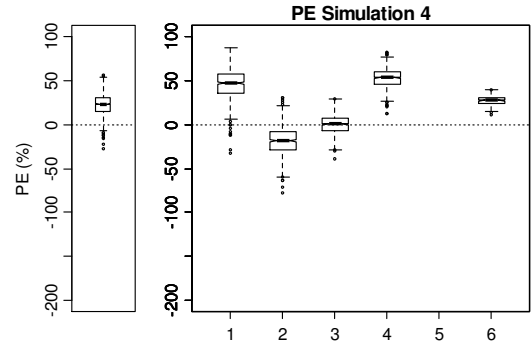
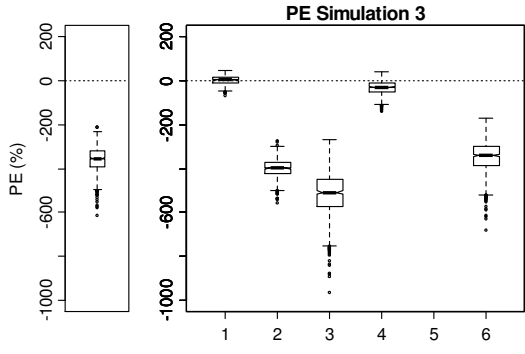
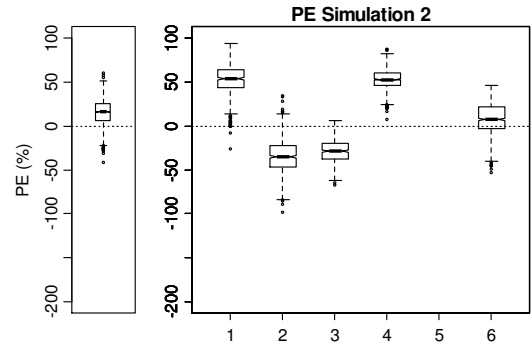
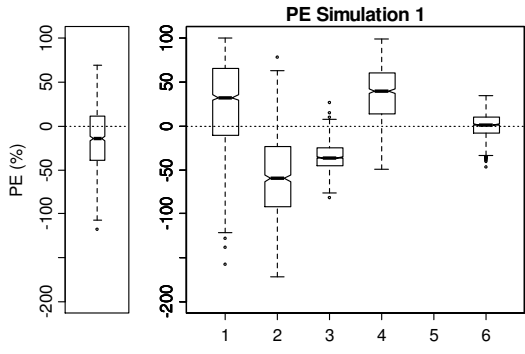


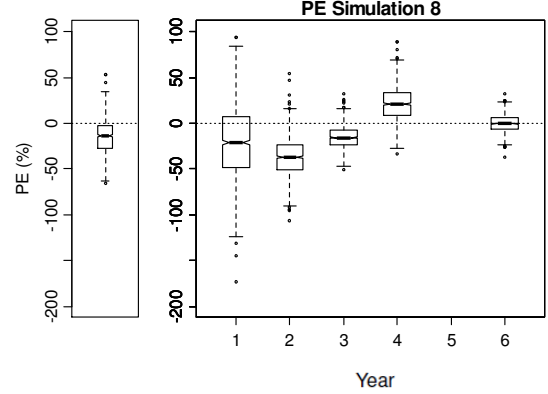
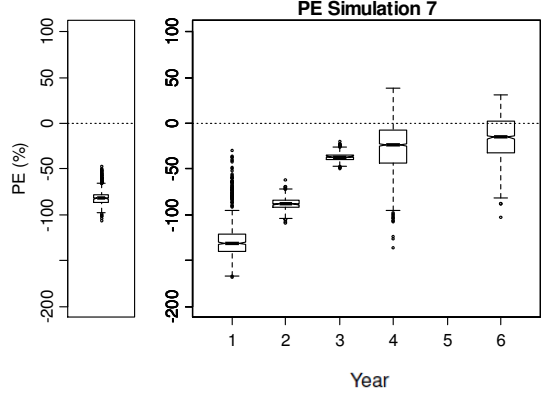
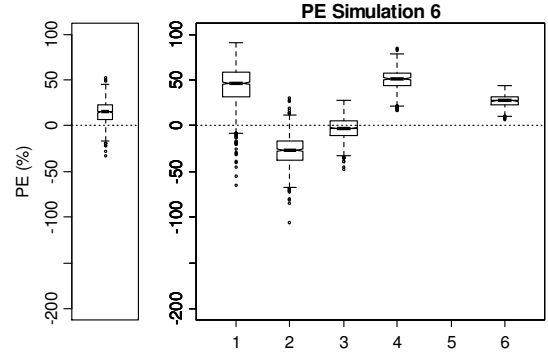
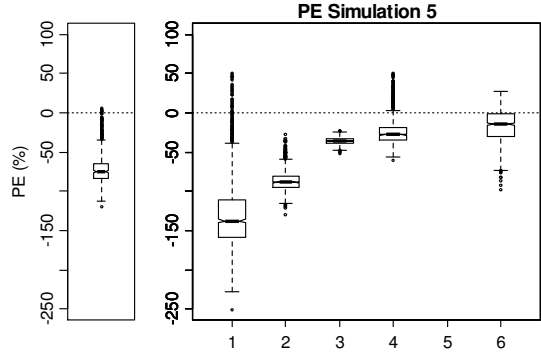
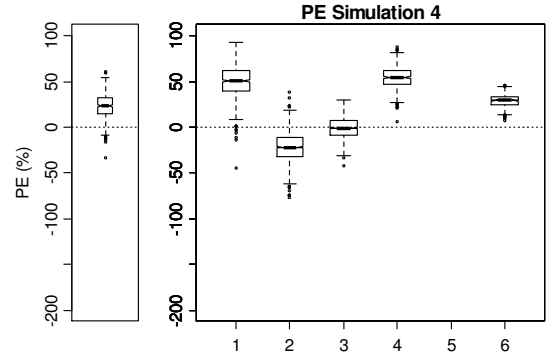
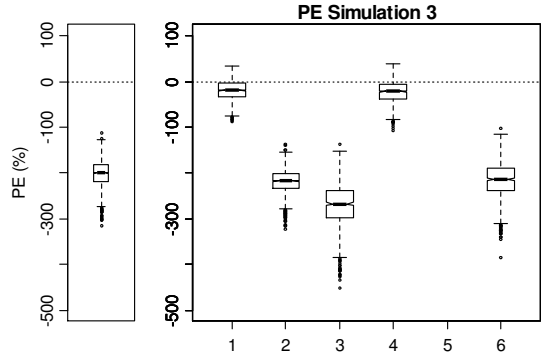
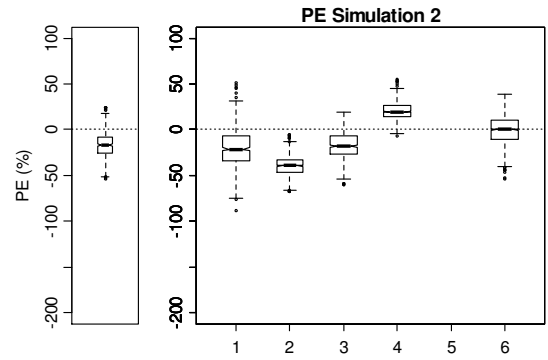
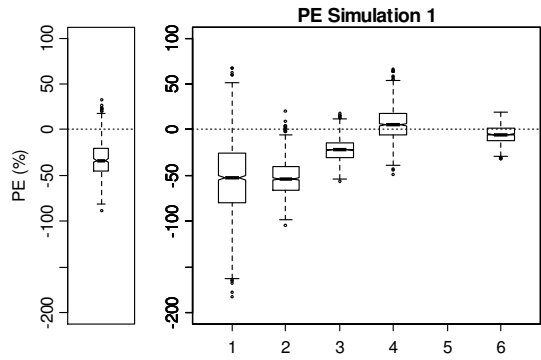
**c parameter**











Year

Year

1 **Table 1.** Model formulations considered in the fitting process.

Abbreviation	Model Formulation	Number Eq.
Model <i>d</i>	$W_s = a D_{10}^b + \varepsilon$	(4)
Model <i>dh</i>	$W_s = a D_{10}^b H^c + \varepsilon$	(5)
Model <i>dhn</i>	$W_s = a D_{10}^b H^c n^d + \varepsilon$	(6)
Model <i>dn</i>	$W_s = a D_{10}^b n^d + \varepsilon$	(7)
Model <i>h</i>	$W_s = a H^c + \varepsilon$	(8)
Model <i>D</i>	$W_s = a D_{10}^{(b_1 I_1 + b_2 I_2 + b_3 I_3 + b_4 I_4 + b_6 I_6)} + \varepsilon$	(9)
Model <i>H</i>	$W_s = a H^{(c_1 I_1 + c_2 I_2 + c_3 I_3 + c_4 I_4 + c_6 I_6)} + \varepsilon$	(10)
Model <i>Dh</i>	$W_s = a D_{10}^{(b_1 I_1 + b_2 I_2 + b_3 I_3 + b_4 I_4 + b_6 I_6)} H^c + \varepsilon$	(11)
Model <i>DH</i>	$W_s = a D_{10}^{(b_1 I_1 + b_2 I_2 + b_3 I_3 + b_4 I_4 + b_6 I_6)} H^{(c_1 I_1 + c_2 I_2 + c_3 I_3 + c_4 I_4 + c_6 I_6)} + \varepsilon$	(12)
Model <i>DHN</i>	$W_s = a D_{10}^{(b_1 I_1 + b_2 I_2 + b_3 I_3 + b_4 I_4 + b_6 I_6)} H^{(c_1 I_1 + c_2 I_2 + c_3 I_3 + c_4 I_4 + c_6 I_6)} n^{(d_1 I_1 + d_2 I_2 + d_3 I_3 + d_4 I_4 + d_6 I_6)} + \varepsilon$	(13)
Model <i>DHn</i>	$W_s = a D_{10}^{(b_1 I_1 + b_2 I_2 + b_3 I_3 + b_4 I_4 + b_6 I_6)} H^{(c_1 I_1 + c_2 I_2 + c_3 I_3 + c_4 I_4 + c_6 I_6)} n^d + \varepsilon$	(14)
Model <i>Dhn</i>	$W_s = a D_{10}^{(b_1 I_1 + b_2 I_2 + b_3 I_3 + b_4 I_4 + b_6 I_6)} H^c n^{(d_1 I_1 + d_2 I_2 + d_3 I_3 + d_4 I_4 + d_6 I_6)} + \varepsilon$	(15)
Model <i>Dhn</i>	$W_s = a D_{10}^{(b_1 I_1 + b_2 I_2 + b_3 I_3 + b_4 I_4 + b_6 I_6)} H^c n^d + \varepsilon$	(16)
Model <i>DN</i>	$W_s = a D_{10}^{(b_1 I_1 + b_2 I_2 + b_3 I_3 + b_4 I_4 + b_6 I_6)} n^{(d_1 I_1 + d_2 I_2 + d_3 I_3 + d_4 I_4 + d_6 I_6)} + \varepsilon$	(17)
Model <i>Dn</i>	$W_s = a D_{10}^{(b_1 I_1 + b_2 I_2 + b_3 I_3 + b_4 I_4 + b_6 I_6)} n^d + \varepsilon$	(18)

2 Where *n* is the number of shoots per stool, *H* is the height of the dominant shoot per

3 stool (m), *D*<sub>10</sub> is the basal diameter of the dominant shoot per stool (mm), *W*<sub>s</sub> is the total

4 aboveground dry biomass per stool (g) and *I*<sub>1</sub>, *I*<sub>2</sub>, *I*<sub>3</sub>, *I*<sub>4</sub> and *I*<sub>6</sub> are the dummy variables.

5 **Table 2.** Statistics for the main variables measured in the 'I-214' clone plots for each  
6 stage of development.

		<b>R2S1</b>	<b>R3S2</b>	<b>R4S3</b>	<b>R5S1</b>	<b>R7S3</b>	<b>ALL</b>
<b><i>n</i></b>	Max <sup>a</sup>	25	11	9	15	17	25
	Min <sup>b</sup>	4	1	1	3	1	1
	Mean	9.09	3.93	4.60	7.10	7.66	6.39
	Devest <sup>c</sup>	4.48	2.30	1.95	3.18	3.74	3.81
<b><i>H (cm)</i></b>	Max <sup>a</sup>	293	563	917	470	1031	1031
	Min <sup>b</sup>	70	115	249	273	331	70
	Mean	215.75	435.71	706.24	408.33	868.10	507.76
	Devest <sup>c</sup>	46.36	109.17	169.22	52.37	180.89	259.11
<b><i>D<sub>10</sub> (mm)</i></b>	Max <sup>a</sup>	18.41	57.36	96.95	29.17	96.00	96.95
	Min <sup>b</sup>	10.31	4.72	16.98	17.48	18.00	4.72
	Mean	15.16	37.66	60.37	25.06	66.41	39.92
	Devest <sup>c</sup>	1.73	12.47	20.74	3.12	20.47	24.13
<b><i>Ws (g)</i></b>	Max <sup>a</sup>	692.02	3602.31	11768.12	2481.22	22757.27	22757.27
	Min <sup>b</sup>	16.15	100.06	245.17	155.08	152.41	16.15
	Mean	340.08	1199.85	4358.56	1188.57	8616.63	2864.28
	Devest <sup>c</sup>	183.40	814.28	3109.71	672.89	5902.23	3989.55
<b><i>N Data</i></b>		44	41	42	30	29	186

7 Where *n* is the number of shoots per stool, *H* is the height of the dominant shoot per  
8 stool (m), *D<sub>10</sub>* is the basal diameter of the dominant shoot per stool (mm), *Ws* is the total  
9 aboveground dry biomass per stool (g) and *N Data* is the number of stools measured.  
10 The stage of development is expressed according to their root (*R*) and their stool age (*S*),  
11 so R2S1 is the first year after coppicing, year 1(2006), R3S2 is year 2 (2007), R4S3 is  
12 year 3 (2008), R5S1 is year 4 (2009) the first year after coppicing in the second rotation  
13 and the last is R7S3, which is year 6 (2011). <sup>a</sup> Max: maximum; <sup>b</sup> Min: minimum; <sup>c</sup>  
14 Devest: mean deviation

15 **Table 3.** Different number of simulations proposed and the sample data used to fit the  
 16 models for each stage of development.

	<b>R2S1</b>	<b>R3S2</b>	<b>R4S3</b>	<b>R5S1</b>	<b>R6S2</b>	<b>R7S3</b>	<b>TOTAL</b>
<b>Sim. 1</b>	13		13	13		13	<b>52</b>
<b>Sim. 2</b>			26			26	<b>52</b>
<b>Sim. 3</b>	26			26			<b>52</b>
<b>Sim. 4</b>			25				<b>25</b>
<b>Sim. 5</b>						25	<b>25</b>
<b>Sim. 6</b>	26		26				<b>52</b>
<b>Sim. 7</b>				26		26	<b>52</b>
<b>Sim. 8</b>	10	10	10	10		10	<b>50</b>
<b>TOTAL DATA</b>	<b>44</b>	<b>41</b>	<b>42</b>	<b>30</b>	<b>0</b>	<b>29</b>	<b>186</b>

17 Where the simulations are abbreviated by Sim. and the number of each one, and the  
 18 stage of development is expressed according to their root (*R*) and their stool age (*S*), so  
 19 R2S1 is the first year after coppicing, year 1(2006), R3S2 is year 2 (2007), R4S3 is year  
 20 3 (2008), R5S1 is year 4 (2009) the first year after coppicing in the second rotation and  
 21 the last is R7S3, which is year 6 (2011).

22 **Table 4.** Mean residuals (MRES, g) (left) and root mean square error (RMSE, g) (right)

23 at stool level for the clone 'I-214' in model *d* and *dn* (Table1), for each simulation.

		MRES						RMSE					
		All ages	R2S1	R3S2	R4S3	R5S1	R7S3	All ages	R2S1	R3S2	R4S3	R5S1	R7S3
Model <i>d</i>	Sim. 1	-211	175	-521	-1569	646	1381	1755	244	951	2461	857	3261
	Sim. 2	-6	230	-352	-1483	759	1490	1153	281	782	2374	948	2867
	Sim. 3	-16252	100	-4986	-26105	-64	-30292	26228	169	6437	34402	396	37483
	Sim. 4	784	219	-114	50	771	3354	2116	272	601	129	962	4718
	Sim. 5	-768	168	-848	-2694	570	-53	2030	229	1222	3610	784	2530
	Sim. 6	860	205	-169	-4	739	3325	2309	259	617	1270	934	4714
	Sim. 7	-1210	105	-1121	-2900	400	-191	2268	183	1467	3691	607	2514
	Sim. 8	-33	223	-307	-1432	760	1477	1842	278	813	2469	950	3306
Model <i>dn</i>	Sim. 1	-160	-16	-425	-511	285	397	1265	157	805	1980	529	2008
	Sim. 2	-33	55	-313	-473	404	482	875	149	709	1876	605	1754
	Sim. 3	-9185	43	-2613	-13036	-48	-19885	15306	132	3283	17045	372	25401
	Sim. 4	842	229	-150	3.77	798	3712	2318	282	675	1329	993	5189
	Sim. 5	-458	-180	-717	-857	-2	-105	1282	252	1052	2144	437	1851
	Sim. 6	921	216	-196	-42	766	3631	2499	270	682	1307	965	5114
	Sim. 7	-551	-180	-728	-852	-23	-65	1368	232	1058	2122	380	1778
	Sim. 8	-20	54	-283	-417	415	489	1323	169	718	1967	620	2119

24 Where the simulations are abbreviated by Sim. and the number of each one, and the

25 stage of development is expressed according to their root (*R*) and their stool age (*S*), so

26 R2S1 is the first year after coppicing, year 1(2006), R3S2 is year 2 (2007), R4S3 is year

27 3 (2008), R5S1 is year 4 (2009) the first year after coppicing in the second rotation and

28 the last is R7S3, which is year 6 (2011).