Compatibility of whole-stand and individual-tree models using composite estimators and disaggregation

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ABSTRACT

This study presents a new approach in linking models with different levels of resolution. Data from 50 permanent sample plots installed in even-aged birch (*Betula alba*) dominated stands were used to develop both, a whole-stand growth model and an individual-tree model. In a first step, six disaggregation approaches to link number of trees per hectare with tree survival were combined with four disaggregation approaches to link stand basal area with tree basal area growth predictions. To analyze the effect of stand variable predictions on disaggregation estimates, two different methods to obtain these predictions were evaluated: (a) 1-fold cross-validation of the stand growth model and (b) a method involving composite estimators. Therefore, altogether 48 different approaches in linking models were analyzed in this first step. In a second step, two common methods based on the use of a threshold to translate the survival tree probabilities into a discrete event, i.e. dead or alive, were combined with the four disaggregation approaches to link stand basal area with tree basal area growth predictions and the two methods to obtain stand variable predictions. Therefore, altogether 16 different approaches in linking models were analyzed in this second step. Finally, the best combinations obtained in each step were compared. Regarding the disaggregation of predicted stand density, the approach based on considering the intercept of the logit function for tree survival as a specific parameter of each sample plot and optimizing its value produced the best results. Regarding the disaggregation of stand basal area among trees, the constrained least squares method was selected, since it showed the best results among four alternative approaches. The use of composite estimators instead of the 1-fold cross validation predictions improved the accuracy of both, tree survival and tree basal area estimates, although the differences were not significant. Finally, disaggregation approaches performed better than the methods based on the use of a threshold. The results show that the combination between composite estimators and disaggregation provided compatible and reliable predictions of stand density, tree survival, stand basal area and tree basal area. The main limitation of this new approach is the dependency of accurate stand growth predictions, therefore, it should be tested in future studies with more complicated stand structures, such as mixed and un-even aged forests, or to include the effect of silvicultural treatments.

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1. Introduction

Growth and yield models for forest management decision support range from relatively simple whole-stand models to detailed individual-tree models. There are advantages and disadvantages associated to each level of resolution. Whole-stand models are generally simpler and more robust, and they are easier to develop, but they have a limited potential for simulating stand structures and management options in multi-species forests (Ritchie and Hann, 1997; Qin and Cao, 2006; Álvarez-González et al., 2009). Individual-tree models, on the other hand, can be used to predict tree growth in complex stand structures and species compositions. However, due to the fact that individual tree predictions are often associated with large errors, aggregate stand-level predictions are generally not as reliable as those from whole-stand models (Ritchie and Hann, 1997).

The selection of the appropriate resolution level depends on the reliability of estimates, the flexibility to simulate management alternatives, the ability to provide detailed information for decision

making and the efficiency to do it (Burkhart and Tomé, 2012). It makes sense, therefore, to combine models with different levels of resolution. Thus, there has been considerable interest in linking individual-tree and whole-stand models to obtain well-behaved projections of overall values, with numeric consistency among the estimates, while maintaining detailed tree information.

According to Weiskittel et al. (2011), three approaches have been used in the past to link stand- and tree-level models: (i) disaggregation; (ii) constrained parameters and (iii) combined. In the disaggregation approach, growth and mortality are projected at the stand level and then adjusted to individual trees (e.g. Clutter and Allison, 1974; Campbell et al., 1979; Harrison and Daniels, 1988; Matney et al., 1990; Nepal and Somers, 1992; Cao and Baldwin, 1999; Qin and Cao, 2006). The constrained approach uses a multi-response parameter estimation technique developed by Bates and Granger (1969) to optimize tree-level predictions at multiple levels (e.g. Zhang et al., 1997a, 1997b; Cao, 2006). The combined approach uses a composite estimator to link estimates of tree and stand level equations to improve both predictions (e.g. Yue et al., 2008; Zhang and Lei, 2010; Zhang et al., 2010, 2011). Further revision of the methods used to link models with different level of resolution using disaggregation can be found in Ritchie and Hann (1997), and the background of the three different approaches described above is presented in Weiskittel et al. (2011, Ch. 10) and Cao (2014).

In this study, which evaluates and extends previously described techniques within a new context, the primary objectives are: (1) to fit a whole-stand model and an individual tree model; (2) compare alternative methods for implementing the stand- and tree-level equations; and (3) evaluate the best method and approach for combining the predictions.

2. Material and methods

2.1. Data set

A network of 137 plots was established in even-aged, birch dominated stands in the winters of 1997–1998, 1998–1999 and 2000–2001. The plots were located throughout the area of distribution of this species in Galicia/Spain, and were subjectively selected to represent a wide range of site qualities, ages and stand densities. The plot size ranged from 625 m² to 1200 m² depending on stand density, in order to achieve a minimum of 50 trees per plot. Because of forest fires or clear cutting, many plots disappeared and only a subset of 50 of the initially established plots was re-measured in the winter of 2007–2008. The intervals between the measurements (7, 9 and 10 years) were considered sufficient to absorb the short-term effects of abnormal climatic extremes. In other studies, an interval of 5 years, as suggested by Gadow and Hui (1999), for example, was found to be appropriate.

All the trees in each sample plot were labeled with a number. Total height (±0.1 m) and two values of diameter at breast height (outside bark; ±0.1 cm) at right angles were measured and the arithmetic mean of the two diameters was calculated. Descriptive variables of each tree were also recorded, e.g. if they were alive or dead. The stand variables calculated for each inventory were: dominant height (H, in m) defined as the mean height of the 100 thickest trees per hectare, stand basal area (G, in m²/ha), number of trees per hectare (N), relative spacing index (RSI), defined as the ratio between the mean distance between trees and dominant height ($RSI = 100/(\sqrt{N}H)$) and site index (SI, in m), defined as the dominant height estimated with the model proposed by Diéguez-Aranda et al. (2006) at a reference age of 20 years. The mean, maximum and minimum values, and the

standard deviation of the main stand and tree variables used in this study are shown in Table 1.

2.2. Model structure

2.2.1. Stand growth model

The dynamic stand growth model that we are presenting is based on the assumption that the behavior of any birch stand evolving over time can be approximated by describing the current state with three state variables: dominant height (H), number of trees per hectare (N) and basal area (G). Transition functions are used to estimate the change of the variables as a function of their current state.

2.2.1.1. Transition function for dominant height.
A site-specific 2-parameter equation, derived from the Hossfeld base model and proposed by Diéguez-Aranda et al. (2006), was used as a transition function for dominant height. This Generalized Algebraic Difference Approach (GADA) model allows simultaneous concurrent polymorphism and multiple asymptotes, two characteristics of site equations that are often desirable (Cieszewski, 2002). The mathematical expression of this model is

$$H_2 = \frac{19.8 + X_0}{1 + 758/X_0 \cdot t_2^{-1.40}}$$

$$\text{where } X_0 = \frac{1}{2} \cdot \left(H_1 - 19.8 + \sqrt{(19.8 - H_1)^2 + 4 \cdot 758 \cdot H_1 \cdot t_1^{-1.40}} \right)$$

$$(1)$$

H_1 and t_1 represent the current height (m) and age (years), and H_2 is the predicted height at some future age t_2.

2.2.1.2. Transition function for mortality.
Natural mortality and tree survival are extremely variable processes and thus particularly difficult to predict. The mortality transition function is based on the assumption that the rate of change of number of trees per ha (N) relative to dominant height (H) increment depends on the current values of H and N as $dN/dH - a_1 H^{a_2} N^{a_3}$, where a_i are parameters to be estimated. That assumption has been broadly used in stand growth models development (e.g. García, 2011, 2013; García et al., 2011 and Tewari et al., 2014). Integration of both sides of the differential equation and equating the resulted invariant for points in time 1 and 2 gives the following transition function for number of trees per ha:

$$N_2 = \left[N_1^{1-a_3} + a_1 \frac{a_3 - 1}{a_2 + 1} \left(H_2^{a_2+1} - H_1^{a_2+1} \right) \right]^{1/(1-a_3)} \quad (2)$$

Number of trees per ha (N) and dominant height (H) in Eq. (2) were rescaled to homogenize the magnitude of both variables, resulting in the following expression:

$$N_2 = 1000 \left[\left(\frac{N_1}{1000} \right)^{1-a_3} + a_1 \frac{a_3 - 1}{a_2 + 1} \left(\left(\frac{H_2}{10} \right)^{a_2+1} - \left(\frac{H_1}{10} \right)^{a_2+1} \right) \right]^{1/(1-a_3)}$$

$$(3)$$

2.2.1.3. Transition function for basal area.
Instead of predicting basal area (G, m²/ha) directly, we choose to model the change of the product $W = GH$. The rate of change of W can be expressed as the difference between two components: gross increment and mortality. In pure and even-aged stands (such as those considered in this study), the gross increment can be written as $b_1 H^{b_2} N^{b_3}$ and the mortality as $-k \frac{W}{N} \frac{dN}{dH} = -kW \frac{d\log N}{dH}$, where log is the natural logarithm, b_i are parameters to be estimated, and k represents the mean size of dying trees relative to the mean size of the survivors,

Table 1
Summarised data corresponding to the sample of 50 plots used for model development.

Variable (plot/tree)	1st inventory				2nd inventory			
	Mean	Max.	Min.	S.D.	Mean	Max.	Min.	S.D.
t (years)	28.93	47.00	12.00	10.00	38.05	56.00	22.00	9.74
H (m)	13.65	21.83	7.22	3.36	18.34	26.69	11.44	3.14
G (m^2/ha)	23.31	66.47	3.34	11.5	28.72	71.75	9.16	10.9
N (stems/ha)	1634.7	5600.0	390.0	1093.4	1369.6	4480.0	350.0	828.6
SI (m)	12.52	19.24	8.08	2.44	–	–	–	–
RSI	0.20	0.59	0.08	0.09	0.17	0.37	0.08	0.06
d (cm)	12.88	37.85	1.00	5.38	15.96	42.35	4.85	5.81
h (m)	13.58	25.25	5.30	3.90	15.09	26.90	7.35	3.69
p_s (%)	–	–	–	–	98.46	100.00	95.24	1.10

t = stand age; H = dominant height; G = stand basal area; N = number of stems per hectare; SI = site index; RSI = relative spacing index; d = diameter at breast height over bark; h = total tree height; p_s = annual survival probability; S.D. = standard deviation.

and is assumed as constant. Therefore, the general model for W is assumed as $\frac{dW}{dH} = b_1 H^{b_2} N^{b_3} + kW \frac{d \log N}{dH}$. A simple closed-form solution of this differential equation is obtained in the special case where k is equal to b_3 (e.g. García et al., 2011; García, 2013; Tewari et al., 2014 or Álvarez-González et al., 2014). In this case, the integration of the differential equation gives the transition equation for basal area:

$$G_2 = N_2^k \left(G_1 H_1 N_1^{-k} + b_1 \left(H_2^{b_2+1} - H_1^{b_2+1} \right) \Big/ (b_2 + 1) \right) \Big/ H_2 \tag{4}$$

In the same way as done in Eq. (4), number of trees per ha and dominant height were rescaled and the result is as follows:

$$G_2 = \left(\frac{N_2}{1000} \right)^k \left[G_1 \frac{H_1}{10} \left(\frac{N_1}{1000} \right)^{-k} + b_1 \left(\left(\frac{H_2}{10} \right)^{b_2+1} - \left(\frac{H_1}{10} \right)^{b_2+1} \right) \Big/ (b_2 + 1) \right] \Big/ \left(\frac{H_2}{10} \right) \tag{5}$$

2.2.1.4. Parameter estimation. The model was fitted based on projections of pairs of consecutive measurements. Predicted, rather than observed, dominant heights at the second inventory were used as H_2 in Eq. (5) to include the error of the estimates in the whole stand growth model. In the present study, mortality is used as a dependent variable in Eq. (2) and as an independent variable in Eq. (5), thus involving a simultaneous system of equations. Therefore, the transition functions for mortality and basal area were fitted simultaneously using the full information maximum likelihood (FIML) in order to obtain estimates that are consistent and efficient and that contribute to increased precision of the model predictions. Because the convergence with this approach is very sensitive to the starting values of the parameters, both transition functions were first fitted separately to obtain good estimates of initial values.

The models were initially fitted under the assumption that the within-equation errors were independent and identically distributed. As only two measures were available for each stand, autocorrelation among measurements within a sample plot was ruled out. However, the mortality model showed problems related to heterocedasticity.

That problem was solved by weighting each observation during the fitting process by the inverse of its variance (σ_i^2). If the variance is unknown, the problem becomes one of estimating the proper weight for each observation. However, it is assumed that the variance of the error of the ith individual can be modeled as a power function of a combination of the independent variables i.e., $\sigma_i^2 = (X_i)^\alpha$. The most reasonable combination of independent variables and corresponding value of the exponential term α should provide the most homogeneous studentized residual plot (Huang et al., 2000). It can be obtained by analyzing different sets of independent variables and optimizing the value of α as suggested by Harvey (1976), by using the estimated errors of the unweighted

model ($\hat{e}_i$) as the dependent variable in the error variance model, i.e. $\hat{e}_i^2 = \gamma (X_i)^\alpha$ or, taking the natural logarithm of the function $\ln \hat{e}_i^2 = \ln \gamma + \alpha \log(X_i)$. The α parameter was estimated using linear regression. The weighting factor for heteroscedasticity $1/(X_i)^\alpha$ was programmed in the MODEL procedure of SAS/ETS® (SAS Institute Inc., 2008).

2.2.2. Individual tree growth model

The components usually identified in individual tree growth models are diameter or basal area increment, mortality, and recruitment (Vanclay, 1994). No regeneration was observed in the plots used in the present study, thus it was not possible to develop a recruitment equation. In order to model mortality, the logistic or logit cumulative distribution function was used (e.g., Monserud, 1976; Monserud and Sterba, 1999; Juma et al., 2014). The basal area and mortality models which were finally selected are:

$$g_2 = g_1 + c_0 g_1^{c_1} G_1^{c_2} \exp \left(c_3 \frac{d_1}{dg_1} \right) \tag{6}$$

$$p_s = \frac{1}{1 + \exp \left(f_o + f_1 d_1 + f_2 G_1 + f_3 \frac{d_1}{dg_1} \right)} \tag{7}$$

where g_1 and g_2 are the basal area at times t_1 and t_2, respectively, G_1 is the stand basal area at time t_1 (m^2/ha); d_1 and dg_1 are the diameter at breast height (cm) and the quadratic mean diameter at time t_1 (cm), respectively, and p_s is the annual survival probability.

In the present study, the re-measurement interval was variable, with either 7, 9 or 10 years between successive inventories. The variable growth rate (VGR) approach was used for fitting the annual individual-tree growth model. This approach uses the methodology developed by Cao (2000), in which the left-hand side of the growth equation represents the observed basal area at the end of the growth period, and the right hand side is a function that adds the annual increments of basal area (ig) to the total value at the start of the growth period. The survival probability was obtained as a product of the annual survival probabilities (e.g. Cao and Strub, 2008). In the VGR approach, interim values of d were obtained on the basis of predicted values of g and interim values of G and dg were obtained from the stand growth model fitted previously.

The system involving Eqs. (6) and (7) was fitted simultaneously using the seemingly unrelated regression procedure (SUR) to account for possible correlated error components, as some terms (e.g., d) were common to both equations. Maximum likelihood techniques were used to fit Eq. (7), with the log likelihood function defined as $\ln(L) = y_0 \log (p_s) + (1 - y_0) \log (1 - p_s)$, where y_0 is a dummy variable assuming a value of 1 for a live tree and 0 for a dead tree. The above maximum likelihood problem can be

reformulated as a regression problem, whose model statement is $0 = sqrt\{-2\ln(L)\}$.

To ensure compatibility between stand and tree models, other interesting stand variables, such as total and merchantable volume or biomass per tree fractions can be estimated by aggregation, after linking the individual-tree and stand growth models.

2.3. Model evaluation

The evaluation of the estimates for models (3), (5) and (6) was based on numerical and graphical analyses of the residuals. Two statistical criteria were examined: adjusted model efficiency (ME_{adj}) and root mean square error ($RMSE$). To evaluate the logistic model (7) the value of the generalized coefficient of determination ($\bar{R}^2$) proposed by Nagelkerke (1991) and the receiver operating characteristic (ROC) curve were calculated. The ROC curve relies on false/true–positive/negative tests, where sensitivity is the proportion of true positives (i.e. a live tree predicted to be alive) and specificity is the proportion of true negatives (i.e., a dead tree predicted to be dead). According to Hosmer and Lemeshow (2000), the area under the ROC curve is a threshold independent measure of model discrimination, where a value of 0.5 suggests no discrimination, 0.7–0.8 suggests acceptable discrimination, and 0.8–0.9 suggests excellent discrimination. The expressions of these statistics are summarized as follows:

$$ME_{adj} = 1 - \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2/(n-p)}{\sum_{i=1}^{n}(y_i - \bar{y})^2/(n-1)} \tag{8}$$

$$RMSE = \sqrt{\frac{\sum_{i=1}^{n}\left(Y_i - \hat{Y}_i\right)^2}{n-p}} \tag{9}$$

$$\bar{R}^2 = \frac{R^2}{R_{max}^2} = \frac{1 - \left[L(0)/L(\hat{\beta})\right]^{2/n}}{1 - L(0)^{2/n}} \tag{10}$$

where y_i, $\hat{y}_i$ and $\bar{y}$ are the observed, estimated and mean values of the dependent variable, n is the total number of observations used to fit the model, p is the number of model parameters, $L(0)$ is the likelihood of the intercept-only model and $L(\hat{\beta})$ is the likelihood of the fitted model.

2.4. Linking models

The disaggregation method used in this study involves adjusting the outputs of the individual-tree growth model to match estimates of number of trees and stand basal area of the stand growth model. Six different approaches to adjust the individual-tree survival and four different approaches to adjust tree basal area growth were evaluated. To assess the validity of these different approaches, an independent data set is sometimes recommended. However, due to the limited number of sample plots available, cross-validation has been used in this study. Each sample plot at age t_2 was predicted from the stand- and tree-level growth models, which were fitted from the data without that plot. In the first step, the stand variables of that sample plot at age t_2 were predicted from Eqs. (3) and (5). In the second step, the survival probability and the basal area growth of each tree in that plot were predicted from Eqs. (6) and (7), employing interim values of G and dg obtained from the stand growth model.

Our comparison between the different approaches was based on two common statistics: mean absolute difference (MAD) and root mean square error (RMSE). In addition to these two statistics, the logarithm of the likelihood function ($-2LL$) for tree survival probability and model efficiency (ME) for tree basal area growth were also computed.

2.4.1. Individual tree survival adjustment

Method 1. According to Cao (2010), the adjusted tree survival probability of tree j within the sample plot i ($\hat{p}'_{ij}$) was assumed as a power function of the unadjusted probability ($\hat{p}_{ij}$), i.e. the probability directly obtained from the individual tree growth model.

$$\hat{p}'_{ij} = \hat{p}_{ij}^{\alpha_i} \tag{11}$$

where α_i is the adjustment coefficient of the sample plot i.

Method 2. According to Qin and Cao (2006), individual tree survival was adjusted based on the ratio of dead and alive probabilities as follows:

$$\frac{1 - \hat{p}'_{ij}}{\hat{p}'_{ij}} = \beta \frac{1 - \hat{p}_{ij}}{\hat{p}_{ij}} \Rightarrow \hat{p}'_{ij} = \frac{\hat{p}_{ij}}{\hat{p}_{ij} + \beta_i(1 - \hat{p}_{ij})} \tag{12}$$

where β_i is the proportional growth coefficient of the sample plot i.

Method 3. The proportional yield method proposed by Qin and Cao (2006) was used and the adjusted survival probabilities were estimated as:

$$\hat{p}'_{ij} = \hat{p}_{ij} \frac{s\hat{N}_{2i}}{\sum_{j=1}^{n_i} \hat{p}_{ij}} \tag{13}$$

where s is the sample plot area in hectares, $\hat{N}_{2i}$ is the estimated number of tree of sample plot i at age t_2 and n_i is the number of trees in sample plot i at age t_1. The adjusted probability obtained with Eq. (13) could be higher than 1 and, therefore, an iterative procedure to constrain the values to ranges between 0 and 1 was used. In each step, the maximum value of the adjusted probability was constrained to 1 and the difference $\sum_{j=1}^{n_i} \hat{p}'_{ij} - s\hat{N}_{2i}$ was distributed among the trees with an adjusted probability lower than 1, proportionally to its adjusted survival probability, $\hat{p}'_{ijk} = \hat{p}'_{ijk-1} + \hat{p}'_{ijk-1}\left[\left(\sum_{j=1}^{n_i}\hat{p}'_{ijk-1} - s\hat{N}_{2i}\right)\big/\sum_{j=1}^{n_i}\hat{p}'_{ijk-1}\right]$ where $\hat{p}'_{ijk}$ is the adjusted probability in the iteration k of tree j within sample plot i. The iterative procedure ended when the difference $\sum_{j=1}^{n_i}\hat{p}'_{ij} - s\hat{N}_{2i}$ was lower than 0.01.

Method 4. The constrained least squares method (Matney et al., 1990; Qin and Cao, 2006) was used to adjust survival probabilities by minimizing $\sum_{j=1}^{n_i}\left(\hat{p}'_{ij} - \hat{p}_{ij}\right)^2$, subject to $\sum_{j=1}^{n_i}\hat{p}'_{ij} = s\hat{N}_{2i}$. Taking into account the described restrictions, the adjusted probabilities were obtained as:

$$\hat{p}'_{ij} = \hat{p}_{ij} - \frac{\sum_{j=1}^{n_i}\hat{p}_{ij} - s\hat{N}_{2i}}{n_i} \tag{14}$$

Using this method the adjusted probability could be higher than 1, therefore an iterative procedure similar to that described for method 3 was used to constrain the values of adjusted probability to range between 0 and 1.

Method 5. According to Cao (2010), the adjusted tree survival probability was assumed to be equal to:

$$\hat{p}'_{ij} = \hat{p}_{ij} + \gamma_i(1 - \hat{p}_{ij}) \tag{15}$$

where γ_i is the adjustment coefficient of the sample plot i, defined as $\gamma_i = \left(s\hat{N}_{2i} - \sum_{j=1}^{n_i}\hat{p}_{ij}\right)\big/\left(n_i - \sum_{j=1}^{n_i}\hat{p}_{ij}\right)$.

Using Eq. (15) the adjusted tree survival probability could be negative. In that case, the adjusted probabilities were estimated in two steps (Cao, 2010). In a first step the adjusted survival probability for the smallest diameter was equaled to 0 to obtain γ_{min} as follows: $0 = \hat{p}_{i\,min} + \gamma_{i\,min}(1 - \hat{p}_{i\,min}) \Rightarrow \gamma_{i\,min} = -\hat{p}_{i\,min}/(1 - \hat{p}_{i\,min})$. In the second step, the final adjusted probability is assumed to be proportional to the adjusted survival probability from step 1:

$$\hat{p}'_{ij} = \delta_i\lfloor \hat{p}_{ij} + \gamma_{i\,min}(1 - \hat{p}_{ij})\rfloor \tag{16}$$

where δ_i is the adjustment coefficient defined as $\delta_i = s\hat{N}_{2i} \Big/ \left[\sum_{j=1}^{n_i} \hat{p}_{ij} + \gamma_{\min} \left(n_i - \sum_{j=1}^{n_i} \hat{p}_{ij} \right) \right]$

Method 6. The intercept of the logistic model (Eq. (7)) fitted to the data was considered as a local parameter (φ_i), i.e. sample plot specific, and its value was estimated for each sample plot.

$$\hat{p}'_{ij} = \frac{1}{1 + \exp\left(\varphi_i + f_1 d_1 + f_2 G_1 + f_3 \frac{d_1}{dg_1} \right)} \qquad (17)$$

where f_1, f_2 and f_3 are the estimates obtained fitting the Eq. (7) to the complete database.

The values of the adjustment coefficients α_i, β_i, and φ_i used in methods 1, 2 and 6, respectively, where estimated for each sample plot using the OPTIM function of the STAT library in R Core Team (2014) such that $\sum_{j=1}^{n_i} \hat{p}_{ij} = s\hat{N}_{2i}$.

2.4.2. Individual tree basal area growth adjustment

Method 1. According to Qin and Cao (2006), the adjusted basal area of each tree within each sample plot ($\hat{g}'_{2ij}$) was proportional to the predicted basal area growth, i.e., the difference between the unadjusted basal area at age t_2 ($\hat{g}_{2ij}$) and the initial observed basal area (g_{1ij}):

$$\hat{g}'_{2ij} = g_{1ij} + \chi_i(\hat{g}_{2ij} - g_{1ij}) \qquad (18)$$

where χ_i is the proportional growth coefficient of the sample plot i calculated as $\chi_i = \left(s\hat{G}_{2i} - \sum_{j=1}^{n_i} \hat{p}'_{ij} g_{1ij} \right) \Big/ \sum_{j=1}^{n_j} \hat{p}'_{ij}(\hat{g}_{2ij} - g_{1ij})$, $\hat{G}_{2i}$ is the estimated basal area of the sample plot i at age t_2 and $\hat{p}'_{ij}$ is the adjusted survival probability estimated with one or more of the six above mentioned methods.

Method 2. The proportional yield method proposed by Qin and Cao (2006) was used and the adjusted basal areas were estimated as:

$$\hat{g}'_{2ij} = \hat{g}_{2ij} \frac{s\hat{G}_{2i}}{\sum_{j=1}^{n_i} \hat{p}_{ij} \hat{g}_{2ij}} \qquad (19)$$

Method 3. The constrained least squares method (Matney et al., 1990; Qin and Cao, 2006) was used to adjust tree basal area by minimizing $\sum_{j=1}^{n_i} \left(\hat{g}'_{2ij} - \hat{g}_{2ij} \right)^2$, subject to $\sum_{j=1}^{n_i} \hat{p}'_{ij} \hat{g}'_{2ij} = s\hat{G}_{2i}$. Taking into account the described restrictions, the adjusted basal areas were obtained as:

$$\hat{g}'_{2ij} = \hat{g}_{2ij} - \hat{p}'_{ij} \left(\sum_{j=1}^{n_i} \hat{p}'_{ij} g_{1ij} - s\hat{G}_{2i} \right) \Big/ \sum_{j=1}^{n_j} \left(\hat{p}'_{ij} \right)^2 \qquad (20)$$

Method 4. The parameter c_0 of the tree basal area growth model (Eq. (6)) fitted to the data was considered as a local parameter (λ_i), i.e. sample plot specific, and its value was estimated for each sample plot.

$$\hat{g}'_{2ij} = g_{1ij} + \lambda_i g_{1ij}^{c_1} G_{1i}^{c_2} \exp\left(c_3 \frac{d_{1ij}}{dg_{1i}} \right) \qquad (21)$$

where c_1, c_2 and c_3 are the estimates obtained fitting Eq. (6) to the complete database.

The values of adjustment coefficients χ_i and λ_i used in methods 1 and 4, respectively, where estimated for each sample plot using the OPTIM function of the STAT library in R Core Team (2014) such that $\sum_{j=1}^{n_i} \hat{p}'_{ij} \hat{g}'_{2ij} = s\hat{G}_{2i}$.

2.5. Effect of stand variable predictions on disaggregation estimates

Due to the disaggregation constraints that tree variables must match predicted stand variables from the stand growth model, the quality of tree-level predictions using disaggregation greatly depends on the accuracy and precision of the stand model predictions (Qin and Cao, 2006; Cao, 2010; Zhang et al., 2011). To analyze this effect, all of the disaggregation methods proposed above were also applied, with stand variables predictions obtained from the forecast combination method (Bates and Granger, 1969; Newbold and Granger, 1974). This method efficiently combines information generated from different models to improve predictions by reducing errors (Zhang et al., 2010). Using this method, the combined estimators of number of trees per ha and stand basal area can be obtained as following:

$$\begin{aligned} N_2^C &= w_N N_2^T + (1 - w_N) N_2^S \\ G_2^C &= w_G G_2^T + (1 - w_G) G_2^S \end{aligned} \qquad (22)$$

where N_2^C and G_2^C are the combined estimators of N and G, respectively; N_2^T and G_2^T are the estimates of N and G obtained with cross-validation from the individual tree model; N_2^S and G_2^S are the estimates of N and G obtained with cross-validation from the stand growth model and w_N and w_G are weights. The optimal weights were calculated by use of the ordinary least-squares method proposed by Zhang et al. (2010).

3. Results

3.1. Stand growth and individual tree growth model

The parameter estimates, their standard errors and the goodness-of-fit statistics obtained for the stand growth model (Eqs. (3) and (5)) and for the individual tree growth model (Eqs. (6) and (7)) are presented in Table 2. All coefficients were significant at the 5% level.

Regarding the stand growth model, Eq. (3) explained more than 95% of the observed variability while Eq. (5) explained more than 96%. All the parameters estimates were highly significant and the plots of weighted residuals against predicted values showed no evidence of heterogeneous variance and no systematic pattern after the correction for heterocedasticity in the mortality model (weighting factor $\alpha = 2.2521$). The trajectories of observed and predicted number of trees over time and basal area for different initial conditions are shown in Fig. 1.

The individual tree basal area growth model explained almost the 92% of the total variability. The generalization of the coefficient of determination ($\bar{R}^2$) proposed by Nagelkerke (1991) for the tree survival model (Eq. (7)) was 0.5635 and the mean predicted survival probability was 98.49% while the observed mean survival

Table 2
Estimates, standard errors of parameters and goodness-of-fit statistics in the stand growth model fitted.

Equation	Parameter	Estimate	SE	RMSE	ME_{adj}	$\bar{R}^2$
3	a_1	0.1756	0.0626	186.3	0.9505	
	a_2	1.6652	0.6871			
	a_3	1.4608	0.2370			
5	b_1	26.3928	1.9747	2.0205	0.9666	
	b_2	1.5201	0.1310			
	k	0.2061	0.0531			
6	c_0	0.0556	0.0110	0.01751	0.9187	
	c_1	0.6083	0.0247			
	c_2	−0.7517	0.0270			
	c_3	0.3661	0.0516			
7	f_0	−1.3723	0.2576			0.5635
	f_1	−0.1154	0.0244			
	f_2	0.0241	0.00494			
	f_3	−2.3639	0.4055			

probability was 98.46%. The receiver operating characteristic (ROC) curve is shown in Fig. 2. According to the values proposed by Hosmer and Lemeshow (2000), the value of the area under the ROC curve obtained in this study (0.8056) indicated that the model discriminated well.

Cross-validation was used to analyze the performance of the stand and individual tree growth models. The cross-validation estimates of number of trees per hectare and basal area obtained with the stand growth model (N_2^S and G_2^S) and the estimates of these variables obtained by aggregating the cross-validation estimates of the individual tree growth model (N_2^T and G_2^T) were combined to obtain the forecast estimators (N_2^C and G_2^C) with Eq. (22). The weights obtained using the ordinary least-squares method (Zhang et al., 2010) were $w_N = 0.2767$ and $w_G = 0.1685$. The cross-validation evaluation statistics for predicted number of trees per ha and stand basal area from the stand- and tree-level growth models and from the forecast estimators are shown in Table 3.

3.2. Linking models

3.2.1. Individual tree survival adjustment

The values of the statistics used to compare the methods are shown in Table 4. The Wilcoxon signed-rank test was used to compare the related samples of RMSEs calculated for each sample plot using the estimates of 1-fold cross validation for the unadjusted method and each of the approaches used to link the models. This is a non-parametric paired difference test to assess whether the population mean ranks differ when the population cannot be assumed to be normally distributed.

All the adjustment methods analyzed produced better values of RMSE and the logarithm of the likelihood function than the unadjusted method (i.e. survival probabilities estimated directly from the individual tree growth model), although, according to the Wicoxon signed-rank test, the differences were not significant ($\alpha = 5\%$) for methods 1, 2 and 5 when the stand variables used for adjustment were predicted from the stand growth model. The
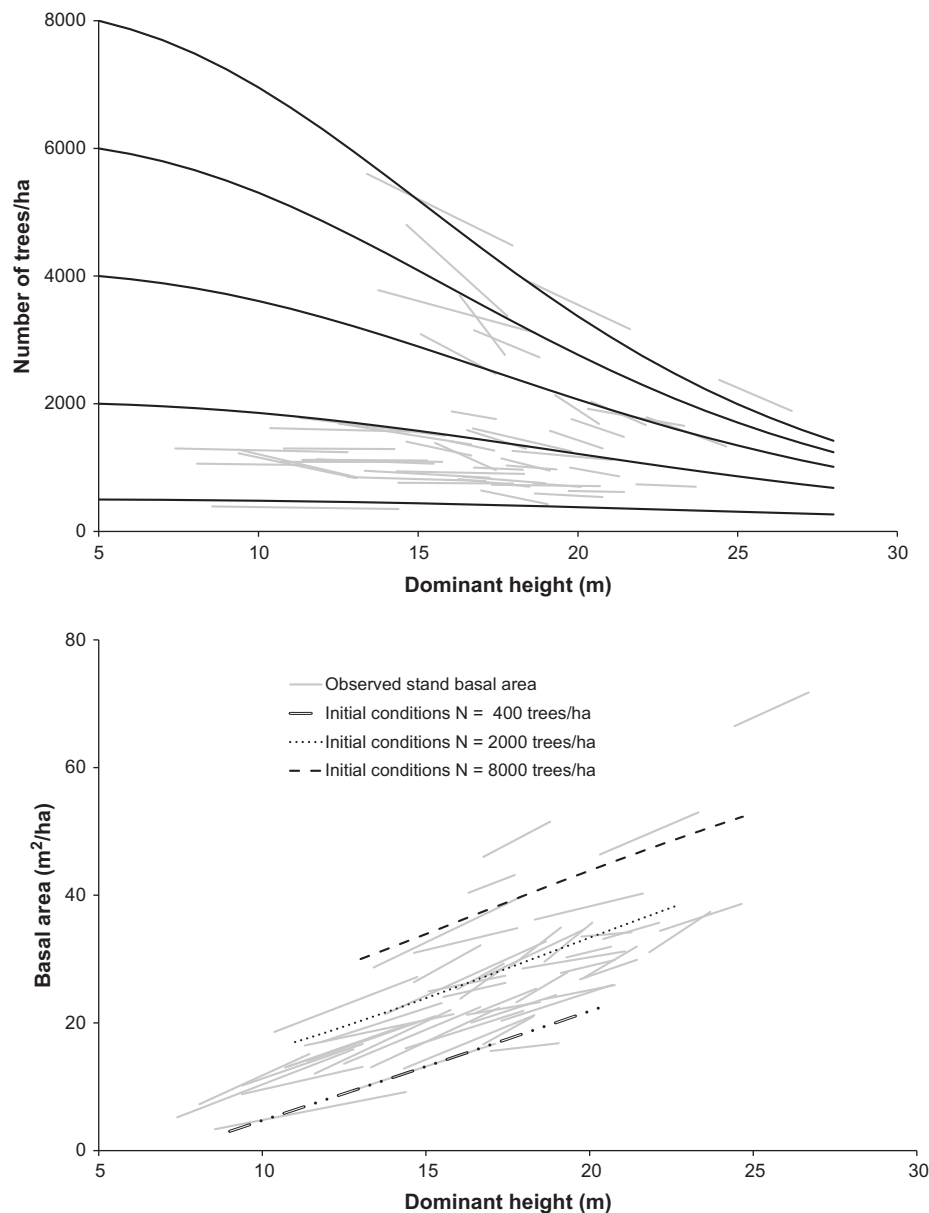

Fig. 1. Trajectories of observed and predicted number of trees per hectare (upper) and stand basal area (lower) for different initial conditions obtained with the fitted Eqs. (3) and (5), respectively.
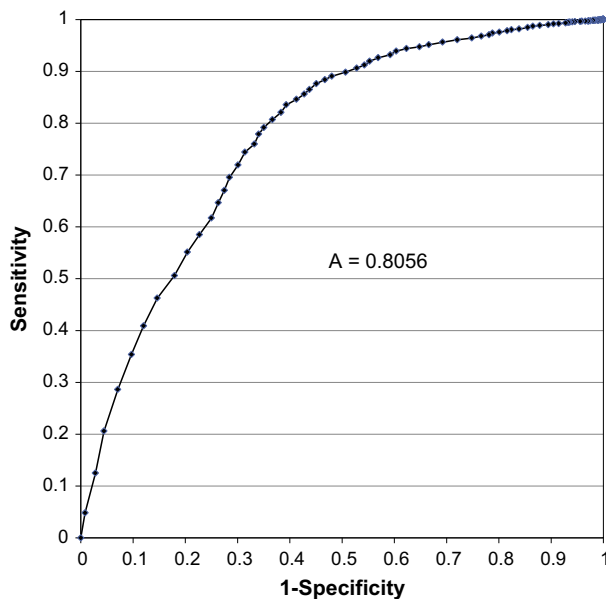
Fig. 2. ROC curve for the individual tree mortality model fitted.

Table 4
Evaluation statistics for the unadjusted and adjusted predictions of tree survival probabilities based on cross-validation.

Adjust	Method	MAD	RMSE	ΔRMSE	−2ln(L)
Unadjusted	–	0.2054	0.3289	–	2878.4717
Adjusted from stand model predictions	Method 1	0.2078	0.3281	−0.24%	2817.8240
	Method 2	0.2076	0.3281	−0.24%	2819.0810
	Method 3	0.2048	0.3241[**]	−1.46%	2754.4398
	Method 4	0.2054	0.3245[**]	−1.34%	2770.1092
	Method 5	0.2080	0.3281	−0.24%	2816.0283
	Method 6	0.1984	0.3240[**]	−1.49%	2671.8382
Adjusted from forecast combination method	Method 1	0.2040	0.3184[**]	−3.19%	2548.1105
	Method 2	0.2042	0.3185[**]	−3.16%	2552.1654
	Method 3	0.2050	0.3187[**]	−3.10%	2559.3712
	Method 4	0.2047	0.3187[**]	−3.10%	2559.1400
	Method 5	0.2038	0.3184[**]	−3.19%	2547.8909
	Method 6	0.2052	0.3185[**]	−3.16%	2550.8993

[**] Indicates significant differences between the proposed method and the unadjusted approach (α = 5%)

best results were obtained from method 6, which considered the intercept of the logit function as a specific parameter of each sample plot and optimized its value.

The results of the forecast combination for all the methods were significantly better than those obtained with the stand growth model estimates for the same method when both values were compared using the Wilcoxon signed-rank test.

3.2.2. Individual tree basal area growth adjustment

The survival probability adjusted with method 6 was used in conjunction with the four methods for adjusting tree basal area growth to link with the stand basal area predictions for the stand growth model. The values of the evaluation statistics are presented in Table 5.

Again, all four adjustment methods produced significantly better results based on the evaluation statistics than the unadjusted method, regardless of which stand variable values were used for adjustment, except for methods 1 and 2 combined with the stand growth model estimates. However, in this case the results of the forecast combination were not significantly better than those of the stand growth model when both values are compared with the Wilcoxon signed-rank test.

The tree-level survival equation predicts the probability of its occurrence and therefore requires a decision to translate these probabilities into a discrete event (i.e. dead or alive) for forest growth simulations. Two different methods have been widely

used: the first one assumes that the survival probability of a specific tree should be multiplied by the tree's expansion factor (in this study, the ratio between the area of the sample plot and a hectare) to get the number of trees per hectare; the second one is based on a survival probability threshold, above which a tree is considered alive. The approaches described above to link stand- and tree-level models use the first method, therefore, the best combination obtained for linking individual tree survival and individual tree basal area growth models with stand variables (i.e. method 6 for the survival model combined with method 3 for the basal area model) was compared with two approaches, based on the use of thresholds for simulating individual tree survival, combined with the four methods for individual tree basal area growth adjustment.

In the first approach (unadjusted threshold approach), a unique threshold (λ) is selected for all the sample plots. If the estimated tree survival probability obtained with Eq. (7) is less than λ, then it was assumed that natural mortality occurs, otherwise, the tree will survive. The threshold was selected to maximize the accuracy of Eq. (7), defined as the proportion of predicted events (correctly classified) to the total events, and a value of 0.53 was obtained (accuracy = 0.8658). This approach has been broadly used in stand and tree mortality models (e.g. Monserud and Sterba, 1999; Álvarez-González et al., 2004; Crecente-Campo et al., 2010). In the second approach (adjusted threshold approach), a specific threshold was selected for each sample plot. If the estimated tree survival probability obtained with Eq. (7) was less than the sample plot specific threshold (λ_i), then natural mortality was assumed to occur, and a value of 0 was assigned to the tree survival probability, otherwise, the tree survival probability was equal to 1. The specific

Table 3
Evaluation statistics for predicted stand variables from the stand and individual-tree growth models and forecast combination based on cross-validation.

	Predicted number of trees per ha (N)			Predicted stand basal area (G)		
	RMSE	ΔRMSE	ME_adj	RMSE	ΔRMSE	ME_adj
Stand growth model	215.3181	–	0.9338	2.2641	–	0.9580
Individual tree growth model	244.2814	13.45%	0.9148	3.9315	73.65%	0.8734
Forecast combination	214.4077	−0.42%	0.9344	2.1642	−4.41%	0.9616

Table 5
Evaluation statistics for the unadjusted and adjusted predictions of tree basal area estimates based on cross-validation.

Adjust	Method	MAD	RMSE	ΔRMSE	ME
Unadjusted	–	0.004395	0.007365	–	0.8229
Adjusted from stand model predictions	Method 1	0.004222	0.007235	−1.77%	0.8291
	Method 2	0.004238	0.007258	−1.45%	0.8280
	Method 3	0.004202	0.007172[**]	−2.62%	0.8320
	Method 4	0.004219	0.007228[**]	−1.86%	0.8294
Adjusted from forecast combination method	Method 1	0.004090	0.007145[**]	−2.99%	0.8334
	Method 2	0.004094	0.007157[**]	−2.82%	0.8328
	Method 3	0.004092	0.007114[**]	−3.41%	0.8348
	Method 4	0.004086	0.007139[**]	−3.07%	0.8336

[**] Indicates significant differences between the proposed method and the unadjusted approach (α = 5%).

threshold of each sample plot was selected to link with the number of trees per ha predicted by Eq. (3):

$$\begin{cases} \hat{p}'_{ij} = 1 & \text{if } \hat{p}_{ij} > \lambda_i \\ \hat{p}'_{ij} = 0 & \text{if } \hat{p}_{ij} \leqslant \lambda_i \end{cases} \text{ such that } \sum_{j=1}^{n_i} \hat{p}'_{ij} = s\hat{N}_{2i} \tag{23}$$

The results of both approaches were significantly worse than those obtained with the combination of method 6 for survival adjustment and method 3 for basal area growth adjustment (Table 6), except for the combination of a common threshold and method 3. The results were especially worse using a sample plot-specific threshold to link with predictions of number of trees per ha. For both approaches, the best method to link with stand basal area predictions (Eq. (5)) was again the constrained least squares method (method 3), irrespective of whether the stand variables used for adjustment were predicted from the stand growth model or were calculated by the forecast combination method.

4. Discussion

4.1. Stand growth and individual tree growth model

The simultaneous fitting combined with the variable growth rate (VGR) approach (Cao, 2000) worked well for fitting the tree basal area growth and tree survival probability. Similar results were also reported for other species (e.g., Cao, 2006; Nord-Larsen, 2006; Cao and Strub, 2008; Crecente-Campo et al., 2010) although only the last named authors applied simultaneous fitting of the components of the model.

The individual tree growth model used in the present study include size variables (d and g), and competition variables (G and d/dg), in their formulation. Similar results were found by Wykoff (1990) and Monserud and Sterba (1996) when developing basal area increment models for individual trees in even- and uneven-aged stands. These authors found that most of the explained variance was due to size factors and the next most important contribution came from competition variables.

Site index had a non-significant effect in the basal area growth model, which may indicate that the key factor driving growth in this study is competition rather than site. The reason could be the inclusion in the model of tree size (ratio between tree diameter and quadratic mean diameter), which could be an indicator of past growth, taken into account site effects. Similar results were reported by other authors (e.g. Crecente-Campo et al., 2010 or Schröder et al., 2002).

The values and signs of the estimates in the individual tree growth model have biological meaning. The projected tree basal area decreases for lower initial diameters; for higher initial stand densities (represented by stand basal area) and for lower social status of the tree (represented by the ratio between tree diameter and quadratic mean diameter). The probability of survival decreases for the smallest trees when the stand basal area increases, or when the social status of the tree decreases.

As expected, prediction errors of the stand variables (N and G) were lower for the stand growth model than for the aggregated estimates of the individual-tree growth model. The *RMSE* of stand density and stand basal area predictions increased 13.45% and 73.65%, respectively, when these stand variables were obtained by aggregating estimates of the individual-tree growth model. Moreover, the forecast combination estimators obtained with Eq. (22) combining the cross-validation estimates of the stand growth model (N_2^S and G_2^S) and the estimates of these variables obtained by aggregating the cross-validation estimates of the individual tree growth model (N_2^T and G_2^T) showed slightly better results than the stand- and individual tree models independently (*RMSE* decreased 0.42% and 4.41% for stand density and stand basal area, respectively). Similar results were obtained by Yue et al. (2008) for stand basal area of Norway spruce (*Picea abies*) in Germany, and by Zhang et al. (2010) and Zhang et al. (2011) for stand basal area and for stand survival of Chinese pine (*Pinus tabulaeformis*) in China, respectively.

Using a forecast combination, we assume that the predictions of both growth models are unbiased and the covariances of the predictions of the models known, such as in this study. However, if the covariances are unknown, they might be ignored and the predictions of each model could be weighted by the inverse of their mean square error (Newbold and Granger, 1974).

Table 6
Evaluation statistics for the unadjusted and the best adjusted predictions of tree basal area compared with adjusted predictions based on two approaches using a threshold to estimate tree survival and cross-validation.

Adjust	Individual tree adjustment methods		MAD	RMSE	ΔRMSE	ME
	Survival model	Basal area growth model				
Unadjusted	–	–	0.004395	0.007365	–	0.8229
Stand model	Method 6	Method 3	0.004202	0.007172[**]	−2.62%	0.8320
Forecast	Method 6	Method 3	0.004092	0.007114[**]	−3.41%	0.8348
Adjusted from stand model predictions	Unadjusted threshold	Method 1	0.004304	0.007319	−0.62%	0.8251
		Method 2	0.004354	0.007360	−0.07%	0.8231
		Method 3	0.004188	0.007198[**]	−2.27%	0.8309
		Method 4	0.004304	0.007314	−0.69%	0.8254
Adjusted from forecast combination method	Unadjusted threshold	Method 1	0.004214	0.007241	−1.68%	0.8288
		Method 2	0.004250	0.007271	−1.28%	0.8274
		Method 3	0.004106	0.007154[**]	−2.86%	0.8329
		Method 4	0.004211	0.007236	−1.75%	0.8291
Adjusted from stand model predictions	Adjusted threshold	Method 1	0.004571	0.007705	4.62%	0.8062
		Method 2	0.004600	0.007734	5.01%	0.8047
		Method 3	0.004498	0.007621	3.48%	0.8104
		Method 4	0.004568	0.007700	4.55%	0.8065
Adjusted from forecast combination method	Adjusted threshold	Method 1	0.004497	0.007643	3.77%	0.8093
		Method 2	0.004518	0.007663	4.05%	0.8083
		Method 3	0.004439	0.007587	3.01%	0.8121
		Method 4	0.004493	0.007638	3.71%	0.8095

[**] Indicates significant differences between the proposed method and the unadjusted approach ($\alpha = 5\%$).
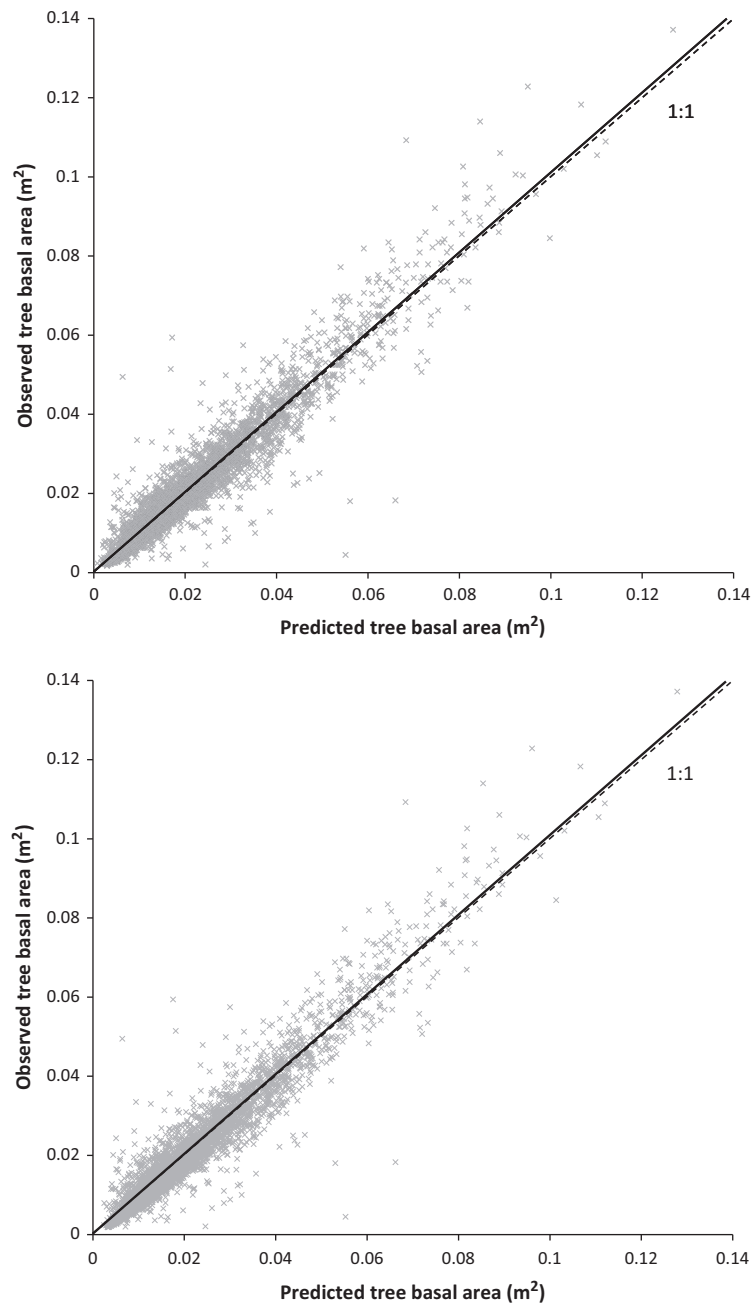
Fig. 3. Observed versus predicted tree basal obtained using the stand growth model estimates (above) and the forecast combination (below) combined with method 6 for survival adjustment and method 3 for tree basal area adjustment. The continuous line corresponds to the linear model fitted, and the broken line corresponds to the diagonal.

4.2. Linking models

4.2.1. Individual tree survival adjustment

The six disaggregation approaches analyzed to link tree survival probability with stand density produced slightly better values of *RMSE* (reductions ranged from 0.24% to 1.49%) and the logarithm of the likelihood function than the unadjusted method (i.e. survival probabilities estimated directly from the individual tree growth model). The best results were obtained considering the intercept of the logit function as a specific parameter of each sample plot and optimizing its value (method 6). This method was also selected by Qin and Cao (2006) to link individual tree and stand growth models for loblolly pine (*Pinus taeda*) in the southern USA.

As expected, again the use of forecast combination estimators for adjustment rather than predictions from the stand model

significantly improved the prediction errors of the tree survival probabilities for all the disaggregation methods. *RMSE* decreased more than 3% for the six disaggregation approaches analyzed (Table 4). These results indicate that the performance of the adjusted tree model depends on the reliability of the stand predictions. Similar results were obtained by Qin and Cao (2006) and Cao (2010) who used both observed and predicted stand variables for disaggregation, and Zhang et al. (2011) who evaluated predicted stand variables against forecast combination estimators as the basis for disaggregation.

4.2.2. Individual tree basal are growth adjustment

The results of combining the survival probability adjusted with method 6 and the four methods for adjusting tree basal area growth to link with the stand basal area predictions were

significantly better than the unadjusted method (RMSE reductions from 1.45% to 2.62%), except for method 2 (Table 5). All the significant methods showed very similar results, however, methods 1 and 4 required an optimization of adjusted coefficients, whereas the adjusted basal areas in method 3 were directly calculated. Therefore method 3 was selected as the best approach for adjusting tree basal area for this data set. As in the case of the individual tree survival adjustment, the results of the forecast combination were better than those of the stand growth model with a *RMSE* reduction ranging from 2.82% to 3.41% (Table 5), although, in this case, the differences were not significant. The scatterplot of observed versus predicted tree basal areas obtained with the proposed approach (method 6 for survival adjustment and method 3 for tree basal area adjustment) linking with the stand growth model estimates and with the forecast combination are shown in Fig. 3. A very slight trend to underestimate for high initial basal areas was observed in both combinations.

Regarding the comparison between different methods to translate the probabilities of the tree survival model into a discrete event (i.e. dead or alive) for forest growth simulations, the results indicate that the use of thresholds to simulate tree survival does not improve the results obtained with the proposed approach (method 6 for survival adjustment and method 3 for tree basal area adjustment). The use of a site-specific threshold could even reduce the accuracy of the linked models with a *RMSE* increment from 3.01% to 5.01%, depending on the method used for tree basal area adjustment (Table 6).

5. Conclusions

In this study, a whole-stand growth model and an individual-tree model were fitted to data from even-aged birch forests. Both models have imposed limitations based on their resolution. Different approaches in linking the estimates of both using disaggregation were evaluated. The methods used to adjust individual-tree survival predictions to match number-of-trees estimates of the whole-stand model produced significantly better results than the unadjusted method. Disaggregation based on the composite estimators instead of the whole-stand model predictions resulted in significantly better values of evaluation statistics, confirming the assumption that the performance of disaggregation is likely to depend on the accuracy of stand variable predictions. The coefficient adjustment (method 6), which considered the intercept of the logit function as a specific parameter of each sample plot, was selected to disaggregate predicted stand density among trees.

The methods used to adjust tree basal area growth showed significantly better results than the unadjusted model and, again, the use of the composite estimators improved tree basal area predictions, although the differences were not significant. The constrained least squares method (method 3) was selected to disaggregate stand basal area among trees. The results show that a combination of composite estimators and disaggregation provided compatible and reliable predictions of stand density, tree survival, stand basal area, and tree basal area.

The main limitation of this approach is the dependency of accurate stand growth predictions, therefore, it deserves further attention in future studies that aim to link models with different resolution levels, especially for more complicated stand structures such as mixed and un-even aged forests, or to include the effect of silvicultural treatments.

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