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:

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

(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,