Research paper

Site-effects on biomass allometric models for early growth plantations of Norway spruce (*Picea abies* (L.) Karst.)

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A B S T R A C T

Although it is commonly assumed that biomass allometric models are site specific, evaluations of site-effects are rarely undertaken. In this paper we develop biomass-allometric models to determine site influences. This study is based on data from 240 Norway spruce trees (*Picea abies* (L.) Karst.), growing in 24 early-growth plantations. A multilevel modelling approach was adopted and intraclass correlation was used to evaluate site effects. Results indicated that biomass allometric models were highly specific to sites and that, depending on the biomass component and the type of predictor adopted, some 33% and 86% of overall model variance could be attributed to forest stand effects. The remaining variance was attributable within stand variability. Stem biomass was the most site-specific biomass component whereas branch biomass was the least influenced by site effects. Diameter at collar height (D) was less site-specific than height (H) in predicting biomass. Using D and H within the same model as distinct predictors, although improving the model fit, increased the model site-specificity. However, when D and H were combined in one predictor expression (i.e. D^2H), this reduced model site specificity, despite requiring fewer parameters than other models. This also compensated for undesirable collinearity effects amongst predictor variables. Furthermore, for the sampled diameter range, the site-specificity was mainly driven by biomass allocation pattern (to branches, needles and roots). The considerable between site variability of allometric relationships suggests that consideration of stand effects is essential for the robust prediction of biomass.

1. Introduction

Forests play an important role in the global carbon cycle [1,2], and it is well established that increasing forest area can immediately influence rates of carbon sequestration by increasing capacity for carbon dioxide uptake through the accumulation of new plant biomass [3]. European forests have expanded in area by 21.2 million hectares since 1990, increasing at a rate of 0.85% per year, as a result of afforestation and natural regeneration [4]. However, despite apparent increase in forest area, other research suggests that the European forest carbon-sink may be at the point of saturation [5], and this is believed to be due to decrease in stem volume increment rate. An increased rate of afforestation is therefore needed if earlier net gains in the forest carbon sink are to be maintained [5]. As one of the most extensively grown and economically important species in Europe, Norway spruce (*Picea abies* [L.] Karst.), it is widely used in afforestation schemes for production, protection and erosion control [6,7].

Biomass allometric models are commonly used to estimate carbon accumulation in forests [1,8]. Despite recent advances in remote sensing and other survey instruments, allometric models remain fundamental to biomass prediction and for calibrating emerging technologies and new approaches to estimation [9–11]. Biomass allometric models are regression models that use tree diameter and/or height to predict biomass [12,13], and due to the importance of Norway spruce throughout Europe, there is considerable interest in their application to this species [14–20].

Developing generalized biomass allometric models with high prediction accuracy and precision is widely regarded to be a challenging undertaking [21–24]. Among other refinements wood density has been used to improve biomass prediction [24,25], as it is well known that wood density is highly heritable [26]. This is consistent with a view that interspecific genetic variability is related to, and can be explained by wood density variation. Height-diameter (H–D) ratio is also used to improve prediction accuracy of allometric models [21,23,24]. As each

forest site has particular environmental conditions, and because it is widely understood that H–D ratio is in part affected by environmental conditions [27–29], it follows that the inclusion of height (together with diameter) in allometric models may explain the site effect. However, wood density and height has been shown to make relatively little contribution to improving prediction of biomass at particular forest stands [30]. It is therefore unlikely that either accurate generalized allometric models will be developed or predictions will improve without first understanding the factors that drive variation in such models and how the variance is partitioned within and between stands.

Because site-specificity is an important constraint in developing accurate generalized allometric models, the development of new allometric models often involves an investment of substantial resources to record and model biomass at individual sites. Investigating the site-specificity of allometric models is potentially useful in many ways, such as: (i) identifying the conditions under which it is fact possible to apply any one given allometric model to other forest stands; (ii) guiding the selection of statistical means and modelling algorithms appropriate to circumstances. Because range of covariates (i.e. diameter at breast height, DBH; tree height) is often limited within a forest stand, researchers commonly sample trees from more than one forest stand. Sampling more than one tree from each of multiple stands, results in clustered data. The decision to allow or adjust for a clustering effect (of forest stand on allometric model), is determined by the extent to which variance is attributable to a forest stand effect. If there is no discernible site-specificity effect, then it is acceptable to apply methods that disregard clustering. Conversely, disregarding site-specificity/forest-stand effects when they are apparent is likely to bias standard errors with downstream consequences for model uncertainty and hypothesis testing.

The aim of this paper was to develop biomass allometric models for Norway spruce trees based on data sampled from multiple forest stands and to evaluate site effects on allometric models, with a view to determining the following:

i) the extent of site-specificity in biomass allometric models;
ii) how site-specificity varies with each of the biomass components being predicted;
iii) how site-specificity varies between individual predictors/indicators;
iv) the underlying causes and possible consequences of site-specificity in allometric models.

2. Material and methods

2.1. Study sites

The study area, in Eastern Carpathians of Romania (Fig. 1), extends some 330 km between southerly and northerly latitudinal extremes of 45.44°N and 47.77°N respectively. Sample site elevations were between 641 and 1543 m above sea level, with mean annual temperature ranging from 2.6 to 7.3 °C and mean annual precipitation from 643 to 933 mm. Data was collected from 24 randomly selected plantations between 2009 and 2010. Ages of sampled trees ranged from 4 to 15 years (Table 1). Species composition was entirely Norway spruce, planted at an initial stand density of 5000 saplings per hectare (on a grid of 2.0 m × 1.0 m). However, due to mortality, stand density at the time of sampling was found to be between 3100 and 4800 trees per hectare. Sampled stands had not been subject to thinning or other forest management intervention to reduce stocking levels.

2.2. Biomass measurements

In each plantation, a 200 m^2 sample plot was selected as being representative of the overall conditions of the immediate forest stand. Root collar diameter and height measurements were taken for all trees

and used to calculate the 'mean height' (i.e. the height of tree of mean collar area; this is analogous to mean basal area but measured at collar instead of breast height). At each stand, ten trees with dimensions that of 'mean height' were selected and destructively sampled for biomass measurements that also included roots. A total of 240 trees were sampled, with root collar diameter (referred hereafter as diameter – D) ranging from 0.6 to 10.0 cm, and height (H) between 53.0 and 552.0 cm. This dataset, therefore, satisfies the minimum requirement that samples should represent a range of one order of magnitude to be useful for allometric studies [31]. Root collar diameter was used instead of diameter at breast height because approximately 50% of sampled trees were less than 1.3 m in height. For each sampled tree total biomass was divided in four categories (stem – ST, branches – BR, needles – ND and roots – RT), which was oven dried at 80 °C to constant weight, and then electronically weighed to a precision of ± 0.1 g.

2.3. Statistical analysis

All variables were expressed as natural log transformations (ln) to ensure a linear relationship between variables and to correct for heteroskedasticity and thereby meet assumptions for purposes of applying a Random Intercept Model. Dependent variables were: ln(TB), ln total biomass; ln(AB), ln aboveground biomass (calculated as the sum of stem, branch and needle biomass); ln(ST), ln stem biomass; ln(BR), ln branch biomass; ln(ND), ln needle biomass; and ln(RT), ln needle biomass. Independent variables were: ln(D), ln root collar diameter; ln(H), ln height; and ln(D^{2}H), the natural logarithm of the product diameter squared and height.

A multilevel modelling approach was used to differentiate the effects of between and within stand variance. The study was designed so that a Random Intercept Model (RIM) could be applied. Within stands, sampled trees were of similar height, maximizing therefore the likelihood of observing the entire range of height-diameter variability (within-stand variability). The RIM allowed intercepts to vary with the forest stand, whereas the slope is fixed for all stands. The distribution of intercepts is assumed to be normal with the mean value α and standard deviation σ_α. The allometric models tested for ln biomass (ln(B)), in their log-linear form, were:

$$\ln(B)_{ij} = \alpha + \beta \times \ln(D)_{ij} + \varepsilon_{ij} + u_i \tag{1}$$

$$\ln(B)_{ij} = \alpha + \beta \times \ln(H)_{ij} + \varepsilon_{ij} + u_i \tag{2}$$

$$\ln(B)_{ij} = \alpha + \beta \times \ln(D^2H)_{ij} + \varepsilon_{ij} + u_i \tag{3}$$

$$\ln(B)_{ij} = \alpha + \beta \times \ln(D)_{ij} + \gamma \times \ln(H)_{ij} + \varepsilon_{ij} + u_i \tag{4}$$

where β and γ are the fixed slopes; α is the fixed part of the intercept (the overall intercept); u_i is the random error component of the intercept, $u_i \sim N(0, \ \sigma_\alpha{}^2)$, and represents the error component at level 2 (at forest stand level); ε_{ij} is the random residual error, $\varepsilon_{ij} \sim N(0, \ \sigma_\varepsilon{}^2)$; $j = 1$ … N (number of stands); $i = 1 \ldots n_j$ (the trees within stand).

Furthermore, the ratios of tree component categories were modelled as:

$$R_{ij} = \alpha + u_i + \varepsilon_{ij} \tag{5}$$

Where R is the dependent variable and is represented by the proportions of tree components (i.e. Root-to-Shoot ratio calculated as RT/AB; and comparable treatments for ST/TB, BR/TB, ND/TB and RT/TB). The parameters may be interpreted similarly to those presented in Eqs. (1)–(4). To find if R was significantly influenced by age, the following model was used:

$$R_{ij} = \alpha + \beta \times Age_{ij} + \varepsilon_{ij} + u_i \tag{6}$$

The use of multilevel model for assessing the effect of age (Eq. (6)) is justified by the need to correct p-values for the 'nuisance effect' of data clustering caused by greater homogeneity of trees within stands than