

Individual tree aboveground biomass for *Castanopsis indica* in the mid-hills of Nepal

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Received: 7 July 2015/Accepted: 27 July 2017/Published online: 31 July 2017 © Springer Science+Business Media B.V. 2017

Abstract Quantitative information of tree biomass is useful for management planning and monitoring of the changes in carbon stock in both forest and agroforestry systems. An estimate of carbon stored in these systems can be useful for developing climate change mitigation strategies. A precise estimate of forest biomass is also important for other issues ranging from industrial forestry practices to scientific purposes. The individual tree-based biomass models serve as fundamental tools for precise estimates of carbon stock of species of interest in forest and agroforestry systems. We developed individual tree aboveground biomass models for Castanopsis indica using thirty-six destructively sampled tree data covering a wide range of tree size, site quality, growth stage, stand density, and topographic characteristics. We used diameter at breast height (DBH) as a main predictor and height-to-DBH ratio (a measure of tree

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slenderness) and wood density (a measure of stiffness and cohesiveness of wood fibres) as covariate predictors in modelling. We, hereafter, termed the biomass models with former two predictors as first category models (density independent models) and the models with all three predictors as second category models (density dependent models). Among various functions evaluated, a simple power function of the form $y_i = b_1 x_i^{b_2}$, in each category, showed the best fits to our data. This formulation, in each category, described most of the biomass variations $(R_{adi}^2 > 0.98)$ and RMSE < 72.2) with no significant trend in the residuals. Since both density dependent and density independent models exhibit almost similar fit statistics and graphical features, one of them can be applied for desired accuracy, depending on the access of the input information required by the model. Our biomass models are site-specific, and their applications should therefore be limited to the growth stage, stand density, site quality, stand condition, and species distribution similar to those that formed the basis of this study. Further research is recommended to validate and verify our model using a larger dataset with a wider range of values for site quality, climatic and topographic characteristics, stand density, growth stage, and species distribution across Nepal.

Keywords Allometric modelling · Destructive sampling · Density dependent biomass model · Heightto-diameter ratio · Wood density

Introduction

In recent years, tree growth and carbon dynamics are important issues especially in the context of climate change, which has drawn the global interest (Meer et al. 2001). Forests reduce the possibility of climate change through sequestration of atmospheric carbon. Majority of forest biomass studies have been carried out for accounting aboveground biomass that covers the greatest fraction of the total living biomass in forest ecosystem (Chave et al. 2005). The agroforestry system, which is also a part of the forest ecosystem, comprises substantial amounts of living biomass (Kumar and Nair 2011; Feyisa et al. 2016). As the Kyoto Protocol recognizes agroforestry system as a greenhouse gas mitigation strategy, the global interest in carbon sequestration through adaption of this system has increased (Albrecht and Kandji 2003; Jose 2009; Nair et al. 2009; Sharrow and Ismail 2004). Landholders realize that agroforestry system could become economically incentive with increased markets of forest biomass and carbon (Oelbermann et al. 2004). An estimate of forest biomass is useful for developing climate change mitigation strategies, planning for sustainable management, and monitoring of carbon-stock changes in agroforestry systems (Jose and Bardhan 2012; Tumwebaze et al. 2013; Beedy et al. 2016). An estimate of aboveground forest biomass is also important for several other issues ranging from industrial forestry practices to scientific purposes (Parresol 1999; Tumwebaze et al. 2013). However, accurate estimation of aboveground forest biomass is much challenging task, and a major challenge in measuring and monitoring carbon sequestration potential of agroforestry systems is measuring aboveground tree biomass, which stores significant amounts of carbon assimilated by these systems (Kumar and Nair 2011; Temesgen et al. 2015).

Tree biomass may be estimated by using direct or indirect methods (Vogt et al. 1998). A direct method requires destructive sampling, which is time consuming and costly, but most accurate. It is suitable for small plants and sample sizes. Since forest area is often large, estimation of tree biomass for an entire forest using destructive sampling is almost impossible. In such a situation, an indirect approach, which involves estimating biomass of a total tree or its components using allometric models (Subedi and Sharma 2012; Sharma et al. 2017). Allometric models are mathematical relationships that estimate total tree biomass or by components based on the variables of standing individuals such as trunk diameter, total height, wood density (Bartelink 1996; Parresol 1999; Lima et al. 2012; Picard et al. 2012; Skovsgaard and Nord-Larsen 2012; Subedi and Sharma 2012; Feyisa et al. 2016; Sharma et al. 2017). The allometric biomass models, which are used for predicting biomass of trees through dendrometric characteristics of easy measuring, are fundamental tools for estimating the contribution of forest ecosystems to carbon cycles (Picard et al. 2012; Tumwebaze et al. 2013). A large number of aboveground forest biomass models for various tree species and geographical areas are reported in the literatures (Ter-Mikaelian and Korzukhin 1997; Zianis et al. 2005; Muukkonen and Mäkipä 2006; Muukkonen 2007; Návar 2009a, b). All of these models, whether intended for application to a single species forest, mixed species forest, specific biogeographical region, or climate-related biomes, are based on the allometric relationships between aboveground biomass and size (diameter, height) and wood density of trees (Tumwebaze et al. 2013). Allometric biomass models can be considered as basic tools for estimating carbon sequestration in agroforestry systems (Albrecht and Kandji 2003; Martin et al. 2010; Nair et al. 2010; Feyisa et al. 2016). However, most of the biomass models developed so far are mainly based on the data collected from either natural forests or plantations. Therefore, they might have some limitations while applying in agroforestry systems, because architecture of the trees in forest and agroforestry systems would be different as consequences of different silviculture tendings applied in the systems (Segura et al. 2006; Tamang et al. 2012; Beedy et al. 2016).

Agroforestry promotes the production and conservation by diversifying products and services (Kumar and Nair 2011). Agroforestry, as a part of the multifunctional working landscape, can play a major role in conserving and enhancing biodiversity from farms to the landscape level in both tropical and temperate regions of the world (Jose 2012). Agroforestry system is potentially important for livelihood strategies and forest conservation, and varies greatly according to the local contexts. Agroforestry system generates substantial income, supports livelihood and biodiversity, and keeps ecological functions in intact (Regmi and Garforth 2010; Oli et al. 2015). The trees growing in agroforestry systems have immense potentialities for

producing timber, fuel wood, fodder, food, sequestrating carbon, conserving soil and water (Dhungana and Bhattarai 2008).

The Indian Chestnut [Castanopsis indica (Roxb.)] is a one of the important evergreen broad-leaved tree species in the mid-hills of Nepal. It grows in a wide geographical range, distributing from 1200 to 2900 m above mean sea level (Jackson 1994). It is a multipurpose species, whose stem is used as construction timber, leaves as fodder and raw materials for plates, branches as fuelwood and fruits as edible food and leaves of this species contain protein (15%) and fiber (29%), making nutrient-rich fodder source (Jackson 1994). Most of the C. indica forests in Nepal were degraded in the recent past, due to policy conflict between the central government and local forest users. However, after introduction of community forestry programs in 1970s (Bartlett 1992), most of C. indica forests were successfully rejuvenated, but they are still in immature stages. Most of the agricultural fields were built after clearing natural C. indica forests and therefore, agricultural fields are adjoining to these forests, and also in some cases, agricultural fields are surrounded by C. indica forests in all directions. Thus, C. indica forests contribute to the nutrient flow to the adjacent agricultural fields, for example, 250 kg leaf litter of Schima-Castanopsis forests may transfer about 11 kg, 1.3 kg, and 6 kg of nitrogen, phosphorus, and potassium, respectively, which may help maintaining fertility in the agriculture fields (Balla et al. 2014). C. indica has a high calorific value, which makes it a potential source of energy. Besides producing valuable material products, C. indica also provides environmental services (soil and water conservation) and carbon sequestration, which play important roles in the climate mitigation functions.

Because of the immense importance of *C. indica* forests, in-depth investigations on this species is necessary. Among various aspects of investigation, developing individual tree-based aboveground biomass models can be one of them. Because, a precise estimate of standing volume and biomass for this species is necessary for effective management of *C. indica* forests. Some previous studies have attempted to develop allometric biomass models for this species, such as biomass models for juvenile stage plants (Bhandari and Neupane 2014) and biomass models and volume tables for all sized-trees (Tamrakar 2000). However, Tamrakar (2000) used only diameter as a

predictor in the models, which would be significantly biased in the stands where trees of *C. indica* with similar diameters have different heights, height-todiameter ratios (tree slenderness coefficients), wood densities, and crown sizes. In order to ensure a high prediction accuracy in such as situations, this study aims to develop the individual tree aboveground biomass models using three important variables: diameter, height-to-diameter ratio, and wood density as predictor variables. The presented models will be applied for a precise prediction of the individual tree aboveground biomass of *C. indica* in both forest and agroforestry systems in the mid-hills of Nepal.

Materials and methods

Study area

We carried out this study in three different community forests (CFs) in Kaski district, one of the mid-hills districts in Nepal (Fig. 1). The CF is defined as the forest managed by local people in line with the CF user group constitution and operation plans. We used three CFs: Bhangara CF, Thulo CF, and Pachabhaiya CF in our study. The forests covers 46% area of the district, and out of which 22% forest is being managed by 497 CF user groups. The altitude of these CFs varies from 637 to 823 m above mean sea level, and slope varies from 10° to 44°. Mean maximum and minimum temperatures are reported to be 33 and 5.6 °C, respectively. Mean annual precipitation varies from 3068 to 3353 mm (DDC 2010). All three CFs have been managed by local people since last 15–20 years. Various silviculture tendings such as weeding, cleaning, climber cutting, thinning were applied to improve the productivity of these CFs. Forests were originated naturally with stand age varying from 25 to 45 years, and they consist of different tree species such as Castanopsis indica, Schima wallichii, Bombax ceiba, Lagerstroemea parviflora, Wrightia arborea, Albizia procera, Shorea robusta, Syzygium cumini. However, Castanopsis indica is a dominating species in terms of its abundance, coverage, stem volume, and biomass in each CF. The lower boundary of these three CFs are attached to the agricultural fields. Therefore, their contribution to the agroforestry system is substantially high either in terms of providing nutrients or in stabilizing slopes of both forests and agricultural fields.



Fig. 1 Study area

Sampling and measurement

Based on the size (diameter and height) of population of a species of interest, sample trees were identified with the help of local people and forest management plans that were formulated by community forest user groups. We applied the stratified sampling technique (Chaturvedi and Khanna 2011) to select the sample trees that properly represent the variabilities in terms of size of trees, site quality, stand density, stand structure, and physiographic features of the stands. The stratified sampling with subjective tree selection method is often used to obtain good representative samples from each stratum of population of a species of interest (Edwards Jr et al. 2006; Chapagain et al. 2014; Sharma et al. 2017). This selection method resulted in the thirty-six sample trees representing all kinds of above-mentioned variabilities. At least three trees in each diameter at breast height (DBH) class were identified and measured for standing height, stump diameter, and DBH. Diameters were measured to a precision of 1 mm. We excluded diseased, deformed, top broken, suppressed, leaning, and wolf trees from being sampled. Since forest consists of a large proportion of small sized trees, size of sample trees selected from small-sized classes were also relatively large. The number of sample trees in each DBH class varied from 3 to 9.

Selected trees were felled through October and November 2013 and total height was measured to a precision of 1 cm. Foliage, branch, stem of each tree were segregated immediately after felling. On the basis of diameter, felled trees were grouped into stem parts (small: 1.5–10 cm, large: ≥ 10 cm), and branch parts (foliage: <1.5 cm, small: 1.5–10 cm, large: ≥ 10 cm). Each of these parts were weighed in situ separately. Stem parts and large branches were segregated to maximum of 3 m length. Within the limit of 3 m, and based on tapering, segments were divided into swollen parts or twisted parts. Diameters on thicker, middle, and thinner ends and total length were measured for each segment. The wood volume of each segment was determined using the Newton's formula (Chaturvedi and Khanna 2011) as below:

$$V = \frac{L(S_1 + 4S_m + S_2)}{6} \tag{1}$$

where *V* is the wood volume of a segment (m³); *L* is the length of a segment (m); S_l is the basal area at thinner end of a segment (m²), S_2 is the basal area at thicker end of a segment (m²), S_m is the basal area at mid-point of a segment (m²);

Discs (wood sub-samples) were cut from thicker, middle and thinner end of the stem of each sampled tree. Following the methods suggested by Nelson et al. (1999), discs were taken in such a way that both inner and outer parts would be properly included. Based on the thickness, one or two discs were cut from a large branch. Also, sub-samples from foliage and small branches of each sampled tree were taken and their fresh weights were measured. Wood volumes of subsamples from stems and branches were determined by using water displacement method. All sub-samples were transported to the laboratory for oven drying. Sub-samples were dried on the oven (102 °C) until their weights decreased to a stable state. Dried subsamples were weighed separately. Wood density of sub-samples from stem and large branch was determined using the following formula (Chave et al. 2006; Mäkipä and Linkosalo 2011):

$$\rho = \frac{W_o}{V_s} \tag{2}$$

where ρ (rho) is the wood density (kg m⁻³); W_o is the oven dry weight of a sub-sample (kg); V_s is the water saturated volume of a sub-sample (m³)

Dry-to-fresh weight ratio was determined and this was multiplied by total fresh weight to estimate dry biomass of foliage and small branches. Biomass of each segment from stem and large branch was estimated as a product of wood volume and wood density. Total dry biomass of each sample tree was obtained by summing up of dry weight of stems, branches, and foliage. A summary of statistics of data is presented in Table 1.

| Variables | Statistics [mean ± DBH class (cm) | SD (range)] | | | | |
|---------------------------------------|--------------------------------------|-----------------------------------|------------------------------------|-------------------------------------|--------------------------------------|-----------------------------------|
| | 5-10 | 10–20 | 20–30 | 30-40 | 40–50 | Overall |
| JBH (cm) | $7.5 \pm 1.7 \ (5.5-9.9)$ | $16.7 \pm 2.2 \ (13.5 - 19)$ | $26.0 \pm 2.3 \ (22.3-28.9)$ | $34.8 \pm 2.3 \ (31.5 - 38.2)$ | $43.6 \pm 2.6 \; (41.0 - 46.3)$ | $22.7 \pm 11.6 \ (5.5-46.3)$ |
| Fotal height (m) | $7.5 \pm 2.3 \ (4.9-10.8)$ | $14.1 \pm 1.5 \ (11.1 - 16.7)$ | $17.9 \pm 3.9 \ (13.3 - 24.8)$ | $18.1 \pm 1.6 \; (16.3 - 20.3)$ | $26.4 \pm 2.5 \ (24.3 - 29.3)$ | $15.4 \pm 5.8 \ (4.9 - 29.3)$ |
| HDR $(m \text{ cm}^{-1})$ | $1.8 \pm 0.4 \; (1.2 - 2.5)$ | $0.9 \pm 0.32 \ (0.3 - 1.4)$ | $0.5 \pm 0.2 \ (0.2 - 0.8)$ | $0.6 \pm 0.2 \ (0.2 - 0.8)$ | $0.3 \pm 0.1 \ (0.2 - 0.4)$ | $0.9 \pm 0.6 \ (0.2 - 2.5)$ |
| Wood density (kg m ⁻³) | 496 ± 33 (451–539) | 534.9 ± 38.3 (482.4-607.9) | 534.5 ± 27.9 (477.9–565.1) | $517.9 \pm 40.4 \ (465.8 - 589.6)$ | 528.7 ± 13.1 ($520.7 - 543.8$) | 529.8 ± 33.1 (465.8–607.9 |
| Dry biomass (kg) | 19.7 ± 9.1 (12.2-36.1) | $142.1 \pm 50.9 \ (72.5 - 229.3)$ | 432.1 ± 132.8 (272.9-667.8) | $825.8 \pm 223.7 \\ (489.4-1104.8)$ | 1815.4 ± 381.4 (1486.3–2233.5) | 459.8 ± 525.6 $(12.2-2233.5)$ |
| Number of trees | 8 | 6 | 6 | 7 | 3 | 36 |
| DBH diameter | at breast height, HDR | ? height-to-DBH ratio, SD s | standard deviation | | | |

 Table 1
 Summary statistics of modelling data

Model development

Since there is allometric relationship between tree variables and tree biomass or its component biomass, this can be modeled as a function of

- 1. diameter alone (Rizvi et al. 2008; Ajit et al. 2011; Sharma 2011; Singh et al. 2011; Kuyah et al. 2012),
- diameter and height (Ketterings et al. 2001; Rizvi et al. 2008; Hosoda and Iehara 2010; Subedi and Sharma 2012; Sharma et al. 2017), and
- diameter, height, and wood density (Chave et al. 2005; Basuki et al. 2009; Alvarez et al. 2012; Chaturvedi and Raghubanshi 2012; Chapagain et al. 2014).

Since our preliminary analyses showed poorer results with use of the first approach compared to other two, we excluded this from further analyses. This would be logical in a sense that even within a small stand, biomass of the trees having similar diameters might be different, because of differing heights and wood densities. Also, biomass of the trees having similar heights and diameters might be different because of differing wood densities. Realizing this, we used all three variables (DBH, height, wood density) to develop biomass models. Instead of total height, we used height-to-DBH ratio (HDR). As HDR is a measure of tree slenderness, it is an appropriate characteristic to describe the form of an individual plant (Sharma et al. 2016, 2017). We categorized predictor variables into two groups: first group: DBH as a main variable and HDR as covariate predictor; second group: DBH as a main variable and product of HDR and wood density as covariate predictors. All candidate models with each variable group fitted to the data. The models developed using variables from the first group are hereafter termed as density independent models (first category models) while models developed from second group are termed as density dependent models (second category models).

We examined the scattered plots of HDR versus DBH and wood density versus DBH to know the patterns of their relationships (i.e., linear or nonlinear) (Fig. 2). We used this figure for covariate modelling purpose. We applied the parameter prediction approach (Chapagain et al. 2014; Sharma et al. 2017), which is slightly different from that used in other biomass modelling works (Rizvi et al. 2008; Basuki et al. 2009; Hosoda and Iehara 2010; Alvarez et al. 2012; Subedi and Sharma 2012). Among various candidate models evaluated, only six model converged with global minimum, and exhibited biologically plausible model curves. However, because of a brevity of space, we have presented only these six models here (Table 2). The parameter b_1 of each of the base models (Table 2) was found significantly correlated to each of the two covariate predictors (HDR, HDR \times wood density). The parameter b_1 of each base model was then modeled as a nonlinear function of a covariate (see Eq. 3 as an example for M2 in Table 2). To make a product value (HDR \times wood density) smaller, wood density was cubed root. This allowed variations between 3 and 9 (Fig. 2, right).

$$b_1 = \alpha_1 z_i^{\alpha_2} \tag{3}$$

where $z_i = HDR_i$ (for first category models), $z_i = HDR_i \times \rho_i^{1/3}$ (for second category models); HDR_i is the height-to-DBH ratio for tree *i* (m cm⁻¹), and ρ_i (*rho*) is the wood density for a tree *i* (kg m⁻³), and b_1 , α_1 , α_2 are parameters to be estimated.





| Table 2 Candidate models used to fit data | Model | Mathematical form | References | |
|---|-------|--|----------------------------|--|
| | M1 | $W_i = b_1 [1 - \exp(-b_2 D_i)]^2 + \varepsilon_i$ | Bertalanffy (1957) | |
| W_i dry biomass of a tree <i>i</i> (kg): <i>D</i> , diameter at breast | M2 | $W_i = b_1 D_i^{b_2} + \varepsilon_i$ | Huxley and Teissier (1936) | |
| height (DBH) of a tree | M3 | $W_i = b_1 \exp(b_2 \sqrt{D_i}) + \varepsilon_i$ | This study | |
| <i>i</i> (cm); $b_1 = \alpha_1 z_i^{\alpha_2}$ with $z_i = HDR_i$ (for first category | M4 | $W_i = \expig(b_1 D_i^{b_2} ig) + arepsilon_i$ | Sharma (2011) | |
| models). $z_i = HDR_i \times \rho_i^{1/3}$ | M5 | $W_i = D_i/(b_1+b_2D_i)+arepsilon_i$ | Hosoda and Iehara (2010) | |
| (for second category models): <i>HDR</i> , height-to- | M6 | $W_i=D_i^2/ig(b_1+b_2D_i^2ig)+arepsilon_i$ | Hosoda and Iehara (2010) | |

Parameter estimation and model evaluation

The model parameters were estimated with nonlinear least square regression using PROC MODEL in SAS (SAS Institute Inc. 2012), applying Marquardt's method. The estimated models were evaluated using various statistical measures and graphical appearances. We used following statistical measures: (1) significance of parameter estimates: this avoids biologically illogical parameter estimates. Unless otherwise specified, 1% level of significance ($\alpha = 1\%$) was used in our analyses. (2) Root mean square error (*RMSE*): this analyzes precision of the estimation. (3) Adjusted coefficient of determination (R_{adj}^2) : this reflects the total variability described by the model considering total number of parameters to be estimated. The expressions of *RMSE* and R_{adj}^2 are found in the standard text books of statistics (e.g., Montgomery et al. 2001). (4) Akaike information criterion (AIC): this compares the estimated models more logically than others as AIC is based on minimizing Kull-back-Lieber distance (Akaike 1972; Burnham and Anderson 2002). Additionally, residual graphs and the model curves produced with each base model were also analyzed. This helps better understanding whether models are attributed to theoretical basis and biological logics (Zeide 1993).

Model validation is one of the important procedures of modelling as this provides credibility and confidence about the developed model. Validation is often carried out by splitting data (Ajit et al. 2011; Sharma and Breidenbach 2015; Sharma et al. 2017). However, we were not able to do this because of small dataset. Even validation by splitting data alone does not provide more information in addition to the respective fit statistics obtained directly from the model fitted with a total dataset (Kozak and Kozak 2003; Yang et al. 2004). Therefore, validating model with external independent data can be the best alternative only, but it would not be possible to get additional destructive samples, because of resource limitations.

Results

The parameter estimates of the models in each model category were significant (p < 0.001) and biologically plausible. There were only smaller differences among the six models within the same category than the models between the different categories (Table 3). Except M6 of the first category models, AIC difference of each model (with respect to that of the best model, M2 of the second category models) was less than 10. As expected, all second category models resulted in better fits than the models in the first category. A simple power function of the form $y_i = b_1 x_i^{b_2}$ (M2), in each category, showed the most promising fit statistics (smallest *RMSE* and AIC, largest R_{adi}^2). Even though this model, in the second category, showed the most promising fit statistics, a significant part of the biomass variations was left unexplained (RMSE = 65.4). The last model (M6), in each category, showed the poorest fit statistics (largest *RMSE* and *AIC*, smallest R_{adi}^2). Two models M1 and M2, in each category, showed very small discrepancies in the fit statistics, but significant differences in the residuals (Fig. 3).

There was no variance heteroscedasticity in data. Compared to other models, the best fitted model (M2), in each category, showed no significant trends in the residuals against the predictor variables (DBH, height, slenderness coefficient, and wood density) (graphs not shown). The histograms and probability plots of the residuals of model M2, in each category, also showed much better bell-shaped pattern than other models (graphs not shown). Due to brevity of space, we Table 3 Parameter estimates and fits statistics of six models (Table 2)

The best performing model in each category is highlighted

RMSE root mean squared errors; R_{adj}^2 adjusted coefficient of determination, AIC Akaike's information criterion; α_1 , α_2 , b_2 , are

* Defined in Table 2 and more description is in a sub-

Fig. 3 Mean residuals of

each model (Table 2) against two tree variables-

10 cm intervals of both height and DBH

(category = 1: first

defined in Table 2)

category = 2: second

category models, both are

category models;

parameters

section "Model

development"

| Category* | Paramet | er estimates | Fit statistics | | | | |
|-----------|---------|--------------|----------------|----------|---------|-------------|-----|
| | Model | α1 | α2 | b_2 | RMSE | R^2_{adj} | AIC |
| First | M1 | 684.2589 | 0.648284 | -0.02444 | 73.6293 | 0.9804 | 314 |
| | M2 | 0.034642 | 0.789939 | 2.980244 | 72.1951 | 0.9811 | 313 |
| | M3 | 2.780965 | 0.570763 | 1.023094 | 76.8374 | 0.9786 | 317 |
| | M4 | 1.500356 | 0.094673 | 0.438494 | 74.9218 | 0.9797 | 316 |
| | M5 | 2.180419 | -0.31858 | -0.03404 | 75.6059 | 0.9793 | 316 |
| | M6 | 1.645352 | -0.33981 | -0.00046 | 79.1907 | 0.9773 | 320 |
| Second | M1 | 190.328 | 0.653222 | -0.02374 | 68.0968 | 0.9832 | 309 |
| | M2 | 0.007598 | 0.778986 | 2.945875 | 65.4181 | 0.9845 | 306 |
| | M3 | 0.87058 | 0.580227 | 1.01461 | 72.1755 | 0.9811 | 313 |
| | M4 | 1.252436 | 0.09428 | 0.433645 | 69.9811 | 0.9823 | 311 |
| | M5 | 4.205852 | -0.3254 | -0.03254 | 71.2643 | 0.9816 | 312 |

-0.35722

-0.00044

75.6122

0.9793

316

M6

3.400865



present only graphs of M2-the best model (Fig. 3). Compared to other models, M2, in each category, showed smaller residual variations than that for larger trees. Trends of the M2-estimated biomass plotted against the measured biomass nicely followed the 1:1 line (Fig. 4). This indicated that two biomass amounts were not substantially different, especially for very small and large trees. The biomass curves produced with M2, in each category, also showed an adequate covering to the measured biomass (Fig. 5). There was a significant differentiation of the curves within the data range, even for the same DBH due to differing tree slenderness coefficients and wood densities.

Discussion

We developed both wood density dependent and density independent biomass models for the prediction of aboveground biomass of the individual C. indica trees growing in forest and agroforestry systems. Both model alternatives show attractive fit statistics



Fig. 5 Biomass curves produced with M2 (Table 2), overlaid on the measured biomass data. The curves were produced using HDRs at 0.1 intervals, with the lowest and highest curves belonging to biomass for trees with *HDR* of 0.2 and 0.9, respectively (category = 1), and $HDR^{1/3} \times rho$ at 1.0 interval

(Table 3) and our data adequately represent wide ranges of tree size (Table 1), site quality, stand conditions, and topographic characteristics in the study area. Like other biomass modelling studies (Chave et al. 2005; Basuki et al. 2009; Návar 2009a, b; Alvarez et al. 2012; Chaturvedi and Raghubanshi 2012; Lindner and Sattler 2012; Chapagain et al. 2014), our density dependent models also show higher accuracies than their density independent counterparts. Only small discrepancies were observed in the fit statistics among the model alternatives (Table 3). If AIC difference of any model relative to that of the best fitted model is <10, these models would have identical prediction accuracies (Burnham and Anderson 2002). Only less than 2% of the total variations in the measured biomass remain unexplained by the best model, because none of the mathematical functions perfectly describe the measured biomass data due to large variations among the individual tree sizes. To capture more and more variations of a response variable, i.e., biomass amount, fitting of several

with the lowest and highest curves belonging to biomass for trees with $HDR^{1/3} \times rho$ of 2 and 9, respectively (category = 2). Dots are the measured biomass values (category = 1: first category models; category = 2: second category models, both are defined in Table 2)

models of different functional forms (e.g. power, exponential, polynomial forms) to the data is necessary and this may offer a good chance of getting suitable models as per the nature of data (Rizvi et al. 2008; Ajit et al. 2011; Sharma 2011; Subedi and Sharma 2012; Chapagain et al. 2014; Sharma et al. 2017). Realizing this, we also evaluated several candidate functions as base models and selected the best performing one, which describes more than 98% biomass variations among the individual trees (Table 3). This indicated that the base model and predictor variables chosen and modelling approach applied were best suited to our data.

Non-existence of significant and systematic trends in the residuals of the best model (Fig. 3), in each category, confirms the model's adequacy and precision (Table 2). A clear differentiation of the curves produced with M2 within the measured data range, even for the same DBH (Fig. 5), is due to the significant effects of other covariate predictors (p < 0.001 for α_1 and α_2 in each category). Because of different heights and wood densities of the sampled trees used (Table 1), their predicted biomasses are expected to be different, even for the same DBH as shown in Fig. 5. Adequate covering of the model curves to the measured biomass also suggests that the selected models are adequate enough to describe biomass variations for all sized trees (Table 1). This suggests that selected model is biologically plausible and mathematically robust. Smaller residual variations for small trees (Fig. 3) suggests that our models can be more accurate for smaller trees than for larger ones. This may be the reason that there were fewer data from larger trees as compared to the smaller ones.

All functions evaluated in this study are nonlinear and some of them have already been used to model aboveground biomass for large individual trees and juvenile stage plants. As in many other studies (e.g., Ketterings et al. 2001; Subedi and Sharma 2012; Chapagain et al. 2014; Sharma et al. 2017), using DBH as a single predictor in the models did not adequately describe the data in this study also. These models would have limited scope of application as they do not provide desired prediction accuracies in the situations where trees of similar DBH have different heights, HDR, wood densities, and crown sizes. This situation commonly exists in each stand, even a stand is very small. Alternatively, inclusion of other predictor variables such as HDR (a measure of tree slenderness), wood density (a measure of stiffness and cohesiveness of wood fibres), and crown size (a measure of tree vigour and health) into the biomass models may increase the model's prediction accuracy and have a wider scope of application. For example, Feyisa et al. (2016) developed allometric biomass models with crown area and crown volume along with other tree variables as predictors for ten woody species in rangelands of southern Ethiopia. However, we were not able to include crown variables into our biomass models because of lack of crown measurements.

If wood density of the modelled species is available, density dependent models or M2 (in second category) could certainly be the first choice. Alternatively, in lacking of the information of wood density of a species of interest, the density independent model or M2 (in first category), which requires information of only DBH and HDR, could be applied. The prediction accuracies of both model types may not be much different, because they exhibit almost identical fit statistics (Table 3) and graphical features (Figs. 3, 4, 5). However, we were not able to compare their prediction accuracies in different growing conditions of *C. indica*, because of lack of external independent data. Since tree height and diameter are more readily measureable than wood density, first category models (density independent models) are often suggested for application (Ketterings et al. 2001; Rizvi et al. 2008; Hosoda and Iehara 2010; Subedi and Sharma 2012; Chapagain et al. 2014). The adequate covering of simulated biomass curves (Fig. 5) to the measured data suggests that models could be applicable with an acceptable accuracy for individual trees having a wide range of HDR and wood density (Fig. 2).

The sampled trees used in this study (Table 1) are fairly representative to various site qualities, sizes, stand conditions, and physiographic characteristics (aspect, slope, altitude). The destructive sampling is usually carried out for biomass studies, but it requires more time and resources. Therefore, this method is rarely applied for a large sample size and geographic area. We argue that our sample size (36 trees) is larger than that used in other biomass studies (Ajit et al. 2011; Sharma 2011; Chaturvedi and Raghubanshi 2012; Subedi and Sharma 2012), which ranged from 27 to 30 individuals. With few exceptions (e.g. Brown et al. 1993; Chave et al. 2005), biomass modeling studies requiring destructive sampling only use small sample size from a small geographic area. Furthermore, most of the allometric biomass models developed so far are mainly based on the data collected from either natural or plantation forests (forest systems). Therefore, some limitations may be realized for their application in agroforestry systems because of the differences in tree statures (or tree architectures) resulted from different silviculture tendings applied in these systems (Segura et al. 2006; Martin et al. Martin et al. 2010; Tamang et al. 2012; Beedy et al. 2016; Feyisa et al. 2016). Thus, it is important to collect data (as we did in this study) from a population of a species of interest, covering both forest and agroforestry systems. This may ensure the adequacy and confidence of the developed biomass models while applying them for either system.

When sample trees are adequately representative to all existing sizes, sites, and stand conditions, measurements from only a few trees could be good enough to secure the desired accuracies of the allometric biomass models. In order to confirm this possibility, modellers need to confirm whether the developed biomass models could be used for precise prediction under different growing conditions. Since biomass is affected by wood density, and wood density by various factors such as site quality, climate, growth stage of trees, and competition stresses, inclusion of site index, age, and competition measure into the biomass models may significantly increase the model's accuracy and scope of application. Further research will be carried out using data from wider ranges of site quality and stand condition, and distribution of *C. indica* when adequate financial resources are available.

Conclusions

A simple allometric model with DBH, height-to-DBH ratio, and wood density included as predictors (density dependent model) showed the best fits to the data. Compared to this model, the same functional form with the former two predictors (density independent model) showed slightly less attractive fit statistics. However, both model alternatives described more than 98% variations in the biomass amounts of individual trees with no significant trend in the residuals. Thus, one of the alternatives may be used for a precise prediction of the individual tree aboveground biomass of C. indica growing in forest or agroforestry systems, depending on the access of input information required by the model. Our models are site-specific, and therefore model users need to take precautions while applying them to a wider geographical range, where conditions for C. indica are different in terms of growth stage, site quality, stand density, and species composition that formed the basis of this study. To make the biomass models more comprehensive, accurate, and broadly applicable, they need to include measurements of site quality (e.g., site index), stand density (e.g., competition index), topographic characteristics (e.g., aspect, slope, and altitude), climate characteristics (temperature and precipitation), and soil properties. Thus, further research is suggested to validate and verify our model using a larger dataset with a wider range of values for site quality, climate and topographic characteristics, stand density, growth stage, and species distribution across Nepal.

Acknowledgements This article is a part of the first author's MSc thesis submitted to the Institute of Forestry, Tribhuwan University in Nepal. We would like to thank the local users of

the three CFs (Bhangara CF, Thulo CF, Pachabhaiya CF) for their participatory supports during sampling and measurements. The Forest Resource Assessment (FRA) Nepal Project provided financial support to this study (Grant No. 08062011). The contribution to this publication was also provided by an Excellent Output Project-2016 (IGA- B02/16) and the project focusing on mitigation of the impact of climatic changes to forests from the level of a gene to landscape level (CZ.02.1.01/ 0.0/0.0/15-003/0000433 financed by OP RDE) in the Faculty of Forestry and Wood Sciences, Czech University of Life Sciences Prague. We are grateful to the editor for constrictive comments and insightful suggestions to improve the manuscript.

Compliance with ethical standards

Conflict of interest No conflict of interest among the authors.

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