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Additive biomass model for *Heritiera fomes* (Buch.-Hum.) in the Sundarbans Reserved Forest, Bangladesh

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Mangroves are recognised as an important carbon sequester and therefore demand accurate biomass and carbon stock estimations. This study aimed to develop additive biomass models for *Heritiera fomes*, the most dominant tree species of the Sundarbans Reserved Forest in Bangladesh. Using a non-destructive method, 219 small branches (diameter < 7 cm) were harvested from 97 individual trees to develop biomass models for leaves and smaller branches. The biomass of bigger branches (diameter > 7 cm) and stem was calculated from the volume and mean wood density value after debarking while the biomass of all other components was derived from the determined fresh to oven dry weight conversion ratio. Finally, the biomass of one individual tree was calculated by adding the biomass of trimmed and untrimmed leaves, small and large branches, foliage and stem. An independent data set was used to validate the best-fit model. A component-wise (leaves, branches, bark and stem) biomass model was developed by recovering subsequent cross-component correlations which were then aggregated using the weighted Gaussian maximum likelihood estimation method. Among the components model, D (diameter at breast height) alone performed best for leaves and branches while the product of D and H (total tree height) proved the better results for stem and bark. Our best-fit model (Biomass = $0.0389D^{2.3773} H^{0.4178} + 0.0492D^{2.3027} + 0.0112D^{1.1144} H^{1.4572} + 0.0306D^{1.8507}$) showed the highest model efficiency with the lowest AIC, RMSE%, MAE, and MPE values. The efficiency of our non-destructive model has shown that it is as effective as other widely used pan-tropical models. Our built models can therefore be used for accurate estimation of biomass and carbon stock in *H. fomes* of the Sundarbans Reserved Forest, Bangladesh.

Keywords: additive model, biomass allocation, mangroves, nonlinear seemingly unrelated model, Sundari

Introduction

Mangroves are among the most productive and carbon-dense ecosystems in the tropics (Hutchings and Sanger 1987; Mahmood 2014). For accurate estimation of this productivity and carbon storage, biomass measurement followed by a species specific and cost-effective biomass model is necessary (Mahmood 2004; Mahmood et al. 2008; Yatskov et al. 2019). However, biomass estimation in mangroves is often driven by common biomass models, which could result in biomass under- or overestimation (Jones et al. 2020; Zhu et al. 2021). A species specific and cost-effective biomass model that is less destructive can minimise this uncertainty in quantification of biomass and thereby contribute to accurate carbon estimation in the technical part of nature-based carbon mitigation projects (e.g. REDD+) (Bernard et al. 2014; Roxburgh et al. 2015).

Allometric biomass models using the destructive method (felling of sample trees) is indisputably accurate, but it is destructive, time-consuming, costly and labour intensive (Ketterings et al. 2001; Dong et al. 2015; Kuyah et al. 2016; Meng et al. 2017), especially in mangroves (Mahmood 2004). Moreover, destructive sampling is carried out in small areas

or for a small number of tree samples and its further use for repeated measurement is also limited (Louhaichi et al. 2018). The semi-destructive method has gained much attention in deriving allometric biomass models as the moratorium on tree felling increases daily (Brown et al. 2001; Mahmood et al. 2019). However, the number of sample trees is highly variable, and mainly depends on the desired precision and accuracy in biomass estimation, size classes of sample trees, and methods used for developing allometric models (Picard et al. 2012; Roxburgh et al. 2015).

The power-law relationship between dry biomass and different biometric variables is most popular for tree biomass estimation (Dong et al. 2015; Meng et al. 2017). Frequent use of logarithmic transformation in many studies is criticised, as such alteration could induce uncertainties due to systematic bias (Lambert et al. 2005; Zhao et al. 2015). Moreover, the calibration of tree component-based equations is intrinsically more complex (Affleck and Diéguez-Aranda 2016). Some researchers suggest using the original data via non-linear regression by least squares as it assumes an additive error structure for the equation (Dong et al. 2015).

In general, for developing biomass models, diameter at breast height (DBH; 1.3 m) is commonly used either alone or in combination with other tree attributes as a predictor (Ketterings et al. 2001; Dong et al. 2015; Affleck and Diéguez-Aranda 2016). The DBH has lenience in measurement and often accounts for the largest share of variation in tree biomass (Affleck and Diéguez-Aranda 2016). In many studies, tree height is used as an additional predictor (Kuyah et al. 2016) though its use as the single parameter is rare (Anitha et al. 2015). Although other tree variables like wood specific gravity, tree crown parameters (e.g. crown length, crown width) and age of the tree can account for additional variation, they are rarely used in model development as they are much more difficult to obtain in practice (Estrada et al. 2014; Dong et al. 2018).

Scientific interest in tree partitioned biomass led to the development of component-wise biomass equations (Sanquetta et al. 2015). Then component-wise biomass was added to get total above-ground biomass (Antonio et al. 2007). But the conventional method of biomass estimation showed irrelevancy while comparing the estimated total above-ground biomass of a tree derived from the TAGB model and the sum of estimated component-wise biomass (Parresol 1999, 2001). Moreover, component-wise biomass models ignore the intrinsic correlations among biomass components (Dong et al. 2015). The additive approach has overcome this disparity, but this method is not adopted frequently for the required statistical analysis and software beyond the least square regression (Parresol 2001; Zhang et al. 2016; Fu et al. 2017).

To date, various models have been proposed to ensure the compatibility property of biomass equations which can be divided into aggregative and disaggregative approaches (Dong et al. 2015). Both of these approaches were later modified by Affleck and Diéguez-Aranda (2016) to provide a valid probabilistic model. The aggregated approach estimates biomass of each component separately with subsequent recovery of cross-component correlations from the original measurements and then jointly fits the total models by using the maximum likelihood option. However, the disaggregated approach first focuses on the development of the total biomass estimation model and then it is disintegrated into components on the basis of their proportions in total to ensure additivity (Zhao et al. 2019). The aggregated approach ensures greater efficiency, and is consequently considered as the de facto standard for non-linear biomass equation estimation (e.g., Sanquetta et al. 2015; Zhao et al. 2015). Even the aggregated approach showed better performance in comparison to other types (Parresol 2001; Widagdo et al. 2020).

The Sundarbans Reserved Forest, the world's largest contiguous mangrove forest, is situated in Bangladesh (59%) and India (Mahmood 2014). Considering higher biodiversity (Rahman et al. 2015a; Islam et al. 2016) and ecosystem services, the Bangladesh part (Sundarbans Reserved Forest) was declared a Ramsar Site in 1992 and, with its three wildlife sanctuaries, as a World Heritage Site in 1997 (UNESCO 2021). *Heritiera fomes* (Buch.-Ham.) is one of the most dominant and single most important tree species of this forest (Hussain and Acharya 1994), covering 67% of the vegetated area of the forest. However, it has been declared an endangered species as its global distribution is declining, (Polidoro et al. 2010). *Heritiera fomes*-dominated sites contain the highest amount of ecosystem carbon per unit area and

hence accurate biomass estimation will play a crucial role in conserving forest resources as well as in getting benefits from various global initiatives (e.g. carbon trading) (Rahman et al. 2015b). Species and site specific allometric biomass models of *H. fomes* are required to minimise over or underestimation of biomass and carbon stock. However, only five multi-species specific models were available for mangroves (Komiyama et al. 2005; Chave et al. 2005; Ray et al. 2011; Chave et al. 2014; Mahmood et al. 2019). Some researchers also used the model of Brown (1997) for moist forests to estimate the biomass of mangroves. Among them, only the model of Mahmood et al. (2019) includes *H. fomes* as the sample. As mangroves experience high site variability leading to variation in structure and architecture of trees (Estrada et al. 2014), it is often recommended to develop species and site specific models. Therefore, our study aimed to: (1) derive component-wise biomass models; (2) develop additive above-ground biomass models for *H. fomes* using the Gaussian Maximum Likelihood approach; and (3) compare the driven model with the frequently used multi-species common models for mangroves.

Materials and methods

Description of the study site

The samples of *H. fomes* were collected from the Sundarbans Reserved Forest (latitude 21.30°–22.30° N and longitude 89.00°–89.55° E) located downstream of the Ganges-Brahmaputra estuary (Figure 1). The land is low and flat, has an average altitude of 0.9–2.1 m a.s.l. (Iftekhar and Islam 2004) and is dominated by silty loam or alluvium (Islam 2003). A significant portion of the forest is inundated by the tide twice a day, but in monsoon time, most of the land goes underwater during the high spring tides (Karim 1994). The soil is geological of recent deltaic origin and hence is poorly drained with no distinct sediment horizon (Das and Siddiqi 1985). The spatio-temporal variation in salinity is prominent here and, in general, salinity increases from east to west during monsoon (minimum salinity in August–September) while it increases from north-east to south-west during other periods. (Wahid et al. 2007). The western part shows few changes even during the monsoon as it has no direct link with the River Ganges, the main freshwater source (Wahid et al. 2007). Salinity controls the vegetation composition (Hussain and Acharya 1994) and growth (Mahmood et al. 2014; Siddique et al. 2017). Rainfall is highly seasonal: May to October is the wet season, contributing 87% of the mean annual rainfall (1 500 mm), and the rest of the months are dry season with no or less rainfall (Hussain and Acharya 1994). Temperature fluctuates between 18 °C and 35 °C in summer and 12 °C and 29 °C in winter.

Description of the species

H. fomes, called Sundari locally, is a non-exclusive evergreen tree species. It can grow up to 25 m in height with dense and robust pneumatophores. It is a shade bearer in its early stages of growth (Mahmood 2015). Since the species prefers a freshwater environment (0–5 practical salinity units, PSU), it is commonly found alongside tidal creeks and channels in coastal swamps (Banerjee and Rao 1990). However, it can tolerate moderate saline conditions (Mahmood 2015). In the Sundarbans Reserved Forest, it occurs with *Excoecaria*

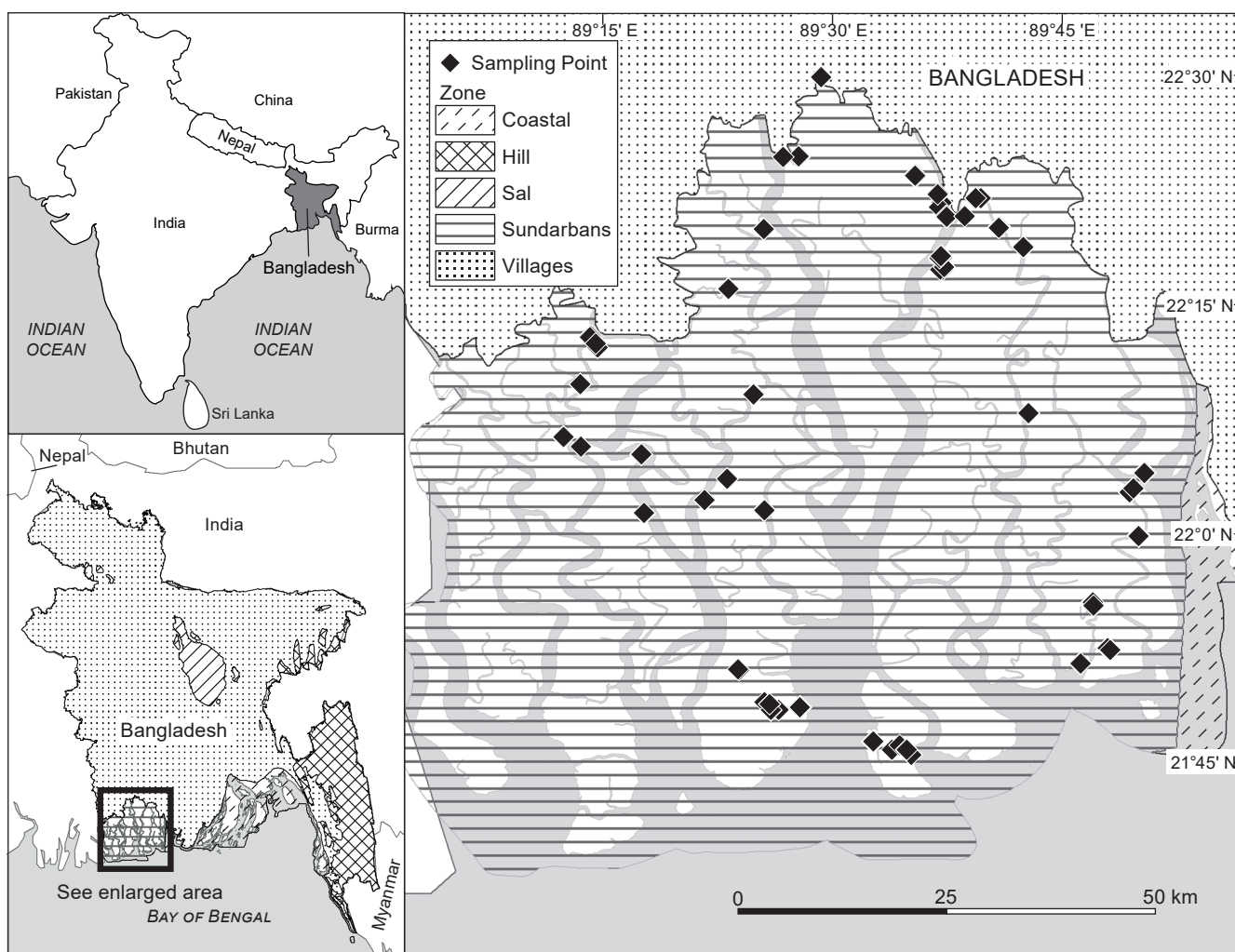


Figure 1: The Sundarbans of Bangladesh and sampling spots of this study

agallocha, *Xylocarpus moluccensis*, *Aglaia cucullata* and *Ceriops decandra*. Unlike other mangrove species, *H. fomes* can act as a biological indicator of climate change related to rises in sea level (Maxwell et al. 2018).

Biomass sampling

A total of 80 healthy individuals of *H. fomes* were selected purposively throughout the Sundarbans Reserved Forest for model development, keeping *D* (DBH) range 2–40 cm and *H* (total tree height) range 4–21 m, respectively. The data collected from these 80 individuals were considered as data set A. Sampling was done using a non-destructive method due to the moratorium on tree felling in the Sundarbans Reserved Forest since 1989.

Sampled trees were climbed to make sections for bigger branches (diameter > 7 cm) and stem using a paint mark. The diameter at the thicker and thinner ends sections was recorded for both stem and bigger branches. Bark thickness at each end of the log section was measured from the bark chip. The volume of all sections of stem and bigger branches was estimated without bark using Smalian's formula except for the last section, which was estimated using the volume formula

of the cone (Mahmood et al. 2017). The buttress volume of each tree was measured using the formula given by Picard et al. (2012). Measurements were taken for all small branches at the base (diameter < 7 cm) and only 2–3 small branches were trimmed per sample tree considering the tree size (Picard et al. 2012). A total of 219 smaller branch samples were harvested and then separated into sections (branches, twigs with leaves, and bark) in the field to determine their fresh weight. From each part of trimmed branches, 10 subsamples (approximately 0.25 kg) of woody portion and 20 subsamples of leaf, bark and buttress, were taken from each part of the trimmed branches and oven dried at 105 °C for seven days to get the conversion ratio for fresh to oven-dry weight.

Biomass determination in the sampled trees

From the trimmed branches, non-linear biomass models were developed for leaves and branches by taking base diameter as independent and oven-dried biomass of leafy branches as dependent variables respectively. Using these developed models, the biomass of untrimmed leaves and branches was determined. The oven-dried biomass of stem and bigger branches without bark were obtained from their calculated

volume (m³) and mean wood density (kg m⁻³) as determined by Sattar et al. (1999). Finally, total above-ground biomass of sample trees was estimated from the biomass of trimmed and untrimmed leaves and smaller branches, bigger branches, stem and bark.

Biomass allocation to leaf, branch, bark and stem was assessed by calculating biomass fractions (ratio of component biomass and total above-ground biomass) for each component. A bivariate relationship between biomass fractions and tree diameter was patterned for each component biomass.

Non-linear model development

The relationship between tree component biomass (leaf, branch, bark and stem) and the predictor variables (D and H) were explored to detect outliers and the nature of correlation from data set A using a scatter diagram. The allometric model was generated from data set A for tree component (leaf, branch, bark and stem) and total above-ground biomass through non-linear regression analysis using nlme function in R (Pinheiro and Bates 2000; R Core Team 2011). Equations 1–3 were used to get the relationship between biomass and predictor variables (Bi et al. 2004; Cai et al. 2013; Menendez-Miguel et al. 2013).

$$W = a \times D^b \quad (1)$$

$$W = a \times (D^2 \times H)^b \quad (2)$$

$$W = a \times (D^b \times H^c) \quad (3)$$

Additive biomass models

The total above-ground biomass model was derived by using the same independent predictor variables that were used to calculate the biomass of tree components. In addition, the component-wise best fit models were added to get the final additive models for total above-ground biomass (Cunia and Briggs 1984; Parresol 1999). Models 1 and 2 included D and H as a single predictor respectively for the biomass models of tree components and additive model according to Bi et al. (2004) as follows:

Model 1

$$Y_1 = e^{\beta_{10}} D^{\beta_{11}} + \varepsilon_1$$

$$Y_2 = e^{\beta_{20}} D^{\beta_{21}} + \varepsilon_2$$

$$Y_3 = e^{\beta_{30}} D^{\beta_{31}} + \varepsilon_3$$

$$Y_4 = e^{\beta_{40}} D^{\beta_{41}} + \varepsilon_4$$

$$Y_5 = e^{\beta_{10}} D^{\beta_{11}} + e^{\beta_{20}} D^{\beta_{21}} + e^{\beta_{30}} D^{\beta_{31}} + e^{\beta_{40}} D^{\beta_{41}} + \varepsilon_5$$

Model 2

$$Y_1 = e^{\beta_{10}} H^{\beta_{11}} + \varepsilon_1$$

$$Y_2 = e^{\beta_{20}} H^{\beta_{21}} + \varepsilon_2$$

$$Y_3 = e^{\beta_{30}} H^{\beta_{31}} + \varepsilon_3$$

$$Y_4 = e^{\beta_{40}} H^{\beta_{41}} + \varepsilon_4$$

$$Y_5 = e^{\beta_{10}} H^{\beta_{11}} + e^{\beta_{20}} H^{\beta_{21}} + e^{\beta_{30}} H^{\beta_{31}} + e^{\beta_{40}} H^{\beta_{41}} + \varepsilon_5$$

Where Y_1 to Y_4 implies the component (leaf, branch, bark and stem) and Y_5 indicates the total above-ground biomass (kg); β_{ij} denotes the regression coefficients. Here, the errors are intrinsically correlated for an individual tree and can be expressed as $\varepsilon = [\varepsilon_1, \varepsilon_2, \varepsilon_3, \varepsilon_4, \varepsilon_5]$ assuming ε equals 0 and the variance and covariance matrix ($\varepsilon\varepsilon'$) will be sum total (Σ).

The cross equation restrictions on the structural parameters compel each coefficient to be shared between two equations.

We also used D and H at combinations (D^2H and D^bH^b) for Models 3 and 4 according to Bi et al. (2004), Williams et al. (2005), Cienciala et al. (2013) and Battulga et al. (2013) in the following way:

Model 3

$$Y_1 = e^{\beta_{10}} (D^2H)^{\beta_{11}} + \varepsilon_1$$

$$Y_2 = e^{\beta_{20}} (D^2H)^{\beta_{21}} + \varepsilon_2$$

$$Y_3 = e^{\beta_{30}} (D^2H)^{\beta_{31}} + \varepsilon_3$$

$$Y_4 = e^{\beta_{40}} (D^2H)^{\beta_{41}} + \varepsilon_4$$

$$Y_5 = e^{\beta_{10}} (D^2H)^{\beta_{11}} + e^{\beta_{20}} (D^2H)^{\beta_{21}} + e^{\beta_{30}} (D^2H)^{\beta_{31}} + e^{\beta_{40}} (D^2H)^{\beta_{41}} + \varepsilon_5$$

Model 4

$$Y_1 = e^{\beta_{10}} D^{\beta_{11}} H^{\beta_{12}} + \varepsilon_1$$

$$Y_2 = e^{\beta_{20}} D^{\beta_{21}} H^{\beta_{22}} + \varepsilon_2$$

$$Y_3 = e^{\beta_{30}} D^{\beta_{31}} H^{\beta_{32}} + \varepsilon_3$$

$$Y_4 = e^{\beta_{40}} D^{\beta_{41}} H^{\beta_{42}} + \varepsilon_4$$

$$Y_5 = e^{\beta_{10}} D^{\beta_{11}} H^{\beta_{12}} + e^{\beta_{20}} D^{\beta_{21}} H^{\beta_{22}} + e^{\beta_{30}} D^{\beta_{31}} H^{\beta_{32}} + e^{\beta_{40}} D^{\beta_{41}} H^{\beta_{42}} + \varepsilon_5$$

Model 5

This model was generated from the component wise (leaf, branch, bark and stem) best fitted model that contained the combination of

$$Y = e^{\beta_{10}} D^{\beta_{11}} + \varepsilon_1,$$

$$Y = e^{\beta_{10}} H^{\beta_{11}} + \varepsilon_1,$$

$$Y = e^{\beta_{10}} (D^2H)^{\beta_{11}} + \varepsilon_1$$

$$\text{and } Y = e^{\beta_{10}} D^{\beta_{11}} H^{\beta_{12}} + \varepsilon_1$$

Model 5 was adopted, as component-wise it contained the best model, according to Magalhães and Seifert (2015), Zhao et al. (2015) and Dimobe et al. (2018). Concurrent estimation of all four components was done by collapsing the four component functions into a single function using logical flags, and the specified variance structure was using the nlme varComb() function of R package (version 3.1-118). With the starting values of the parameters, β were obtained from the non-linear component models, the aggregative model parameters were then estimated by maximum likelihood using the gnls function of the nlme package (Pinheiro et al. 2014) of R environment (R Core Team 2014) for Gaussian maximum likelihood.

Weighting functions for heteroscedasticity

Heteroscedasticity of the residuals of tree biomass or volume data usually corresponds to the power relation between tree size and residual variance. Heteroscedasticity of our biomass data was corrected by a power variance $\text{var}(\varepsilon_{ij}) = \sigma^2 \times I(W_j)^{2\delta}$ and was used in tree biomass models where $\text{var}(\varepsilon_{ij})$ is the residual of the model, δ requires to be estimated, $\hat{W}$ has estimated biomass of j component of each tree and σ^2 is a scaling factor (Fu et al. 2013; Zhao et al. 2019).

Model evaluation and validation

Data set A was used to develop component-wise models and the five candidate additive models. The fitness of the component models was evaluated by five goodness-of-fit statistics: the Akaike information criterion (AIC), the adjusted

coefficient of determination (adjusted R^2), residual standard error (RSE), mean absolute error (MAE) and root mean square error (RMSE) (Soares and Schaeffer-Novelli 2005; Mahmood et al. 2016). The biomass model with the lowest AIC, RSE, RMSE and MAE, and the highest adjusted R^2 was considered as best-fit. Residual distribution homogeneity and bias were checked visually by residual plots with LOESS regression lines overlaid on the plots.

The validation of the additive model was done by using a separated data set B (containing biomass of 17 individual trees) that was collected during the second visit. Model validation with a smaller number of the testing data sets may yield overfitting or underfitting of the derived model. Mugasha et al. (2013) reported that as few as 10 individual sample trees could be used to validate the biomass model. However, data set B of this study may not be able to capture the desired confidence in model validation considering the extent and variabilities (salinity, tidal inundation, vegetation types, etc.) of the Sundarbans Reserved Forest, which can be a source of uncertainty in model validation of this study.

The model fitting was evaluated by the model efficiency (ME), AIC, RMSE (%), MAE and the mean prediction error (MPE) values obtained from the independent biomass observations and the predicted biomass value of the additive model. Fitted values were compared against independent biomass observation (t -test) to test the validity of the model. Again, data set B was used to compare ME, MPE, bias (%) and mean absolute percentage error (MAPE) of the most commonly used allometric models that are used for mangroves (Brown 1997; Komiya et al. 2005; Chave et al. 2005; Chave et al. 2014; Ray et al. 2011). Regression line Y_p (in Y-axis) and Y_o (in X-axis) was drawn for the best-fit model to compare with other frequently used models according to Piñeiro et al. (2008). A 1:1 line for each model also helped to realise over- or underestimation of the predicted biomass (Sileshi 2014). The alpha level was always kept at 0.05 for statistical analysis.

Results

Biomass partitioning

Biomass allocations to three different components were 61.70 ± 10.31 , 24.12 ± 7.44 , 9.17 ± 6.64 and 5.0 ± 2.55 (mean $\pm$ sd) for the stem, branch, bark and leaf respectively. The biomass proportion of leaf, branch and bark showed a decreasing pattern with increasing diameter while stem showed an opposite relationship (Figure 2).

Biomass additive systems

Both DBH (D) and total height showed a non-linear trend for leaf, branch, bark and stem as displayed in Figure 3. Models for each component were significant ($p < 0.001$) with a range of adjusted R^2 value (0.6867–0.9884) (Table 1). The inclusion of total tree height in any form (alone or in combination with D) did not improve the evaluation statistics for leaves and branches, while the combination of D and H (D^p , H^p) worked better for model evaluation (Adj. R^2 , AIC, RMSE, MAE and RSE) statistics of stem and bark. Models considered with H as a single predictor variable, on the other hand, failed to meet the criterion for model selection of all components (Table 1).

Additive Models 1, 3, 4 and 5 showed an insignificant difference between the predicted and observed total above-ground

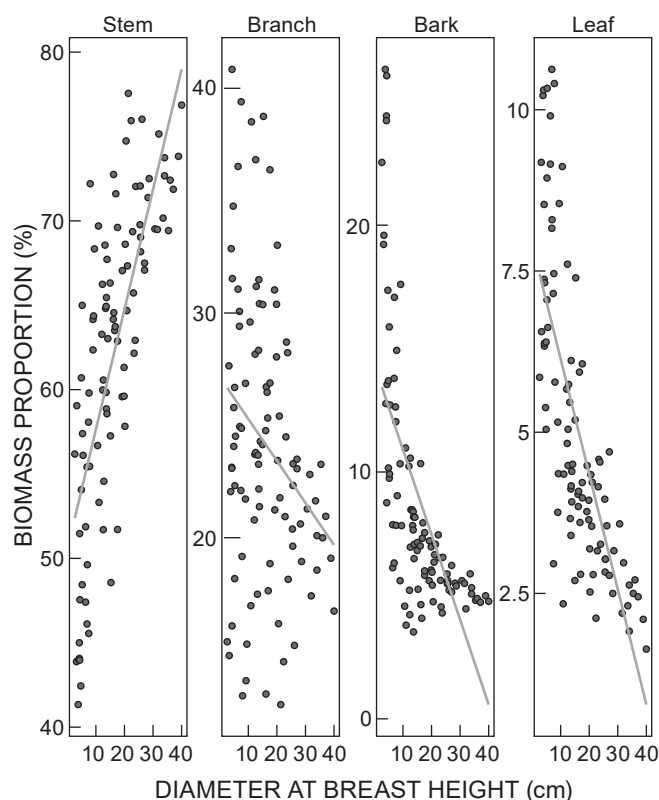


Figure 2: Relationship of the component mass fraction with DBH

biomass values (paired t -test, $p > 0.05$), while Model 2 showed a significant difference. Although all the additive equations showed an acceptable model efficiency value (0.535–0.984), the component-wise best-fit additive model (Model 5: Biomass = $0.0389D^{2.3773}H^{0.4178} + 0.0492D^{2.3027} + 0.0112D^{1.1144}H^{1.4572} + 0.0306D^{1.8507}$), yielded the highest efficiency value (0.984) with the lowest AIC (116.797), RMSE% (1.987), MPE (1.374) and MAE (12.938) values. Additive Model 4 was a very close competitor of Model 5 having a close model efficiency (0.982) and MAE (13.063) values, and secured the second lowest AIC (118.392), RMSE% (2.211) and MPE (1.439) values. The other three models (Models 1, 2 and 3) displayed lower model efficiency value (0.972; 0.535; 0.981) with higher AIC (122.877; 173.942; 119.732), RMSE % (2.85; 13.872; 1.152), MAE (18.185; 81.634; 15.583) and MPE (1.742; 7.375; 1.497) values respectively (Table 2). However, the graphical presentation of the studied additive models also indicated that diameter alone (Model 1) can explain the relationship, but Model 5 was the best-fit (Figure 4). The best model (Model 5) yielded the component-wise regression line (Figure 5a). The dots of the component were close to the 1:1 line (Figure 5b).

Evaluation of existing biomass equation

Our additive Model 5 showed the highest model efficiency value (0.9839) and lowest MPE (1.2465), MAPE (13.6876) and bias (1.9865%) compared to the common biomass models that are frequently used for biomass estimation of mangroves. However, the common biomass model of Chave et al. 2005 and Mahmood et al. (2019) were close competitors of the derived additive model of *H. fomes* (Table 3).

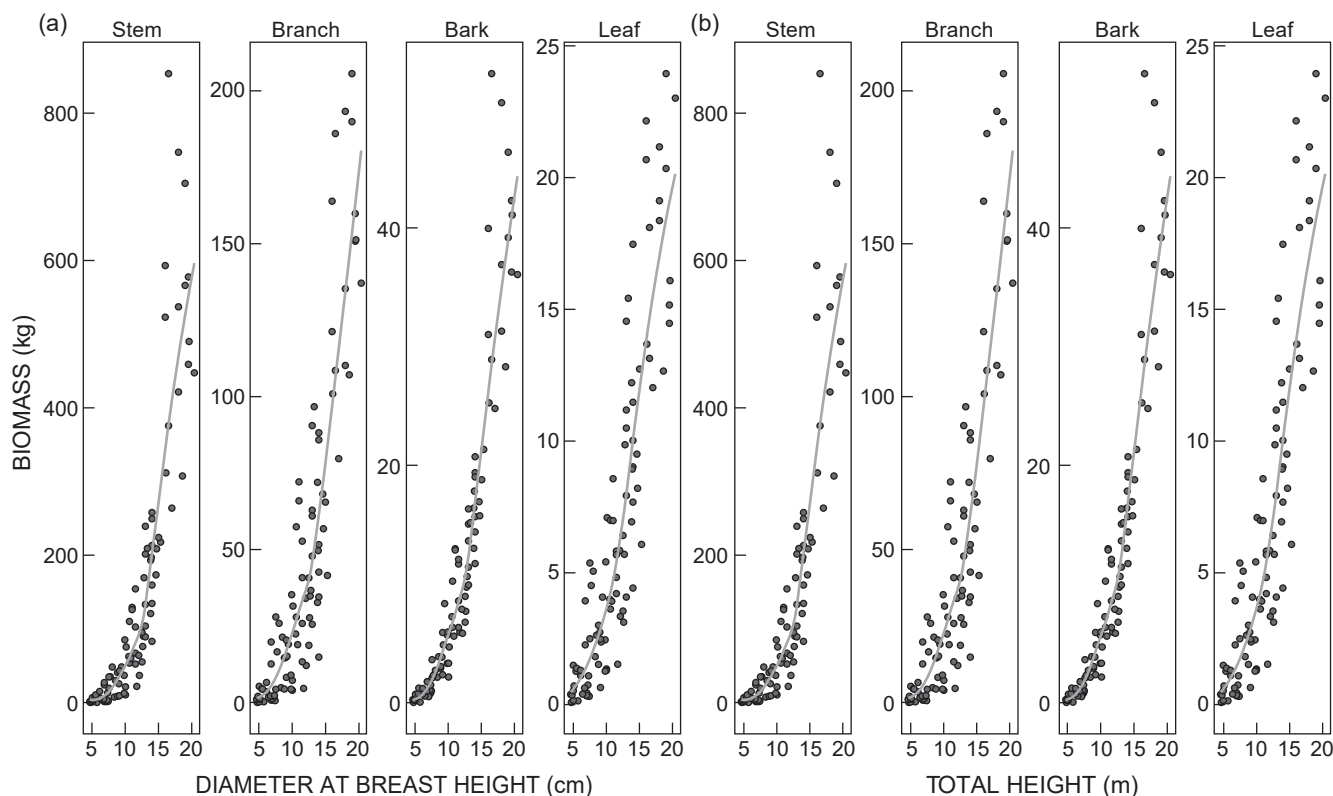


Figure 3: Relationship between leaf, branch, bark and stem biomass with (a) DBH and (b) H respectively

Discussion

Accurate estimation of total biomass and biomass partitioning among the components of trees are prerequisite for studying the photosynthate allocation to plant growth, forest productivity, nutrient and carbon cycling, and stock assessment (Kozłowski et al. 1991; Mahmood 2004; Bi et al. 2015). Our study showed a higher proportion of leaf, branch and bark biomass for the trees with a lower diameter. Conversely, a higher proportion of stem biomass was observed for trees with higher diameter. Collectively, stem biomass had the greatest contribution (approximately 41–78%), whereas the leaf represents the lowest portion (2–11%). Similar results were obtained for *Rhizophora apiculata* (Ong et al. 2004), *R. mangle*, *Laguncularia racemosa* and *Avicennia germinans* (Sherman et al. 2003), *Kandelia candel* and *Excoecaria agallocha* (Mahmood et al. 2015; Mahmood et al. 2016). Biomass partitioning among the tree components is highly variable by geographical location and microclimate (Tomlinson 1986), age, plant size (height and diameter) (Clough et al. 1997; Peichl and Arain 2007), species, tree architecture at different growing stages (sapling, pole and tree), and competition for the common resources like light, water, nutrients, etc. (Zeide 1995; Mahmood 2004; Wang et al. 2013; Mensah et al. 2016).

Species specific biomass models usually include D and H as predictor variables to consider the variabilities of tree size (Picard et al. 2012). However, models having only the D as a single predictor variable were the best-fit model for leaf and branch. Biomass models with D as a single predictor variable

are more convenient for biomass estimation in the field (Chave et al. 2014). The best-fit model of stem and bark contained a combination of D and H ($D^b H^c$) that indicates a single predictor variable has failed to capture the variabilities among the size of the sample trees in terms of their diameter and height. The inclusion of total height as an additional parameter for estimating the stem biomass of mangroves can minimise the overestimation (Ketterings et al. 2001; Feldpausch et al. 2012). The goodness of fit statistics was poor for biomass models of leaf and branch in this study. In comparison, the fit statistics (Adj. R^2) for leaf and branch of *Kandelia candel* and *Excoecaria agallocha* from the Sundarbans Reserved Forest (Mahmood et al. 2015; Mahmood et al. 2016) were similar to those for this study. Therefore it can be expected that the best-fit models of leaf and branch will be able to satisfactorily estimate biomass. The biomass of leaves and branches is highly influenced by internal and external factors, which varies naturally in comparison with the biomass proportion of other components (Satoo and Madgwick 1982; Sanquetta et al. 2015). This could be the reason to get poor goodness-of-fit statistics for leaf and branch models compared to stem and bark of this species.

Additivity in the biomass model is a desirable characteristic for predicting component as well as total above-ground biomass (Parresol 2001; Dong et al. 2015; Riofrio et al. 2015). Our study reveals that tree diameter alone can be used as an indispensable predictor of biomass models (Figure 4), findings similar to those of Henry et al. (2011) and Vahedi et al. (2014). Moreover, the additive Models 1, 3, 4 and 5 (having D alone and a combination of D and H) showed an insignificant

Table 1: Regression coefficients with goodness-of-fit statistics of the component-wise biomass allometric equations

Model	Component	Regression coefficients			Evaluation statistics			
		a (SE)	b (SE)	c (SE)	Adj. R ²	AIC	RSE	MAE
W ~ a * D ^b	Leaf	0.0343 (0.0051)	1.8056 (0.051)		0.9000	247.3797	0.0231	0.1110
W ~ a * H ^b		0.0011 (0.00056)	3.330 (0.196)		0.6925	353.2762	0.0497	1.198
W ~ a * (D ² H) ^b		0.0181 (0.0034)	0.7043 (0.0222)		0.8955	264.2498	0.0299	0.0063
W ~ a * D ^b * H ^c		0.0415 (0.0096)	1.9243 (0.1212)	-0.2131 (0.1983)	0.8977	254.2435	0.0221	0.1098
W ~ a * D ^b	Branch	0.0495 (0.0071)	2.2952 (0.0499)		0.9382	509.3821	0.0273	1.2019
W ~ a * H ^b		0.0003 (0.0002)	4.4378 (0.2532)		0.7418	641.5938	0.08505	11.2805
W ~ a * (D ² H) ^b		0.0217 (0.0045)	0.8961 (0.0242)		0.9503	538.8689	0.0509	0.0353
W ~ a * D ^b * H ^c		0.0726 (0.0157)	2.5308 (0.1152)	-0.4245 (0.188)	0.9240	512.6489	0.0226	1.1396
W ~ a * D ^b	Stem	0.0586 (0.0042)	2.6002 (0.0253)		0.9883	558.9729	0.0132	2.0601
W ~ a * H ^b		0.00016 (0.00008)	5.1189 (0.2146)		0.6867	771.8468	0.0659	39.3786
W ~ a * (D ² H) ^b		0.0229 (0.0023)	1.0173 (0.0118)		0.9785	578.4053	0.0336	0.2269
W ~ a * D ^b * H ^c		0.0418 (0.0051)	2.3945 (0.0575)	0.3713 (0.0992)	0.9884	553.5616	0.0173	2.0230
W ~ a * D ^b	Bark	0.0399 (0.0068)	1.9448 (0.0543)		0.9677	331.2225	0.0843	0.0066
W ~ a * H ^b		0.00098 (0.00023)	3.6151 (0.0972)		0.8425	347.0696	0.0169	1.7056
W ~ a * (D ² H) ^b		0.021 (0.0028)	0.7564 (0.0151)		0.9799	281.8299	0.0504	0.0738
W ~ a * D ^b * H ^c		0.0104 (0.0019)	1.0879 (0.0774)	1.5175 (0.145)	0.9696	266.5119	0.0201	0.0799

a, b and c = model coefficients with SE (standard error) in parentheses

D = diameter at breast height (cm)

H = total height (m)

Adj. R² = adjusted coefficient of determination AIC = Akaike information criterion RSE = residual standard error MAE = mean absolute error RMSE = root mean square error**Table 2:** Coefficients with standard error (SE) and goodness-of-fit statistics of the additive allometric equations

Model	Regression coefficients						Evaluation statistics			
	Leaf			Stem			Bark			
	a (SE)	b (SE)	c (SE)	a (SE)	b (SE)	c (SE)	a (SE)	b (SE)	c (SE)	Model efficiency
Model 1	0.031 (0.004)	1.8462 (0.0446)		0.0495 (0.0064)	2.3009 (0.0445)		0.0538 (0.0037)	2.6282 (0.0238)		0.9722
							0.0346 (0.0054)	1.9927 (0.0486)		
Model 2	0.00059 (0.00027)	3.5399 (0.1762)		0.00032 (0.00017)	4.4473 (0.2076)		0.001 (0.0002)	3.5979 (0.0841)		0.5347
							0.0213 (0.0025)	0.7548 (0.0133)		
Model 3	0.0154 (0.0025)	0.7254 (0.0193)		0.0206 (0.0036)	0.9042 (0.0205)		0.0214 (0.002)	1.0247 (0.0107)		0.9808
							0.0112 (0.0018)	1.1145 (0.0679)		
Model 4	0.0352 (0.0074)	1.9351 (0.1086)	-0.1534 (0.1792)	0.0643 (0.0130)	2.4656 (0.1064)	-0.2944 (0.1752)	0.0391 (0.0045)	2.3816 (0.0547)	0.4101 (0.0932)	0.9823
							0.0389 (0.0044)	2.3773 (0.0544)	0.4178 (0.0926)	
Model 5	0.0306 (0.004)	1.8507 (0.0451)		0.0492 (0.0064)	2.3027 (0.0447)		0.0389 (0.0044)	2.3773 (0.0544)	0.4178 (0.0926)	0.9839

a, b and c = model coefficients with SE (standard error) in parentheses

AIC = Akaike information criterion

RMSE % = per cent root mean square error

MAE = mean absolute error

MPE = mean prediction error

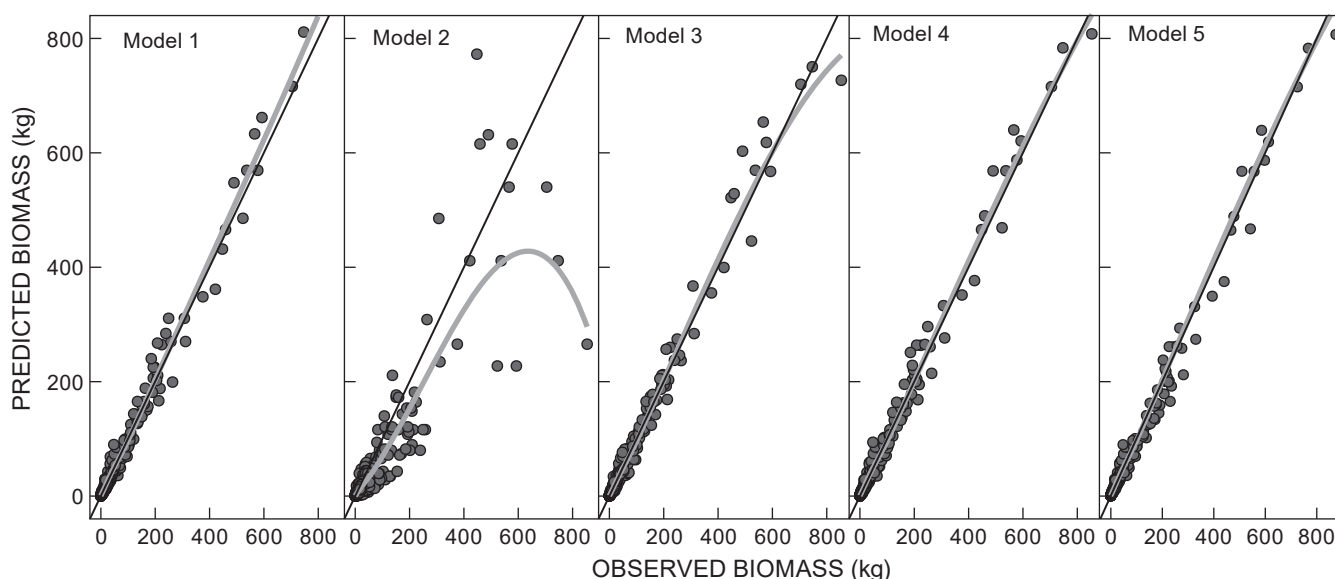


Figure 4: Graphical illustrations of the additive models through scatterplots of the observed (X-axis) and the predicted (Y-axis) biomass values. The black line denotes 1:1 equivalence

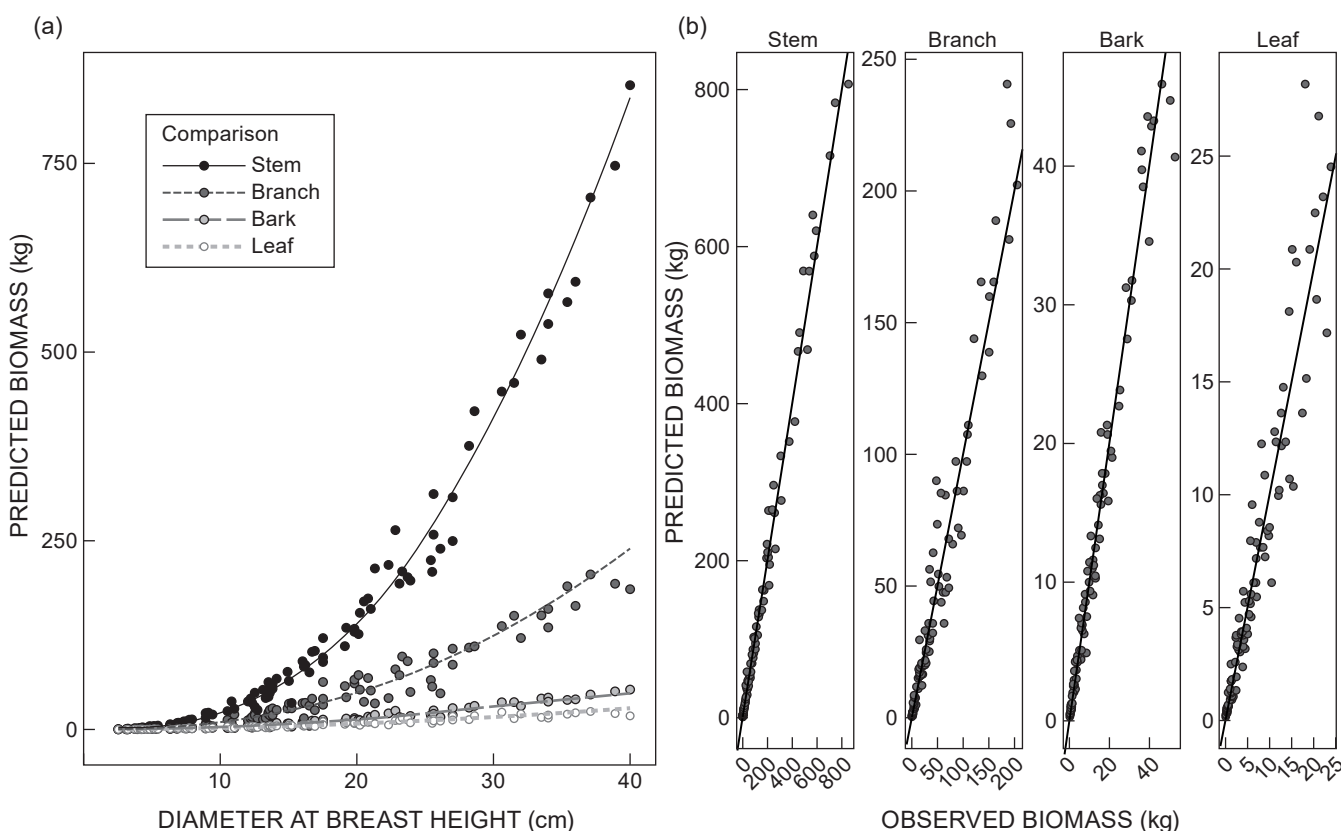


Figure 5: Component-wise relationship of the best fit model (a) with DBH; (b) Component-wise scatterplots of the observed (X-axis) and the predicted (Y-axis) biomass values of the best fit model. The black line denotes 1:1 equivalence

difference between the predicted and observed biomass values. Model 2 (H as single predictor) showed a significant difference. This could be the reason we observed least biomass prediction using Model 2 compared to other models.

But, Model 4 was a close competitor of Model 5 considering the model evaluation statistics, which can also be used for total above-ground biomass estimation (Magalhães and Seifert 2015; Zhao et al. 2015; Dimobe et al. 2018).

Table 3: Comparison with some existing common biomass equations usually used for mangroves biomass estimation

Source model	Predictor	Model efficiency	MPE	Bias	MAPE
Brown (1997)	DBH	0.9452	2.2977	−11.5511	16.6241
Komiyama et al. (2005)	DBH	0.5815	6.3475	−47.2914	57.8171
Chave et al. 2014	DBH, height and wood density	0.9384	2.4345	−11.3548	16.0644
Chave et al. 2005	DBH, height and wood density	0.9633	1.8798	−4.2263	13.4661
Ray et al. 2011	DBH, height and wood density	0.1738	8.9185	60.2184	122.0214
Mahmood et al. 2019	DBH, height and wood density	0.9817	1.3277	4.6402	15.7294
Best-fit additive model	DBH and height	0.9839	1.2465	1.9865	13.6876

DBH = diameter at breast height MPE = mean prediction error MAPE = mean absolute percentage error

Our best-fit additive model (Model 5) exhibited higher efficiency in biomass estimation compared to frequently used pantropical models (Table 3). The model of Mahmood et al. (2019) was a very close competitor for biomass estimation of *H. fomes* as only this local model included this species. Among the others, the model of Chave et al. (2005) yielded an acceptable approximation. The species and site specific biomass models generate less uncertainty than pantropical models, as evidenced in a biomass study from Indonesia (Basuki et al. 2009; Manuri et al. 2014; Maulana et al. 2016), Sarawak (Kenzo et al. 2009), Columbia (Alvarez et al. 2012), south-western Amazon (Goodman et al. 2013), Gabon (Ngomanda et al. 2014) and Vietnam (Nam et al. 2016). Therefore we can recommend using the derived best-fit additive model (Model 5) to estimate the biomass of *H. fomes* in the Sundarbans Reserved Forest instead of using other common models if the size range falls within the data material of our study (Nam et al. 2016).

Conclusions

The derived best-fit additive biomass model using the non-destructive method shows higher efficiency in biomass estimation compared to the other regional and pantropical models. Our developed model will therefore have implications for forest inventory and for the Measurement, Reporting and Verification Section of the REDD+ programme in Bangladesh. The findings of this study will contribute to climate change mitigation programmes in Bangladesh. Moreover, this non-destructive method can also be used for deriving additive biomass models for other species with greater accuracy compared to the available regional and pantropical models.

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