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An allometric equation for estimating stem biomass of *Acacia auriculiformis* in the north-eastern region of Bangladesh

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Tree biomass plays an important role in sustainable management and in estimating forest carbon stocks. The objective of this study was to select the best model for measuring stem biomass of *Acacia auriculiformis* in the study area. Data from five hillocks and 120 individual trees from each hillock were used in this study. Twelve different forms of linear, power and exponential equations were compared in this study to select the best model. Two models (VI and XI) were selected based on R^2 , adjusted R^2 , the Akaike information criterion, F-statistics and the five assumptions of linear regression. Model VI was discarded based on the Durbin-Watson value of autocorrelation of the residuals, then the ARIMA (2, 0, 1) model was used to remove the autocorrelation from the model and the final bias-corrected model XI was derived. The model was validated with a test data set having the same range of DBH and stem height of the training data set on the basis of linear regression, Morisita's similarity index, and E-test for mean difference between predicted and expected biomass. A comparison between the best logarithmic and non-linear allometric model shows that the non-linear model produces systematic biases and overestimates stem biomass for larger trees. The overall results showed that the bias-corrected logarithmic model XI can be used efficiently for estimating stem biomass of E. E-test for mean difference between predicted and expected biomass.

Keywords: Acacia auriculiformis, allometry, Bangladesh, stem biomass

Introduction

High levels of carbon dioxide are one of the major threats to the Earth where climate change is concerned. Carbon dioxide can be released into the Earth's atmosphere either by combustion of fossil fuels or by removal/transformation of biomass through deforestation. Climate change during the last decades has increased the need for information on the amount of forest biomass in different regions for climate policy definition. This requires reliable estimation of carbon pools in forest ecosystems. The estimation of above- and below-ground biomass pools is of great importance for the characterisation of structure and function of ecosystems. Quantitative information on biomass helps not only to understand energy accumulation within forest ecosystems (Chave et al. 2005) but also serves as an ecological indicator for sustainability. These estimates can also help to assess forest productivity, carbon pools, and carbon sequestration in biomass components. The determination of aboveground tree biomass helps to ensure sustainable planning of forest resources, and foresters apply different methods to obtain such estimations (Zianis and Mencuccini 2004). For scientific purposes, standing biomass is a fundamental variable in several ecological and ecophysiological models. Estimation of aboveground biomass is an essential aspect of studying carbon stocks, and the effects of deforestation and carbon sequestration on the global carbon balance. It also provides valuable information for many global issues. It can also be a useful measure for comparing structural and functional attributes of forest ecosystems across a wide range of environmental

conditions (Brown et al. 1989). Most of the studies estimating aboveground biomass concentrate on stem biomass because it constitutes around 83% of the total aboveground biomass, and the biomass of tree compartments (leaves, reproductive parts, twigs, branches, trunks and prop roots) constitutes the remainder (Zhou and Hemstrom 2009).

Since measuring tree biomass in the field is extremely time consuming and potentially limited to a small tree sample size, rapid and easily implementable methods are needed for the assessment of stem biomass. Although the destructive (direct) method of biomass estimation is more precise than the non-destructive (indirect) method, it is very time consuming, labour intensive, eco-unfriendly and depends on very small samples. That is why allometric equations and theoretical relationships for estimating stem biomass, based on non-destructive methods, have been gaining popularity over the last two decades.

For the development of an allometric equation, empirical relationships between stem biomass and some predictive biometric variables (most frequently: DBH and height) are used (Curtis 1967, Zianis and Mencuccini 2004). The most commonly used forms of allometric functions are polynomials, power and their combinations. Polynomials have the disadvantage that their shapes are not biologically interpretable. The power function ($y = ax^b$) form is widely used in biological sciences particularly for tree biomass estimation (Ketterings et al. 2001, Niklas 2006). Traditionally, allometric models are developed by fitting a

linear relationship between log-transformed diameter and biomass data. As opposed to the traditional approach, non-linear models are increasingly fitted directly to untransformed diameter and biomass data (Mascaro et al. 2011). Although the log-transformed linear equation is mathematically equivalent to the power equation, they are not identical in the statistical sense (Zar 1968). Moreover, fitting linear models on log-transformed data leads to results that are biased and misleading. Such models operate in geometric rather than arithmetic space and the statistical analysis should be performed on the original scale (Packard and Boardman 2008). In this context, the non-linear approach may be favoured in part because it avoids the need for transformation and back transformation. However, in practice, the default non-linear technique assumes homogeneity of errors that cannot be safely assumed with most allometry data. Ideal tree allometric data are strongly heteroscedastic and exhibit increasing variation in biomass with increasing diameter. When non-linear fitting techniques are applied without accounting for heteroscedasticity, the resulting models may include substantial biases even while maintaining high r^2 and low mean square errors. Moreover, fitting non-linear biomass allometry models assuming additive errors can produce systematic biases in estimates for smaller diameter trees (Mascaro et al. 2011). However, many allometric characteristics of organisms are multiplicative by nature and thus fitting models to log-transformed data is perfectly acceptable because accounting for proportional rather than absolute variation is most important (Kerkhoff and Enquist 2009).

To cope with the continuous population pressure and increasing demands for timber and fuel wood, Acacia auriculiformis was introduced to Bangladesh from Australia during the 1980s (Das and Alam 2001). It is a fast-growing, short-rotation and nitrogen-fixing species that can provide moderate graded timber and fuel wood. Considering its performance, A. auriculiformis has been planted all over the country including road verges and denuded hills. Therefore, the accurate estimation of its stem biomass is crucial for many applications, from the commercial exploitation of timber to the global carbon cycle, which requires the development of an allometric equation. We can use a national or regional protocol for estimating biomass of this species but site- and species-specific equations are preferred because different species may differ substantially in their architecture and wood properties. This may propagate erroneous estimation of the biomass. The allometric biomass equation of this frequently planted species is virtually unavailable. With the current trend of carbon trading for the financial interest of Bangladesh, the accuracy in biomass estimation is more than an academic interest.

A substantial portion of the total afforested area (16%) is located in the north-eastern region of Bangladesh. Although there is no scientific record yet, our experience is that *A. auriculiformis* covers a considerable portion of the forest cover of this region. It is frequently planted in home gardens, next to roads, on institutional premises, and on bare forest lands. Shahjalal University of Science and Technology (SUST) is the largest educational institute of the north-eastern region of Bangladesh. It is a green campus enriched with a diversity of more than 30 tree species

dominated by *A. auriculiformis*. The main goal of our study was to develop an allometric equation for *A. auriculiformis* that will help to estimate stem biomass of the species planted in the areas that fall within the same microclimatic zone of SUST, Bangladesh.

Materials and methods

Study area

The study was conducted at SUST, Sylhet, which is located between 24.8917° N and 91.8833° E, in the north-eastern region of Bangladesh (Figure 1). Its area is 129.5 ha. It falls within the monsoon climatic zone with annual average highest temperatures of 23 °C and average lowest temperature of 7 °C. Mean annual rainfall is 3 334 mm (SCC 2011). This humid subtropical climate supports diverse trees. The geological formation of this area dates from the Pleistocene era and the soil type is slightly acidic (Banglapedia 2006). The five hillocks of the campus are widely planted with a number of tree species, mostly with A. auriculiformis because of its ability to grow on very poor soil. It is a tropical arborescent species native to northern Australia and southern New Guinea. It is widely planted in different plantation forests in a number of countries with tropical environments (Sedgley et al. 1992). At SUST, most of the A. auriculiformis are mature with an average DBH of 26.17 cm and stem height of 4.29 m. The heartwood, which is yellowish-brown in colour, occupied an average 76-85% of the cross-sectional area. The wood is moderately hard and moderately dense, with shallowly interlocked grain and medium texture. Wood structure is diffused porous. In the Indian plantations mean moisture content of 8- to 13-year-old A. auriculiformis trees is 48.67% (Shukla et al. 2007).

Field data collection

For the study, the individual trees were systematically sampled sequentially following predesigned transect-lines. A total of 600 individuals (120 per hillock) of A. auriculiformis were selected, and DBH (cm), stem height (m), and wood samples were collected from these trees. A total of 13 trees at each 50-tree interval were selected for measurement of the form factor. For estimating the wood density, sample cores were collected to a depth of half the DBH (1.37 m) using an increment borer. Sunnto Clinometer, tree caliper, and Haga altimeter were used for measuring stem height, DBH, and form factor respectively. Data of DBH (cm), height (m), form factor, and wood samples from an additional 17 trees were collected and used as a test data set for validating the models. All the collected wood samples were measured in the field for their fresh weights, and oven-dried weights were taken after drying them in 105 °C for 72 h.

Data analysis

Procedure of stem biomass estimation Wood density (ρ) was calculated following King et al. (2006):

The stem biomass was estimated following King et al. (2006):

$$SB = ff \frac{\pi}{4} \rho D^2 H$$

where SB = stem biomass (kg), ff = form factor, defined as the ratio of the volume of the tree to the volume of a cylinder with the height and DBH of the tree, ρ = wood density (kg m⁻³), D is the diameter at breast height (cm), and H is the stem height (m).

Model development and evaluation

Among the different predictive biometric variables, we selected the most frequently used variables, i.e. DBH, stem height, and their combinations. While fitting these variables in the regression models considering 'stem biomass' as a response variable, we tested them for linear, power and exponential regression equations. The following 12 models were tested to find the best allometric relationship between the response and predictors (Table 1).

The following five regression assumptions were used to judge the consistency of the models (Robinson and Hamann 2011):

- (1) the linear model captures the relationship
- (2) error terms are independent
- (3) error terms have constant variance
- (4) error terms are normally distributed
- (5) the sample represents the population from which it was drawn.

Diagnostic plots were used to check these regression assumptions, except for assumption 2. The Durbin-

Watson (d value) test for autocorrelation and a diagnostic plot (residual vs previous residuals) were used to check assumption 2. In addition to the above assumptions, R^2 , adjusted R^2 , F-statistics, the Akaike information criterion (AIC) and d values were used to select the best model. There was a good probability of having serial autocorrelation within the residuals of the best models, based on the assumptions and all criteria except assumption 2. Therefore, if a model should show serial autocorrelation among the residuals, we would apply Autoregressive integrated moving average (ARIMA) regression models. Predictions based on ARIMA models comprise the following stages (Cryer and Chan 2008):

Table 1: Different models used in this study

Model no.	Structure
iio.	Stem Biomass (kg) = a + b * DBH (cm)
II	Stem Biomass (kg) = $a + b * DBH (cm) + c * Stem Height (m)$
Ш	Stem Biomass (kg) = $a + c$ * Stem Height (m)
IV	ln(Stem Biomass (kg)) = a + b * ln(DBH (cm))
V	ln(Stem Biomass (kg)) = a + c * ln(Stem Height (m))
VI	ln(Stem Biomass (kg)) = a + b*ln(DBH (cm)) + c*ln(Stem Height (m))
VII	In (Stem Biomass (kg)) = $a + b * (DBH (cm))$
VIII	In (Stem Biomass (kg)) = $a + c$ * (Stem Height (m))
IX	In (Stem Biomass (kg)) = $a + b * (DBH (cm)) + c * (Stem Height (m))$
X	Stem Biomass (kg) = $a + b*(DBH (cm)*Stem Height (m))$
ΧI	ln(Stem Biomass (kg)) = a + b*In ((DBH (cm)*Stem Height (m))
XII	In (Stem Biomass (kg)) = $a + b^*$ ((DBH (cm)*Stem Height (m))

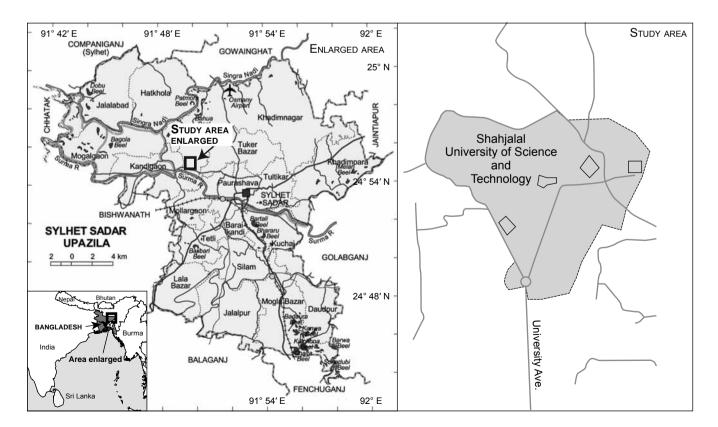


Figure 1: Map of the study area (source of lefthand map: Banglapedia 2006)

- · model identification
- · parameter estimation
- · diagnostic checking.

We completed the three steps with the forecast package version 2.19 for R (Hyndman 2011). For model identification the *auto.arima* code was used. This procedure returns the best ARIMA model according to either the AIC, corrected AIC or Bayesian information criterion value. The program conducts a search over the possible model within the order (p, d, q) of constraints provided where, p is the number of autoregressive terms, d is the number of non-seasonal differences, and q is the number of lagged forecast errors. After selecting the best order (p, d, f), the *Arima* code estimates the parameters (intercept and slope) with other related statistics. The *tsdiag* code was used to draw diagnostic plots for the desired model.

For model identification we used the power and exponential equations, which were transformed into their natural logarithmic (In) equivalent of the usual allometric forms. Parameters in the original allometric equations (power and exponential) were estimated by regressing In(stem biomass) on In(predictors) and then back-transforming them to the arithmetic scale (Zar 1968, Smith 1984). There is an inherent bias in this process that detracts from the accuracy of associated predictions. For correcting this bias from the estimation of the model, we multiplied the obtained result by e^{ε} , where ε is the random error term. The regression residuals are normally distributed (based on normal Q-Q plot) and ε was obtained from the following equations (Newman 1993):

 $\varepsilon = \frac{\text{Mean square of the error (MSE) from the regression}}{2}$

$$MSE = \frac{\left(\sum_{i=1}^{N} e_i^2\right)}{N-3} = \frac{\sum_{i=1}^{N} e_i^2 \left(\ln Y_i - \ln \hat{Y}_i\right)^2}{N-3}$$

where e_i^2 = regression residuals from the *i*th data pair squared, and N = total number of pairs.

The performance of the relevant selected model was assessed using a test data set containing DBH (cm), stem height (m), and stem biomass (kg) (n = 17).

Model validation

For validating the models, we regressed the observed stem biomass (SB_t) of the test data against the predicted stem biomass data (\widehat{SB}_t) as: $SB_t = a + b \times \widehat{SB}_t$. To judge the consistency of the model, we conducted a *t*-test to measure whether the observed intercept and slope differed significantly from the expected intercept and slope (Amaro 1998). As a measure of distance between observed and predicted values, we calculated Morisita's (1959) dissimilarity index (D_M):

$$D_{M} = \frac{\frac{1}{n} \sum_{i=1}^{n} (y_{i} - y_{i}^{p})^{2}}{\frac{1}{n} (\sum_{i=1}^{n} y_{i}^{2} + (\sum_{i=1}^{n} y_{i}^{p})^{2})}$$

where y_i = observed stem biomass of the test data and y_i^p = predicted stem biomass

Note that $1 - D_{\rm M}$ is essentially Morisita's measure of niche overlap or similarity (Smith and Rose 1995). Moreover, to assess the performance of the models at the stand level, we conducted a Welch two-sample t-test to find out if there was any significant mean difference between the observed and predicted stem biomass of A. auriculiformis.

We developed a best fit non-linear least square model using the *nls* code of R (R Development Core Team 2011) for the stem biomass. This model was then compared with the relevant logarithmic model with bias correction.

Results and discussion

The range of DBH and stem height data for the model validation data set fell within the boundary of training data set (Table 2), so it could be used for proper model validation. From Figure 2, it was evident that both DBH and stem height of the training data set were not normally distributed (for DBH: Shapiro-Wilk p=4.49e-07; for stem height p=5.999e-05 at $\alpha=0.05$). Figure 3 shows that the test data set was normally distributed (for DBH: Shapiro-Wilk p=0.496; for stem height p=0.318 at $\alpha=0.05$).

Model development

For the development of the best model, we tried 12 different equation forms. Some of the combinations of independent variables were univariate and some were bivariate. For the univariate models we estimated only intercepts (a) and regression coefficients (b or c), but for the bivariate models we estimated regression coefficients of the respective explanatory variables along with their intercepts (Table 3).

Although the estimates showed that all intercepts and regression coefficients for all the models were significant, the values of R^2 , adjusted R^2 , AlC and F-statistics indicated that models VI and XI were better than the others. Between these two models, it might seem that model VI was better than model XI. To avoid any confusion, we checked the five regression assumptions to select the best model. A good model should conform to all valid statistical assumptions (Robinson and Hamann 2011).

Assumption 1: The linear model captures the relationship In order to check whether the linear model captures the relationship, we plotted regression residuals versus fitted value with a smooth curve superimposed on it (top left panel

 Table 2: Descriptive statistics for the different variables of Acacia auriculiformis at SUST Campus

Variables	N	Minimum	Maximum	Mean	SD	Skewness	Kurtosis
DBH (cm)	600	10.10	54.70	26.18	8.20	0.483	-0.085
Stem height (m)	600	1.30	8.40	4.30	1.33	0.302	-0.199
DBH validation (cm)	17	17.30	33.80	26.44	4.54	-0.551	-0.175
Stem height validation (m)	17	2.70	6.30	4.76	1.05	-0.329	-0.982

of Figures 4 and 5). In these figures we looked for evidence of curvature and outliers. Figure 5 shows a comparatively smooth straight line compared to Figure 4. A bit of curvature in the Figure 4 indicates a possible substantial local bias in the model, which contradicts the first assumption above. According to the assumption 1, model XI was judged to be better than the model VI. These residuals were not standardised, therefore the possibility of local bias of model VI alone could not prove it as invalid (Robinson and Hamann 2011).

Assumption 2: Error terms are independent

If any model does conform to assumption 2, then its standard error will be wrong and the test and confidence interval will be unreliable. The basic diagnostic plot cannot check assumption 2 because it doesn't have the option to check the independence of the error terms. To check this assumption, the Durbin-Watson test for autocorrelation among the residuals showed that for model VI d=0.1194 (autocorrelation = 0.94) and for model XI d=1.425 (autocorrelation = 0.285). For two independent variables, n=600 and $\alpha=0.01$; the critical lower and upper limits of d were 1.50 and 1.58, respectively. Thus, we could say

that model VI was more positively correlated than model XI (Figure 6). However, the fact was that the residuals of model XI were also slightly positively correlated. This problem would need attention.

Assumptions 3 and 4: The error terms have constant variance and are normally distributed

We plotted the normal Q-Q plot (the top right panel of Figures 4 and 5) of the standardised residuals against the normal distribution in order to check whether the error terms have constant variance and were normally distributed. It was clear that all points in Figure 4 were not in a straight line. Departures from a straight line in this plot indicate the non-normality of the residuals or non-constant variance, or both (Robinson and Hamann 2011). According to largesample theory, modest departures from a straight line are often acceptable, which is found in the case of Figure 5. Moreover, to check assumption 3, we plotted the square root of the absolute residuals against the fitted values, along with a smooth line (the bottom left panel of Figures 4 and 5). In this plot, deviations from a horizontal line signify heteroskedasticity, which was a violation of the third assumption and is more evident in Figure 4 than in Figure 5.

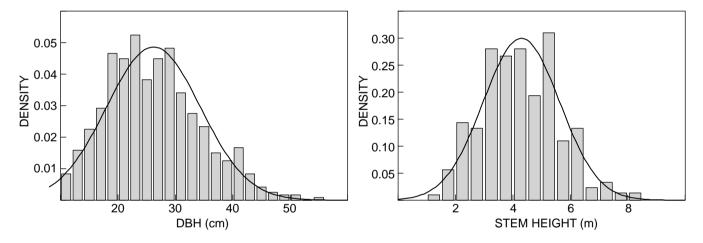


Figure 2: Diameter at breast height (DBH; cm) and stem height (m) distributions of the training (model fitting) data set

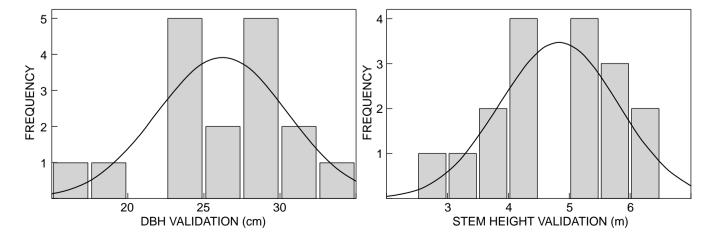


Figure 3: Diameter at breast height (DBH; cm) and stem height (m) distributions of the validation (test) data set used in the study

Assumption 5: The sample represents the population from which it was drawn

The bottom-right panel of Figures 4 and 5 shows a plot of the leverage of the observations against the standardised residuals, which are the two components of Cook's distance. Cook's distance >1 contradicts assumption 5 (Robinson and Hamann 2011). It is evident from both figures that the

sample represents the population from which it was drawn. However, Figure 5 supports assumption 5 more appropriately than Figure 4.

Fixing the problems of autocorrelation in model XI

The problems with autocorrelation can be fixed in two ways: (1) by adding new variables to the model (usually a lurking

Table 3: Estimated parameters of the different models tested in the study

Model	а	b	С	R ²	Adjusted R ²	AIC	F-statistic
	-157.3487***	10.5088***	_	0.8048	0.8045	6205.033	2465
II	-99.742***	_	50.632***	0.4927	0.4919	6778.014	580.8
III	-210.2582***	8.5299***	24.3780***	0.8905	0.8901	5860.287	2427
IV	-3.62978***	2.51050***	_	0.8864	0.8862	223.3344	4667
V	-1.57869***	_	2.03508***	0.6076	0.6069	967.2375	925.8
VI	-3.296178***	1.959321***	1.022794***	0.9971	0.9971	-1985.766	1.044e+05
VII	1.919372***	0.096303***	_	0.8402	0.8399	428.294	3143
VIII	2.32084***	_	0.49343***	0.5817	0.581	1005.493	831.7
IX	1.3493404***	0.0749822***	0.2626409***	0.9638	0.9637	-460.7517	7947
Χ	-56.20103***	1.47551***	_	0.9294	0.9293	5595.025	7869
XI	-2.41952***	1.48460***	_	0.9674	0.9673	-525.6211	1.775e+04
XII	2.93946***	0.01273***	_	0.8601	0.8599	348.2685	3677

Significance codes: 0 '*** 0.001 '** 0.01 '*

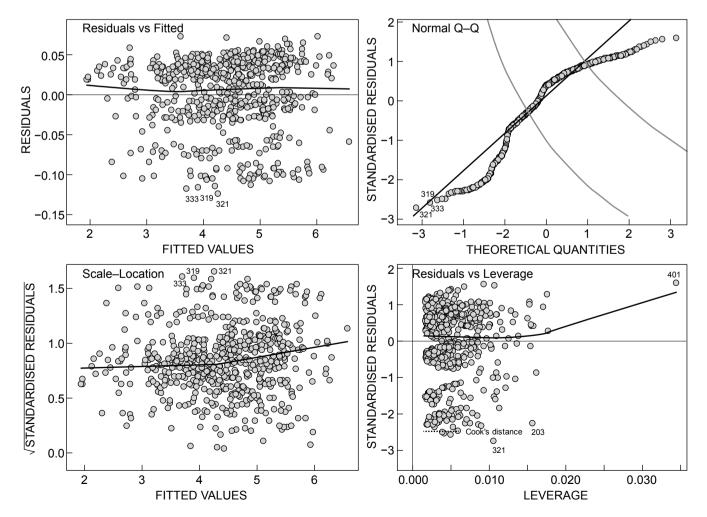


Figure 4: Diagnostic plots for model VI

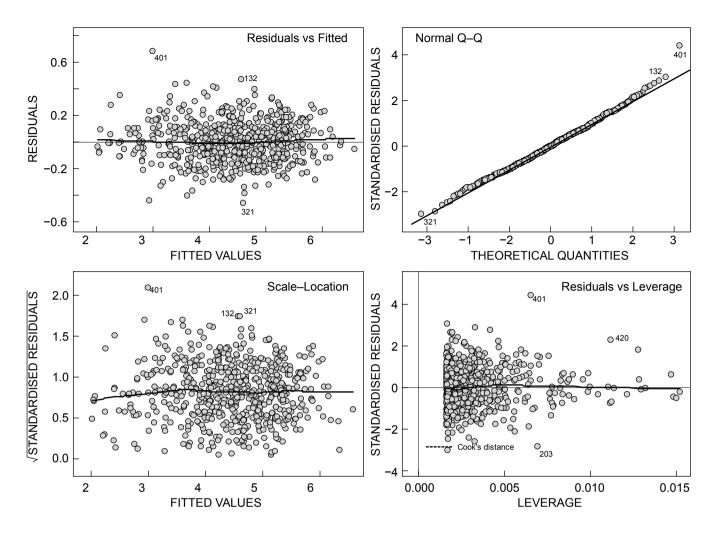


Figure 5: Diagnostic plots for model XI

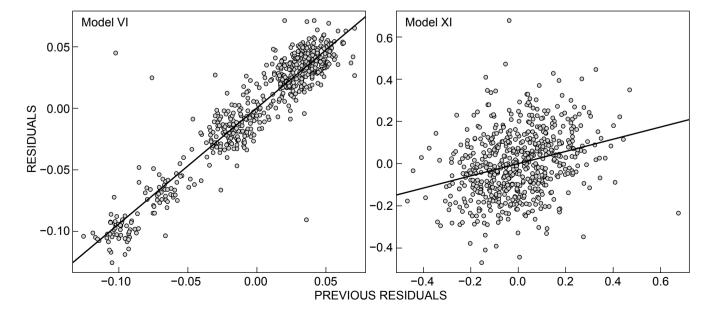


Figure 6: Showing the serial autocorrelation of the residuals of models VI and XI

variable), and (2) by using ARIMA instead of the least squares regression procedure (Cryer and Chan 2008). In our case, we used the most important regressors (DBH and height) in our model, therefore it was logical to go for the second option. We tested all possible combinations of order (p, d, q) and found the ARIMA (2, 0, 1) model with non-zero mean as the best option. Using this model we obtained estimates for the parameters of model XI (as shown in Table 4) with the associated statistics.

Table 4 showed that the ARIMA (2, 0, 1) model was better than the LSR model and had corrected the autocorrelation problems of model XI (1.50 $< d_c < 1.58$) (Figures 7 and 8).

Therefore, the final model is:

SB = exp (
$$-2.3807 + 1.4765 \times In(DH)$$
)
or SB = $0.092486 \times (DH)^{1.4765}$

Bias correction = $e' = e^{0.01060398} = 1.01066$ Therefore, the bias corrected model is:

$$SB = 0.092486 \times (DH)^{1.4765} \times 1.01066$$
$$= 0.09347 \times (DH)^{1.4765}$$

Model validatation

Figure 9 shows a comparison of actual vs predicted values using the test data set. For our model, we obtained 'a' = 4.33290, 'b' = 0.94398, adjusted R^2 = 0.9864. A *t*-test result showed that there was no significant difference between the expected intercept (0) and observed intercept (p = 0.0616, α = 0.05), and the expected slope (1) and observed slope (p = 0.3032, α = 0.05). This means that there was no significant difference between the predicted and observed stem biomass.

Table 4: Precision of model XI using the ARIMA (2, 0, 1) model in comparison with the least squares method (LSR)

Regression	Intercept	SE _I	Slope	SE _s	AIC	Durbin-Watson (d)
LSR	-2.41952	0.0519	1.4846	0.01114	-525.62	1.425
ARIMA	-2.3807	0.0539	1.4765	0.011	-600.02	2.0024

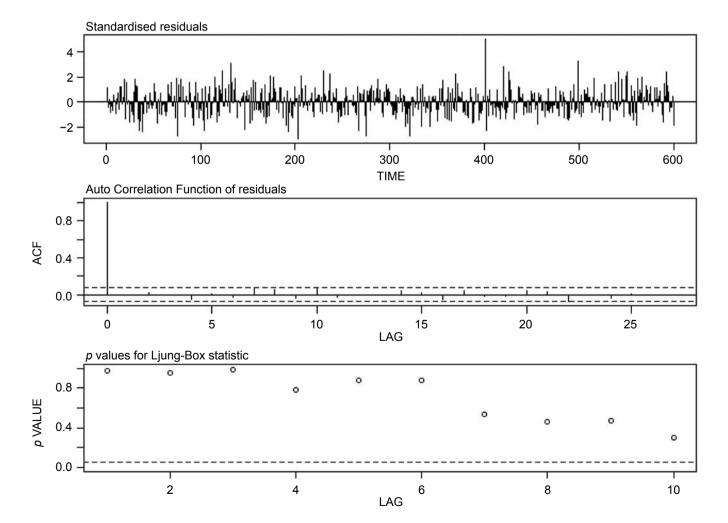


Figure 7: Diagnostic plots for the ARIMA (2, 0, 1) model XI

Morisita's (1959) index of similarity (1 – $D_{\rm M}$) was 0.9989157 (almost 1), which indicated that the model can predict stem biomass, outside the training data, effectively.

We know that non-destructive theoretical biomass models are used to predict the biomass of a stand and not of a single tree (IPCC 2003). That is, for evalution of a model, it is essential to judge whether the mean difference between the observed and predicted stem biomasses are significant or not. A Welch two-sample t-test showed that there was no significant difference between the mean observed and predicted stem biomasses (t = 0.1429, p-value = 0.8873).

Comparison between best fitted nonlinear and the bias corrected logarithmic models

For contrasting linear and nonlinear approaches, we first developed a best fit non-linear regression model for estimating stem biomass from the candidate models used in logarithmic modeling. The estimated parameters of the best fit non-linear model (power function) is given in Table 5.

The adjusted R^2 and AIC values for the non-linear allometric model were 0.95 and 5374.95, whereas for the logarithmic model they were 0.97 and -525.62. Moreover,

from Figure 10 it is evident that the non-linear allometric model has the tendency to overestimate stem biomass with an increase in DBH or height. These facts indicate that the logarithmic model can predict the variation in stem biomass more accurately than the non-linear model. The findings of Mascaro et al. (2011) also support our findings.

This means that the logarithic model can be used effectively at the stand level for estimation of stem biomass of *A. auriculiformis* quickly, accurately and non-destructively.

Conclusion

In this study, different combinations and forms of equation of diameter and stem height were used to select the best model for measuring stem biomass of *A. auriculiformis*. Moreover, a comparison between the best fitted logarithmic and non-linear allometric models was made. Fitting a non-linear biomass allometric model produces systematic biases in estimates for larger DBH/height trees. This can lead to a huge overestimation of biomass at the landscape level if they are based on stand-level data sets dominated by large trees. Since the models were compared based on the same assumptions, the final model can be used with

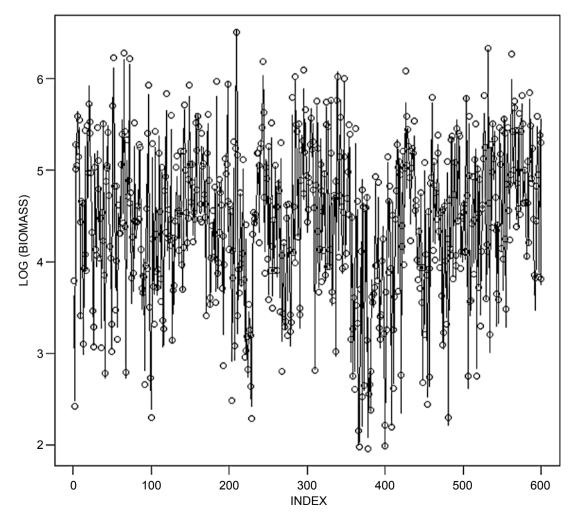


Figure 8: Observed vs predicted In(biomass)

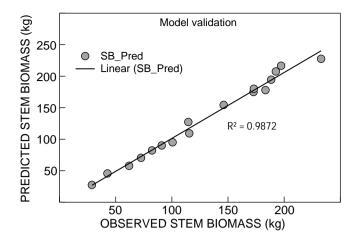


Figure 9: Linear regression between observed and predicted stem biomass (kg)

Table 5: Estimated parameters for the best fit nonlinear model XI

Parameters	Estimate	SE	t- value	<i>p</i> -value
Intercept	0.092467	0.007115	13	<2e-16 ***
Power	1.479986	0.014507	102	<2e-16 ***

^{***} Significant at $\alpha = 0.00$

confidence to estimate the stem biomass of *A. auriculi-formis* in the north-eastern region of Bangladesh. The final model can be used within a DBH range of 10–55 cm and a stem height range of 1–9 m. This model will be very helpful to the forest manager for decision-making as the species is well-acclimatised throughout the country.

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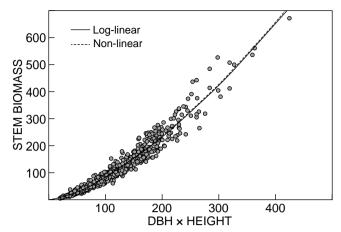


Figure 10: Best fit logarithmic and nonlinear allometric models

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