The book ***"Allometric Tree Biomass and Volume Models in Tanzania"*** documents biomass and volume models and various processes involved in their development for different vegetation types and some tree species in Tanzania. This book is organized into 14 chapters:

- Chapter 1 is an introductory part which covers forests and forest types in Tanzania and the importance of forest biomass and volume models in Tanzania;
- Chapter 2 gives background information on development of biomass and volume models;
- Chapter 3 is on biomass and volume models for the vast miombo woodlands in Tanzania;
- Chapter 4 provides models for predicting biomass of individual trees in lowland and humid montane forests *(AGB, BGB, twigs and leaves, branches and stem);*
- Chapter 5 presents general and species-specific models for AGB and BGB for three main mangrove species *(Avicennia marina, Rhizophora mucronata and Sonneratia alba);*
- Chapter 6 focuses on AGB and BGB biomass models and total volume models for Itigi thickets of central Tanzania dominated by *Pseudoprosopi fischeri and Combretum celastroides;*
- Chapter 7 is on *Acacia-Commiphora* woodlands biomass and volume models. Site-specific *(AGB and BGB)* and general *(AGB, BGB and stem)* biomass models are presented;
- Chapter 8 is about general and site-specific allometric models for estimating biomass of *Pinus patula;*
- Chapter 9 describes models for predicting biomass and volume of *Tectona grandis.*
- Chapter 10 deals with biomass and volume allometric models for coconut trees *(Cocos nucifera);*
- Chapter 11 presents cashewnut trees *(Anacardium occidentale)* biomass and volume allometric models;
- Chapter 12 is on biomass and volume models of baobab *(Adansonia digitata)*. AGB and total volume allometric models are presented;
- Chapter 13 compares biomass and volume estimates for different vegetation types and forests obtained by applying models presented in this book with corresponding previously published estimates; and
- Chapter 14 expresses concluding remarks.

The book covers useful knowledge for scholars who wish to engage in tree allometric modelling, and expert practicing forestry for the determination of forest stocking levels needed for forest planning and other processes such as forest carbon trading. It is a book of great interest not only for forest experts but also for forestry students undertaking forest resources assessment at different levels.

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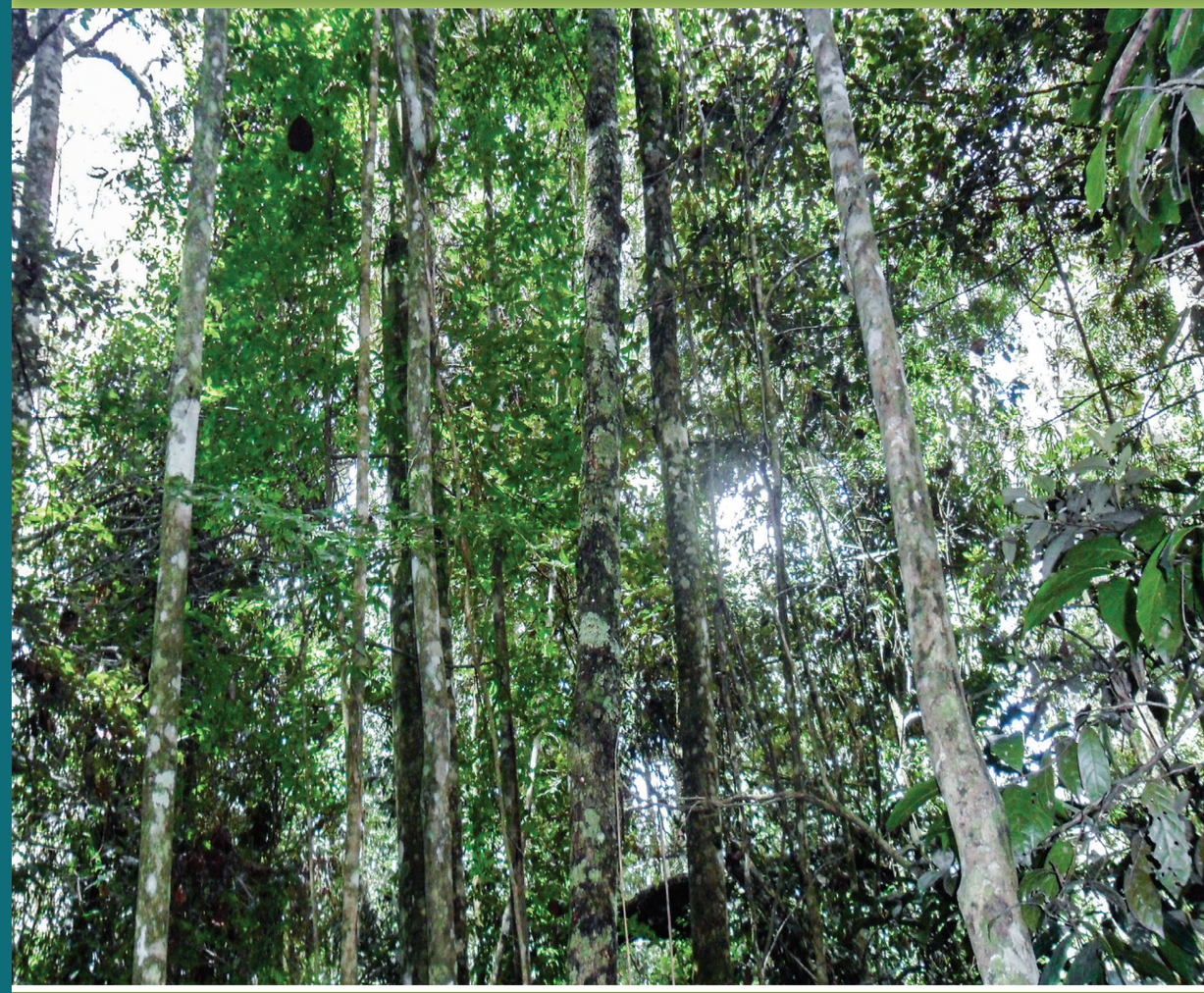

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2 Background on the Development of Biomass and Volume Models

Bollandsås, O.M., Zahabu, E. and Katani, J.Z.

2.1 History and approaches on the determination of biomass and volume

There are two main approaches to estimation of tree biomass. One is to obtain biomass as a product of tree volume and wood basic density. However, since most of the volume equations consider only the merchantable part of the tree, a biomass expansion factor that expands merchantable volume directly to total aboveground biomass is usually applied. The second approach is the direct use of biomass models.

The development of both biomass- and volume models has been based on relating easily measurable tree variables, such as diameter at breast height (dbh) and total tree height (ht), to biomass or volume. These variables are considered to be the most efficient input variables for tree level biomass and volume prediction (Brown, 1997; IPCC, 2003; Chave et al., 2014).

Global models have the advantage of being, in principle, applicable anywhere. However, due to great variation in climatic and edaphic factors, such models can yield large errors locally. Thus, a model developed on data from a smaller region, will within that region give more accurate estimates. Similarly, a model developed generally for a large number of species is more versatile in the application phase, but will yield estimates with large errors for those species that are atypical relative to the mean relationship between the response and the input variables. A species specific model has a more narrow range

of application, but will give better estimates for that particular species. A recent review of biomass and volume models for sub-Saharan African forests done by Henry et al. (2011) revealed that for tropical forests, a large number of species-specific and few general models existed. However, in Tanzania, development of biomass and volume models has been limited in terms of coverage of tree species, tree components, tree sizes and sample sizes (Temu, 1979; Malimbwi and Temu, 1984; Malimbwi, 1987; Malimbwi and Mbwambo, 1990; Malimbwi et al., 1994; Malimbwi et al., 1998; Chamshama et al., 2004; Munishi and Shear, 2004; Malimbwi et al., 2005).

In highly diverse ecosystems such as tropical forests, global models (Brown, 1997; Chave et al., 2005; Chave et al., 2014) have been applied in the absence of general- or species-specific local models. Species-specific models are generally more desirable. In a tropical natural forest with a large number of different species, though, developing species-specific models is almost impossible and consequently general models are the most appropriate.

2.2 Basic steps in the development of allometric models

Several important issues need to be considered before developing allometric biomass and volume models (see for example Vanclay, 1994). First of all one should decide exactly for what purpose the model is needed and what kind of results are expected from the model. This is then followed by a decision on what data is needed in order to develop a model that is in accordance with expectations and requirements. A consideration of the available resources for developing the model should also be done to enable planning and assessment of the magnitude of data collection. Already existing data sets could be supplementary to the final pool of data and should therefore be considered. However, it is important that sampling and measurement protocols are harmonised between the existing data and the planned data collection.

Both biomass and volume models are developed from empirical observations of sample trees. The response (biomass or volume) is accurately measured for each sample tree using destructive methods. Easily measurable variables such as dbh and ht are also recorded for each sample tree, and these measurements are later regressed against the response. This results into models that by means of easily measurable variables can predict biomass or volume.

The first consideration that has to be made in the model development process is to know the geographical extent and tree species for which the model will be applied. This is important because tree allometry varies with

location, tree sizes and species. Thus, it is important to do the sampling so that the population ranges of these factors are covered when selecting sample trees for biomass and volume modelling. If these guidelines are followed, extrapolations in the model application phase are minimised. This is particularly important to avoid if the model has a linear relationship between the response and the input variables.

Selection of sites and sample trees

As indicated above, the selection of sample trees should be carefully planned so that all tree species and size ranges are covered. However, in tropical forests where there are many tree species within small areas, a prioritisation of species that are important to be sampled has to be done because of limited resources. Such a decision can either be made on the basis of how frequent different species are or how important different species are for various uses. Either way, information on the frequency and distribution of species is necessary to make this prioritisation. A forest inventory of some kind prior to selection of sample trees is therefore required. If no local inventory has been carried out in the area of interest, sample plot information from the national forest inventory (NFI) can be used, if it exists. If no prior information is available, a separate sample plot inventory should be carried out with plots systematically distributed throughout the area of interest. Diameter and species registration on each plot enable the establishment of both species and size range for the area of interest. Later, sample trees can be purposely selected for destructive sampling according to the species frequency and size range information. The selection of sample trees can be carried out as single observations over the area of interest. However, it is possible to plan which trees to sample before even going to the field if a plot inventory has already been carried out and the sample trees selected among these trees. Additional plots can be established in-between the inventory plots for selection of additional sample trees if needed. Furthermore, selecting sample trees from plots where also information on the neighbouring trees is available enables calculation of stand variables, such as stand basal area, that can be included in the model single tree biomass or volume. Even if such variables are not directly included as an input variable in the final model, they can be informative with respect to giving insight to the accuracy assessment of the model, and with respect to learning for which forest conditions the model works particularly well.

The most important aspect when it comes to selection of sample trees is to cover the range of tree sizes, which is approximated from the prior inventory plot information. There will always be trees with more extreme sizes than

those measured in sample plots, but extremely big trees will also occur quite rarely when the model is applied later on. If there is a concern that the upper tail of the tree size distribution is underrepresented, additional extreme value observations can purposely be selected subsequent to the main sampling effort. The reason for this is that it is important to cover the size range in order to avoid extrapolations in the application phase. Using a model calibrated for small trees to do predictions for larger trees can result in large systematic errors.

Aboveground biomass and volume models

The development of biomass and volume models requires that the biomass or volume of each sample tree be measured accurately through destructive sampling procedures, even though terrestrial laser scanning can be used to build three dimensional models of trees which can be used to calculate volume of the different tree components. If information on wood basic density is also available, for example from a core sample, biomass can also be established. However, destructive sampling where the sample trees are felled and separated into different components (stem, branches, twigs and leaves) and further into billets, so far been the most common way of establishing the observed biomass or volume. For the determination of aboveground biomass (AGB), each billet is weighed in the field immediately after cutting. The weights of billets from different tree components are summed up for each tree. To estimate the biomass of tree components, samples are then taken from each component of each tree, measured for fresh weight in the field and later taken to the laboratory for oven drying. Thereafter, each sample is once again weighed, followed by calculation of a dry to fresh weight ratio (DF-ratio). The biomass of each tree component is obtained by multiplying component specific DF-ratios with the corresponding fresh weight, while tree biomass is obtained by summing the biomass values of different tree components.

The determination of the volume of sample trees is carried out as follows: The sample tree is divided into two main components, namely merchantable stem and branches. Subsequently, these components are divided into billets and measured for length and mid diameter. Then, the cross sectional area is calculated and volume determined by multiplying with the length of the billet (Huber's formula). It can be shown that this formula slightly underestimates the volume and that the underestimation increases with increasing section length. Sections should therefore be kept short, typically less than 1 m.

Belowground biomass models

The determination of belowground biomass (BGB) values basically follows the same procedures as for the AGB with regard to separation into different components (root crown, main roots and side roots) and with regard to determination of DF-ratios. However, there is a huge difference with regard to the resources needed to get the samples available for measurements because of the excavation need. Not only is the excavation work demanding in itself, but it can also be difficult to retrieve all of the root biomass from the ground. Thus, with a limited budget and if the goal is to get as much as possible model accuracy out of that budget, it may be more effective to do sampling of the BGB rather than doing an exhaustive excavation.

The sampling procedure indicated above can be carried out in the following way (see also Mugasha et al., 2013): First, the root crown is excavated and each root that is therefrom (main root) is cut at the base and the diameter is measured. Three of the main roots; one small, one medium, and one large with respect to basal diameter are selected for excavation in full length. Side roots branching from the excavated main roots are also sampled in the same fashion. Other unexcavated main and side roots are measured for their basal diameters. The excavated root components are further processed in the same way as the aboveground components. First, the roots are weighed fresh in field and then samples are taken to the laboratory for oven drying and are subsequently weighed. Then DF-ratio is calculated for each root and multiplied with the corresponding fresh weight. However, as opposed to the aboveground procedures, models must be developed to predict the biomass of the roots that are not excavated and weighed. Models for the side roots biomass are first developed. Such models cannot be made for each tree because the observations are too few, so they must be developed by species and/or within some geographical limits. The root basal diameters are regressed against the observed biomass of corresponding roots. The models are then applied to estimate the biomass of unexcavated roots. These side roots biomass predictions are then added to the biomass of their respective main root to adjust for the entire main roots which were not excavated. Having established the total biomass of every main root, main root biomass models are developed. As for the side root model, also these models must be developed by species and/or geographical area. The main root models are then applied to the base diameters measured for non-excavated main roots. A sample is also taken from the root crown itself, and a DF-ratio is calculated and multiplied by the fresh weight of the root crown. By summing the partly measured and partly estimated biomass of the different belowground components, BGB is obtained.

The advantage of carrying out this procedure, as opposed to excavating every root in full, is that more observations can be made available for the final development of the model for BGB. This ensures that more between-tree variation is covered in the data material and that more combinations between tree size and site factors are covered. However, since the observed biomass values used as response in the modelling partly are results of model predictions, an error is imposed. This is an error that to some degree will draw the observed biomass towards the mean for a given tree size. But, if the modelling is sound, the only effect is that the criteria of model fit will seem a little bit better compared to if the sample were excavated in full.

The procedure described above, was used in several previous studies. Kuyah et al. (2012) for example, did not excavate roots that went deeper than 2 m below the ground surface. Instead diameters were measured and the weight estimated by regression equations. Later the estimated weights were added to the observed biomass and BGB models were developed. Similarly in Niiyama et al. (2010) (Illustration Pg. 275), the stump was pulled from the ground and a lot of roots were broken. The weights of broken roots were estimated using a similar approach as described above, and finally estimated and observed biomass was added together and a model for BGB was developed.

Model form selection, fitting, selection and evaluation

Model is a general term that means simplification of reality. The allometric models that are the topic of the current book are simplifications in the sense that they yield approximations of the true biomass and volume with the use of measurements of dbh and ht. These are direct, easy to obtain, measurements of tree size, and they correlate quite closely to both biomass and volume. An empirical, statistical relationship between biomass or volume and the input variables, dbh and ht, can then be fitted using regression analysis. This estimates parameter coefficients for the input variables so that the residual errors between fitted values and the corresponding observed response values are minimised. Equation 1 displays a linear model form. This is a simple model where the response (Y) is linearly dependent on the input variables (dbh and ht) through constants β_1 and β_2, and an intercept term, β_0.

$$Y = \beta_0 + \beta_1 \times dbh + \beta_2 \times ht \quad (1)$$

However, the relationship between dbh and/or ht and biomass and/or volume is not linear. For some tree species, or for parts of a diameter range, the relationship may be close to linear, but in most cases a model needs to have the capability to describe non-linear patterns between the response

and measurements that are taken in the field. This does not mean that the model form displayed in Equation 1, cannot be used. Linear regression (e.g. Montgomery et al., 2001) is easy to use, and the ordinary least square estimation of the parameter coefficients, always ensures that the best solution is obtained. Thus, if the relationship between the measurements of dbh and ht are non-linear to biomass or volume, transformations of dbh and ht can be carried out. Potential transformations could be for example square, square root or logarithmic. Equation 2 shows an example of a model where the response is linearly dependent on square transformations of dbh and ht. A square transformation of dbh is equivalent to using basal area as an input variable.

$$Y = \beta_0 + \beta_1 \times dbh^2 + \beta_2 \times ht^2 \quad (2)$$

Interaction terms can also be used. Products of dbh and ht or even products of transformations of dbh and ht can sometimes prove to be good input variables. Equation 3 shows an example where the response is linearly dependent on dbh and ht and an interaction term between dbh and ht.

$$Y = \beta_0 + \beta_1 \times dbh + \beta_2 \times ht + \beta_3 \times dbh \times ht \quad (3)$$

However, in many cases a linear model is not sufficient to represent the relationship between response and the input variables. Non-linear functional forms are more flexible than linear models and there are many that have been used previously. Equation 4 gives an example of a multiplicative model where the parameter coefficient estimates can be determined by a non-linear regression technique. This particular model could actually be fitted on a linear form by logarithmic transformation of both response and input variables, but this will introduce the need for correcting bias introduced when transforming the response. Nevertheless, many non-linear functional forms are not possible to fit linearly through transformation.

$$Y = \beta_0 \times dbh^{\beta_1} \times ht^{\beta_2} \quad (4)$$

Fitting of non-linear models requires more knowledge and skills compared to fitting of linear models. The parameter coefficients are estimated through some iteration procedure based on, for example, minimising of root mean square error (RMSE). Basically non-linear regression procedures start with some values (random or pre-selected) for the parameter coefficients and then they are changed. Subsequent to each change, a goodness-of-fit criterion is evaluated and it is decided if the change made the model better or worse. The changing of parameters is carried out until a marginal change ceases to improve the goodness of fit criterion any more. For some non-linear functional forms, though, there exists many combinations of parameter

coefficients that give local solutions where the goodness-of-fit criterion becomes worse in any direction. Thus, it is therefore important to use a range of different starting values for the parameter coefficients in order to ensure that the best solution is global one.

If the modelling data originate from field plots, where several sample trees are selected from each plot, trees within the same plot will tend to be similar in terms of allometry since they have the same growing conditions. This is a challenge to the modelling, since observations that originate from a particular plot will have a similar effect on the model. For example, if the number of sample trees varies between plots, those plots where many trees were sampled will have a considerable impact on the model. This means that the growing conditions on plots with many sampled trees will be over represented. In the modelling this can be dealt with by allowing for random effects in the model to take into account that the observations were sampled in clusters where observations are correlated. Such models are called mixed effects models and they treat the different hierarchical levels specified by the modeller as different populations. The model parameters are affected by the choice of the modelling technique which may also alter input variables that are statistically significant.

There are always assumptions related to every modelling technique. If these assumptions are not fulfilled, the resulting model may perform badly in the application phase. Thus a careful check of the assumptions should always be carried out. An example is the assumption that the variance of the residual error should be homoscedastic (equal). In those cases where it is not homoscedastic, a variance function can be applied in the fitting of the model, see for example Mugasha et al. (2013).

In order to select which model form to use, a lot of initial scrutiny of the data should be done. First, graphical plots of the relationship between the response and the input variables should be made. Such plots will easily give the researcher an impression of the relationships investigated. Similar plots with transformed variables should also be made to see if there might be linear relationships on a transformed scale. Different alternative models should also be fitted, both linear and non-linear, and assess which form fits best to the data. To be able to compare the models, common criteria for evaluation must be used. One option could be to do a leave-one-out cross validation of all alternative models and compare RMSE and mean prediction error (MPE). Graphical plots of the residuals are also useful, especially with relation to

the selection between a linear and a non-linear model. The distribution of the residuals will reveal in many cases quite clearly if a linear model form does not fit the data at hand.

When models for large areas (say, countries) are developed, considerations about stratification have to be made. More specifically, the relationships between response and input variables may change with factors that are known. Forest type, climate and soil type are examples of such factors, and the model developer must consider if stratified models should be chosen over models fitted for the entire data set. A model fitted on soundly stratified data will fit better to the data compared to a common model because the stratification itself will define parts of the variation in the response. The downsides are that the model will be based on fewer observations, and that the stratification information must be available also in the application phase.

Evaluations of the final models are carried out just like the evaluation of alternative models explained above. A cross validation and calculation of RMSE will give an indication of the expected error that will occur when the model is applied. For a linear model, it is common to report the coefficient of determination (R^2), which expresses the proportion of variance of the response that is explained by the input variables. For non-linear models, a pseudo-R^2 can be computed from the residuals. Both of these enable comparisons between the goodness-of-fit for different models. For non-linear models, there are many more criteria indicating goodness of fit, such as the Akaike Information Criterion (AIC) and the Bayesian Information Criterion (BIC) that enable selection between alternative models. Before models are finally selected, the model behaviour outside the range of the data material should also be tested. In the application phase, there will be certain situations when the models are applied to much larger trees than those sampled in the calibration data set. It is therefore of interest to push the model beyond this limit by applying it to a diameter range that goes towards values that can be considered as what is maximum.

Documentation of data, model fit and model application

Documentation of both data material and models is important so that the user is not only able to apply the model within its ranges of validity, but also is informed of its expected accuracy. This section only briefly describes the documentation requirements for further elaboration and details the reader is referred to Jara et al. (2015) which provides an excellent compilation of guidelines for documentation of allometric equations.

The location from which the data set used for model development is collected, needs to be clearly reported since it defines the core area where the model can be used. A simple way of providing this information is to give the coordinates of the outer edges and/or refer to location names in addition to a map displaying the origin of the data. Further information about the location like elevation, climate (average precipitation, mean temperatures), soil types and landscape characteristics are very useful.

Furthermore, the documentation must include information on definitions of the response values. This means that for each tree component for which biomass or volume is modelled must be clearly defined. For example, does the AGB include the stump or not, and what is the cut-off diameter between stem and branches? Moreover, it is essential to report the units of measurement for both the response and input variables (kilogramme vs tonne, cm vs mm, m^3 vs dm^3). Otherwise it will be difficult for the users to interpret the results from the models.

The sampling scheme and the samples themselves must also be described. Which were the criteria for selecting the different sample sites? How were the sample trees selected within sites? Information on the distribution of tree species and tree sizes is also essential, because it enables the user of the model to disclose where the models might be more prone to yield errors. Both scientific and local species names should be reported too.

Preparation of the sample trees and subsequent measurements are important to document. For biomass models this includes the cutting into billets and the weighing in field. How large were the billets and what was the accuracy of the scale used in field? The number of samples taken from each tree component for drying in the laboratory must also be disclosed.

Documentation of the modelling is also important because it gives information on how trustworthy the models are. As a minimum, the model fit as described by R^2, RMSE and MPE should be reported together with the functional form of the model and a table with all parameter coefficients. A leave-one-out cross validation of the model could also add useful documentation of the model accuracy.

Lastly, recommendations on the use of the model should also be included in the model documentation. This will certainly ensure that the models are appropriately applied.

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