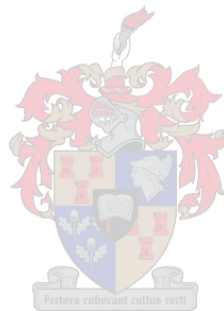


Modeling above-ground biomass of selected tree species within a Mistbelt forest in KwaZulu Natal

By

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Thesis presented in partial fulfilment of the requirements for the degree of Master of Science in Forestry at the Faculty of AgriSciences, University of Stellenbosch.



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DECLARATION

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ABSTRACT

The objective of this study was to develop species-specific allometric models for selected natural forest species within a forest forming part of the Southern Mistbelt Forest Group, close to the town of Richmond in KwaZulu Natal. The objective was met by determining the tree dimensions (diameter at breast height (DBH) and tree height) of the forest. The collected variables were used and the most dominant species in terms of their basal area coverage: *Xymalos monospora* and *Celtis africana* were selected for biomass modeling. The allometric models were developed from a two-step stratified sampling approach. Population dimensions were determined from sample plots, where-after trees were sampled for biomass representing the collected dimensions. The dry mass of the sampled components were used in a regression modeling approach to develop a set of species-specific and combined species linear models. The best models were selected based on goodness-of-fit model evaluation criteria (GOF) and parsimony principles and a two-step upscaling process was used to upscale samples to tree level and from tree to stand level. DBH and basic density were significant predictors of total above-ground biomass (AGB) and diameter as single predictor produced consistently good results. Diameter was used throughout the upscaling process to determine the biomass per ha. The estimated AGB for *X. monospora*, *C. africana* and all the species were 62.98, 93.56 and 230.86 Mg ha⁻¹ respectively. Estimated AGB for all species compared well with results from other biomass studies. Future research can investigate remote sensing applications in combination with the field sampling to estimate forest biomass more cost effectively over larger areas.

Keywords: *Xymalos monospora*, *Celtis africana*, species-specific models, combined-species models, diameter, basic density, AGB, remote sensing.

OPSOMMING

Die doel van hierdie studie was om spesie-spesifieke allometric modelle vir geselekteerde natuurlike woudspesies te ontwikkel in 'n woud wat deel vorm van die Suidelike Misbelt woudgroep, naby die dorp Richmond in KwaZulu-Natal. Die doel was bereik deur die bepaling van die boom dimensies (deursnee op die bors hoogte en boomhoogte) van die woud en deur gebruik te maak van die versamelde veranderlikes, is die mees dominante spesies in terme van hul basale area dekking: *Xymalos monospora* en *Celtis africana* gekies vir modellering. Die allometriese modelle is ontwikkel uit 'n twee-stap gestratifiseerde steekproefneming benadering. Bevolkings dimensies is bepaal van die monster erwe, waar-na 'n steekproef van die bome verteenwoordigend van die versamelde dimensies bemonster is vir biomassa bepaling. Die droë massa van die monster komponente is in 'n regressie modelerings benadering tot 'n stel van spesie-spesifieke en gekombineerde spesies lineêre modelle ontwikkel. Die beste modelle is gekies op grond van beste model evalueringskriteria en model spaarsamigheidsbeginsels en 'n twee-stap opskaling is gebruik om monsters op te skaal tot boom vlak en van boom tot vlak staan. Deursnee op borshoogte en basiese digtheid was beduidende voorspellers van die totale bogrondse biomassa en deursnee as enkele voorspeller het konsekwent goeie resultate gelewer. Deursnee is dwarsdeur die opskalings proses gebruik om die biomassa per ha te bepaal. Die beraamde totale bogrondse biomassa vir *X. monospora*, *C. africana* en al die spesies tesame was 62.98, 93.56 en 230.86 Mg ha⁻¹ onderskeidelik. Beraamde totale bogrondse biomassa vir alle spesies het goed vergelyk met die resultate van ander biomassa studies. Toekomstige navorsing kan afstandswaarnemings tegnieke in kombinasie met die veld steekproefneming ondersoek om biomassa meer koste-effektief oor groter gebiede te bepaal.

Sleutelwoorde: *Xymalos monospora*, *Celtis africana*, spesies-spesifieke modelle, gekombineer spesies modelle, deursnee, basiese digtheid, bogrondse biomassa, afstandswaarneming

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DEDICATIONS

I dedicate this thesis in memory of my belated father

1939 to

2006

Thank you for your continuous encouragement to further my studies and helping me to reach my full potential. You will always be an inspiration to me and although you are not here, your presence will always be felt.

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LIST OF ABBREVIATIONS

AIC	Akaike's Information Criteria
BEF	Biomass Expansion Factors
CBD	Convention on Biological Diversity
CF	Biomass Correction factors
CGA	Centre for Geographical Analysis
CSFM	Committee for Sustainable Forest Management
CV	Coefficient of Variance
DAFF	Department of Agriculture, Forestry and Fisheries
DBH	Diameter at Breast Height
DEM	Digital Elevation Model
DWAF	Department of Water Affairs and Forestry
GOF	Goodness of Fit
IPCC	Intergovernmental Panel on Climate Change
LiDAR	Light Detection and Ranging
MAX CI	Maximum Confidence Interval
MIN CI	Minimum Confidence Interval

PCI&S	Principles, Criteria's, Indicators and Standards
PLM	Pantropical Level Model
UNCED	United Nations Convention on Environment and Development
UNFCCC	United Nations Framework Convention on Climate Change
QGIS	Quantum Geographical Information Services
RMSE	Root Mean Square Error
RSS	Residual Sum of Squares
TSS	Total Sum of Squares

1. INTRODUCTION

1.1 BACKGROUND

Forests play an important role in the global carbon cycle and in the mitigation of carbon dioxide emissions and as a result, the need to accurately measure carbon stored in forests has increasingly gained recognition (Brown 2002; IPCC 2006). During the process of photosynthesis trees sequester carbon which is stored as part of the structural biomass, thus making them carbon sinks (Goicoa et al. 2011). Considering the above, the estimation of above-ground tree biomass by using allometric equations (Henry et al. 2010) or biomass expansion factors (IPCC 2006; Dovey 2009) is an essential aspect of the evaluation of carbon stocks (Goicoa et al. 2011).

Biomass equations are developed for industrial and scientific purposes. These models evaluate tree characteristics that are relatively difficult to measure, like crown and stem mass, from easily collected data like DBH, height and basic density (Saint-André et al. 2005; Chave et al. 2005; Parresol 1999) or tree volume (Dovey 2009).

Information on carbon stocks is important for studying forest productivity; nutrient cycling and quantities of fuel wood (Terakunpisut et al. 2007). Forests can be influenced by natural or human causes that can lead to forest degradation. In cases of severe disturbance, forests can become sources of CO₂ where the net primary production (NPP) is exceeded by oxidation and respiration. Where the disturbed forest or agricultural land is established to forest, the forested land can become carbon sinks where oxidation or respiration is exceeded by NPP (Brown 2002).

Considering the important role that forests play in the carbon cycle, various national and international legislation and agreements make provision for the protection of forests in South Africa. Documents produced at the United Nations Convention on Environment and Development (UNCED) also known as the Earth Summit held in Rio de Janeiro, Brazil in 1992 includes (1) Forestry Principles (non-legally binding statement of principles designed to commit governments to the management, conservation and sustainable development of all types of forest, (2) Convention on Biological Diversity (CBD) for the conservation of biological diversity and the sustainable use of its components and (3) Framework Convention on Climate Change (UNFCCC) where forests are recognized for their role in mitigating industrial carbon emissions. South Africa is a signatory to the CBD and the UNFCCC (DWAFF 1996).

Since forest activities are both sources and sinks of carbon, it was also included in the Kyoto Protocol (United Nations 1998). Article 3.3 of the Kyoto Protocol discusses carbon emissions by sources and removals by sinks from direct induced human activities limited to afforestation, reforestation and deforestation. Article 3.4 discusses additional human induced activities in forestry. Article 6 discusses the trading of emission reduction units in any sector of the economy while Article 12 discusses the emission offset trading between developed and developing countries (Brown 2002; DEA 2011). In this context, it is significant that the South African government endeavours to protect the scarce natural forest resources in South Africa.

1.2 DEFINITION OF THE RESEARCH PROBLEM

Forests play an important role in the global carbon cycle and accurate biomass and carbon assessments by using allometric equations (Henry et al. 2010) are important for industrial and scientific purposes and environmental sustainability (Saint-André et al. 2004).

Various general allometric equations have been developed to assess the biomass of single tropical and temperate forest tree species and for combinations of tree species (Chave et al. 2005; Navar 2008). Since tropical forests consist of a variety of species, generic multi-species equations are often used to estimate total mass per ha of all species (Chave et al. 2005). Species-specific equations provide more reliable results (Cole and Ewel 2006) and require fewer trees to be sampled as compared to multi-species equations (Picard et al. 2012).

Very few allometric equations exist for forest species of sub-Saharan Africa and generalised equations developed for forests in other continents are often applied to the forests of sub-Saharan Africa (Henry et al. 2010).

1.3 OBJECTIVES OF THE STUDY

This study aims to develop biomass models for selected natural forest tree species within an important South African forest type, the Southern Mistbelt Forest Group, close to Richmond, KwaZulu Natal and thus contribute towards better resource use and environmental management practices.

1.3.1 Specific Objectives

The specific objectives of the study were to:

1. Determine the species composition and tree dimensions of a Mistbelt forest.
2. Collect tree dimensional and biomass data in order to develop species-specific biomass models for two selected species and combined species biomass models from the combined data of the two selected species.
3. Scale up the biomass of the forest based on the inventory data and the developed biomass functions.

The objectives will be met by answering the following research questions:

- Which species are the most dominant in terms of the basal area contribution and what is their DBH and height class distribution?
- Which models are the most suitable to estimate the biomass throughout the upscaling process?
- What are the stand level dry weight values for each of the selected species and for all the species and how does it compare to other natural forests?

1.4 RESEARCH APPROACH

A stratified plot and biomass sampling approach were used to estimate the biomass of the study area. With the stratified random plot sampling, homogeneous segments with similar site characteristics were created by making use of a 2009 aerial photo digitized according to the natural forest coverage of the study area. Within these segments, sample points were randomly selected to determine the species and size class dimensions of the forest. With the collected dimensions, a stratified sampling approach based on DBH and height was used to select trees to sample for biomass covering the DBH and height variation. With the collected biomass data, species-specific and combined species allometric equations were developed and the AGB

was estimated by up-scaling tree based samples to the individual tree plot and stand level.

To apply the models developed in this study to other sites, inventory data would have to be available. This is generally unlikely, and hence these results must be considered applicable in a specific and limited set of contexts. However, the data and models developed in this study can be extended to allow calibration remote sensed applications to enable biomass estimation of other sites.

2. LITERATURE REVIEW

2.1 FORESTS AS CARBON STORES

Forests store large amounts of carbon, but the quantitative contribution forests make to the global carbon cycle is still not well estimated (Brown 2002). A study by the IPCC (2001) found that forests store approximately 80% of all above ground and 40% of all below ground terrestrial carbon. For this reason the UNFCCC and its Kyoto Protocol recognise the important role forests play in carbon sequestration and accurate biomass assessments are important for reporting purposes (Brown 2002).

Carbon can be measured for two policy related reasons: (1) to comply with the requirements for the UNFCCC and (2) as part of the implementation of the Kyoto Protocol (Brown 2002).

Aboveground carbon content is closely related or proportional to AGB and carbon storage of the forest can be derived from the biomass since approximately 50% of the dry weight of the forest is carbon (West 2009). Tree biomass information is important for the assessment of forest structure and condition (Chave et al. 2003), forest productivity and carbon sequestration in roots, stems, branches and foliage (Chave et al. 2003; Cole and Ewel 2006). Biomass assessments can establish the annual gain or loss in carbon storage. Biomass increment contributes to annual gain, while annual losses are caused by activities such as harvesting activities, fuel wood collection or burning practices (IPCC 2003).

Information collected from biomass assessments can be used for resource use and environmental management purposes. Collected information can be used to quantify how much of the resource is available for utilization purposes to ensure that management practices do not lead to an annual loss in stored carbon (Parresol 1999).

2.2 CARBON STORAGE IN SOUTHERN AFRICAN INDIGENOUS FORESTS

Data and information is particularly lacking about carbon stocks of indigenous forests in Sub-Saharan Africa, and equations to assess such forests are not readily available (Henry et al. 2010). South Africa has 19 indigenous forest types, classified based on floristic composition, bio-geographical relationship and climate, substrate and water dynamics (Mucina and Geldenhuys 2006) (Figure 2.1). Forest patches are generally small to very small, with few exceeding 100 ha (Cooper 1985; Geldenhuys 1991). Unfortunately, much of the information on the conservation status of forests in South Africa is outdated and there is a general concern about the loss of protected forest, lack of adequate measures to protect the needs of local communities and the protection of national forest assets (DWAF 1996).

The climate and the effect of fires have confined the natural forest areas to a total forest area of 3 000 - 4 000 km² (Geldenhuys 2004). Large areas of natural forests have been destroyed over the last few centuries with the settlement of Europeans in southern Africa since 1652 (Mucina and Geldenhuys 2006). Much of the natural forest areas survived, but destruction of natural forest areas still continues as a result of growing human need (Geldenhuys 2004). Most of the natural forest areas occur in

the Eastern Cape (140 000 ha), followed by KZN (91 200 ha), the Western Cape (60 000 ha), Northern Province and Mpumalanga (35 000 ha each).

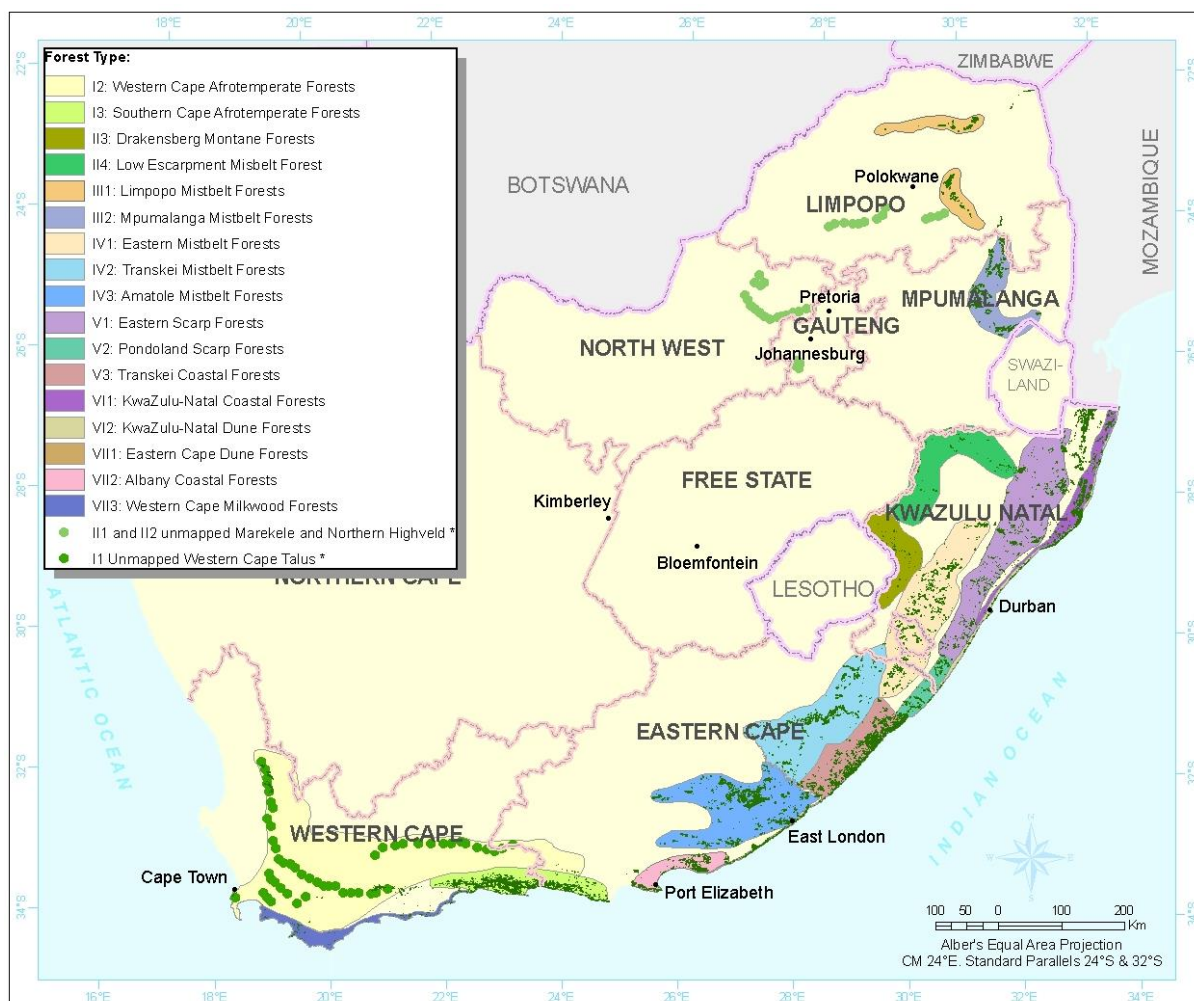


Figure 2.1 National forest types in South Africa (DWAf 2000)

A forest group of particular interest is the Southern Mistbelt Forest group consisting of the Eastern, Transkei and the Amathole Mistbelt Forest types. Southern Mistbelt Forests can be considered to represent a major indigenous carbon store with considerable differences between primary and secondary forests and are important for biomass assessments to determine their carbon stocks (Adie et al. 2013).

The Southern Mistbelt Forests are multi-layered high forests of 10 to 30 m high, occurring mainly on mountain foothills, scarp slopes and gullies. The soils are generally deep, loamy and with high nutritional status. Approximately 8% of the forest type is protected in South Africa and smaller patches are protected on private nature reserves. A study by von Maltitz et al. (2003) (cited in Geldenhuys and Mucina (2006) found that the current threats to the forest group are uncontrolled harvesting of timber, firewood collection and burning and fire regimes originating from adjacent grasslands. All Mistbelt forests contain a high biodiversity and unique composition of Afrotropical tree species (Mucina and Geldenhuys 2006).

Some of the important and dominant species to be found in the forest type include tall trees such as *Xymalos monospora* and *Celtis africana* (Mucina and Geldenhuys 2006; Adie et al. 2013).

X. monospora is commonly called Lemonwood and belongs to the family *Monimiaceae*. It is a medium to large evergreen tree, 8 - 25 m in height (Coates Palgrave 2005), sexes are bared on separate trees and the species can often be found in coastal and montane forests (van Wyk and van Wyk 2013).

The flowers are greenish and in short axillary spikes. The fruit is fleshy oval, 15 mm long, red and often eaten by birds. The wood is yellow, durable and suitable for furniture while the bark is used medicinally (van Wyk and van Wyk 2013). The bark ranges from light greyish brown to brown and often flaking off in round patches marked with concentric rings, rectangles and whirls. The species is generally fire resistant and the old stumps coppice. With the coppice growth after disturbances and its dense foliage, the species generally forms dense stands often excluding

other species. This is often an indication of a disturbed forest (Coates Palgrave 2005).

C. africana is commonly called White Stinkwood and belongs to the family *Celtidaceae*. It is a medium to large deciduous tree (12 - 30 m) which often occurs in forest, bushveld and grassland. The leaves are ovate, dull green and sparsely to densely covered with hairs, with the upper half of the leaves toothed. The flowers are small, greenish and appear with the new leaves while the fruit is drupe, ovoid and about 6mm in diameter (van Wyk and van Wyk 2013). The bark ranges from pale grey to white and is smooth. The wood is white to yellow of color and of a medium hardness (Coates Palgrave 2005).

2.3 PRINCIPLE METHODS TO ASSESS FOREST BIOMASS

Assessment of biomass, undertaken for a variety of reasons, involves a number of components. In this section, a review is provided of the approach, in general terms, involved in conducting a biomass assessment and model development procedure for forests (Figure 2.2). This section of the theses addressed points II – VII. Points I and VIII were not addressed in the review as a country wide carbon mapping and assessment for this forest type is out of the scope of this thesis.

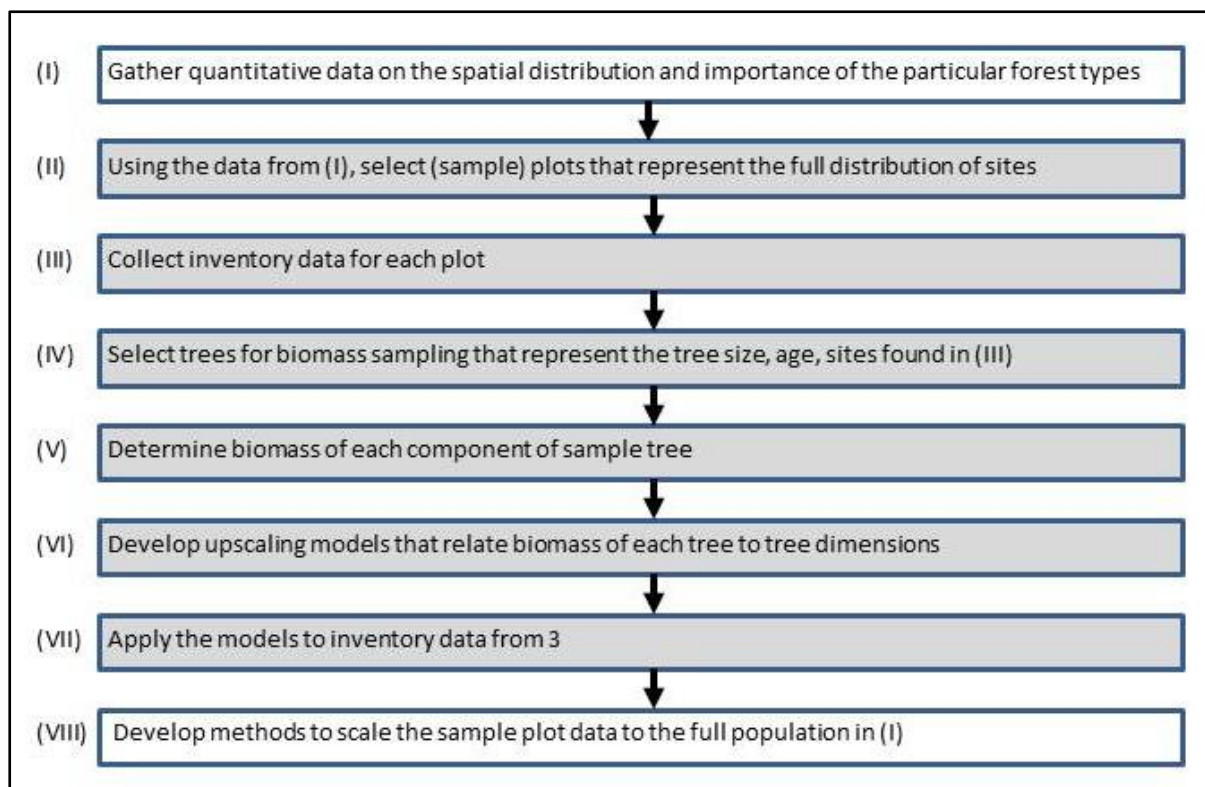


Figure 2.2: Approach used in conducting biomass assessment

2.3.1 Selecting representative sample plots

Forest inventories are time consuming and expensive and complete inventories of whole forest areas are rarely done. A representative sample of the population is measured instead, which provides a cost effective alternative compared to a full forest inventory. Sample plots and are dependent on the variability of the resource and the level of accuracy required. Higher accuracies are associated with higher cost and time spent in field (van Laar and Akça 2007; Kunneke et al. 2014).

In biomass studies forest inventory plots are selected based on simple random sampling and stratified random sampling approaches (Gibbs et al. 2007; Condit 2008). With simple random sampling, plots are randomly selected (Gibbs et al. 2007) and biomass estimations are unbiased, provided that there are no other sources of

bias during the data collection (van Laar and Akça 2007). When using the random sampling approach without stratification, over or under-sampling may occur as data in nature may not exhibit a normal distribution and can be skewed (Gibbs et al. 2007). With stratified random sampling, a study area is divided into homogeneous segments based on site variability factors that include stand composition, slope, elevation, and species (Gibbs et al. 2007; van Laar and Akça 2007; Condit 2008; Picard et al. 2012). Forest areas can be delineated and thereafter stratified into homogeneous segments by using information about the area, often obtained from remote sensing , e.g. aerial photos or satellite images. Using a stratified sampling approach, the sampling intensity can be reduced, while improving population estimates (van Laar and Akça 2007; Gibbs et al. 2007).

Various plots shapes are used to describe forest composition (Condit 2008) and sample plots may be circular, rectangular or squared in shape. Trees are considered to be part of the plot if the centre of the base of the bole falls within the plot. Circular plots are efficient and easy to measure, as a circle has the smallest perimeter per plot size, less borderline trees and the boundaries of the plot can easily be measured. Concentric circular plots are often used in inventories of multi-aged forests since they provide a better efficiency without compromising the representativeness. The same centre is used for plots with different radii, when this technique is applied. Trees with different diameter classes are measured within each circular plot (van Laar and Akça 2007).

2.3.2 Collecting inventory data for each plot

Once representative plots have been selected, measurements of tree dimensions are made on all (or in some cases sub-sets of) trees within the plots. Ultimately, forest biomass is meaningful at the “stand” level. But as a forest stand comprises individual trees, the biomass needs to be assessed on an individual tree level during the biomass assessment stage, where after the total of the individual tree biomass is calculated to get an estimation of the biomass of the stand per ha. Thus, typically, the development of allometric functions for estimation of biomass involves two stages where basic tree dimensions are measured within sample plots of known area and where sample trees are selected to measure tree biomass and data (Parresol 1999; Kunneke et al. 2014). During the first stage, all trees in sample plots are measured including basal area and tree height. During the second stage, the same tree variables are measured for the selected sample trees and biomass material are collected. The biomass material collected during the second stage is used to develop biomass models. The biomass of the plot is then determined by applying the biomass models to all trees measured during the first stage. In this way the biomass of the forest can then be scaled up (Chave et al. 2005; Samalca 2007).

2.3.3 Selecting representative sample trees

The number of trees selected for biomass sampling will depend on the variability of the resource and the size class distribution of the species in the forest (Picard et al. 2012). According to Steward et al. (1992) at least 12 trees should be sampled for each species within a specific site type to develop species-specific models. However, the optimal number of sample trees should be determined by a coefficient

of variation (CV) test and sample size should be increased until an acceptable level of error is achieved (Chave et al. 2004).

Since the determination of above ground biomass is more difficult than determining stem volume, fewer observations are used to construct models for biomass than for stem volume (Picard et al. 2012). Some biomass tables or models have been derived from few observations due to various constraints (seven trees from Kajimoto et al. 1999 in Siberia, eight trees from Brown et al. 1995 in Brazil, 12 trees from Ebuy et al. 2011 in the Democratic Republic of the Congo and 19 trees from Segura and Kanninen 2005 in Costa Rica).

A study by Kunneke et al. (2014) found that selecting trees for biomass sampling is a substantial task and requires knowledge of the independent variables. Stratified random sampling techniques can be utilized for selecting sample trees over the whole range by ranking trees within the inventory plots by DBH and dividing them into three diameter classes: small, medium and large (Köhl et al. 2006). Kunneke et al. (2014) recommended the use of DBH and height in parallel as independent variables for stratification as illustrated in Figure 2.3. DBH and height data can be divided into classes in a stratified sampling procedure and the trees selected for biomass sampling should cover the full range of DBH and height variation found in the inventory. In stand inventories, a common approach used is to plot a DBH and height curve for each separate stand in order to produce an unbiased estimate. For this approach it is recommended to measure at least 20 - 25 heights in each stand to produce unbiased estimates (van Laar and Akça 2007).

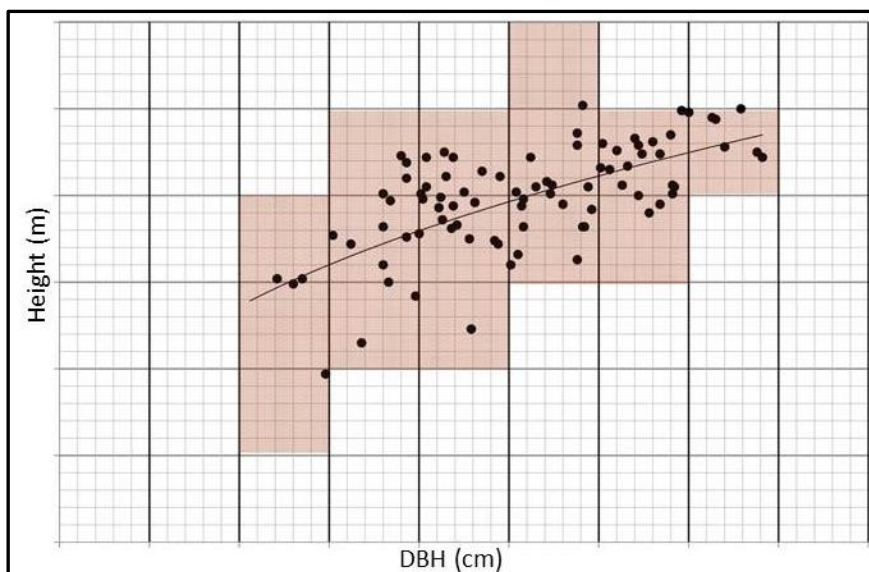


Figure 2.3: Stratified sampling process based on height and DBH to select sample trees to cover all DBH and height variation. The colour areas represent the DBH and height variation that was covered (Kunneke et al. 2014).

Typically trees in an unrepresentative environment (*i.e.* close to the road side) are not selected as their architecture (*i.e.* stem form and branching) often differs from the other trees. In biomass studies, sample trees can be mistakenly selected in groups clustered in close proximity to each-other or close to roads to simplify the sampling and transportation of material. This means that the variability in the sample set is biased as selected trees do not represent the true/full variability of the stands or site (Köhl et al. 2006). Various studies have shown that the allometric relationships between tree components can vary between species and different site conditions. In some cases it was found that there is a consistency in the allometry across a range of sites (Medhurst et al. 1999). General field conditions (slope, accessibility etc.) often require the sampling plan to be adjusted to include sample trees from accessible forest areas to simplify sampling and transportation of material (Picard et al. 2012).

2.3.4 Biomass determination of sample trees

Biomass sampling for trees can be broadly divided into bulk sampling where more than one tree is sampled and individual tree sampling (Figure 2.4). With bulk sampling, whole trees are chipped in the forest and the method is normally applied for industrial purposes in short rotation plantations to determine the fresh weight (Seifert and Seifert 2014). The biomass of individual sample trees can be estimated by destructive whole tree sampling (Goicoa 2011) or minimal invasive sampling. With the destructive sampling method the whole tree is felled and the dry weight of the components (stem, branch and foliage) is determined (Seifert and Seifert 2014). Minimal invasive sampling is used where the tree species are protected or rare or of high saw timber value and cannot be destructively sampled (Goicoa 2010). When minimal invasive sampling methods are applied, the trees are climbed and total volume is computed from measuring the stem sections and larger branches. Wood density is determined by core sampling along the stem. To obtain branch biomass data, the diameters of the branches are measured by the tree climber who cuts a smaller number of branches for dry weight determination (Samalca 2007).

Statistical regression procedures are then used to develop models for scaling dimensional variables of the standing tree to biomass (Parresol 1999; Picard et al. 2012). Statistical regression procedures can also be applied to minimal invasive sampling, where the basic density of core samples, volume of stem sections and dry mass of branches are upscaled to the rest of the tree. Destructive and minimal invasive sampling of biomass still remain a time consuming and expensive process, but are necessary to develop baseline biomass estimates against which other less costly methods can be calibrated (Yavaşlı 2012).

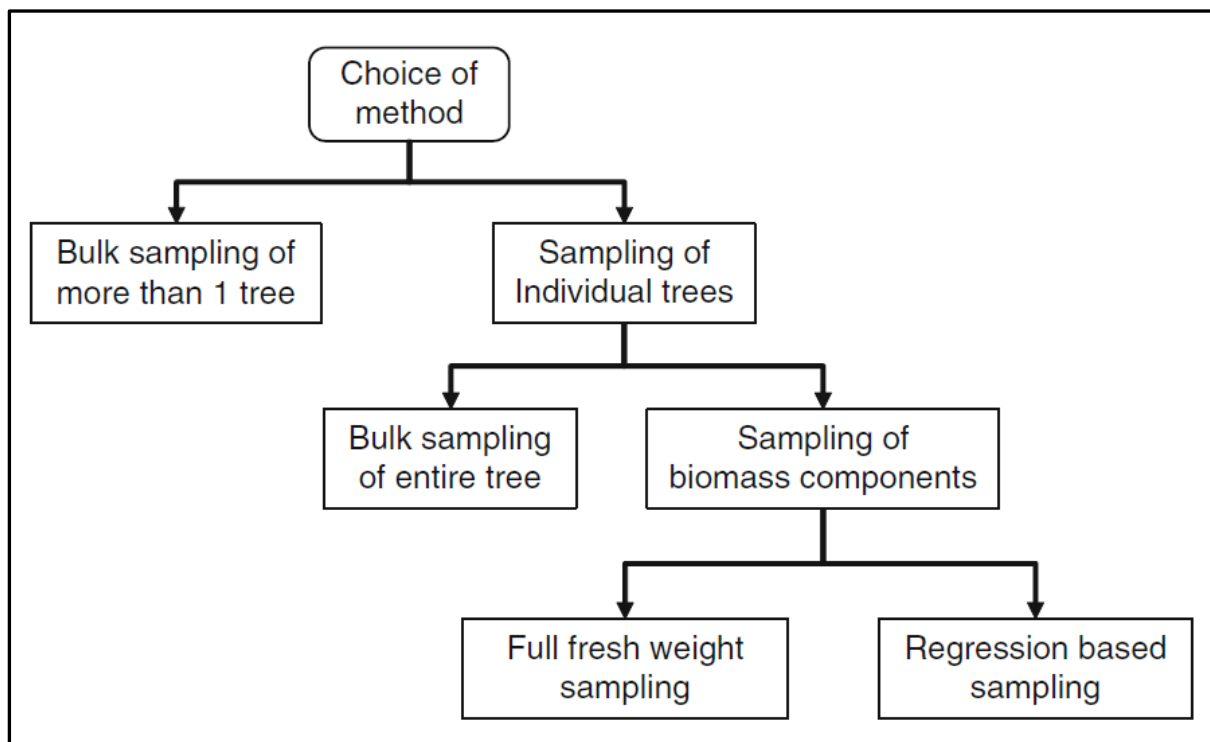


Figure 2.4: Biomass sampling methods for trees (Seifert and Seifert 2014).

Forest biomass is determined by an upscaling process using statistical modeling. The upscaling process is usually done in two stages to obtain tree and stand level estimates (Figure 2.5) (Seifert and Seifert 2014).

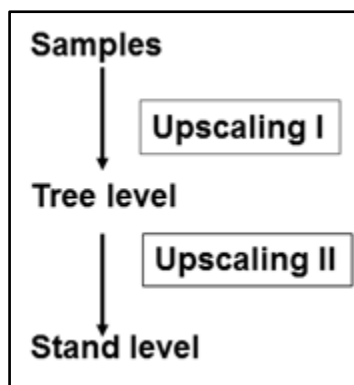


Figure 2.5: Upscaling steps for field samples from sample to tree to stand level (Ackerman et al. 2013).

To simplify the calculation of above-ground tree biomass, selected sample trees are divided into different components and each component is measured separately (Picard et al. 2012). Trees can be divided into stem and crown and the crown into branches and foliage, whereas the stem is often separated in stem wood and bark (Parresol 1999; He et al. 2003; Phiri et al. 2015). Allometric equations can then be developed separately for each biomass component (Seifert and Seifert 2014).

Stem biomass is estimated from reconstructing collected stem samples. The oven dry biomass (dried at 105°C until constant weight) is a function of stem volume (m^3) calculated with a volume equation and basic density ($kg\ m^{-3}$) calculated from the volume and oven dry mass of stem samples (American Society for Testing and Materials 2008, Picard et al. 2012). Inconsistencies in the drying temperature or the lack thereof is one of the main problems in comparing the results of biomass studies (Williamson and Wiemann 2010). Sample biomass can only be quantified once an equilibrium mass has been reached according to laboratory standards. Various tree components are dried at various temperatures for various purposes and drying temperatures range from 40°C to 105°C. Oven dry weight refer to drying of samples

to a constant weight at $103\pm 2^{\circ}\text{C}$. Using drying temperatures of less than 105°C leads to an overestimation of biomass (Seifert and Seifert 2014).

The volume of stem samples are often determined by using the water displacement technique and the weight of the water replaced after full immersion, represents the volume of the sample in cm^3 (American Society for Testing and Materials 2008; Seifert and Seifert 2014). Within broad leaved multi-stemmed trees, it is difficult to differentiate between stem and branch sections and the larger branches are often treated as stem sections by measuring their volume (Seifert and Seifert 2014).

For practical purposes, stem volume equations are widely applied to estimate the total and merchantable volume of stems from limited diameter measurements along the stem (van Laar and Akca 2007).

Stems of trees often assume the following frustums: neiloids, cones or paraboloids (Figure 2.6) (Husch et al. 2003). Various equations (Table 2.1) make provision for the calculation of frustums of various forms. Newton's formula can be applied to all the frustums while Smalian and Hubert's formula can be applied when the frustums are that of a Paraboloid. In a previous study (Young et al. 1967 in Husch et al. 2003), the three equations were tested against the water displacement method and a zero percent error was found with Newton's equation while a +9 and -3, 5 % error was found with the Smalian and Hubert equations respectively.

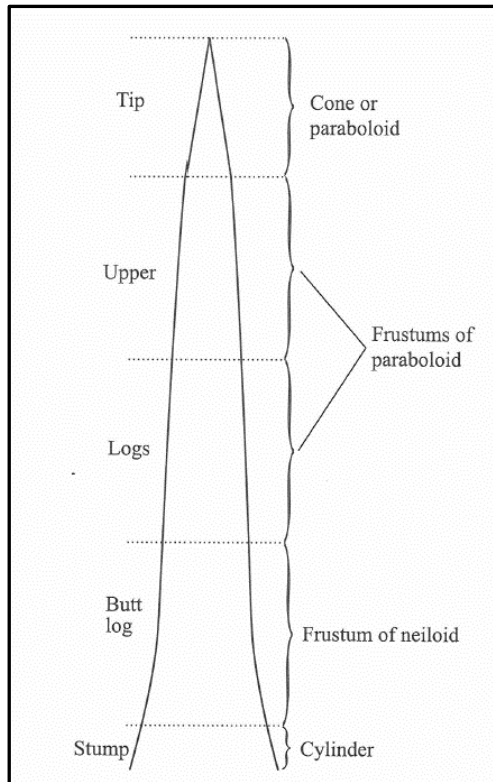


Figure 2.6: General frustum forms and their position along the stem (Husch et al. 2002)

Frequently used volume equations include the so-called Smalian, Huber and Newton functions (Table 2.1). Volume of stem sections are often calculated using Smalian's formula, or alternatively by using the geometric formula for the truncated cone (Equation 2.4) (Seifert and Seifert 2014).

Table 2.1: Volume equations frequently used to calculate the volume of stem sections (van Laar and Akca 2007; Seifert and Seifert 2014).

Equation no.	Name	Formula
2.1	Smalian's formula	$V = \frac{g_u + g_l}{2} \cdot l$
2.2	Huber's formula	$V = g_m l$
2.3	Newton's formula	$V = \frac{g_u + 4g_m + g_l}{6} \cdot l$
2.4	Geometric formula for truncated cone	$V = \frac{\pi l}{3} (R^2 + Rr + r^2)$

Where g_m is the cross sectional area at the midpoint of the stem section, g_l , g_u cross sectional area at the lower and the upper end; l is the length of stem sections, V is the volume and R , r the diameters at the thick and the thin end of the log.

Regression based sampling is used when the crown mass is sampled. The foliage is manually separated and scaled up separately from the branch material. This is a time consuming and labour intensive exercise. Leaves are sampled separately from the branch material for trees with small canopies or where the project objective requires full canopy sampling. A regression based sampling approach is used whereby all the branch diameters and branch lengths are measured and a sub-sample of the branches are used to determine the oven dry mass. It should be

recorded whether the branches were measured perpendicular, or with the axis of the stem since the two methods provide different results. Measurements taken perpendicular to the stem axis yields smaller values than measurements taken with the axis of the stem. The branch and foliage mass are then regressed against the branch diameter, and sometimes the branch length (Parresol 1999) as an additional independent variable.

2.3.5 Upscaling models relating biomass of sample trees to tree dimensions

Forest biomass can be estimated from using allometric models or biomass expansion factors (West 2009) and applying them to forest inventory data (Brown 2002). Biomass expansion factors (BEFs) are calculated as the ratio between the mass of a tree component or whole tree and a stem volume or stem mass. Expansion factors are usually applied at the stand level and allometric functions at the tree level. Multiplying the stem volume, determined from a volume function with the BEF of the component will result in the biomass of the component. The biomass can also be calculated at the stand level by multiplying stand volume with the BEFs (West 2009). AGB estimates are often derived from calculated stem volume from forest inventories and default BEFs (Brown 2002). This may result in unreliable estimates, since BEFs may vary with tree age, size and site conditions. In contrast to these findings, a study by Magalhães and Seifert (2015a) found that the BEFs were weakly related to tree size. Errors with the application of BEFs on a country level may be large and difficult to quantify, as developed BEFs are site and stand specific (Jalkanen et al. 2005).

The most common method to estimate forest biomass is through the use of regression models, often using logarithmically (ln) transformed linear models (Parresol 1999; Seifert and Seifert 2014). Both simple linear regression (Equation 2.5) and multiple linear regression (Equation 2.7) equations and ln-transformed simple (Equation 2.6) and multiple linear regression (Equation 2.8) as proposed by Picard et al. (2012) (equations 2.5, and 2.6) and Parresol (1999) (equations 2.7, and 2.8) are used to model forest biomass. Allometric models are used to relate tree biomass to variables like DBH, height and basic density.

$$Y = \beta_0 + \beta_1 X + \epsilon \quad (2.5)$$

$$\ln(Y) = \beta_0 + \beta_1 \ln(X) + \epsilon \quad (2.6)$$

$$Y = \beta_0 X_1^{\beta_1} X_2^{\beta_2} \dots X_j^{\beta_j} \epsilon \quad (2.7)$$

$$\ln(Y) = \ln \beta_0 + \beta_1 \ln(X_1) + \dots + \beta_j \ln(X_j) + \ln \epsilon \quad (2.8)$$

Where:

Y= Tree component mass (kg)

X= Tree dimensional variables

β_j = Model parameter

β_0 = Intercept value

β_1 = Slope value

ln= The natural logarithm

ϵ = Error term

Additivity is a desirable attribute of models that cover different biomass components. (Picard et al. 2012). Additivity of regression models means that the biomass estimates of the various biomass components should add up and produce the same estimate, as if only one total mass equation has been used (Parresol 1999), therefore the sum total mass of the parts should not exceed the sum total of the whole (Cunia and Briggs 1984).

Goodness of fit model evaluation criteria is used to compare biomass models and to select the best models. Parresol (1999) recommended the following GOF (Table 2.2):

Table 2.2: Goodness of fit for allometric models (Parresol 1999)

Equation	Statistic	Formula
2.9	Fit Index (FI)	$FI = 1 - (RSS/TSS)$
2.10	Standard Error (S_e)	$S_e = \sqrt{RSS/(n - p)}$
2.11	Coefficient of Variation (CV)	$CV = (S_e / \bar{Y}) \times 100$
2.12	Furnivals Index (I)	$I = [f(Y)]^{-1} \times RMSE$
2.13	Percent Error (P_e)	$P_e = \left[\frac{(196)^2}{X^2(n-p)} \sum_{i=1}^n \left(\frac{\hat{Y}_i}{Y_i} - 1 \right)^2 \right]^{1/2}$

2.14	Mean Percent Standard Error \bar{S} (%)	$\bar{S} (\%) = \frac{100}{n} \sum_{i=1}^n Y_i - \hat{Y}_i / \hat{Y}_i$
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Where (TSS) is the Total Sum of Squares; (RSS) is the Residual Sum of Squares; p is the number of model parameters; $f(Y)$ is the derivative of the dependent variable with respect to biomass; \bar{Y} = the arithmetic mean of Y ; RMSE is the Root Mean Square Error of the fitted equation.

The Akaike's Information Criteria (AIC), Root Mean Square Error (RMSE) and Coefficient of Determination (R^2) are also used in many biomass studies to evaluate models and models with the lowest AIC and RMSE values and highest R^2 values are selected (Chave et al. 2005; Picard et al. 2012; Goodman et al. 2014). The AIC uses a penalized likelihood criteria and penalizes models based on the number of included independent variables and cannot be used to compare transformed to untransformed models (Burnham and Anderson 2002; Picard et al. 2012). The R^2 measures the explained variance of the model compared to the total variance (Picard et al. 2012), but should be used with caution in models with many parameters as the R^2 values often increase with the addition of independent variables without increasing the explanation value due to multi-collinearity (Sileshi 2014). The RMSE gives larger weight to bigger errors as it squares the errors before they are averaged (Sileshi 2014).

2.3.6 Application of biomass models to inventory data

Selected models can be applied to a particular species, multi-species mixed forest or a specific site (Chave et al. 2005; Navar 2008).

Where species-specific information is available with measurements including height over all the size classes, single-species allometric models can give more reliable estimates of AGB than applying a multi-species model to estimate the biomass. Single species models are often applied to high value tree species or when precise estimates are required, and requires less sample trees to develop the model than for a multi-species model to estimating carbon stocks (Cole and Ewel 2006; Picard et al. 2012).

Many allometric models relating biomass to tree diameter or diameter combined with total height have been developed in the past (Overman et al. 1994). DBH is easy to measure and is the most commonly used independent variable in biomass estimation, explaining most of the variation in stand biomass (Montagu et al. 2005; Segura and Kanninen 2005; Cole and Ewel 2006).

In a study by Jonson and Freudenberger (2011), allometric equations were developed from eight native Australian tree species from remnant woodland stands of unknown age. Trees were selected to cover a wide range diameters. Measured dimensions included DBH (1.3 m), stem diameter at ground height (D_0), stem diameter at 10 cm above ground (D_{10}), stem diameter at 30 cm above ground (D_{30}), total tree height, canopy width and canopy length. Measured dimensions were regressed separately against total mass. The study concluded that all stem diameters were highly correlated with total biomass with the strongest relationships being: D_0 , D_{30} , D_{10} and DBH. Crown diameter was highly correlated with total biomass, especially in trees with relatively uniform canopies, while height was not well correlated. According to Madgwick and Satoo (1975) In Montagu et al. (2005), including height as an additional variable in allometric equations make a small

contribution to the predictive capability. Phiri et al. (2015) points out that if stands with small height variability are sampled, height sometimes does not contribute to biomass estimation.

Height as an additional independent variable may not explain more of the variation in biomass where the allometric model originated, but might make the model more applicable when transferred to other sites where a difference in DBH and height allometry exists (Ketterings et al. 2001). In contrast to the findings of Ketterings et al. (2001), Montagu et al. (2005) tested the allometric relationships of *Eucalyptus pilularis* across seven contrasting sites in Australia using the independent variables DBH and height. The study found that DBH was the most stable and that the inclusion of height decreased the performance of the model. Where tree height is incorporated in models, the biomass is often underestimated (Segura and Kanninen 2005; Goodman et al. 2014). Tree height is more difficult to measure in closed canopy broad-leaved forests with higher associated costs and error (Brown 2002; Chave et al. 2004), and incorporating height in the model requires all trees in the first phase forest inventory to be measured for height (Brown 2002).

To estimate aboveground biomass over multiple sites over a broad geographical range with many different species, non-site specific allometric equations are required. Generally, published allometric regression equations are site-specific (Montagu et al. 2005). Sampling a sufficient and representative number of trees to generate local multi-species models in a mixed-forest is time consuming and expensive (Brown 2002). Existing generic multi-species models often have four shortcomings: (1) They are constructed from limited samples, (2) they are often applied beyond their valid diameter range, (3) they don't take into account wood

specific gravity (Chave et al. 2004) and (4) they don't have a sufficient number of large trees (Brown 2002).

According to Chave et al. (2005), the most important predictors of AGB in decreasing order are: Trunk diameter, wood specific gravity, total height and forest type (wet or dry forest). When total tree height, diameter and wood specific gravity are included in the generic biomass equation, the biomass of any species from any site can be easily estimated. There is a difference in wood density between species and within species along the bole length, therefore, multispecies models will generally benefit from the inclusion of wood specific gravity as an independent variable (Navar 2008). Brown (1997) found that when species groups (tropical moist or wet hardwood species) are pooled together, highly significant prediction equations can be produced between only DBH and individual tree biomass with R^2 values of 0.98 and more. In a study by Segura and Kanninen (2005) in Costa Rica, allometric multi-species models were developed from seven species and 19 sample trees using DBH and total height as independent variables to determine total biomass. The combination of total height and DBH produced the best results compared to using only DBH in terms of the GOF. IN this case, however, models using only DBH were selected for estimating the biomass, because of the simplicity of the models using only one independent variable that is easy to measure and readily available in forest inventories.

With the constructing of generic multi-species models at least 100 trees should be included in the models, as smaller sample sizes result in higher errors. A study with the aim of developing generic multi-species models concluded that a 3.1% coefficient of variation (CV) was obtained when 300 trees were sampled to construct

volume tables in a wet tropical forest, whereas an acceptable 5% error was achieved with 150 sample trees across different species (Chave et al. 2004).

3. MATERIALS AND METHODS

3.1 STUDY AREA

3.1.1 Location and Topography

This study was carried out in patches of natural forest occurring within a plantation forest estate (Enon), managed by NCT Forestry Group (Figure 3.1). Enon is located 8 km northwest of the town of Richmond within the KwaZulu Natal Midlands (29°48'38.14"S, 30°13'33.14"E) with topography ranging from fairly flat areas to steep cliffs on the western side of the estate with slopes up to 33 degrees. The elevation of the study area extends from 964 to 1 554 m above sea level.

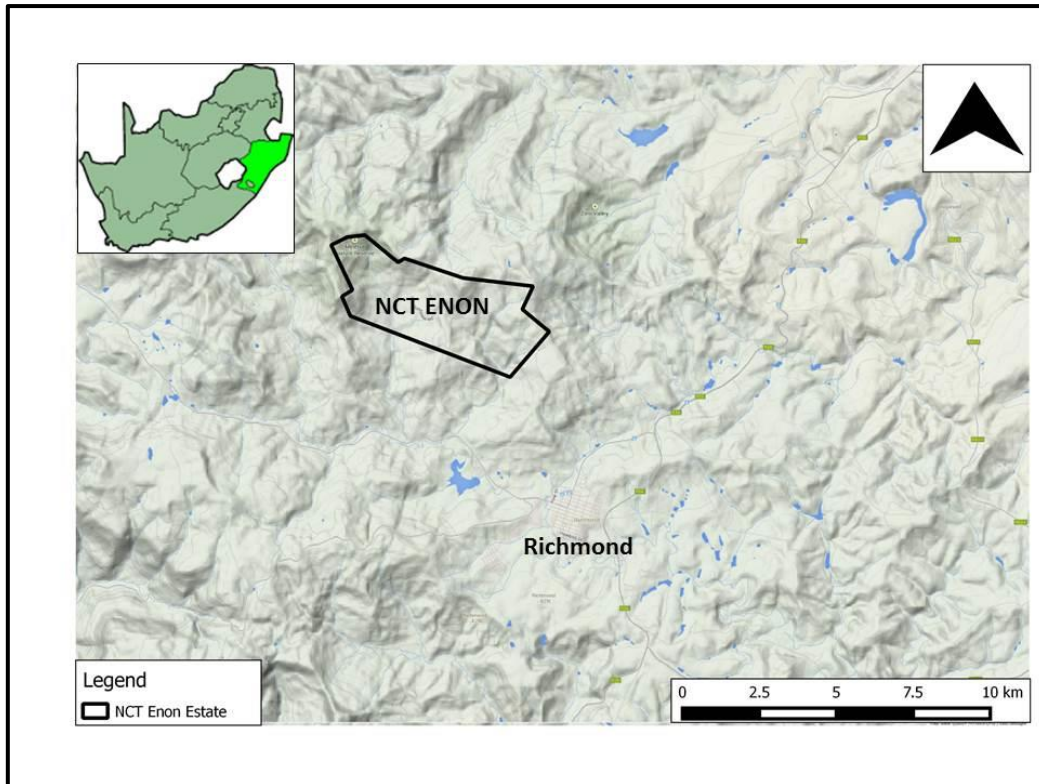


Figure 3.1: Location of NCT Enon Estate in relation to Richmond in KwaZulu Natal.

3.1.2 Climate and natural vegetation

NCT Enon estate consists of a mosaic of *Pinus*, *Eucalyptus* and *Acacia* plantations surrounded by natural forest patches. The natural forest consists of various patches varying in size, topography, species composition and forest development. The total natural forest area is 475 ha in size and the biggest portion of the indigenous forest area (>200 ha) is located on the western side of the estate. The forest patches surrounding Enon plantation are classified as being part of the Southern Mistbelt Forest Group. Forest trees occurring in the study area exhibits a variety of growth forms and are often multi-stemmed (Figure 3.2).



Figure 3.2: The variety of tree growth and architectural forms to be found within the natural forest in the NCT Enon study site. (a) Multi-stemmed trees with many stems branching below the 1.3 m DBH level, (b) Single-stemmed trees growing upright. (c) Multi-stemmed leaning trees and (d) Multi-stemmed trees growing horizontal to ground level on a slope.

The annual rainfall of Richmond is about 852 mm per annum and most of the rainfall occurs during the summer months. The average midday temperatures range from 19.4°C in June to 26°C in February (SA Explorer 2000-2004).

3.2 DEMARCATION AND STRATIFICATION OF THE STUDY SITE

3.2.1 Digitizing the natural forest areas

A 2009 aerial photo of the NCT Enon Estate was obtained from NCT Forestry Ltd. and the natural forest areas within the estate boundary were manually digitized by making use of the QGIS® (Quantum Geographical Information Services) 2.2.0 *Valmiera* program (QGIS Development Team 2014) to create a class for natural forest areas (Figure 3.3).

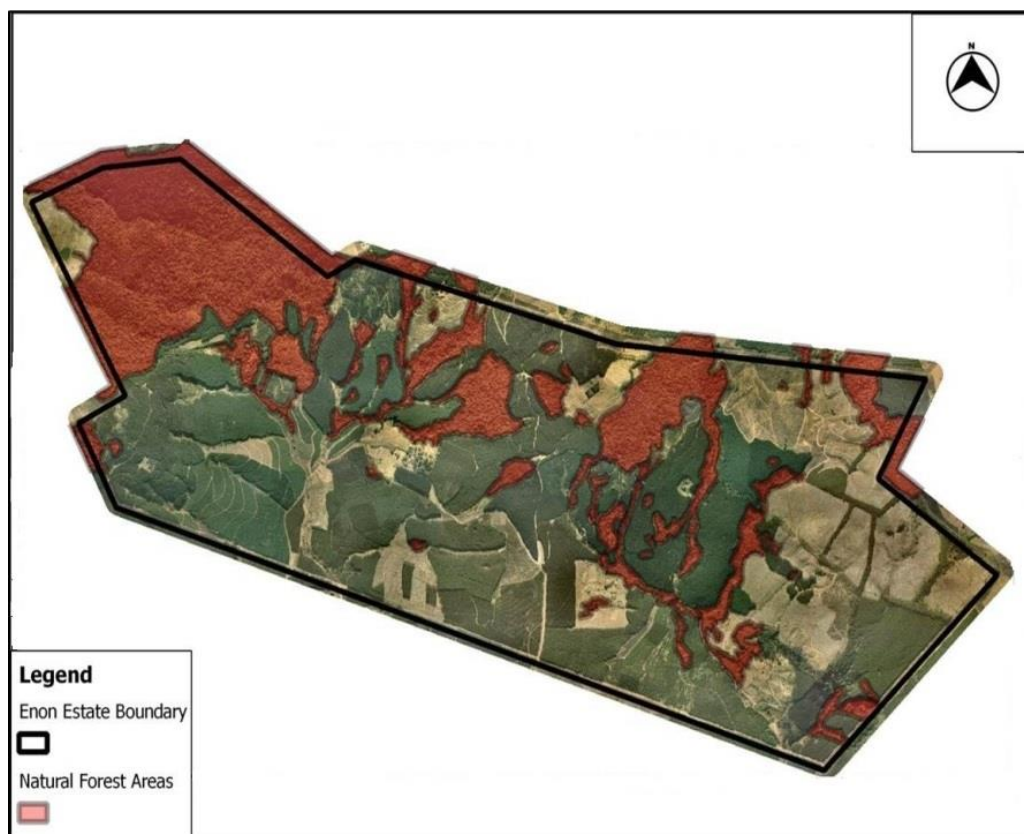


Figure 3.3: Enon Forest Estate with boundary and digitised natural forest areas.

3.2.2 Stratification of the study area

Plots were selected randomly, without having any prior knowledge of the forest area (Condit 2008). Where researchers have a choice as to where the sample plots should be located, the site variability is often not covered, leading to biased estimates (Chave et al. 2004).

Three site factors: slope, aspect and elevation were used in a stratified random sampling approach (Gibbs et al. 2007). Homogeneous segments were created, based on the selected site factors (CIFOR 2012). This pre-stratification was done to increase the sampling efficiency and to ensure the representation of the sample for different sites in the population. A digital elevation model (DEM) with 5 m resolution were obtained from the University of Stellenbosch Centre for Geographical Analysis- (CGA) and the digitized natural forest areas were stratified by the following classes based on the selected site factors using ArcView® GIS software (ESRI 2014):

- 3 Slope classes: 1) 0 – 10 degrees
2) 11 – 20 degrees
3) 21 degrees and more

- 4 Aspect classes: 1) North: 0 - 45 degrees and 315 - 360 degrees
2) East: 45 - 135 degrees
3) South: 135 - 225 degrees
4) West: 225 - 315 degrees

- 5 Elevation classes: 1) 964 – 1 082 m
2) 1 083 – 1 201 m
3) 1 202 – 1 319 m
4) 1 320 – 1 437 m
5) 1 438 – 1 555 m

Buffers 20 m width were created around the entire road network to exclude areas of high disturbance from the sampling. The site attributes (stratification and classes) were used to create 52 segments with all possible combinations between the various classes. A total of 80 points were randomly generated within the segments by using ArcView® GIS (ESRI 2014), and the points were downloaded onto a GPS to locate the points in field. During the field sampling, a further 21 points were eliminated due to insufficient forest cover and inaccessible terrain conditions leaving a total of 59 points.

During the plot inventory, data were collected from 34 sample plots covering a total of 31 segments. Due to time and money constraints, more random points could not be sampled (Figure 3.4).

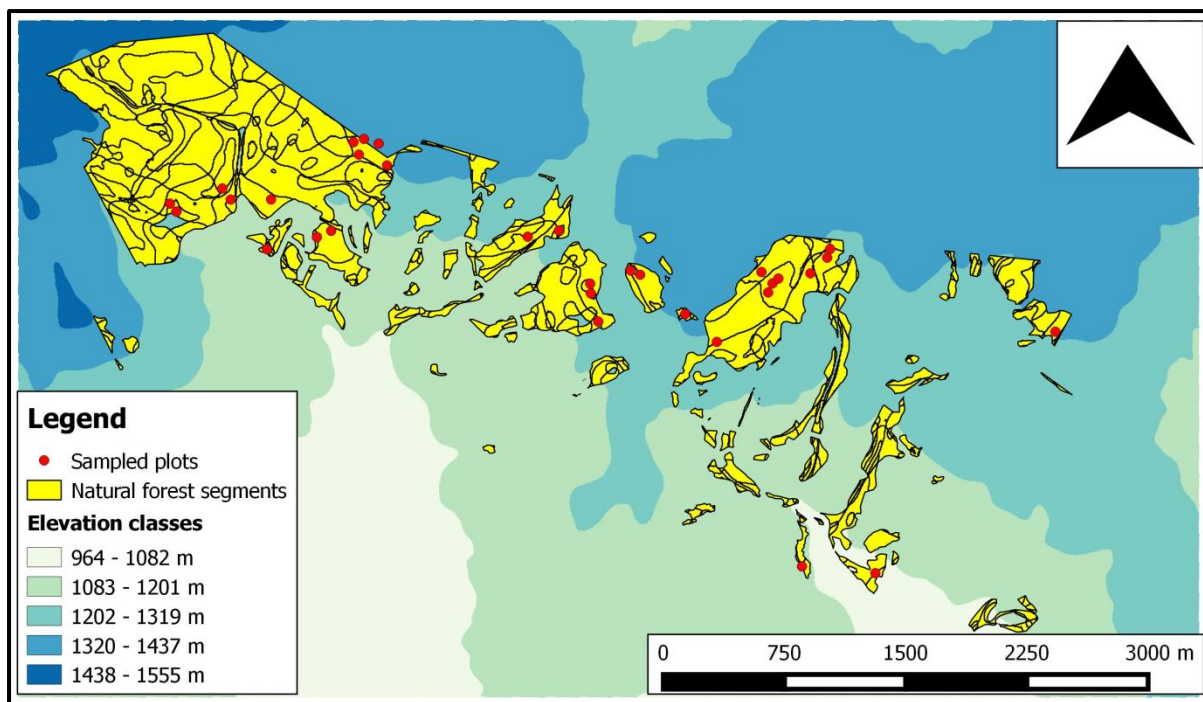


Figure 3.4: Stratified forest segments based on slope, aspect and elevation with the collected field points.

3.3 DATA COLLECTION

3.3.1 Plot sampling

34 nested forest plots with two concentric circular plots of radius 5.65 m (100 m²) and 11.28 m (400 m²) were laid out in each randomly selected plot (Figure 3.5). Within the 100 m² plots, all stems with 5 cm ≤ DBH but <10 cm were measured while in the 400 m² plots all trees with DBH ≥ 10 cm were measured. DBH of all stems within the nested plots were measured starting from the middle point of the plot moving to the outer boundary in a clockwise fashion to ensure that all trees are captured. Trees located on slopes were measured for DBH on the uphill side (CIFOR 2012). Where stem swellings occurred at DBH level, measurements for DBH were taken below and above the swelling and the average of the two readings were

reported as the true diameter (van Laar and Akça 2007). A white line and tree number were painted at 1.3 m above-ground level on the trunk for all trees measured in the plots to indicate the exact point of measurement and to facilitate future re-measurements.

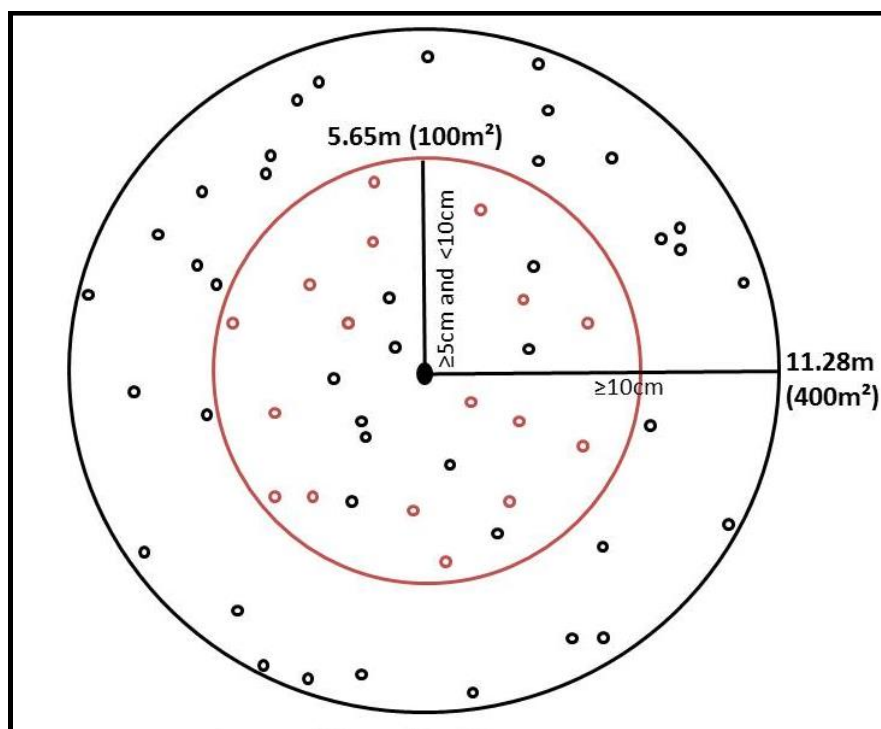


Figure 3.5: Layout of concentric circular plots used for the plot sampling. The blue dots indicate trees with DBH ≥ 5 cm and < 10 cm within the 100m² plot, while the black dots indicate trees ≥ 10 cm DBH within the 400 m² plot.

DBH, basal area and species names were recorded for all trees in the inner and outer plots. Where the main stem of trees forked below 1.3 m above-ground, all stems were measured provided that they fell within the diameter range of the nested plots as discussed above. Plot correction factors (Equation 3.1) were applied to the main sample plots and sub-sample plots, based on the slope of the plot and trees located outside the adjusted plot sizes were excluded from the inventory.

$$\text{Plot correction factor: } Plot \text{ size } (m^2) \times \cos\left(\frac{Slope}{180} \times \pi\right) \quad (3.1)$$

Where:

Plot size: Size of sub-plot (100 m²) or main plot (400 m²)

Slope: Slope in degrees

The species and basal area (m²) data collected during the inventory were then summed per plot and were ranked in from the species with the highest basal area contribution to the lowest. The two selected species were then sampled for height and AGB.

3.3.2 Height sampling of the selected species

Following methods in van Laar and Akça (2007), a minimum of 25 total tree heights (m) and crown base heights (m) were measured. Heights were measured to cover variation in site and size class distribution. The height measurements were not restricted to the sample plots, but were collected over the whole NCT Enon forest area to capture as much DBH and height variation as possible. The DBH and height curves as proposed by Kunneke et al. (2014) have been used as a stratification guide to select trees for the biomass sampling phase to ensure that as much as possible DBH and height variation are covered. A Haglöf Vertex IV hypsometer was used to measure the tree heights and special care has been used to measure the heights from the tree base. Leaning trees and trees with abnormal shapes were avoided as far as possible.

3.3.3 Selection of trees for biomass sampling

Trees were sampled according to the DBH and height stratification to cover variation in size classes across the study area. Whole tree destructive sampling was not used in alignment with DAFF conservation regulations for the area. Instead, the minimal invasive sampling approach was applied for the biomass sampling and a total of 30 trees (15 trees for each of the two selected species: *X. monospora* and *C. africana*) were selected across six sites (Figure 3.6). Trees sampled for biomass were not restricted to the sampled plots, but were selected from the whole NCT forest area according to their coverage of the observed differences in DBH, tree height, terrain variability factors and the ease of access for sampling. Trees were sampled in intervals of 10 cm DBH classes and 5 m height classes to cover the observed DBH and height variation over the whole size range. DBH, crown diameter (m), total tree height and crown base height were determined for each selected sample tree prior to sampling. Crown diameters were measured from below the canopy with a measurement tape on a north to south and east to west axis, making sure to measure the complete canopy diameter in each direction. The canopy diameter in both directions were summed and divided by two to get the average diameter.

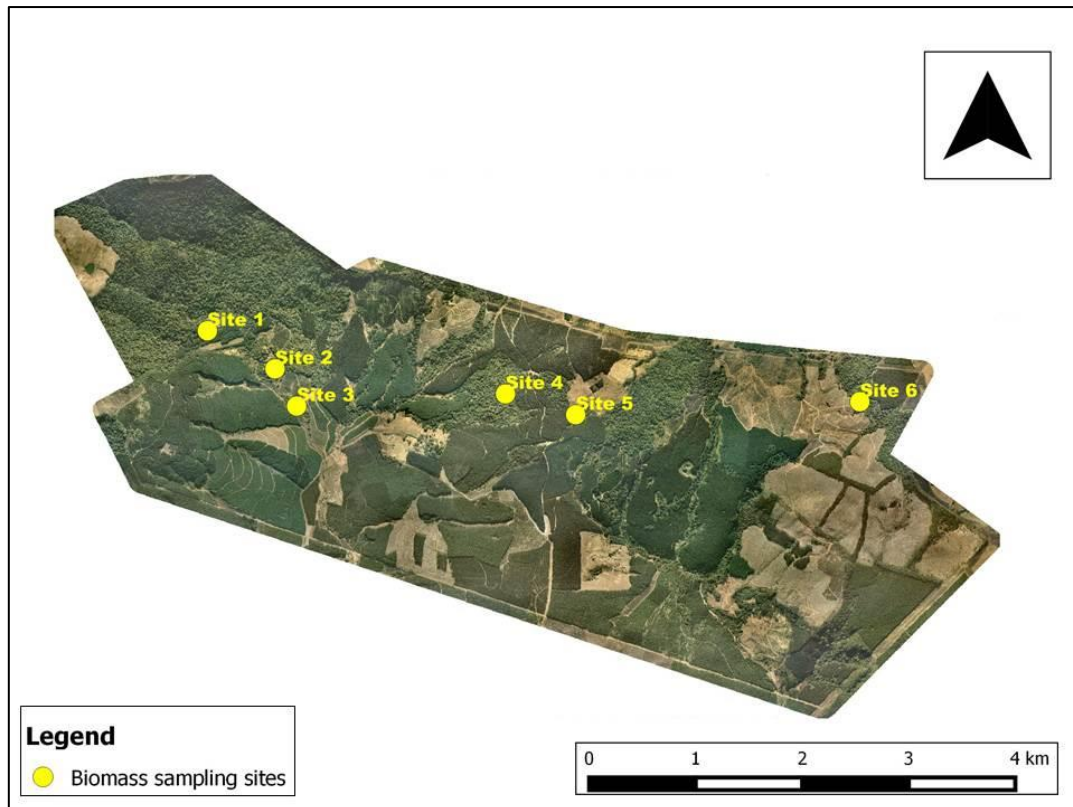


Figure 3.6: Biomass sampling sites for *Xymalos monospora* and *Celtis africana* at NCT Enon Estate

3.3.4 Trees sampled for biomass

Sampling of stemwood for volume and density

Since whole tree destructive harvesting was not used, basic density determination was restricted to the collection of core samples along the stem of sample trees. Two core samples of 5 mm diameter each were collected from each sampled tree: one at DBH level and one at crown base height to determine the stem density, making sure to reach the pith of the tree. All core samples were collected on the northern side of the tree. Where sample trees were located on a slope, the DBH and crown base core samples were collected perpendicular to the slope. The stem diameters (cm)

were recorded at the specific point where the core sample was taken. The stem samples were collected for later processing in the laboratory to determine basic density.

To calculate the stem volume, the sample trees were divided in topological levels: The main stem section is Level 1, where the main stem forks is Level 2 and where level two forks is Level 3 etc. A tree climber equipped with harness, ropes and all necessary safety equipment (Figure 3.7) was contracted to measure the over bark stem diameters of the stem sections at least every 2 m along the stem, starting from ground level and moving to the top of the tree. The lengths of all stem sections between nodes and their thick and thin end diameter were recorded as far as it was within reach and safe for the tree climber to access. Branch sections on which the thick and thin end diameters (cm) and lengths (m) could be measured were treated and measured as stem sections to overcome difficulties in differentiating between stem and branch sections, which is a common problem in broad-leaved multi-stemmed trees (Seifert and Seifert 2014). Where stem lengths between nodes could not be measured due to safety and accessibility issues, the sections were treated as branches and measured for thick end diameters. Stem volume was calculated by making use of the geometric formula for the truncated cone (Equation 3.5) (Seifert and Seifert 2014). Sketches with the branching pattern and positions for each of the selected trees were created for future referencing purposes.



Figure 3.7: The tree climber equipped with safety equipment, progressing towards the top of the tree.

Sampling of branches

On average, three to five branches per tree were randomly sampled over a range of branch diameters and horizontal and vertical distributions within the tree to cover as much variation as possible between branch mass and foliage mass, and exposure of branches to sunlight. A total of 35 branches were sampled for *C. africana* and 33 branches for *X. monospora* and branch diameter (cm) and length (m) recorded for all sampled branches. Apart from the sample branches all branch diameters for each tree were measured with a diameter tape, 10 cm from the branching point or at the point above the branch buttress. All branch diameter measurements were taken

perpendicular to the axis of the branch to be consistent and avoid ovality effects (Seifert and Seifert 2014).

Branch lengths of sampled branches were measured with a measuring tape, starting from the cutting point and measuring all along the axis of the branch to the tip. Foliage was manually separated from the sampled branches and stored in separate paper bags from the branches, for mass and density determination in the lab. The paper bags were marked with the tree number, branch number and contents (foliage or branches) for identification purposes.

3.4 LABORATORY PROCEDURES

3.4.1 Determining the volume and basic density of the core samples

To determine the volume (cm^3) of the core samples, three methods were tested and the standard deviations (SD) of the measurements were compared on a sub-set of five samples: (1) Water displacement, with measuring the displaced water volume (2) water displacement with a balance and, (3) multiplying the basal area (mm^2) and length (mm) of core samples measured with Vernier calliper. The SD for the three respective methods was: 1.55, 1.52 and 1.43. Method three was selected since the method is quick, showed the lowest SD and can be used for objects uniform in shape (American Society for Testing and Materials 2008) (Figure 3.8).

To determine the dry weight in grams for the core samples, the cores were dried at $103 \pm 2^\circ\text{C}$ (American Society for Testing and Materials 2008) until constant weight. The basic density cm^3 was determined by dividing the total dry weight of the core sample by the total volume determined. To determine the basic density of stem

sections for each sample tree, the densities obtained from the core samples at DBH level and crown base height were averaged and scaled up to the complete stem section of the tree calculated by Equation 3.2 (Seifert and Seifert 2014).

$$BM = V \cdot R \quad (3.2)$$

Where:

BM = Oven dry biomass (kg)

V = volume of stem sections (m³)

R = basic density of the stem samples (kg/m³)

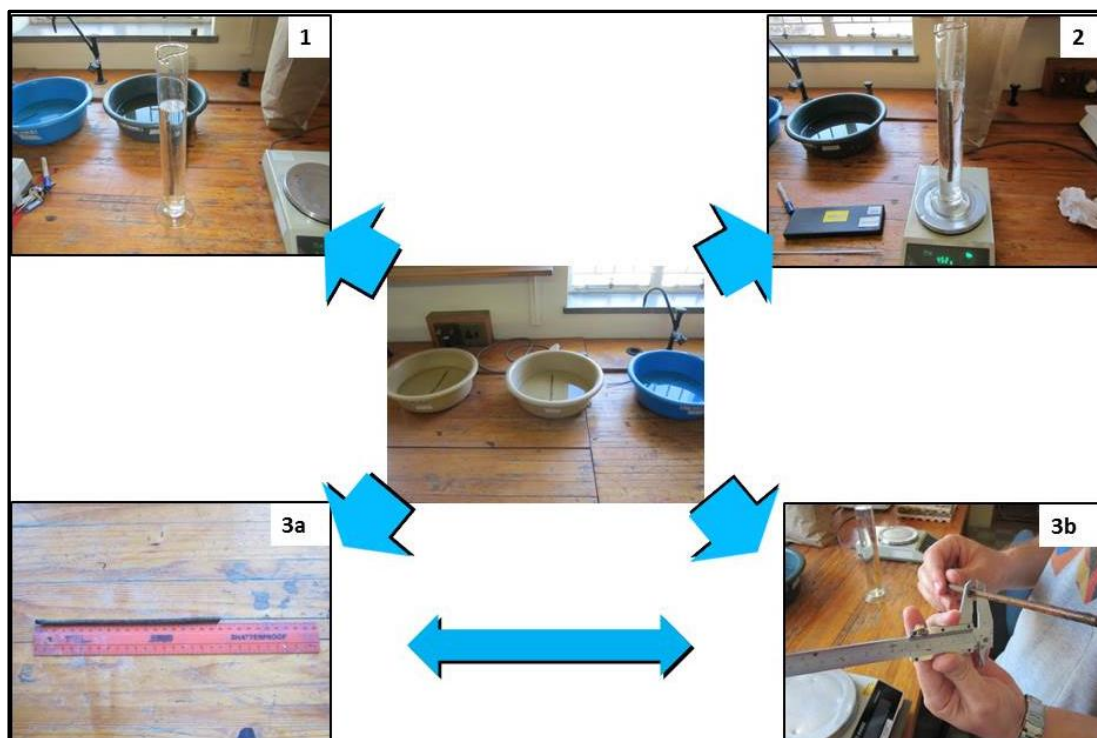


Figure 3.8: Methods tested to determine the volume of the core samples. Picture 1 indicates the water displacement method with only the volumetric flask while picture 2 indicates the water displacement method with the volumetric flask and balance and picture 3a and 3b indicates volume determination with the Vernier calliper where the core sample is measured for length and diameter.

3.4.2 Determining the dry mass of the branch and foliage material

Foliage and branch material were dried at two drying regimes in the drying ovens, first at 60°C and thereafter 103±2°C until constant weight. Branch and foliage material were first pre-dried at 60°C in a kiln (Kiefer) for practical purposes, since the Kiefer has more space compared to the limited oven-space available for the laboratory ovens operating at 103±2°C (Figure 3.9). Oven operating temperatures were regularly confirmed with thermometers to ensure that the ovens operate at the

recommended temperatures. Paper bags with branch and foliage material were weighted and weights of all bags (kg) across the time period of the drying regime were recorded.

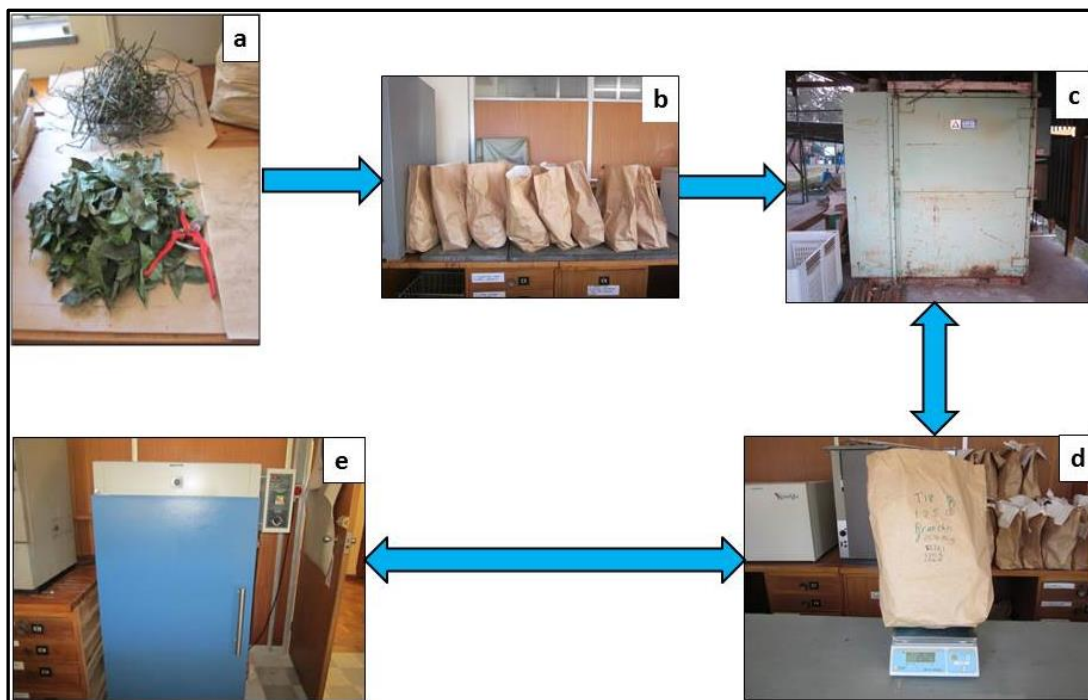


Figure 3.9: Process flow for drying the branch and foliage material. Separating the branch and the foliage material (a), storing the foliage and branch material in separate paper bags (b), drying the material first at 60°C in the Kiefer (c) and then at 103±2°C (e), weighing the samples (d) until equilibrium weight first at 60°C and then 103±2°C.

3.5 UPSCALING OF SAMPLES

The biomass upscaling procedures discussed by Seifert and Seifert (2014) were implemented to upscale from sample to tree level (Upscaling I) and from tree to stand level (Upscaling II). Upscaling of samples were done separately for the crown

and stem sections and for the two selected species. The crown components were further separated into foliage and branch material.

Both simple linear regression (Equation 2.5) and multiple linear regression (Equation 2.7) equations and ln-transformed simple (Equation 2.6) and multiple linear regression (Equation 2.8) equations were used and various independent variables were tested.

3.5.1 Upscaling I: From sample to tree level

Branch length models

Three branch length models were developed for each of the two selected species. The branch length models were used as an additional independent variable to estimate the branch and foliage mass of branches from the sample trees measured for diameter but not sampled for biomass. Independent predictor variables used in the developed models include branch diameter in cm (d), d^2 and the ln-transformed d (Table 3.1).

Table 3.1: Branch length models developed for *Xymalos monospora* and *Celtis africana*.

Species	Dependent variable	Independent variables	References
<i>X. monospora</i> <i>C. africana</i>	length	d	(van Laar and Akça 2007)
	ln (length)	ln (d)	(Medhurst et al. 1999; van Laar and Akça 2007)
	length	d ² , d	(van Laar and Akça 2007)

Note: d is branch diameter (cm). Branch length was recorded in m.

Branch length models were evaluated and the best models were selected based on their compliance with the assumptions of linear regression and goodness of model fit.

Upscaling of stem biomass

Volume of stem sections was calculated by making use of the geometric formula for a truncated cone (Seifert and Seifert 2014). The thick and thin end diameters of all stem sections and branch sections that could be measured were measured at least every two meters or between nodes. The calculated volumes (m³) of the measured stem sections were then multiplied with the average basic density values (kg m⁻³) obtained from the core samples at DBH and crown base height for the specific sample tree. The total stem mass was obtained by adding all stem section volumes.

Upscaling of crown biomass

Branches were divided into branch and foliage material and the components were upscaled separately for each species. After the material was physically divided into components and dried, regression models were developed to estimate branch and foliage biomass. The mass of the branches and foliage of sample trees of each species were pooled separately and the data was used to develop allometric models to estimate the branch and foliage of branches which were only sampled for diameter. Branch diameter (cm), branch length (m) and basal area (cm²) were then used as independent variables to estimate the biomass (Table 3.2).

Table 3.2: Branch and foliage mass models for *Xymalos monospora* and *Celtis africana*.

Species	Dependent variable	Independent variable	References
<i>X. monospora</i> <i>C. africana</i>	B _{bm}	ba	(Grote 2002; van Laar and Akça 2007)
	ln (B _{bm} / F _{bm})	ln (d)	(van Laar and Akça 2007)
	ln (B _{bm} / F _{bm})	ln (d ² l)	(Parresol 1999)
	ln (B _{bm} / F _{bm})	ln (d), ln (l)	(van Laar 1973)

Note: d is branch diameter (cm), l is branch length (m), B_{bm} is branch biomass (kg) and F_{bm} is foliage biomass (kg) for individually estimated branches of sampled trees measured for branch diameter, but not sampled.

The branch and foliage mass models were evaluated and the best models were selected based on compliance with the assumptions of linear regression and GOF model evaluation criteria.

3.5.2 Upscaling II: From tree to stand level

Height Models

Two total height candidate models were parameterised for each of the selected species. These models can potentially be used to estimate the height of trees sampled during the plot sampling as an additional predictor variable to estimate the mass of the tree components. Independent variables in the models include DBH, DBH² and the ln-transformed DBH (Table 3.3).

Table 3.3: Fitted total height models for *Xymalos monospora* and *Celtis africana*

Species	Dependent variable	Independent variable	References
<i>X. monospora</i> <i>C. africana</i>	ln (Height)	ln (DBH)	(Chave et al. 2005; van Laar and Akça 2007)
	Height	DBH, DBH ²	(van Laar and Akça 2007)

Note: DBH is diameter at breast height (cm). Total height was recorded in (m).

The height candidate models were evaluated and models were selected based on compliance with the assumptions of linear regression and GOF criteria.

Upscaling of stem biomass

The combined total stem mass of each sampled tree of the two selected species was used to develop models to estimate the stem mass of the other trees measured only for DBH during the plot sampling. Species-specific stem mass models were developed to estimate the stem mass on the individual tree level for each of the two selected species. The stem mass of the two selected species were then combined

and models were developed to estimate the total stem mass of other forest tree species measured during the plot sampling (Table 3.4). Independent predictor variables included in the models were DBH and total height.

Table 3.4: Stem mass models for *Xymalos monospora*, *Celtis africana* and all the tree species sampled during the plot sampling.

Species	Dependent variable	Independent variable	References
<i>X. monospora</i> <i>C. Africana</i> All species	ln (Stem)	ln (DBH)	(Verwijst 1991; Segura and Kanninen 2005)
	ln (Stem)	ln (DBH, h)	(van Laar and Akça 2007)
	ln (Stem)	ln (DBH ² h)	(Verwijst 1991; Cole and Ewel 2006)

Note: DBH is diameter at breast height (cm) and h is total tree height (m). Stem mass were recorded in kg.

The stem mass models were evaluated and models for upscaling to the ha level were selected based on their compliance with the assumptions of linear regression, GOF model evaluation criteria and parsimony concepts.

Upscaling of crown biomass

The combined branch and foliage mass estimated from the upscaling step one were used to fit models to estimate the total branch and foliage crown mass of trees sampled during the plot sampling. Species-specific and combined-species models were fitted with a selection of independent variables including DBH and total tree height to estimate the total branch and foliage crown mass at the plot and ha level (Table 3.5).

Table 3.5: Total branch and foliage crown mass models for *Xymalos monospora*, *Celtis africana* and all the forest tree species measured during the plot sampling.

Species	Dependent variable	Independent variable	References
<i>X. monospora</i> <i>C. africana</i> All Species	Branch / Foliage	DBH	(van Laar and Akça 2007)
	ln (Branch /Foliage)	ln (DBH)	(Brandeis et al. 2006)
	ln (Branch / Foliage)	ln (DBH ² h)	(Overman et al. 1994; Cole and Ewel 2006; Brandeis et al. 2006)
	ln (Branch /Foliage)	ln (DBH), h	(van Laar and Akça 2007)

Note: Total branch and foliage mass was estimated in kg. DBH is diameter at breast height (cm) and h is total tree height (m).

The total branch and foliage crown mass models were evaluated and the best models were selected based on their compliance with the assumptions of linear regression, GOF model evaluation criteria and parsimony concepts and used to upscale the branch and foliage mass to plot and ha level.

Estimating the above-ground biomass

The total stem, branch and foliage biomass for each of the selected species were combined and four species-specific total biomass models were developed. Thereafter the mass of the two selected species were combined and four total mass models were developed for the combined species (Table 3.6). The species-specific models were used to estimate the total aboveground dry mass in Mg ha⁻¹ for the selected species and the combined model for all the species measured during the plot sampling.

Table 3.6: Total mass models for *Xymalos monospora*, *Celtis africana* and all the forest tree species.

Species	Dependent variable	Independent variable	References
<i>X. monospora</i> <i>C. africana</i> All species	ln (TOTAL)	ln (CrDm)	(Jonson and Freudenberger 2011; Goodman et al. 2014)
	ln (TOTAL)	ln (DBH,h, ρ)	(Chave et al. 2015)
	ln (TOTAL)	ln (DBH)	(Verwijst 1991; Specht & West 2003; Segura and Kanninen 2005; Brandeis et al. 2006)
	ln (TOTAL)	ln (DBH ² h)	(Verwijst 1991; Overman et al. 1994; Cole and Ewel 2006; Brandeis et al. 2006)

Note: Total is total aboveground biomass (kg), CrDm is crown diameter (m), DBH is diameter at breast height (cm), h is total tree height and ρ is basic density (kg m^{-3}).

The total mass models were evaluated according to the same principles as the other models.

Although the total mass models were fitted, the models were not used for the purpose of this study to estimate the total mass per ha. Total mass per ha was calculated by adding the estimated total stem, branch and foliage biomass for the species-specific models and for the combined model. The total mass was then calculated per plot by multiplying the total estimated weight of each tree in the plot sampling phase with the respective plot expansion factor to get the weight of the specific tree per ha. The average mass per ha was then calculated by calculating the sum of the tree mass in each plot and by obtaining the average between all the plots.

3.6 DATA ANALYSIS

For statistical analysis and upscaling of biomass components, R-Statistical software was used (R Core Team 2014) in R Studio (RStudio 2014). Various models were tested with various combinations of independent variables for each biomass component. Models were evaluated for compliance to the assumptions of linear modelling and by GOF model evaluation criteria.

3.6.1 Assumptions in linear regression

Selected linear models were tested to confirm whether they comply with the assumptions of linear regressions and further desirable traits of biomass models: (1) Additivity (2) Residuals that are normally distributed and of constant variance (homoscedasticity), and (3) residuals that are independent of each other (Picard et al. 2012; Gentleman et al. 2011). Biomass data often exhibits heteroscedasticity meaning that as the tree dimensions increase, an increase in variability of the biomass can also be expected (Picard et al. 2012; Seifert and Seifert 2014). With the application of \ln -transformations to the data, the variance was equalised, in an attempt to satisfy the assumptions of homoscedasticity (Verwijst 1991; Sileshi 2014) and linear regression was used instead of non-linear regression (Seifert and Seifert 2014). Within this study, both simple linear regression models and multiple linear regression models using \ln -transformed and un-transformed variables were used. The residuals were plotted against the predicted values and plots were visually assessed to determine whether there was any structure or pattern amongst the residuals indicating heteroscedasticity or dependence (Picard et al. 2012). A Shapiro-Wilk test was performed to test that the residuals were normally distributed.

3.6.2 Biomass correction factors

Ln-transformed models can in principle be used for estimating the mass of the biomass components if the residuals are normally distributed (Chave et al. 2005). Ln-transformed data exhibits a bias in the estimation of biomass when transformed back to the arithmetic unit. Uncorrected biomass values often underestimate the actual biomass value (Seifert and Seifert 2014). The biased estimations from using ln-transformed models in this study were corrected by multiplying the estimated value with the following correction factor (CF) (Equation 3.3) (Baskerville 1972 as also used by Chave et al. 2005):

$$CF = \exp\left(\frac{RSE^2}{2}\right) \quad (3.3)$$

Where:

CF= Biomass Correction Factor

RSE= Residual Standard Error of the regression

3.6.3 Extrapolation beyond the regression range of samples in the upscaling process

Due to the constraints inherent in the sampling procedure, such that branches above a certain point in the trees could not be reached and had to be sampled at lower heights, samples for all components in the calibration range did not span the size range in the final data set. Because of this reason a solution needed to be obtained for a model that needed to be applied outside its calibration range. No precedent for this problem could be found in the literature on which to draw. A solution was

therefore devised to ascertain, with the greatest possible confidence, the reasonableness of extrapolating of the biomass model. The approach assumed is based on allometric theory that states that biomass scales with other tree dimensions such as DBH or branch diameter and this relationship follows an allometric principle. Thus, a specific allometric coefficient can be identified (Niklas 1994), which describes these proportions. In this study it means if stabilisation of the allometric coefficient with increasing data points is observed the assumption that the allometric coefficient will stay stable in the extrapolation range can be made with reasonable confidence.

In practice it was done with the stepwise inclusion of more samples, with prior samples retained in each subsequent step, but with newly introduced samples of a larger size class. If the slope between the predicted (biomass) and predictor variable stabilised with increasing size classes that were included, it would reasonably be expected to remain stable for larger classes. That is, where the mass of tree components needed to be estimated beyond the range of dimensions used to develop the allometric regression, the respective sampled tree components were divided in five diameter classes to test the stability of allometric relationships of the selected model across the diameter range.

The slope of the allometric regression with minimum and maximum confidence intervals (Equation 3.4) were assessed by incrementally fitting regressions (Equation 2.6) on the first, on the first and second, on the first, second and third diameter class, etc. When the curve stabilizes, it can be expected with a certain confidence that the selected allometric equation will also produce reliable results in the extrapolation region beyond the parameterization range.

$$CI = \text{Slope} \pm Se * t \quad (3.4)$$

Where:

CI= Min/Max confidence intervals

Slope= Slope of the independent variable

Se = Estimated standard error

t = Factor from the T-table, depending on the significance level (0.05 here) and the sample number

3.6.4 Additivity of regression models

Additivity of models were assured by using the same independent variables and model form throughout upscaling step one and two for each of the respective biomass components (Cunia and Briggs 1984; Parresol 1999; Magalhães and Seifert 2015b).

3.6.5 Goodness of fit model evaluation criteria

To select the best model in this study, AIC, RMSE and R^2 have been used as GOFs for this study. The results obtained from the GOFs can be used to compare the results of biomass studies. Models with less independent variables have also been selected, as they are more parsimonious (Burnham and Anderson 2002; Sileshi 2014). Models were selected on the basis of having the least number of variables, explaining most of the variation in the AGB. The more variables a model have the more will the accumulated error be, since each variable contains measurement error and error in the estimation of the parameters (Sileshi 2014).

4. RESULTS

4.1 PLOT SAMPLING

4.1.1 Diameter distribution of all species during the plot sampling

A test of kurtosis performed on the DBH distribution (Figure 4.1), indicated a leptokurtic distribution with values >3 (8.497) with a high probability for extreme values. A test of skewness performed indicated a value >0 (2.027) where the distribution is skewed to the right and that most values are concentrated left of the mean with extreme values to the right. Thus, most of the recorded stems were in the smaller DBH range of between 10 - 20 cm while the fewest stems were recorded within the DBH range between 70 - 120 cm DBH (Figure 4.1).

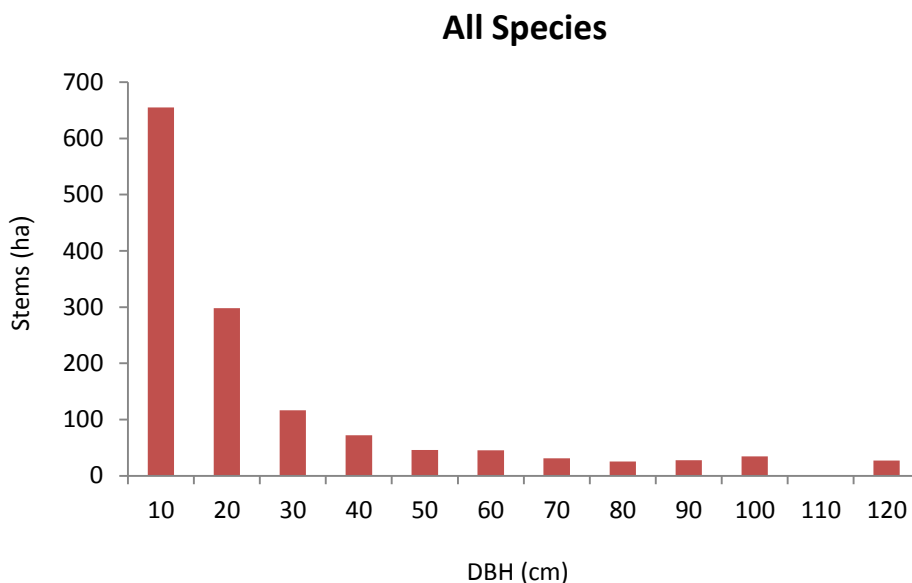


Figure 4.1: Diameter distribution of all species with a total of 1379 stems ha^{-1} .

4.1.2 Basal area coverage for all recorded species

Seven of the recorded species contributed to 72.74% of the total basal area (Figure 4.2). *Xymalos monospora* had the highest basal area contribution of 29.09% followed by *Celtis africana* and *Combretum kraussii*, each contributing to 17.87% and 8.36%.

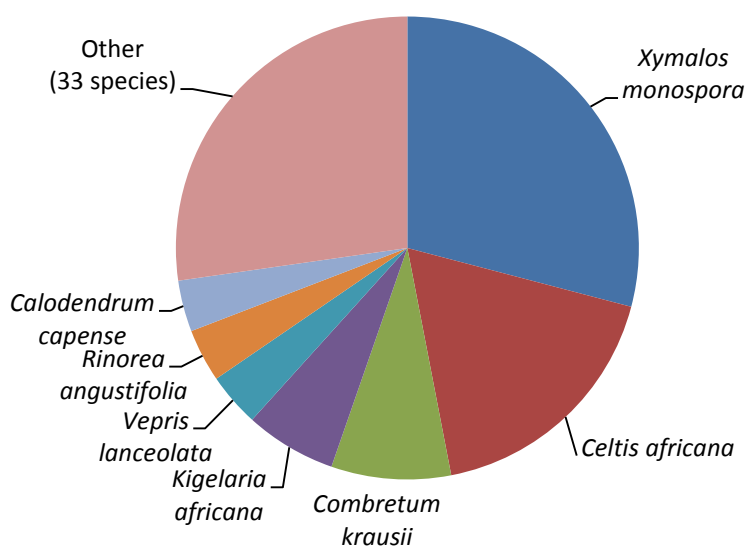


Figure 4.2: Percentage basal area coverage of the recorded species within the 34 nested plots.

4.1.3 Diameter distribution of the two top basal area contributors

Most of the measured stems were in the 10 - 20 cm DBH classes with no recorded stems for the 90 - 100 cm and 100 - 110 cm DBH classes. A test of kurtosis performed, indicated a leptokurtic distribution with values >3 (9.103) with a high probability for extreme values. A test of skewness performed indicated a value >0

(1.923) where the distribution is skewed to the right and that most values are concentrated left of the mean with extreme values to the right (Figure 4.3).

X. monospora

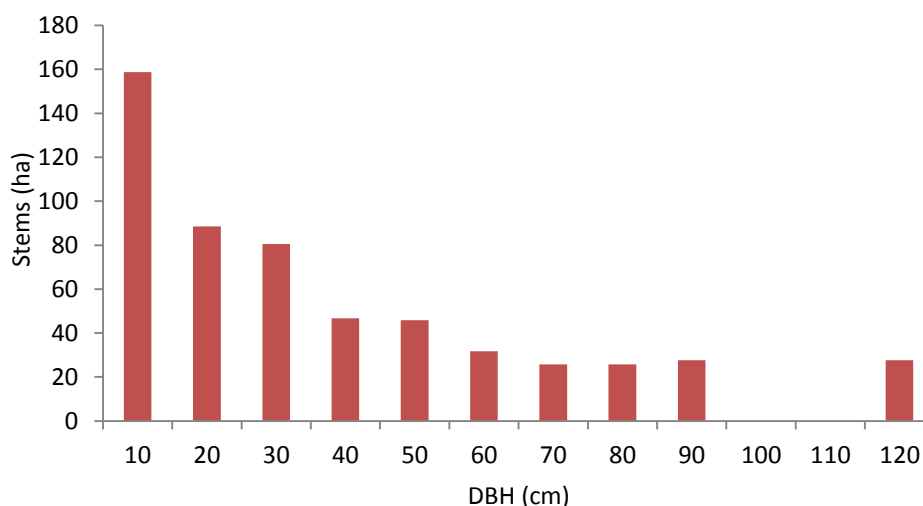


Figure 4.3: Diameter distribution of *Xymalos monospora* with a total of 559 stems ha⁻¹.

The majority of the recorded stems for *C. africana* were between 10 - 20 cm and 20 - 30 cm DBH. No stems were recorded for the DBH range between 70 - 80 cm and 80 - 90 cm. However, a small number of very large (100 - 110 cm) *C. africana* trees were found in the plots. A test of kurtosis indicated a leptokurtic distribution with value >3 (5.236) indicating a high probability for extreme values. A test of skewness performed indicated a value >0 (1.428) indicating that the distribution is skewed to the right and that most values are concentrated left of the mean with extreme values to the right (Figure 4.4).

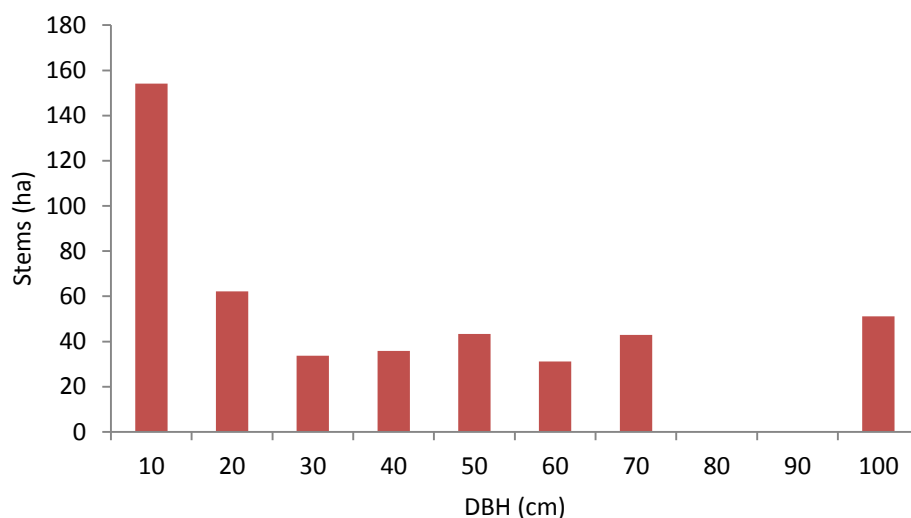
C. africana

Figure 4.4: Diameter distribution of *Celtis africana* with a total of 454 stems ha⁻¹.

The inventory results in Table 4.1 indicate that the maximum recorded DBH for *X. monospora* is higher than the maximum value for *C. africana*, but the standard deviation from the mean is higher for *C. africana* than for *X. monospora*. Mean calculated stems per ha were also higher for *X. monospora* than for *C. africana*.

Table 4.1: Measured DBH and stems per ha of all the species, *Xymalos monospora* and *Celtis africana* measured in inventory plots.

Species	<i>n</i>	Measured DBH (cm)				Measured stems/ha			
		Min	Max	Mean	SD	Min	Max	Mean	SD
All species	902	5	113	20.2	15.3	258	3 640	1379	667

<i>X. monospora</i>	187	6	110	26	15	51	787	559	195
<i>C. africana</i>	93	5	97	27.47	18.27	25	678	454	137

Note: *n* is the number of measured stems, Min is the minimum and Max is the maximum value, the mean and SD is the standard deviation from the mean.

4.2 BIOMASS SAMPLING

4.2.1 Height sampling of trees

Diameter and height distribution of Xymalos monospora and Celtis africana sampled for height and biomass

Larger trees with higher DBH values were sampled as part of the DBH and height stratification for *X. monospora* than the ones that were sampled for biomass as reflected in the maximum and the mean values. The height range between trees sampled for the DBH and height stratification and biomass were very similar (Table 4.2). Figure 4.5 shows the DBH and height distribution of trees sampled for the DBH and height stratification and for biomass.

C. africana trees sampled for the DBH and height stratification showed very similar values compared to trees sampled for biomass *i.t.o.* their DBH and height distribution (Table 4.2). Figure 4.6 shows the DBH and height distribution of trees sampled for the DBH and height stratification and for biomass.

Table 4.2: Diameter and height distribution of *Xymalos monospora* and *Celtis africana* measured for height and biomass

Species	Sampling type	Sample size (<i>n</i>)	Measured DBH (cm)				Measured Height (m)			
			Min	Max	Mean	SD	Min	Max	Mean	SD
<i>X. monospora</i>	Height	35	5.7	74.5	33.03	16.80	4.9	19.6	12.58	3.46
	Biomass	15	2	54.5	26.93	16.63	2.8	19.2	12.94	5.12
<i>C. africana</i>	Height	40	2.4	97	35.30	21.90	4.1	27.3	16.92	5.72
	Biomass	15	2.8	94.5	34.33	25.98	3.5	22.4	15.13	6.03

Note: Min is the minimum and Max is the maximum value, the mean and SD is the standard deviation from the mean.

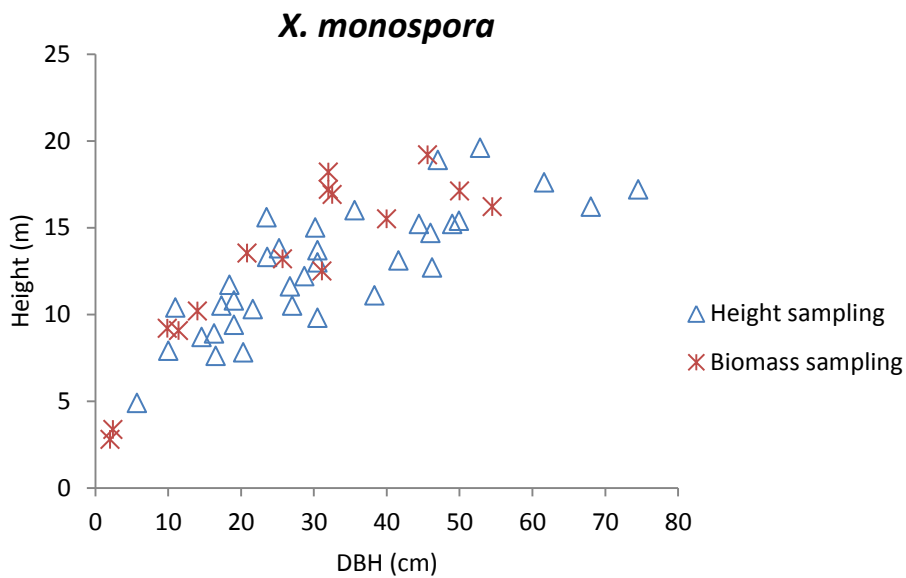


Figure 4.5: *Xymalos monospora* trees sampled for height and biomass

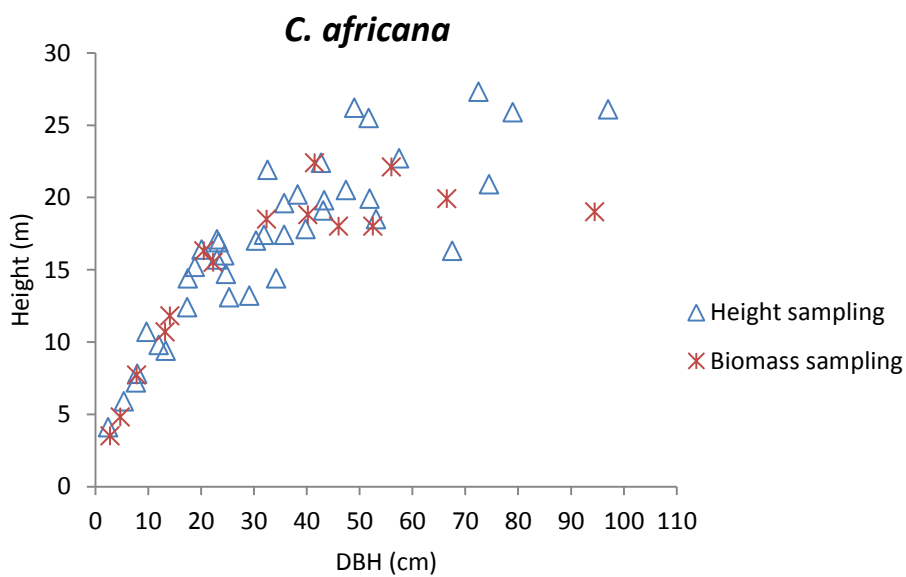


Figure 4.6: *Celtis africana* trees sampled for height and biomass

4.2.2 Mean wood density of sampled trees

The mean wood density value for *X. monospora* was lower than for *C. africana* and *X. monospora* had a lower standard deviation from the mean than *C. africana* (Table 4.3).

Table 4.3: Mean wood density for *Xymalos monospora* and *Celtis africana*

Average core wood density (kg m ⁻³)				
Species	Min	Max	Mean	SD
<i>X. monospora</i>	396	543	459.63	41.22
<i>C. africana</i>	301	655	573.07	88.76

Note: Min is the minimum and Max is the maximum value, SD is the standard deviation from the mean

Two outliers were also present in the dataset for *C. africana*. A t-test comparing the mean wood density between species showed that the difference in density was highly significant ($p < 0.05$) (Figure 4.7).

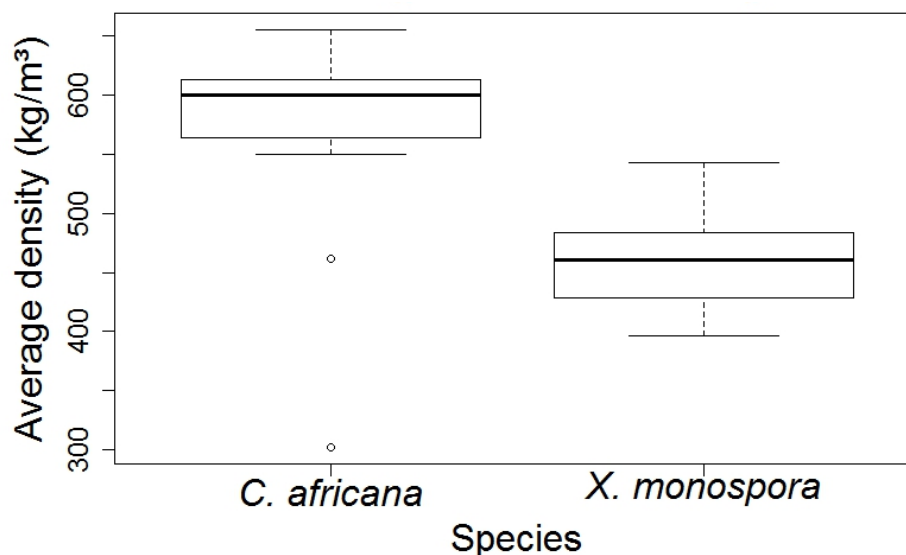


Figure 4.7: Mean wood density of *Celtis africana* and *Xymalos monospora*. The bold lines represent the average wood density, the whiskers the minimum and maximum values while the bottom and top of the box shows the 25th and 75th percentiles respectively.

4.2.3 Biomass models to scale up from sample to tree level

Branch length models

Three branch diameter and length models were fitted for *C. africana* and *X. monospora* (Table 4.4). Models include In-transformed models (models 4.2, and 4.5), untransformed models (models 4.1, and 4.4) and models incorporating d and d^2 variables (models 4.3, and 4.6). The untransformed models (models 4.1, and 4.4) hold R^2 values of 0.75 and 0.83 for *X. monospora* and *C. africana* respectively, while the transformed models (models 4.2, and 4.5) hold R^2 values of 0.95 and 0.91 respectively.

Table 4.4: Branch length models for *Xymalos monospora* and *Celtis africana*

Species	Model	Dependant variable	Independent variable	Parameter estimates (with p-values in parentheses)			CF	R ²	RMSE
				b ₀	b ₁	b ₂			
<i>X. monospora</i>	4.1	length	d	1.005 (<0.001)	0.380 (<0.001)			0.75	0.780
	4.2	ln(length)	ln(d)		0.694 (<0.001)		1.029	0.95	0.230
	4.3	length	d ² , d		0.795 (<0.001)	-0.029 (<0.001)		0.96	0.623
<i>C. africana</i>	4.4	length	d	1.091 (<0.001)	0.556 (<0.001)			0.83	0.735
	4.5	ln(length)	ln(d)	0.248 (<0.001)	0.704 (<0.001)		1.016	0.91	0.176
	4.6	length	d ² , d		1.026 (<0.001)	-0.038 (<0.001)		0.97	0.682

Note: d is branch diameter (cm) and length (m). The b₀, b₁ and b₂ values are the parameter values with the p-values in parentheses.

The parameter values for all models were significant ($p < 0.05$), except for the intercept values of models 4.2, 4.3 and 4.6, which were not significantly different from 0 ($p > 0.05$). The models with not significant intercept values were all re-fitted without the intercept. The RMSE values were the lowest for the ln-transformed models (models 4.2, and 4.5) and highest for models 4.1 and 4.4.

Model 4.2 [$\ln(\text{length}) = 0.694 \ln(d)$] and Model 4.5 [$\ln(\text{length}) = 0.248 + 0.704 \ln(d)$] were selected as the best performing models since the models having relatively good R² values and low RMSE values. Although the intercept of model 4.2 proved to be not significant and refitted without the intercept, the model was not rejected. Figure 4.8 shows the relationship between the transformed model (Model 4.2) for *X. monospora* and the ln-transformed branch diameter and length model (Model 4.5) for *C. africana*.

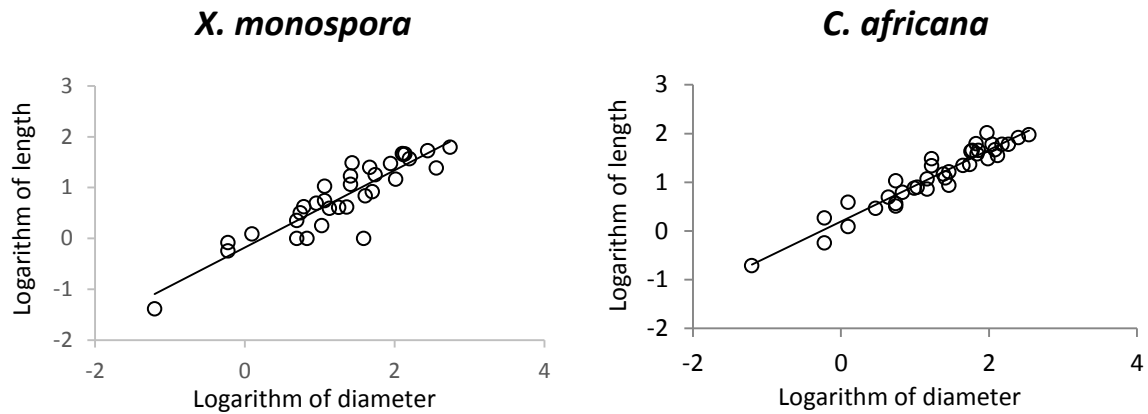


Figure 4.8: Diameter and length linear models for *Xymalos monospora* (Model 4.2) and *Celtis africana* (Model 4.5).

The predicted branch length values for the two selected models plotted against the residuals, show that there were no clear pattern and that there was visually no obvious heteroscedicity (Figure 4.9). A Shapiro-Wilk test performed on the residuals confirmed that the residuals were normally distributed ($p > 0.05$). There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

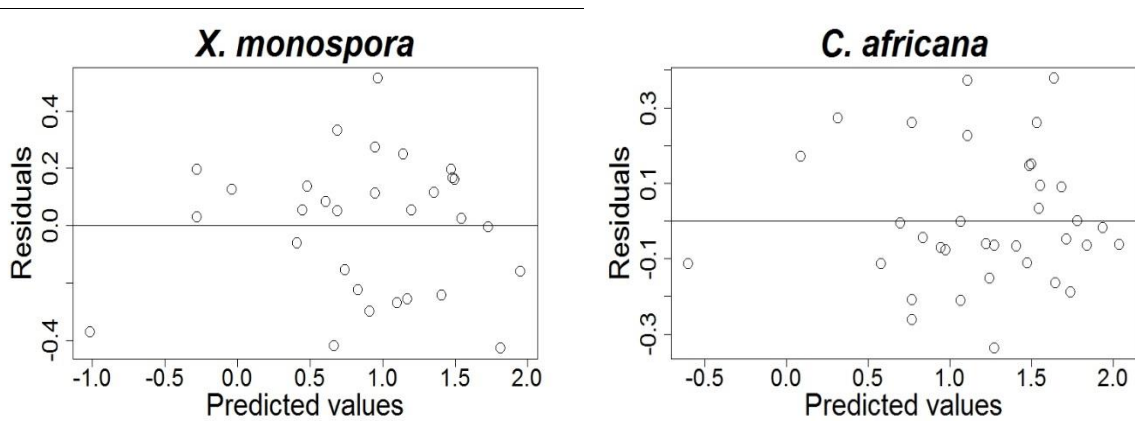


Figure 4.9: *Xymalos monospora* (Model 4.2) and *Celtis africana* (Model 4.5) predicted vs. residual plots for predicted branch length.

Branch mass models

The range of branch diameters sampled for *X. monospora* is well within the range of diameters that need to be estimated for branches measured, but not sampled. For *C. africana* the maximum branch diameter to estimate the branch mass from is significantly larger than the maximum branch diameter sampled (Table 4.5).

Table 4.5: Diameter range of branches sampled and diameter of branches to estimate.

Species	Sample size (<i>n</i>)	Diameter of sampled branches (cm)				Diameter of branches to estimate (cm)			
		Min	Max	Mean	SD	Min	Max	Mean	SD
<i>X. monospora</i>	33	0.3	15.5	4.92	3.61	0.6	16.4	6.92	4.12

<i>C. africana</i>	35	0.3	12.7	4.91	3.01	0.3	36.2	9.34	5.73
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Note: Min is the minimum and Max is the maximum value, SD is the standard deviation

Estimations of branch mass for *X. monospora* were all within the regression range, but for *C. africana* estimations had to be made for branches with diameters above the regression of the sampled branches. By studying the graph (Figure 4.10), it is evident that the slope of the DBH and biomass relationship stabilizes. Thus it can be expected that the allometric equation will produce reliable results in the extrapolation region beyond the parameterization range.

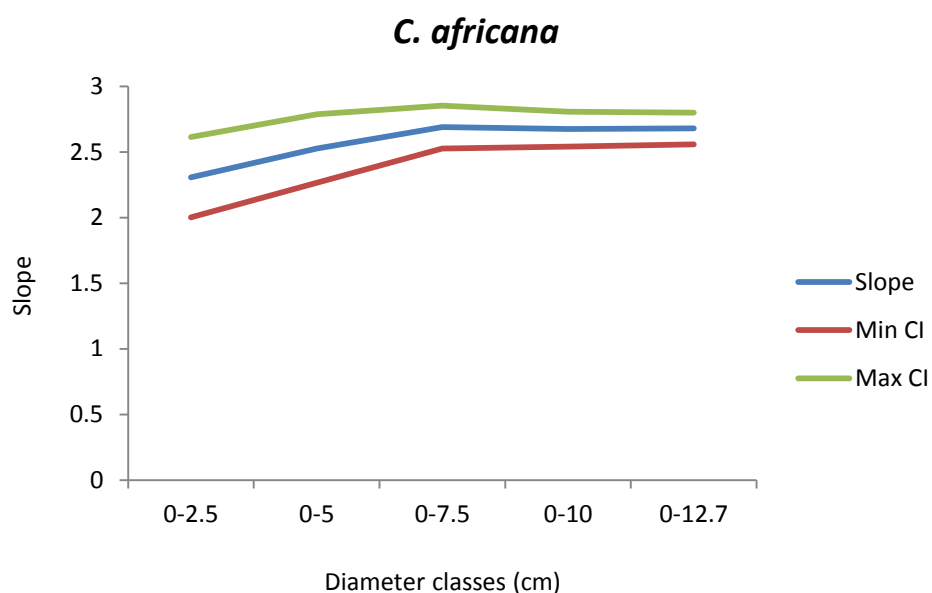


Figure 4.10: Slope with minimum and maximum confidence intervals (CI) for *Celtis africana* branch mass

To estimate branch biomass, three models were fitted for estimating branch mass (Table 4.6). Single (models 4.7, 4.10 and 4.11) and two predictor variable models

(models 4.8, 4.9, 4.12 and 4.13) were used. Model 4.8, 4.9, 4.12 and 4.13 had the highest R^2 values, while models 4.9 and 4.13 had the lowest RMSE values. The ln-transformed models with ln-diameter (d) as predictor variable (models 4.7, and 4.11) had R^2 values of 0.92 and 0.93 and RMSE values of 0.806 and 0.652. Model 4.8 and model 4.13 had the lowest AIC values, while models 4.7 and 4.11 had the highest AIC value.

Table 4.6: Branch mass models for *Xymalos monospora* and *Celtis africana*

Species	Model	Dependant variable	Independent variable	Parameter estimates (with p-values in parentheses)			CF	R^2	RMSE	AICc
				b_0	b_1	b_2				
<i>X. monospora</i>	4.7	ln(B _{bm})	ln(d)	-3.630 (<0.001)	2.587 (<0.001)		1.231	0.92	0.806	68.58
	4.8	ln(B _{bm})	ln(d ² l)	-3.494 (<0.001)	0.932 (<0.001)		1.215	0.93	0.776	60.82
	4.9	ln(B _{bm})	ln(d), ln(l)	-3.494 (<0.001)	1.861 (<0.001)	0.939 (-0.073)	1.224	0.93	0.752	62.82
<i>C. africana</i>	4.10	B _{bm}	ba	-1.222 (-0.0185)	0.248 (<0.001)			0.92	2.097	
	4.11	ln(B _{bm})	ln(d)	-3.314 (<0.001)	2.680 (<0.001)		1.170	0.93	0.652	62.71
	4.12	ln(B _{bm})	ln(d ² l)	-3.589 (<0.001)	0.999 (<0.001)		1.111	0.96	0.506	48.89
	4.13	ln(B _{bm})	ln(d), ln(l)	-3.831 (<0.001)	1.210 (<0.001)	2.088 (<0.001)	1.093	0.96	0.45	43.81

Note: B_{bm} is branch biomass (kg), d is branch diameter (cm), l is length (m) and ba is basal area (cm²). The b_0 , b_1 and b_2 values are the parameter values with the p-values in parentheses.

Model 4.8 and model 4.13 were the best performing models having high R^2 values and low RMSE and AIC values. Although the ln-transformed models, Model 4.7 [$\ln(B_{bm}) = -3.630 + 2.587 \ln(d)$] and model 4.11 [$\ln(B_{bm}) = 3.314 + 2.680 \ln(d)$] were inferior, the models were selected as the best models for both species since all

the model parameters were significant and because of the simplicity of the models having only one predictor variable (parsimony concept) (Burnham and Anderson 2002). Parameters for all models were significant ($p < 0.05$), except for model 4.9 where the logarithm of branch length did not contribute significantly to the prediction ($p > 0.05$). Figure 4.11 shows the relationship for the transformed branch diameter and mass models for the two species.

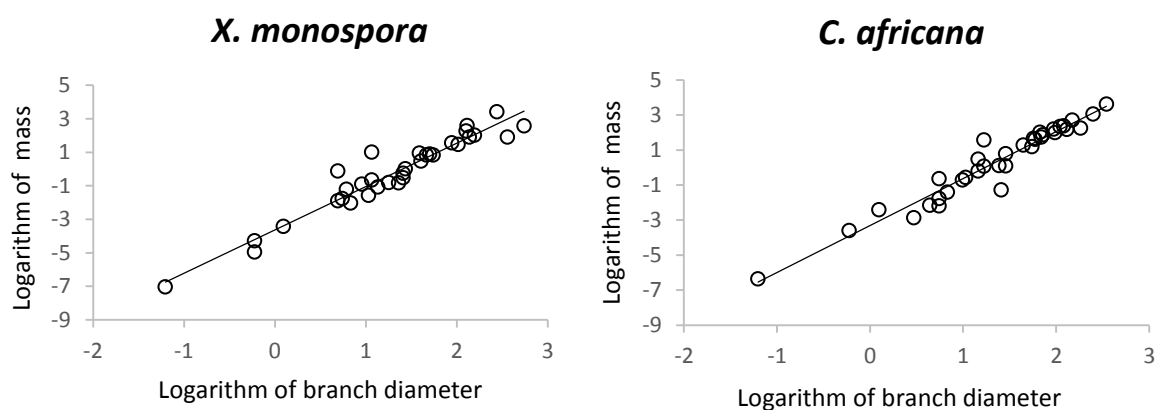


Figure 4.11: Transformed branch diameter and branch mass linear models for *Xymalos monospora* (Model 4.7) and *Celtis africana* (Model 4.11).

The predicted branch mass values plotted against the residuals, shows that there were no clear pattern and that the residuals were not visually heteroscedastic (Figure 4.12). A Shapiro-Wilk test performed on the residuals, confirmed that the residuals were normally distributed ($p > 0.05$) and that the residuals were homoscedastic. There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

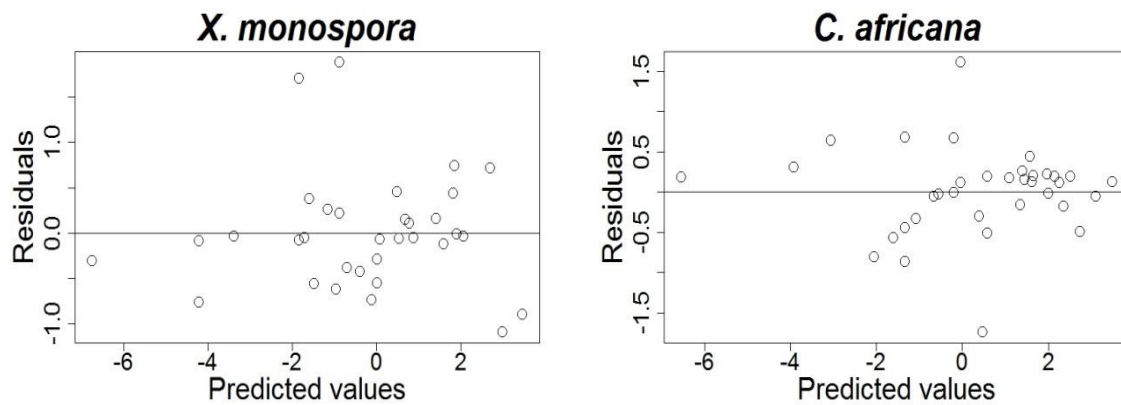


Figure 4.12: *Xymalos monospora* (Model 4.7) and *Celtis africana* (Model 4.11) predicted vs. residual plots for predicted branch mass.

Foliage mass models

Foliage mass for *C. africana* had to be estimated beyond the regression range of the sampled branches. By looking at the graph it is evident that the slope between the foliage biomass and branch diameter stabilized beyond the 0 - 7.5 cm branch diameter range (Figure 4.13). Estimation of foliage mass outside of the regression range was assumed to have low error, given the smaller confidence limits at the upper end of the regression range in Figure 4.13.

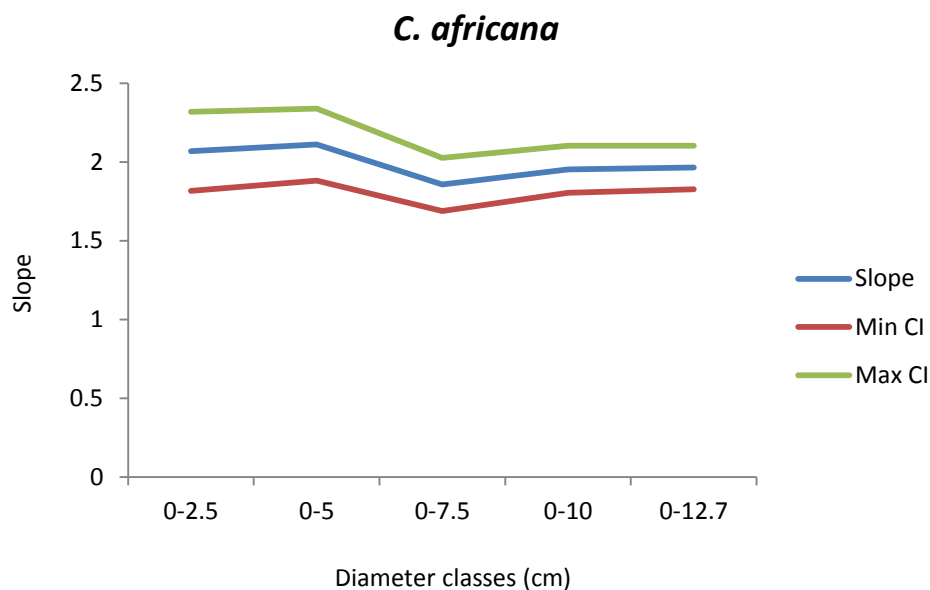


Figure 4.13: Slope with minimum and maximum confidence intervals (CI) for *Celtis africana* for foliage mass

Three models were fitted to estimate the foliage mass of *X. monospora* and *C. africana* (Table 4.7). Single (models 4.14, and 4.17) and two predictor variable models (models 4.15, 4.16, 4.18 and 4.19) were used. All models were In-transformed using branch diameter (models 4.14 and 4.17) or a combination of branch diameter and branch length (models 4.15, 4.16, 4.18 and 4.19). Models 4.15 and 4.18 having a combined predictor variable (d^2h) and the two predictor variable models (models 4.16, and 4.19) had the highest R^2 values. Models 4.16 and 4.18 had the lowest RMSE values. Models 4.15 and 4.18 had the lowest AIC values, while models 4.14 and 4.17 had the highest. Parameter values for models were all significant ($p < 0.05$), except for the logarithm of branch length in model 4.19, where branch length did not contribute significantly to the prediction ($p > 0.05$).

Table 4.7: Foliage mass and branch diameter models for *Xymalos monospora* and *Celtis africana*

Species	Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)			CF	R ²	RMSE	AICc
				b ₀	b ₁	b ₂				
<i>X. monospora</i>	4.14	ln(F _{bm})	ln(d)	-4.688 (<0.001)	1.958 (<0.001)		1.322	0.84	1.135	76.95
	4.15	ln(F _{bm})	ln(d ² l)	-4.656 (<0.001)	0.717 (<0.001)		1.277	0.86	1.016	67.60
	4.16	ln(F _{bm})	ln(d), ln(l)	-4.587 (<0.001)	1.059 (-0.024)	1.200 (-0.040)	1.280	0.86	1.015	68.76
<i>C. africana</i>	4.17	ln(F _{bm})	ln(d)	-4.560 (<0.001)	1.964 (<0.001)		1.218	0.86	0.809	70.70
	4.18	ln(F _{bm})	ln(d ² l)	-4.750 (<0.001)	0.729 (<0.001)		1.197	0.87	0.756	67.46
	4.19	ln(F _{bm})	ln(d),ln(l)	-4.833 (<0.001)	1.187 (-0.010)	1.104 (-0.068)	1.201	0.87	0.759	69.01

Note: F_{bm} is foliage biomass (kg) , l is length (m) and d is diameter (cm). The b₀, b₁ and b₂ values are the parameter values with the p-values in parentheses.

Models 4.14 and 4.17 were the best performing models due to high R² value and low RMSE and AIC values. Although Model 4.14 [ln (F_{bm}) = -4.688 + 1.958 ln (d)] and model 4.17 [ln (F_{bm}) = -4.560 + 1.964 ln (d)] were inferior, they were selected as the preferred models since branch length was not available for all the branches in minimal invasive sampling and because parsimonious models are preferred (Figure 4.14).

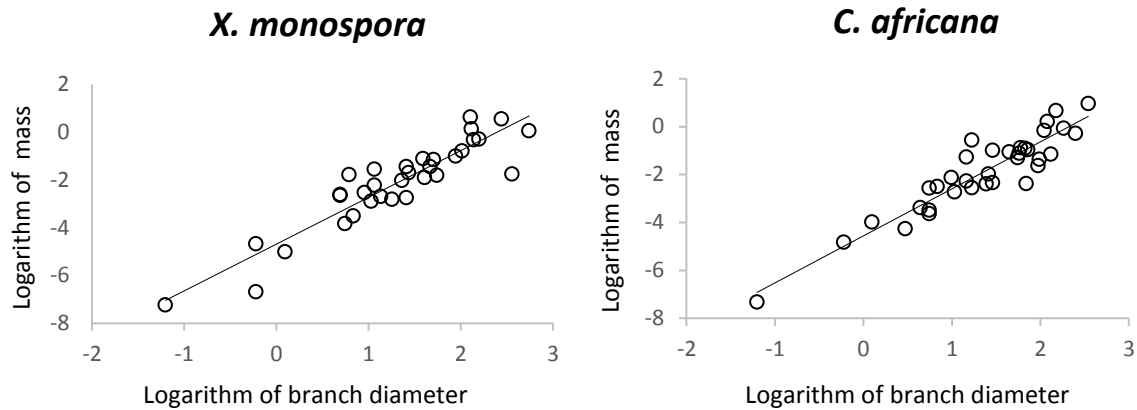


Figure 4.14: Ln-transformed branch diameter and foliage mass linear models for *Xymalos monospora* (Model 4.14) and *Celtis africana* (Model 4.17).

The predicted foliage mass values plotted against the residuals, shows that there were no obvious pattern and that the residuals were not visually heteroscedastic (Figure 4.15). A Shapiro-Wilk test performed on the residuals confirmed that the residuals were normally distributed ($p > 0.05$) and that the residuals were homoscedastic. There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

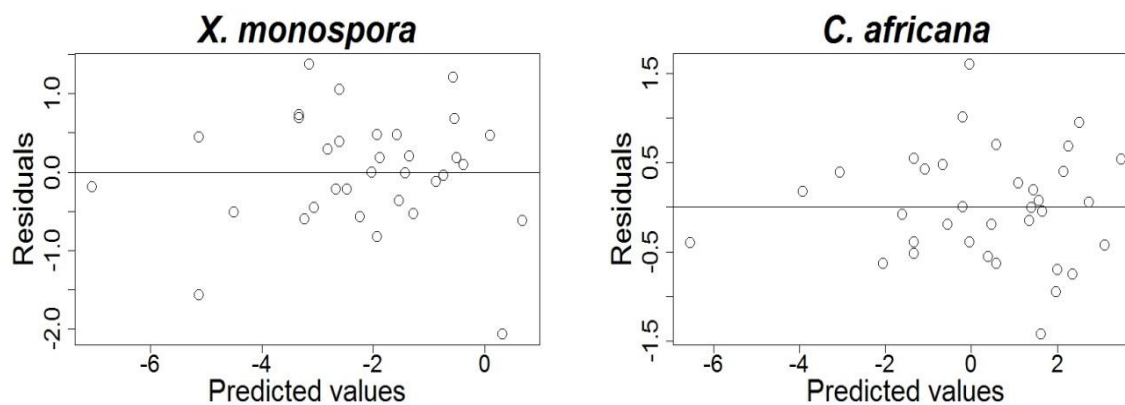


Figure 4.15: *Xymalos monospora* (Model 4.14) and *Celtis africana* (Model 4.17) predicted vs. residual plots for predicted foliage mass.

4.2.4 Biomass models to scale up from tree to stand level

Height models

Two models were formulated for predicting the height of both *X. monospora* and *C. africana* (Table 4.8). Models 4.21 and 4.23 were ln-transformed models with DBH as independent variables while two-predictor variable models (models 4.2 and 4.4) were untransformed using d^2 and d as independent variables. CF's were applied to the ln-transformed models as a back-transformation.

Table 4.8: DBH and height models for *Xymalos monospora* and *Celtis africana*

Species	Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)			CF	R ²	RMSE
				b ₀	b ₁	b ₂			
<i>X. monospora</i>	4.20	ln(h)	ln(DBH)	0.887 (<0.001)	0.494 (<0.001)		1.014	0.83	0.165
	4.21	h	DBH, DBH ²	3.445 (<0.001)	0.450 (<0.001)	-0.003 (<0.001)		0.74	1.963
<i>C. africana</i>	4.22	ln(h)	ln(DBH)	1.026 (<0.001)	0.514 (<0.001)		1.013	0.88	0.168
	4.23	h	DBH, DBH ²	4.481 (<0.001)	0.518 (<0.001)	-0.003 (<0.001)		0.81	2.432

Note: DBH is diameter at breast height (cm) and h is height (m). The b₀, b₁ and b₂ values are the parameter values with the p-values in parentheses.

The ln-transformed models (models 4.20 and 4.22) were superior with regards to their R² and had lower RMSE values than models 4.21 and 4.23. All the model parameters were highly significant (p <0.05).

Model 4.20 [$\ln(h) = 0.887 + 0.494 \ln(\text{DBH})$] and model 4.22 [$\ln(h) = 1.026 + 0.514 \ln(\text{DBH})$] were considered as the best performing models because all the model parameters were significant (p <0.05), the RMSE values were lower than the other fitted models and both models had a high R² fit. Figure 4.16 shows the ln-transformed DBH and height distribution for *X. monospora* and *C. africana*.

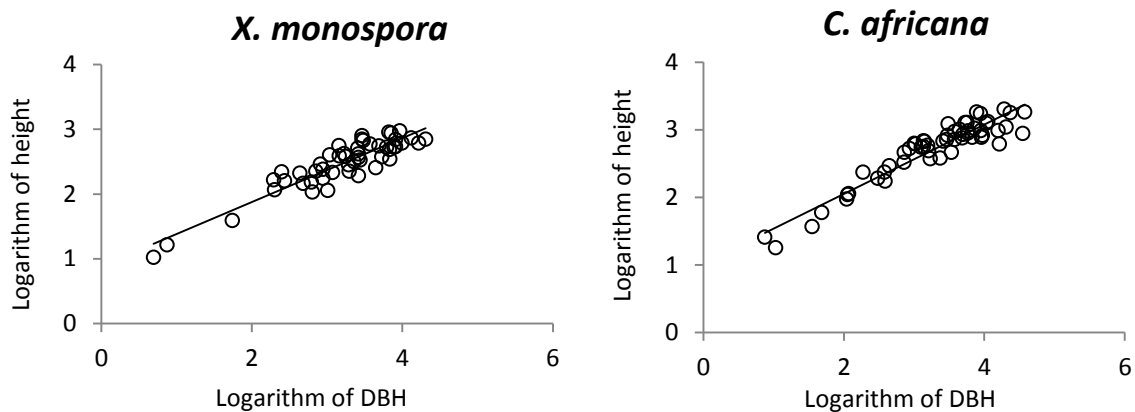


Figure 4.16: Transformed DBH and height linear models for *Xymalos monospora* (Model 4.20) and *Celtis africana* (Model 4.22)

The predicted height values of the best fitting models (models 4.20, and 4.22) plotted against the residuals, shows that there are no clear pattern for *X. monospora* but a slightly visible pattern for *C. africana*. A Shapiro-Wilk test performed on the residuals of *C. africana* confirmed that the residuals were normally distributed ($p=0.1451$) and that the residuals were homoscedastic (Figure 4.17). There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

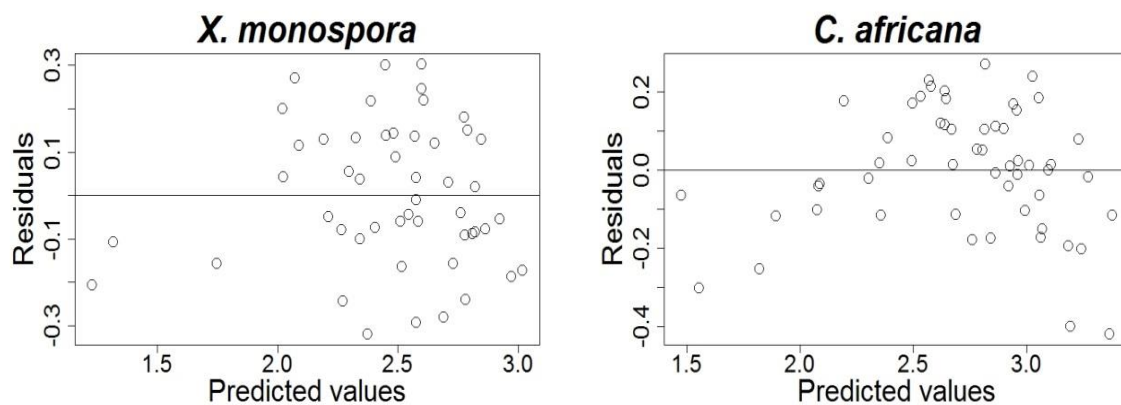


Figure 4.17: *Xymalos monospora* (Model 4.20) and *Celtis africana* (Model 4.22) predicted vs. residual plots for predicted height

Stem biomass models

Since stem mass had to be estimated beyond the range for the stem mass regression, a stability check on the allometric slope parameter was constructed as described before. It is evident that the slope of the DBH and biomass relationship stabilized. That is, the relationship appears to be constant across larger classes. By looking at the graph for *C. africana*, a slight shift between the maximum and minimum confidence interval lines is visible within the 0 - 94.5 cm DBH class. This could be due to the fact that only one tree was sampled within the 90 - 100 cm DBH range or a natural divergence that occur in such data.

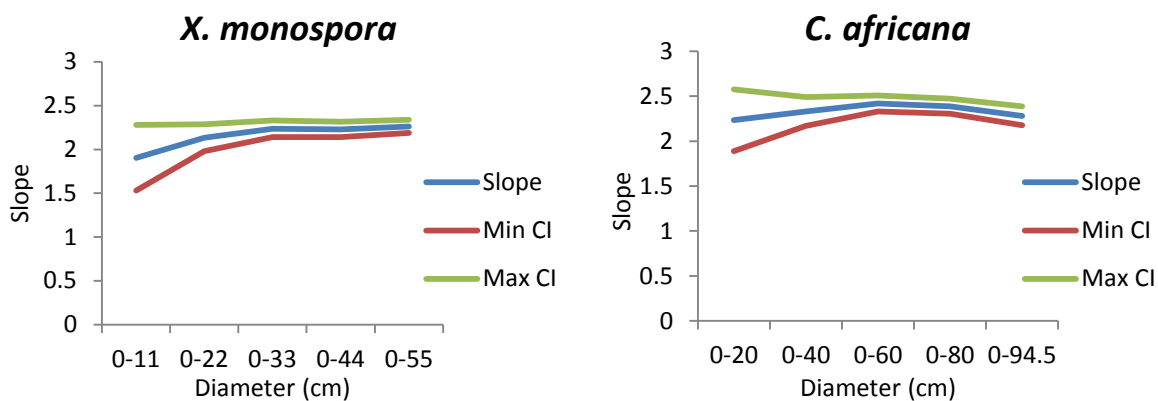


Figure 4.18: Slope with minimum and maximum confidence intervals (CI) for *Xymalos monospora* and *Celtis africana* stem mass.

Three stem mass models were formulated for *C. africana* and *X. monospora*, having only DBH (models 4.24, and 4.27) and DBH and h as predictor variables (models 4.25, 4.26, 4.28 and 4.29) (Table 4.9). Height parameters fitted in the logarithmic form but did not produce a good fit. The R^2 values were high for all models, except for model 4.27 where the R^2 fit was slightly lower.

Table 4.9: Stem biomass models for *Xymalos monospora* and *Celtis africana*

Species	Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)			CF	R ²	RMSE	AICc
				b ₀	b ₁	b ₂				
<i>X. monospora</i>	4.24	ln(Stem)	ln(DBH)	-2.407 (<0.001)	2.263 (<0.001)		1.042	0.99	0.338	9.08
	4.25	ln(Stem)	ln(DBH), h	-2.361 (<0.001)	2.078 (<0.001)	0.039 (0.446)	1.044	0.98	0.336	10.32
	4.26	ln(Stem)	ln(DBH ² h)	-3.064 (<0.001)	0.880 (<0.001)		1.059	0.98	0.427	13.98
<i>C. africana</i>	4.27	ln(Stem)	ln(DBH)	-2.162 (<0.001)	2.281 (<0.001)		1.081	0.97	0.581	18.58
	4.28	ln(Stem)	ln(DBH), h	-1.872 (<0.001)	1.655 (<0.001)	0.112 (0.033)	1.059	0.98	0.443	14.64
	4.29	ln(Stem)	ln(DBH ² h)	-3.017 (<0.001)	0.904 (<0.001)		1.062	0.98	0.47	14.61

Note: DBH is diameter at breast height (cm) and h is tree height (m). Stem mass was recorded in kg. The b₀, b₁ and b₂ values are the parameter values with the p-values in parentheses.

The p-values of all models were significant (p <0.05) except for the height parameter in model 4.25 (p >0.05). Models 4.24 and 4.29 had the lowest AIC values, while models 4.26 and 4.27 had the highest AIC values. In the case of *C. africana*, models including height (models 4.28, and 4.29) were performing better in terms of AIC, RMSE and R² and might be the better models to utilize in other forest areas to adapt to changing DBH and height relations.

Model 4.24 [ln (Stem) = -2.407 + 2.263 ln (DBH)] and model 4.27 [ln (Stem) = -2.162 + 2.281 ln (DBH)] were selected for the purpose of this study since both models have significant parameters, both models have high R² values and because of the simplicity of the models using only DBH as predictor variable, making them immediately applicable to all trees without a modeling step of height in between.

Figure 4.19 illustrates the relationship between the ln-transformed stem DBH and stem mass for the two selected models.

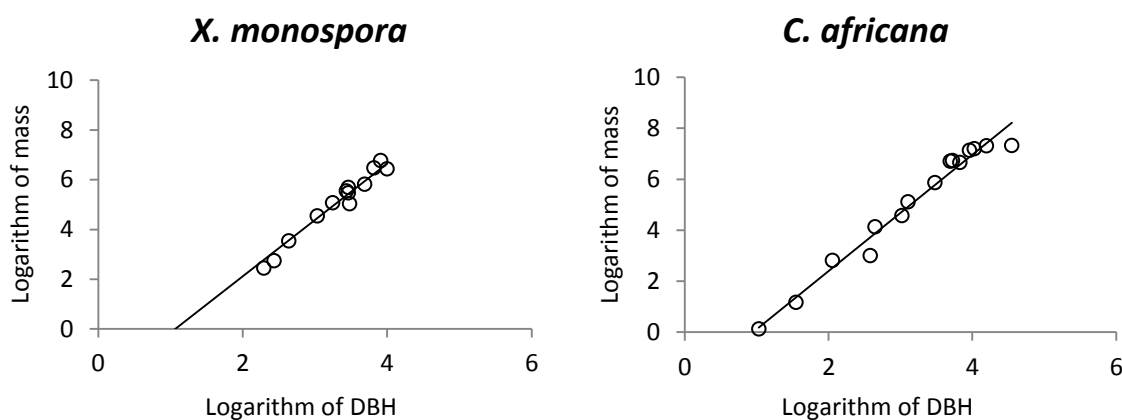


Figure 4.19: Ln-transformed DBH and stem mass linear models for *Xymalos monospora* (Model 4.24) and *Celtis africana* (Model 4.27).

The predicted stem mass values plotted against the residuals, shows that there were no clear pattern and that the residuals were not visually heteroscedastic. A Shapiro-Wilk test performed on the residuals of *C. africana* confirmed that the residuals were normally distributed ($p > 0.05$) and that the residuals were homoscedastic (Figure 4.20). There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

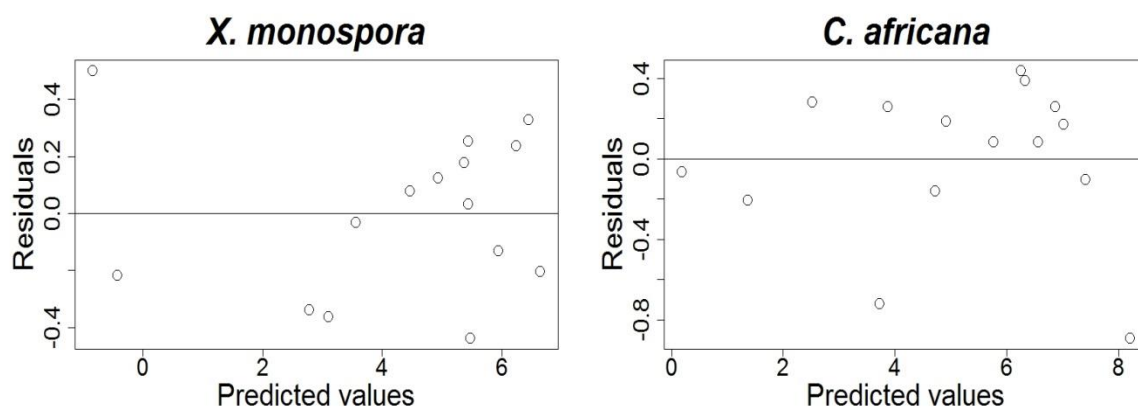


Figure 4.20: *Xymalos monospora* (Model 4.24) and *Celtis africana* (Model 4.27) predicted vs. residual plots for predicted stem mass.

Branch biomass models

Since the total branch biomass had to be estimated beyond the range of the sampled DBH, the DBH - values were divided into five classes and regression equations were fitted (Equation 2.6) to determine slope behavior over the various DBH classes. It is evident that the slope between branch biomass and diameter stabilized beyond the 0 - 33 cm DBH class for *X. monospora* and beyond the 0 - 60 cm DBH class for *C. africana*. The drop visible for *C. africana* in the 0 - 94.5 cm DBH range and the divergence between the maximum and minimum confidence interval is likely due to the fact that only one tree was sampled between 0 - 90 cm DBH range (Figure 4.21).

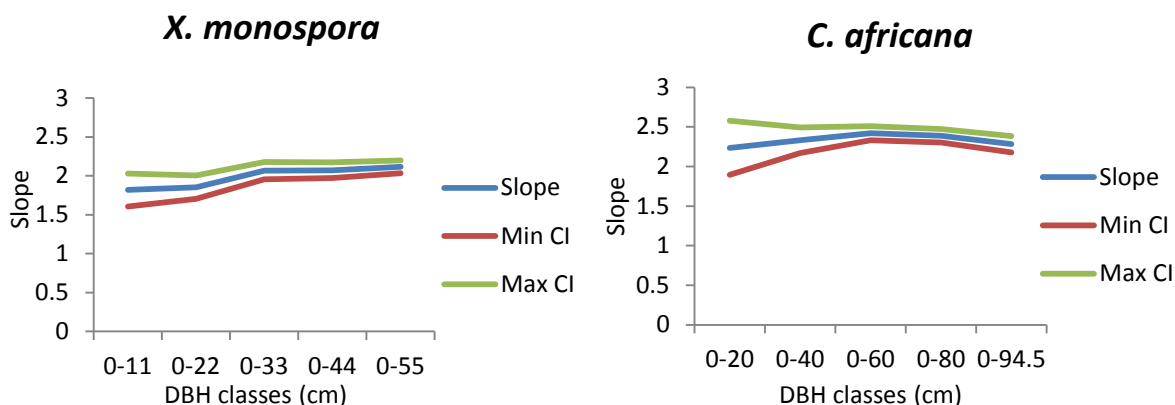


Figure 4.21: Slope with minimum and maximum confidence intervals (CI) for *Xymalos monospora* and *Celtis africana* branch biomass

Three branch mass models were fitted for *X. monospora* and *C. africana*, having either a single predictor variable (models 4.30, and 4.33) or two predictor variables (models 4.31, 4.32, 4.34 and 4.35) (Table 4.10). The R^2 values for all models were above 0.98, with the R^2 values for *C. africana* being the highest. Both models including height as a predictor variable (models 4.32, and 4.35) were not significant. Height parameters were first fitted in the logarithmic form but did not exhibit a good fit. Models 4.32 and 4.35 had the lowest RMSE values while models 4.31 and 4.34 had the highest RMSE values. Models 4.32 and 4.33 had the lowest AIC values while models 4.31 and 4.34 had the highest AIC values.

Table 4.10: Total branch biomass models for *Xymalos monospora* and *Celtis africana*

Species	Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)			CF	R ²	RMSE	AIC
				b ₀	b ₁	b ₂				
<i>X. monospora</i>	4.30	ln(Branch)	ln(DBH)	-2.885 (<0.001)	2.116 (<0.001)		1.052	0.98	0.911	11.98
	4.31	ln(Branch)	ln(DBH ² h)	-3.508 (<0.001)	0.824 (<0.001)		1.060	0.98	1.351	14.10
	4.32	ln(Branch)	ln(DBH),h	-2.775 (<0.001)	1.671 (<0.001)	0.093 (0.080)	1.043	0.98	0.309	9.98
<i>C. africana</i>	4.33	ln(Branch)	ln(DBH)	-3.777 (<0.001)	2.564 (<0.001)		1.038	0.99	0.318	7.52
	4.34	ln(Branch)	ln(DBH ² h)	-4.694 (<0.001)	1.011 (<0.001)		1.051	0.99	0.390	11.84
	4.35	ln(Branch)	ln(DBH),h	-3.660 (<0.001)	2.312 (<0.001)	0.045 (0.245)	1.037	0.99	0.302	7.76

Note: DBH is diameter at breast height (cm) and h is tree height (m). Branch biomass is given in kg dry mass. The b₀, b₁ and b₂ values are the parameter values with the p-values in parentheses.

The ln-transformed models 4.30 [$\ln(\text{Branch}) = -2.885 + 2.116 \ln(\text{DBH})$] and 4.33 [$\ln(\text{Branch}) = -3.777 + 2.564 \ln(\text{DBH})$] having DBH as predictor variable were selected since all the parameters were significant, the AIC values of both models are relatively low, and both have high R² values. Model 4.32 was slightly better with regards to AIC but had an additional independent variable. Thus model 4.30 was preferred for reasons of parsimonious modeling. Figure 4.22 illustrates the relationship between the ln-transformed DBH and total branch biomass of the two chosen models.

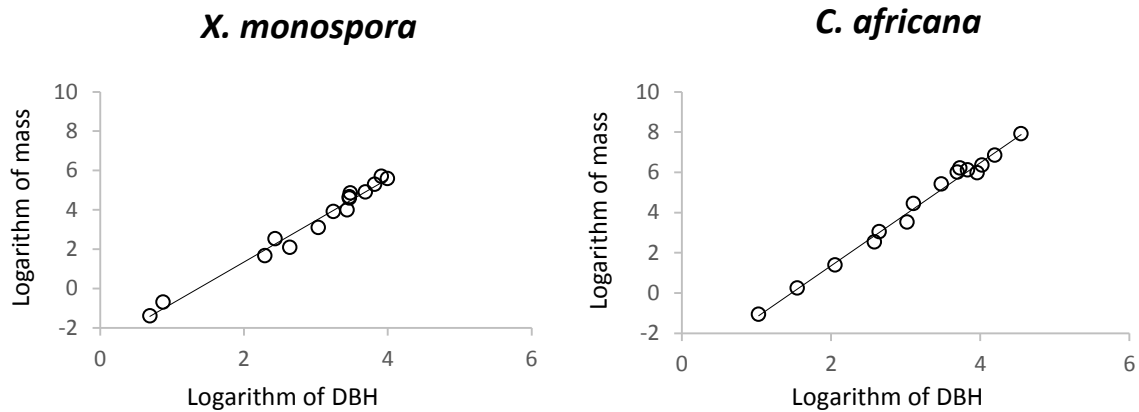


Figure 4.22: Ln-transformed DBH and branch biomass linear models for *Xymalos monospora* (Model 4.30) and *Celtis africana* (Model 4.33).

The predicted branch mass values of models 4.30 and 4.33 plotted against the residuals, showed that there were no clear pattern and that the residuals were not obviously heteroscedastic (Figure 4.23). A Shapiro-Wilk test performed on the residuals confirmed that the residuals were normally distributed ($p > 0.05$) and that the residuals were homoscedastic. There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

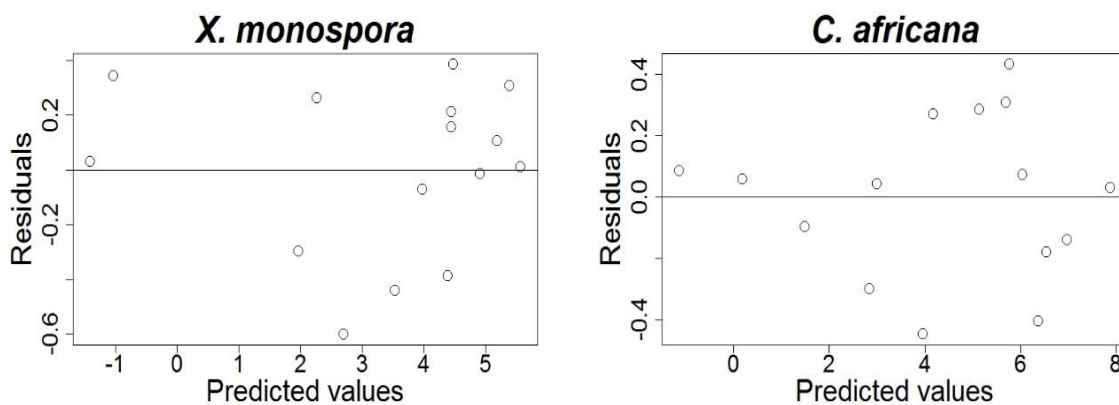


Figure 4.23: *Xymalos monospora* (Model 4.30) and *Celtis africana* (Model 4.33) predicted vs. residual plots for predicted branch mass.

Foliage biomass models

Since total foliage biomass had to be predicted beyond the DBH range of the regression of sample trees, the DBH range of sample trees was divided within five classes and regression equation were fitted (Equation 2.6) to determine how the slope behaved in relation to the DBH and foliage biomass over the regression range (Figure 4.24). It evident that the slope stabilizes beyond the 0 - 33 cm DBH class for *X. monospora* and beyond the 0 - 60 cm DBH class for *C. africana*. The slight tendency of the slope to move downwards at DBH values larger than 80 as observed in *C. africana* is not significant.

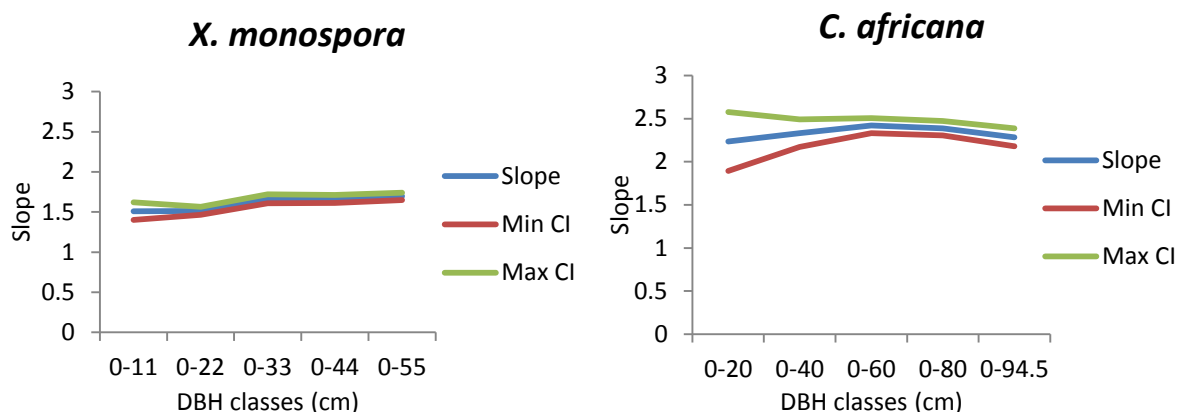


Figure 4.24: Slope with minimum and maximum confidence intervals (CI) for *Xymalos monospora* and *Celtis africana* foliage mass

Three models were fitted for *X. monospora* and four models for *C. africana* to predict the total foliage mass (Table 4.11). Single (models 4.36, 4.39, and 4.40) and two predictor variable models (models 4.37, 4.38, 4.41 and 4.42) were fitted using DBH and height as independent variables. Height parameters were first fitted in the logarithmic form but did not exhibit a good fit. The R^2 values for all models were high, except for models 4.39 and 4.41 having slightly lower R^2 values. Models 4.38 and 4.42 had the lowest RMSE values and models 4.37 and 4.39 had the highest RMSE values. Models 4.38 and 4.40 had the lowest AIC values. Parameters for all models were significant ($p < 0.05$), except for the p -values of the height variables in model 4.38 and 4.42 which were not significant ($p > 0.05$).

Table 4.11: Total foliage biomass models for *Xymalos monospora* and *Celtis africana*

Species	Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)			CF	R ²	RMSE	AICc
				b ₀	b ₁	b ₂				
<i>X.monospora</i>	4.36	ln(Foliage)	ln(DBH)	-3.777 (<0.001)	1.695 (<0.001)		1.015	0.99	0.165	-6.04
	4.37	ln(Foliage)	ln(DBH ² h)	-4.270 (<0.001)	0.659 (<0.001)		1.023	0.99	0.207	0.38
	4.38	ln(Foliage)	ln(DBH),h	-3.731 (<0.001)	1.510 (<0.001)	0.039 (0.199)	1.014	0.99	0.154	-6.18
<i>C. africana</i>	4.39	Foliage	DBH	-9.356 (0.0037)	0.801 (<0.001)			0.92	5.611	100.31
	4.40	ln(Foliage)	ln(DBH)	-4.538 (<0.001)	1.987 (<0.001)		1.031	0.99	0.245	4.60
	4.41	ln(Foliage)	ln(DBH ² h)	-5.248 (<0.001)	0.783 (<0.001)		1.042	0.98	0.287	8.81
	4.42	ln(Foliage)	ln(DBH),h	-4.427 (<0.001)	1.746 (<0.001)	0.043 (0.220)	1.030	0.99	0.230	4.64

Note: DBH is diameter at breast height (cm) and h is tree height (m). Foliage biomass is given in kg dry mass. The b₀, b₁ and b₂ values are the parameter values with the p-values in parentheses.

Model 4.36 [$\ln(\text{Foliage}) = -3.777 + 1.695 \ln(\text{DBH})$] and model 4.40 [$\ln(\text{Foliage}) = -4.538 + 1.987 \ln(\text{DBH})$] with the ln-transformed DBH predictor variable were selected for modeling because of the simplicity of the models using only one predictor variable and the high R² value. Figure 4.25 shows the relationship between the ln-transformed DBH and foliage biomass for the selected models.

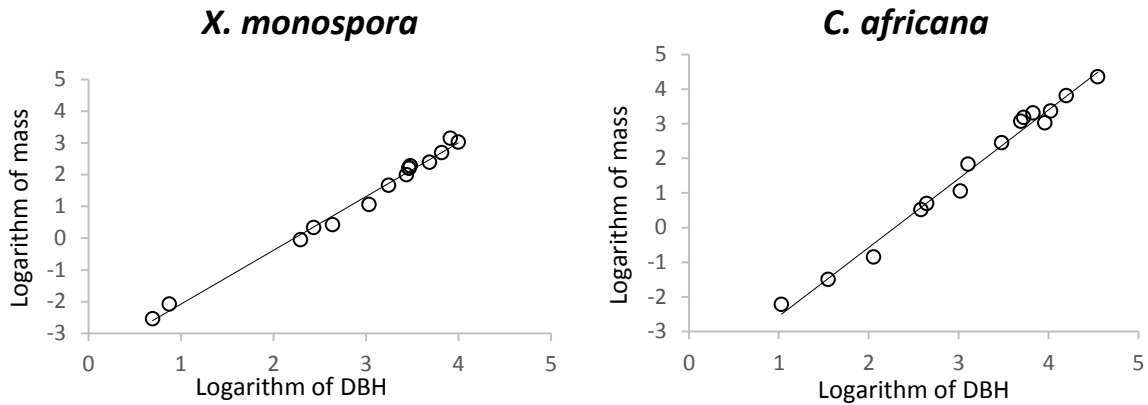


Figure 4.25: Ln- transformed DBH and foliage biomass linear models for *Xymalos monospora* (Model 4.36) and *Celtis africana* (Model 4.40).

The predicted foliage mass values plotted against the residuals for model 4.36 and 4.40, shows that there were no clear pattern and that the residuals were not visually heteroscedastic (Figure 4.26). A Shapiro-Wilk test performed on the residuals confirmed that the residuals were normally distributed ($p > 0.05$) and that the residuals were homoscedastic. There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

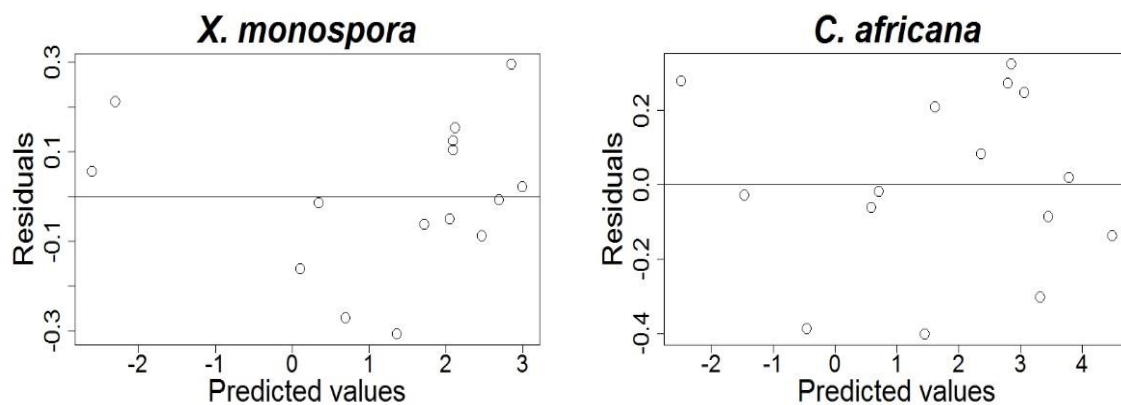


Figure 4.26: *Xymalos monospora* (Model 4.36) and *Celtis africana* (Model 4.40) predicted vs. residual plots for predicted foliage mass.

Total biomass models

The total biomass had to be estimated beyond the sampled DBH range. By looking at the graphs (Figure 4.27) it is evident that *X. monospora* stabilizes beyond the 0 - 33 cm diameter range and *C. africana* stabilizes after the 0 - 60 cm DBH range. The slight downwards trend in *C. africana* was ignored since it was not significant. The results provided some confidence that the total biomass could be extrapolated beyond the parameterization range of the DBH.

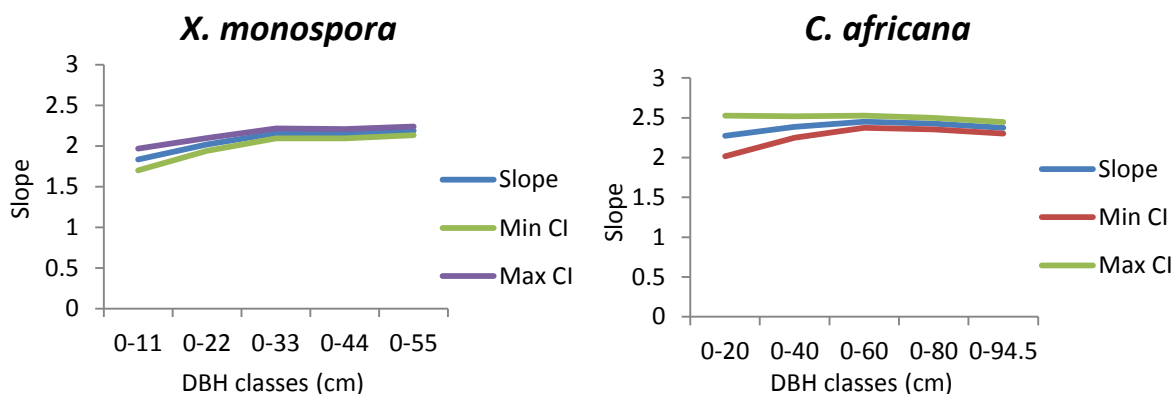


Figure 4.27: Slope with minimum and maximum confidence intervals (CI) for *Xymalos monospora* and *Celtis africana* total mass.

Four models were each fitted for *X. monospora* and *C. africana* to estimate the AGB. Single (models 4.43, 4.45, 4.47 and 4.49) two (model 4.46 and 4.50) and three predictor variable models (models 4.44, and 4.48) were used (Table 4.12). The R^2 fit for all models were relatively high with lower R^2 values for crown diameter as a predictor variable. Models 4.45 and 4.48 had the lowest RMSE and AIC values. The parameter p-values of all models were significant ($p < 0.05$), except for models 4.43, 4.44 and 4.47 having not significant values ($p > 0.05$) for the intercepts. The models were fitted without the intercepts. The height parameters of Model 4.44 and model 4.48 were not significant.

Table 4.12: Total above-ground models for *Xymalos monospora* and *Celtis africana*.

Species	Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)				CF	R ²	RMSE	AICc
				b ₀	b ₁	b ₂	b ₃				
<i>X. monospora</i>	4.43	ln(Total)	ln(CrDm)		2.837 (<0.001)			1.461	0.97	2.503	41.40
	4.44	ln(Total)	ln(DBH,h,ρ)		2.427 (<0.001)	-0.415 (0.363)	-0.243 (0.003)	1.023	0.99	0.226	0.97
	4.45	ln(Total)	ln(DBH)	-1.782 (<0.001)	2.186 (<0.001)			1.021	0.99	0.219	-1.28
	4.46	ln(Total)	ln(DBH ² h)	-2.419 (<0.001)	0.850 (<0.001)			1.035	0.99	0.302	6.10
<i>C. africana</i>	4.47	ln(Total)	ln(CrDm)		2.712 (<0.001)			1.319	0.98	2.027	36.68
	4.48	ln(Total)	ln(DBH,h,ρ)	-8.574 (<0.001)	1.985 (<0.001)	0.601 (0.064)	0.984 (0.008)	1.020	0.99	0.210	-0.28
	4.49	ln(Total)	ln(DBH)	-2.009 (<0.001)	2.374 (<0.001)			1.040	0.99	0.350	8.00
	4.50	ln(Total)	ln(DBH ² h)	-2.876 (<0.001)	0.938 (<0.001)			1.037	0.99	0.334	7.06

Note: CrDm is crown diameter (m), DBH is diameter at breast height (cm), h is tree height (m) and ρ is basic density of the specific tree. The b₀, b₁, b₂ and b₃ values are the parameter values with the p-values in parentheses. Total mass is given in kg drymass.

The ln-transformed models, Model 4.45 [$\ln(\text{Total}) = -1.782 + 2.186 \ln(\text{DBH})$] and Model 4.49 [$\ln(\text{Total}) = -2.009 + 2.374 \ln(\text{DBH})$], having DBH as independent variable have been selected. They had high R² values and are relatively simple to use, since the models use only one predictor variable. Figure 4.28 shows the relationship between the ln-transformed DBH and AGB for *X. monospora* and *C. africana* for the two selected models.

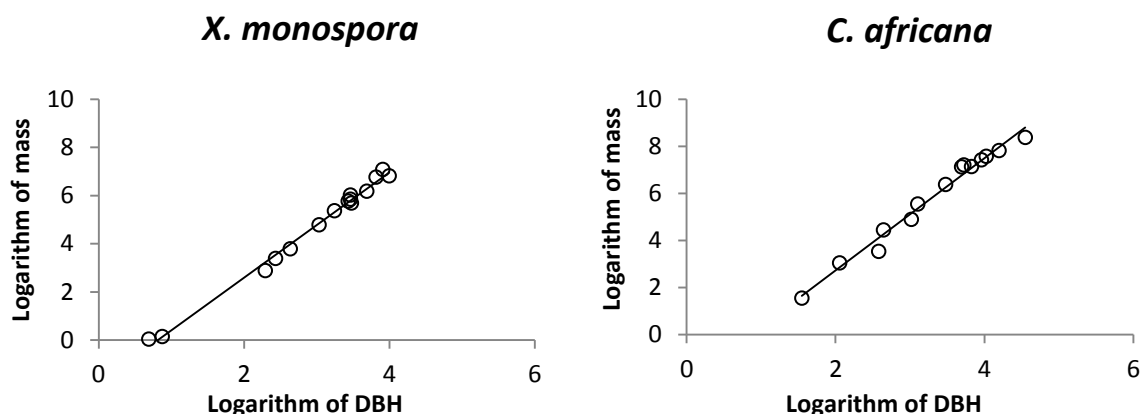


Figure 4.28: Ln-transformed DBH and total biomass linear models for *Xymalos monospora* (Model 4.45) and *Celtis africana* (Model 4.49).

The predicted total mass values of the two best fitting models (models 4.45, and 4.49) plotted against the residuals, shows that there were no clear pattern and that the residuals were not visually heteroscedastic (Figure 4.29). A Shapiro-Wilk test performed on the residuals confirmed that the residuals were normally distributed ($p > 0.05$) and that the residuals were homoscedastic. There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

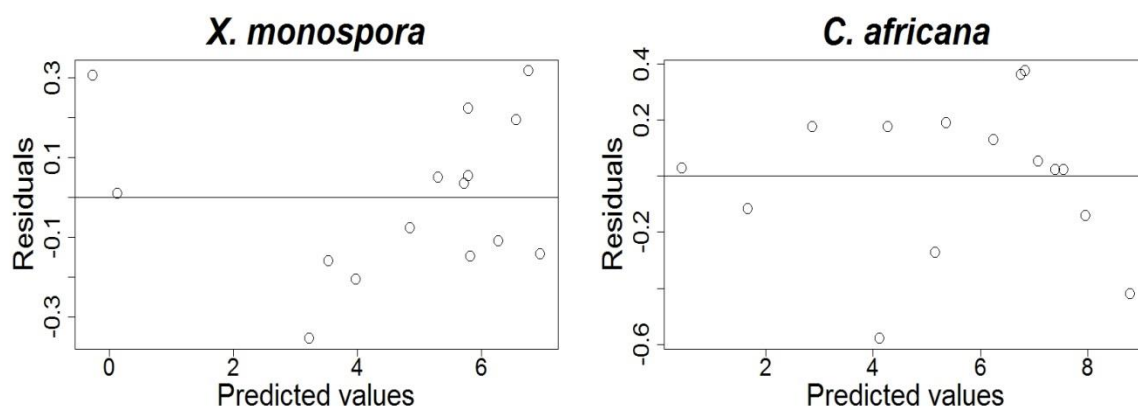


Figure 4.29: *Xymalos monospora* (Model 4.45) and *Celtis africana* (Model 4.49) predicted vs. residual plots for predicted total mass.

4.2.5 Combined species models

Stem biomass models

Three stem mass models have been formulated to estimate the stem mass of the combined species model (Table 4.13). The predictor variables that have been used include DBH (Model 4.51) and a combination of DBH and height (models 4.52 and 4.53). Height parameters were first fitted in the logarithmic form but did not exhibit a good fit. The R^2 fit of all models were the same (0.98). Model 4.53 had the lowest RMSE value followed by model 4.52 and 4.51. Model 4.53 had the lowest AIC value and model 4.51 the highest.

Table 4.13: Combined-species stem mass models

Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)			CF	R ²	RMSE	AICc
			b ₀	b ₁	b ₂				
4.51	ln(Stem)	ln(DBH)	-2.329 (<0.001)	2.287 (<0.001)		1.070	0.98	0.509	29.06
4.52	ln(Stem)	ln(DBH ² h)	-3.082 (<0.001)	0.898 (<0.001)		1.066	0.98	0.485	27.18
4.53	ln(Stem)	ln(DBH), h	-2.134 (<0.001)	1.780 (<0.001)	0.097 (0.005)	1.054	0.98	0.414	22.15

Note: DBH is diameter at breast height (cm) and h is height (m). The b₀, b₁ and b₂ values are the parameter values with the p-values in parentheses. Stem mass is given in kg drymass.

The p-values of all parameters and models were significant ($p < 0.05$). Model 4.53 was the superior model, having a high R² value and low AIC and RMSE values. The ln-transformed model having DBH as only predictor variable, model 4.51 [$\ln(\text{Stem}) = -2.329 + 2.287 \ln(\text{DBH})$] was selected to estimate stem biomass, since the model has a high R² fit and all the parameter values are significant ($p < 0.05$). Model 4.51 is also a more parsimonious model since it only has one independent variable and complies with the concept of parsimony. Figure 4.30 shows the relationship between the ln-transformed DBH and stem biomass.

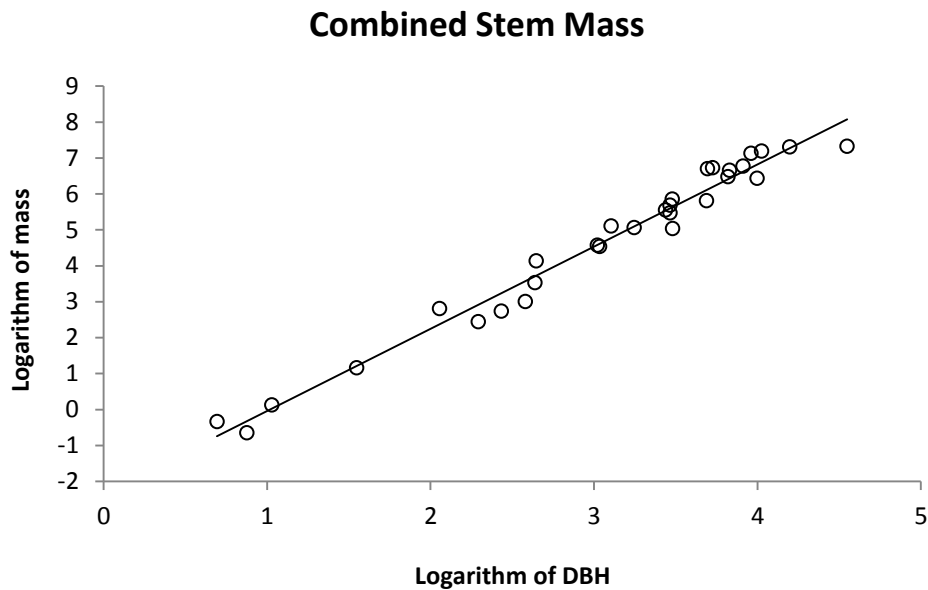


Figure 4.30: Ln-transformed stem mass and DBH linear model for the combined- species model (Model 4.51).

The predicted stem mass values of the best performing model (Model 4.51) plotted against the residuals, shows that there was no clear pattern and that the residuals were not visually heteroscedastic (Figure 4.31). A Shapiro-Wilk test performed on the residuals confirmed that the residuals were normally distributed ($p > 0.05$) and that the residuals were homoscedastic. There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

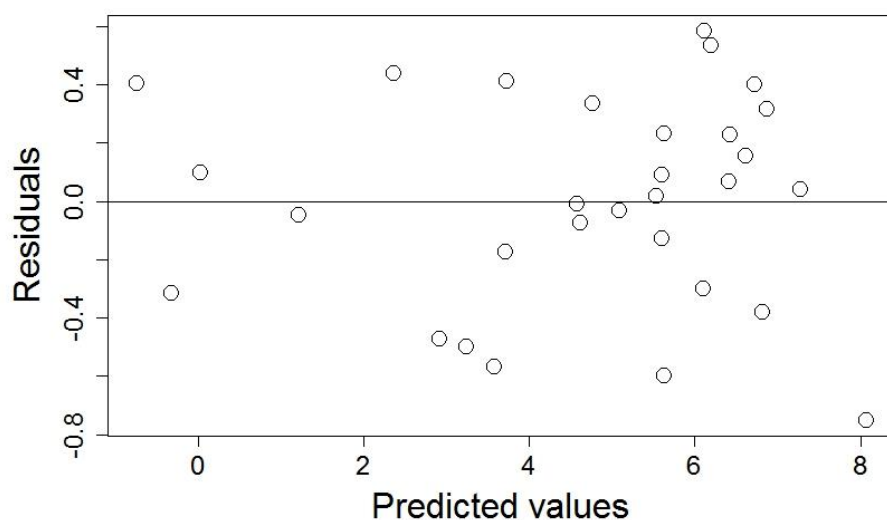


Figure 4.31: Combined model predicted vs. residual plots for predicted stem mass (Model 4.51).

Branch biomass models

Three branch biomass models were formulated to estimate the total branch mass for the combined model (Table 4.14). Developed models had DBH only (Model 4.54) and a combination of DBH and height (models 4.55, and 4.56) as predictor variables. Height parameters were first fitted in the logarithmic form but did not exhibit a good fit. Model 4.56 had the highest R^2 value, followed by model 4.54 and model 4.55. Model 4.56 had the lowest RMSE value, followed by model 4.54 and 4.55. Model 4.56 had the lowest AIC value. The parameters and model p-values of all models were significant ($p < 0.05$).

Table 4.14: Combined species branch biomass models

Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)			CF	R ²	RMSE	AICc
			b ₀	b ₁	b ₂				
4.54	ln(Branches)	ln(DBH)	-3.380 (<0.001)	2.363 (<0.001)		1.103	0.97	0.630	40.05
4.55	ln(Branches)	ln(DBH ² h)	-4.142 (<0.001)	0.925 (<0.001)		1.110	0.96	0.665	42.10
4.56	ln(Branches)	ln(DBH),h	-3.134 (<0.001)	1.725 (<0.001)	0.122 (0.003)	1.075	0.98	0.497	32.15

Note: DBH is diameter at breast height (cm) and h is tree height (m). The b₀, b₁ and b₂ values are the parameter values with the p-values in parentheses. Branch mass is given in kg drymass.

Model 4.56 was the superior model due to having a high R² value and low RMSE and AIC values. Model 4.54 [ln (Branches) = -3.380 + 2.363 ln (DBH)] was selected for upscaling since the model has a high R² value, comparatively low RMSE and AIC value, with all parameters significant (p <0.05) and because of the simplicity of the model using only DBH as independent variable. Figure 4.32 shows the relationship between the ln-transformed DBH and branch biomass of the best performing model.

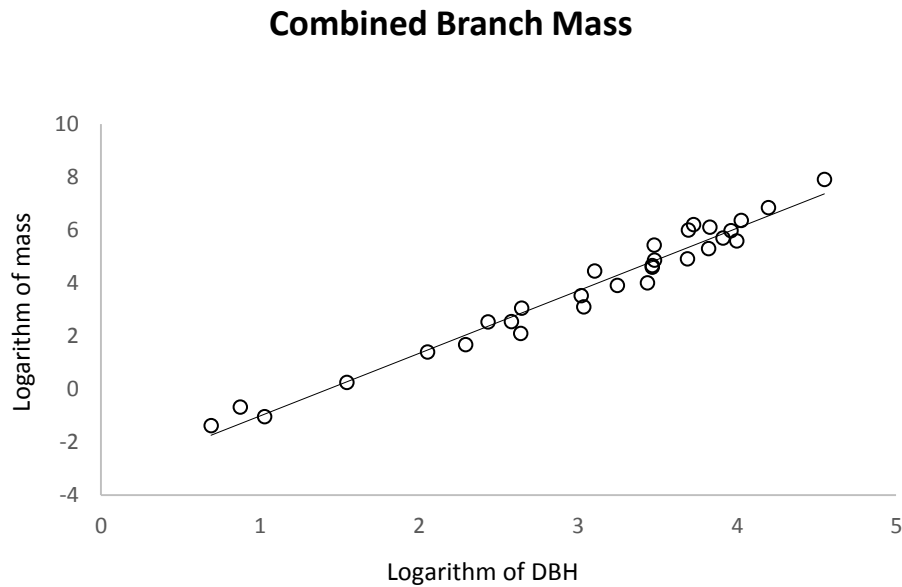


Figure 4.32: Ln-transformed DBH and branch mass linear model for the combined species model (Model 4.54).

The predicted branch mass values plotted against the residuals, shows that there were no clear pattern and that the residuals were not visually heteroscedastic (Figure 4.33). A Shapiro-Wilk test performed on the residuals confirmed that the residuals were normally distributed ($p > 0.05$) and that the residuals were homoscedastic.

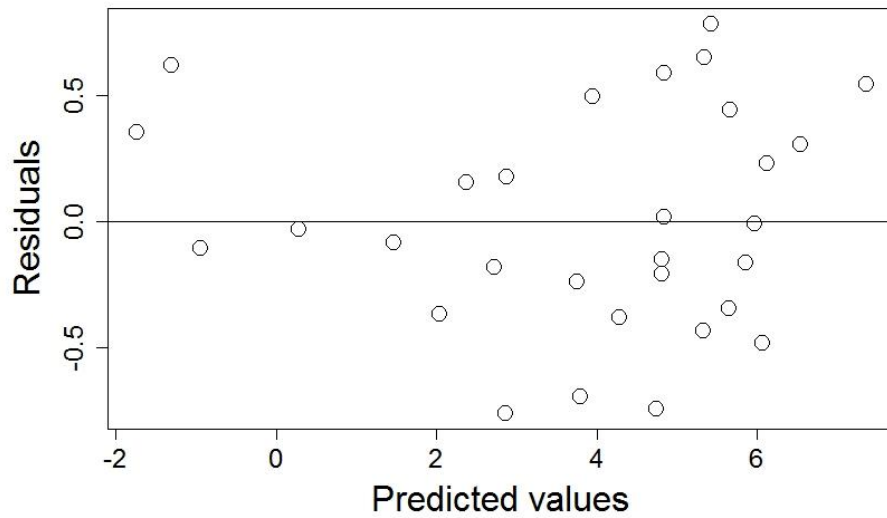


Figure 4.33: Combined model predicted vs. residual plots for predicted branch mass (Model 4.54).

Foliage biomass models

Three models were formulated to estimate total foliage biomass for the combined species model (Table 4.15). Developed models had only DBH (Model 4.57) and combinations of DBH and height (models 4.58, and 4.59) as predictor variables. Height parameters were first fitted in the logarithmic form but did not exhibit a good fit, where after it was fitted in the arithmetic form. The R^2 values of all the models were the same (0.98). The model p - values and p - values of all parameters were significant ($p < 0.05$). The AIC value of model 4.59 was the lowest.

Table 4.15: Combined species foliage biomass models

Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)			CF	R ²	RMSE	AICc
			b ₀	b ₁	b ₂				
4.57	ln(Foliage)	ln(DBH)	-4.162 (<0.001)	1.846 (<0.001)		1.035	0.98	0.267	8.91
4.58	ln(Foliage)	ln(DBH ² h)	-4.750 (<0.001)	0.722 (<0.001)		1.045	0.98	0.304	15.94
4.59	ln(Foliage)	ln(DBH), h	-4.034 (<0.001)	1.515 (<0.001)	0.063 (0.012)	1.029	0.98	0.235	3.69

Note: DBH is diameter at breast height (cm) and h is height (m). The b₀, b₁ and b₂ values are the parameter values with the p-values in parentheses. Foliage mass is given in kg dry mass.

Model 4.59 was the best performing model and had the lowest AIC and RMSE values and a high R². The ln-transformed model, model 4.57 [ln (Foliage) = - 4.162 + 1.846 ln (DBH)], only having DBH as predictor variable have been selected to model the total foliage biomass since it has a high R² value and because of the simplicity of the model, having only one parameter that is easy to measure. Figure 4.34 shows the best fitting model's relationship between the transformed DBH and total foliage biomass.

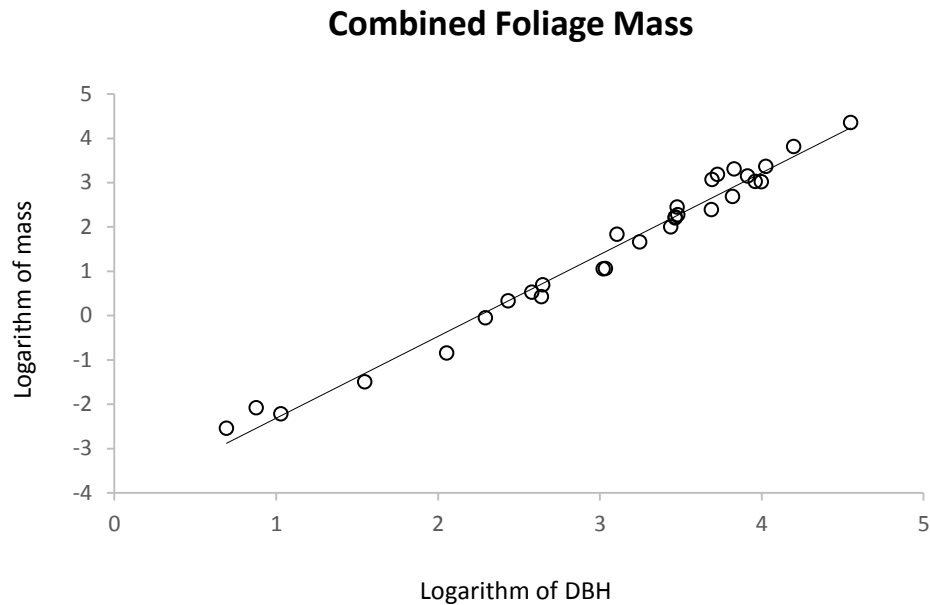


Figure 4.34: Ln-transformed DBH and foliage mass linear model for the combined species model (Model 4.57).

The predicted foliage mass values of the best fitting model (Model 4.57) plotted against the residuals, shows that there were no clear pattern and that the residuals were not visually heteroscedastic (Figure 4.35). A Shapiro-Wilk test performed on the residuals confirmed that the residuals were normally distributed ($p > 0.05$) and that the residuals were homoscedastic. There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

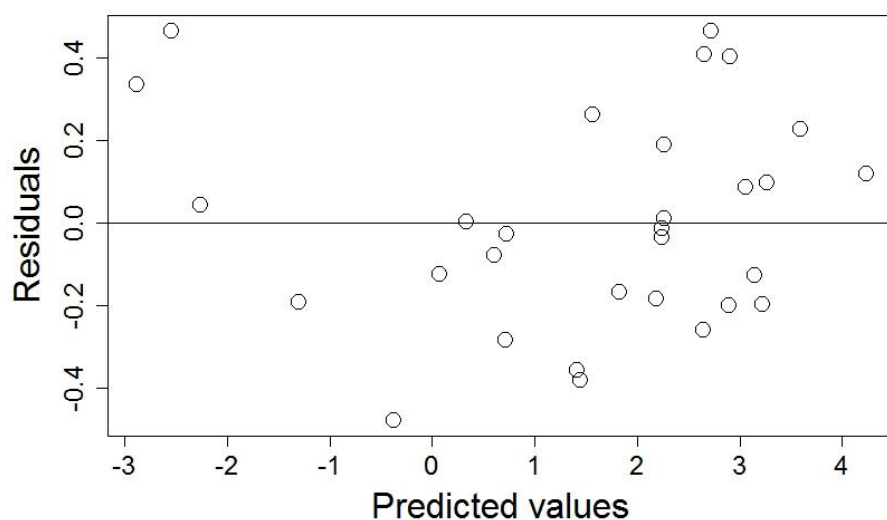


Figure 4.35: Combined model predicted vs. residual plots for predicted foliage mass of Model 4.57.

Total biomass models

Four models were developed to estimate the total biomass of the combined model (Table 4.16). Models having single (Model 4.62), two (models 4.61, and 4.63) and three predictor variables (Model 4.60) have been fitted. Predictor variables include DBH, height and basic density. All models had R^2 values of 0.99, except for models 4.62 and 4.63 having R^2 values of 0.98. Model 4.61 had the lowest RMSE value, followed by model 4.62, 4.60 and 4.63. Model 4.61 had the lowest AIC value followed by models 4.60, 4.62 and 4.63.

Table 4.16: Combined species above-ground biomass models

Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)				CF	R ²	RMSE	AICc
			b ₀	b ₁	b ₂	b ₃				
4.60	ln(Total)	ln(DBH,h,ρ)	-9.733 (<0.001)	2.093 (<0.001)	0.203 (0.451)	1.270 (<0.001)	1.026	0.99	0.424	2.29
4.61	ln(Total)	ln(DBH,ρ)	-9.681 (<0.001)	2.202 (<0.001)	1.289 (<0.001)		1.026	0.99	0.260	0.96
4.62	ln(Total)	ln(DBH)	-1.939 (<0.001)	2.297 (<0.001)			1.050	0.98	0.410	19.12
4.63	ln(Total)	ln(DBH ² h)	-2.685 (<0.001)	0.900 (<0.001)			1.053	0.98	0.427	20.80

Note: DBH is diameter at breast height (cm), h is height (m) and ρ is basic density of the specific tree. The b₀, b₁, b₂ and b₃ values are the parameter values with the p-values in parentheses. Total biomass is given in kg drymass.

All the parameter and model p-values were significant ($p < 0.05$), except for the height parameter in model 4.60 having a not significant ($p < 0.05$) value. Model 4.61 was the best performing model, having low RMSE and AIC values. Model 4.62 [$\ln(\text{Total}) = -1.939 + 2.297 \ln(\text{DBH})$] having the ln-transformed DBH as predictor variable were selected since it has a high R² value and because of the simplicity of the model using only DBH as a predictor variable. Figure 4.36 shows the relationship between the ln-transformed DBH and total mass of the combined species model (Model 4.62).

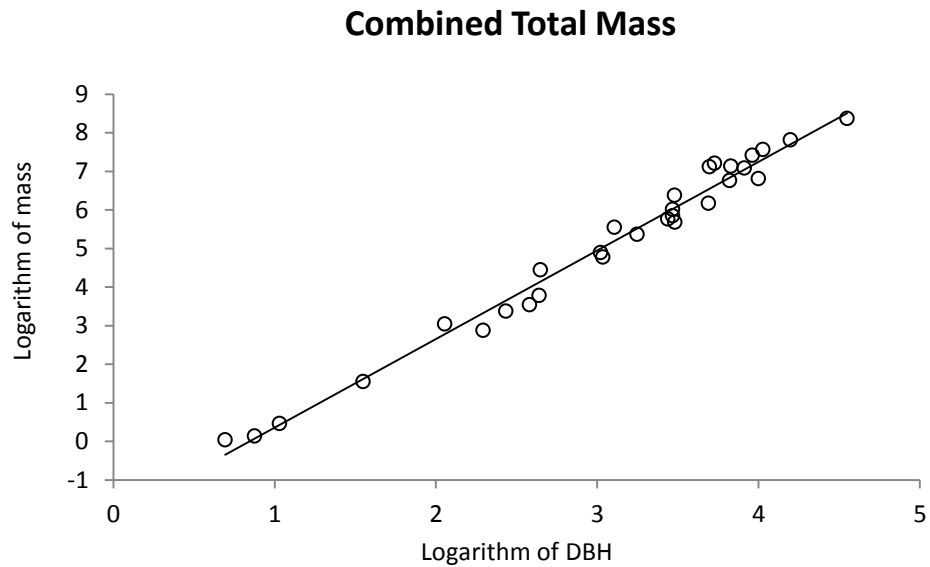


Figure 4.36: Ln-transformed DBH and total mass linear model for the combined species model (Model 4.62).

The predicted total mass values of the selected Model 4.62 plotted against the residuals, shows that there were no clear pattern and that the residuals were not visually heteroscedastic (Figure 4.37). A Shapiro-Wilk test performed on the residuals confirmed that the residuals were normally distributed ($p > 0.05$) and that the residuals were homoscedastic. There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

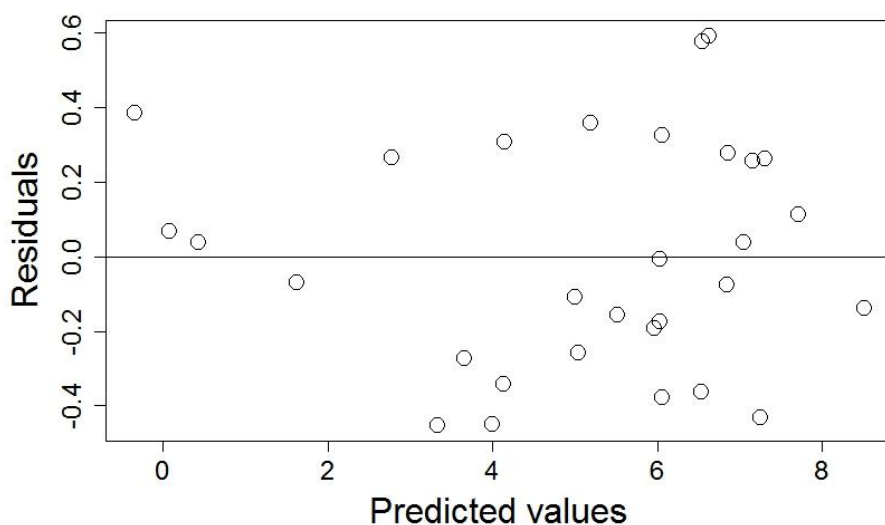


Figure 4.37: Combined model predicted vs. residual plots for predicted total mass (Model 4.62).

4.3 BIOMASS PER HECTARE

4.3.1 *Xymalos monospora* and *Celtis africana* biomass per hectare

The biomass of each of the biomass components (stem, branches and foliage material) were upscaled to the plot level and then to the ha level for each of the 34 sample plots by using the applicable upscaling factor for the plot. Models 4.24, 4.30 and 4.36 were used to estimate the stem, branch and foliage biomass respectively for *X. monospora*. Models 4.27, 4.33 and 4.40 were used to estimate the stem, branch and foliage biomass for *C. africana* respectively. Mean mass for each of the components per ha were obtained. The mean total mass per ha was calculated by adding the mean stem, branch and foliage biomass. Figure 4.38 shows the relationship between the different biomass components to the total mass. The recorded foliage and branch mass percentages were lower for *X. monospora* than

for *C. africana*, while the percentage stem mass was more for *X. monospora* than for *C. africana*.

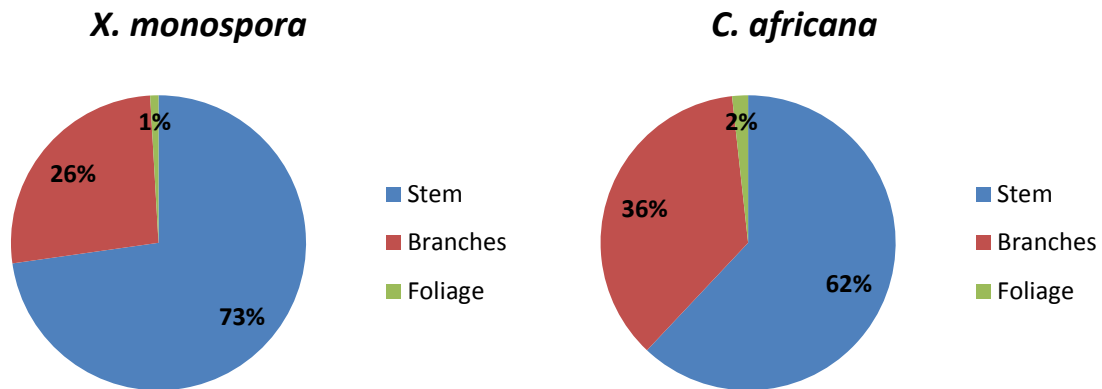


Figure 4.38: Percentages of biomass components for *Xymalos monospora* and *Celtis africana*.

The total mass of all components were higher for *C. africana* than for *X. monospora* (Figure 4.39).

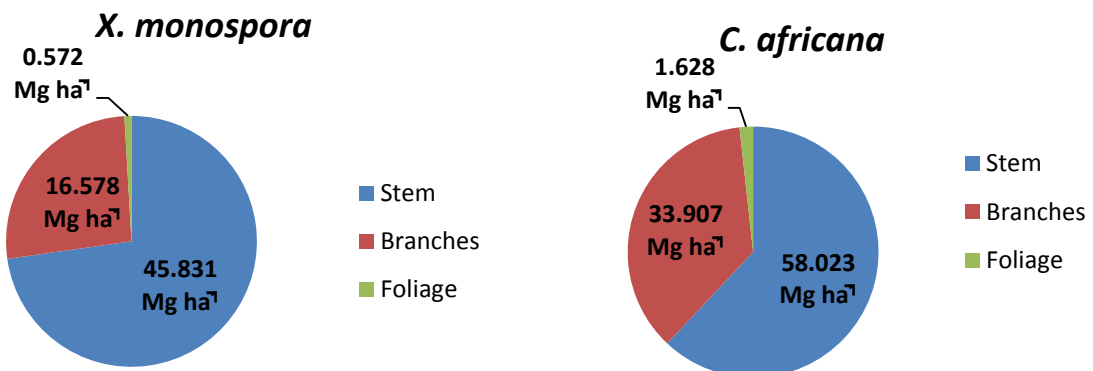


Figure 4.39: Mass of biomass components per ha for *Xymalos monospora* and *Celtis africana*

4.3.2 Total biomass for all species, *Xymalos monospora* and *Celtis africana*

The combined species model was used to estimate the mass of the biomass components (foliage, branch and stem) of all species on all the 34 nested plots. Models 4.51, 4.54 and 4.57 were used to estimate the stem, branch and foliage biomass. The mass of the components were first calculated on a plot level basis and then up scaled to the ha level by making use of the applicable plot correction factor. An average mass was obtained between the 34 sampled plots up scaled to the ha level. Figure 4.40 shows the relation of the different biomass components to the total mass and the total mass of each component per ha.

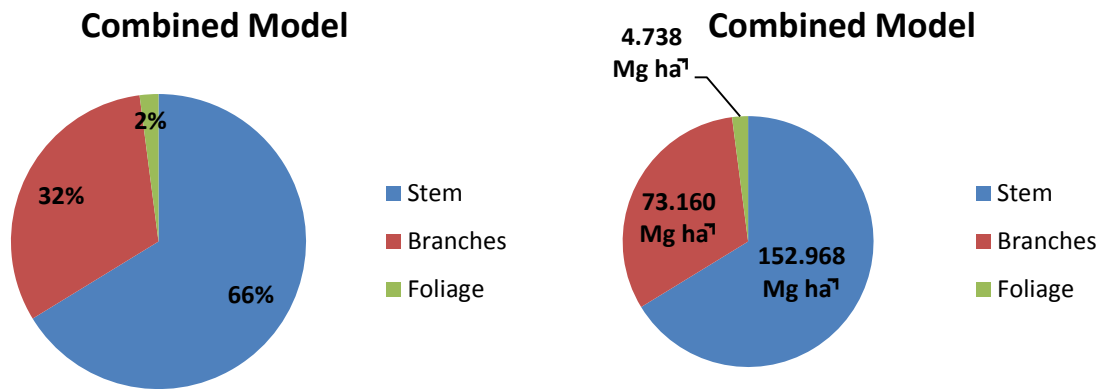


Figure 4.40: Percentages of the biomass components and Mg ha⁻¹ for the combined model.

The mean total mass per ha were obtained by adding up the average mass of the stem, foliage and branch material. The mean mass per ha and the standard deviation from the mean was significantly higher for *C. africana* than for *X. monospora* (Table 4.17).

Table 4.17: Mean biomass per ha for all the species, *Xymalos monospora* and *Celtis africana*

Species	Biomass per ha (Mg ha ⁻¹)			
	Min	Max	Mean	SD
All species	64	826	231	144.22
<i>X. monospora</i>	4	269	63	65.33
<i>C. africana</i>	1	799	94	164.88

Note: Min is minimum and max is maximum. SD is the standard deviation from the mean.

5. DISCUSSION AND CONCLUSIONS

5.1 SAMPLE SIZE AND VARIABILITY OF SAMPLED TREES

The sample size of trees selected for biomass sampling is dependent on the variability of the resource and higher accuracies are associated with higher costs (Kunneke et al. 2014). Fewer sample trees are necessary for species-specific models than for generic multi-species models (Picard et al. 2012). Steward et al. (1992) tested the variability in stand biomass of Central American dry zone species using three site and species-specific allometric models developed from three different sample sizes of 16, 12 and eight sample trees respectively. They found that estimates using allometric models developed from 16 sample trees were as accurate as models developed from 12 trees, but that the biomass estimates became more variable when eight trees were used. Considering the findings above, the sample size used in this study to develop site and species-specific allometric models are sufficient to estimate the biomass of the selected species with reasonable accuracy.

Saint-André et al. (2005) and Samalca (2007) recommended that trees sampled for biomass should follow an even distribution of size classes covering all size classes measured during the plot sampling and that allometric equations should not be applied beyond the valid regression range from which it was developed (Chave et al. 2005). Trees sampled for biomass were sampled following a stratified approach to cover an even distribution of DBH and height variation (Kunneke et al. 2014). With the stratification, a wide range of DBH and height variation was covered. Due to time constraints during the biomass sampling, all trees fitting the stratification plan could

not be located and included; therefore extrapolation beyond the sampled DBH and height range was necessary by assuming limited deviations from the confidence interval.

5.2 EXTRAPOLATION BEYOND THE SAMPLED SIZE RANGE

In principle, extrapolations to estimate biomass should not be made outside the diameter range of the sample trees used to develop the model. However, given constraints inevitable in some environments, there may be instances where it is necessary to make estimates for trees of sizes outside the calibration range. This was the case in this work where biomass had to be estimated for trees above 54.5 cm. In order to assess how reasonable such an extrapolation was the allometric slope coefficient was analysed. The first involved a novel approach to testing stability of the slope of the biomass regression across increasing ranges of tree sizes. This analysis showed that the slope parameter stabilised and the error of the estimate converged. This approach, which has not been applied to this analysis previously, gave a good indication that the slope of the regression would continue to hold beyond the range. However this assumption should be tested against independent data in a further study to fully validate this novel method.

Second, studies have shown in multiple forest types that the relationship between transformed stem dimensions (diameter) and transformed biomass is highly linear across a very broad range. Hence, it is reasonable to assume the same would be true here. Furthermore, Zianis and Mencuccini (2004) discussed the value of using small trees for estimation of biomass given the smaller error of the estimates within the smaller diameter range. A study by Aboal et al. (2005) also found that there is an

almost perfect linear relationship between ln-transformed DBH and biomass and that extrapolations beyond the sampled diameter range will yield reliable results.

Branch mass also had to be extrapolated substantially beyond the sample branch diameter range for *C. africana*. Extrapolation of branch mass yielded the same results than for the DBH range as described above.

All model types are not subjected to the same degree of error when used to extrapolate beyond the sample range (Picard et al. 2012). The finding by Zianis and Mencuccini (2004) and Aboal et al. (2005) supports the findings of this study and that the application of an ln-transformed model can be used to extrapolate beyond the valid range and still achieving reliable results.

5.3 BIOMASS MODELS TO SCALE UP FROM SAMPLE TO TREE LEVEL

5.3.1 Height models

The relationship of DBH and height is often used to describe characteristics of a forest stand and height is often a required predictor in biomass equations (Mugasha et al. 2013; Chave et al. 2015). Height models were developed for the selected species to aid in future AGB estimations, since development of such DBH and height prediction equations may save on future measuring costs (Mugasha et al. 2013). Two species-specific height models each were fitted for *X. monospora* and *C. africana*. Ln-transformed models with DBH and height are the most frequently used (Brown et al. 1989; Feldpausch et al. 2011). Midgley (2003) recommended against using transformed height models, since tree height is not linearly related to

DBH increment and limitations in height growth can be found, especially with the larger diameter trees.

The transformed models, using DBH as a predictor variable proved to be the best fitting models. The findings were also supported in a study by Feldpausch et al. (2011) who found that the ln-transformed model had the least deviation, irrespective of the diameter class it has been applied to. The R^2 fit for the two models are in line with the R^2 fit of other species-specific DBH and height models developed in temperate and tropical regions (Colbert et al. 2002, Wang et al. 2006) and species-specific models generally showed a better R^2 fit than models for grouped species (Mugasha et al. 2013).

Various models of forms other than the ln- transformations are used, relating height to DBH. Polynomial functions are often included in models to set a maximum attainable height, instead of a linear relationship as with the ln-transformed DBH and height models (Chave et al. 2005; Sileshi 2014). Variables additional to DBH are also used to predict tree height (Feldpausch et al. 2011). Larsan and Hann (1987) In Colbert et al. (2002) used non –linear regression models of the Monserud's model form on Midwest riparian tree species, enforcing the constraint that as DBH approaches zero, the tree height approaches breast height (1.37 m), provided that the parameters of the model are negative. The models produced S-shaped height curves for two of the species and in general the models performed well and consistent with the natural behavior of the species. Feldpausch et al. (2011) tested a pantropical level model (PLM). This model is also a ln-transformed DBH and height model incorporating various site factors including stand level basal area, precipitation coefficient of variation, dry season length, annual average temperature and DBH.

The PLM provided less robust estimates than the In-transformed DBH and height models, using only DBH as an independent variable.

Mugasha et al. (2013) compared height and DBH from natural forests in Tanzania using species type and forest type as additional explanatory variables in the development of species and forest type specific models. The species-specific models performed better than the forest-type specific models. Mugasha et al. (2013) concluded that forest-type specific models can be used as a good alternative to species-specific type models, where species information are not available. Bollandsås (2007) included stems per ha as an additional variable to DBH, but Mugasha et al. (2013) concluded that DBH explains most of the variation and other variables in the model will only provide a marginal improvement.

Considering the findings of the various developed height models above, DBH explains most of the variation in height and the In-transformed DBH and height models used in this study and other studies delivered consistently good results.

5.3.2 Branch and foliage mass models

There is ongoing discussion about which predictive variables should be included in regression based modelling of branch biomass. Parresol (1999) determined the branch mass of sampled branches by using a combined independent predictor variable with branch base diameter and length (d^2l). He also measured all the other branches on the sampled trees for branch base diameter and length and used the allometric equation to upscale the branch mass to crown level. In a study by van Laar (1973) on *Pinus radiata*, the addition of branch length to branch diameter as

independent variables to predict branch mass was significant, but the moderate increase in R^2 fit did not justify including branch length as a variable.

In this study the independent variable, branch length for estimating the branch mass of *C. africana* (Model 4.13) and the foliage mass of *X. monospora* (Model 4.16) showed significant results. Measuring the branch lengths of all the branches is not feasible if the tree is not felled. When the tree is felled, many of the branches break and diameter measurements of branches are problematic. In a study by Seifert et al. (2006), height of the branches in the crown was used as an additional variable, but using this approach would be more suitable to conifers than broad-leaved species due to the symmetrical architecture of conifers.

5.4 BIOMASS MODELS TO SCALE UP FROM TREE TO STAND LEVEL

5.4.1 Stem mass

Height as an independent variable proved to be not significant for *X. monospora* (Model 4.25) and significant for *C. africana* (Model 4.28). With the combined species model, height was a significant predictor of stem mass and models with height as an independent variable showed better R^2 , AIC and RMSE goodness of fit criteria (models 4.52, and 4.53). Tree height as an additional predictor variable was not really practical for determining the total stem mass since there was no defined cut-off diameter for stem sections and bigger branch sections were also treated as stem sections. Within broad-leaved multi-stemmed species it is often difficult to differentiate between stem and branch sections (Seifert and Seifert 2014).

Models with only DBH as predictor variable were selected for the modeling. An advantage of a model with only DBH is the simplicity of the estimation in practice.

Height did not substantially improve the estimation as the trees were all sampled from one forest area in this study. DBH and height relationships are often very site-specific (Mugasha et al. 2013). Similar observations were made by Phiri et al. (2015) and Montagu et al. (2005) on *Eucalyptus* species. An application of the models in another area might make it necessary to apply models with predictors, DBH and height to cater for differences in the height-diameter relationships.

5.4.2 Branch and Foliage Biomass

Height was a not significant predictor of total branch and foliage biomass for *X. monospora* and *C. africana* but a significant predictor for the combined species model.

The fact that height did not emerge as a good predictor of branch and foliage mass could be ascribed to the fact that there was no clear definition or cut-off diameter for branch or stem material and branch material was often treated as stem material. In broad-leaved multi-stemmed forests it is also difficult to differentiate between stem material and branch material (Seifert and Seifert 2014).

5.4.3 Total above-ground biomass

The AGB models using crown diameter were marginally better for *C. africana* than for *X. monospora* in terms of the R^2 fit. Various studies investigated the inclusion of crown diameter as a predictor variable rather than tree height (Goodman et al. 2014), since crown diameter predicts AGB better than total tree height (Henry et al.

2010). A study by Jonson and Freudenberger (2011) found that crown diameter was highly correlated with total tree biomass, especially in trees with uniform canopy diameters. These results suggest that the crown diameters of *C. africana* are slightly more uniform than that of *X. monospora*.

Chave et al. (2005) stated that according to his results on tropical trees the most important predictors for AGB in generic multi-species models were in decreasing order of importance stem diameter, basic density, height and forest type (moist or dry forest). Models with three independent variables incorporating DBH, height and basic density were fitted for *X. monospora* (Model 4.44), *C. africana* (Model 4.48) and for the combined species model (Model 4.60). Sileshi (2014) warns against the use of complex models incorporating multiple independent variables such as models 4.44, 4.48 and 4.60, since collinearity may be a problem between the variables and may influence the parameter estimates. Picard et al. (2015) contradicted this statement by saying additional variables to DBH in a model will have no influence on the statistical correctness of the p-values and that collinearity between independent variables *i.e.* DBH and height will not influence the predictability of a model. He further concluded that collinearity between independent variables only means that the parameters of the independent variables cannot be studied separately. However it must be stated in this context that collinearity artificially increases the R^2 values, which might lead to wrong assumptions about the explanatory value of the model.

Chave et al. (2005) developed various biomass models with or without the inclusion of height, but recommended that height should be included since height explains a significant amount of variation in tree biomass (Feldpausch et al. 2011). Where height data from directly harvested trees are not available, estimated height from

DBH and height allometric models can be used (Chave et al. 2005). Sileshi (2014) suggested that the inclusion of estimated height in allometric equations as an additional variable is not reliable since the height estimate is directly derived from the DBH data and collinearity might exist between these two variables. Introducing additional parameters in the model, with each parameter's measurement error (Magalhães and Seifert 2015c) will contribute to the total accumulated error in the model.

Height predictors within *X. monospora*, *C. africana* and the combined species models were non-significant independent variables ($p > 0.05$) of AGB. DBH and basic density were significant independent predictor variables for *X. monospora*, *C. africana* and the combined model (models 4.44, 4.48 and 4.60). It was not surprising that basic density was an important contributor to the combined model, as the two species had significantly different densities. In any general model applied to this forest type, density should be taken into account as an important determinant of total biomass. For the species-specific models, it is likely that the differences in basic density can be ascribed to the range of size and age classes of trees sampled for biomass (van Laar and Akça 2007). That is to say, diameter and density may vary independently to some extent. For the *C. africana* model where DBH, height and basic density values were included (Model 4.48), the model had the lowest AIC and RMSE values with the highest R^2 value. Sileshi (2014) warns that the R^2 fit of a model can be deceiving since the R^2 value will increase with the addition of independent variables, even if there are no correlation between the independent and dependent variable and if multi-collinearity exists between the independent variables. However, basic density is a variable that is probably the most expensive

and time-consuming to measure of the three (DBH, h, basic density) and the question arises as to whether any increase in the GOF on a species-specific model would be warranted by its measurement.

The ln-transformed models with DBH as single predictor variable were selected for both species-specific models and the combined species models as the best models due to the simplicity of the model using a single variable that explains most of the AGB variation (Picard et al. 2015), to having high R^2 values and a low AIC value (Model 4.45). The same model form and DBH as independent variable have been used for each component in each upscaling step thereby ensuring additivity of biomass components (Cunia and Briggs 1984; Parresol 1999; Magalhaes and Seifert 2015b). DBH can also be measured more accurately in-field than measuring total height (Segura and Kanninen 2005) or basic density and a model with only DBH will have less error than a combined model with other variables (Sileshi 2014). Sileshi (2014) recommended that the parameters of a model should be restricted to two to four parameters with one to three independent variables. He further suggested that fewer variables in a model are better, since less parameters will reduce error in the estimation of parameters in the model and will also reduce measurement errors in field by measuring the independent variables.

5.5 THE NEXT STEP BEYOND GROUND-BASED BIOMASS DETERMINATION: REMOTE SENSING AS AN EMERGING ALTERNATIVE

During the study reported in this thesis, biomass models were developed from inventory data and ground-based biomass sampling below the canopy of the forest.

Locating the random points and accessing the terrain to collect the tree dimensional data proved to be very time consuming and expensive.

However, various methods exist whereby biomass can be assessed including remote sensing and field measurements (Parresol 1999; Yavaşlı 2013). Remote sensing is a useful tool whereby biomass of forestry resources can be assessed cost effectively over large areas (Parresol 1999; Lu 2006; Yavaşlı 2013; Kunneke et al. 2014), in contrast to field measurements that are costly and time consuming (Picard et al. 2012).

Remote sensing technologies used to assess forest biomass include photogrammetry and Light Detection and Ranging (LiDAR) (Yavaşlı 2013; Kunneke et al. 2014). Recently, for example, LiDAR remote sensing methods have been used to determine the height of trees and by using high resolution aerial photos, crown diameter dimensions can be measured (Kunneke et al. 2014). Considering these variables is of importance. A study by Goodman et al. (2014) found that including total height within allometric models underestimated total tree mass by 11% to 14% especially within the larger diameter classes. This might suggest that there are limits in terms of tree height growth with increasing DBH and the tree might allocate resources to crown width expansion instead of height growth (Midgley 2003; Goodman et al. 2014). In another study canopy diameter explained more of the variation in biomass than total tree height (Henry et al. 2010). Height data can be derived from these LiDAR images (Lefsky et al. 2002; Gautam et al. 2010; Hansen et al. 2015) and also crown dimensions of individual images from small footprint LiDAR images (Gibbs et al. 2007; Kunneke et al. 2014) and aerial photography (van Laar and Akça 2007). The combined tree height and canopy diameter data can be

used to estimate biomass, although remote sensing applications require strong computers and skilled operators (Goodman et al. 2014).

Biomass assessments with remote sensing have limitations, however, relying on available field data to calibrate the biomass estimates derived from remote sensed data (Picard et al. 2012). To estimate the biomass on a landscape scale or greater and for the development of biomass models, field measurements are needed (Picard et al. 2012; Kunneke et al. 2014). Biomass data collected in field is more accurate than data collected from remote sensing applications (Lu 2006). High costs are associated with remote sensed applications like LiDAR, but an increase of vendors in the market will drive down the costs and improved algorithms will address accuracy concerns around the data (Kunneke et al 2014).

Overall, considering the good R^2 fit of the models using crown diameter as an independent variable, crown diameter proved to be a good predictor of AGB especially for *C. africana* which seems to have a slightly better fit than *X. monospora*. Remote sensing applications can potentially be used to cost effectively determine the biomass of these species across large areas (Jonson and Freudenberger 2011) in combination with scientifically robust biomass studies to calibrate the biomass models derived from the remote sensed data.

5.6 TOTAL MASS PER HECTARE

Biomass per ha was estimated for *X. monospora* and *C. africana* using species-specific allometric equations and the mass of all measured species during the plot sampling was calculated using equations developed from the combined data of *X. monospora* and *C. africana*. Estimates of total mass is a product of basic density

and stem volume (Munishi and Shear 2004) and estimates of regression equations developed from the dried mass of sample branches and the density of the stems per ha. The total estimated mass for *X. monospora* was 63 Mg ha⁻¹ and 94 Mg ha⁻¹ for *C. africana* while the total mass for all species during the plot sampling was 231 Mg ha⁻¹. Munishi and Shear (2004) reported an average estimate of 872 Mg ha⁻¹ and 648 Mg ha⁻¹ AGB for all recorded species from two Afromontane rainforests in Tanzania, while the AGB for individual species ranged from 13 Mg ha⁻¹ - 227 Mg ha⁻¹. A study by Brown et al. (1991) found that only about 6% of tropical forests in Asia had biomass of larger than 500 Mg ha⁻¹, while more than 61% of tropical forests had biomass values smaller than 250 Mg ha⁻¹. The exceptionally high mass ha⁻¹ estimated in the study by Munishi and Shear (2004) can be attributed to intact forest conditions with little disturbance and really big trees. Brown (1994) further estimated the AGB in a forest in south-western Amazonia to be 285 Mg ha⁻¹, while Nascimento and Laurance (2002) estimated the AGB in the forests of the central Amazon to be 325 Mg ha⁻¹. Brown (1997) found the estimated AGB in closed moist forests in Bolivia, Guyana and Malaysia to be 230, 254 and 275 Mg ha⁻¹. Considering the estimated mass calculated by Brown (1991,1997), the estimated AGB per ha calculated within the present study is in line with the findings.

5.7 CONCLUSIONS AND RECOMMENDATIONS

- Considering the positive correlation between crown diameter and AGB, remote sensing applications such as high resolution aerial photography can be explored in further research projects to estimate the biomass of the two species more cost effectively over larger areas. Remote sensing estimates can be

combined with field measurements to calibrate the models developed from the remote sensed data.

- Higher accuracies with less variability can be obtained by sampling more plots during the plot sampling phase. More accurate inventories will result in more accurate biomass estimates during the upscaling of biomass from the tree level biomass to the stand level.
- By increasing the sample of larger trees in the biomass sampling scheme, more precise measurements can be obtained especially from the larger trees since variability of biomass is higher especially in the larger size classes.
- According to findings in the literature, the number of sample trees was sufficient for the development of species-specific allometric equations. The developed equations are site and species-specific and to estimate the biomass of the species on other sites, or within other forest types, allometric models need to be developed for each specific site by sampling at least 12 trees per species on each site. More sample trees can potentially be included to further reduce the variability in biomass estimates. The site-specific data can then be pooled and with the inclusion of total height, soil type and climate in the model, the biomass for the species can be estimated across many sites.
- To develop multi-species allometric equations to use across many sites, the same principles can be used as for the development of species-specific allometric models, but with the exception that a range of species are included in the pooled data. With the inclusion of the independent variables height and basic density as recommended by Chave et al. (2005), variability between different sites and species can be effectively captured.

- Since the minimal invasive sampling technique used in this study is very time consuming and expensive, destructive sampling should be employed where possible. Although extrapolation beyond the sample range indicated no large bias; employing destructive sampling will ensure ease of access for measurement of all tree components thereby illuminating the need to extrapolate beyond the sampled range.

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APPENDIX I

BRANCH BIOMASS DATA SHEET (*Xymalos monospora*)

BRANCH_NO.	SPECIES	DIAMETER(cm)	D ² H	BASAL AREA(cm ³)	D ²	BRANCH LENGTH(m)	FOLIAGE(kg)	BRANCH(kg)	TOTAL(kg)
1.3.1	<i>X. monospora</i>	2.80	10.04	6.16	7.84	1.28	0.0555	0.2054	0.2609
1.4	<i>X. monospora</i>	3.90	28.14	11.95	15.21	1.85	0.1321	0.4312	0.5633
1.5.1	<i>X. monospora</i>	0.80	0.59	0.50	0.64	0.92	0.0093	0.0136	0.0230
1.1.2	<i>X. monospora</i>	8.20	356.37	52.81	67.24	5.30	1.8901	9.5085	11.3986
1.4.2	<i>X. monospora</i>	3.10	17.30	7.55	9.61	1.80	0.0678	0.3369	0.4048
1.4.7	<i>X. monospora</i>	4.20	77.62	13.85	17.64	4.40	0.1834	1.0143	1.1977
1.2.2.1	<i>X. monospora</i>	9.00	388.80	63.62	81.00	4.80	0.7472	7.5189	8.2660
1.2.5	<i>X. monospora</i>	2.90	17.66	6.61	8.41	2.10	0.2109	2.7296	2.9405
1.1.1.2	<i>X. monospora</i>	4.10	48.75	13.20	16.81	2.90	0.2349	0.7642	0.9991
1.1.5	<i>X. monospora</i>	2.00	5.68	3.14	4.00	1.42	0.0711	0.8737	0.9448
1.1.6	<i>X. monospora</i>	2.20	9.00	3.80	4.84	1.86	0.1694	0.2987	0.4681
1	<i>X. monospora</i>	2.30		4.15	5.29		0.0299	0.1303	0.1603
1.1	<i>X. monospora</i>	0.30	0.02	0.07	0.09	0.25	0.0007	0.0009	0.0016
1.1.5	<i>X. monospora</i>	11.50	740.60	103.87	132.25	5.60	1.7407	29.9824	31.7231
1.1.2	<i>X. monospora</i>	2.60	13.52	5.31	6.76	2.00	0.0799	0.4065	0.4864
1.1.1.5	<i>X. monospora</i>	8.50	380.04	56.75	72.25	5.26	0.7255	6.6667	7.3922
1.1.1.3	<i>X. monospora</i>	2.90	23.38	6.61	8.41	2.78	0.1086	0.5185	0.6271
1.3.1	<i>X. monospora</i>	12.90	665.64	130.70	166.41	4.00	0.1737	6.6213	6.7950
1.2.1	<i>X. monospora</i>	15.50	1441.50	188.69	240.25	6.00	1.0581	13.0033	14.0614
1.5	<i>X. monospora</i>	7.00	213.15	38.48	49.00	4.35	0.3691	4.7639	5.1330
1.6	<i>X. monospora</i>	5.00	57.50	19.63	25.00	2.30	0.1488	1.6032	1.7520
1.7	<i>X. monospora</i>	2.10	7.28	3.46	4.41	1.65	0.0217	0.1722	0.1939

BRANCH_NO.	SPECIES	DIAMETER(cm)	D ² H	BASAL AREA(cm ³)	D ²	BRANCH LENGTH(m)	FOLIAGE(kg)	BRANCH(kg)	TOTAL(kg)
1.7	<i>X. monospora</i>	5.30	113.20	22.06	28.09	4.03	0.2371	2.2997	2.5369
1.3.2	<i>X. monospora</i>	4.10	57.15	13.20	16.81	3.40	0.0642	0.5861	0.6504
1.1.1	<i>X. monospora</i>	2.00		3.14	4.00		0.0739	0.1481	0.2219
1.2	<i>X. monospora</i>	4.90		18.86	24.01		0.3311	2.5611	2.8922
1.1.2	<i>X. monospora</i>	7.50	180.00	44.18	56.25	3.20	0.4545	4.3198	4.7743
1.2	<i>X. monospora</i>	8.30	358.23	54.11	68.89	5.20	1.1406	13.3121	14.4527
1.2.1	<i>X. monospora</i>	5.70	113.72	25.52	32.49	3.50	0.1637	2.2726	2.4363
1.3.1	<i>X. monospora</i>	5.50	75.63	23.76	30.25	2.50	0.3158	2.4323	2.7481
1.4	<i>X. monospora</i>	3.50	22.54	9.62	12.25	1.84	0.0602	0.4452	0.5054
1.1.1	<i>X. monospora</i>	0.80	0.50	0.50	0.64	0.78	0.0012	0.0070	0.0082
1.2.3	<i>X. monospora</i>	1.10	1.32	0.95	1.21	1.09	0.0066	0.0327	0.0393

APPENDIX II**BRANCH BIOMASS DATA SHEET (*Celtis africana*)**

BRANCH_NO.	SPECIES	DIAMETER(cm)	D ² H	BASAL AREA	D ²	BRANCH LENGTH(m)	FOLIAGE(kg)	BRANCH(kg)	TOTAL(kg)
1.2	<i>C. africana</i>	0.30	0.04	0.07	0.09	0.49	0.0007	0.0017	0.0024
1.3	<i>C. africana</i>	0.80	0.83	0.50	0.64	1.30	0.0080	0.0271	0.0351
1.2.1	<i>C. africana</i>	1.10	2.18	0.95	1.21	1.80	0.0187	0.0886	0.1073
1.1.2	<i>C. africana</i>	1.60	4.07	2.01	2.56	1.59	0.0140	0.0569	0.0710
1.2.1.1	<i>C. africana</i>	1.90	7.22	2.84	3.61	2.00	0.0340	0.1149	0.1490
1.2.1.2	<i>C. africana</i>	2.10	7.72	3.46	4.41	1.75	0.0305	0.1119	0.1423
1.1.1	<i>C. africana</i>	2.10	12.35	3.46	4.41	2.80	0.0773	0.5243	0.6016
1.1.1	<i>C. africana</i>	2.10	7.32	3.46	4.41	1.66	0.0266	0.1695	0.1961
1.2.1.1	<i>C. africana</i>	2.30	11.64	4.15	5.29	2.20	0.0820	0.2423	0.3243
1.4.1	<i>C. africana</i>	2.70	17.50	5.73	7.29	2.40	0.1190	0.4917	0.6107
1.8	<i>C. africana</i>	2.80	19.21	6.16	7.84	2.45	0.0654	0.5612	0.6266
1.5.1.1	<i>C. africana</i>	3.20	29.70	8.04	10.24	2.90	0.2811	1.6094	1.8905
1.2.1	<i>C. africana</i>	3.20	24.06	8.04	10.24	2.35	0.1028	0.8133	0.8133
1.3	<i>C. africana</i>	3.40	43.93	9.08	11.56	3.80	0.0783	1.0817	1.1600
1.3.2.1	<i>C. africana</i>	3.40	50.86	9.08	11.56	4.40	0.5728	4.8232	5.3960
1.4	<i>C. africana</i>	4.00	51.20	12.57	16.00	3.20	0.0915	1.1027	1.1942
1.3.1	<i>C. africana</i>	4.10	49.93	13.20	16.81	2.97	0.1379	0.2783	0.4162
1.5.2	<i>C. africana</i>	4.30	47.15	14.52	18.49	2.55	0.0972	1.0849	1.1821
1.1.3	<i>C. africana</i>	4.30	61.94	14.52	18.49	3.35	0.3703	2.2025	2.5727
1.4.2	<i>C. africana</i>	5.20	103.29	21.24	27.04	3.82	0.3488	3.5926	3.9413
1.3.1	<i>C. africana</i>	5.70	126.71	25.52	32.49	3.90	0.2748	3.2764	3.5512

BRANCH_NO.	SPECIES	DIAMETER(cm)	D ² H	BASAL AREA	D ²	BRANCH LENGTH(m)	FOLIAGE(kg)	BRANCH(kg)	TOTAL(kg)
1.1	<i>C. africana</i>	5.80	171.90	26.42	33.64	5.11	0.3301	5.2199	5.5499
1.5.1	<i>C. africana</i>	5.90	181.01	27.34	34.81	5.20	0.4130	4.9563	5.3693
1.6	<i>C. africana</i>	6.20	230.64	30.19	38.44	6.00	0.4050	7.4709	7.8759
1.4.1	<i>C. africana</i>	6.30	192.10	31.17	39.69	4.84	0.0934	5.6996	5.7929
1.2.1.3	<i>C. africana</i>	6.40	212.99	32.17	40.96	5.20	0.3811	6.4235	6.8046
1.2.1	<i>C. africana</i>	7.20	388.80	40.72	51.84	7.50	0.1952	8.9985	9.1936
1.2.1	<i>C. africana</i>	7.30	234.48	41.85	53.29	4.40	0.2574	7.3704	7.6279
1.1.3	<i>C. africana</i>	7.70	349.81	46.57	59.29	5.90	0.8568	10.4314	11.2881
1.1	<i>C. africana</i>	8.00	337.28	50.27	64.00	5.27	1.2311	10.7640	11.9951
1.2.1.1	<i>C. africana</i>	8.30	323.78	54.11	68.89	4.70	0.3160	8.8154	9.1314
1.3.1	<i>C. africana</i>	8.80	458.44	60.82	77.44	5.92	1.9424	14.9205	16.8629
1.2.1.3	<i>C. africana</i>	9.60	543.74	72.38	92.16	5.90	0.9396	9.4696	10.4092
1.7.1	<i>C. africana</i>	11.00	822.80	95.03	121.00	6.80	0.7578	21.2019	21.9597
1.3.1	<i>C. africana</i>	12.70	1161.29	126.68	161.29	7.20	2.6303	37.3132	39.9435

APPENDIX III**BIOMASS DATA SHEET (*Celtis africana* and *Xymalos monospora*)**

TREE NO.	SPECIES	DBH(cm)	D ² H	HEIGHT(m)	CROWN DIAMETER(m)	DENSITY(kg ⁻³)	STEM(kg)	FOLIAGE(kg)	BRANCHES(kg)	TOTAL(kg)
1	C.afr	32.40	19420.56	18.50	10.40	609.50	349.55	11.58	227.05	588.18
2	C.afr	7.80	468.47	7.70	4.55	612.50	16.55	0.43	4.02	20.99
3	C.afr	41.50	38578.40	22.40	13.98	600.00	834.47	24.06	495.51	1354.04
4	C.afr	40.20	30381.55	18.80	11.25	655.00	814.91	21.46	403.33	1239.69
5	C.afr	22.30	7708.00	15.50	7.80	549.50	165.33	6.24	85.69	257.27
6	C.afr	46.00	38088.00	18.00	14.45	569.00	776.63	27.37	450.57	1254.57
7	C.afr	4.70	106.03	4.80	3.93	461.50	3.19	0.22	1.28	4.70
8	C.afr	20.50	6850.08	16.30	5.90	594.50	96.48	2.87	33.68	133.03
9	C.afr	52.50	49612.50	18.00	10.80	610.50	1250.84	20.54	391.85	1663.24
10	C.afr	66.50	88002.78	19.90	18.23	646.50	1496.30	45.31	937.74	2479.35
11	C.afr	56.00	69305.60	22.10	14.08	575.50	1331.93	28.98	579.78	1940.69
12	C.afr	14.10	2345.96	11.80	4.60	614.00	62.41	2.00	21.07	85.48
13	C.afr	94.50	169674.75	19.00	20.53	637.00	1515.90	77.82	2730.52	4324.24
14	C.afr	13.20	1864.37	10.70	4.64	301.50	20.16	1.69	12.63	34.47
15	C.afr	2.80	27.44	3.50	1.25	559.50	1.13	0.11	0.35	1.59
16	X.mon	9.90	901.69	9.20	3.73	414.50	11.49	0.95	5.31	17.74
17	X.mon	31.10	12090.13	12.50	6.03	482.00	257.03	7.38	54.52	318.93
18	X.mon	32.00	17612.80	17.20	7.35	485.00	237.25	9.22	99.64	346.11
19	X.mon	14.00	1995.28	10.18	5.73	460.50	34.17	1.53	8.14	43.84
20	X.mon	2.40	19.35	3.36	2.23	396.00	0.53	0.12	0.50	1.15
21	X.mon	32.50	17850.63	16.90	9.60	505.00	153.48	9.73	129.55	292.76

TREE NO.	SPECIES	DBH(cm)	D ² H	HEIGHT(m)	CROWN DIAMETER(m)	DENSITY(kg ⁻³)	STEM(kg)	FOLIAGE(kg)	BRANCHES(kg)	TOTAL(kg)
22	X.mon	50.00	42750.00	17.10	11.18	543.00	873.69	23.28	298.48	1195.45
23	X.mon	40.00	24800.00	15.50	7.33	425.00	333.15	10.88	134.96	478.99
24	X.mon	45.60	39923.71	19.20	9.45	432.50	648.58	14.71	200.59	863.88
25	X.mon	11.40	1177.44	9.06	4.06	449.50	15.43	1.40	12.51	29.33
26	X.mon	25.70	8718.47	13.20	7.00	471.00	158.31	5.27	49.95	213.54
27	X.mon	20.80	5849.29	13.52	5.05	480.00	93.55	2.88	22.10	118.53
28	X.mon	54.50	48118.05	16.20	9.08	432.50	624.26	20.51	266.38	911.16
29	X.mon	32.00	18636.80	18.20	5.30	505.00	295.48	9.03	105.47	409.98
30	X.mon	2.00	11.12	2.78	1.13	413.00	0.71	0.08	0.25	1.04