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Model Selection and Fitting for Basal
Area Increment in a Vietnamese
Tropical Forest

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List of Acronyms (used in Models)

d: DBH_(cm)

dsqr: $DBH_cm^{(0.5)}$ or DBH exponential $^ 0.5$

d2: DBH_cm^2 or DBH exponent $^ 2$

dex: $DBH_cm^{(-1)}$ or DBH exponent $^ -1$

dex2: $DBH_cm^{(-2)}$ or DBH exponent $^ -2$

H: Total height (m)

InH: log transformation f Total height

CR: Crown Ratio

Ming: Mingling Diversity Index

Shan: Shannon Diversity Index

Simp: Simpson Diversity Index

Even: Evenness Diversity Index

Abun: Abundance Diversity Index

RESUMEN

La modelización del crecimiento forestal es fundamental para comprender la dinámica de los bosques y predecir la productividad futura. En este estudio, se ajustaron modelos para seis (6) especies y tres (3) grupos diferentes llamados clase I, II y otros. Las especies de las que no se disponía de suficientes observaciones se agruparon según sus valores de densidad de la madera y se clasificaron de acuerdo con el sistema vietnamita de agrupación de especies. Se ajustaron relaciones altura diámetro para los árboles (por especie y clase) presentes en el aula de señalamiento. El ancho de copa se modelizó mediante el diámetro normal y la fracción de copa. Con el objeto de estudiar la influencia de la diversidad sobre el tamaño se incluyeron índices de diversidad como variables independientes en los modelos anteriores. Los modelos así ajustados fueron significativos. Los modelos lineales candidatos se clasificaron según el criterio de información de Akaike y el R-ajustado. Los índices de diversidad afectaron el tamaño de la copa y la relación altura-diámetro. A partir del crecimiento de cinco estaciones de crecimiento de *Cinnamomum iners* se encontró que el incremento en el área basimétrica solo está afectado por el diámetro normal y no por la ratio de copa.

PALABRAS CLAVE: Bosque tropical, Aula de señalamiento, Selección de modelos, Crecimiento, Diversidad de Estructuras

ABSTRACT

Modeling forest growth is essential to understand the dynamics of forests and predict future productivity. In this study, models were adjusted for six (6) species and three (3) different groups called class I, II and others. The species for which there were not enough observations were grouped according to their wood density values and classified according to the Vietnamese system of grouping of tree species wood quality by density. Height diameter relationships were adjusted for the trees (by species and class) present in the marteloscope. The crown width was modeled by using the normal diameter and the crown ratio as independent variables. In order to study the influence of diversity on size, diversity indices were included as independent variables in the previous models. The models thus adjusted were significant. The linear candidate models were classified according to the Akaike information Criterion and the R-adjusted. The diversity indexes affected the size of the crown and the height-diameter relationship. From the growth of five growing periods of *Cinnamomum iners* we found that the basal area increment is affected only by the diameter at breast height and not by the crown ratio.

KEYWORDS: Tropical Forest, Marteloscope, Model Selection, Incremental Core, Structural Diversity

1. INTRODUCTION

The composition of Vietnamese tropical forest is characterized by well diversified flora and fauna. This points out the important the forest ecosystem. The forest ecosystem functionalities are influenced by the structure, diversity, natural habitat, socio-cultural heritage role, many other services and products. Hung (2018) argues and discusses an encapsulated history in detail how the development on Vietnamese tropical forest has evolved. Studies have elucidated that, typically, the climate topography and soils influence the diversity and abundance of the forest vegetation (Luong, 2018) resulting in a fair distribution across provinces in the entire country.

Meyfroidt and Lambin (2008) structured a classified and homogenized Vietnamese forest cover into the types, namely: pure forest, mixed and non-forest. Elevation pattern richly determines the ecosystem this forest type, the dominate forest formation namely; evergreen, semi-deciduous (Luong, 2014). A common preview of forest cover globally in tropical ecosystems (as shown in figure 2) is its species richness and capacity of multifunctional roles such as carbon storage, etc. However, part of the challenges faced with tropical forests are deforestation (Meyfroidt and Lambin, 2008; Minh and Kono, 2017; Hung, 2018) to meet various need of society such as agriculture (Minh and Kono, 2017). Nonetheless, in the case of Vietnam, forest cover in has increased in the past decades (Nagendra and Southworth, 2010). While some authors argue in favor of bourgeoned forest cover (Nagendra and Southworth, 2010; Luong, 2014).

Policy interventions through development planning is noted to have intervened deforestation (Rompaey et al., 2013; Luong, 2014; Hung, 2018) accounting for the sustainable timber processing, and land-use (GIZ, 2017) particularly when the need of the Vietnamese local communities and population's participation were to be prioritized (Boissière et al., 2009). Largely, forest management strategies (as shown in figure 3 below) which might have involved range of stakeholders including policy makers, forest managers among others directly involved or otherwise (SelectFor, 2013; Bravo et al., 2018) are essential in this regard. However, sometimes, the main challenge could partly be non-compliance or unclear role play my stakeholders involved (Schaltenbrand and Seiber, 2007).

Literature confirms that, through international collaboration and national commitments between 1990-2010, there has been rapid forest recovery trajectory observed in Vietnam surged with forest protection and rehabilitation program, thus, a total area of about 13.3 million ha according to Luong (2014). Silvicultural treatments and techniques contributed enormously during this regime. Schaltenbrand and Seiber (2007) reported in a study where it was observed that, Community Forest Management (CFM) in Vietnam aided a novel participatory approach of forest resource owing to legal permission and acknowledgement through Vietnamese Government to decentralize forest management,

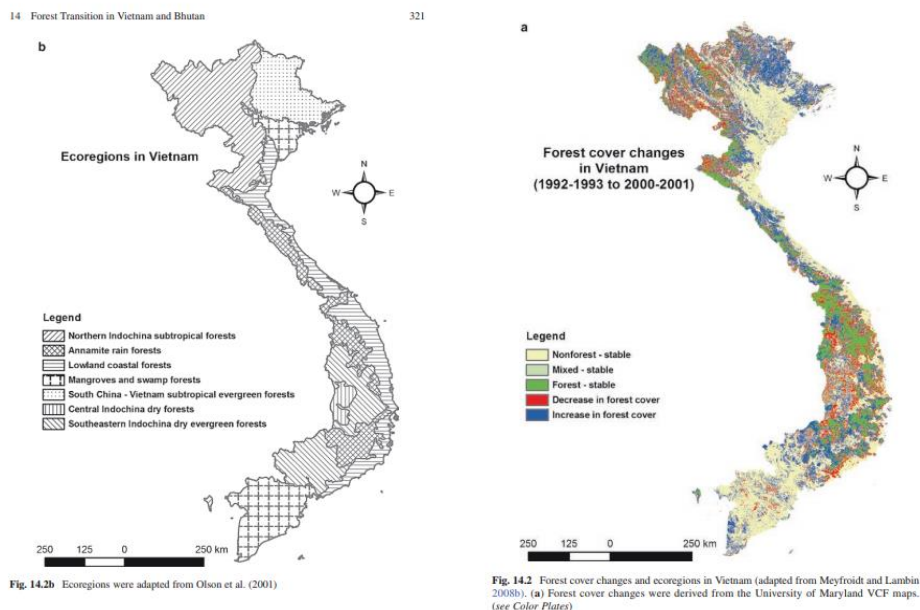
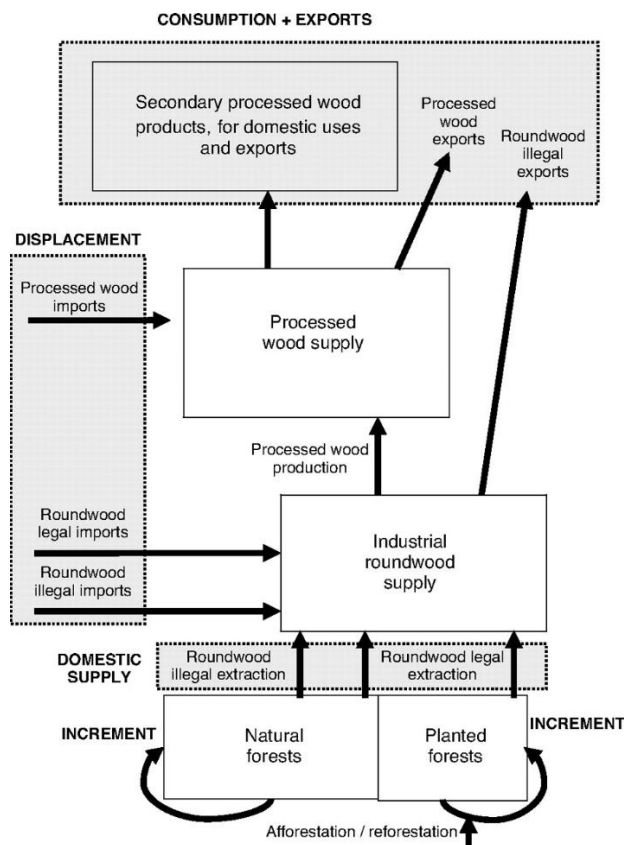


Figure 1: Preview of Forest Transition in Vietnam
Source: Nagendra and Southworth (2010)



Marteloscope in forest data science and management could be one essential key component for ensuring these sustainability measures in the long term in Vietnam. The term marteloscope is of French origin (SelectFor, 2013; Soucy et al., 2016) where *mardeaux* (hammer) is used to mark the trees that are mature and should be harvested.

The term is defined by concept as a permanent plot established within a forest dedicated for tree measurements. Principally, an associated software (example: Smartelo, I+ software) is tailored to provide a complete framework for training purposes such as marking and selection exercises (SelectFor, 2013; Integrate+, 2014; Rodríguez et al., 2015). This concept not only applies to on-field sense of practice but also, it could be in virtual mode through videography (Soucy et al., 2013; Mangelsdorf et al., 2018) where students are cultured in the form of a standard didactic process (Kraus et al., 2018). A standard marteloscope by dimension is a hectare (1 ha) rectangular plot split into 16 subplots or otherwise named quadrants labeled from 1 to 16 of 25 x 25 meters wide.

In recent years, Marteloscope has gained worldwide recognition in sustainable forest management didactics. Further than that, Soucy et al., (2016) believes marteloscope may be more than just a permanent plot. The author argued further on the definition it inner of itself as a terminology in forestry is uncommonly recognized coupled with the fact that attempts by publishers to universalize its definition received less attention. However, it was further referred as “*the combination of a permanent plot (i.e., forest area) with a means to summarize and visualize the outcomes of a virtual tree selection within that plot* (Soucy et al., 2016)” for training students in and perhaps to aid discussions with stakeholder belonging to the forestry sector about forest growth and modeling efforts.

Modeling forest structure can be very sensitive and complicated and thus, expert’s firm knowledge is required. Mathematical equations are established in this case. Consequently, from the perspective of different forest biomes at different ecological zone, varied logically approaches would be imminent to model forest structure. Hung (2018) reveals that, several mathematical functions; both linear and non-linear are expressed to cement relationship between two or more variable/parameters. Notably logistic function using R statistical application (Hung and Doi, 2017; R Core Team, 2019). In regression, Height and Diameter (h-d) are integral part of growth and yield models as basic variable input (Temesgen et al., 2007; Lida et al., 2012; Riofrío et al., 2019) as dependent and independent in the analysis. Mate et al., (2014) argued about h-d per species are probably the best fit for growth/biomass models in combination with stand composition variables such as Basal Area (Riofrío et al., 2019), crown architecture (Pretzsch et al., 2015) including the relationship with wood density (Lida et al., 2012) giving rise to improved model coefficients. This argument could be said to be unanimous as growth models developed for tropical and temperature forest structures relies on similar variables.

1.2 Problem Statement and Justification

The understanding of forest structure is essential and cannot be discounted in forest research (Hung, 2018) particularly with species diversity indices, vertical and horizontal spatial pattern, species mingling (Del Rio et al., 2018), height-diameter relationships and canopy structure among others. In tropical region of the south eastern Asian country of Vietnam, for instance, comprehending the analytical scope of forest structure (Del Rio et al., 2018), including growth modeling has chiefly been part of the limitation to fully explore forests from management perspective. Hung (2018), considered that, in tropical forest such a Vietnam, key attributes worth associating to structural analysis are height-diameter relationship, gap analysis, spatial distribution among others. Meyfroidt and Lambin (2008) structured a classified and homogenized Vietnamese forest cover into the types, namely: pure forest, mixed and non-forest. Mixed forests’ wide range of potential services and products make it appealing to users (Cattaneo et al., 2018; Bravo et al., 2001) in recent discourse. in this regard, indicators of key functional biodiversity measurement and its dynamics in mixed forest such as competition, evenness, vertical structure and competitions are essential. Rendering the inclusion of competition indices an enhancement of growth model quality (Cattaneo et al., 2017).

As part of Vietnam’s commitment to UN REDD program, collaborative effort by the UN and local government sectors such as the nation’s forest service and leading local Universities carried out intensified quantitative research for forest management. Among the science-based activities included development of allometric equations for some major

forest types (Hung et al., 2012b). Modelling above diameter growth of tropical forests species has quite been tricky and mostly the less successful; usually requiring sound technical knowledge in determining the incremental growth. For instance, comprehending the analytical scope of forest structure, including growth modeling has chiefly been part of the limitation to fully explore forests from management perspective. Researchers' skills/ability, financial constraint, quality and availability of world-class literature are cited as impediment (Hung, 2018). Forest managers and engineers heavily rely on parameters such as: basal area, height, stand density, volume layers/social status, etc. (Sánchez-González et al., 2007; Bravo et al., 2011; Hung, 2018). Hung (2018), considered that, in tropical forest such a Vietnam, key attributes worth associating to structural analysis are height-diameter relationship, gap analysis, spatial distribution among others.

Above ground biomass (Ketterings et al., 2001; Huy et al., 2016) growth measurements in these tropical forest ecosystems are quite complex and complicated in detecting the annual rings (Ogden, 1981) as compared to temperate tree species. Potentially, this is owed to the fact that, site conditions of tropical forest tree species significantly differ from temperate forest ecosystems and thus, creating such difference particularly when incremental cores are sampled to determine ring growth from respective biome. Antecedent factor known to perhaps influence forest growth as such could be for example, tropical climatic condition characterized by rainy and dry seasons. Nonetheless, a primal precursor feature in many unsuccessful diameter growth measurements of tropical tree species could be due to some extent, underdeveloped dendrochronological scientific research (technological and modelling) advancement in the forest management mainly in developing countries. In latest development in Vietnam, a 10-year long term forestry development strategy between 2010-2020 seeks to meet a targeted 16.24 million ha of forest and forest land (Luong, 2014) which intend to serve timber production and or nature conservation purposes. This implies that, a research capacity and infrastructural resources are required for such daunting objective. This status-quo is no different for Vietnam (Hung 2018). Thus, further prompting the need of advanced scientific investigation to detect these dynamic and paramount stages of forest growth in the tropics (Huy et al., 2016). Moreover, little is done in modelling growth Vietnamese forest species. This study therefore adopts a state-of-the-art dendrochronological scientific approach to measure the incremental annual ring growth for some selected Vietnamese tropical species, subsequently candidate tree species are fitted in growth models to ascertain the best explained Basal Area Increment (BAI) in the species under examination.

2. RESEARCH OBJECTIVES

The objective of the study was to analyze Basal Area Increment (BAI) and structural characteristics for a secondary Vietnamese tropical forest tree species.

2.1 Specific Objective

The study specifically sought to:

1. Generate a linearize model of Total Height (H) – Diameter at Breast Height (DBH) for the candidate species and groups/classes including structural variables as explanatory variables
2. To examine the relationship between structural diversity on height-diameter growth
3. To examine the effect of diversity on crown size.
4. Obtain diameter growth of *Cinnamomum iners* for the past 5-years.

3. MATERIALS AND METHODS

3.1 Research Framework

The study was carried out in a stepwise approach beginning from data collections through to discussion of results a scope elaborated and as shown in fig. 1 below with pragmatic effort to achieving the intended study/research objectives.

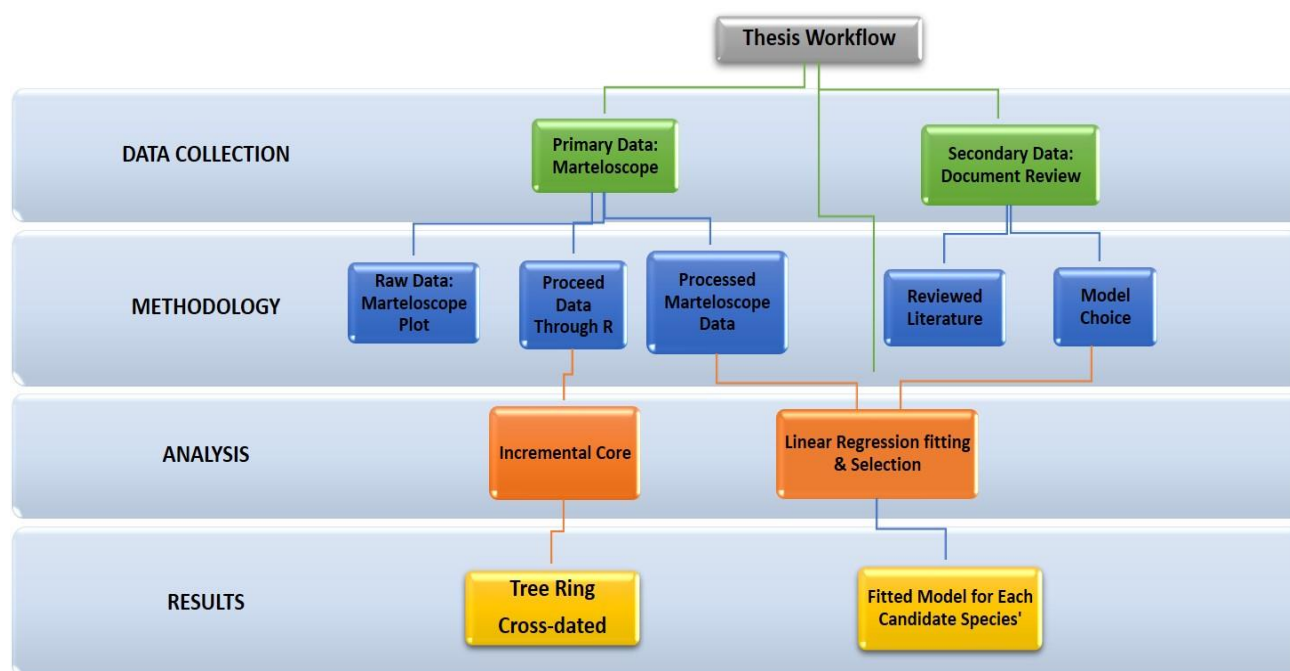


Figure 3: Thesis Workflow- Model Selection and Basal Area Increment for Vietnamese Tropical Forests

3.2 Study Area and Natural Conditions

The research activities were carried out in Vietnam which is one of the South-Eastern Asian countries. Geographically, the study area (Marteloscope) as shown on a map in figure 4 lies on latitude 20°54'37.70"N and longitude 105°33'57.38"E in the Xuan Mai township within Chuong My administrative district of Hanoi, Vietnam. The size or total land-area of the marteloscope covers about one hectare (100 x 100 m). By standardized practice, the marteloscope had not been thinned or heavy utilized for the past 10 years. The natural site condition of the country and therefore with respect to the study area is typical tropical monsoon climate (Giang, 2017). Hence, the rainfall is abundant (Giang, 2017; Schneider et al., 2017) with an average of about 1612mm per year. While an annual average temperature is about 23°C. The study area has an elevation of about 113 meters (m) above sea level.

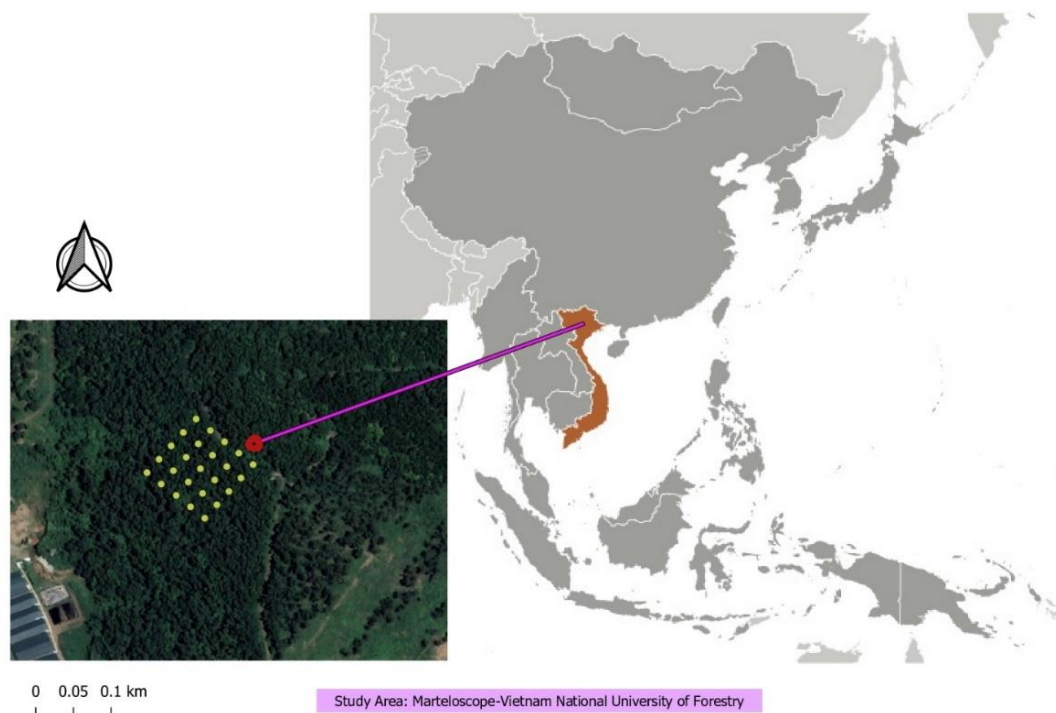


Figure 4: Map of Study Area

3.3 Data Collection

The data collection from the marteloscope were focused on two main approaches, namely; the Static and Dynamic approach. Here, the static approach implied the compartment of the thesis work which relied on the dimensions of the forest’s structural features (such as measuring DBH, total height, etc.) and species compositions.

3.3.1 Static Approach

The principles of setting up a marteloscope involves an intensive and accurate amounts of primary data collection. Bravo et al., (2018) highlights some guidelines that is composed of all the essential parameters to be collected in such exercise. According to the author, there are two main important segments of the parameters which are termed as Basic and Extended variables. Regarding the study area, the following data were collected in accordance with Bravo et al., (2018) recommendation as shown in the Table 1 below.

Table 1: Standard Parameter Measured in a Marteloscope

Basic Variable	Extended variables
1. Identification (ID) Number	1. Diameter Increment
2. Species	2. Microhabitat
3. Diameter at Breast Height (DBH)	3. Health Status
4. Total Height	4. Potential Uses
5. Height to Crown Base	5. Timber Quality
6. Crown Height	6. Social Status

Modified from Bravo et al., 2018



Figure 5: Example of Tree Identification (Tag) in the Marteloscope



Figure 6: Study Area: Overview of the Forest Structure

3.3.2 Species composition

Species identification were investigated in the marteloscope (study area) to ascertain its tree compositions and diversity that existed. At the end of the identification exercise, about 36 different tropical species were identified in the marteloscope (see Fig.7) and labelled with unique species identification (ID). This was an indication and true reflectance of a typical tropical forest of varied forest stories. Further, such composition undoubtedly influences the biodiversity and functional role in terms of ecosystems services in the marteloscope. As mentioned earlier, the marteloscope comprised of a total area of 1 ha with no thinning activity at least for the past 10 years.

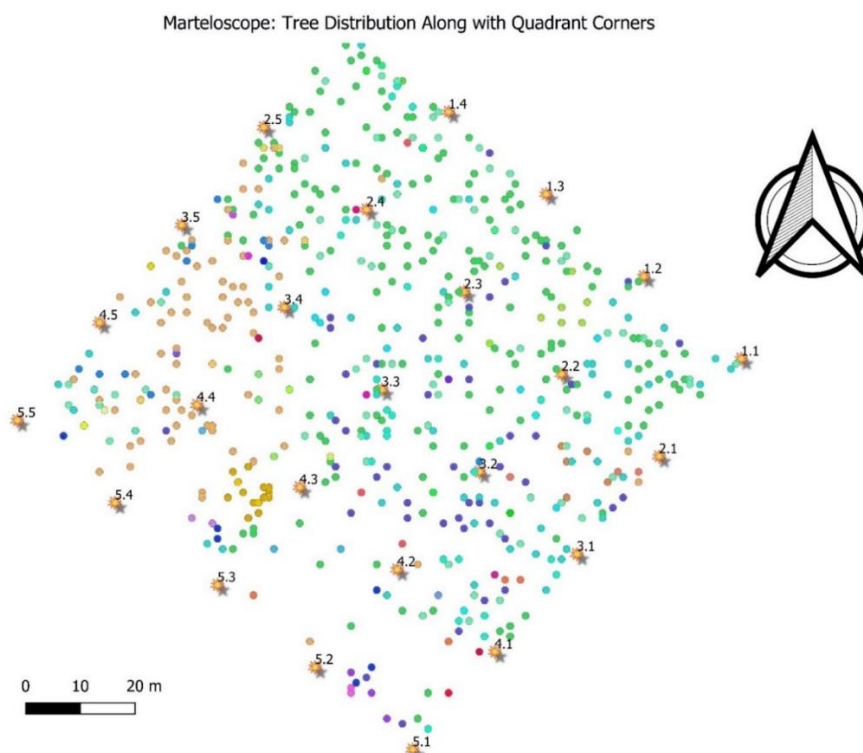


Figure 7: Overview Tree Species Distribution per Quadrant in the Marteloscope (Study Area).

3.3.2 Dynamic Approach: Diameter Growth Quantification

The Dynamic approach could be referred to as; the growth measurement/estimation. Incremental core samples were obtained from the marteloscope to enable the quantification of the diameter growth from trees. Two categorizations were made based on two systematic features; first a target species and secondly, the target tree's neighboring or surrounding trees. Therefore, the targeted tree species and its surrounding or neighboring trees were subsequently cored at 1.3m at breast height (Riofrío et al., 2017; Bravo et al., 2018).

A sub-plot of dimension 900m² was set-up within the marteloscope with distinctive markings (red and yellow colors) for the plot boundary and cored tree respectively, as shown in figure 9. Expert judgement was adopted to select the targeted species namely; *Cinnamomum iners*. The justification behind the selection of *Cinnamomum iners* as the target tree species of interest is chiefly due to the fact that, it among one of the most important tree species in Vietnam due to its several socio-economic, ecological and medicinal benefits (FIPI, 2009). Secondly, it is the single most abundant species with over one hundred and ninety (190) observations present in the marteloscope. These two justifications, nonetheless, is ample to examine or explore further. Consequently, to likewise be able to identify a relationship between its diameter growth pattern over the past five (5) growth periods (backdated) as per the study objective, the surrounding trees within the entire sub-plot of 900m² dimension were also taken into account for quantification of their diameter growth (Bravo et al., 2018).

In more detail, thirty-five (35) *Cinnamomum iners* trees were cored, two (2) sample per tree making a total of seventy (70); sample from the sub-plot. It is worth mentioning that, as per the natural orientation of the trees, it was observed that sloppy nature of the land area may influenced extensively the rings at DBH (for example, see figure 8) and thus making it inclined proportionally, hence, it was prudent to core from two (2) angles or direction per tree at first angle on upslope seconded by another sampling at 120^o angle

from the initial point of sampling. By following this approach, it is ensured that the growth upslope and downslope are taking into account during ring detection and for that matter, diameter growth pattern could be known. Slope orientation could have effect on tree growth and ring pattern.

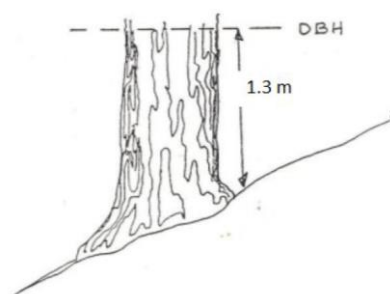


Figure 8: Typical Example of Slope Orientation’s Influence on Trees in the Marteloscope
Source: Bravo et al., 2018

Consequently, twenty-two (22) neighboring trees of *Cinnamomum iners* were as well cored, of which two (2) sample per tree was extracted accounting to a total of Forty-four (44) species indicated on map in figure 13. In summary, One-hundred and fourteen (114) ring core were extracted, adding up to fifty-seven (57) trees were entailing two (2) samples per tree species. Partly, the number of sampling were constrained by the overall number of species observed within the plot. That being said, we exercised prudence to ensure that setting up of the plot justifiably contain greater number of diverse trees. As presented in figure 13 depicting the incremental core plot, sampled trees were noted to have encompassed quadrant 1, 2, 3, 6 and 7. Albeit, some quadrant contained more observations than other.



Figure 9: Sub-plot Setting; Cored Tree (both Target and Neighboring) Marked Yellow in Sub-plot During Exercise



Figure 10: Coring Activity

The processed incremental core samples were scanned at 2400 dpi resolution. This high scanning image resolution is justified by virtue of the complexities to delineating ring formation. tropical rings usually uneasy to be detected. As per dendrochronological standard practices (Cattaneo et al., 2017; Riofrio et al., 2017) in ring detection (Cherubini 2015), 'measuRing' (Lara et al., 2015) coupled with 'dplyRs' (Bunn, 2008) packages in R software to obtain from the scanned rings image a five (5) annual (diameter increment) growth (see Annex 4).

The incremental cores were facilitated in an oven-dried (as indicated in figure 11 below) overnight at 40°C (Cherubini, 2015). These samples were then withdrawn from the oven after successful drying to allow further air-drying (Cattaneo et al., 2018)



Figure 11: Readied Samples Packed for Oven-Dry

Samples were polished manually with sandpapers to reveal the ring pattern or orientations in the incremental core samples. Sanding (as indicated in figure 12) after oven drying core samples is one of the integral dendrochronological procedurals to detect rings (Cherubini, 2015; Cattaneo et al., 2018).



Figure 12: Sanding Core Sample in the Laboratory

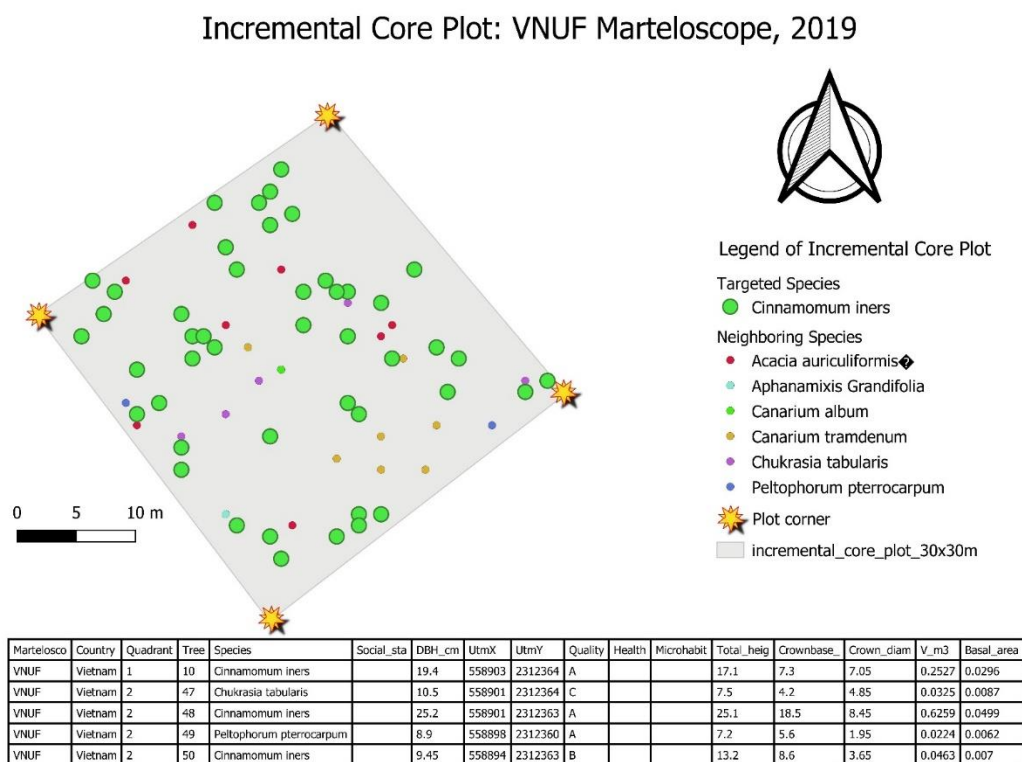


Figure 13: Map of Sub-plot Designated for Incremental Coring Activity within the Marteloscope (Study Area)

3.3.3 Incremental Core Nomenclature

The incremental coring for each individual tree species in the dedicated plot earmarked for the activity was executed following a personalized protocol developed by the research student. The first and foremost task was to develop a nomenclature which will ensure a systematic naming that will facilitate tracking each core sample obtained during the field data collection owing to the complexities that exists and more importantly, to avoid errors and ensure quality data records. To begin with, a template was created to assist genuine labeling of raw and processed core (polished and scanned). As mentioned earlier, the purpose of this innovative technique was to ensure sound and standardized approached to detecting and monitoring accuracy of the work done.

Based on previous experiences, the nomenclature took the following structure. The name of the Study Area (Marteloscope); preferably called the VNUF, Tree ID, Sample Number (also based on the slope of the terrain), Year of core extraction respectively and by exact order of arrangements.

For example:

A core-holder with label 'VNUF_47_1_19' and 'VNUF_47_2_19' implies an interpretation as shown in table below. Consequently, the following interpretation below further denotes the nomenclature table indicated in table 2.

1. **Marteloscope name:** VNUF
2. **Tree ID:** 47
3. **Sample Number:**
 - 1: Upslope/uphill @ first angle and 2: Downslope @ 120-degree angle on the tree at DBH of 1.3m
4. **Year of extraction:** 2019

Table 2: Example of Incremental Core Nomenclature

Marteloscope	Tree	Species	Sample Number	Year	DBH_cm	Total height (m)
VNUF	47	<i>Chukrasia tabularis</i>	1	2019	10.5	7.5
VNUF	47	<i>Chukrasia tabularis</i>	2	2019	10.5	7.5

3.4 Data Processing and Analysis

The primary data collected in the field were compiled in a Microsoft excel workbook and cleaned to poise and assure the quality of the data was uncompromised. Species name correction, repetition, among other were corrected. As indicated earlier about the static and dynamic approaches adopted for the study, likewise, the analysis and data processing procedures varied accordingly with software (analytical tool), technique, etc.

Generally, the data analysis was performed with R statistical application (R Core Team (2019). According to the latest and common practice in data science and management applied to forestry, forest biometricians have relied on R language for analysis. This is so because, R is proven to usually ensure and handle the possibility to feature an enormous to statistical computation (Hung and Doi, 2017) for which emphatically, many pre-conditions statistically application may not allow or be able to.

3.4.1 Static Approach

In this approach, the study explored the forest structural characteristics in terms of diversity indices (ie. Shannon (Shannon, 1948), Simpson (Simpson, 1949) and mingling among others (Del Río et al., 2018) as well as develop model equations that could be used or adopted to establish relationship with between parameters. In this view, a relationship between Total height (H) and Diameter at Breast Height (DBH) was first established for the entire marteloscope dataset and thereafter for each candidate species within the study area. Therefore, the following equations were used to quantify the forest structural diversity within the marteloscope which were further categorized into structural characteristics/diversity and Height-DBH relationship.

3.4.1.1 Structural Characteristics/Diversity

Simpson Diversity Index (1-D)

$$D = 1 - \frac{\sum_{i=1}^R ni(ni - 1)}{N(N - 1)} \quad \text{Equation (1)}$$

Where:

- D= Mathematical characterization of species diversity
- R= Richness; an indication of the total number of types
- ni= Number of entities of the *i*th type
- N= Total number of observations in the dataset

Berger-Parker Index (D)

$$D = Nmax/N \quad \text{Equation (2)}$$

Where:

- D= Abundance of species
- Nmax= Number of observations in the most abundant species
- N= Total number of observations

Evenness Index (E)

$$E = \frac{H'}{\ln S} \quad \text{Equation (3)}$$

Where:

E= Evenness

H' = Diversity index

lnS = Species count expressed in terms of natural logarithm

Shannon Index (H')

$$H' = - \sum_{i=1}^s P_i \ln P_i \quad \text{Equation (4)}$$

Where:

H' = Diversity index

Pi= Proportion of S made up of the *i*th species

3.4.1.2 Height-DBH relationship

Different height-diameter equations and largest crown equations have tested. diameter equations included diameter at breast height as independent variables with different exponent such as squared, square root, inverse or squared inversed (see table 3 for details). These height-diameter equations have been linearized by log transformation. Largest crown equations included diameter and crown ration as independent variable. Crown ration (CR) accounted for tree vigor while diameter (with different exponent) accounted for tree size (see details in table 4). To examine the effects of diversity on h-dbh and crown size in the marteloscope, diversity indices such as Mingling, Evenness, Simpson, Abundance and Shannon would be modelled with the allometries proposed for h-dbh and largest crown width to attest if there would be any significance.

All the model fitted were studied and the best model selected following the procedures used before in forest research by different authors as Allen, (1971), Harville et al., (1992), Chave et al., (2005) Djomo et al., (2010), El Mamoun et al., (2012) or Nam et al., (2016) in regression analysis. Model selection is based in the following criteria:

- Significance Parameter coefficient at 95%
- The adjusted R-square (R_{adj}^2) value
- The Akaike Information Criterion (AIC) value
- The level of significance (P-value)
- Mean Square Error (MSE) value

Based on these sets of methodology, candidate species are ranked (for example see Cattaneo et al., 2018) to select best fitted model amongst the five (5) linearized allometric models as referred and as elaborated from the table ..above.

$$AIC = (-2) \times \ln(L) + (2 \times k) \quad \text{.....Equation 5}$$

Where:

k is the number of model parameters

L is maximized likelihood function for the estimated model

$$(R_{adj})^2 = 1 - \frac{(1-R^2)(n-1)}{n-p-1} \quad \text{.....Equation 6}$$

Where,

R_{adj}^2 = Adjusted R-square

R²=sample R-square

p=Number of predictors

n= Total sample size

The five (5) generic models were transformed from originally non-linear state to linear to suit our objective through logarithmic transformation (Deb et al., 2012). The fitted linear regression models (Vanclay, 1989; O'Brien et al., 1995; Chazdon et al., 2005; Martínez-Garza et al., 2005) included exponential and polynomial models (Gourlet-Fleury and Houllier, 2000; Deb et al., 2012); a widely accepted statistical operation to quantify dependence of variables and their effects (Palomaki et al., 2006).

Table 3: Generic Allometric Structure for Height (H) - Diameter at Breast Height (DBH) Model

Non-Linear Model	Linearized Model	Model No.
$H = e^{\beta_0 + \beta_1 * DBH^{-1}}$	$\ln H = \beta_0 + \beta_1 * (DBH^{-1})$	1
$H = e^{\beta_0 + \beta_1 * DBH^{-2}}$	$\ln H = \beta_0 + \beta_1 (DBH^{-2})$	2
$H = e^{\beta_0 + \beta_1 * \sqrt{DBH}}$	$\ln H = \beta_0 + \beta_1 (DBH^{0.5})$	3
$H = e^{\beta_0 + \beta_1 * DBH + \beta_2 * DBH^2}$	$\ln H = \beta_0 + \beta_1 (DBH) + \beta_2 (DBH^2)$	4
$H = e^{\beta_0 + \beta_1 * DBH + \beta_2 * DBH^{-2}}$	$\ln H = \beta_0 + \beta_1 (DBH) + \beta_2 (DBH^{-2})$	5

Table 4: Generic Allometric Structure for Largest Crown Width (LCW), DBH, and Crown Ratio (CR) Model

Linearized Model	Model No.
$LCW = \beta_0 + \beta_1 * CR + \beta_2 * (DBH^{-1})$	1
$LCW = \beta_0 + \beta_1 * CR + \beta_2 * (DBH^{-2})$	2
$LCW = \beta_0 + \beta_1 * CR + \beta_2 * (DBH^{0.5})$	3
$LCW = \beta_0 + \beta_1 * CR + \beta_2 * (DBH) + \beta_3 * (DBH^2)$	4
$LCW = \beta_0 + \beta_1 * CR + \beta_2 * (DBH) + \beta_3 * (DBH^{-2})$	5

3.4.1.3 Species Grouping

The collective sum of species and its observation for regression analysis (statistical computation) from the data collected in the marteloscope was observed to have a limitation during a pre-test analysis. Due to the low number of observations for some candidate species as low as less than twenty (20), the pretested analysis revealed an adequate level of undefined (N/A) variations for allometric equations co-efficient. Therefore, grouping the species (Vanclay, 1991; Akindele and LeMay, 2006; Pretzsch et al., 2015; Nam et al., 2016) became a valuable option based on standardized similarity within species with the low number of observations owing to the fact that, species grouping are widely practiced particularly in forest data science (Phillips et al., 2002). The usefulness of data in forest science is paramount for prudent decision making (Hung and Doi, 2017). In tropical forest (Köhler and Huth, 1998) ecosystems, wood density is frequently cited to exhibit distinctions for wood quality (Nam et al., 2018), a key functional trait which influences biomass in tropical forest (Brown et al., 1989). Wood density values were obtained from global wood density database (Zanne et al., 2009). It contained studies conducted to estimate tropical wood densities particularly of southeast Asian origin (Chave et al., 2009; Huy et al., 2012). Selection of the specific species wood density values for our dataset was through this method tailored with the predefined Vietnamese wood density classification (Nam et al., 2016) system, these density values were classed/grouped accordingly.

Consequently, based on Vietnamese wood density classifications adopted for logging regulations and wood quality grades (MARD, 2004; Nam et al., 2016), the following classes of wood density with respect to the dataset candidate species were re-grouped as shown in Table 5. Nonetheless, not all the classes of wood density were found for the species present in our dataset, hence some of the classes excluded and other merged. Candidate species having inadequate number of observations coupled with species lists whose density values could not be obtained from the database were subjected to different class of undefined density values (class others) and therefore considered as separate group sufficient for the analysis.

Nam et al., (2016) indicated that, the forest service of Vietnam classed wood density into five (5) classes: “*class I* ($WD \leq 0.50 \text{ g cm}^{-3}$), *class II* ($0.51 - \leq 0.65 \text{ g cm}^{-3}$), *class III* ($0.66 - \leq 0.80 \text{ g cm}^{-3}$) *class IV* ($0.81 - \leq 0.95 \text{ g cm}^{-3}$) and *class V* ($>0.95 \text{ g cm}^{-3}$)”. Since our dataset did not capture classes of III, IV and V, all those candidate species were classed as ‘Others’ for our model fitting and selection regression analysis (Stephenson et al., 2014; Pretzsch et al., 2015)

Wood density is one of the plausible characteristics to determine biophysical interaction in species within a given forest plot. Lida et al., (2012) highlighted in their paper which examine the architectural differentiation in tropical tree species, it noted that, species with high wood density were more inclined/tolerant to shade. In the event of having to necessary group tree species especially in the situation where number of species observations are less represented for a given dataset for statistical inferences, shade and light tolerance, wood density classification, among other could become standardized basis.

Table 5: Species Grouping for H-DBH Allometric Modelling

Individual Species	Class I (WD ≤ 0.50 g cm ⁻³)	Class II (WD 0.51 - ≤ 0.65 g cm ⁻³)	Class Other
<i>Cinnamomum iners</i> (191)	<i>Alangium chinense</i> (6) _a	<i>Antidesma ghaesembilla</i> (1) _a	<i>Mallotus philippinensis</i> (2) _a
<i>Peltophorum pterocarpum</i> (76)	<i>Bombax ceiba</i> (1) _a	<i>Bauhinia variegata</i> (1) _a	<i>Microcos paniculata</i> (1) _a
<i>Chukrasia tabularis</i> (44)	<i>Canarium album</i> (10) _a	<i>Cassia siamea</i> (2) _a	<i>Aphanamixis grandiflora</i> (4) _b
<i>Manglietia conifera</i> (78)	<i>Cryptocarya lenticellata</i> (1) _a	<i>Litsea glutinosa</i> (4) _a	<i>Aporosa dioica</i> (2)
<i>Dracontomelon duperreanum</i> (23)	<i>Ficus hispida</i> (4) _a	<i>Khaya senegalensis</i> (3) _a	<i>Castanopsis cerebrina</i> (3)
<i>Acacia auriculiformis</i> (70)	<i>Liquidambar formosana</i> (5) _a	<i>Canarium tramdenum</i> (8) _b	<i>Chisocheton paniculatus</i> (2)
	<i>Litsea cubeba</i> (1) _a	<i>Acacia mangium</i> (1) _a	<i>Dalbergia tonkinensis</i> (2)
	<i>Macaranga denticulata</i> (1) _a	<i>Cinnamomum camphora</i> (2) _b	<i>Fernandoa brilletii</i> (2)
	<i>Prunus arborea</i> (1) _a		<i>Madhuca pasquieri</i> (9)
	<i>Michelia mediocris</i> (2) _a		<i>Rauvolfia verticillate</i> (2)
	<i>Oroxylum indicum</i> (16) _a		
	<i>Pinus massoniana</i> (3) _a		
482	51	22	29

Where: WD is Wood Density, *Parenthesis is number of observations for each species, _a: source of wood density values (Chave et al., 2009; Zanne et al., 2009), _b: source of wood density values (Huy et al., 2012). -Total Number of Observation is: 584 -Total Number of species: 36
Models were independently fitted for each species under individual species column and for the classes I, II and Other with all its species together. In total 9 set of models (6 species plus 3 classes)

Table 6: H-D Summary Statistics of Candidate Species from Regression Analysis by Grouping

Independent Candidate Species and Grouping	No. of Obsv.	Total Height (m)	DBH (cm)	Crown Diameter (m)	Crown-Base Height (m)
		Mean±SD	Mean±SD	Mean±SD	Mean±SD
A. Individual Species					
1. <i>Chukrasia tabularis</i>	44	10.6±3.9	10.0±3.0	4.4±1.3	5.7±2.7
2. <i>Acacia auriculiformis</i>	70	23.1±4.7	30.6±7.6	8.0±2.5	12.0±4.2
3. <i>Dracontomelon duperreanum</i>	23	17.0±4.6	20.9±7.4	7.4±2.2	7.0±3.1
4. <i>Cinnamomum iners</i>	191	16.3±7.9	17.3±8.2	6.3±2.2	8.8±4.0
5. <i>Manglietia conifera</i>	78	18.8±4.7	21.92±6.8	5.6±1.5	13.3±4.8
6. <i>Peltophorum pterocarpum</i>	76	13.5±4.0	11.4±4.6	4.2±1.7	8.2±3.1
B. Class I					
	51	12.6±3.8	12.9±6.0	4.5±1.7	7.3±4.0
C. Class II					
	22	13.9±4.9	13.3±7.1	4.4±1.7	8.6±3.9
D. Class Others					
	29	9.6±3.7	10.7±9.5	3.7±1.5	4.0±1.9
		584.00			

Where SD: standard deviation

3.4.2 Dynamic Approach

To obtain the basal area increment (BAI) (Dean, 2004), the growth of targeted species (*Cinnamomum iners*) was derived from past five (5) growth periods (backdated) from the incremental core rings through estimation by the measuRing R package (Lara et al., 2015). The model took the general form (as shown in equation 7):

$$BAI = e^{\beta_0 + \beta_1 * \ln(DBH) + \beta_1 * DBH^2 + \beta_3 * \ln(\frac{CR+0.2}{1.2})} \dots \dots \dots \text{Equation 7}$$

Where:

ln is natural logarithm, DBH is the diameter at breast height at the beginning of the five (5) year growth seasons period and CR is the crown ratio (we consider as constant the CR in this 5 growth period so relation between tree total height and crown base height at the measurement moment was used)

This model was linearized by taking natural logarithm and after variable selection and different exponent applied to DBH, the models fitted were the following:

Model	Model No.
$\ln BAI = \beta_0 + \beta_1 * \ln(DBH)$	1
$\ln BAI = \beta_0 + \beta_1 * \ln(DBH) + \beta_2 * \ln\left(\frac{CR+0.2}{1.2}\right)$	2
$\ln BAI = \beta_0 + \beta_1 * \ln(DBH) + \beta_1 * DBH^2$	3
$\ln BAI = \beta_0 + \beta_1 * DBH^2$	4
$\ln BAI = \beta_0 + \beta_1 * \ln(DBH) + \beta_1 * DBH^2 + \beta_3 * \ln\left(\frac{CR+0.2}{1.2}\right)$	5

4. RESULTS

4.1 Height-Diameter (h-d) Relationship

Linear regression analysis was conducted to test five (5) candidate models to ascertain the best explained relationship for six (6) individual species and three (3) classes/groups aggregating selected species as delineated in the methodology and table 6. Out of the five (5) tested models, models 1 (as shown in table 6 and 7) had the best results across all the h-dbh relationship for all individual species and classes. The selection of best fitted model was adjudged according the parameter significance at 95%, Akaike Information Criterion (AIC), R-adjusted and Mean Square Error (MSE) and P-values respectively of its associated co-efficient values. The regression analysis indicated that MSE for all candidate models were <0.08, indicating good performance as the lower the MSE value the better. Adjusted R-squared values ranged from 0.72-0.2 but varied with model type. *Cinnamomum iners*, *Chukrasia tabularis*, *Peltophorum pterocarpum*, *Dracontomelon duperreanum*, Class I and II performed well with model 1. *Acacia auriculiformis* with model 2, *Manglietia conifera* and Class Others with model 4.

The study's examination on the interaction between h-dbh and diversity indices in the marteloscope revealed that, species diversity do have relationship with the tree size relationship. Diversity indices namely; Shannon, Simpson, Evenness, Mingling and Abundance were fitted with the observations already made with h-dbh. The Mingling and Shannon indices relationship with h-dbh was best explained by model 1, Evenness and Simpson by model 2 and Abundance by model 3. The adjusted R-squared values for all the models (1 to 5) were between 0.60-0.69. this indicates the model goodness of fitting. The Abundance and Evenness indices did not have significant coefficients for all of its parameter except for their best-fit models, models 3 and 2 respectively as shown in table 8 and 9. The Mean Square Error for the all the h-d and diversity were between 0.05 to 0.07. These MSE values, however, are good since it approaches zero because the lower the better. Overall, the models performed well with all candidate models respective p-values for h-d relationship and h-d and diversity were <0.01.

4.1.1 Height-Diameter relationship Models

Table 7a: Fitted Models for on h-d Relationship

	β_0	d	d ²	d ⁻¹	d ⁻²	d ^{0.5}	MSE	R ²	P-Value	AIC
Independent Candidate Species and Grouping										
1. <i>Chukrasia tabularis</i>										
Model 1	3.42***			-10.44***			0.040	0.71	<0.01	-12.9
Model 2	2.86***				-44.9***		0.046	0.67	<0.01	-7.09
Model 3	0.12					0.69***	0.039	0.72	<0.01	-13.8
Model 4	0.62	0.22***	-0.00				0.039	0.72	<0.01	-13.1
Model 5	1.86***	0.06**			-18.64		0.039	0.72	<0.01	-12.5
2. <i>Acacia auriculiformis</i>										
Model 1	3.53***			-11.8***			0.032	0.29	<0.01	-38.36
Model 2	3.31***				-149.6***		0.032	0.30	<0.01	-39.33
Model 3	2.28***					0.15***	0.034	0.24	<0.01	-34.10
Model 4	1.84***	0.07***	-0.0009**				0.031	0.30	<0.01	-38.9
Model 5	3.42***	-0.002			-172**		0.032	0.29	<0.01	-37.49
3. <i>Dracontomelon duperreanum</i>										
Model 1	3.24***			-7.99***			0.033	0.61	<0.01	-9.23
Model 2	2.98***				-46.84***		0.035	0.58	<0.01	-7.77
Model 3	1.64***					0.25***	0.038	0.55	<0.01	-5.86
Model 4	1.77***	0.07*	-0.001				0.038	0.55	<0.01	-4.95
Model 5	2.67***	0.01			-32.55*		0.034	0.60	<0.01	-7.88
4. <i>Cinnamomum iners</i>										
Model 1	3.35***			-8.39***			0.045	0.61	<0.01	-47.46
Model 2	3.02***				-47.03***		0.049	0.57	<0.01	-29.88
Model 3	1.68***					0.26***	0.057	0.50	<0.01	0.45
Model 4	1.71***	0.08***	-0.01***				0.046	0.60	<0.01	-41.83
Model 5	2.82***	0.008**			-37.98***		0.047	0.59	<0.01	-36.61
5. <i>Manglietia conifera</i>										
Model 1	3.35***			-8.96***			0.084	0.35	<0.01	23.4
Model 2	3.06***				-53.3***		0.084	0.36	<0.01	32.2
Model 3	1.80***					0.23***	0.100	0.24	<0.01	45.6
Model 4	1.08***	0.15***	-0.003***				0.077	0.41	<0.01	25.9
Model 5	3.05***	0.0004			-52.87***		0.085	0.35	<0.01	34.2

Table 7b: Fitted Models for on h-d Relationship

	β_0	d	d ²	d ⁻¹	d ⁻²	d ^{0.5}	MSE	R ²	P-Value	AIC
6. <i>Peltophorum pterrocarpum</i>										
Model 1	3.22***			-7.34***			0.046	0.54	<0.01	-13.95
Model 2	2.92***				-34.81***		0.050	0.50	<0.01	-8.57
Model 3	1.32***					0.36***	0.049	0.51	<0.01	-9.95
Model 4	1.56***	0.11***	-0.002**				0.047	0.53	<0.01	-11.84
Model 5	2.52***	0.022*			-21.65**		0.047	0.53	<0.01	-12.11
7. CLASS I										
Model 1***	3.11***			-7.04***			0.053	0.50	<0.01	-1.23
Model 2***	2.81***				-35.84***		0.056	0.47	<0.01	1.31
Model 3***	1.46***					0.28***	0.058	0.44	<0.01	3.74
Model 4	1.55***	0.10***	-0.001*				0.056	0.46	<0.01	2.84
Model 5	2.53***	0.01			-25.18**		0.054	0.49	<0.01	0.71
8. CLASS II										
Model 1	3.30***			-7.97***			0.042	0.68	<0.01	-3.57
Model 2	2.951***				-38.8***		0.049	0.62	<0.01	-0.12
Model 3	1.37***					0.33***	0.047	0.64	<0.01	-0.99
Model 4	1.51***	0.11***	-0.001*				0.042	0.68	<0.01	-2.63
Model 5	2.55***	0.01		-24.7*			0.042	0.67	<0.01	-2.40
9. CLASS OTHERS										
Model 1	3.01***			-6.79***			0.043	0.59	<0.01	-5.18
Model 2	2.70***				-32.60***		0.044	0.58	<0.01	-4.35
Model 3	1.61***					0.18**	0.074	0.30	<0.01	10.72
Model 4	1.26***	0.12***	-0.001***				0.029	0.72	<0.01	-15.57
Model 5	2.78***	-0.031			-35.08***		0.045	0.57	<0.01	-2.699

NB: ***, **, * indicates the model had all parameters significant at 100, 99 and 95% respectively. All models had P-value of <0.001. Coefficients without associated indications were not significant. Best and Selected Model in bold font

4.1.2 Height-Diameter relationship with Diversity

Table 8: fitted Models for H-DBH relationship with Evenness Index

Model	(Intercept)	dex	evenness	dex2	dsqr	d	d2	R.adj	MSE	AICc
M1	4.10***	-8.86***	-0.77					0.69	0.05	-69.35
M5	3.59***		-0.86	-36.70***		0.01***		0.67	0.05	-43.22
M4	1.57**		0.03			0.09***	0.00***	0.67	0.05	-42.91
M2	4.54***		-1.58**	-48.20***				0.65	0.06	-0.81
M3	1.34*		0.18		0.29***			0.60	0.07	80.84

NB: Models are arranged by order of AIC ranking, NB: ***, **, * indicates the model had all parameters significant at 100, 99 and 95% respectively. All models had P-value of <0.001. Coefficients without associated indications were not significant.. Best and Selected Model in bold font

Table 9: fitted Models for H-DBH relationship with Abundance Index

Model	(Intercept)	abundance	dex	dex2	dsqr	d	d2	R.adj	MSE	AICc
M1	3.38***	-0.01	-8.89***					0.69	0.05	-67.79
M4	1.65***	-0.01				0.09***	0.001***	0.68	0.05	-44.89
M5	2.77***	-0.01		-35.61***		0.01***		0.67	0.05	-42.21
M2	3.03***	0.00		-48.47***				0.64	0.06	7.87
M3	1.59***	-0.04***			0.29***			0.61	0.07	67.77

NB: Models are arranged by order of AIC ranking, NB: ***, **, * indicates the model had all parameters significant at 100, 99 and 95% respectively. All models had P-value of <0.001. Best and Selected Model in bold font Coefficients without associated indications were not significant.

Table 10: Fitted Models for H-DBH relationship with Mingling Index

Model	(Intercept)	dex	mingling	dex2	dsqr	d	d2	R.adj	MSE	AICc
M1	3.40***	-8.86***	-0.07*					0.69	0.05	-72.01
M4	1.69***		-0.01***			0.09***	0.001***	0.68	0.05	-55.23
M5	2.77***		-0.08*	-34.90***		0.01***		0.68	0.05	-46.60
M2	3.05***		-0.02	-48.29***				0.64	0.06	7.37
M3	1.61***		-0.16***		0.29***			0.61	0.06	56.12

NB: Models are arranged by order of AIC ranking, NB: ***, **, * indicates the model had all parameters significant at 100, 99 and 95% respectively. All models had P-value of <0.001. Best and Selected Model in bold font. Coefficients without associated indications were not significant.

Table 11: Fitted Models for H-DBH relationship with Shannon Index

Model	(Intercept)	dex	shannon	dex2	dsqr	d	d2	R.adj	MSE	AICc
M1	3.14***	-8.95***	0.06*					0.69	0.05	-70.93
M4	1.31***		0.08*			0.09***	0.00***	0.68	0.05	-49.08
M5	2.45***		0.08*	-35.45***		0.01***		0.68	0.05	-45.99
M2	2.98***		0.01	-48.47***				0.64	0.06	7.79
M3	0.96***		0.15***		0.30***			0.61	0.06	64.44

NB: Models are arranged by order of AIC ranking, NB: ***, **, * indicates the model had all parameters significant at 100, 99 and 95% respectively. All models had P-value of <0.001. Best and Selected Model in bold font. Coefficients without associated indications were not significant.

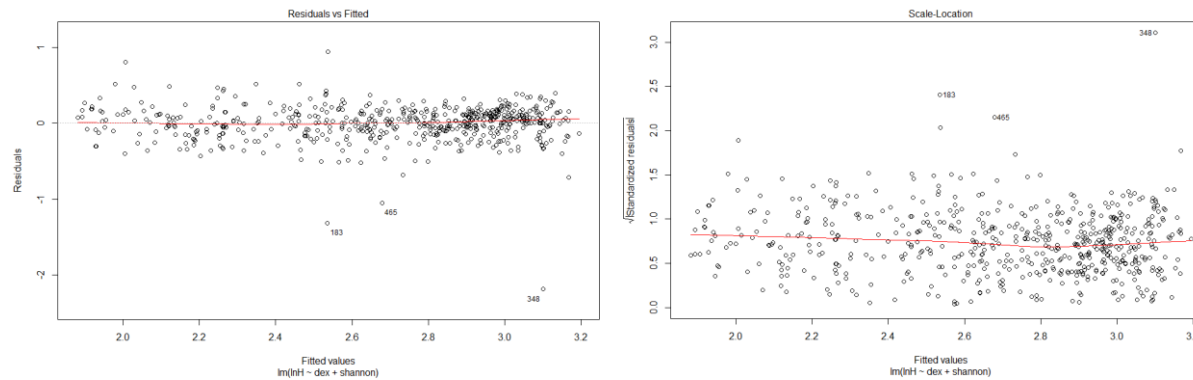


Figure 14: Plot of H-DBH-Shannon index Residual vs Fitted for Best and Selected Model (Model 1)

Table 12: Fitted Models for Height-DBH with simpson Index relationship

Model	(Intercept)	Dex	simp	dex:simp	dex2	dex2:simp	dsqr	dsqr:simp	d	d2	d:simp	d2:simp	R.adj	MSE	AICc
Model1	5.17***	-46.86***	-1.88	39.33**									0.69	0.05	-73.87
Model4	-4.41		6.22*						0.42	-0.01	-0.34	0.00	0.68	0.05	-52.33
Model5	2.23		0.53		-182.55	151.56			0.04		-0.03		0.68	0.05	-43.23
Model2	4.74***		-1.76*		-303.82***	264.65**							0.65	0.06	1.18
Model3	-2.90		4.55				0.81	-0.53					0.60	0.07	72.32

NB: Models are arranged by order of AIC ranking, NB: ***, **, * indicates the model had all parameters significant at 100, 99 and 95% respectively. All models had P-value of <0.001. Best and Selected Model in bold font. Coefficients without associated indications were not significant.

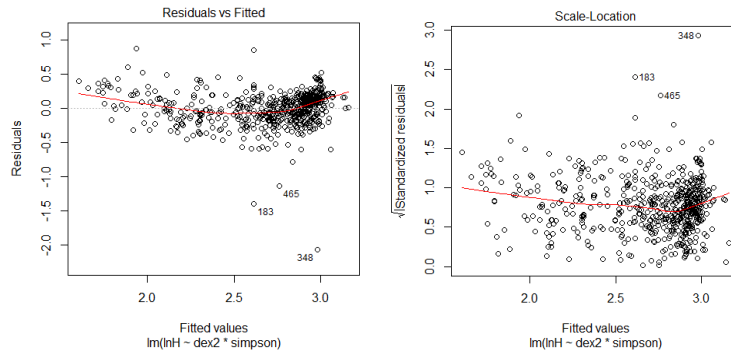


Figure 15: Plot of H-DBH-Shannon index Residual vs Fitted for Best and Selected Model (Model 2)

4.2 Largest Crown Width (LCW), Crown Ratio (CR) and Diameter at Breast Height (DBH) Relationship

Crown dimensions are key variables in modelling growth. Five (5) models fitted as shown in table 4 to analyze the effect of largest crown width/crown diameter, crown ratio and dbh to ascertain if there would a relationship. The results from this test as shown in table 13 below indicated that, there were significant interactions between these parameters. In all, model 3 performed best and thus, was selected among the other five candidate models since it fulfilled the conditions as elaborated in model selection criteria in methodology. Crown ratio which is the difference total height and crown base height divided by total height was found to have all parameter coefficient significant in the entire models.

The best-fitted model (model 3) had an adjusted R-squared value of 0.55 and Mean Squared Error value of 2.5. it can be inferred that, the all the model performed adequately well taking into account that, the associated adjusted R-squared values were around the same figure and also, the AIC of model 3 and 4 were had value difference of only two (2) points as shown in table 13. Moreover, the results revealed that, crown ratio had much influence in the models in comparison with DBH even though, this may not always be the case.

Further, examining the effect of diversity on the LCW, CR and DBH showed a positive relationship on each other. Generally, the results revealed that, abundance index had the most influence on the LCW, CR and DBH. The parameter coefficients of crown ratio and abundance index were significant at 100% and associated p-value of <0.01 as shown in table 15. Nonetheless, similar trend of parameter coefficient's significance for other diversity indices such as Simpson and Shannon, Evenness and mingling were significant, but not were mostly associated with the best-fit models. The overall performances of models were sufficient but not absolute as models MSE were higher as compared to those of h-d and diversity models. Also, the adjusted R-squared values for all the candidate models ranged between 0.49 to 0.57.

According to the model selection criteria, effects of diversity on crown size and DBH were best explained relative models, model 3 was selected to adequately reveals the abundance and mingling diversity effect as shown in table 15 and 17 respectively. Model

1 consequently, was the best-fit model for Shannon and Simpson indices as shown in table 14 and 16 respectively. Whiles model 4 explained evenness index as shown in 18.

Table 13: Fitted Models for Largest Crown Width, Crown Ratio, and DBH

Model	(Intercept)	CR	dex	dex2	dsqr	D	d2	R.adj	MSE	AICc
Model3	-0.61*	0.10***			1.16***			0.55	2.50	2197.771
Model4	1.22***	0.10***				0.19***	-0.001*	0.57	2.50	2199.265
Model5	2.18***	0.11***		-27.23		0.11***		0.55	2.51	2201.446
Model1	5.46***	0.14***	-25.72***					0.51	2.72	2248.418
Model2	3.34***	0.19***		-92.25***				0.49	2.88	2280.907

NB: ***, **, * indicates the model had all parameters significant at 100, 99 and 95% respectively. All models had P-value of <0.001. Models are arranged by order of AIC ranking. Best and Selected Model in bold font. Coefficients without associated indications were not significant.

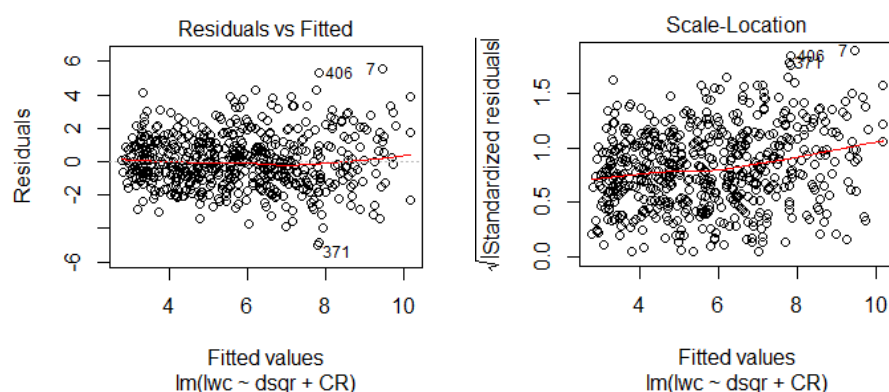


Figure 16: Crwonsize-DBH Plot of Residual vs Fitted for Best and Selected Model (Model 3)

Table 14: Fitted Models for Largest Crown Width, Crown Ratio, DBH and Shannon Index

Model	(Intercept)	CR	dex	shannon	dex2	dsqr	d	d2	R.adj	MSE	AICc
M3	0.02	0.11***		-0.17		1.15***			0.56	2.50	2199.26
M4	1.77*	0.10***		-0.16			0.20***	-0.002*	0.56	2.51	2200.85
M5	2.74**	0.11***		-0.15	-28.51		0.11***		0.56	2.52	2203.08
M1	7.38***	0.14***	-25.39***	-0.55*					0.52	2.71	2244.94
M2	5.72***	0.19***		-0.66**	-92.91***				0.50	2.85	2275.45

NB: ***, **, * indicates the model had all parameters significant at 100, 99 and 95% respectively. All models had P-value of <0.001. Coefficients without associated indications were not significant. Models are arranged by order of AIC ranking. Best and Selected Model in bold font

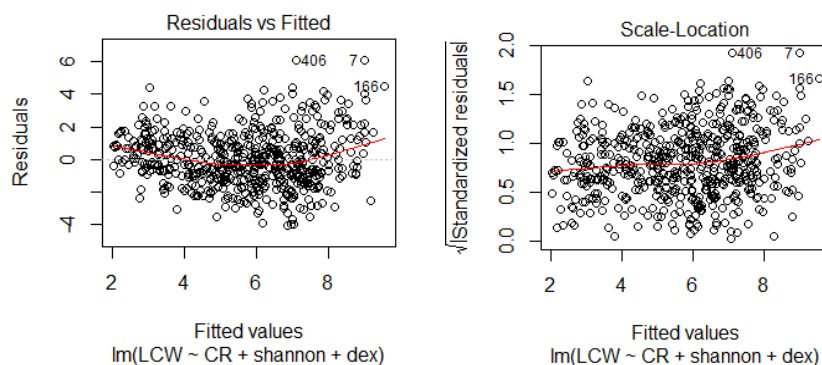


Figure 17: Plot of Crown Size-Shannon index Residual vs Fitted for Best and Selected Model (Model 1)

Table 15: Fitted Models for Largest Crown Width, Crown Ratio, DBH and Abundance Index

Model	(Intercept)	abundance	CR	dex	dex2	Dsqr	d	d2	R.adj	MSE	AICc
M3	-1.14***	0.24***	0.11***			1.13***			0.57	2.44	2185.27
M4	0.47	0.24***	0.10***				0.22***	-0.002**	0.57	2.45	2186.68
M5	1.82***	0.24***	0.11***		-39.22*		0.10***		0.57	2.46	2189.56
M1	4.77***	0.34***	0.14***	-26.69***					0.54	2.61	2223.09
M2	2.66***	0.35***	0.19***		-101.75***				0.51	2.75	2255.11

NB: ***, **, * indicates the model had all parameters significant at 100%, 99 and 95% respectively. All models had P-value of <0.001. Coefficients without associated indications were not significant. Models are arranged by order of AIC ranking. Best and Selected Model in bold font

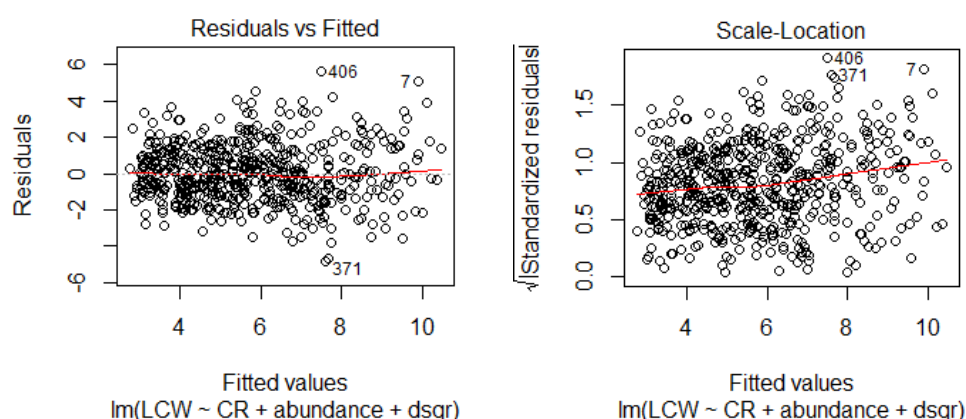


Figure 18: Plot of Crown Size-abundance index Residual vs Fitted for Best and Selected Model (Model 3)

Table 16: Fitted Models for Largest Crown Width, Crown Ratio, DBH and Simpson Index

Model	(Intercept)	CR	dex	simpson	dex2	dsqr	D	d2	R.adj	MSE	AICc
M3	2.36	0.10***		-3.04		1.16***			0.56	2.50	2199.30
M4	3.88	0.10***		-2.75			0.20***	-0.002*	0.56	2.51	2200.90
M5	4.84	0.11***		-2.71	-28.49		0.11***		0.56	2.52	2203.10
M1	14.49***	0.14***	-25.60***	-9.33*					0.52	2.71	2245.98
M2	13.97**	0.19***		-10.93*	-93.57***				0.49	2.86	2277.14

NB: ***, **, * indicates the model had all parameters significant at 100%, 99 and 95% respectively. Coefficients without associated indications were not significant. All models had P-value of <0.001. Models are arranged by order of AIC ranking. Best and Selected Model in bold font

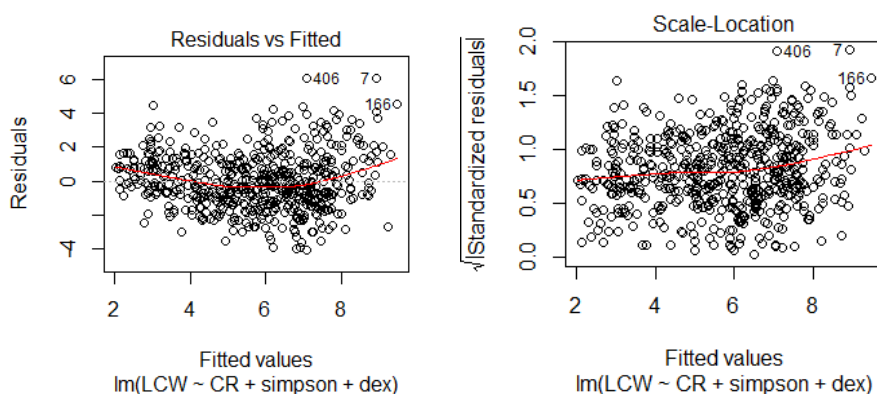


Figure 19: Plot of Crown Size-simpson index Residual vs Fitted for Best and Selected Model (Model 1)

Table 17: Fitted Models for Largest Crown Width, Crown Ratio, DBH and Mingling Index

Model	(Intercept)	CR	dex	mingling	dex2	dsqr	d	d2	R.adj	MSE	AICc
M3	-0.86**	0.11***		0.41*		1.14***			0.56	2.49	2195.79
M4	0.90**	0.11***		0.39			0.20***	-0.002*	0.56	2.49	2197.72
M5	2.01***	0.12***		0.42*	-33.69*		0.11***		0.56	2.50	2199.53
M1	4.99***	0.14***	-26.13***	0.75***					0.53	2.67	2237.65
M2	2.89***	0.19***		0.83***	-98.71***				0.50	2.82	2268.43

NB: ***, **, * indicates the model had all parameters significant at 100%, 99 and 95% respectively. Coefficients without associated indications were not significant. All models had P-value of <0.001. Models are arranged by order of AIC ranking. Best and Selected Model in bold font

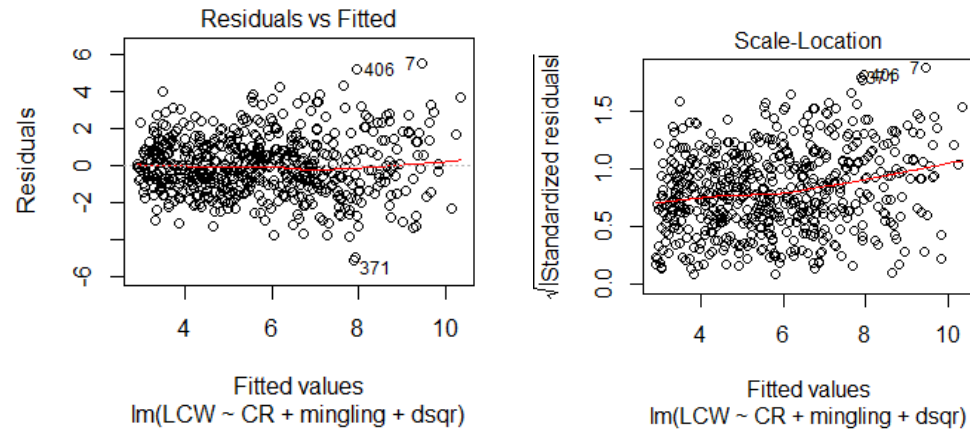


Figure 20: Plot of Crown Size-Mingling index Residual vs Fitted for Best and Selected Model (Model 3)

Table 18: Fitted Models for Largest Crown Width, Crown Ratio, DBH and Evenness Index

Model	(Intercept)	CR	dex	even	CR:even	dex:even	dex2	dex2:even	Dsqr	dsqr:even	d	d2	d:even	d2:even	R.adj	MSE	AICc
M4	32.68*	2.77**		-32.91*	-2.80**						-7.16***	0.14***	7.72***	-0.14***	0.57	2.43	2186.66
M5	-57.84**	1.37		62.88**	-1.32		2743.23**	-2902.38**			1.18*		-1.12		0.56	2.48	2198.77
M3	-11.08	0.81		10.97	-0.74				0.51	0.69					0.56	2.51	2202.39
M1	-62.92*	2.85**	363.61**	71.75**	-2.84**	-408.14*									0.52	2.70	2246.21
M2	-49.11*	2.73**		55.06**	-2.66**		2210.34*	-2414.43**							0.50	2.85	2277.72

NB: Even implies evenness index. : ***, **, * indicates the model had all parameters significant at 100%, 99 and 95% respectively. Coefficients without associated indications were not significant. All models had P-value of <0.001. Models are arranged by order of AIC ranking. Best and Selected Model in bold font

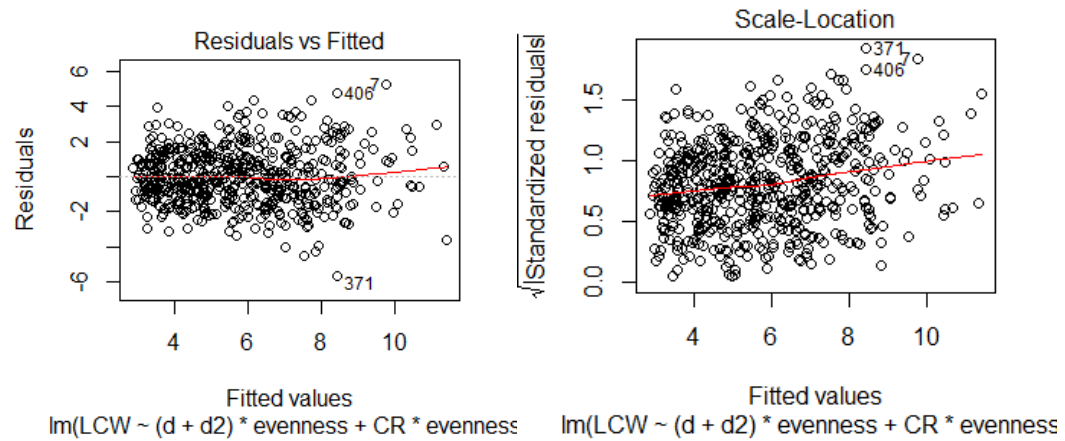


Figure 21: Plot of Crown Size-Evenness index Residual vs Fitted for Best and Selected Model (Model 4)

4.3 Basal Area Increment (BAI)

The analysis revealed that; the basal area increment was best explained by model 4 (as shown in table 19 below) where Basal Area Increments was associated with size (DBH). The best-fit model had all parameters coefficient significant and p-value of <0.01. The Mean Squared Error (MSE) were within 0.41-0.53 which is an indication of model fitness, the adjusted R-squared values were relatively low; ranging between 0.41 to 0.53. crown ratio constant had none of its parameter coefficient significant.

Table 19: Basal Area Increment (BAI) relationship with diameter growth (DBH) Models

Model	(Intercept)	ln (DBH_5)	DBH ² _5	ln (CR+0.2/1.2)	R.adj	RSE	AICc
M1	-8.99***	1.22***			0.42	0.49	42.07
M2	-9.04***	1.19***		-0.144	0.49	0.41	43.66
M3	-6.21***	0.27	0.005*		0.43	0.54	36.67
M4	--6.744***		0.004***		0.42	0.56	34.91
M5	-6.25***	-0.294	0.005*	-0.138	0.53	0.44	38.17
M6	-9.03***	1.188***		0.114	0.41	0.49	43.66

NB: ***, **, * indicates the model had all parameters significant at 100%, 99 and 95% respectively. Coefficients without associated indications were not significant. All models had P-value of <0.001, DBH_5 is dbh 5-years ago, CR=crown ratio. Best and Selected Model in bold font

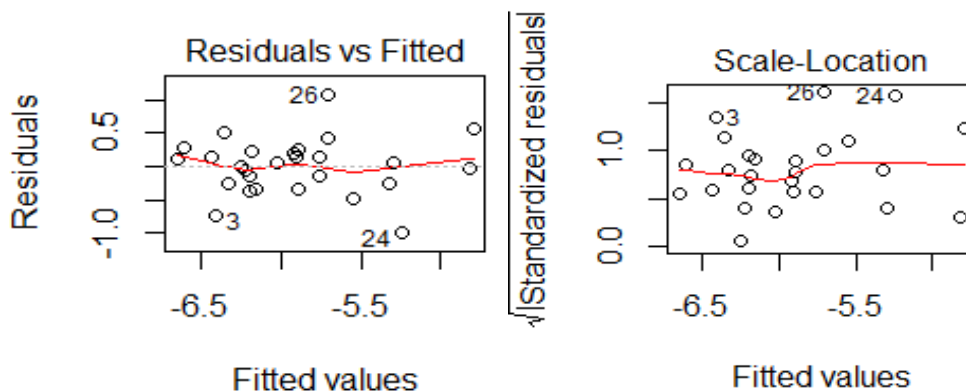


Figure 22: Plot of Basal Area Increment-Size (DBH) Residual vs Fitted for Best and Selected Model (Model 4)

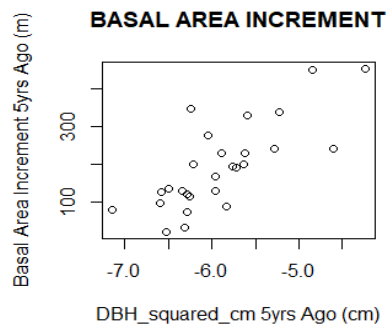


Figure 23: Relationship Between BAI and Size 5-years Ago

5. DISCUSSION

Static and dynamic models have been fitted for tree species in a forest plantation in Northern Vietnam. Static study was based on the development of height-diameter relationships and largest crown width equations for 6 individual species and 3 species groups. Dynamic study was focused on *Cinnamomum iners* due to its abundance in the study area and its interest as fast growing species useful for ecosystem restoration and its potential production of non-wood products (essential oil and incense), Agroforestry and timber (Gowda et al., 1980; TPD, 2019).

Largest crown width (LCW) was modelled as a function of crown ratio (CR) and diameter at breast height (DBH). Our results supported the findings by Moeur (1981) that established that LCW depends on DBH and crown ratio (CR). Our model is not spatially explicit, but the results are sound (as the lower AIC values support). Spatially explicit models have been proposed by Sharma et al., (2016) but the improvement over the non-spatially explicit models is not clear when using only tree measurements. Crown ratio was highly significant in all the analyzed models but the effect of DBH cannot be discounted. Hann (1997) working on the mixed forest of the United States mixed forests confirms the relationship between largest crown width and crown ratio which are widely used for prediction and imputation of missing data in forest growth models (Hann 1999). The importance of CR in the LCW prediction is also supported by Russell and Weiskittel (2011) who found that the inclusion of CR in LCW (besides DBH) improve the predictions. However, Russell and Weiskittel (2011) warned that the close correlation between DBH and CR for its species of interest (hardwood and conifers in the mixed forests of North East United States) can explain this fact while in other cases the inconsistency in the measurement protocols can bias their results.

Growth and productivity of forest largely depends on crown size (Pretzsch et al., 2015) that is a proxy of tree vigor. Forest ecosystem services provision depend upon the tree vigor due to its high impact on tree dynamic. Diversity impacts on tree size as we confirm by adding different diversity measures in the LCW models. This implies that, estimating the relationship or effects of diversity of crown sizes in tropical forest are paramount for sustainable management. Our results proved that, functional role in the species composition regarding Shannon index which takes into account both evenness and abundance (Del Rio et al., 2018) had all parameter coefficient significant indicating the positive effect on crown size. Osorio et al., (2009) found out that, there were no significant relationship between plant diversity in maritime pine (*Pinus pinaster* Ait.). However, the obvious reason could be that, the forest structures are different; thus, our significance gave rise from a tropical forest structure as opposed to temperate structure where the results were contrary.

Height-diameter equations are key tools for forest assessment as regularly dbh measurements are done in every tally tree but not total height. For imputation of missing total height values, we need adequate and accurate height-diameter equations. Our results showed a strong relationship between height and DBH. According to Bravo et al., (2011), h-dbh function are used to estimate/predict future height of trees. Since all our five (5) models indicated a conclusive parameter (DBH) coefficient significance (as shown in table 7a, 7b and Annex 1: h—d Plot of residual vs fitted values) with p-value of <0.01, and residuals suggests adequate goodness of fit (Sánchez-González et al., 2007), we could adopt the models for use in tropical tree species in the study area in Northern Vietnam.

As far as we know, the size models presented here is the most complete catalogue of equations to predict height and largest crown width for South Asian Tropical Forest species (6 species individually and other species grouped by wood density, an important functional trait used for species grouping in forest research in Vietnam). Additionally, the insight of the importance of diversity indices on tree size also show that size is related with diversity in an inconsistent way. A positive relationship between size and diversity was

found when Abundance or Mingling Indices were used as diversity indices while the reverse (negative relationship) was detected when Evenness, Shannon or Simpson Indices were used. The best model (as the parameter significance and AIC value indicates) to predict LCW included abundance (table 15) but the value is very close to the AIC for the model that included Evenness (table 18) so our results are not conclusive for LCW. On the other hand, for the height diameter equations all diversity indices but Shannon Index hold a negative parameter in the tested models.

Tree size equations jointly with growth equations are very important for forest dynamic forecast. Between tree growth dimensions height and diameter growth are the key variable to be properly predicted. Height growth models development is out of the scope of this work because suitable data (repeated measures) are lacking. Tropical tree rings are difficult to measure due to the lack of seasonality in the climate, however it is not impossible (Nath et al, 2016, Worbes et al, 2017). In this study, 5 growth seasons, defined by 2 two consecutive mark indicating ring growth start-end, were used to define the basal area increment. For tree diameter growth studies, the use of diameter growth models or basal area increment (BAI) models is normally a personal election but BAI models are often easily linearized and correlation between predictors and the dependent variable are normally higher (see Alder, 1995 for details) Basal area increment models normally are based exponential equations with DBH (with different exponents and transformation) and CR (normally log transformed after sum a small value and divided by a factor over 1 to avoid zero values) as predictors. In this study, only data for *Cinnamomum iners* were available for the last five growth periods by analyzing tree cores. CR was no significant in any of the five models tested while DBH (log transformed or squared) was positively related with BAI. Model including squared DBH shows the lowest AIC thus was selected. However, due to its exponential growth behavior the model should be corroborated with a wider dataset.

6. CONCLUSION

The finding of the study established that, the dynamics of the Vietnamese secondary tropical forest growth was dependent on tree size and site conditions. In the linear regression analysis where indices of structural diversity such as Simpson, Shannon, Evenness, Abundance and Mingling were tested in relation with their effect on forest growth (Height-Diameter at Breast Height), a positive correlation was found. This is not surprising because tropical forest biome is believed to be well-diversified (Couvreur et al., 2011) our data (sourced from marteloscope) analysis confirmed. Likewise, structural diversity in the marteloscope revealed the existence and influence on crown size and tree size (diameter). Basal Area Increment (BAI) obtained from ring growth from last five (5) growing period of *Cinnamomum iners* indicated that Diameter at Breast Height (DBH) not influenced BAI whiles Crown Ratio did not show any significant effect in all the models. Ultimately, proposed fitted models and selected based on parameter significance and Akaike Information Criterion (AIC) could be adopted for local forest growth modeling in South-east Asian regions.

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“To God (Allah) belongs all sovereignty this day, The One, The Prevailing”.

“Limanil mulkul yawm, Lillaahil waahidul qahhar” Q. 40:16

“Praise be to Allah, the Lord of the worlds! (Alhamdulillah lillahi rabil alameen!)” Q. 1:2

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Weber, P., Bugmann, H., Fonti, P., & Rigling, A. (2008). Using a retrospective dynamic competition index to reconstruct forest succession. *Forest Ecology and Management*, 254(1), 96-106.

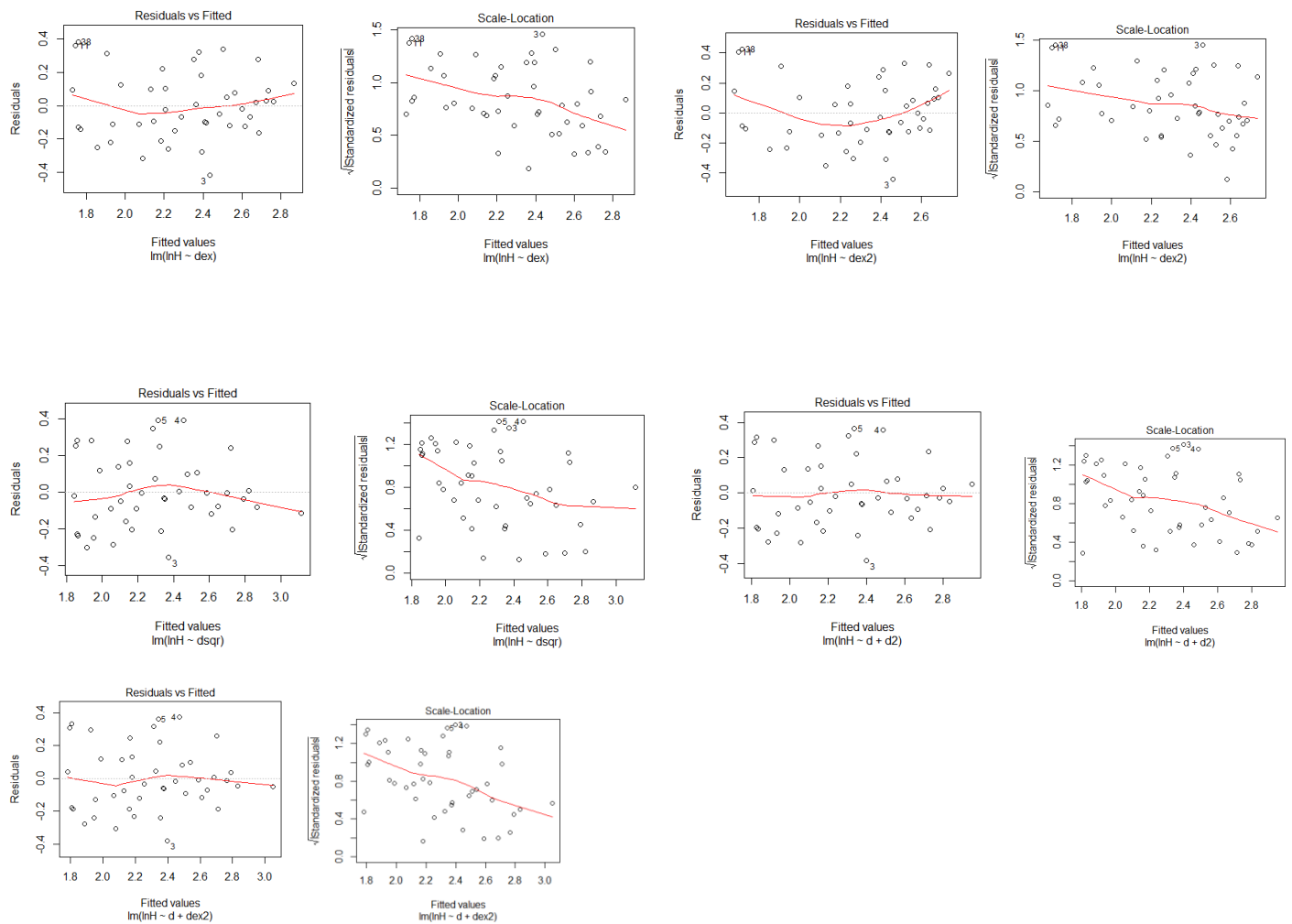
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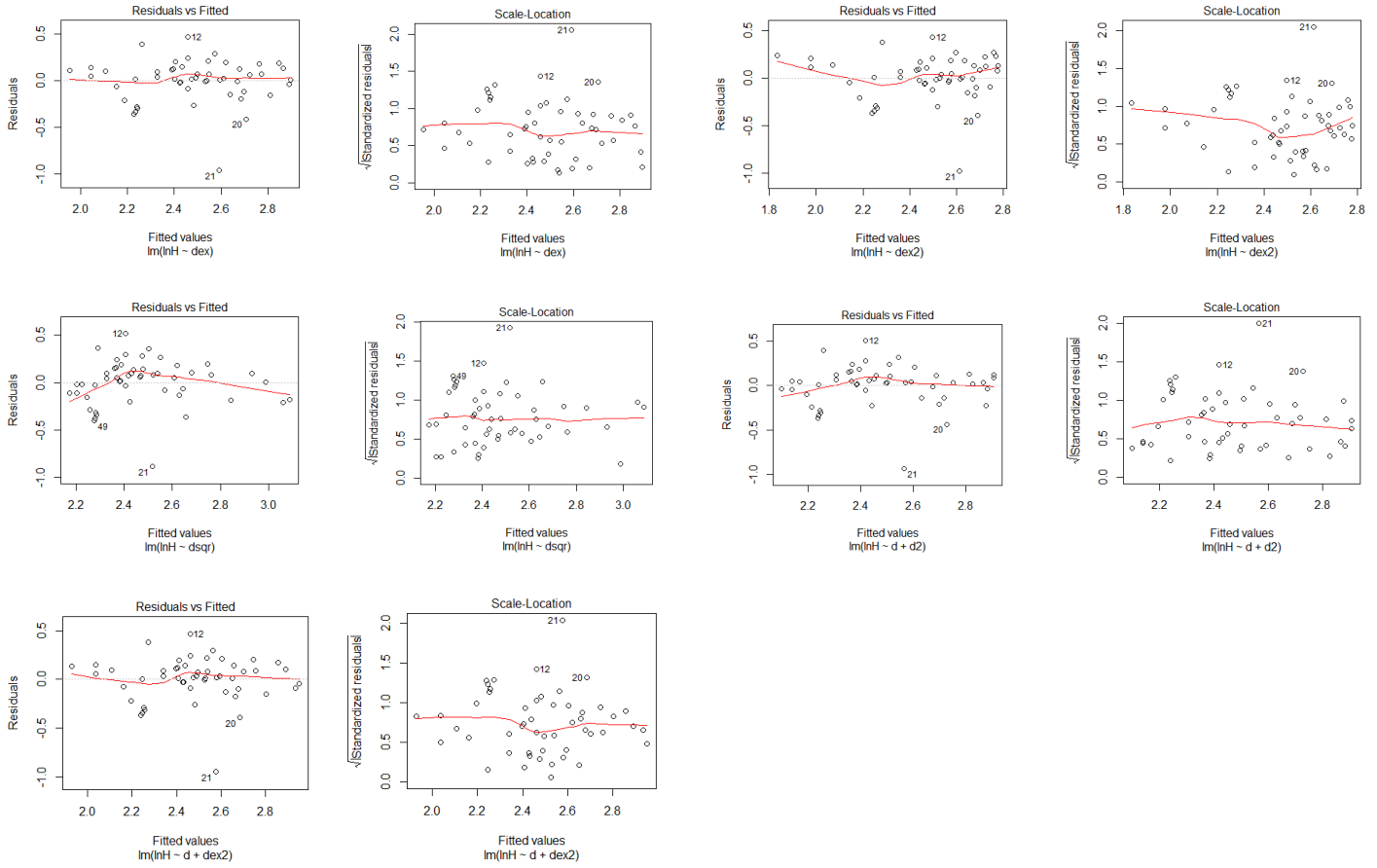
ANNEXES

Annex 1: Height-DBH Plot of Residual vs Fitted Models: Individual Species and Grouping

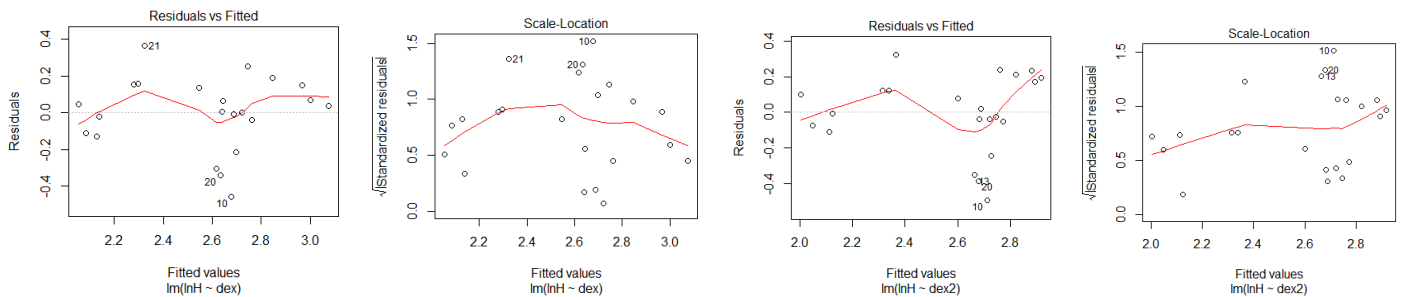
Chukrasia tabularis

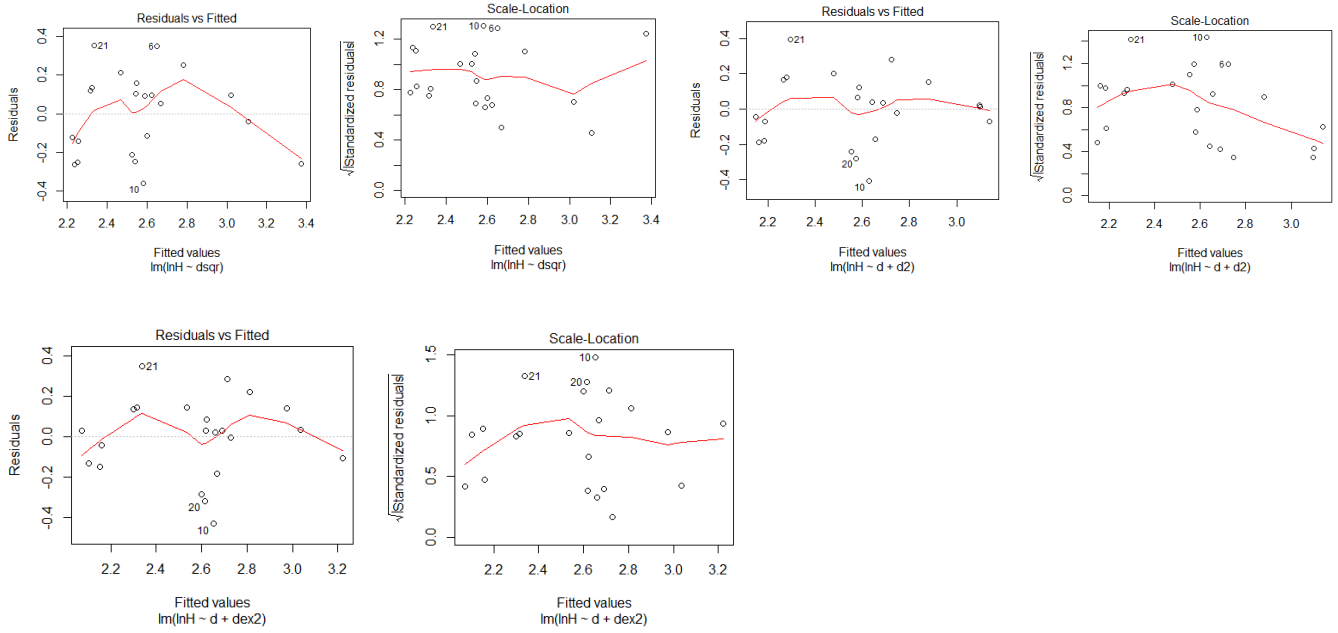


Class I

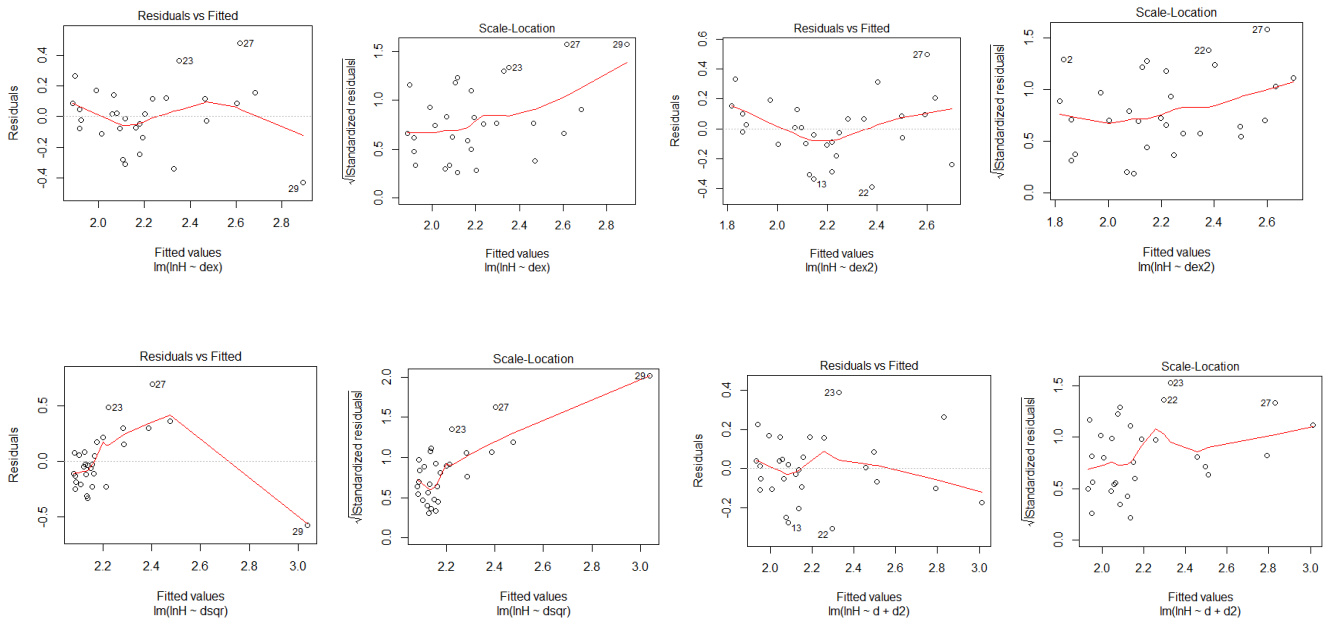


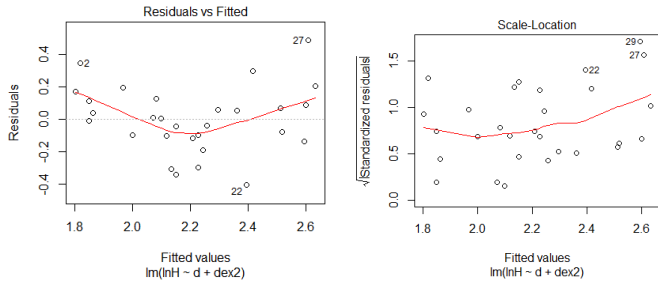
For class II



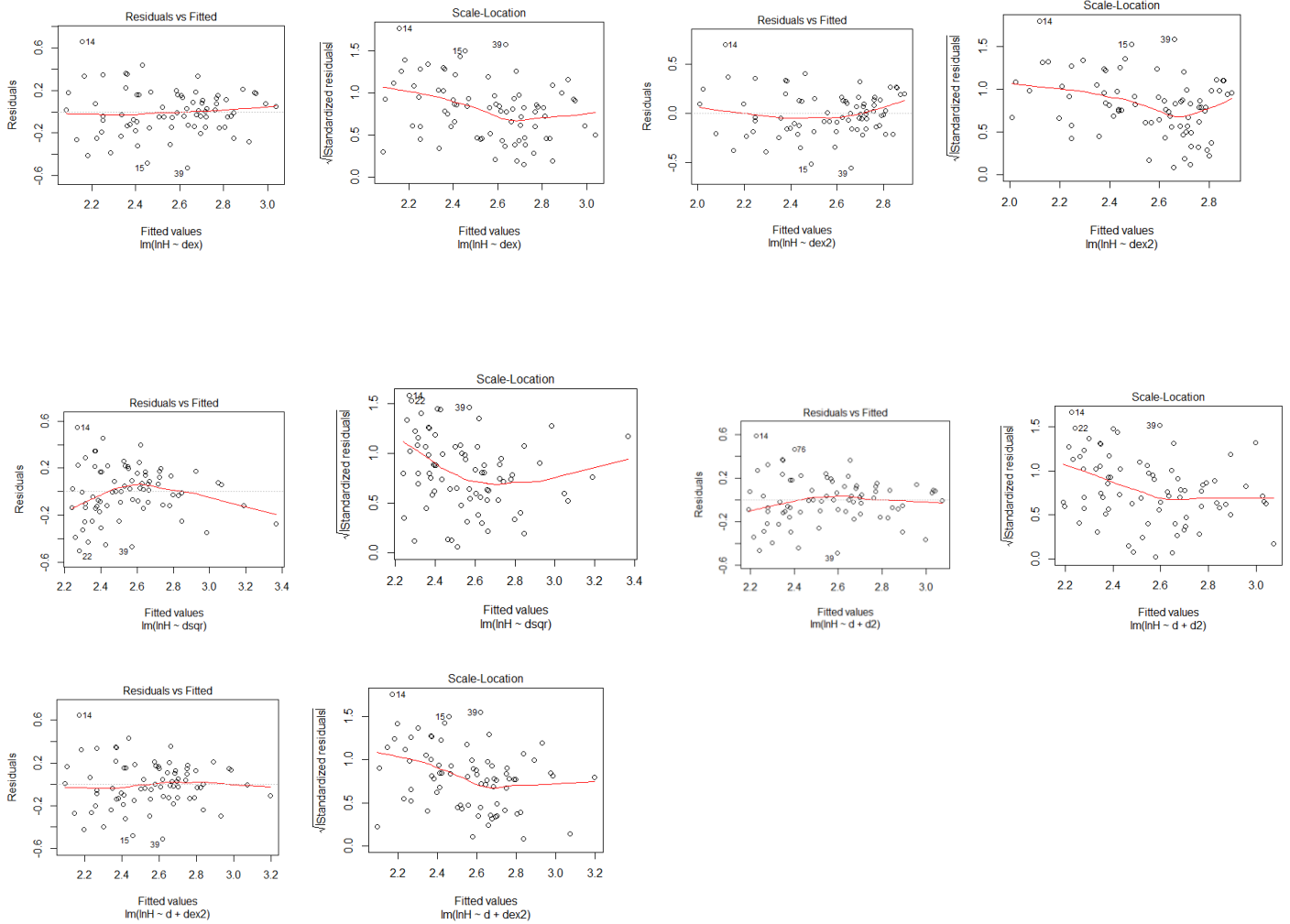


Class others

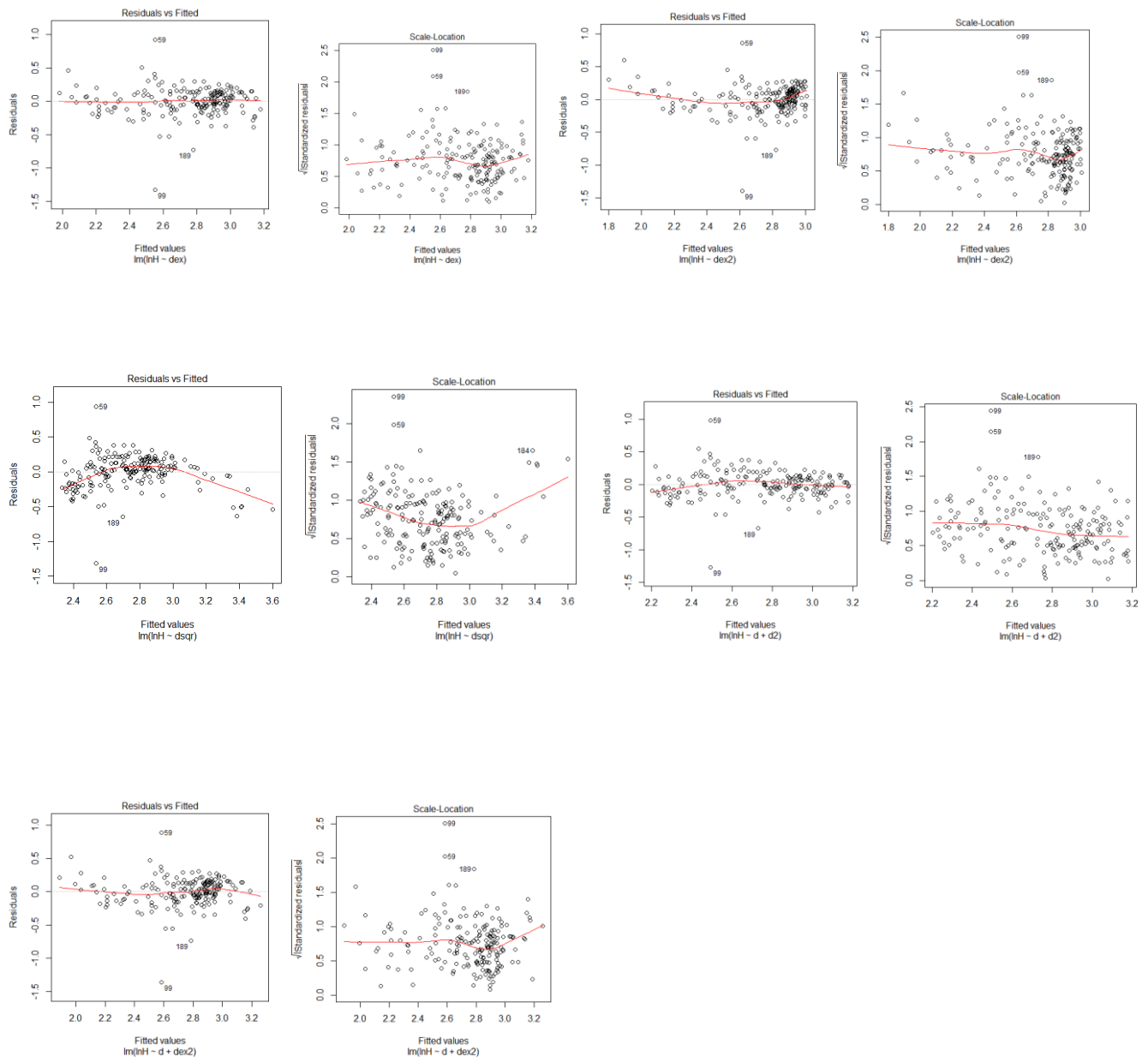




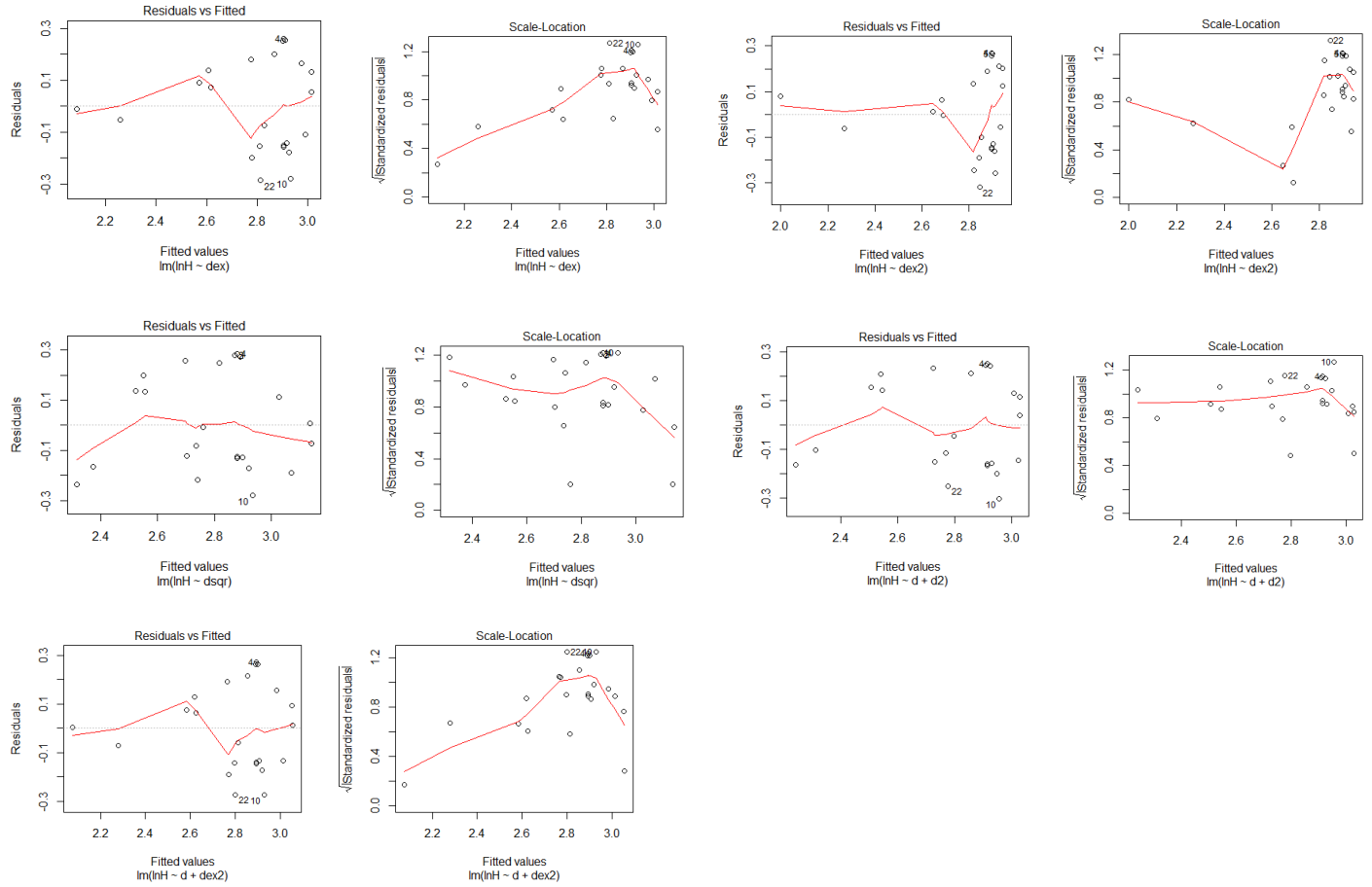
Peltophorum pterrocarpum



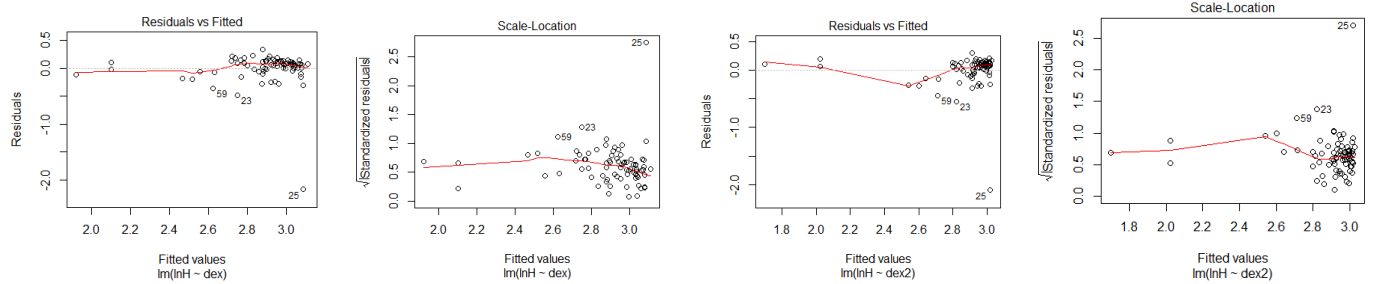
Cinnamomum iners

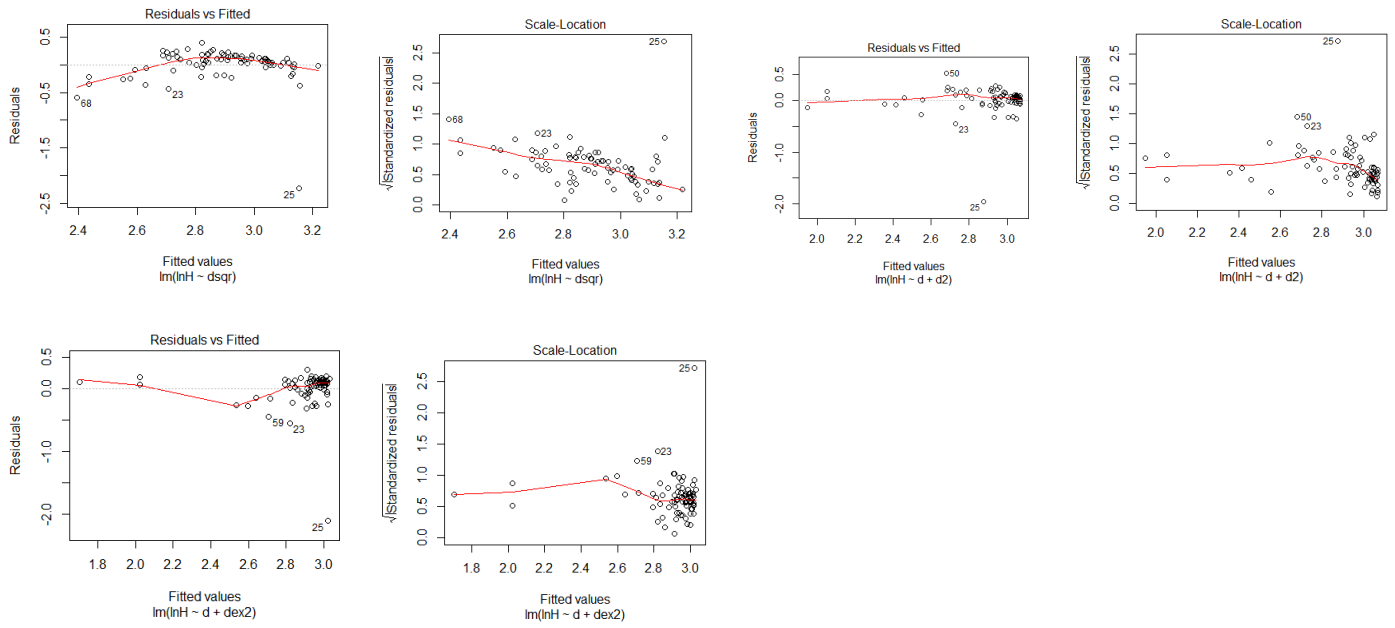


Dracontomelon duperreanum

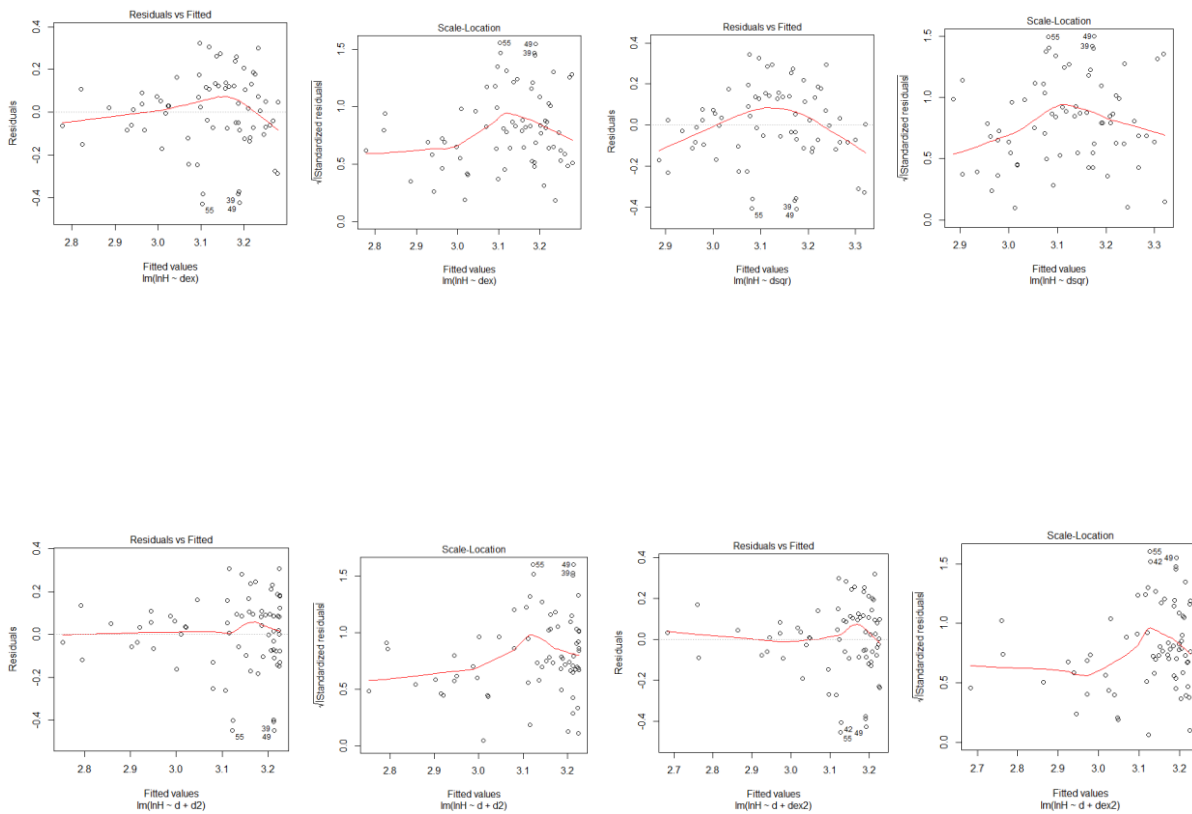


Manglietia confiera

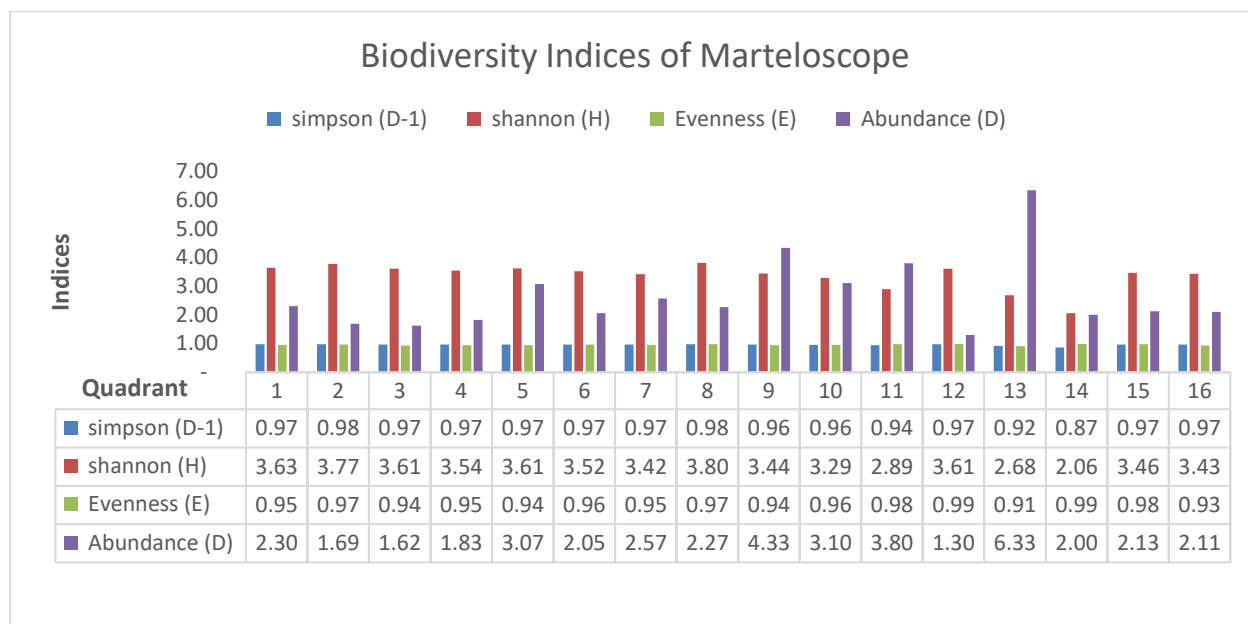




For: *Acacia auriculiformis*

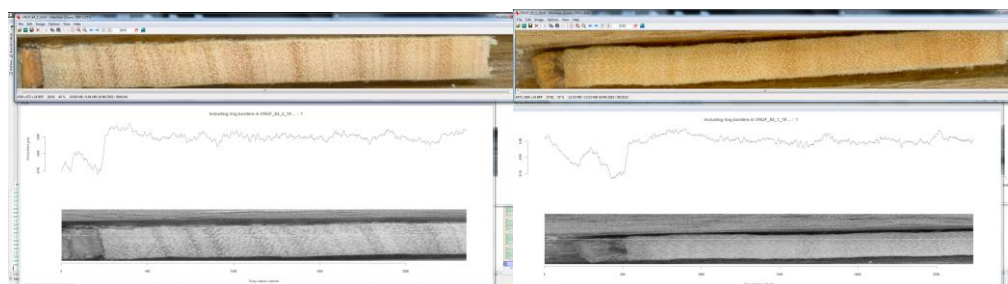


Annex 2: STRUCTURAL DIVERSITY INDICES PER QUADRANT



Overview of Biodiversity Indices in the Marteloscope

Annex 3: Ring Detection using measuRing R-package



Ring detection of *Cinnamomum iners*

Annex 4: Sample of R-Script Developed for Data Analysis

####---- Author: Yusif Habib

----- Thesis Title: Model Selection and Fitting for Basal Area Increment in a Vietnamese Tropical Forest

-----Institution: University of Valladolid, Campus Palencia.

##-----MSc. Mediteranean Forestry and Natural Resources (MEDFOR), 2017-2019

Crownsizes ~ STRUCTURAL INDICES AND DBH MODEL FITTING AND SELECTION

1. For Entire species in Marteloscope

2. For Crwonsizes and structural diversity indices

Abundance Index

Shannon Index

Simpson Index

Mingling Index

Evenness Index

setting up working directory

setwd("C:/MScThesis_MEDFOR_UVa/Data/Processed")

#calling data file for directory

data<-read.csv("Marteloscope_data_VNUF.csv", header = TRUE)

#installed packages required for analysis

installed.packages("dplyr")

installed.packages("ggplot2")

installed.packages("MuMIn")

installed.packages("AICcmodavg")

installed.packages("coefplot")

#call [ackages into working environment

library(dplyr)

library(ggplot2)

library(AICcmodavg)

library(MuMIn)

library(coefplot)

library(AICcmodavg)

#Having a look at what data we have in the dataframe

str(data)

summary(data) # summary statistics

#extreacting standard deviation paramerters

sd(data\$Total_height_m, which[(Species=="Manglietia conifera")], na.rm=TRUE)

sd(data\$Total_height_m=="Acacia auriculiformis", na.rm=TRUE)

sd(data\$Total_height_m=="Peltophorum pterrocarpum", na.rm=TRUE)

sd(data\$Total_height_m=="Cinnamomum iners", na.rm=TRUE)

#View(data)

Definition of Parameters

d <- data\$DBH_cm #DBH

dsqr <-data\$DBH_cm^(0.5) #DBH exponential ^ 0.5

d2 <-data\$DBH_cm^2 #DBH exponential ^ 2


```

dex <- data$DBH_cm^(-1) #DBH exponential ^ -1
dex2 <- data$DBH_cm^(-2) #DBH exponential ^ -2
H <- data$Total_height_m #total height
lnH <- log(H) #represents the natural log of Total height
Y <- ((log(data$Total_height_m)/(data$Crownbase_height_m))-1) # Nat. log of [(Total
Height/crownbase height) - 1]
y <- (((data$Total_height_m)/(data$Crownbase_height_m))-1)
CL <- ((data$Total_height_m)-(data$Crownbase_height_m)) #Crown length
CR <- ((data$Total_height_m)-(data$Crownbase_height_m))/(data$Total_height_m)
#crown ratio
LCW <- data$Crown_diameter_m #Largest Crown Width or Crown Diameter

```

```

#####.....          LCW and Abundance index Model: all 5 Models
.....#####

```

```

#M1 <- lm(LCW ~ CR*abundance+dex*abundance, data=data) #expressing
#summary(M1)

```

```

M1 <- lm(LCW ~ CR+dex+abundance, data=data) #expressing largest crown width as a
function of Crwon ratio + DBH exponential ^ -1 + abundance index
summary(M1)

```

```

#M2 <- lm(LCW ~ CR*abundance+dex2*abundance, data=data) #expressing
#summary(M2)

```

```

M2 <- lm(LCW ~ CR+dex2+abundance, data=data) #expressing largest crown width as a
function of Crwon ratio + DBH exponential ^ -2 + abundance index
summary(M2)

```

```

#M3 <- lm(LCW ~ CR*abundance+dsqr*abundance, data=data) #expressing
#summary(M3)

```

```

M3 <- lm(LCW ~ CR+abundance+dsqr, data=data) #expressing largest crown width as a
function of Crwon ratio + squared root of DBH + abundance index
summary(M3)
plot(M3)

```

```

#M4 <- lm(LCW ~ (d+d2)*abundance+CR*abundance, data=data) #expressing
#summary(M4)

```

```

M4 <- lm(LCW ~ (d+d2)+abundance+CR, data=data) #expressing largest crown width as
a function of DBH + DBH squared+ crown ratio + abundance index
summary(M4)

```

```

#M5 <- lm(LCW ~ abundance*(d+dex2)+CR*abundance, data=data) #expressing
#summary(M5)

```

```
M5 <- lm(LCW ~ (d+dex2)+CR+abundance, data=data) #expressing largest crown width
as a function of DBH exponential ^ -2 +DBH+ Crwon ratio + abundance index
summary(M5)
```

```
#Extracting AIC information for model ranking
AIC(M1, M2, M3, M4, M5, k=2)
```

```
AICc(M1, M2, M3, M4, M5)
```

```
R.adj <- function(x) summary(x)$adj.r.squared # define R^2
MSE <- function(x) (summary(x)$sigma)^2
#Std.Dev<-function(x) (summary(x)$sd)
Ldbh_abun <- model.sel( M1, M2, M3, M4, M5, extra = c("R.adj", "MSE"))
#Ldbh_even <- model.sel( Model1, Model2, Model3, Model4, Model5, extra = c("R.adj",
"MSE"))
Ldbh_abun$model<-rownames(Ldbh_abun)
# replace Model name with formulas little tricky so be careful
for(i in 1:nrow(Ldbh_abun)) Ldbh_abun$model[i]<-
as.character(formula(paste(Ldbh_abun$model[i])))[3]
# let's see what is in there
View(Ldbh_abun) #-->> Model4 is the best model with lowest AICc
```

```
#saving uotput file on computer
write.csv(Ldbh_abun,
file=("C:/MScThesis_MEDFOR_UVa/outputs/FINAL/LM_LCW_DBH_AbundanceIndex_e
ntire_Marteloscope_MSc_Yusif_medfor_20190708.csv"))
```

```
#####..... LCW and Mingling index Model: all 5 Models
.....#####
```

```
#M1 <- lm(LCW ~ CR*mingling+dex*mingling, data=data) #expressing
#summary(M1)
```

```
M1 <- lm(LCW ~ CR+mingling+dex, data=data) #expressing
summary(M1)
```

```
#M2 <- lm(LCW ~ CR*mingling+dex2*mingling, data=data) #expressing
#summary(M2)
```

```
M2 <- lm(LCW ~ CR+mingling+dex2, data=data) #expressing
summary(M2)
```

```
#M3 <- lm(LCW ~ CR*mingling+dsqr*mingling, data=data) #expressing
#summary(M3)
```

```
M3 <- lm(LCW ~ CR+mingling+dsqr, data=data) #expressing
summary(M3)
```

plot(M3)

```
#M4 <- lm(LCW ~ (d+d2)*mingling+CR*mingling, data=data) #expressing
#summary(M4)
```

```
M4 <- lm(LCW ~ (d+d2)+CR+mingling, data=data) #expressing
summary(M4)
```

```
#M5 <- lm(LCW ~ mingling*(d+dex2)+CR*mingling, data=data) #expressing
#summary(M5)
```

```
M5 <- lm(LCW ~ mingling+(d+dex2)+CR, data=data) #expressing
summary(M5)
```

```
#Extracting AIC information for model ranking
AIC(M1, M2, M3, M4, M5, k=2)
AICc(M1, M2, M3, M4, M5)
```

```
R.adj <- function(x) summary(x)$adj.r.squared # define R^2
MSE <- function(x) (summary(x)$sigma)^2
```

```
Ldbh_ming <- model.sel( M1, M2, M3, M4, M5, extra = c("R.adj", "MSE"))
Ldbh_ming$model<-rownames(Ldbh_ming)
# replace Model name with formulas little tricky so be careful
for(i in 1:nrow(Ldbh_ming)) Ldbh_ming$model[i]<-
as.character(formula(paste(Ldbh_ming$model[i])))
# let's see what is in there
View(Ldbh_ming) #---> Model4 is the best model with lowest AICc
write.csv(Ldbh_ming,
file=("C:/MScThesis_MEDFOR_UVa/outputs/FINAL/LM_LCW_DBH_minglingIndex_entire_Marteloscope_MSc_Yusif_medfor_20190708.csv"))
```

```
#####..... LCW and Shannon index Model: all 5 Models
.....#####
```

```
#M1 <- lm(LCW ~ CR*shannon+dex*shannon, data=data) #expressing
#summary(M1)
```

```
#M2 <- lm(LCW ~ CR*shannon+dex2*shannon, data=data) #expressing
#summary(M2)

#M3 <- lm(LCW ~ CR*shannon+dsqr*shannon, data=data) #expressing
#summary(M3)

#M4 <- lm(LCW ~ (d+d2)*shannon+CR*shannon, data=data) #expressing
#summary(M4)

#M5 <- lm(LCW ~ shannon*(d+dex2)+CR*shannon, data=data) #expressing
#summary(M5)
```

```
#####-----
```

```
M1 <- lm(LCW ~ CR+shannon+dex, data=data) #expressing
summary(M1)
plot(M1)

M2 <- lm(LCW ~ CR+shannon+dex2, data=data) #expressing
summary(M2)

M3 <- lm(LCW ~ CR+shannon+dsqr, data=data) #expressing
summary(M3)

M4 <- lm(LCW ~ (d+d2)+shannon+CR, data=data) #expressing
summary(M4)

M5 <- lm(LCW ~ shannon+(d+dex2)+CR, data=data) #expressing
summary(M5)
```

```
#####-----
```

```
#Extracting AIC information for model ranking
AIC(M1, M2, M3, M4, M5, k=2)
```

```
AICc(M1, M2, M3, M4, M5)
```

```
R.adj <- function(x) summary(x)$adj.r.squared # define R^2
MSE <- function(x) (summary(x)$sigma)^2
```

```
Ldbh_shan <- model.sel( M1, M2, M3, M4, M5, extra = c("R.adj", "MSE"))
#Ldbh_even <- model.sel( Model1, Model2, Model3, Model4, Model5, extra = c("R.adj",
"MSE"))
Ldbh_shan$model<-rownames(Ldbh_shan)
# replace Model name with formulas little tricky so be careful
for(i in 1:nrow(Ldbh_shan)) Ldbh_shan$model[i]<-
as.character(formula(paste(Ldbh_shan$model[i])))[3]
# let's see what is in there
View(Ldbh_shan) #--->> Model4 is the best model with lowest AICc
```

```
write.csv(Ldbh_shan,
file=("C:/MScThesis_MEDFOR_UVa/outputs/FINAL/LM_LCW_DBH_ShannonIndex_enti
re_Marteloscope_MSc_Yusif_medfor_20190708.csv"))
```

```
#####.....          LCW and simpson index Model: all 5 Models
.....#####
```

```
#M1 <- lm(LCW ~ CR*simpson+dex*simpson, data=data) #expressing
#summary(M1)
```

```
#M2 <- lm(LCW ~ CR*simpson+dex2*simpson, data=data) #expressing
#summary(M2)
```

```
#M3 <- lm(LCW ~ CR*simpson+dsqr*simpson, data=data) #expressing
#summary(M3)
```

```
#M4 <- lm(LCW ~ (d+d2)*simpson+CR*simpson, data=data) #expressing
#summary(M4)
```

```
#M5 <- lm(LCW ~ simpson*(d+dex2)+CR*simpson, data=data) #expressing
#summary(M5)
```

```
##-----
```

```
M1 <- lm(LCW ~ CR+simpson+dex, data=data) #expressing
summary(M1)
plot(M1)
```

```
M2 <- lm(LCW ~ CR+simpson+dex2, data=data) #expressing
summary(M2)
```

```
M3 <- lm(LCW ~ CR+simpson+dsqr, data=data) #expressing
summary(M3)
```

```
M4 <- lm(LCW ~ (d+d2)+simpson+CR, data=data) #expressing
summary(M4)
```

```
M5 <- lm(LCW ~ simpson+(d+dex2)+CR, data=data) #expressing
summary(M5)
```

```
###-----
```

```
#Extracting AIC information for model ranking
AIC(M1, M2, M3, M4, M5, k=2)
```

```
AICc(M1, M2, M3, M4, M5)
```

```
R.adj <- function(x) summary(x)$adj.r.squared # define R^2
MSE <- function(x) (summary(x)$sigma)^2
```

```
Ldbh_simp <- model.sel( M1, M2, M3, M4, M5, extra = c("R.adj", "MSE"))
#Ldbh_even <- model.sel( Model1, Model2, Model3, Model4, Model5, extra = c("R.adj",
"MSE"))
Ldbh_simp$model<-rownames(Ldbh_simp)
# replace Model name with formulas little tricky so be careful
for(i          in          1:nrow(Ldbh_simp))          Ldbh_simp$model[i]<-
as.character(formula(paste(Ldbh_simp$model[i]))) [3]
# let's see what is in there
View(Ldbh_simp) #--->> Model4 is the best model with lowest AICc
write.csv(Ldbh_simp,
file=("C:/MScThesis_MEDFOR_UVa/outputs/FINAL/LM_LCW_DBH_SimpsonIndex_entire_Marteloscope_MSc_Yusif_medfor_20190708.csv"))
```

```
#####.....          LCW and evenness index Model: all 5 Models
.....#####
```

```
M1 <- lm(LCW ~ CR*evenness+dex*evenness, data=data) #expressing
summary(M1)
```

```
#M1 <- lm(LCW ~ CR+evenness+dex, data=data) #expressing
#summary(M1)
```

```
M2 <- lm(LCW ~ CR*evenness+dex2*evenness, data=data) #expressing
summary(M2)
```

```
#M2 <- lm(LCW ~ CR+evenness+dex2, data=data) #expressing
#summary(M2)
```

```
M3 <- lm(LCW ~ CR*evenness+dsqr*evenness, data=data) #expressing
summary(M3)
```

```
M4 <- lm(LCW ~ (d+d2)*evenness+CR*evenness, data=data) #expressing
summary(M4)
plot(M4)
```

```
M5 <- lm(LCW ~ evenness*(d+dex2)+CR*evenness, data=data) #expressing
summary(M5)
```

```
#Extracting AIC information for model ranking
AIC(M1, M2, M3, M4, M5, k=2)
```

```
AICc(M1, M2, M3, M4, M5)
```

```
R.adj <- function(x) summary(x)$adj.r.squared # define R^2
MSE <- function(x) (summary(x)$sigma)^2
```

```
Ldbh_even <- model.sel( M1, M2, M3, M4, M5, extra = c("R.adj", "MSE"))
#Ldbh_even <- model.sel( Model1, Model2, Model3, Model4, Model5, extra = c("R.adj",
"MSE"))
Ldbh_even$model<-rownames(Ldbh_even)
# replace Model name with formulas little tricky so be careful
```

```
for(i in 1:nrow(Ldbh_even)) Ldbh_even$model[i]<-
as.character(formula(paste(Ldbh_even$model[i])))[3]
# let's see what is in there
View(Ldbh_even) #--->> Model4 is the best model with lowest AICc
write.csv(Ldbh_even,
file=("C:/MScThesis_MEDFOR_UVa/outputs/FINAL/LM_LCW_DBH_EvennessIndex_ent
ire_Marteloscope_MSc_Yusif_medfor_20190713.csv"))

##### END OF LCW INDICES, CROWN RATIO AND DBH EFFECT
#####3
```