Universidad de Valladolid

Máster
Gestión Forestal basada en Ciencia de Datos**/**
Forest Management based on Data Science
(DATAFOREST)

Aboveground tree biomass, carbon stocks and tree diversity in a mixed forest plantation in Northern Vietnam

Student: Doan Thi Nhat Minh

Co-advisors: Prof. Felipe Bravo Oviedo– University of Valladolid

Prof. Vu Van Manh – Vietnam National University, University of Science

July, 2019

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BioEcoN

Co-funded by the
Erasmus+ Programme
of the European Union

TABLE OF CONTENTS

ABSTRACT

Tropical forests reserve a huge amount of carbon stocks and contribute to the amount of biomass accumulation above- and below-ground and the global carbon cycle. Forest plantations in the tropics have long been recognized as an effective solution in reducing the rate of increase in CO2 in the atmosphere. Moreover, the information on forest biomass and carbon content is necessary to support sustainable forest resource management in the world generally and in Vietnam particularly. Most of the forest plantations included only one tree species nevertheless, the use of two or more tree species during the planting phase and the plantation diversification are becoming more and more frequent. Within the framework of BioEcoN project, a Marteloscope, covered an area of 1 hectare, was set up in Hoa Lac Campus of Vietnam National University, Hanoi, Vietnam. Data collected from the Marteloscope include diameter at breast height (1,3 m above the ground), total height, species identity and position of 507 trees. Carbon stocks and above ground tree biomass by compartments were calculated using different biomass equations obtained from the relevant literature. The relationship between above ground tree biomass and species diversity were examined using regression analysis in which predictor variables are a set of parameters for the characterization of mixed stand structure include stand density and diversity, species intermingling, horizontal and vertical tree distribution pattern. The results show that the study area embraces 110.66 tons/ha of tree aboveground biomass and 55.33 tons/ha of carbon. Furthermore, results from the calculation of indices for characterizing species richness and diversity indicates high diversity and high evenness in the community. Although the study area is said to be a plantation, the results from a set of measures, indices, and methods for characterization of tree distribution patterns illustrate random distribution patterns. The sensitivity analysis of the optimum model fitted to explain the relationship between above ground tree biomass and species diversity indicates that above-ground biomass and carbon content decrease as the species diversity increase.

Key words: Tropical forests, marteloscope, model selection, spatial pattern, forest structure

RESUMEN

Los bosques tropicales almacenan una gran cantidad de reservas de carbono y contribuyen a la acumulación de biomasa tanto aérea como subterránea y al ciclo global del carbono. Las plantaciones forestales en los trópicos han sido reconocidas durante mucho tiempo como una solución efectiva para reducir la tasa de aumento del CO2 en la atmósfera. Además, la información sobre la biomasa forestal y la concentración de carbono es necesaria para apoyar la gestión sostenible de los recursos forestales tanto a nivel global como en Vietnam en particular. La mayoría de las plantaciones forestales incluyen solo una especie arbórea, sin embargo, el uso de dos o más especies arbóreas durante la fase de plantación y la diversificación de las plantaciones es cada vez más frecuente. En el marco del proyecto BioEcoN se estableció, en el Campus Hoa Lac de la Universidad Nacional de Vietnam, Hanoi, Vietnam, un aula de señalamiento (*Marteloscope*) de una superficie igual a 1 hectárea. Los datos recopilados en esta aula de señalamiento fueron el diámetro a la altura del pecho (1.3 m sobre el suelo), la altura total, la identidad de la especie y la posición de 507 árboles. Las reservas de carbono y la biomasa arbórea sobre el suelo por compartimientos se calcularon utilizando diferentes ecuaciones de biomasa obtenidas de la literatura relevante. La relación entre la biomasa arbórea aérea y la diversidad de especies se estudió mediante modelos lineales, en los que las variables predictoras fueron un conjunto de parámetros que caracterizan la estructura de los rodales como son la densidad y la diversidad del rodal, la mezcla de especies, el patrón de distribución horizontal y vertical de árboles. Los resultados muestran que en el área de estudio se almacenan 110.66 toneladas / ha de biomasa aérea y 55.33 toneladas / ha de carbono. Además, los resultados del cálculo de los índices para caracterizar la riqueza y diversidad de las especies indican una alta diversidad y una alta uniformidad en el rodal. Aunque el área de estudio es una plantación, los resultados de un conjunto de medidas, índices y métodos para la caracterización de patrones de distribución espacial de árboles se hayo un patrón de distribución aleatorio. El análisis de sensibilidad del modelo óptimo ajustado para explicar la relación entre la biomasa aérea y la diversidad de especies indica que la biomasa aérea y la cantidad de carbono disminuyen a medida que aumenta la diversidad de especies.

Palabras clave: Bosque tropical, aula de señalamiento, selección de modelos, patrón espacial, estructura forestal.

LIST OF FIGURES

LIST OF TABLES

1.- INTRODUCTION

Biomass was defined as all organic matter in the living form (still in the tree) and died on or below ground (Brown et al., 1997). It is also material from flora and fauna which are used for energy production or in different industrial processes as raw material for various products. (Ur-Rehman et al., 2015)

According to the European Commission and the European Biomass Association (AEBIOM), biomass provides an efficient source of energy and a neutral carbon source, with can ensure up to 15% of the industrial demand of industrialized countries by 2020 (AEBIOM, 2017; European Commission, 2014). Additionally, biomass could reduce emissions of CO2 (the main gas causing global warming) by nearly 1000 tons/nm - equivalent to the combined emissions of Canada and Italy combined (Bauen et al., 2004).

Forests play an important part in the global carbon cycle because it contributes 80% of the above ground biomass. Intergovernmental Panel on Climate Change (IPPC) determines the carbon pools in ecosystem biomass, namely biomass on the surface soil, below ground biomass, litter, woody debris and organic matter in the soil Among all carbon pools, above-ground biomass accounts for the majority or 45% of dry biomass of plant parts, forest ecosystems, about 72% of the earth's carbon stocks. (Malhi et al., 2002). The carbon in biomass of forest ecosystems is often concentrated in four main parts: the terrestrial vegetation, down debris, tree roots, and forest soil. Determining the amount of carbon in the forest is usually done through the determination of forest biomass (Mckenzie et al., 2000). Due to difficulties in collecting below ground biomass, most studies predict biomass based only on above ground biomass (AGB) (Lu, 2006). Forest biomass estimation is important for many applications, from trade to timber use (Morgan & Moss, 1985) to the analysis of the global carbon cycle. Forest biomass assessment and management play a key role in sustainable use of forest ecosystems. Biomass is an important source of energy in Vietnam, approximately 90% of domestic energy consumption in rural areas is derived from biomass such as fuel wood, agricultural residues (e.g. rice straw and husks) and charcoal. (Zwebe, 2012)

It is well known that tree biomass is closely related with diameter at breast height and total height (Brown et al., 1989; Chave et al., 2005; Picard et al., 2012). However, different approaches have been used leading to different biomass compartment definitions, scope of the analyisis (local vs regional studies) and statistical approaches (system equations, proportion estimation, …). Beside the ground data, forest biomass has been assessed base on satellite an other remote sensing data (Roy & Ravan, 1996). Biomass were also determined by using carbon dioxide method in which biomass is assessed by determining the rate of CO_2 assimilation. Parts of shrubs and trees under the forest canopy contribute a significant part of the biomass of the forest. There are many methods for estimating biomass for this unit, including the following methods: (1) Sampling whole plants (Quadrants); (2) Line and planar intersect method; (3) Objective measurement; (4) Double sampling method using correlation (Ali et al., 2015; J. K. Brown, 1976; Catchpole & Wheeler, 1992; Pitt & Schwab, 1988). However, the assessment of biomass is not easy, especially the forest subterranean biomass, such as the root system, so the clarification of the problem requires more and more intensive research.

Whether in any different regions such as tropical or temperate, terrestrial or aquatic, all species are not equally common. Various methods of mensuration have been created in order to empirically measure biodiversity. The basic purpose of a diversity index is to obtain a quantitative estimation of biological variability (Help et al., 1998). For tropical ecology, the understanding of how species diversity, species distribution and structural pattern change across different environmental regions is very important. In the past 40 years, many studies were carried out focused on the relationship between species diversity and the ecosystem functions in which one of the most common topics is the relationship between productivity and species richness (Hooper et al., 2005; Keddy, 2005; Mittelbach et al., 2001). Although from many studies, it is said that the relationship between species diversity and productivity are commonly positive. A reverse case was found in Central Europe which indicates a negative relationship between above ground biomass and species diversity (Szwagrzyk & Gazda, 2007). Along with various studies on the productivity and species diversity relationship, another topic which has been much less studied is the relationship between forest stand structural diversity and productivity. Stand structure can be described in terms of the stand density or vertical and horizontal tree distribution patterns. For mixed-species stands, many aspects of structural were increased which led to higher productivity compared to monocultures (Riofrío et al., 2017). A positive relationship between aboveground biomass and stand structural diversity in Canadian forest were also found although the relationship was showed to be a quite weak correlation (Wang et al., 2011).

In recent years, research methods for quantifying, building models for forecasting forest tree biomass have been applied through the relationship between tree biomass and basic measurement factors such as diameter at breast height, tree height which help to quickly predict biomass and save costs ((Bảo, 2017; S. Brown et al., 1989; Huy et al., 2016; Riofrío et al., 2015; Vũ Tấn, 2005). Methods based on biomass measurement can be divided into two groups, which are direct and indirect (Overman et al., 1994). Direct measurement methods include felling trees to identify births. The block is used to measure the actual weight of plant parts such as stems, branches, leaves and weigh the biomass weight after being dried (Supriya Devi & Yadava, 2009). Direct measurement method regional limits and small sample size, accurate biomass determination but it takes a lot of time and effort, large costs. The method is not feasible for large area sizes and does not apply to species that are threatened, much applied to the subjects of vegetation, shrubs and grassland. Other indirect methods aimed at building a relationship between biomass with parameters such as diameter, height, plant density by or wood density regression analysis method (Brown et al., 1989; Vũ et al., 2016).

Correlation equation is one of the most attractive methods of quantifying carbon accumulation in forest biomass because it allows easy use of variables such as diameter, height and tree volume. This method allows the estimation of individual tree biomass from measuring tree size. The development and application of the correlation equation are the criteria for estimating above ground biomass (Návar, 2009). Correlation equations were developed and applied for forest inventories to assess forest biomass and carbon stocks. Many researchers have developed the method of predicting the overall biomass for different forest types and species (Basuki et al., 2009). Some construction works for mixed forest with many different trees, some for specific species on a small scale or for regional and global.

Tropical forests have the largest carbon stock and are the habitat for various world's species (Baccini & Asner, 2013). Up to the present, most researches in the world has showed that although tropical forests cover only less than 10% of the Earth's surface area, it contains up to 70-90% of the total number of flora and fauna species on the earth and store 25 % of global terrestrial carbon (C) and account for 34 % of terrestrial gross primary productivity (B. Bonan, 2008; Malhi, 2012). Forestry activities and changes in land use practices, especially degradation of tropical forests, are an important cause of increasing atmospheric CO_2, estimated at 1.6 billion tons / year in total. The amount of 6.3 billion tons of CO_2 gas per year is emitted by human activities. Therefore, tropical forests and its fluctuations have a great significance in limiting the process of global climate change (S. Brown, 1996; Lasco & Pulhin, 2003; Pearce & Pearce, 2001).

Due to the complex structure of tropical forest stands, tropical forest mensuration is quite challenging in terms of even just basic variable such as the tree height or crown width. The dense understory trees, tall canopies, and closed-canopy conditions are factors which might obstruct the line of sight during field measurement (Hunter et al., 2013). Therefore, research on biomass for tropical forests makes extensive use of destructive sampling method and conversion of volume into the allometric equations (S. Brown et al., 1989; Chave et al., 2005; Hunter et al., 2013; Ketterings et al., 2001)

Vietnam ratified the United Nations Framework Convention on Climate Change on November 16, 1994 and Kyoto Protocol on September 25, 2002 and is considered one of the most active countries (United Nations, 1992, 1998). In Vietnam, studies on biomass and carbon stocks of forests are being paid attention in recent years and have remarkable achievements such as some case studies include research on carbon stocks in vegetation such as grasses and shrub in plantations of *Acacia mangium, Acacia auriculiformis, Eucalyptus urophylla, Acacia hybrid, Pinus kesiya, …* (Nguyễn & Võ, 2008; Võ, 2007, 2009). By accumulating CO_2 in the tree biomass, forest plantation compensates carbon emissions in an efficient way. Most of the forest plantations included only one tree species but it more and more frequent the use of two or more tree species during the planting phase and the platation diversification with individuals belonging to different tree species from adjacent patches or resprouting or germination from the local seed bank. So it is not strange to observe in tropical forest platations that the main planted species (*Acacia sp., Pinus sp. Eucalyptus sp*, …) is mixed with native tree species.

REDD+ program was launched as an initiativavite to reduce emissions due to deforestation and forest degradation avoiding biodiversity loss and reduction. Vietnam has been part of this initiative since the beginning and implementing the policy instruments. As part of this effort biomass equations have been developed for the main forest types in Vietnam. However, the relationship between tree biomass at tree level and the surrounding tree diversity has not been study until now.

2.-OBJECTIVES

The aim of this study is to research on above ground tree biomass and carbon stocks in plantations in Vietnam and to address the relationship between above ground tree biomass and species diversity mixed forest plantation in Vietnam.

The specific objectives are to:

1) Determining Above ground biomass of individual trees by compartments
2) Determining carbon stocks from the amount of tree above ground biomass
3) Characterize species diversity by different indices

4) Examining the relationship between above ground tree biomass and species diversity

3.- MATERIAL AND METHODS

3.1. Study site

Within the frame work of BioEcoN project, a Marteloscope, covered an area of 10000 m^2 (100m x 100m), was set up in Hoa Lac Campus of Vietnam National University, Hanoi (fig. 1) following the framework from University of Valladolid where three different marteloscopes were established previously and are currently mantained. Marteloscopes are sites for training and research purpose that usually cover one hectare in which all trees are numbered, mapped, recorded & measured. The term Marteloscopes is derived from French word *marteaux* (or hammer that it is used to mark the trees to be harvested) and describes a more detailed examination of tree selections and their consequences for the remaining stand.(Bravo et al., 2018).

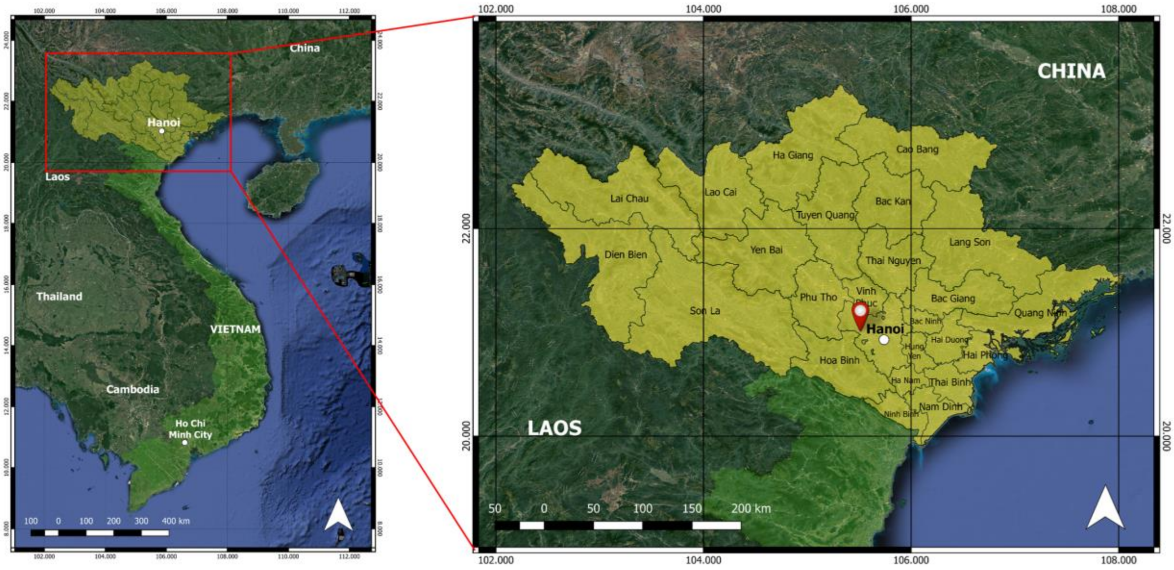


Figure 1: Study area location (105º30'51''E and 21º0'35''N)

Figure 2: Marteloscope A43 of VNU

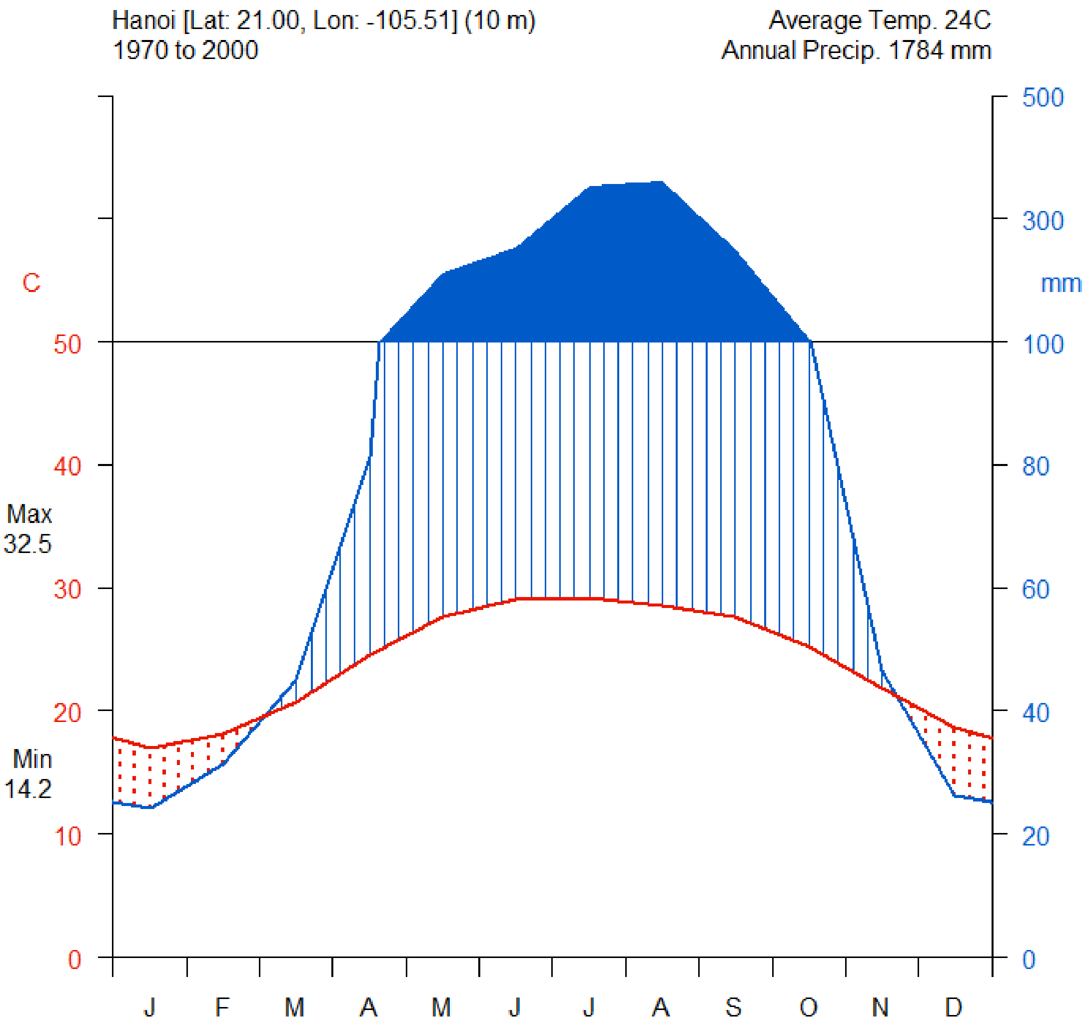


Figure 3: Walter and Lieth climate diagrams of study area (data obtained from The Centre for Environmental Data Analysis)

This marteloscope is located in Hoa Lac, Hanoi (Thach That Disctrict) on a transition area between mountainous and midland areas in the North and the plains. Climate is characterized as a monsoon tropical with wet and cold winters and relatively dry, hot and humid summers (fig. 3). Average annual temperature in the area is 24^{o}C. Average annual rainfall is 1784 mm, unevenly distributed during the year, concentrated in July, August, the precipitation is lowest inDecember and January. From height above 400m no dry season. North wind in the winter with a frequency is greater than 40%. Southeast winds in summer with 25% frequency and the southwest direction. The average air humidity is 84%. From June to November is the highest humidity period of the year. The months of 2,3,4 are dry periods, the average monthly humidity is below 77%. The rock types in Thach That include Precambrian, Paleozoic, Mesozoic, and Kainozoic rocks. The soil types comprise red yellow, brown red and yellow feralite soils, red brown basaltic soils, alluvial soils, valley soils, and gley soils.

The area is among the average sunshine hours in Vietnam. The total number of average hours of sunshine observed is 1595.1 hours. The sunniest period is the rainy season in which the average number of sunshine hours is about 168 to 205 hours. The least sunny month has about 43.3 hours of sunshine. The average total hour of sunshine is 1464 hours. Total annual radiation volume is 122Kcal / cm^2. (N. L. Nguyễn et al., 2009). The rock types in Thach That include Precambrian, Paleozoic, Mesozoic, and Kainozoic rocks. The soil types comprise red yellow, brown red and yellow feralite soils, red brown basaltic soils, alluvial soils, valley soils, and gley soils.

3.2. Data gathering and preparation

3.1.1. Tree level

Following BioEcon marteloscope instalaction protocol (Bravo et al., 2018) for each tree in the marteloscope the diameter at breast height (1,3 m above the ground), total height, species identity and position for every trees with DBH > 5cm were measured and recorded.

The tree diameter at breast height (dbh) was measured by using a measuring tape to measure the perimeter (C) at breast height (accuracy of 0.1cm) then calculate the diameter at breast height with the following equation

$$DBH = \frac{C}{3.14}$$

The tree total height (h) was measured by using the DendroFlexómetro (Reque & Manso, 2003) in combination with a 2m pole (accuracy of 0.1 m).

Tree coordinatex (x – y) were determined using Total station and Real-time kinematic (RTK) positioning. RTK were used to enhance the precision of position data derived from Global Positioning System (GPS). The reference coordinate system used by GPS is the latest World Geodetic System done in 1984 and known as WGS84..

Tree form was recorded following this classification:

– Straight tree (S0): Trees that are not topless, twisted, pestilent, canopy or participate in creating the main canopy of the stand.

- Average tree (S1): Trees that are leaning tree, not topless, crooked, pests, participating in creating the main canopy of the stand.
- Bad trees (S3): Trees that are crooked, pests, which are pressed by other trees.
- Dead tree (Died)

Tree Biomass (total and per compartment: stem, branches and leaves) was calculated from dbh and height using existing allometric biomass equations as shown in Table 1. Tree component biomass values were computed for each individual tree, and summed up to derive a summary of tree biomass for each quadrat and for the marteloscope as a whole.

To obtain the carbon in each tree, the biomass values previously obtained were used. Following (Kollmann, 1959), the percentage of carbon content (C) in the dry biomass was considered as 50 % so the carbon stored in each tree was computed as follows:

$$C\ (kg)\ =\ Biomass\ \times 0.5$$

Finnally, to determine the weight of carbon dioxide sequestered in the tree, the relation between atomic weights of C (12.001115) and O (15.9994) were used to calculate the relation between CO_2 and C as follows:

$$CO_2(kg) = C\ (kg)\ \times 3.666$$

Table 1: Biomass allometric equations for different species in the Marteloscope

Components	**Biomass equation**	**R²**
Acacia auriculiformis (Phạm, 2014)		
Above ground biomass	$AGB = -2.1737 + 0.5109 \times (0.1911 \times DBH^{1,9710} \times H^{0.5391})$	0.95
Stem	$W_s = -1.4322 + 0.5072 \times (0.0984 \times DBH^{1.8862} \times H^{0.7628})$	0.94
Branches	$W_b = 0.0840 + 0.4973 \times (0.1911 \times DBH^{1,9710} \times H^{0.5391}) - (0.0984 \times DBH^{1.8862} \times H^{0.7628} + 0.0434 \times DBH^{1.9294} \times H^{0.2828})$	0.99
Leaves	$W_l = -0.1051 + 0.5135 \times (0.0434 \times DBH^{1.9294} \times H^{0.2828})$	0.98
Acacia mangium (Traoré et al., 2018)		
Above ground biomass	$AGB = exp(-1.073 + 2.081 \times ln(DBH))$	0.97
Stem	$W_s = exp(-3.228 + 1.681 \times ln(DBH) + 1.056 \times ln(H))$	0.98
Branches	$W_b = exp(-0.865 + 0.498 + ln(DBH^2 \times H))$	0.71
Leaves	$W_l = exp(-0.882 + 1.339 + ln(DBH))$	0.57
***Eucalyptus camaldulensis* Dehnh.** (Ounban et al., 2016)		
Above ground biomass	$AGB = 0.035 \times (DBH^2 \times H)^{0.953}$	0.982
Stem	$W_s = 0.019 \times (DBH^2 \times H)^{1.005}$	0.977

Branches	$W_b = 0.015 \times (DBH^2 \times H)^{0.697}$	0.757
Leaves	$W_l = 0.013 \times (DBH^2 \times H)^{0.721}$	0.750
Litsea glutinosa (Đ. H. Nguyễn et al., 2012)		
Above ground biomass	$AGB = 0.1142 \times DBH^{2.4451}$	
Stem	$W_s = 0.1274 \times DBH^{2.3655}$	0.8686
Branches	$W_b = 0.0102 \times DBH^{2.5848}$	0.7188
Leaves	$W_l = 0.0785 \times DBH^{1.4696}$	0.5330
Senna siamea (S. Brown et al., 1989)		
Above ground biomass	$AGB = exp(-3.1141 + 0.9719 \times ln(DBH^2 \times H))$	0.97
Averrhoa carambola (S. Brown et al., 1989)		
Above ground biomass	$AGB = exp(-3.1141 + 0.9719 \times ln(DBH^2 \times H))$	0.97
Aporosa villosa (S. Brown et al., 1989)		
Above ground biomass	$AGB = exp(-3.1141 + 0.9719 \times ln(DBH^2 \times H))$	0.97

For each tree different measures (Table 2) of tree diversity and mixture around it were computed to estimate species richness and diversity, species intermingling and tree distribution pattern (vertical and horizontal). Here the used indices are listed but in (Río et al., 2018) a full list of indices with potential value to define mixtures is presented.

Table 2: Categorization of different indices used

Species Richness & diversity	**Tree Distribution pattern**		
	Species intermingling	**Vertical spatial pattern**	**Horizontal spatial pattern**
Simpson diversity index (1-D)	Segregation index (S)	Vertical Species Profile (A)	L-function
Shannon index (H')	Mingling index (Mi)	Height Differentiation index (TH)	Aggregation index (R)
Berker-Parker index (D)	Spatial Diversity Status (MS)		Uniform Angle Index (W)
Evenness index (E)			

Simpson's Diversity index (1-D) (Simpson, 1949) is a dominance mensuration because rather than providing a measure of species richness, the index is weighted towards the abundance of the most common species in the sample. It indicates the probability of any two individuals randomly selected from a large population belonging to different species. Therefore, the index is less sensitive to species richness. Simpson's index was calculated as follows:

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

Where:

- ni is the total number of a particular species
- N is the total number of all species in the dataset
- *R* – richness (total number of species types in dataset).

The value of Simpson's Diversity index ranges between 0 and 1. The greater value indicates the greater sample diversity. Value close to 1 indicates high diversity and low value (close to 0) indicates low diversity.

Shannon's index (H') accounts for abundance and evenness of the species observed in the stand. (Shannon et al., 1949). The Shannon index reflects the manner in which abundance is distributed amongst the different species constituting the community. The index is based on the relative frequencies of species in the population, thus taking into account both species richness and evenness. However, the value of the index is most strongly related to species richness. Shannon's index was calculated as follows:

$$H' = -\sum_{p_i}^{s} p_i \times \ln(p_i)$$

Where:

$-s$ is the number of a particular species in the stand.

$-p_i$ is the proportion of individuals found in species i. For a well-sampled community, we can estimate this proportion as $pi = ni/N$, where ni is the number of individuals in species i and N is the total number of individuals in the community.

$-ln(p_i)$ is natural logarithm of this p_i which value ranges from 0 to $\ln(S)$. When all species in the dataset are equally common, all p_i values equal $1/S$, and the Shannon index then equal to $In(S)$. If practically all abundance is concentrated in one species, and the other species area very rare (even if there are many of them), the value approaches 0. If there are only one species in the dataset, the value equals to 0

Berger-Parker index (D) (Berger & Parker, 1970) focuses on quantifying the abundance of individuals of each species in the stand. If the Berger-Parker index is high, this means that the stand dominated by the most common species. Berger-parker index was calculated as follows:

$$D = \frac{N_{max}}{N}$$

Where:

$-Nmax$ is the number of individuals in the most abundant species

$-N$ is the total number of individuals in the stand

$1/D$ is the reciprocal of the index, which is often used in order to illustrate that, an increase of the value of the index followed by an increase in diversity and a reduction in the dominance.

Species evenness tells us how evenly the species are distributed in the stand. The Evenness index (E) (Pielou, 1975) compares the actual diversity value (the Shannon-Wiener Index, H') to the maximum possible diversity value (when all species are equally common, $H_{max} = ln\,S$, where S is the total number of species). Evennes index is computed as follows:

$$E = \frac{H'}{ln\,S}$$

Where:

– H' is the number derived from the Shannon index

– $H_{max} = ln\,S$ where H_{max} is the maximum possible value of H'

The Evenness index is constrained between 0 and 1. The more variation in abundances between different species within the community, the lower the Evenness index.

The segregation index (S) by (Pielou, 1961) is commonly used to describe the intermingling of two tree species A and B. The Segregation index (S) describes the relative mixing of two species regardless of their spatial pattern. This method is based on the nearest neighbor distances and compares the observed number of mixed pairs with the one expected under random conditions. S is considered as the ratio of the observed propability (p_{ij}) that the reference tree i and its neareast neighbor j belong to different species along with the same probaility for completely random distributed or independent species attributes (Río et al., 2018) .The segregation index S is computed as follows:

$$S = 1 - \frac{p_{ij}}{E(p_{ij})} = 1 - \frac{Number\ of\ observed\ mixed\ pairs}{Number\ of\ expected\ mixed\ pairs}$$

$$= 1 - \frac{N(b+c)}{m_1n_2 + m_2n_1}$$

Values of S vary between –1 and 1.

- If $0 < S < 1$ indicates that the nearest neighbors are always different species (spatial separation of species)
- If $-1 < S < 0$, spatial association between two species is observed.
- If both species are randomly distributed, then $S = 0$
- $S = -1$ indicates that all neighbours are of different species
- $S = 1$ indicates that the reference tree is surrounded by the same speciess

Table 3: Contingency table summarizing the number of trees of both species (A and B) (adapted from (Pielou, 1961))

		Nearest-neighbor species (j)		
		Species A	Species B	Species A+B
Reference tree (i)	Species A	a	b	$n_1 = a + b$
	Species B	c	d	$n_2 = c + d$
	Species A+B	$m_1 = a + c$	$m_2 = b + d$	N

Quantification of species diversity is an important aspect connected with forest management. Several parameters have been developed to describe species diversity. The Mingling index (M_i) (Füldner, 1995) describes the species pattern around the reference tree. Mingling index is expressed by the proportion of the n nearest neighbour trees of the i^{th} reference tree that do not belong to the same species. This index is generall used to derive a distribution of trees that belong to a certain structure class. (Aguirre et al., 2003). The Mingling index was calculated as follow:

$$M_i = \frac{1}{n}\sum_{j=1}^{n} v_j \qquad v_j = \begin{cases} 1, specie_j \neq specie_i \\ 0, \ specie_j \ is \ the \ same \ as \ specie_i \end{cases}$$

Where:

- n is the number of nearest neighbor trees considered
- v_j produces binary output

The Mingling index range from 0 to 1 ($0 \leq M_i \leq 1$). The larger the mingling variable Mi, the more the different tree species are intermingled. A high value of mean mingling Mi represents a high intermingling of the different species. On the other hand, a small value near 0 will indicates large groups of one single species and segregation.

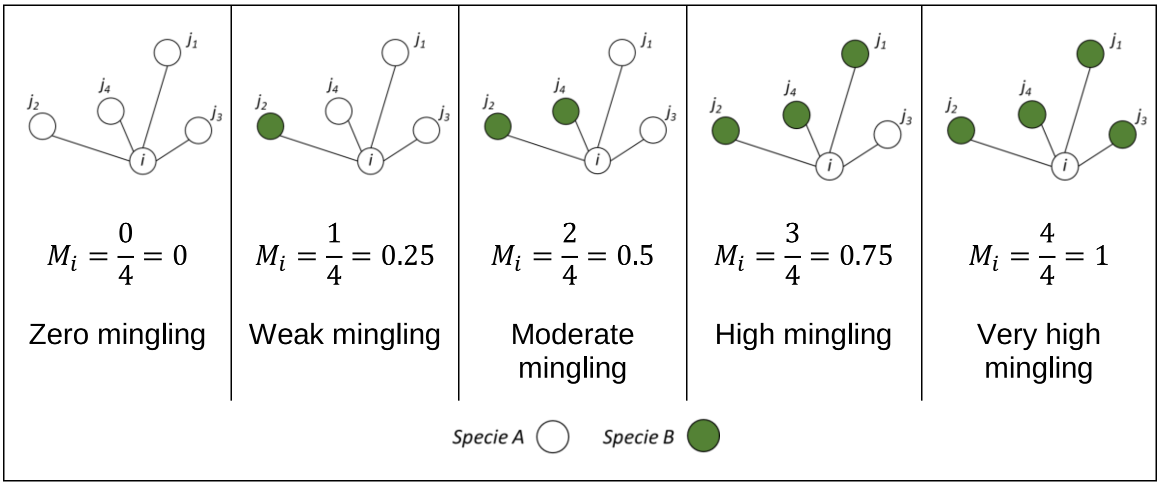


Figure 4: Illustration of the Mingling index for $\boldsymbol{n = 4}$ neighbours. n = neighbours. The neighbours are numbered according to increasing distance from the reference tree (adapted from (Pommerening & Stoyan, 2006))

Spatial diversity status (MS) is improvement of the Mingling index, which considers not only the spatial mingling, but also the number of tree species. Spatial diversity status of a particular tree species is determined by the relative species richness within the stand or analyzed spatial unit i and the degree of mingling of the reference tree (Río et al., 2018). The Spatial diversity status was calculated as follow:

$$MS_i = \frac{S_i}{n_{max}} \times M_i$$

Where:

- S_i is the number of tree species in the neighborhood of the reference tree i, including tree i
- n_{max} is the maximum number of species in this structure unit

- M_i is the species Mingling value.

The Spatial diversity status range from 0 to 1 ($0 \leq MS_i \leq 1$). A reference tree of a common species is more likely to have neighbors of the same species, which is reflected by low values of MS_i. In contrast, a rare species is likely to produce a high proportion of high MS_i values. Thus, MS_i is especially sensitive to rare species. (Gadow & Hui, 2002)

Tree spatial distribution pattern and population structure of trees are the direct consequence of comprehensive interactions among characteristics of species, environmental factor, and intraspecific and interspecific interactions between each individual tree over a long time. Tree spatial distribution pattern depends on the biological characteristics of the tree at a small scale and on environmental heterogeneity, such as soil, pH, nutrition, water, canopy cover, and terrain, at large scales. (Condit et al., 2000)

Vertical species profile (A) (Pretzsch, 1995) is based on the common diversity index of Shannon (Shannon, 1948). A index takes into account the presence of the species in different height zones in addition to the proportion of the species within a stand. The Vertical species profile was calculated as follow:

$$A = -\sum_{i=1}^{S}\sum_{i=1}^{Z} p_{ij} \times \ln(p_{ij})$$

Where

- S is the number of species present in the stand
- Z is the number of height zones (in this study Z = 3)
- N is the total number of individual trees
- p_{ij} is the proportion of a species in the height zone $p_{ij} = n_{ij}/N,$
- n_{ij} is the number of individuals of the species i in the zone j

The value of Vertical species profile is greater than 0 ($A > 0$) is for a single-layered pure stand. The more heterogeneous the vertical profile, the higher the A value. In order to calculate the Vertical Species profile A by using R-studio, the Height were devided into 3 zones. Assume the height of the highest tree in the stand is 100%, zone I extends from 100% to 80% of maximal tree height (H_{max}), zone 2 from 80% to 50% of H_{max} and zone 3 from 50% to the forest ground which is 0% of H_{max}. A tree is considerd in the zone where the top of the tree is located.

Standardization of A can be calculated as follow:

$$A_{rel} = \frac{-\sum_{i=1}^{S}\sum_{i=1}^{Z} p_{ij} \times ln(p_{ij})}{ln(S \times Z)} \qquad \text{where } A_{max} = ln(S \times Z)$$

A_{rel} indicates how close a given stand stucture is to the maximum structuring posible with the given species abundance.

Height Differentiation index (TH) was developed by (Klaus v. Gadow, 1993).It measures the differences of size between the reference tree i and its neighboring trees on a continuous scale and describes spatial distribution of tree sizes. TH reveals small-scale variability in the height for the i reference tree and its n nearest neighbours j ($j = 1 \ldots n$). The average of TH can be calculated at a whole stand level and at species level by summing up TH values and divided it by the number of trees or individuals of the subpopulation. Further, it can be demonstrated in frequency histogram by each species based on its classes defined. The Height Differentiation index was calculated as follow:

$$TH_{ij} = 1 - \frac{MIN(H_i,\ H_j)}{MAX(H_i,\ H_j)}$$

Where

- H_i the height of reference tree i
- H_j the height of neighbour tree j

The Height Differentiation index (TH) range from 0 to 1 $(0\ \leq\ TH\ \leq\ 1)$

- If TH=1, the neighbour trees have high differentiation in height
- If TH=0 means the neightbour trees have an equal height

To define the spatial distribution of the trees the L-function defined by Besag (1977) was used. L-function was calculatedby dividing the K – function (Ripley, 1977) by π and by taking the square root of the quotient, which yields the L -function with both statistical and graphical advantages over the K -function. The L – function allowed tree distribution patterns to be quantified more precisely. For n tres on an experimental plot with size A , the L-function is calculated as follows:

$$\hat{L}(r) = \sqrt{\frac{\hat{K}(r)}{\pi}}, for\ r \geq 0$$

$$\hat{K}(r) = \frac{1}{\lambda} \times \sum_{i=1}^{n}\sum_{j=1}^{n}\frac{P_{ij}(r)}{n-1}, with\ P_{ij}(r) = \begin{cases} 1\ if\ r_{ij} \leq r \\ 0\ if\ r_{ij} > r \end{cases}$$

Where:

$-r$ denotes radius centred at the typical point (tree) i of the point pattern

$-r_{ij}$ is the distance between tree i and tree j

$-\lambda = n/A$ represents the mean point density

In this study The L – function was applied at whole stand level, quadrant level and species level (within and between interactions of species) in each quadrant.

Point patterns can vary from complete random patterns $(\hat{L}(r) = 0)$ by being either aggregated $(\hat{L}(r) > 0)$ or regular $(\hat{L}(r) < 0)$ (Butt, 2010). Therefore, if $\hat{L}(r)$ falls on the expected values (dotted diagonal lines), the trees have a random distribution; if $\hat{L}(r)$ r falls above the expected values (dotted diagonal lines), the trees have a clumpy distribution; if $\hat{L}(r)$ r falls below the expected values (dotted diagonal lines), the trees have a uniform distribution.

The Aggregation index (R) (Clark & Evans, 1954) is a crude measure of clustering or order of a point pattern. Aggregation index (R) is the ratio of the observed mean nearest neighbor distance in the pattern to that expected mean distance in a random tree distribution.

$$R = \frac{\bar{r}_{observer}}{E(r)}, with\ E(r) = 0.5 \times \sqrt{\frac{A}{N}}$$

Where:

$-\bar{r}_{observer}$ is mean of distance between reference tres and neighbours
$-E(r)$ is the average distance to be expected when tres are randomly distributed
$-N$ is the number of trees in the plot
$-A$ is the size of the plot

Aggregation index (R) range between 0 (greatest clumping, all objects occur at the same point) and 2.1491 (strictly regular hexagonal pattern), and indicates wherther the trees are distributed regularly, randomly or in clumps across an area. $R > 1$ describe a tendency towards regular distribution, $R < 1$ indicates a tendency towards clustering and Value around 1 shows random distribution.

In this study Aggregation index (R) was calculated in R-studio softwear at whole stand level, quadrant level and species level (within and between interactions of species) in each quadrant. In R-studio, correction for edge effects is necessary. Aggregation index R will be positively biased without correction for edge effects because edge effects arise due to a case for a point of X located close to the edge of the plot, its nearest neighbour can be outside the plot. Therefore, the observed distances to nearest neighbour tend to be larger than the distances to the true nearest neighbour. The nearest neighbour distance distribution function G(r) of the stationary point process is estimated by Gest using the Kaplan-Meier type edge correction. Then the mean of the distribution is calculated from the cumulative distribution function.

The Uniform Angle Index (W) developed by (Klaus v. Gadow, 1993) describes the degree of regularity in the spatial distribution of individuals tree. This index is based on the classification of angles between nearest neighbours tree of the reference tree (K von Gadow et al., 2002)

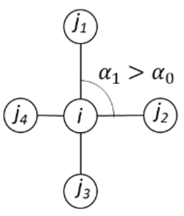
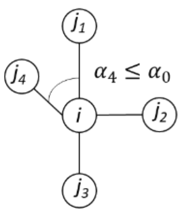
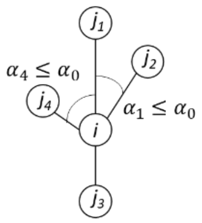
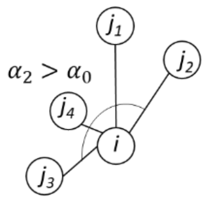
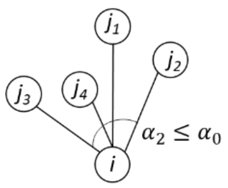
$$W_i = \frac{1}{n}\sum_{j=1}^{n} v_j \ where\ v_j = \begin{cases} 1, \alpha_j < \alpha_0 \\ 0, otherwise \end{cases}$$

Where:

$-n$ is number of nearest neighbours around the reference tree i
$-\alpha_0 = 360^o\ /n$ is the expected standard angle between reference tree and its neighbour

The Uniform Angle Index (W) range from 0 to 1:

- $W < 0.5$ shows regular tree distribution pattern.
- $0.5 \leq W \leq 0.6$ illustrate random distribution
- $W > 0.6$ can be considered as clumpled.

 $W_i = \frac{0}{4} = 0$	 $W_i = \frac{1}{4}$ $= 0.25$	 $W_i = \frac{2}{4} = 0.5$	 $W_i = \frac{3}{4} = 0.75$	 $W_i = \frac{4}{4} = 1$

Very regular	Regular	Random	Irregular	Very irregular

Figure 5: Calculation of uniform angle index W and possible values for structural group of 4 neighbours around the reference $\boldsymbol{i}$-tree (adapted from (K von Gadow et al., 2002))

3.2.2. Stand level

Derived from the diameter at breast height is the basal area. The basal area of a tree is defined as the cross-sectional area of a stem measured at breast height. The basal area of each tree (G_i) in the Marteloscope was calculated using the following equation:

$$G_i = \pi \times \left(\frac{DBH_i}{2}\right)^2$$

The Number of tree per hectare (N) is calculated by multiply the number of tree in the area (n) with the expansion factor which is defined by taking the size of 1 hectare in adequate mensuration unit dividing by the area of the plot (A). The number of tree per hectare is computed as follow:

$$N = n \times \frac{10000}{A}$$

3.3. Statistical Ananlysis

Pearson’s correlation coefficient is a statistical measure of the strength of a linear relationship between paired data. In order to insight into the strength of the linear relationship betweet paired date, the correlation coefficient was defined as follows:

$$-1 \leq r \leq 1$$

Furthermore:

- Positive values denote positive linear correlation;
- Negative values denote negative linear correlation;
- A value of 0 denotes no linear correlation;
- The closer the value is to 1 or –1, the stronger the linear correlation.

In this study, in order to avoid correlation between parameters when fitting different models, we test the maxtrix correlation coefficient in R-studio. Although the significance of parameters does not only be effected by the correlation between parameters, the pairs of variables which have the correlation coefficient (r) out of the range of $-0.5 \leq r \leq 0.5$ will not be included together in the fit models to avoid insignificant results in parameters t-test.

Regression analyses are conducted using the R-open software in order to explain the relationships between tree above ground biomass and trees density, species richness & diversity, species intermingling and tree distribution pattern. Therefore, in each equation, the dependent variable is tree above ground biomass when the independent varibles include basal area of each quadrant, number of tree per hectar of each quadrant and the calculated indices. 3 forms of equations in Table… were used to develop various model for the two most abundant species which are *Acacia mangium* and *Acacia auriculiformis.* The log transformation homogenized the variance about the regression surface and linearized the parameters of the equation to meet the assumptions of linear regression techniques.

Table 4: Model forms for statistical annalysis

Linear form	
$ABG = \beta_0 + \sum_{i=1}^{n} \beta_i X_i + \varepsilon \quad (I)$	
Non-linear form	
Original form	**Log-tranformed form**
$AGB = \exp(\beta_0 + \sum_{i=1}^{n} \beta_i X_i + \varepsilon) \quad (II)$	$ln\, AGB = \beta_0 + \beta_1 G + \beta_2 N$
$AGB = \beta_0 \times {X_1}^{\beta_1} \times \ldots \times {X_n}^{\beta_n} + \varepsilon \quad (III)$	$ln\, AGB = ln\beta_0 + \beta_1 lnX_1 + \cdots + \beta_n lnX_n$

The p-value of the coefficients (Pr(>|t|)) indicates whether the independent variable has statistically significant predictive capability. It essentially shows the probability of the coefficient being attributed to random variation. The lower the probability, the more significant the impact of the coefficient. In R–studio, the p-value is automatically calculated by comparing the t-value against the Student's T distribution table. A p-value of less than 5% ($p\text{-value}<0.05$) indicates the significance of the indepentdent variables.

It is important to select the optimum model because under-fitting a model might not capture the true nature of the variability in the outcome variable. On the other hand, an over-fitted model loses generality. Optimal equation selection was based on the following criteria:

Akaike’s information criterion (AIC) was first developed by (Akaike, 1973) as a way to compare different models on a given outcome. AIC compares the quality of a set of statistical models to each other. tries to formulate the bias variance trade off that every statistical modeler faces when fitting a model to finite set of data. In other words, while fitting a model if the number of parameters is increased, the log likelihood would be improved but might run into the danger of over fitting. The AIC penalizes for increasing the number of parameters thus minimizing the AIC selects the model where the improvement in log likelihood is not worth the penalty for increasing the number of parameters.

$$AIC = -2\log(L(\hat{\theta})) + 2k$$

Where:

- k is the number of estimated parameters included in the model.
- $\hat{\theta}$ represents the maximum likelihood estimates of the model parameters
- $\log(L(\hat{\theta}))$ is the log-likelihood of the model given the data

AIC is computed for every candidate model and the optimum model is the candidate model which has the smallest AIC. The $-2\log(L(\hat{\theta}))$ is the first component in calculating AIC which indicates the value of the likelihood function. Because the value of the likelihood function is multiplied by –2, the model with the minimum AIC is the one with the highest value for the likelihood function when we ignore the second component, However, we add an adjustment based on the number of estimated parameters to the first component, therefore, parameters lead to the greater amount added to the first component, hence the value for the AIC increased. Thus, there is a trade-off: the better fit, created by making a more complex model by adding more parameters, must be considered in light of the penalty imposed by adding more parameters. This is the reason why the second component of the AIC is thought of in terms of a penalty

Bayesian information criterion (BIC) proposed by (Schwarz, 1978) is a criterion for model selection. When fitting models, overfitting might occur if the likelihood is increased by adding parameters, but doing so may result in. The BIC can solve this problem by bringing a penalty term for the number of parameters in the model. The best model is the one that provides the minimum BIC

$$BIC = 2log(L(\hat{\theta})) + klog(N)$$

The coefficient of determination (denoted by R^2) is a key output of regression analysis. It is interpreted as the proportionate amount of variation in the response variable y explained by the independent variables X in the linear regression model. R^2 range from 0 to 1, the larger the R^2 is, the more variability is explained by the linear regression model.

Ordinary — Ordinary (unadjusted) R^2

$$R^2 = \frac{SSR}{SST} = 1 - \frac{SSE}{SST}$$

Adjusted — R-squared adjusted for the number of coefficients

$$R^2 = 1 - \left(\frac{n-1}{n-p}\right) \times \frac{SSE}{SST} = 1 - \left(\frac{n-1}{n-p}\right) \times (1 - R^2)$$

Where:

- *SSE* is the sum of squared error: $SSE = \sum_{i=1}^{n}(y_i - \hat{y}_i)^2$
- *SSR* is the sum of squared regression: $SSR = \sum_{i=1}^{n}(\hat{y}_i - \bar{y})^2$
- *SST* is the sum of squared total: $SSE = \sum_{i=1}^{n}(y_i - \bar{y})^2 = SSR + SSE$
- *n* is the number of observations
- *p* is the number of regression coefficients. Note that *p* includes the intercept, so for example, *p* is 2 for a linear fit. Because R-squared increases with added predictor variables in the regression model, the adjusted R-squared adjusts for the number of predictor variables in the model. This makes it more useful for comparing models with a different number of predictors.
- y_i represents observed values
- $\hat{y}_i$ represents predicted values

Mean square error (MSE) is the average of the squares of the deviations which is also the gap between the observation and fitted value. Due to the randomness or the lack of information which could give a more accurate estimation, there exist differences between actual values and expected values.

The mean square error supports in determinating the quality of a predictor with a non-negative value. If the value of the MSE is close to 0, then it indicates that the quality of the predictor is better. The value of MSE is used to compare the two or more than two models of statistics. The result indicates how well the observations are explained by candidate models is provided afterward. In the regression analysis, the MSE is measured to analyse variance and to determine the significance of the predictor or estimator. MSE is calculated for every candidate model and the optimum model is the candidate model which has the smallest MSE.

$$MSE = \frac{1}{n} \times \sum_{i=1}^{n}(y_i - \hat{y}_i)^2$$

Where:

- *n* is the number of observations
- y_i represents observed values
- $\hat{y}_i$ represents predicted values

Once the best model is selected, the sensitivity analysis of the model is carried out. Sensitivity analysis includes a series of procedures to quantify how the variability in the output of a model is related to that in its inputs. In this study, the sensitivity analysis of the optimal model was done in order to assess how sensitive the tree above ground biomass is to the fluctuations of parameters and data on which the model is built. The results of sensitivity analysis have vital implications in inspecting more broadly the relationship between the parameters and the tree above ground biomass. The sensitivity analysis was conducted by fixing one of the parameters of the model and obtain the results indicating the behaviour of the dependant variable when the remaining independent varies.

4.- RESULTS

4.1. Stand characteristic

The total study area includes 1 hectare (10.000 m^2), with 507 trees were measured. Seven different sepcies were found in the Marteloscope including *Acacia mangium, Acacia auriculiformis, Eucalyptus camaldulensis, Senna siamea, Litsea glutinosa, Aporosa villosa* and *Averrhoa carambola*. Due to the condition of the dead trees, it was impossible to identify the species of the died tree. The location of each species is presented in Figure 7.

Acacia mangium is the most abundant species in the Marteloscope with 300 individuals, accounting for 59.17% of the total trees, followed by *Acacia auriculiformis* with 108 individuals, accounting for 21.30% of the total trees (Table5). The largest DBH (78.62 cm) and height (24.800m) are in *Acacia mangium*, and the smallest are in *Eucalyptus camaldulensis* and *Acacia mangium* (2.45 cm and 1.70 m, respectively). As shown in Figure 6 the smallest diameter class (5-10 cm) accounting for 5.50% of the stand total and with the largest DBH class (>50 cm) only for 0.15% of the stand total. The largest average DBH and height are in *Senna siamea* and *Acacia auriculiformis* (38.87 cm and 15.00 m, respectively) and the smallest are in *Aporosa villosa* (11.46 cm and 4.70 m, respectively).

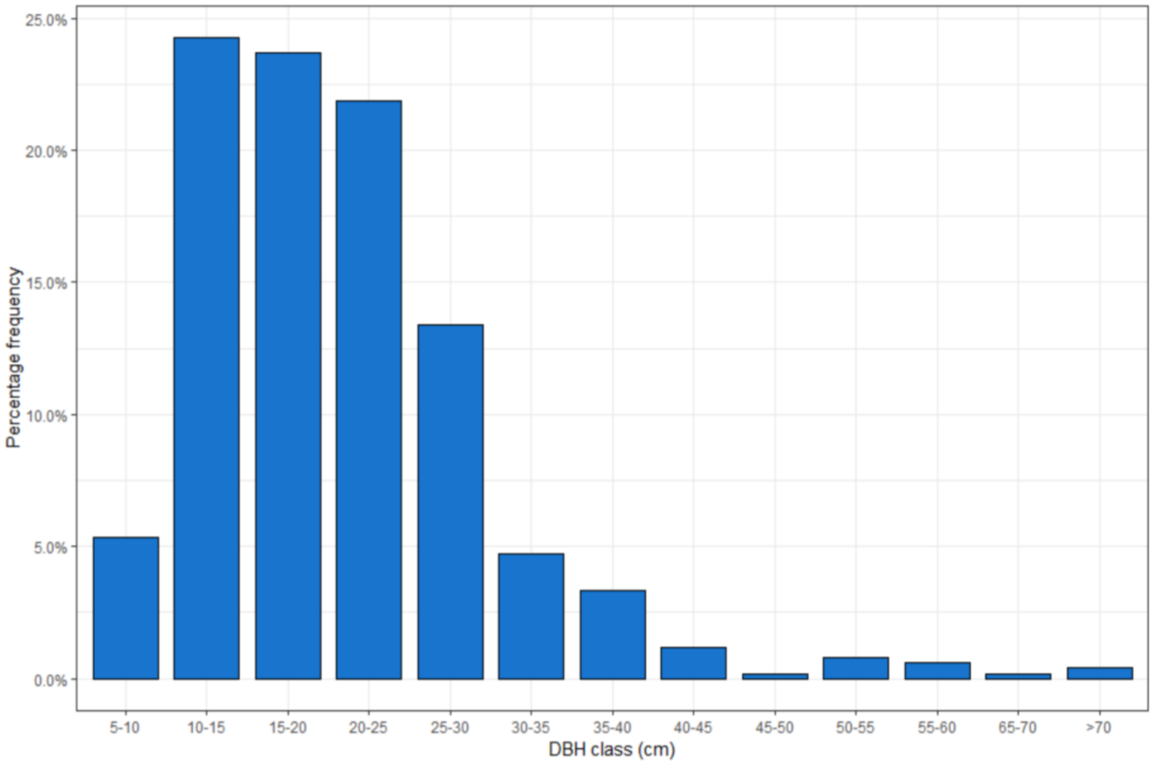


Figure 6: DBH distribution of the Marteloscope

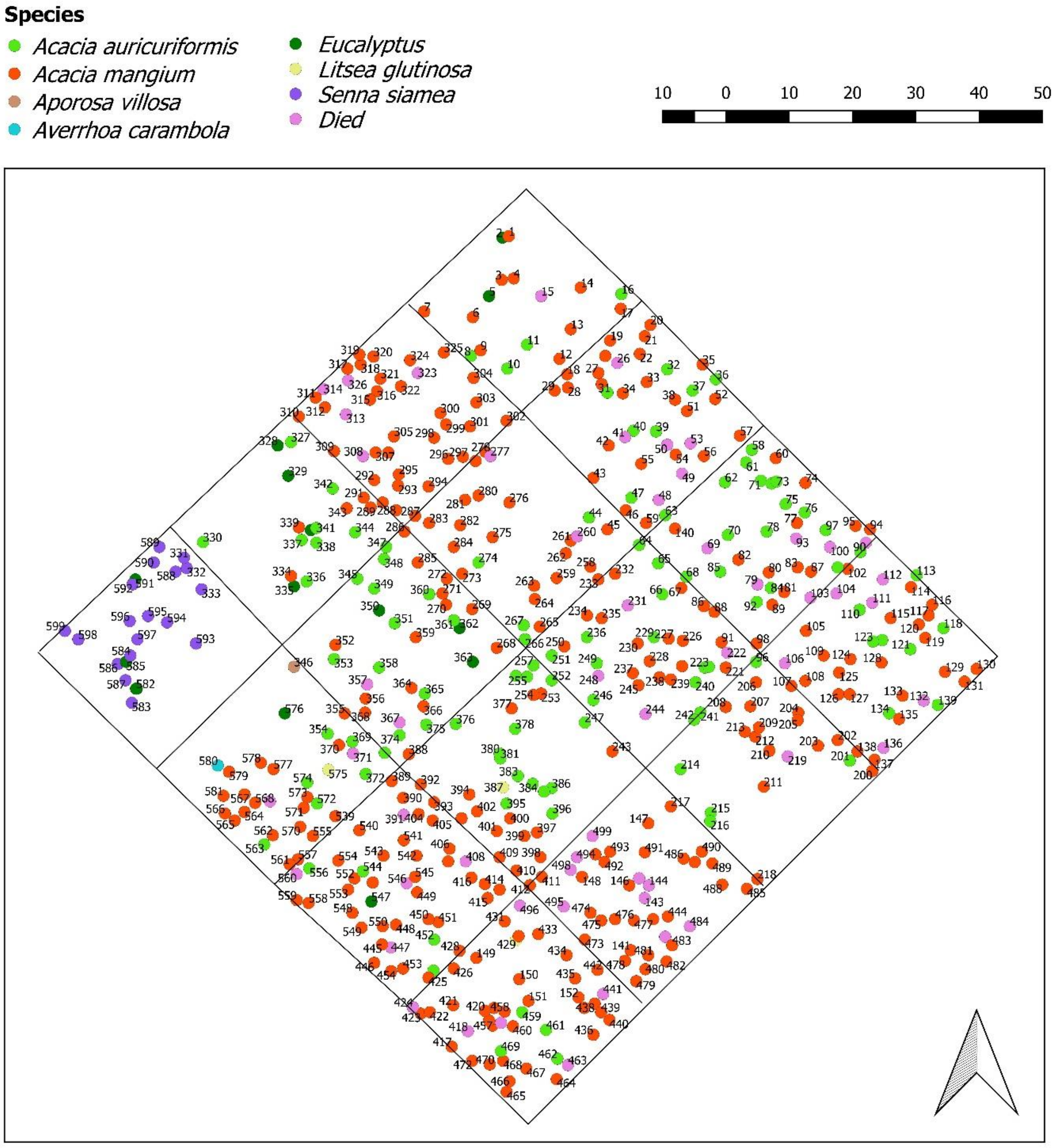


Figure 7: Tree position in the VNU A43 Marteloscope

Table 5: General characteristic of each species

Species	**n**	**DBH (cm)**				**Height (m)**				**AGB**	**C**	**CO_2**
		Mean	**Median**	**Max**	**Min**	**Mean**	**Median**	**Max**	**Min**			
Acacia mangium	300	20.61	19.74	78.62	6.05	15.06	14.90	24.00	1.70	65.71	32.86	120.45
Acacia auriculiformis	108	22.07	21.96	49.97	6.68	15.24	15.00	22.50	6.00	23.70	11.85	43.45
Eucalyptus camaldulensis	15	17.76	18.14	30.88	7.00	15.41	13.50	22.00	8.50	2.05	1.02	3.75
Senna siamea	18	38.87	39.15	75.12	15.92	12.00	11.75	16.00	7.50	13.64	6.82	25.00
Litsea glutinosa	3	11.46	11.46	15.60	7.32	8.60	6.80	12.50	6.50	0.15	0.08	0.28
Aporosa villosa	1	11.46	-	-	-	4.70	-	-	-	0.02	0.01	0.04
Averrhoa carambola	1	11.46	-	-	-	7.50	-	-	-	0.04	0.02	0.07
Died trees	61	15.35	13.85	56.98	6.37	9.25	9.00	17.50	1.30	5.35	2.67	9.80

n: number of individual; DBH: diameter at breast height (cm); AGB: total above ground biomass (tons); C: weight of carbon (tons); CO_2: weight of carbon dioxide sequestered (tons)

Table 6: General characteristics of each quadrants

					Ac_ma		**Ac_au**		**Eu_ca**		**Se_si**		**Li_gl**		**Ap_vi**		**Av_ca**		**Died trees**	
Q	**G**	**Mean DBH**	**Mean H_t**	**N**	**n**	***%G***	**n**	***%G***	**n**	***%G***	**n**	***%G***	**n**	***%G***	**n**	***%G***	**n**	***%G***	**n**	***%G***
1	11.05	21.81	14.65	272	10	63.33	4	22.06	2	5.90	-	-	-	-	-	-	-	-	1	8.71
2	22.53	20.63	13.35	608	22	60.40	8	26.86	-	-	-	-	-	-	-	-	-	-	8	12.74
3	18.88	19.07	14.13	592	14	36.05	17	56.36	-	-	-	-	-	-	-	-	-	-	6	7.59
4	17.42	18.00	14.45	576	22	72.80	8	18.77	-	-	-	-	-	-	-	-	-	-	6	8.43
5	17.31	23.64	13.52	320	12	45.99	4	26.60	-	-	-	-	-	-	-	-	-	-	4	27.41
6	18.01	19.05	13.80	576	19	55.98	13	36.78	-	-	-	-	-	-	-	-	-	-	4	7.23
7	18.33	22.01	15.12	400	19	82.56	4	12.88	-	-	-	-	-	-	-	-	-	-	2	4.55
8	25.82	21.88	15.95	592	32	90.69	-	-	-	-	-	-	-	-	-	-	-	-	5	9.31
9	16.21	26.16	18.05	272	5	23.13	8	60.86	4	16.01	-	-	-	-	-	-	-	-	-	-
10	21.42	22.00	15.96	496	14	44.48	12	50.48	3	6.10	-	-	-	-	-	-	-	-	2	2.33
11	27.57	23.75	15.31	496	15	63.38	15	36.02	-	-	-	-	1	0.60	-	-	-	-	-	-
12	17.61	18.06	14.03	624	30	87.64	-	-	-	-	-	-	-	-	-	-	-	-	9	12.36
13	18.81	17.14	12.68	704	32	74.42	4	12.53	-	-	-	-	1	1.63	-	-	-	-	7	11.42
14	18.09	16.96	13.73	720	35	82.57	4	11.52	1	1.36	-	-	-	-	-	-	-	-	5	4.55
15	18.96	20.19	12.91	512	19	73.79	7	22.37	1	0.32	-	-	1	0.36	1	0.87	1	0.87	2	1.42
16	43.23	35.09	12.15	352	-	-	-	-	4	3.81	18	96.19	-	-	-	-	-	-	-	-

Q: quadrant; G: basal area of the quadrant (m^2/ha); Mean DBH: mean of diameter at breast height (cm); Mean H_t: mean of total height (m); N: number of tree per hectare (tree/ha); n: number of individual tree; %G porpotion of basal area of each species in each quadrant (%); Ac_ma: *Acacia mangium*

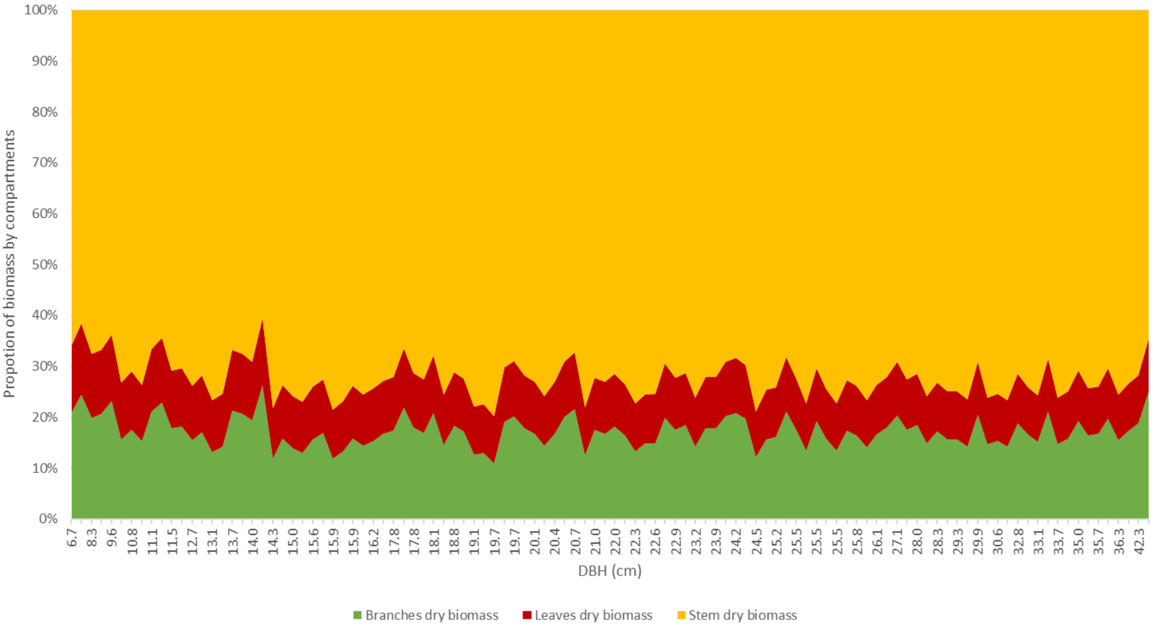


Figure 8: Propotion of biomass by compartments from total ABG of *Acacia auriculiformis*

As can be seen from Figure 8 and Figure 9 the stem biomass is the main components of the total tree above ground biomass for *Acacia auriculiformis* (108 observations) and *Acacia mangium* (300 observations), followed by branches biomass and leaves biomass respectively. For *Acacia auriculiformis*, the proportion of biomass by compartments does not show a clear trend when the DBH increase. On the other hand, it is clearly indicated from Figur 9 that for the *Acacia mangium,* the larger the value of DBH, the higher the proportion of stem biomass, while the proportion of branches biomass decrease and the proportion of leaves biomass seems to remain stable.

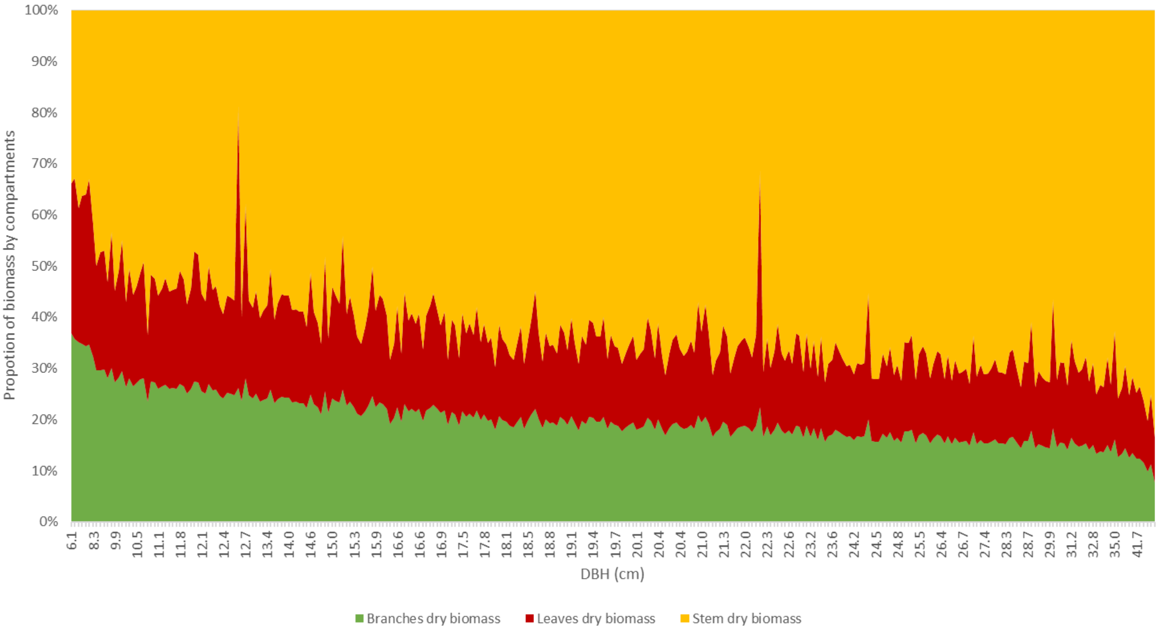


Figure 9: Propotion of biomass by compartments from total ABG of *Acacia mangium*

4.2. Stand diversity

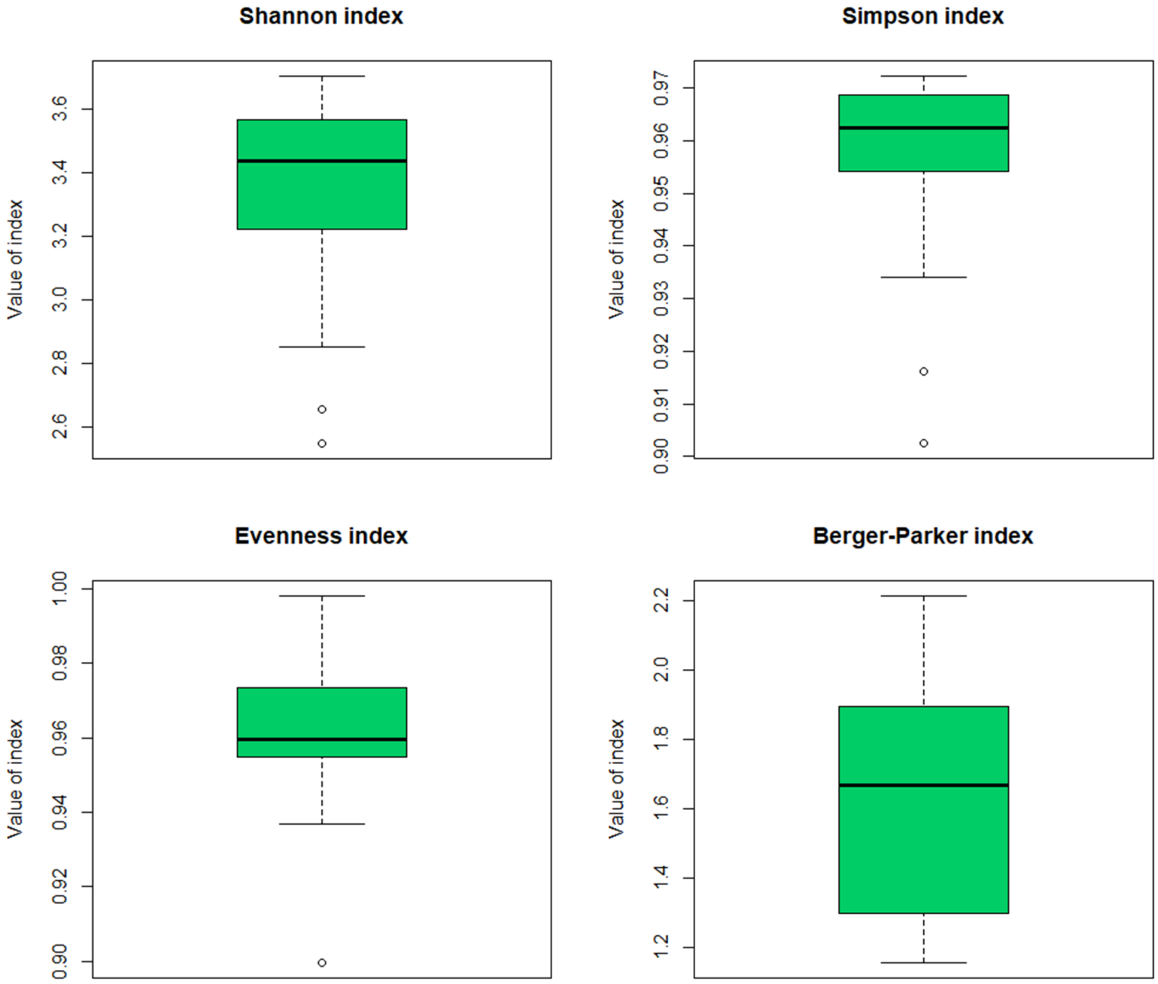


Figure 10: Stand diversity indices of the Marteloscope

The Shannon Index, Simpson diversity Index, Evennes index and Berger-Parker index were calculated for each quadrant. It is observed in Figue 10 that for the Shannon Wiener index, which expressed the richness and evenness of the species that the Shannon index of the Marteloscope range from 2.55 to 3.71 and the median value of the Shannon index is 3.43. Only 25% of Shannon index has a value of less than 3.22. This indicates abundance is distributed amongst the different species constituting the Marteloscope. Reflecting the similar results, the Simpson index range between 0.90 and 0.97 in which the median is 0.96, indicates high diversity in the study stand. Although the Shannon Wiener index also presents meaning for species evenness as species richness and evenness increase, so diversity increases, the Evenness Index, in addition, can shows a clear result of high evenness to complete evenness in the community. The result shows that the range of Evenness index calculated to lies between 0.90 and 1. The importance of the most abundant species was illustrated by the Berger-Parker species, the value of the index range from 1.156 to 2.21. The results of diversity index for each quadrant can be found in Annex 1

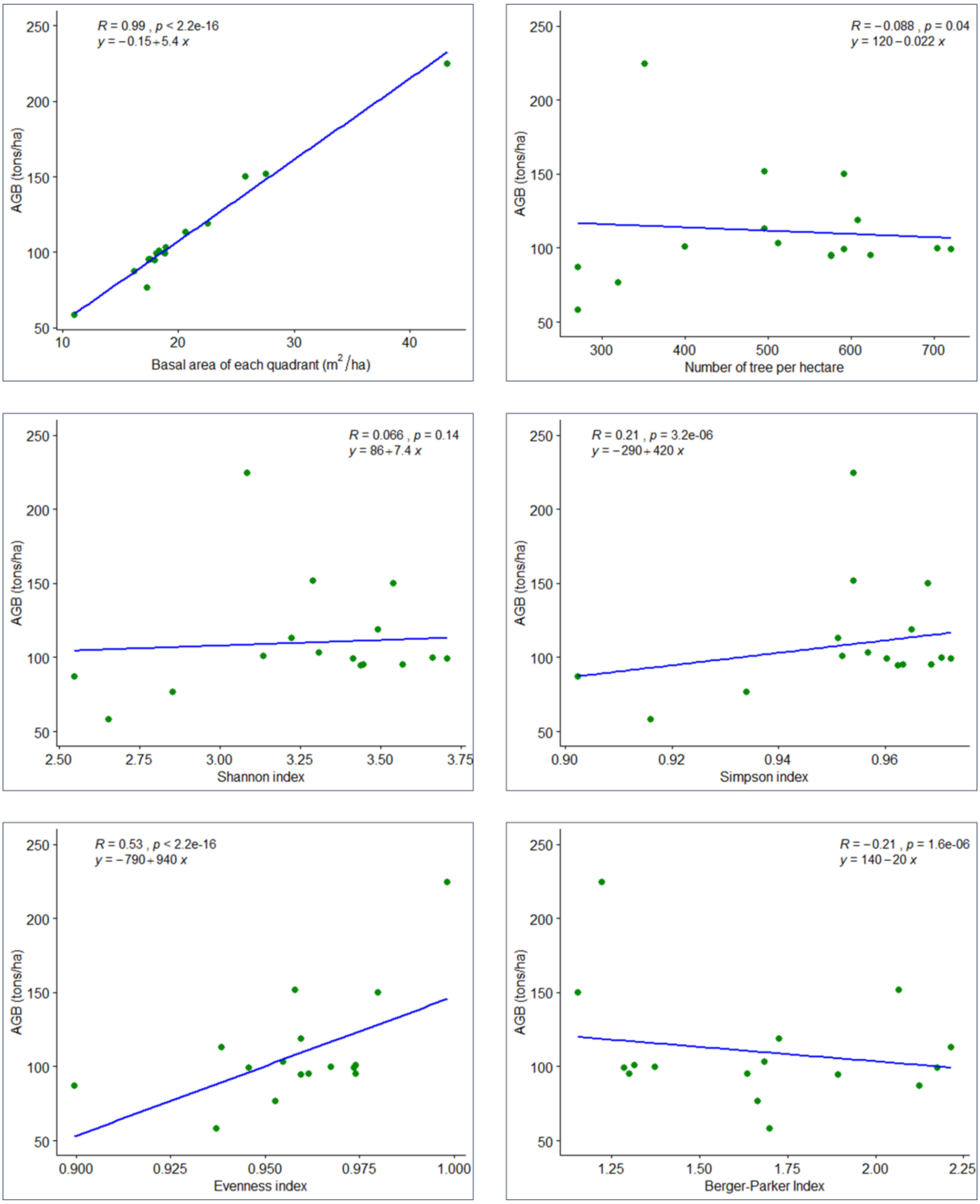


Figure 11: Above ground biomass vs stand density and stand diversity

4.3. Tree distribution pattern

4.3.1. Species Intermingling

From Figure 12, It can be observed that most of the species in the Marteloscope has a trend toward segration since the value of mostly greater than 0. For Senna siamea only located in quadrant 16 and distributed close to eachother, hence the Segregation index of this species close to one means that the reference tree is surrounded by the same species.

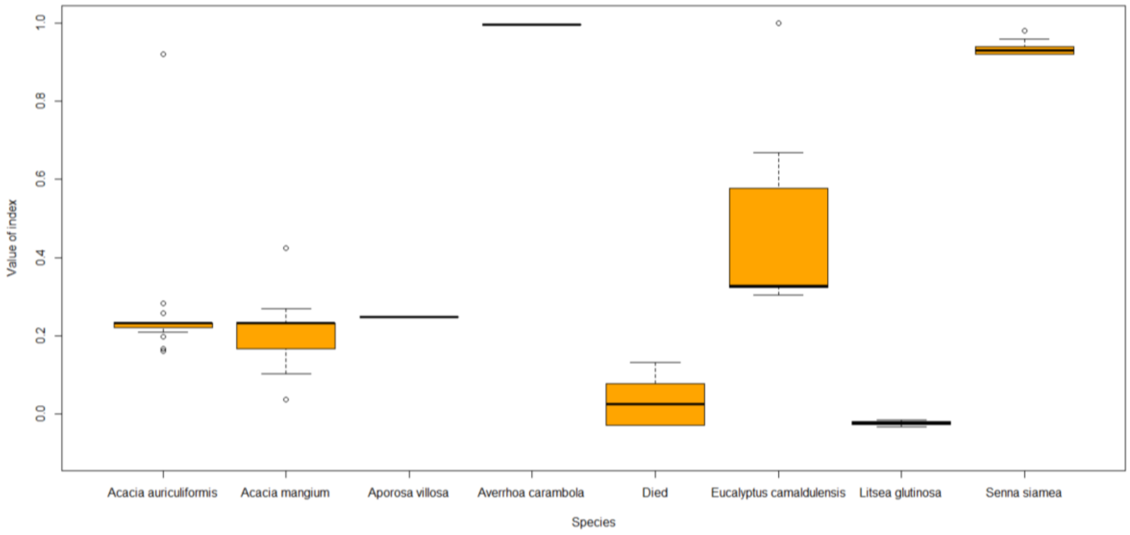


Figure 12: Segregation index for each species

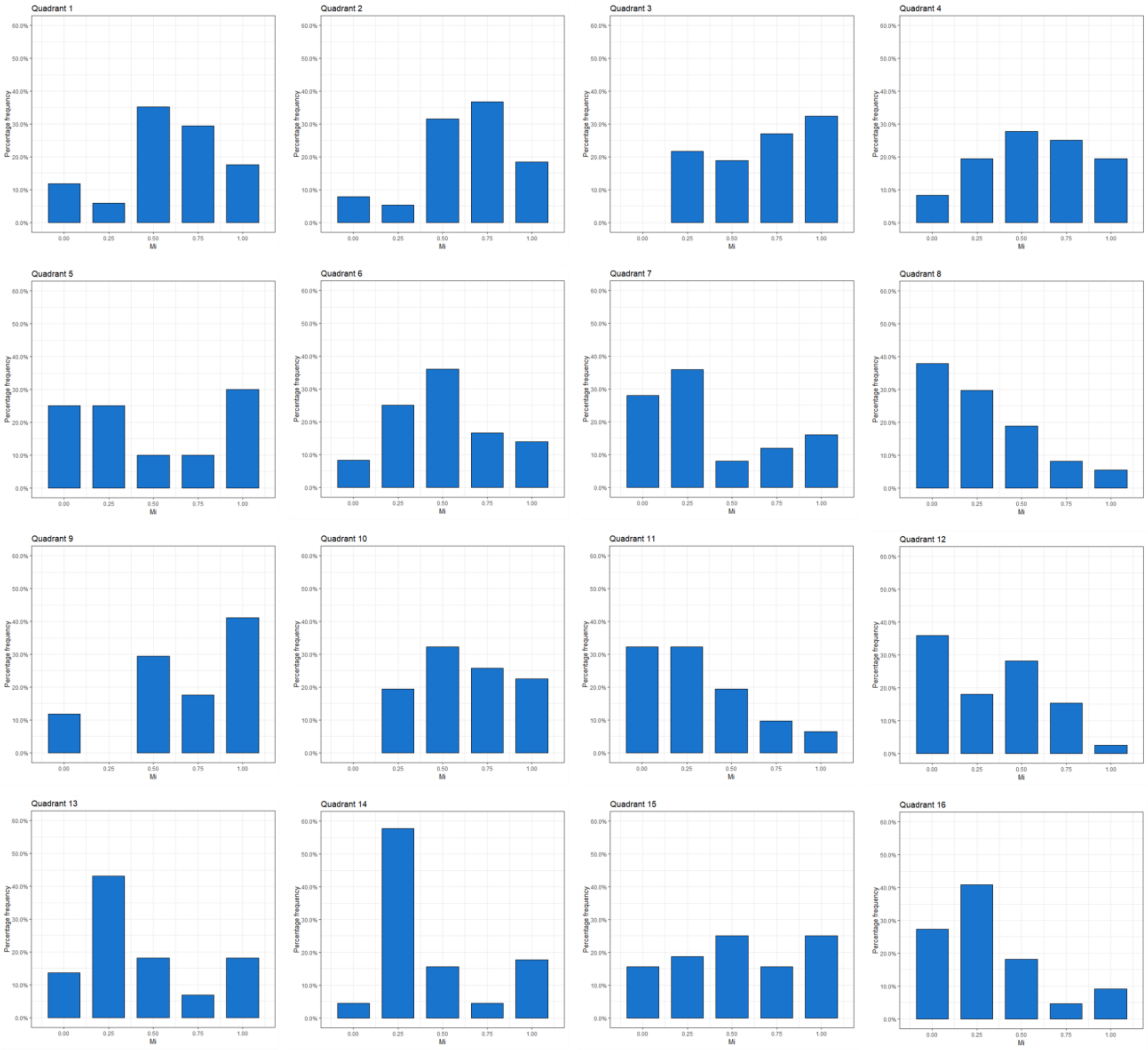


Figure 13: Percentage frequency distribution of Mingling Index (Mi) in each quadrants

The tree distribution situations depicted by Mingling index seem to have a considerable variability throughout the 16 quadrants (Figure 13). In quadrant: 2, 7, 13, 14, 16 we can see a higher component in 0.25-value class in which only two of four nearest neighbours j belongs to different species compared to the reference tree i; in other words it is indicated by a higher presence of weak mingling; or a low mixture measured at small scale. On the other hand, in some other cases (quadrants 8 and 12) small monospecific groups are more present in which the mingling index has 0-value. Generally, considering quadrant, we can notice a trend of the mingling values distribution towards monospecific groups such as quadrants in 2, 7, 8, 11, 12, 13, 14, 16; towards mean mingling such as quadrants in 1, 4, 6, 10, 15 or towards multi-specific groups such as quadrants 3, 5, 9.

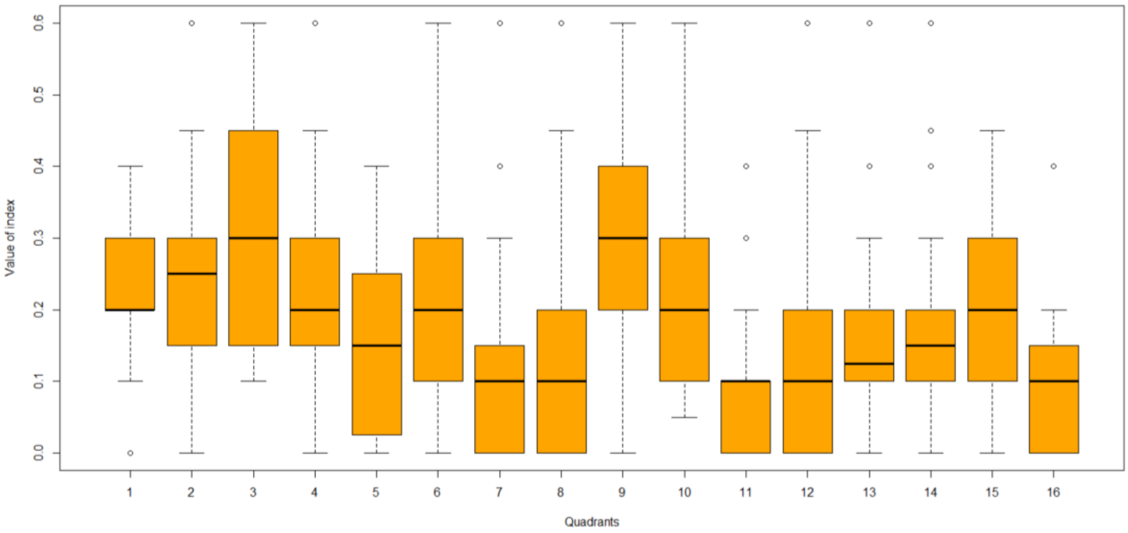


Figure 14: Spatial Diversity Index (MS_i) of each quadrant

The Spatial Diversity Index (MS_i) measures the tree species richness as well as an important spatial characteristic of each quadrant. As can be seen from Figure 14 that the reference trees in quadrant 7, 11, 13, 14 and 16 are more likely to have neighbors of the same species, which is reflected by low MS value. On the other hand, quadrant 3, 6, 9 and 10 seems to have high MS value, indicates a high diversity and as the reference trees are observed to be more likely to have neighbours of the different species.

4.3.2. Vertical Spatial Pattern

The Vertical Species profile A for 3 height zones (100-80%, 80-50%, 50-0% of the maximu height) in each quadrant were illustrated in Figure 15. It is clear that for most of the quadrant, Zone 2 which range from 80-50% of the maximum height has the highest value of A, indicates that for all quadrant, the vertical profile in zone 2 is more heterogeneous than other zones. For quadrant 9, there was no value of A in zone 1 because all trees this quadrant has the total height above 50% of the maximum height

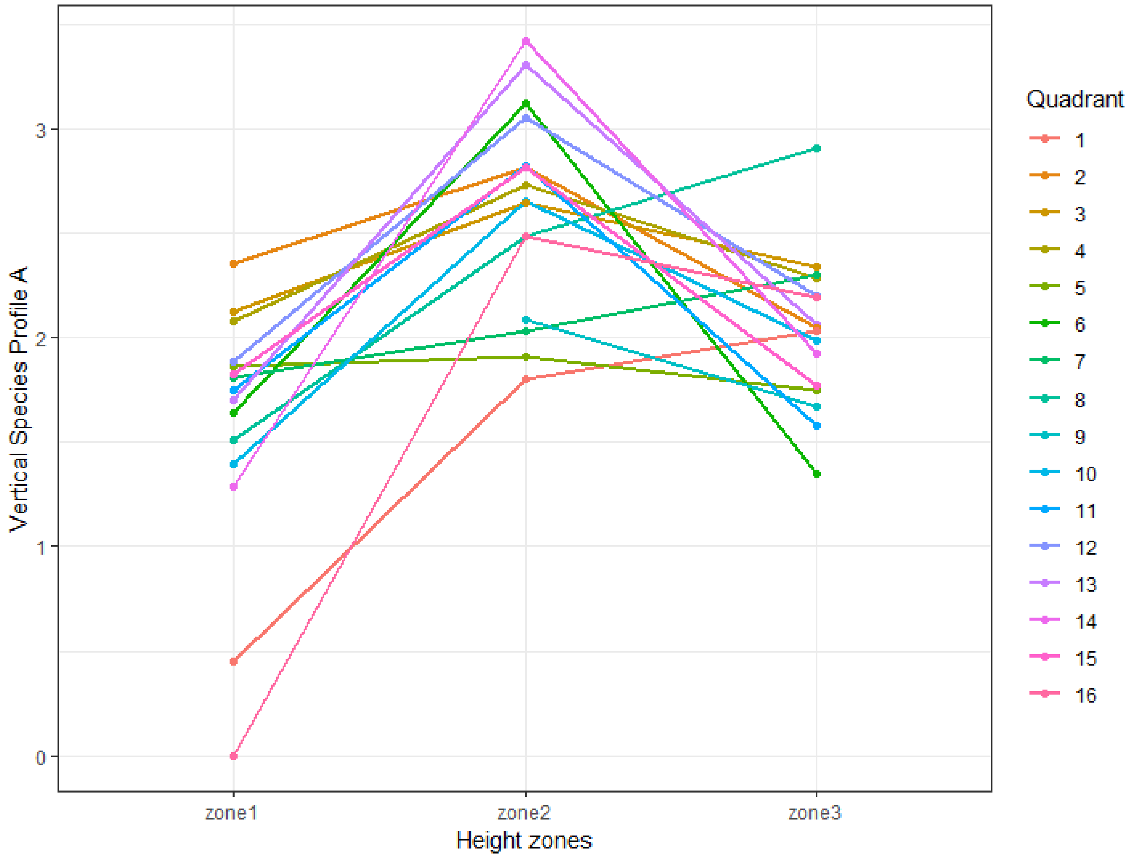


Figure 15: Vertical Species profile A for each zone in each quadrants

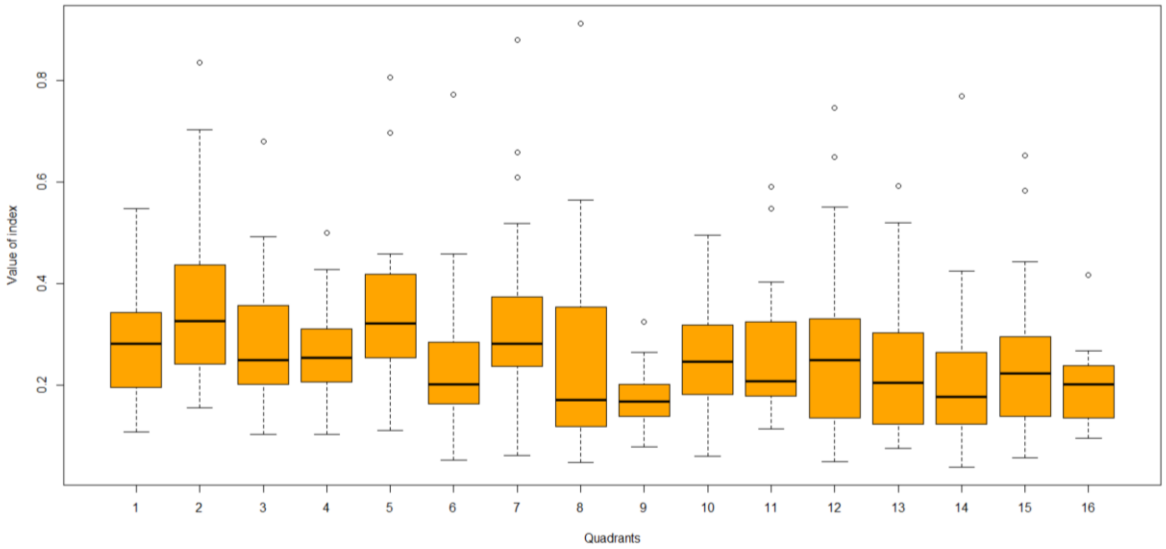


Figure 16: Height Differentiation Index (TH) in each quandrant

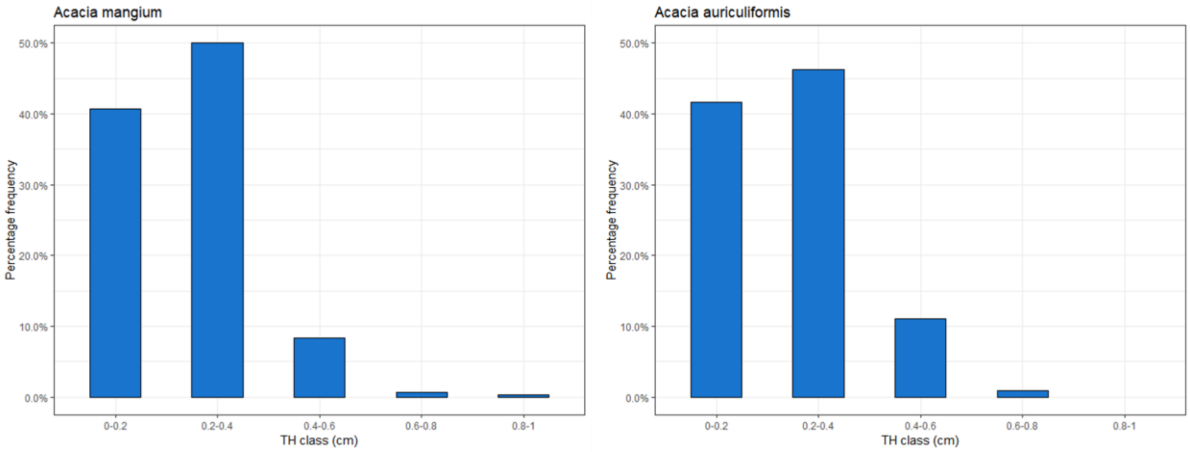


Figure 17: TH class by two most abundant species

As can be seen from Figure 16, the value of Height Differentiation Index is relatively low, although in some quadrants, the outliers with high value were observed. TH class by two most abundant species which are *Acacia auriculiformis* (108 observations) and *Acacia mangium* (300 observations) is presented in Figure 17. As can be observed for both species, more than 40% of the TH value fall between 0 to 0.2 and 0.2 to 0.4. This means that only limited height differences between neighboring trees were be observed.

4.3.3. Horizontal Spatial Pattern

According to the results presented in Figure 18, for the whole Marteloscope with clumply distributions, the L-function line slightly deviates from the expected values, which is inevident and almost invisible, and thus it is very easy to wrongly consider this L-function line as a random distribution or uniform distribution. Therefore, it is needed to have closer look at the L-funtion line in quadrant level.

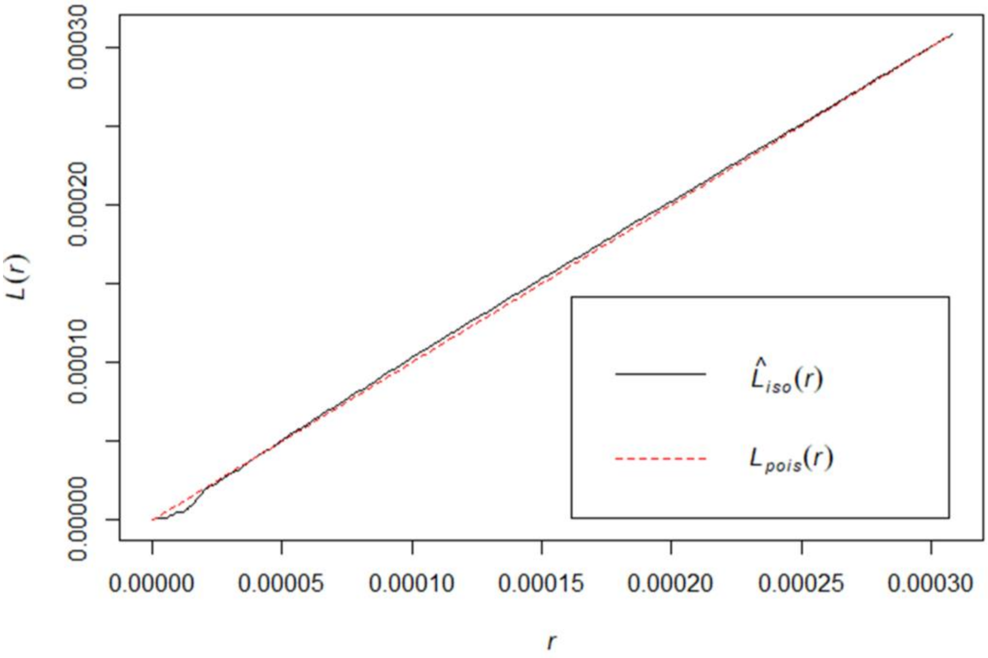


Figure 18: L – function for the whole Marteloscope

Figure 19 presents results of the 16 quadrants in the Marteloscope. The L-function line very slightly deviates from the expected values (dotted diagonal lines); for small r, the actual values are very slightly below the expected values. Althought this might indicate a uniform distribution, I would rather say that this is reflecting a random distribution since the deviation are not are not big enough to be considered as uniform distribution. For bigger r, the actual values mostly fall on the expected values, indicating random distribution. This can be observed in almost all quadrant, except for quadrants 1 and 9 which will need for a closer evaluation in Figure 19. However, the extent of the deviations is very small, so the probability of being wrongly determined distribution pattern is very high. Therefore, an extra test for distribution pattern is inneed

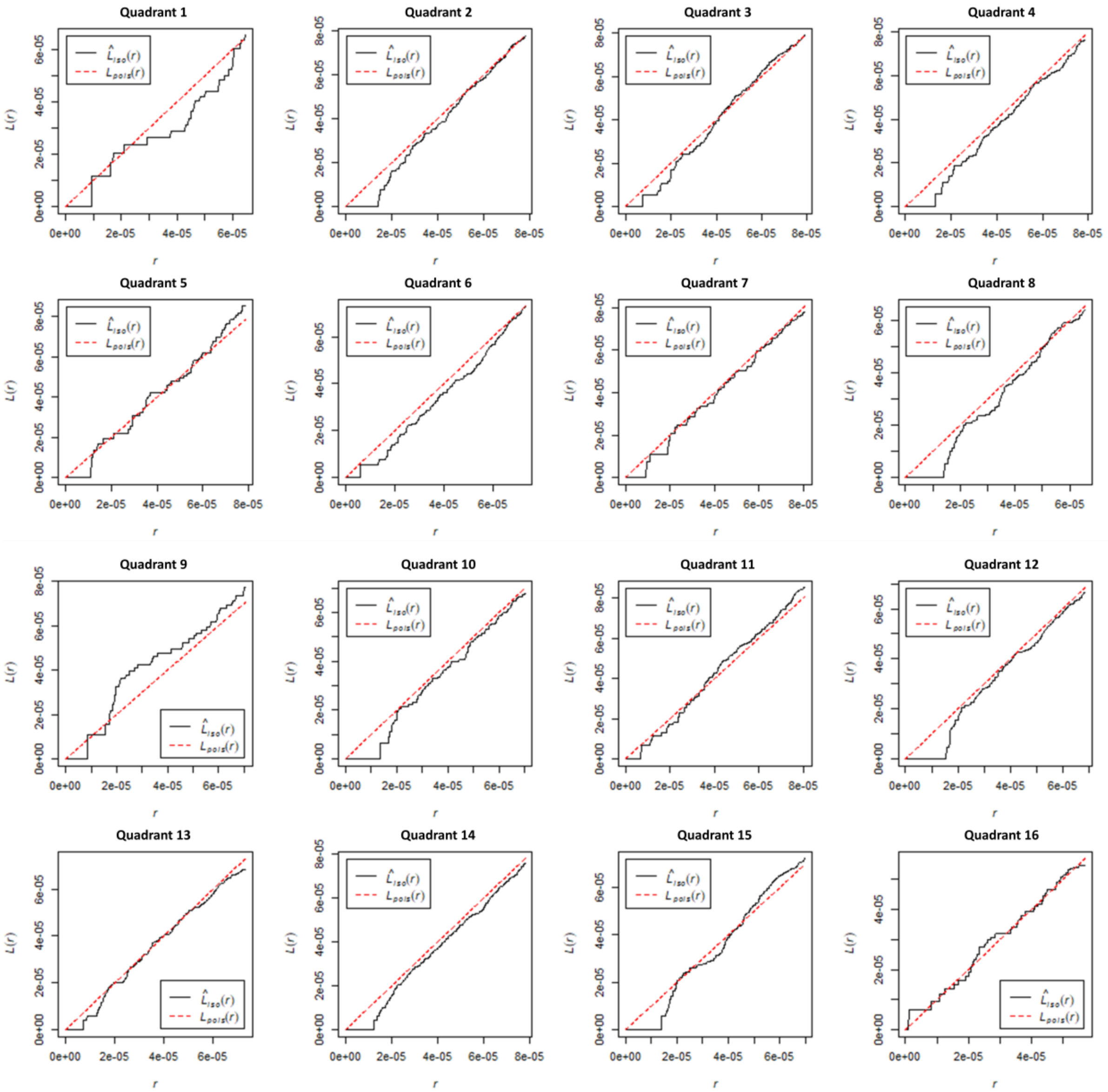


Figure 19: L – function for quandrants 1 to 16

The result from the distribution pattern test of quadrant 1 and 9 which showing random distribution in both quadrants (Figure 20). For small r around $1e - 05$, althought the actual values falls below the expected values (dotted diagonal lines) but the deviation is still very small, it was not clearly wheather this indicate random or uniform distribution.

For incresing r, the actual values in the two quadrants performed differently. While the actual line in quadrant 1 tend to fall below the expected values, the actual line in quadrant 9 falls above the expected values. However, as the deviation from the expected value is small, thus it is very easy to wrongly consider this L-function line as whether a random, uniform or clumpy distribution.

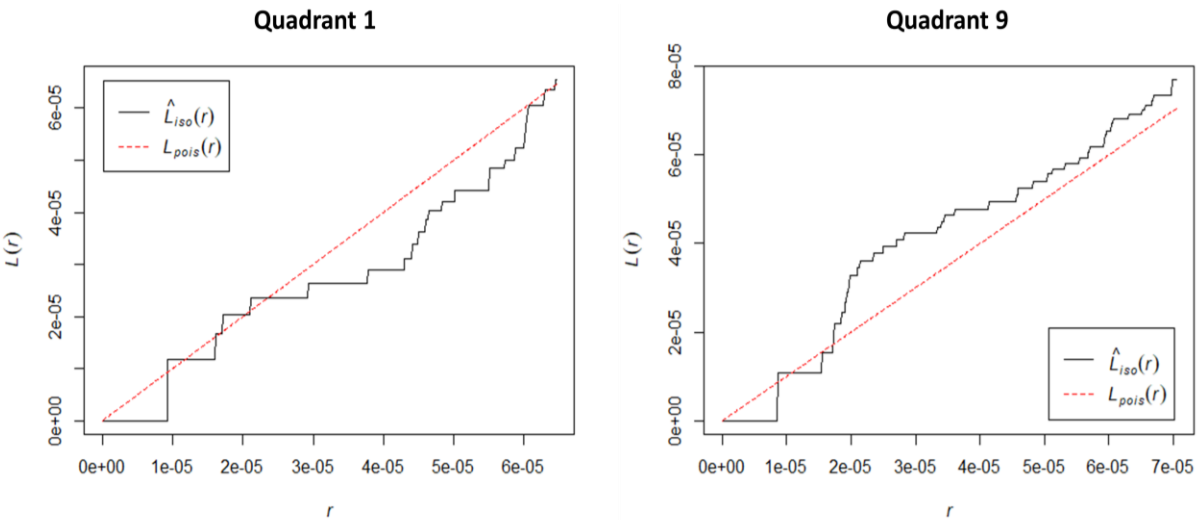


Figure 20: L – function for quandrants 1 and 9

The Clark and Evans aggregation index of the whole Marteloscope was done in R (R Core Team, 2019) and the result (Figure21) shows that the aggregation index is R=1.110826 indicates a Random distribution for the whole stand. For each quadrant, the Agrregation index range from 0.8248 to 1.199 as showed in Figure 20 which indicates that all quadrant and species in the Marteloscope has a tendency toward random distribution. The full results of Aggregation index calculated for each quadrant and species is presented in Annex 2. Although the study site is said to be a plantation acoording to the staff in Campus Hoa Lac of Vietnam National University, the result of L-function and Aggregation index indicates randon distribution for the whole Marteloscope.

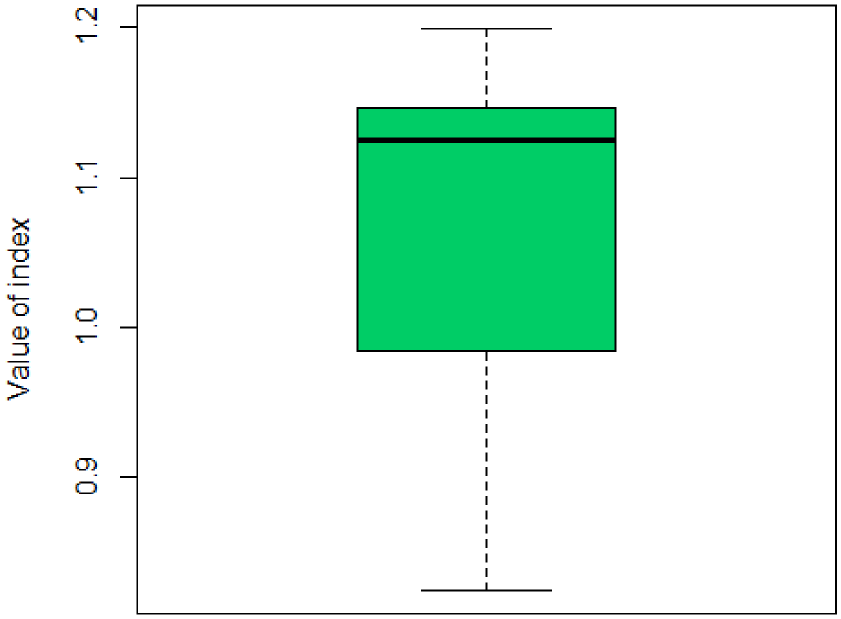


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Figure 21: Agregation index calculated for each quadrant and species

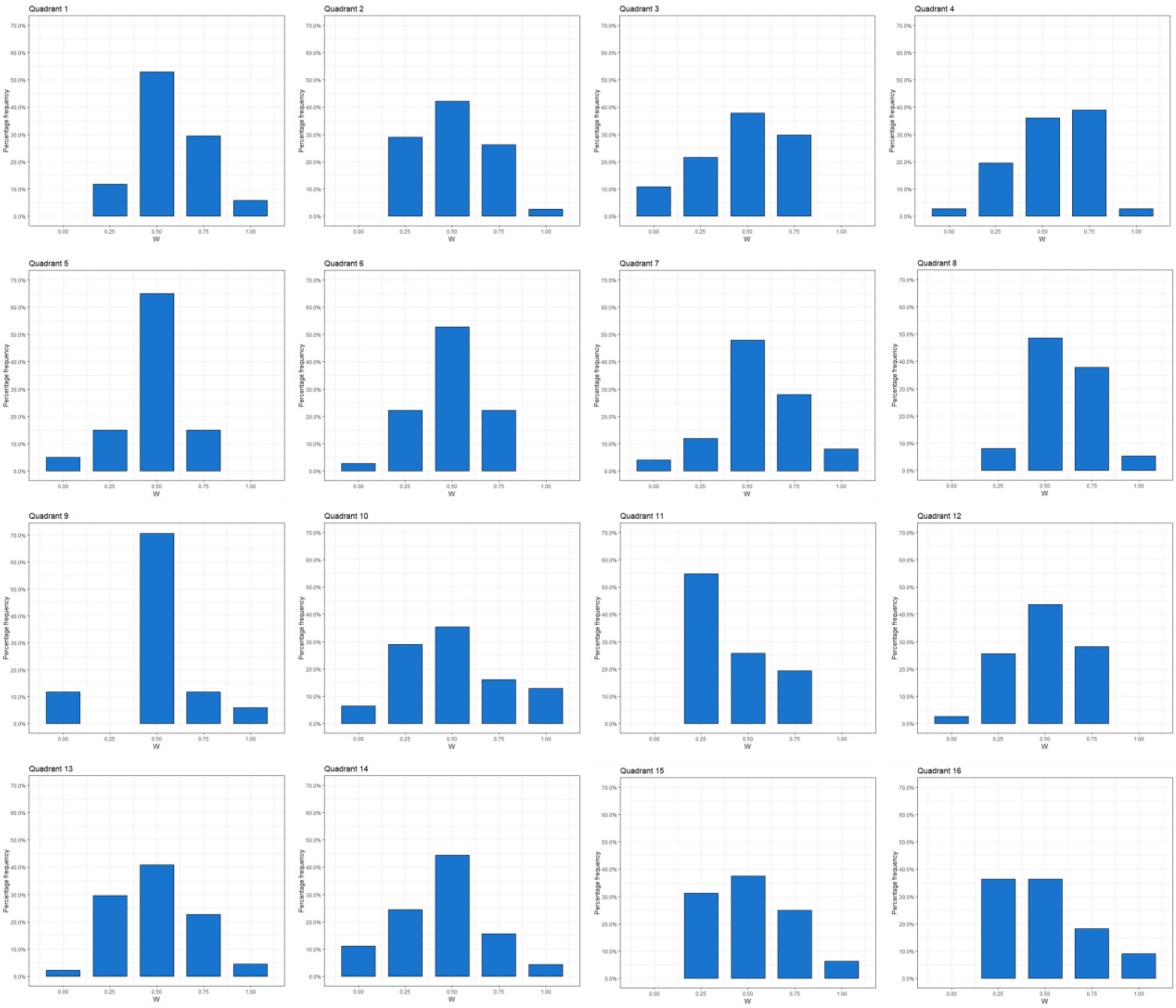

Figure 22: Percentage frequency distribution of Uniform Angle Index (W) in each quadrants

As presented in Figure 22 the percentage frequency distribution of Uniform Angle Index (W) values in each quadrant displayed in order to describe and characterize the horizontal structure and to evaluate differences in 16 quadrants in the stand. According to (Klaus v. Gadow, 1993), the random distribution (0.5 value) represents the more frequent value for most of the quadrant, except for quadrant 4 and quadrant 7. Moreover, in most quadrants, the distribution of W usually resembles a symmetric distribution. The frequency of random distribution (0.5 value) registered in each quadrant can vary, in some quadrant the amount of this distribution can have higher values (>50%) such as quadrant 1, 5, 6, 9 with values respectively of: 53%, 65%, 58%, 72%, or lower values like quadrant 10 with value of 36%, resulting in higher values for the other components. In some cases, we can appreciate the skewness of the distribution, such as the regular distribution represented in quadrant 11 the irregular distribution represented in quadrant 4. Furthermore, some quadrant can be oriented towards a regular distribution for examples quadrants 2, 10, 13, 14, 15 or towards an irregular or clumped distribution such as quadrants 3, 8, 16.

4.4. Statistical Analysis

4.4.1. Statistical analysis for *Acacia mangium*

As presented in the Figure, the value of the correlation and the bivariate scatter plots with a fitted line indicates the high correlation pairs in which the value of r is significantly and $-0.5 < r < 0.5$. Thus, the pairs which need to be avoided adding together when developing models are N-Sh, N-Sm, N-E, N-R, N-A, Sh-Sm, Sh-E, Sh-R, Sh-A, Sm-E, Sm-R, E-D, E-R, D-R and Mi-MS (Figure 23)

Various model were explored and tested, but only those that meet regression assumption such as homogeneity of variance, normality, linearity and non-autocorrelation with high goodness of fit were retained. The list 10 best fitted models is presented in Table 7, the full list of fitted equation is presented in Annex 3

For all model, the R^2 is low, indicates a weak relationship between Above ground biomass and the predictor variables. This is acceptable because these models were built in order to explain the relationship between the above-ground biomass and the species diversity, not to predict that. On comparing AIC, BIC, R^2 and MSE, model (1.1) is selected as the optimal model for explaining the relationship between tree above ground biomass and species diversity.

$$AGB = \exp(6.098 + 0.001 \times G^2 - 0.113 \times Sh^2 - 1.555 \times TH^2) \qquad \text{Model (1.1)}$$

Model (1.1) requires basal area of each quadrant, Shannon index and Height differentiation index. To have an insight on model (1.1), regression diagnostic plots of model (1.1) are presented in Figure 23 In which indicates that Residuals are almost horizontal and well spread, the spread is almost uniform and no point has excess the leverage, residuals have passed the test of Normality since it follows a Normal distribution.

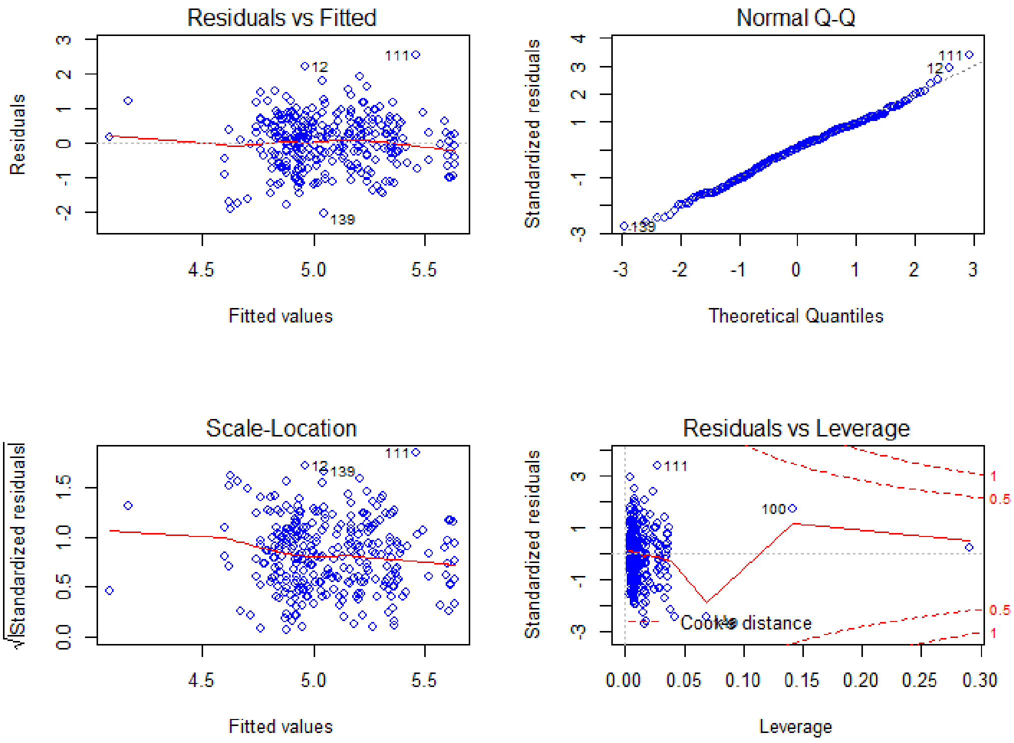

Figure 23: Regression diagnostic plots of Model (1.1)

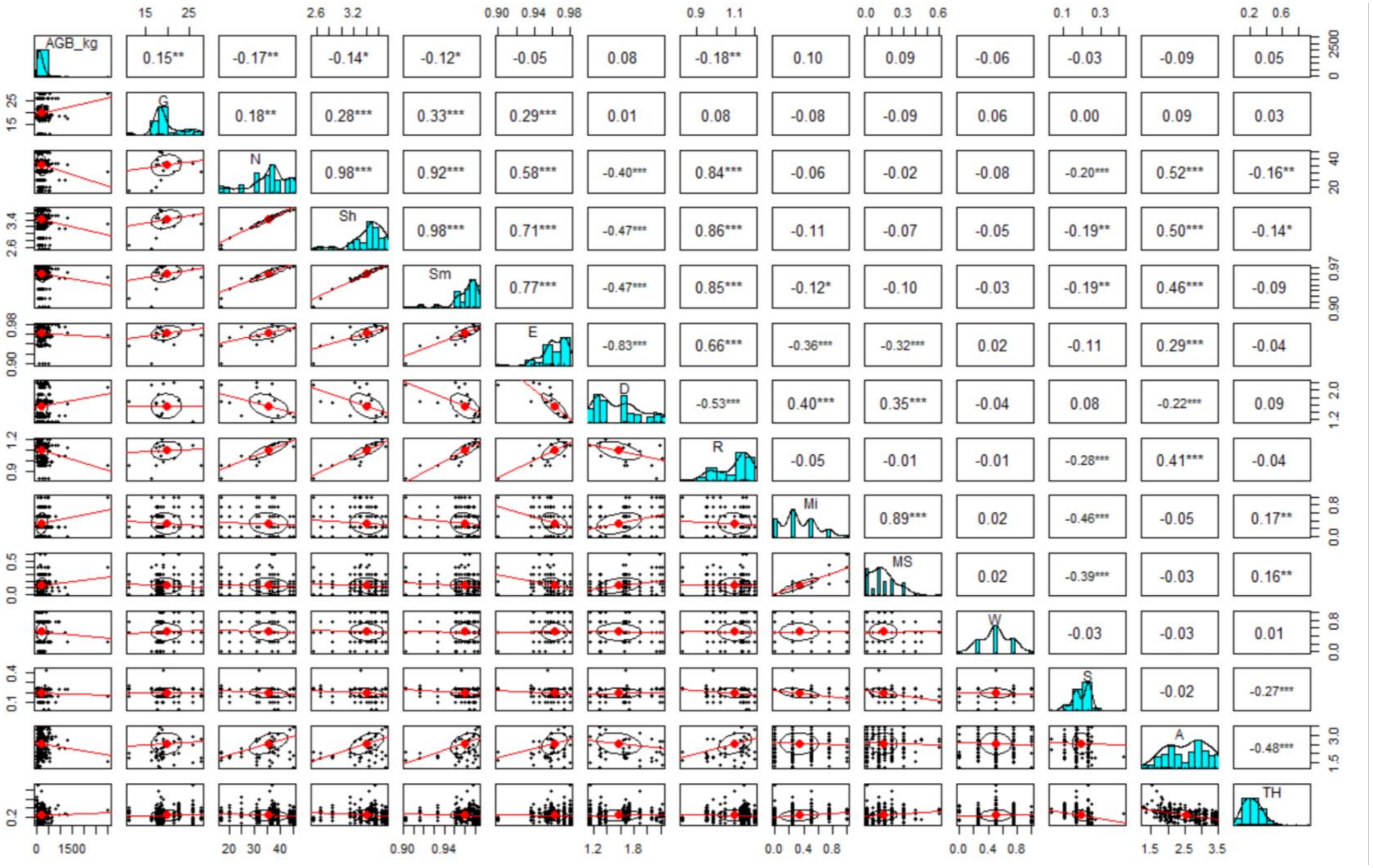

Figure 24: Pearson's correlation matrix between tree above ground biomass and input variables for *Acacia mangium* (G is basal area of each quadrant (m^2/ha); N is number of tree per hectare, Sh is Shannon index; Sm is Simpson index; E is Evenness index; D is Berger-Parker index; R is Aggregation index; Mi is Mingling index; MS is Spatial diversity status; W is Uniform Angle index; S is segregation index; A is Vertical species profile; TH is Height differentiation index; p-values(0, 0.001, 0.01, 0.05, 0.1, 1) associated with symbols("***", "**", "*", ".", " ") respectively

Table 7: 10 best fitted model for *Acacia mangium*

No.	Model	β_0	β_1	β_2	β_3	p-value	R^2	MSE	AIC	BIC
1.1	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 TH^2)$	6.098	0.001	-0.113	-1.555	<0.0001	0.096	0.575	691.506	710.025
1.2	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 TH^2)$	7.231	0.001	-0.725	-1.540	<0.0001	0.095	0.576	692.003	710.522
1.3	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 TH^2)$	9.510	0.001	-2.578	-1.532	<0.0001	0.094	0.577	692.288	710.807
1.4	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 \frac{1}{A})$	6.799	0.001	-0.137	-1.226	<0.0001	0.093	0.578	692.628	711.147
1.5	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 \frac{1}{A})$	8.164	0.001	-0.876	-1.210	<0.0001	0.092	0.578	693.140	711.659
1.6	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 \frac{1}{Sh} + \beta_3 TH^2)$	2.643	0.001	7.091	-1.506	<0.0001	0.091	0.579	693.281	711.799
1.7	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 \frac{1}{A})$	10.916	0.001	-3.117	-1.200	<0.0001	0.091	0.579	693.452	711.971
1.8	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 \frac{1}{\sqrt{A}})$	7.277	0.001	-0.137	-1.546	<0.0001	0.090	0.580	693.710	712.229
1.9	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 \frac{1}{\sqrt{A}})$	8.628	0.001	-0.876	-1.520	<0.0001	0.088	0.581	694.242	712.760
1.10	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 \frac{1}{\sqrt{A}})$	11.368	0.001	-3.112	-1.504	<0.0001	0.087	0.581	694.561	713.080

AGB is tree above ground biomass (kg); TH is Height differentiation index; Sh is Shannon index; G is basal area of each quadrant (m^2/ha); A is Vertical species profile

Sensitivity analysis of Model (1.1) was carried out by fixing basal area at different levels which are 25 m^2/ha, 21 m^2/ha, 17 m^2/ha and 13 m^2/ha and obtain the behavior of tree above ground biomass when Shannon index (Sh) and Height differentiation index (TH) varied. As can be observed from Figure 25, a negative relationship between tree above ground biomass and Species diversity were found in which the higher the value of índices, the lower the value of tree above ground biomass. Since the carbon sequestration was derived from tree above groumg biomass, the species diversity will have similar negative effect on carbon storage in *Acacia mangium.*

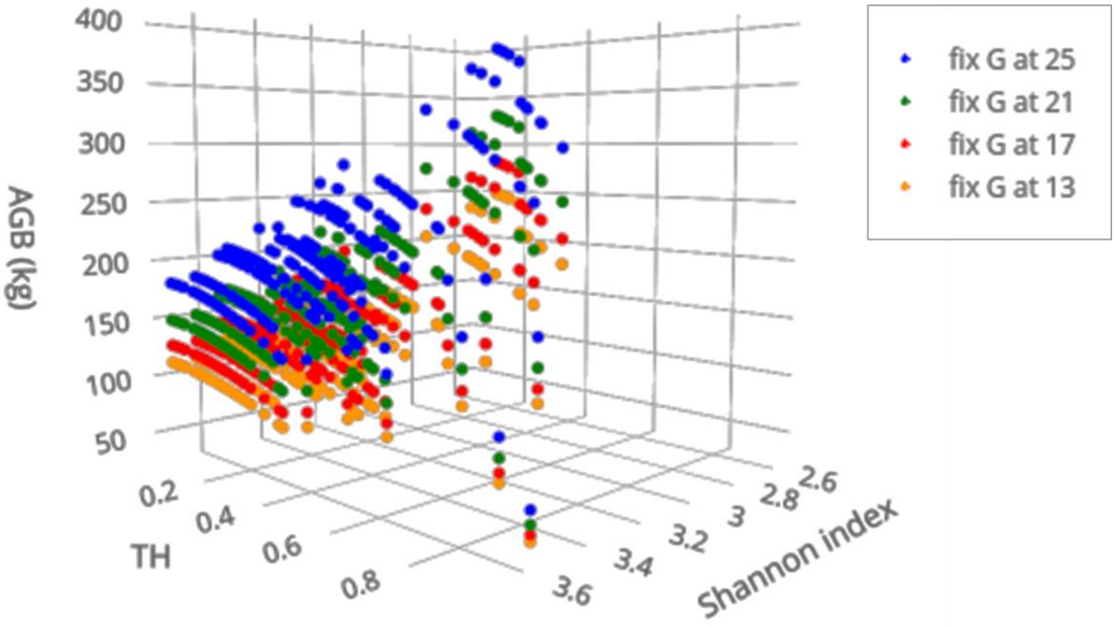

Figure 25: Sensitivity analysis 3D plot of Model (1.1) in different angles

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4.4.2. Statistical analysis for *Acacia auriculiformis*

Althought for two different species, the results of Pearson's correlation matrix (Figure26) between tree above ground biomass and input variables for *Acacia auriculiformis* is quite similar to *Acacia mangium*. Therefore, the pairs predictor variables which need to be avoided adding together when developing models are N-Sh, N-Sm, N-E, N-R, N-A, Sh-Sm, Sh-E, Sh-R, Sh-A, Sm-E, Sm-R, E-D, E-R, D-R, Mi-MS.

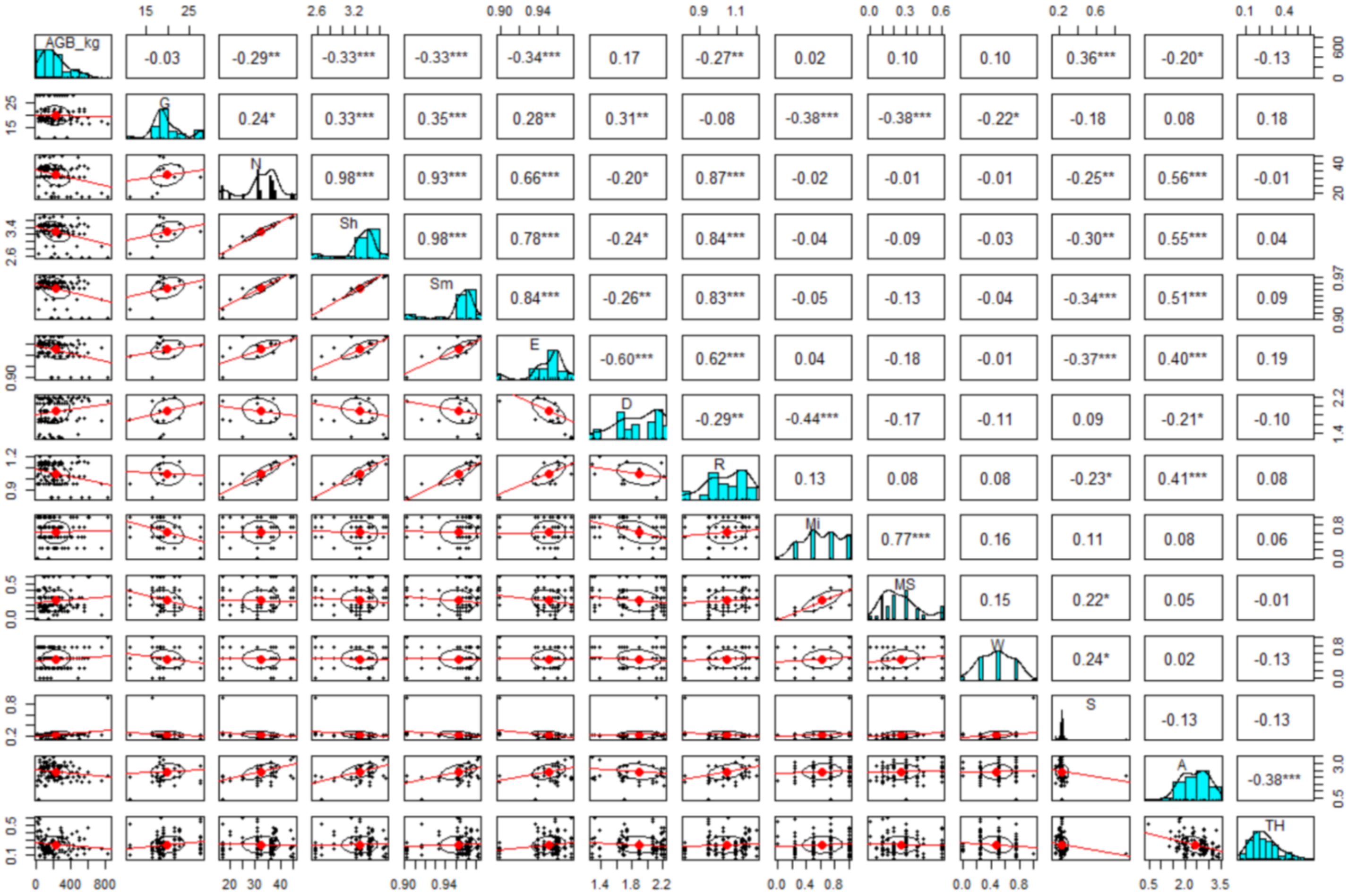

Figure 26: Pearson's correlation matrix between tree above ground biomass and input variables for *Acacia auriculiformis* (G is basal area of each quadrant (m^2/ha); N is number of tree per hectare, Sh is Shannon index; Sm is Simpson index; E is Evenness index; D is Berger-Parker index; R is Aggregation index; Mi is Mingling index; MS is Spatial diversity status; W is Uniform Angle index; S is segregation index; A is Vertical species profile; TH is Height differentiation index; p-values(0, 0.001, 0.01, 0.05, 0.1, 1) associated with symbols("***", "**", "*", ".", " ") respectively)

Table 8: 10 best fitted model for *Acacia auriculiformis*

No.	Model	β_0	β_1	β_2	R^2	p-value	MSE	AIC	BIC
2.1	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sh^2)$	6.713	-4.128	-0.125	0.170	<0.0001	0.693	271.810	282.539
2.2	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sh)$	7.875	-4.099	-0.768	0.169	<0.0001	0.693	271.870	282.599
2.3	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 \frac{1}{Sh})$	3.215	-4.041	6.951	0.167	<0.0001	0.695	272.142	282.870
2.4	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 \sqrt{N})$	7.148	-4.226	-0.315	0.166	<0.0001	0.696	272.322	283.050
2.5	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sm^2)$	11.277	-3.972	-6.527	0.166	<0.0001	0.696	272.347	283.075
2.6	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sm)$	16.961	-3.967	-12.187	0.165	<0.0001	0.697	272.389	283.118
2.7	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 N^2)$	26.771	-3.673	-21.994	0.154	<0.0001	0.706	273.818	284.546
2.8	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 \sqrt{E})$	16.128	-3.673	11.361	0.154	<0.0001	0.706	273.824	284.552
2.9	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E)$	10.805	-3.675	-6.059	0.154	<0.0001	0.706	273.838	284.567
2.10	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E^2)$	5.904	-4.295	0.000	0.162	<0.0001	0.700	272.859	283.587

AGB is tree above ground biomass (kg); TH is Height differentiation index; Sh is Shannon index; Sm is Simpson diversity index; N is number of tree per hectare; E is Evenness index

Different models were explored and tested, but only those that meet regression assumption such as homogeneity of variance, normality, linearity and non-autocorrelation with high goodness of fit were retained. The 10 best fitted models for *Acacia auriculiformis* is presented in Table 8 The full list of fitted equation is presented in Annex 4

On comparing different models by the four criteria AIC, BIC, $R^2$and MSE, Model (2.1) is optimal model to explain the relationship between tree above ground biomass and species diversity.

$$AGB = exp(6.713 - 4.128 \times TH^2 - 0.125 \times Sh^2) \qquad \text{Model (2.1)}$$

Model (2.1) requires Shannon index and Height differentiation index. Regression diagnostic plots of model (2.1) are presented in Figure 27 to have an insight on model (2.1). As can be seen from Figure 26 Residuals are almost horizontal, the spread is almost uniform and no point has excess leverage, residuals have passed the test of Normality since it follow Normal distribution although there are some outliers.

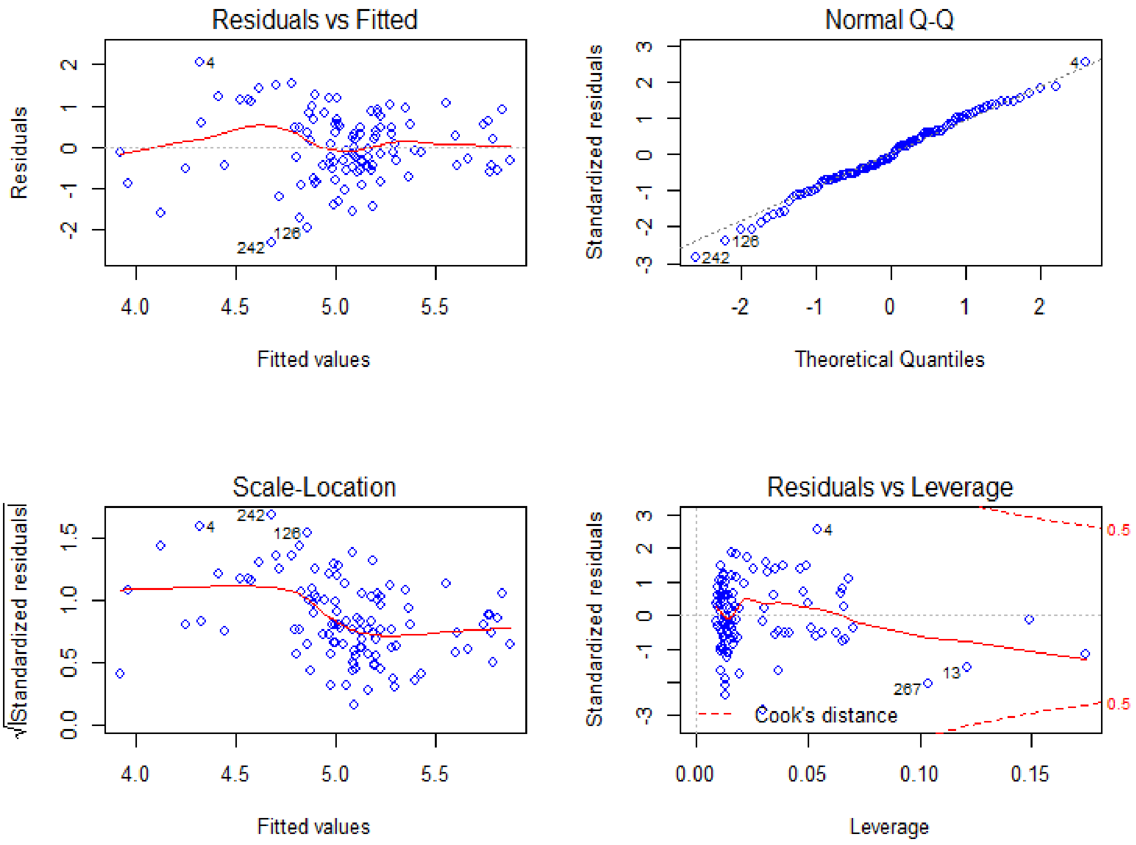

Figure 27: Regression diagnostic plots of Model (2.1)

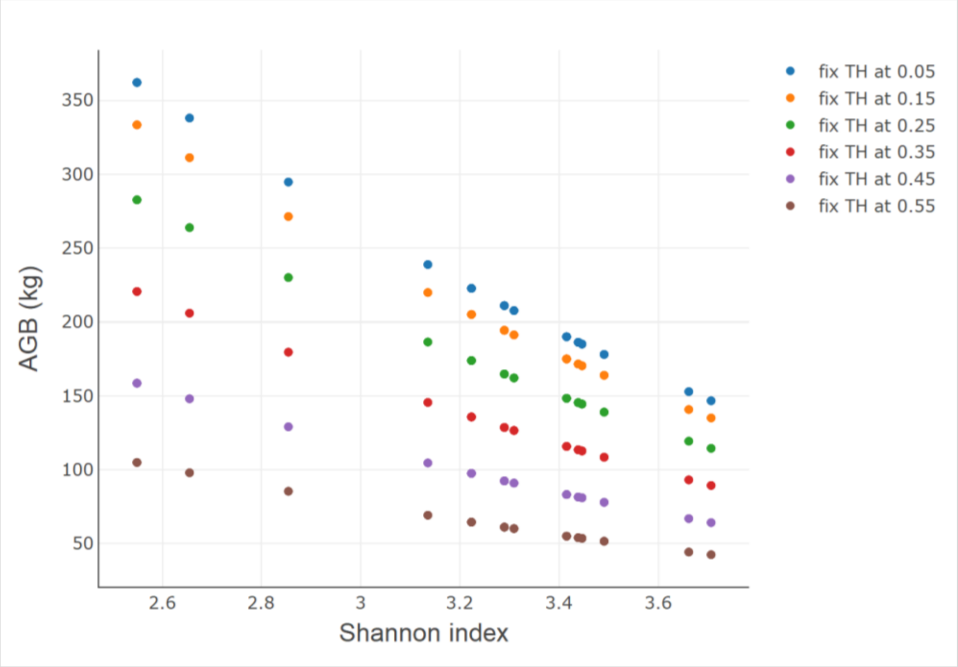

Figure 28: Sensitivity analysis plot of Model (2.1)

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The result of sensitivity annalysis for model (2.1) is presented in Figure 28 The height differentiation index (TH) were fixed at 6 levels (0.05, 0.15, 0.25, 0.35, 0.45, 0.55) in order to analyze the sensitivity of above ground biomass to the change of Shannon index. Figure 27 indicates a negative relationship between above ground biomass and species diversity in which the higher the species diversity, the lower the biomass. As the carbon sequestration was derived from tree above groumg biomass, the species diversity will have similar negative effect on carbon storage in *Acacia auriculiformis.*

5.- DISCUSSION

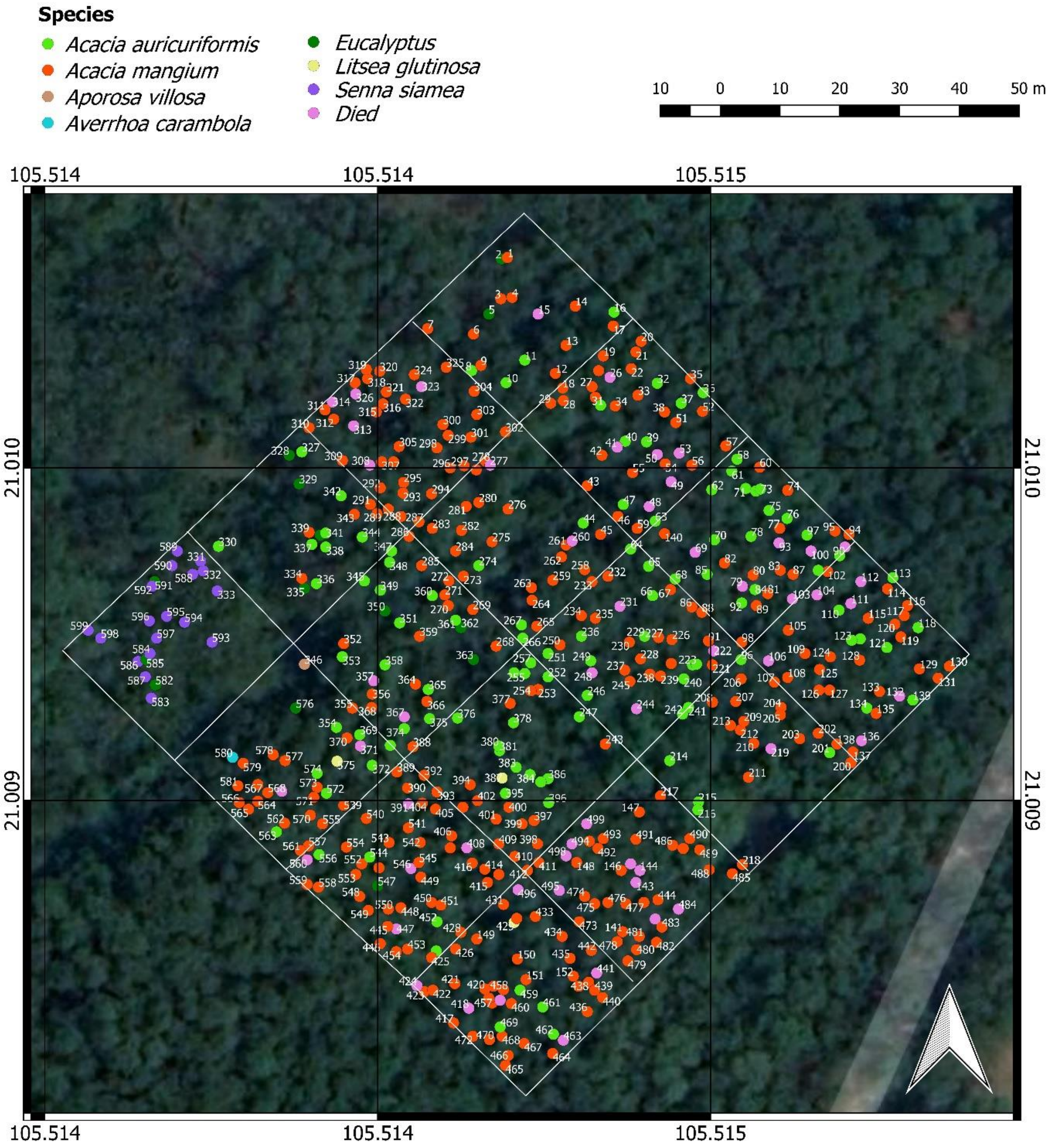

Figure 29: Distribution of Acacia species

Although the Marteloscope is confirmed to be a plantation by the staffs and managers of the Hoa Lac Campus of Vietnam National University, the value of aggregation index together with L-function calculated for the whole Marteloscope and for each quadrants indicates that, the trees distribution in the Marteloscope has a trend towards random (Poisson) distribution. It is hardly to see any clear pattern of trees distribution wheather in terms of species or quandrants or at whole stand level (Figure 28). There a possibility in consideering the historical status of the stand that some trees in the plantation died from natural events, overmature or harvested in the past which leads to the random distribution observed from this Figure 29 and also proven from the calculated trees distrbution pattern indices.

The result of Biomass calculation indicates that the total tree above ground biomass calculated by above ground biomass equations is not equal to the total above groud biomass calculated by the sum of biomass in compartments (Figure 30). This lack of additivity is a common issue in many studies due to the method used in developing biomass allometric equations.

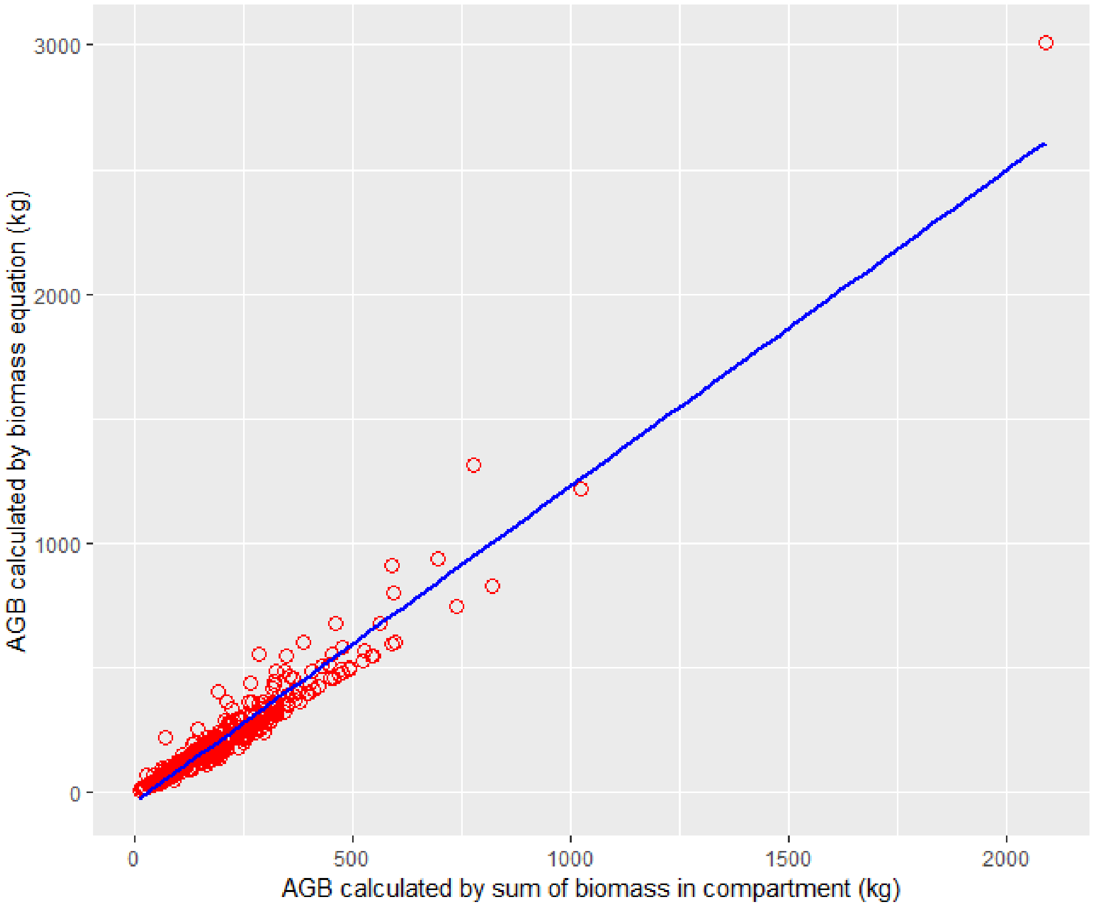

Figure 30: Relation between tree above ground calculated by biomass equations and by sum of biomass in compartments

In general, in order to estimate total biomass and compartments biomass, most studies usually regress the total tree biomass and compartments biomass such as stem, branches, leaves, and bark biomass against basic mensuration of tree attributes such as diameter at breast height (DBH) and tree total height using linear and nonlinear regression. This method was also used in (Đ. H. Nguyễn et al., 2012; Ounban et al., 2016; Phạm, 2014; Traoré et al., 2018) where the tree above ground biomass equations by compartments was adopted to calculate tree above ground biomass for *Acacia mangium, Acacia auriculiformis, Eucalyptus camadulensis,* and *Litsea glutinosa*. However, this method does not ensure that the sum of the total above ground biomass calculated from models for compartments biomass is equal to the biomass calculated from the total aboveground biomass model. This issue is called additivity which is a common issue found in many biomass or carbon allometric equations. The problem of additivity can be solved by fitting compartments models and total biomass models as a simultaneous system. Such methods ignore the inherent correlations among the component models if fitted with the ordinary least squares approach (Parresol, 1999). Hence, another method to estimate total biomass and compartments biomass is a regression-based approach in which a system of equations should be used in order to deal with the issue of non-additivity. In recent years, the popularity of the seemingly unrelated regression (SUR) and non-linear seemingly unrelated regression (NSUR) have been increasing immensely, in which various estimation methods have been proposed in order to ensure the additivity in a system of biomass equations for both linear and nonlinear models (Parresol, 2001; Ruiz-Peinado et al., 2012, 2011).

Shannon Weaver index, Simpson diversity index, Evenness index, and Berger-Parker index resulting from indices calculation indicate that the study area has high species diversity and high species evenness. For the past 10 years, various studies were carried out to insight into the effect of species richness and species diversity on productivity in the forests using data from different sources in different regions of the world (Scherer-Lorenzen et al., 2007; Vila et al., 2005; Vilà et al., 2007; Woodroffe et al., 2014)

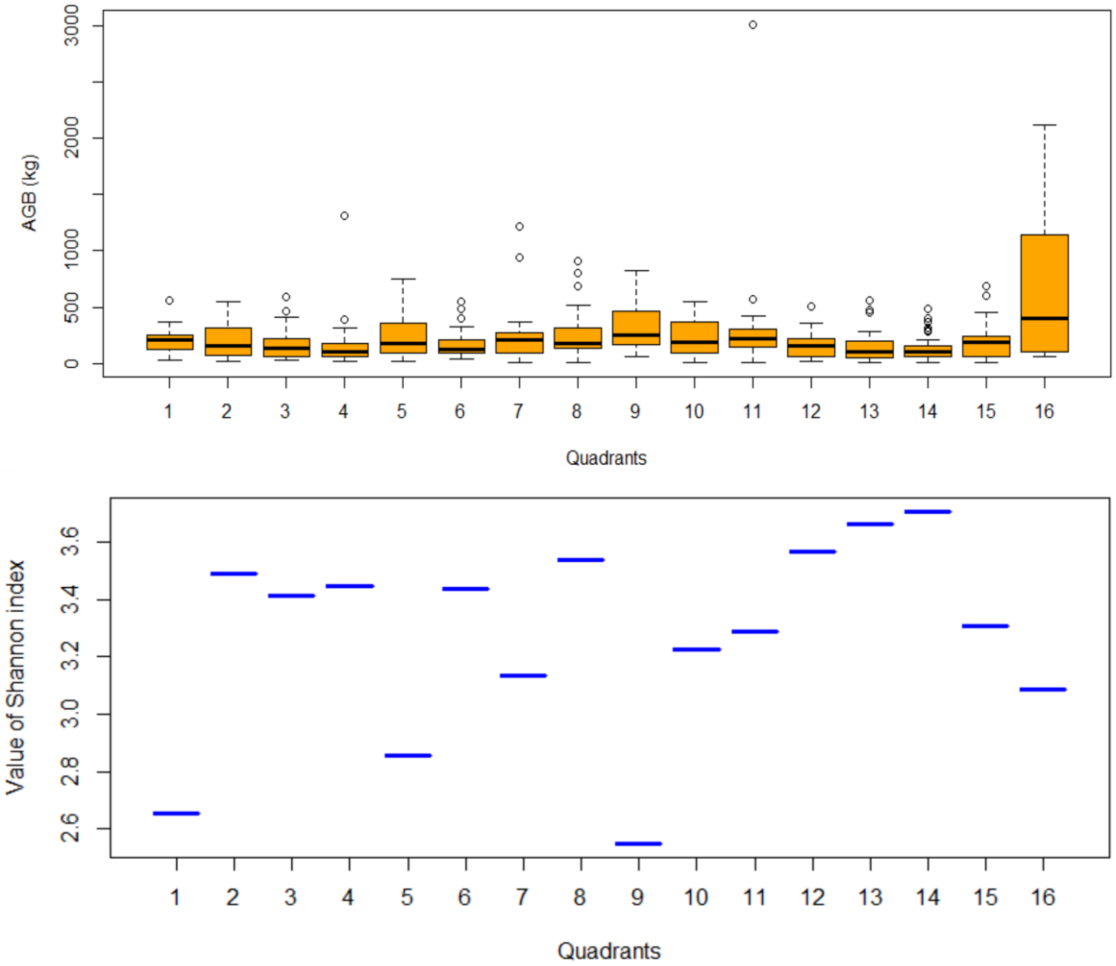

Figure 31: Tree above groud biomass and Shannon index of each quadrants

The negative relationships between species diversity and the tree above ground biomass as well as carbon sequestration in *Acacia mangium* and *Acacia auriculiformis* were indicated from the results of statistical analysis. While the statistical analysis for *Acacia mangium* was carried out with 300 observations, the number of observation for

Acacia auriculiformis was only 107. Due to the differences in the dataset for the two different species, the model forms fitted for these two species also have dissimilarities.

For both species, 3 model forms were fitted using linear regression in R (R Core Team, 2019). However, only model form II $AGB = exp(\beta_0 + \sum_{i=1}^{n} \beta_i X_i + \varepsilon)$ shows the good result in terms of regression assumption such as homogeneity of variance, normality, linearity, and non-autocorrelation with a high goodness of fit. The other two forms mostly show the none-significant relationship between fitted variables in different forms (power of 2; -1; -0.5 and 0.5). The optimal models for both species contain similar independent variables which are TH^2 and Sh^2 (power of two of Height differentiation index and Shannon index). Propaly due to the distribution of each species, the Basal area of each quadrant was inly well fitted for *Acacia mangium.*

While our results of sensitivity analysis for both models fitted for *Acacia mangium* and *Acacia auriculiformis* show that the species richness and diversity had a negative efect on tree above ground biomass and carbon sequestration, the study of (Li et al., 2018) on the relationship between species richness and aboveground biomass in a primary Pinus kesiya forest indicated a reverse result across forest strata, and widely exists in all forest vegetation strata in primary *Pinus kesiya* forests. Another interesting finding compares to the results of this study can be seen from (Day et al., 2013) in which the outcomes illustrate a complex and highly variable relationship between species diversity and above ground biomass in Central African rainforests. In this study, the effect trend of species diversity to above ground biomass varied in different locations within the study area. While some plots with high diversity had relatively low biomass, other plots with low diversity had high biomass since the study areas located in different forest types, and the conditions of the plots were also different in terms of management designations, altitudinal and climate conditions. However, despite this variability, the author claimed that, in general, there was evidence of a positive relationship between biomass and species diversity. This is similar with the general relation ship observed from Figure 30. The similar results were found for a positive correlation between above ground biomass and species richness/ diversity in (Liang et al., 2016; Zhang et al., 2015, 2017). The differencies in outcomes of our study compare to others might be cecause of the effect from the covariation of the number of tree species with other variables such as stand age, environmental factors, species complementary and so on

The result from the calculation of species Evenness index indicates that the species have equal abundance in the study area. Although Evenness index was included in the model development process, the results show that it was not able to address the clearer the relationship between Evenness and tree above ground biomass. Despite this fact, the Shannon index which accounts for both abundance and evenness of the species were successfully showed the negative correlations with tree above ground biomass. On the other hand, in the study of (Zhang et al., 2012), species evenness together with species richness was found to be able to explain the productivity of forest.

Carbon sequestration in forests has been acknowledged to perform the main role to reduce the effect of global climates changes. It has been studied that, depending on different conditions of the forest stand, forest structure, species composition, stand age, etc., the unmanaged forest may store a larger amount of carbon than a forest under management (Krug et al., 2012; Pukkala, 2017). However, carbon sequestration is usually not the only objective in forest management designation. Additionally, the managers also take into account biodiversity conservation, possible ecosystem services and other products provided by the forest systems when considering adequate the management regimes. (Bellassen & Luyssaert, 2014; Ruiz-peinado et al., 2017) indicates that well-managed forests are able to hold as much carbon as unmanaged forests.

The study area embraces 110.66 tons/ha of tree aboveground biomass and 55.33 tons/ha of carbon which is considered as a large amount of carbon sequestration. In Vietnam, it is obvious that positive relationship between species diversity and tree above ground biomass/ carbon concentration will have an important impact on management policy designations and implementation since it would support the assertion in which the REDD+ schemes can provide extraordinary co-benefits for biodiversity conservation. However, for the cases of negative correlation, there would be many trade-offs between biodiversity conservation and biomass accumulation/ carbon sequestration.

6. - CONCLUSION

1. Tree above ground biomass by compartments was calculated using different developed biomass equations and the carbon sequestration was derived from tree above ground biomass. The results show that the study area embraces 110.66 tons/ha of tree aboveground biomass and 55.33 tons/ha of carbon.
2. For each tree, different measures of tree diversity and mixture around it were computed to estimate species richness & diversity, species intermingling, and tree distribution pattern (vertical and horizontal). The result shows that the study area has high species diversity with relatively high evenness. Although the study area is confirmed to be a plantation the results from functions and indices for depicting the horizontal spatial patterns indicate that the distribution of trees in the Marteloscope follows a trend towards random (Poisson) distribution.
3. The relationship between above ground tree biomass and species diversity were examined by regression analysis using a set of parameters for the characterization of mixed stand structure include stand density and diversity, species intermingling, horizontal and vertical tree distribution pattern. As a result, a negative relationship between above ground tree biomass and species diversity was obtained from the outcomes of optimum model sensitivity analysis. Such relationship was not common when compared to other studies and would lead to many trade-offs between biodiversity conservation and biomass accumulation/ carbon sequestration.

7.- AKNOWLEDGES

I would like to extend thanks to the many people who so generously contributed to the work presented in this thesis.

Firstly, I would like to express my sincere gratitude to my supervisors Professor Felipe Bravo Oviedo from University of Valladolid and Professor Vu Van Manh from Vietnam National University - University of Sciences for their patience and the continuous support of my study.

Besides my supervisors, I would like to express my thanks and sincere to Irene Ruano, Cristóbal Ordóñez, Narangarav Dugarsuren, people and other students in ETS Agricultural Engineering University of Valladolid for their assistance and supports in many aspects of the study.

A special thank goes to the professors, staffs and students in Vietnam National University - University of Sciences who have been involved in the planning, establishment, and measurement of the Marteloscope in the framework of the BioEcoN project. The study has been made possible through the BioEcoN project financed by the Erasmus+, Capacity Building in the Field of Higher Education.

Finally, but by no means least, my deep appreciation to my family and friends for providing me with unconditionally support and continuous encouragement throughout my years of study.

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ANNEX

Annex 1: Species diversity índices of each quadrant

Quadrant	Simpson Index (1-D)	Shannon Index (H')	Berger – Parker Index (D)	Evenness Index (E)
1.	0.92	2.65	1.70	0.94
2.	0.97	3.49	1.73	0.96
3.	0.96	3.41	2.18	0.95
4.	0.96	3.45	1.64	0.96
5.	0.93	2.85	1.67	0.95
6.	0.96	3.44	1.89	0.96
7.	0.95	3.14	1.32	0.97
8.	0.97	3.54	1.16	0.98
9.	0.90	2.55	2.12	0.90
10.	0.95	3.22	2.21	0.94
11.	0.95	3.29	2.07	0.96
12.	0.97	3.57	1.30	0.97
13.	0.97	3.66	1.38	0.97
14.	0.97	3.71	1.29	0.97
15.	0.96	3.31	1.68	0.96
16.	0.95	3.09	1.22	1.00

Annex 2: Aggregation indices of each quadrant

Quadrant	R	p- value at quadrant level	p- value at species level	Distribution
1	0.9494	0.460	0.464	Random
2	1.1597	0.940	0.950	Random
3	1.1402	0.918	0.921	Random
4	1.1244	0.880	0.896	Random
5	0.9529	0.427	0.451	Random
6	1.0935	0.829	0.820	Random
7	1.0483	0.689	0.683	Random
8	1.1466	0.920	0.911	Random
9	0.8248	0.209	0.236	Random
10	1.0243	0.642	0.620	Random
11	0.9506	0.410	0.392	Random
12	1.1714	0.959	0.957	Random
13	1.1994	0.989	0.971	Random
14	1.1326	0.922	0.914	Random
15	0.9845	0.472	0.496	Random
16	0.9166	0.347	0.320	Random

Annex 3: Model fitted for *Acacia mangium* (*** indicates p-value>0.05)

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
1	$AGB = \exp(\beta_0 + \beta_1 G^2)$	4.7825	0.0007	-	-	0.0185	0.0184	0.6208	712.4091	723.4394
2	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_1 TH)$	7.3467	0.0010	-0.7307	-0.8128	0.0848	<0.0001	0.5828	695.5585	713.8733
3	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 TH^2)$	7.2306	0.0011	-0.7249	-1.5399	0.0950	<0.0001	0.5763	692.2072	710.5220
4	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 A)$	7.1542	0.0010	-0.8513	0.1614***	0.0796	<0.0001	0.5861	697.2402	715.5551
5	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 A^{-1})$	8.1637	0.0010	-0.8762	-1.2104	0.0915	<0.0001	0.5785	693.3443	711.6591
6	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 A^{-0.5})$	8.6284	0.0010	-0.8756	-1.5201	0.0882	<0.0001	0.5806	694.4456	712.7604
7	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 A^{0.5})$	6.7268	0.0010	-0.8624	0.5543	0.0822	<0.0001	0.5845	696.4167	714.7315
8	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 TH)$	6.2092	0.0010	-0.1145	-0.8278	0.0864	<0.0001	0.5818	695.0438	713.3587
9	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 TH^2)$	6.0982	0.0011	-0.1135	-1.5549	0.0965	<0.0001	0.5754	691.7097	710.0246
10	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 TH^{0.5})$	6.3253	0.0010	-0.1137	-0.6727***	0.0808	<0.0001	0.5853	696.8537	715.1686
11	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 A)$	5.8155	0.0010	-0.1339	0.1673***	0.0813	<0.0001	0.5850	696.6837	714.9986
12	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 A^{-1})$	6.7986	0.0010	-0.1370	-1.2259	0.0931	<0.0001	0.5775	692.8318	711.1466
13	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 A^{-0.5})$	7.2766	0.0010	-0.1370	-1.5461	0.0898	<0.0001	0.5796	693.9139	712.2287
14	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 A^{0.5})$	5.3581	0.0010	-0.1354	0.5703	0.0839	<0.0001	0.5834	695.8627	714.1775
15	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{-1} + \beta_3 TH)$	2.7219	0.0011	7.1321	-0.7787	0.0808	<0.0001	0.5853	696.8636	715.1784
16	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{-1} + \beta_3 TH^2)$	2.6432	0.0011	7.0914	-1.5056	0.0911	<0.0001	0.5788	693.4847	711.7995
17	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{-1} + \beta_3 A^{-1})$	2.6016	0.0011	8.5640	-1.1598	0.0871	<0.0001	0.5813	694.8019	713.1168
18	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{-1} + \beta_3 A^{-0.5})$	3.0485	0.0011	8.5309	-1.4403	0.0837	<0.0001	0.5835	695.9285	714.2434
19	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{-0.5} + \beta_3 TH)$	0.4288***	0.0011	8.1146	-0.7877	0.0819	<0.0001	0.5846	696.5051	714.8199
20	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{-0.5} + \beta_3 TH^2)$	0.3642***	0.0011	8.0638	-1.5147	0.0922	<0.0001	0.5781	693.1320	711.4468
21	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{-0.5} + \beta_3 A^{-1})$	-0.1484***	0.0011	9.7449	-1.1748	0.0884	<0.0001	0.5805	694.3862	712.7010
22	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{-0.5} + \beta_3 A^{-0.5})$	0.3134***	0.0011	9.7154	-1.4635	0.0849	<0.0001	0.5827	695.5086	713.8234
23	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 TH)$	9.6399	0.0011	-2.5972	-0.8048	0.0839	<0.0001	0.5834	695.8514	714.1662
24	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 TH^2)$	9.5096	0.0011	-2.5781	-1.5319	0.0941	<0.0001	0.5769	692.4921	710.8070
25	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 A^{-1})$	10.9158	0.0010	-3.1168	-1.2001	0.0906	<0.0001	0.5791	693.6558	711.9706
26	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 A^{-0.5})$	11.3680	0.0010	-3.1122	-1.5035	0.0872	<0.0001	0.5812	694.7653	713.0802

No.	Model	$\boldsymbol{\beta_0}$	$\boldsymbol{\beta_1}$	$\boldsymbol{\beta_2}$	$\boldsymbol{\beta_3}$	$\boldsymbol{R^2}$	$\boldsymbol{p-value}$	MSE	AIC	BIC
27	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 A^{0.5})$	9.4419	0.0010	-3.0605	0.5447	0.0812	<0.0001	0.5851	696.7431	715.0579
28	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sm + \beta_3 TH^2)$	17.0535	0.0011	-12.8270	-1.4467	0.0865	<0.0001	0.5817	694.9976	713.3124
29	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sm + \beta_3 A^{-1})$	19.9613	0.0011	-15.4751	-1.0862	0.0821	<0.0001	0.5845	696.4492	714.7640
30	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sm^2 + \beta_3 TH^2)$	11.0233	0.0011	-6.8155	-1.4502	0.0869	<0.0001	0.5814	694.8539	713.1687
31	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sm^2 + \beta_3 A^{-1})$	12.6941	0.0011	-8.2280	-1.0934	0.0826	<0.0001	0.5842	696.2700	714.5848
32	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sm^{-1} + \beta_3 TH^2)$	-7.0746	0.0011	11.3370	-1.4395	0.0856	<0.0001	0.5823	695.2957	713.6105
33	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sm^{-1} + \beta_3 A^{-1})$	-9.1332	0.0011	13.6576	-1.0710	0.0809	<0.0001	0.5852	696.8225	715.1373
34	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sm^{-0.5} + \beta_3 TH^2)$	-19.1368	0.0011	23.3904	-1.4413	0.0858	<0.0001	0.5821	695.2199	713.5347
35	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sm^{-0.5} + \beta_3 A^{-1})$	-23.6738	0.0011	28.1890	-1.0749	0.0812	<0.0001	0.5851	696.7273	715.0421
36	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 Sm^{0.5} + \beta_3 TH^2)$	29.1157	0.0011	-24.8800	-1.4449	0.0863	<0.0001	0.5818	695.0708	713.3856
37	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 R + \beta_3 A^{-1})$	7.9404	0.0007	-2.4646	-1.0738	0.0833	<0.0001	0.5837	696.0472	714.3621
38	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 TH^2)$	5.9971	0.0008	-0.9482	-1.3476	0.0853	<0.0001	0.5824	695.3755	713.6904
39	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 A^{-1})$	6.6610	0.0007	-1.1723	-1.0808	0.0838	<0.0001	0.5834	695.8917	714.2065
40	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 A^{-0.5})$	7.0065	0.0007	-1.1523	-1.2851	0.0796	<0.0001	0.5861	697.2393	715.5541
41	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 R^{-1} + \beta_3 TH^2)$	2.8930	0.0008	2.1244	-1.3144	0.0829	<0.0001	0.5840	696.1674	714.4822
42	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 R^{-1} + \beta_3 A^{-1})$	2.8049	0.0007	2.6326	-1.0465	0.0813	<0.0001	0.5850	696.7005	715.0154
43	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 R^{-0.5} + \beta_3 TH^2)$	0.8254***	0.0008	4.1983	-1.3202	0.0835	<0.0001	0.5836	695.9850	714.2998
44	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 R^{-0.5} + \beta_3 A^{-1})$	0.2455***	0.0007	5.2033	-1.0552	0.0819	<0.0001	0.5846	696.4892	714.8041
45	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 R^{0.5} + \beta_3 TH^2)$	9.0981	0.0008	-4.0630	-1.3315	0.0844	<0.0001	0.5830	695.6848	713.9996
46	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 R^{0.5} + \beta_3 A^{-1})$	10.5015	0.0007	-5.0336	-1.0688	0.0829	<0.0001	0.5840	696.1646	714.4795
47	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S + \beta_3 N^{0.5})$	6.6692	0.0010	-1.3504***	-0.2890	0.0770	<0.0001	0.5877	698.0938	716.4087
48	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S + \beta_3 Sh)$	7.3886	0.0010	-1.3266***	-0.7225	0.0754	<0.0001	0.5888	698.6171	716.9319
49	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S + \beta_3 Sh^2)$	6.2547	0.0010	-1.3300***	-0.1126	0.0765	<0.0001	0.5881	698.2724	716.5872
50	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^2 + \beta_3 N)$	5.7205	0.0009	-2.3115***	-0.0257	0.0748	<0.0001	0.5892	698.8291	717.1439
51	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^2 + \beta_3 N^2)$	5.3710	0.0008	-2.3064***	-0.0004	0.0763	<0.0001	0.5882	698.3208	716.6356
52	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 N^{-1})$	3.7821	0.0011	0.0411	21.1331	0.0799	<0.0001	0.5859	697.1657	715.4806
53	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 N^{-0.5})$	3.0159	0.0010	0.0414	8.2389	0.0823	<0.0001	0.5844	696.3759	714.6907
54	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 N^{0.5})$	6.1869	0.0009	0.0415	-0.2908	0.0861	<0.0001	0.5820	695.1331	713.4479

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
55	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 Sh)$	6.9181	0.0010	0.0411	-0.7272	0.0844	<0.0001	0.5830	695.6768	713.9916
56	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 Sh^2)$	5.7754	0.0010	0.0411	-0.1132	0.0854	<0.0001	0.5824	695.3526	713.6674
57	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 Sh^{-1})$	2.2963	0.0011	0.0410	7.1867	0.0815	<0.0001	0.5849	696.6217	714.9366
58	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 Sh^{-0.5})$	-0.0026***	0.0011	0.0411	8.1512	0.0824	<0.0001	0.5843	696.3494	714.6642
59	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 Sh^{0.5})$	9.2166	0.0010	0.0411	-2.5927	0.0838	<0.0001	0.5834	695.8762	714.1911
60	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 Sm)$	17.1570	0.0011	0.0410	-13.2659	0.0787	<0.0001	0.5867	697.5447	715.8596
61	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 Sm^2)$	10.9139	0.0011	0.0410	-7.0419	0.0791	<0.0001	0.5864	697.4252	715.7400
62	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 Sm^{-0.5})$	-20.3068	0.0011	0.0409	24.2259	0.0781	<0.0001	0.5870	697.7313	716.0461
63	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 Sm^{0.5})$	29.6443	0.0011	0.0410	-25.7437	0.0785	<0.0001	0.5868	697.6060	715.9208
64	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 R)$	6.9775	0.0008	0.0480	-2.2594	0.0852	<0.0001	0.5825	695.4151	713.7299
65	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 R^2)$	5.8000	0.0008	0.0482	-1.0742	0.0857	<0.0001	0.5822	695.2735	713.5883
66	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 R^{-1})$	2.2780	0.0008	0.0473	2.4205	0.0835	<0.0001	0.5836	695.9809	714.2957
67	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 R^{-0.5})$	-0.0753***	0.0008	0.0475	4.7792	0.0840	<0.0001	0.5833	695.7997	714.1146
68	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 R^{0.5})$	9.3305	0.0008	0.0479	-4.6167	0.0849	<0.0001	0.5827	695.5186	713.8334
69	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 N)$	5.1113	0.0009	0.2349	-0.0266	0.0856	<0.0001	0.5823	695.2859	713.6008
70	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 N^{-1})$	3.4650	0.0011	0.2318	21.2774	0.0780	<0.0001	0.5871	697.7722	716.0870
71	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 N^{-0.5})$	2.6893	0.0010	0.2340	8.2981	0.0805	<0.0001	0.5855	696.9694	715.2843
72	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 N^{0.5})$	5.8811	0.0010	0.2356	-0.2930	0.0844	<0.0001	0.5831	695.7008	714.0156
73	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 Sh)$	6.6213	0.0010	0.2329	-0.7326	0.0827	<0.0001	0.5841	696.2557	714.5705
74	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 Sh^2)$	5.4705	0.0010	0.2327	-0.1141	0.0837	<0.0001	0.5835	695.9266	714.2414
75	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 Sh^{-1})$	1.9676	0.0011	0.2318	7.2387	0.0797	<0.0001	0.5860	697.2119	715.5268
76	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 Sh^{-0.5})$	-0.3489***	0.0011	0.2323	8.2106	0.0806	<0.0001	0.5855	696.9366	715.2514
77	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 Sh^{0.5})$	8.9368	0.0010	0.2329	-2.6118	0.0820	<0.0001	0.5845	696.4578	714.7726
78	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 R)$	6.6253	0.0008	0.2779	-2.2857	0.0835	<0.0001	0.5836	695.9650	714.2798
79	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 R^2)$	5.4321	0.0008	0.2792	-1.0866	0.0840	<0.0001	0.5833	695.8272	714.1420
80	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 R^{-1})$	1.8770	0.0008	0.2736	2.4489	0.0818	<0.0001	0.5847	696.5271	714.8419
81	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 R^{-0.5})$	-0.5058***	0.0008	0.2749	4.8353	0.0824	<0.0001	0.5843	696.3462	714.6611
82	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 R^{0.5})$	9.0070	0.0008	0.2771	-4.6707	0.0832	<0.0001	0.5838	696.0670	714.3818

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
83	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 W^{0.5})$	4.5269	0.0008	0.1547***	-0.1629***	0.0260	0.0503	0.6202	714.2445	732.5594
84	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 N)$	6.2233	0.0009	-1.3010***	-0.0265	0.0807	<0.0001	0.5854	696.9102	715.2251
85	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 N^2)$	5.8520	0.0008	-1.2800***	-0.0004	0.0820	<0.0001	0.5846	696.4775	714.7923
86	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 N^{0.5})$	6.9897	0.0010	-1.3005***	-0.2915	0.0793	<0.0001	0.5863	697.3516	715.6664
87	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 Sh)$	7.7106	0.0010	-1.2800***	-0.7286	0.0776	<0.0001	0.5873	697.8910	716.2058
88	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 Sh^2)$	6.5665	0.0010	-1.2811***	-0.1135	0.0787	<0.0001	0.5867	697.5502	715.8651
89	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 Sh^{0.5})$	10.0113	0.0010	-1.2779***	-2.5970	0.0770	<0.0001	0.5877	698.0975	716.4123
90	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 R)$	7.9374	0.0008	-1.5861	-2.2596	0.0775	<0.0001	0.5874	697.9394	716.2542
91	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 R^2)$	6.7635	0.0008	-1.5933	-1.0738	0.0779	<0.0001	0.5872	697.8191	716.1339
92	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 R^{-1})$	3.2197	0.0008	-1.5583***	2.4226	0.0759	<0.0001	0.5884	698.4557	716.7706
93	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 R^{-0.5})$	0.8701***	0.0008	-1.5671***	4.7826	0.0764	<0.0001	0.5881	698.2877	716.6026
94	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 R^{0.5})$	10.2886	0.0008	-1.5810	-4.6182	0.0772	<0.0001	0.5876	698.0313	716.3462
95	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 E^2 + \beta_3 TH^2)$	8.7756	0.0010	-4.3151	-1.3031	0.0579	0.0005	0.5999	704.2526	722.5675
96	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 E^{-1} + \beta_3 TH^2)$	-2.9025***	0.0010	7.3909	-1.2988	0.0578	0.0005	0.6000	704.2863	722.6012
97	$AGB = \exp(\beta_0 + \beta_1 G^2 + \beta_2 E + \beta_3 TH^2)$	12.6732	0.0010	-8.2034	-1.3017	0.0579	0.0005	0.5999	704.2597	722.5746
98	$AGB = \beta_0 + \beta_1 G^2$	111.2538	0.2704	-	-	0.0285	0.0033	53980.7767	4124.3525	4135.3828
99	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 Mi$	572.0256	0.3456	-152.8159	90.8462***	0.0721	0.0001	51905.6872	4114.6954	4133.0102
100	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 Mi^2$	539.9327	0.3368	-141.0055	139.5531	0.0804	<0.0001	51442.9412	4112.0089	4130.3237
101	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh + \beta_3 MS^2$	589.5807	0.3393	-152.6341	477.4073***	0.0717	0.0001	51930.7666	4114.8403	4133.1551
102	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 Mi$	332.5423	0.3395	-23.8261	89.7512***	0.0727	0.0001	51876.7194	4114.5279	4132.8427
103	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 Mi^2$	318.7797	0.3312	-21.9799	138.2643	0.0808	<0.0001	51420.7839	4111.8796	4130.1944
104	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh^2 + \beta_3 MS^2$	350.3588	0.3333	-23.8198	472.7873***	0.0723	0.0001	51898.3246	4114.6528	4132.9677
105	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh^{-1} + \beta_3 Mi^2$	-354.5409	0.3463	1385.7435	142.2634***	0.0790	<0.0001	51520.2270	4112.4592	4130.7741
106	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh^{-0.5} + \beta_3 Mi$	-879.8592	0.3538	1707.2342	92.4724***	0.0710	0.0001	51971.4281	4115.0751	4133.3899
107	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh^{-0.5} + \beta_3 Mi^2$	-799.2580	0.3442	1574.7164	141.5787	0.0794	<0.0001	51496.8729	4112.3232	4130.6380
108	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 Mi$	1053.9582	0.3485	-544.3562	91.3939***	0.0718	0.0001	51924.6429	4114.8049	4133.1198
109	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 Mi^2$	984.6544	0.3394	-502.2726	140.2196	0.0801	<0.0001	51458.1630	4112.0976	4130.4124
110	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sh^{0.5} + \beta_3 MS^2$	1070.5672	0.3421	-543.4282	479.6880***	0.0713	0.0001	51951.5602	4114.9604	4133.2752

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
111	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sm + \beta_3 Mi^2$	2423.7656	0.3436	-2465.7444	140.1278	0.0761	<0.0001	51682.1758	4113.4008	4131.7156
112	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sm^2 + \beta_3 Mi^2$	1265.4259	0.3432	-1311.0766	139.8578	0.0763	<0.0001	51670.7236	4113.3343	4131.6491
113	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sm^{-1} + \beta_3 Mi^2$	-2210.8547	0.3443	2175.9214	140.6728	0.0757	<0.0001	51706.1088	4113.5397	4131.8545
114	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sm^{-0.5} + \beta_3 Mi^2$	-4527.8443	0.3441	4491.1863	140.5360	0.0758	<0.0001	51699.9997	4113.5042	4131.8190
115	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 Sm^{0.5} + \beta_3 Mi^2$	4740.7572	0.3438	-4780.9377	140.2635	0.0760	<0.0001	51688.0321	4113.4348	4131.7496
116	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R + \beta_3 Mi$	612.0602	0.2944	-494.8133	96.6393	0.0763	<0.0001	51673.8089	4113.3522	4131.6670
117	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R + \beta_3 Mi^2$	589.8170	0.2895	-468.0241	147.3425	0.0856	<0.0001	51152.9359	4110.3128	4128.6277
118	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R + \beta_3 (Mi+1)^{-1}$	764.2193	0.2944	-506.2785	-137.5924***	0.0719	0.0001	51917.5119	4114.7637	4133.0786
119	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R + \beta_3 (Mi+1)^{-0.5}$	878.5821	0.2945	-503.9158	-255.2357***	0.0728	0.0001	51867.7028	4114.4758	4132.7906
120	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R + \beta_3 Mi^{0.5}$	629.8858	0.2954	-511.1425	65.6077***	0.0715	0.0001	51940.1676	4114.8946	4133.2094
121	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R + \beta_3 MS$	630.3659	0.2951	-506.7116	203.4404***	0.0742	<0.0001	51788.7944	4114.0190	4132.3339
122	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R + \beta_3 MS^2$	634.8697	0.2881	-498.5333	522.3695	0.0765	<0.0001	51663.3592	4113.2915	4131.6064
123	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R + \beta_3 (MS+1)^{-1}$	889.1875	0.2957	-509.8489	-256.4631***	0.0727	0.0001	51875.3379	4114.5199	4132.8348
124	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R + \beta_3 (MS+1)^{-0.5}$	1119.5123	0.2956	-509.0726	-487.5323***	0.0731	0.0001	51853.3233	4114.3926	4132.7074
125	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 Mi$	354.0280	0.2936	-234.7952	96.3161***	0.0764	<0.0001	51666.1757	4113.3079	4131.6227
126	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 Mi^2$	346.0359	0.2887	-222.4186	147.3346	0.0858	<0.0001	51140.6807	4110.2410	4128.5558
127	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 (Mi+1)^2$	499.3140	0.2935	-240.1425	-136.7070	0.0720	0.0001	51910.8371	4114.7252	4133.0400
128	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 (Mi+1)^{-0.5}$	614.3543	0.2936	-239.0379	-253.8009***	0.0729	0.0001	51860.9062	4114.4365	4132.7513
129	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 Mi^{0.5}$	363.3159	0.2945	-242.3958	65.1171***	0.0716	0.0001	51934.0030	4114.8590	4133.1738
130	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 MS$	366.1669	0.2942	-240.5168	202.9551***	0.0744	<0.0001	51779.1996	4113.9634	4132.2783
131	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 MS^2$	375.1126	0.2873	-236.8561	522.6159	0.0767	<0.0001	51650.3901	4113.2162	4131.5310
132	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 (MS+1)^{-1}$	622.3858	0.2948	-241.9470	-255.5205***	0.0728	0.0001	51866.5425	4114.4691	4132.7839
133	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 (MS+1)^{-0.5}$	852.4364	0.2948	-241.5919	-485.9069***	0.0732	0.0001	51844.3548	4114.3407	4132.6555
134	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 MS^{0.5}$	368.2703	0.2954	-244.8714	97.1280***	0.0710	0.0001	51967.4510	4115.0522	4133.3670
135	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^2 + \beta_3 W^2$	425.2118	0.2890	-244.2001	-84.9516***	0.0710	0.0001	51966.4684	4115.0465	4133.3613
136	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-1} + \beta_3 Mi$	-418.9905	0.2963	530.9160	97.1903	0.0753	<0.0001	51727.1053	4113.6615	4131.9763
137	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-1} + \beta_3 Mi^2$	-383.2320	0.2911	500.0452	147.3247	0.0845	<0.0001	51215.0065	4110.6767	4128.9915
138	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-1} + \beta_3 (Mi+1)^{-1}$	-289.9981***	0.2964	543.9073	-139.1393***	0.0710	0.0001	51968.8620	4115.0603	4133.3751

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
139	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-1} + \beta_3 (Mi+1)^{-0.5}$	-169.5955***	0.2965	541.2426	-257.7341***	0.0719	0.0001	51919.3106	4114.7741	4133.0889
140	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-1} + \beta_3 Mi^{0.5}$	-436.3972	0.2975	549.4483	66.4554***	0.0706	0.0001	51990.7297	4115.1865	4133.5013
141	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-1} + \beta_3 MS$	-424.9545	0.2969	543.2963	203.8034***	0.0732	0.0001	51848.0139	4114.3619	4132.6767
142	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-1} + \beta_3 MS^2$	-402.1960	0.2898	533.3399	520.6724	0.0753	<0.0001	51729.2142	4113.6737	4131.9885
143	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-0.5} + \beta_3 Mi^2$	-870.2518	0.2907	988.4786	147.3297	0.0848	<0.0001	51194.3491	4110.5556	4128.8705
144	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-0.5} + \beta_3 (Mi+1)^{-1}$	-818.3283	0.2958	1073.4493	-138.7864***	0.0713	0.0001	51950.7328	4114.9556	4133.2705
145	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-0.5} + \beta_3 (Mi+1)^{-0.5}$	-695.6395	0.2960	1068.2667	-257.1645***	0.0722	0.0001	51901.1198	4114.6690	4132.9838
146	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-0.5} + \beta_3 Mi^{0.5}$	-969.5684	0.2969	1084.2109	66.2642***	0.0709	0.0001	51972.7545	4115.0828	4133.3976
147	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-0.5} + \beta_3 (MS+1)^{-1}$	-703.6709	0.2971	1080.0198	-257.3553***	0.0720	0.0001	51912.8631	4114.7369	4133.0517
148	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{-0.5} + \beta_3 (MS+1)^{-0.5}$	-470.2086***	0.2970	1078.2543	-489.0033***	0.0724	0.0001	51891.1526	4114.6114	4132.9262
149	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{0.5} + \beta_3 Mi$	1127.8547	0.2949	-1011.7672	96.7897	0.0761	<0.0001	51682.0655	4113.4001	4131.7150
150	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{0.5} + \beta_3 Mi^{0.5}$	1163.0420	0.2959	-1045.5530	65.8387***	0.0714	0.0001	51947.6940	4114.9381	4133.2529
151	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{0.5} + \beta_3 MS$	1158.4149	0.2955	-1035.9217	203.6097***	0.0741	<0.0001	51798.2773	4114.0739	4132.3888
152	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{0.5} + \beta_3 MS^2$	1153.8916	0.2885	-1018.6822	522.0933	0.0763	<0.0001	51674.5368	4113.3564	4131.6713
153	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{0.5} + \beta_3 (MS+1)^{-1}$	1421.0125	0.2962	-1042.4866	-256.8337***	0.0725	0.0001	51884.3847	4114.5722	4132.8871
154	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 R^{0.5} + \beta_3 (MS+1)^{-0.5}$	1650.7525	0.2961	-1040.8648	-488.1579***	0.0729	0.0001	51862.4663	4114.4455	4132.7603
155	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S + \beta_3 N$	386.9866	0.3117	-336.8901***	-6.3800	0.0689	0.0001	52086.4654	4115.7384	4134.0532
156	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S + \beta_3 N^2$	297.1966	0.2877	-330.4407***	-0.0975	0.0690	0.0001	52082.6214	4115.7163	4134.0311
157	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S + \beta_3 R$	823.1657	0.2829	-433.7118	-576.2434	0.0712	0.0001	51955.6716	4114.9841	4133.2990
158	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S + \beta_3 R^2$	523.4011	0.2820	-435.7339***	-273.8443	0.0715	0.0001	51939.8825	4114.8930	4133.2078
159	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S + \beta_3 R^{-1}$	-377.2639	0.2849	-424.8738***	616.3951	0.0699	0.0001	52032.1125	4115.4252	4133.7400
160	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S + \beta_3 R^{-0.5}$	-976.5124	0.2844	-427.7444***	1217.9208	0.0703	0.0001	52006.8054	4115.2793	4133.5941
161	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S + \beta_3 R^{0.5}$	1422.6781	0.2834	-432.1385***	-1177.3788	0.0710	0.0001	51968.8171	4115.0600	4133.3749
162	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^2 + \beta_3 N$	346.8661	0.3111	-703.7564***	-6.2957	0.0673	0.0001	52177.2809	4116.2610	4134.5759
163	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^2 + \beta_3 N^2$	259.4547	0.2875	-696.6044***	-0.0964	0.0675	0.0001	52167.6026	4116.2054	4134.5202
164	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^2 + \beta_3 R$	762.8839	0.2827	-936.3257***	-563.9398	0.0690	0.0001	52082.1923	4115.7138	4134.0286
165	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^2 + \beta_3 R^2$	469.2446	0.2818	-940.5999***	-267.9460	0.0692	0.0001	52067.5223	4115.6293	4133.9441
166	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^2 + \beta_3 R^{0-1}$	-411.2575	0.2846	-915.6041***	603.4464	0.0677	0.0001	52154.8145	4116.1318	4134.4467

No.	Model	$\boldsymbol{\beta_0}$	$\boldsymbol{\beta_1}$	$\boldsymbol{\beta_2}$	$\boldsymbol{\beta_3}$	$\boldsymbol{R^2}$	$\boldsymbol{p-value}$	MSE	AIC	BIC
167	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^2 + \beta_3 R^{-0.5}$	-998.0954	0.2841	-922.4699***	1192.2378	0.0681	0.0001	52130.6747	4115.9929	4134.3078
168	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^2 + \beta_3 R^{0.5}$	1349.8645	0.2832	-932.7647***	-1152.3471	0.0688	0.0001	52094.5897	4115.7852	4134.1000
169	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 N$	274.1192	0.3090	8.1857***	-6.3154	0.0712	0.0001	51955.2646	4114.9818	4133.2966
170	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 N^2$	187.3738	0.2854	7.9754***	-0.0963	0.0711	0.0001	51960.8829	4115.0142	4133.3291
171	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 N^{0.5}$	458.3938	0.3212	8.2344***	-69.8699	0.0706	0.0001	51988.9401	4115.1762	4133.4910
172	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 R$	676.8613	0.2800	10.0184***	-570.1519	0.0740	<0.0001	51798.9938	4114.0781	4132.3929
173	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 R^2$	379.7481	0.2791	10.0735***	-271.0967	0.0744	<0.0001	51781.0371	4113.9741	4132.2889
174	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 R^{-1}$	-507.6997	0.2820	9.8311***	609.3986	0.0726	0.0001	51879.4976	4114.5440	4132.8588
175	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 R^{-0.5}$	-1101.1888	0.2815	9.8883***	1204.2787	0.0731	0.0001	51853.2313	4114.3921	4132.7069
176	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-1} + \beta_3 R^{0.5}$	1270.2509	0.2805	9.9816***	-1164.6539	0.0738	<0.0001	51813.2023	4114.1604	4132.4752
177	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 N$	209.3312	0.3101	48.0941***	-6.3706	0.0709	0.0001	51974.2189	4115.0912	4133.4061
178	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 N^2$	123.5679***	0.2861	46.8398***	-0.0972	0.0708	0.0001	51979.0419	4115.1191	4133.4339
179	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 N^{0.5}$	394.8919	0.3223	48.3340***	-70.4734	0.0703	0.0001	52008.8330	4115.2910	4133.6058
180	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 R$	601.1183	0.2810	60.0430***	-577.9815	0.0739	<0.0001	51808.9004	4114.1355	4132.4503
181	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 R^2$	299.4492	0.2801	60.3712***	-274.8018	0.0742	<0.0001	51791.1005	4114.0324	4132.3472
182	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 R^{-1}$	-598.0083	0.2830	58.8632***	617.7604	0.0724	0.0001	51889.9603	4114.6045	4132.9193
183	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 R^{-0.5}$	-1200.1985	0.2824	59.2293***	1220.8308	0.0729	0.0001	51863.4330	4114.4511	4132.7659
184	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 R^{0.5}$	1202.9967	0.2815	59.8169***	-1180.6666	0.0736	<0.0001	51823.1311	4114.2179	4132.5327
185	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 TH$	41.2647***	0.2688	23.6780***	63.8102***	0.0319	0.0221	54155.2727	4127.4235	4145.7383
186	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 TH^2$	43.4152***	0.2716	29.8742***	-31.4520***	0.0310	0.0251	54206.6113	4127.7077	4146.0226
187	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 TH^{0.5}$	17.4941***	0.2692	20.3958***	98.0652***	0.0333	0.0182	54078.2511	4126.9965	4145.3113
188	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 Mi^2$	98.2250	0.2828***	-10.2062	172.1548***	0.0561	0.0007	52800.3845	4119.8224	4138.1373
189	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 MS^2$	66.2694***	0.2793	10.6751***	531.7566***	0.0427	0.0047	53550.1243	4124.0523	4142.3671
190	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{-0.5} + \beta_3 W^{0.5}$	85.5245***	0.2769	28.9852***	-64.8295***	0.0335	0.0176	54064.5403	4126.9204	4145.2353
191	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 N$	453.0672	0.3114	-299.4290***	-6.3966	0.0696	0.0001	52046.4034	4115.5076	4133.8224
192	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 N^2$	361.2387	0.2874	-292.6967***	-0.0977	0.0696	0.0001	52045.7470	4115.5038	4133.8186
193	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 R$	909.7418	0.2826	-382.2239***	-579.5761	0.0722	0.0001	51899.8085	4114.6614	4132.9762
194	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 R^2$	608.7247	0.2817	-384.1110***	-275.4705	0.0725	0.0001	51883.3305	4114.5661	4132.8810

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
195	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 R^{-1}$	-299.1193***	0.2845	-374.5010***	619.7842	0.0708	0.0001	51978.1387	4115.1138	4133.4287
196	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 R^{-0.5}$	-901.2194	0.2840	-376.9741***	1224.6984	0.0713	0.0001	51952.2939	4114.9646	4133.2795
197	$AGB = \beta_0 + \beta_1 G^2 + \beta_2 S^{0.5} + \beta_3 R^{0.5}$	1512.3204	0.2830	-380.8160***	-1184.0994	0.0720	0.0001	51913.3614	4114.7397	4133.0546
198	$AGB = \beta_0 \times (G^2)^{\beta_1}$	3.8184	0.2122	-	-	0.0091	0.0996	0.6268	715.2793	726.3096
199	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh)^{\beta_2}$	5.4650	0.4284	-2.3930	-	0.0655	<0.0001	0.5930	699.7364	714.4159
200	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm)^{\beta_2}$	1.9111	0.4437	-13.1461	-	0.0611	0.0001	0.5958	701.1442	715.8238
201	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (E)^{\beta_2}$	2.9005	0.3168	-7.7992	-	0.0291	0.0124	0.6161	711.1950	725.8746
202	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D)^{\beta_2}$	3.5519	0.2246***	0.4451	-	0.0220	0.0365	0.6206	713.3836	728.0631
203	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R)^{\beta_2}$	3.5576	0.2892	-2.1943	-	0.0608	0.0001	0.5961	701.2630	715.9425
204	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (TH)^{\beta_2}$	3.7416	0.2115***	-0.0519***	-	0.0103	0.2136	0.6281	716.9507	731.6303
205	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (TH^2)^{\beta_2}$	3.7416	0.2115***	-0.0260***	-	0.0103	0.2136	0.6281	716.9507	731.6303
206	$AGB = \beta_0 \times (G^2)^{\beta_1} \times ((Mi+1)^2)^{\beta_2}$	3.6852	0.2233***	0.1250***	-	0.0129	0.1444	0.6264	716.1588	730.8384
207	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh)^{\beta_2} \times (TH)^{\beta_3}$	5.3882	0.4390	-2.5265	-0.1140***	0.0715	0.0001	0.5913	699.8963	718.2111
208	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh)^{\beta_2} \times (Mi+1)^{\beta_3}$	5.3407	0.4347	-2.3656	0.1979***	0.0679	0.0001	0.5935	701.0269	719.3417
209	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh)^{\beta_2} \times (MS+1)^{\beta_3}$	5.3378	0.4376	-2.3751	0.4265***	0.0683	0.0001	0.5933	700.9041	719.2189
210	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh)^{\beta_2} \times ((W+1)^{-0.5})^{\beta_3}$	5.5801	0.4382	-2.4342	0.6165***	0.0688	0.0001	0.5930	700.7571	719.0720
211	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh)^{\beta_2} \times ((W+1)^{0.5})^{\beta_3}$	5.5801	0.4382	-2.4342	-0.6165***	0.0688	0.0001	0.5930	700.7571	719.0720
212	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh)^{\beta_2} \times (A)^{\beta_3}$	5.7214	0.4432	-3.0153	0.4587	0.0809	<0.0001	0.5852	696.8254	715.1402
213	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^2)^{\beta_2} \times (TH)^{\beta_3}$	5.3882	0.4390	-1.2632	-0.1140***	0.0715	0.0001	0.5913	699.8963	718.2111
214	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^2)^{\beta_2} \times (Mi+1)^{\beta_3}$	5.3407	0.4347	-1.1828	0.1979***	0.0679	0.0001	0.5935	701.0269	719.3417
215	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^2)^{\beta_2} \times (W+1)^{\beta_3}$	5.5801	0.4382	-1.2171	-0.3083***	0.0688	0.0001	0.5930	700.7571	719.0720
216	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^2)^{\beta_2} \times (A)^{\beta_3}$	5.7214	0.4432	-1.5076	0.4587	0.0809	<0.0001	0.5852	696.8254	715.1402
217	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^2)^{\beta_2} \times (A^2)^{\beta_3}$	5.7214	0.4432	-1.5076	0.2294	0.0809	<0.0001	0.5852	696.8254	715.1402
218	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{-1})^{\beta_2} \times (TH^2)^{\beta_3}$	5.3882	0.4390	2.5265	-0.0570***	0.0715	0.0001	0.5913	699.8963	718.2111
219	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{-1})^{\beta_2} \times (Mi+1)^{\beta_3}$	5.3407	0.4347	2.3656***	0.1979	0.0679	0.0001	0.5935	701.0269	719.3417
220	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{-1})^{\beta_2} \times (MS+1)^{\beta_3}$	5.3378	0.4376	2.3751***	0.4265	0.0683	0.0001	0.5933	700.9041	719.2189
221	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{-1})^{\beta_2} \times ((W+1)^{0.5})^{\beta_3}$	5.5801	0.4382	2.4342***	-0.6165	0.0688	0.0001	0.5930	700.7571	719.0720
222	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{-1})^{\beta_2} \times (A^{0.5})^{\beta_3}$	5.7214	0.4432	3.0153	-0.9175	0.0809	<0.0001	0.5852	696.8254	715.1402

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
223	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{-0.5})^{\beta_2} \times (TH^{-1})^{\beta_3}$	5.3882	0.4390	5.0529	0.1140***	0.0715	0.0001	0.5913	699.8963	718.2111
224	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{-0.5})^{\beta_2} \times ((Mi+1)^2)^{\beta_3}$	5.3407	0.4347	4.7312	0.0990***	0.0679	0.0001	0.5935	701.0269	719.3417
225	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{-0.5})^{\beta_2} \times ((MS+1)^{0.5})^{\beta_3}$	5.3378	0.4376	4.7502	0.8530***	0.0683	0.0001	0.5933	700.9041	719.2189
226	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{-0.5})^{\beta_2} \times (W+1)^{\beta_3}$	5.5801	0.4382	4.8685	-0.3083***	0.0688	0.0001	0.5930	700.7571	719.0720
227	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{-0.5})^{\beta_2} \times (A)^{\beta_3}$	5.7214	0.4432	6.0305	0.4587	0.0809	<0.0001	0.5852	696.8254	715.1402
228	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{0.5})^{\beta_2} \times (TH)^{\beta_3}$	5.3882	0.4390	-5.0529	-0.1140***	0.0715	0.0001	0.5913	699.8963	718.2111
229	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{0.5})^{\beta_2} \times ((Mi+1)^2)^{\beta_3}$	5.3407	0.4347	-4.7312	0.0990***	0.0679	0.0001	0.5935	701.0269	719.3417
230	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{0.5})^{\beta_2} \times ((MS+1)^2)^{\beta_3}$	5.3378	0.4376	-4.7502	0.2132***	0.0683	0.0001	0.5933	700.9041	719.2189
231	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{0.5})^{\beta_2} \times ((W+1)^{-0.5})^{\beta_3}$	5.5801	0.4382	-4.8685	0.6165***	0.0688	0.0001	0.5930	700.7571	719.0720
232	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sh^{0.5})^{\beta_2} \times (A^{0.5})^{\beta_3}$	5.7214	0.4432	-6.0305	0.9175	0.0809	<0.0001	0.5852	696.8254	715.1402
233	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm)^{\beta_2} \times (TH^{0.5})^{\beta_3}$	1.6876***	0.4518	-13.6775	-0.1980***	0.0657	0.0002	0.5950	701.7658	720.0807
234	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm)^{\beta_2} \times (Mi+1)^{\beta_3}$	1.8418	0.4484	-12.9514	0.1831***	0.0632	0.0002	0.5965	702.5518	720.8667
235	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm)^{\beta_2} \times ((MS+1)^{0.5})^{\beta_3}$	1.8291	0.4508	-12.9903	0.7771***	0.0635	0.0002	0.5964	702.4702	720.7850
236	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm)^{\beta_2} \times (W+1)^{\beta_3}$	1.9675	0.4519	-13.2979	-0.2785***	0.0638	0.0002	0.5961	702.3597	720.6745
237	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm)^{\beta_2} \times (A^2)^{\beta_3}$	1.3477***	0.4582	-16.0049	0.1986***	0.0731	0.0001	0.5902	699.3764	717.6913
238	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (TH^{0.5})^{\beta_3}$	1.6876***	0.4518	-6.8388	-0.1980***	0.0657	0.0002	0.5950	701.7658	720.0807
239	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((Mi+1)^{-1})^{\beta_3}$	1.8418	0.4484	-6.4757	-0.1831***	0.0632	0.0002	0.5965	702.5518	720.8667
240	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((MS+1)^{0.5})^{\beta_3}$	1.8291	0.4508	-6.4951	0.7771***	0.0635	0.0002	0.5964	702.4702	720.7850
241	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (W+1)^{\beta_3}$	1.9675	0.4519	-6.6490	-0.2785***	0.0638	0.0002	0.5961	702.3597	720.6745
242	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((W+1)^2)^{\beta_3}$	1.9675	0.4519	-6.6490	-0.1393***	0.0638	0.0002	0.5961	702.3597	720.6745
243	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((W+1)^{-1})^{\beta_3}$	1.9675	0.4519	-6.6490	0.2785***	0.0638	0.0002	0.5961	702.3597	720.6745
244	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((W+1)^{-0.5})^{\beta_3}$	1.9675	0.4519	-6.6490	0.5570***	0.0638	0.0002	0.5961	702.3597	720.6745
245	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((W+1)^{0.5})^{\beta_3}$	1.9675	0.4519	-6.6490	-0.5570***	0.0638	0.0002	0.5961	702.3597	720.6745
246	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (A)^{\beta_3}$	1.3477***	0.4582	-8.0024	0.3972***	0.0731	0.0001	0.5902	699.3764	717.6913
247	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (A^2)^{\beta_3}$	1.3477***	0.4582	-8.0024	0.1986***	0.0731	0.0001	0.5902	699.3764	717.6913
248	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (A^{-1})^{\beta_3}$	1.3477***	0.4582	-8.0024	-0.3972***	0.0731	0.0001	0.5902	699.3764	717.6913
249	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (A^{-0.5})^{\beta_3}$	1.3477***	0.4582	-8.0024	-0.7943***	0.0731	0.0001	0.5902	699.3764	717.6913
250	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (A^{0.5})^{\beta_3}$	1.3477***	0.4582	-8.0024	0.7943***	0.0731	0.0001	0.5902	699.3764	717.6913

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
251	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{-1})^{\beta_2} \times (TH)^{\beta_3}$	1.6876***	0.4518	13.6775	-0.0990***	0.0657	0.0002	0.5950	701.7658	720.0807
252	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{-1})^{\beta_2} \times ((Mi+1)^{0.5})^{\beta_3}$	1.8418	0.4484	12.9514	0.3662***	0.0632	0.0002	0.5965	702.5518	720.8667
253	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{-1})^{\beta_2} \times ((MS+1)^{0.5})^{\beta_3}$	1.8291	0.4508	12.9903	0.3885***	0.0635	0.0002	0.5964	702.4702	720.7850
254	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{-1})^{\beta_2} \times ((W+1)^{0.5})^{\beta_3}$	1.9675	0.4519	13.2979	0.2785***	0.0638	0.0002	0.5961	702.3597	720.6745
255	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{-1})^{\beta_2} \times (A^2)^{\beta_3}$	1.3477***	0.4582	16.0049	0.1986***	0.0731	0.0001	0.5902	699.3764	717.6913
256	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{-0.5})^{\beta_2} \times (TH)^{\beta_3}$	1.6876***	0.4518	27.3551	-0.0990***	0.0657	0.0002	0.5950	701.7658	720.0807
257	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{-0.5})^{\beta_2} \times ((Mi+1)^2)^{\beta_3}$	1.8418	0.4484	25.9029	0.0916***	0.0632	0.0002	0.5965	702.5518	720.8667
258	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{-0.5})^{\beta_2} \times ((MS+1)^{0.5})^{\beta_3}$	1.8291	0.4508	25.9806	0.7771***	0.0635	0.0002	0.5964	702.4702	720.7850
259	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{-0.5})^{\beta_2} \times ((W+1)^{-1})^{\beta_3}$	1.9675	0.4519	26.5958	0.2785***	0.0638	0.0002	0.5961	702.3597	720.6745
260	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{-0.5})^{\beta_2} \times (A^2)^{\beta_3}$	1.3477***	0.4582	32.0097	0.1986***	0.0731	0.0001	0.5902	699.3764	717.6913
261	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (Sm^{0.5})^{\beta_2} \times (TH^{-0.5})^{\beta_3}$	1.6876***	0.4518	-27.3551	0.1980***	0.0657	0.0002	0.5950	701.7658	720.0807
262	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (E)^{\beta_2} \times (A^{-1})^{\beta_3}$	2.7828	0.3118	-8.3583	-0.1387***	0.0308	0.0259	0.6172	712.7528	731.0676
263	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (E^2)^{\beta_2} \times (W+1)^{\beta_3}$	2.9615	0.3205	-3.8867	-0.2058***	0.0306	0.0266	0.6173	712.8124	731.1272
264	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (E^{-1})^{\beta_2} \times ((Mi+1)^2)^{\beta_3}$	2.8994	0.3157	7.4689	0.0375***	0.0295	0.0311	0.6180	713.1666	731.4815
265	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (E^{-0.5})^{\beta_2} \times (TH^2)^{\beta_3}$	2.7541	0.3199	16.2037	-0.0375***	0.0318	0.0226	0.6166	712.4577	730.7726
266	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (E^{0.5})^{\beta_2} \times (Mi+1)^{\beta_3}$	2.8994	0.3157	-14.9379	0.0751***	0.0295	0.0311	0.6180	713.1666	731.4815
267	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (E^{0.5})^{\beta_2} \times ((Mi+1)^2)^{\beta_3}$	2.8994	0.3157	-14.9379	0.0375***	0.0295	0.0311	0.6180	713.1666	731.4815
268	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D)^{\beta_2} \times (A^{-1})^{\beta_3}$	3.5011	0.2165***	0.4687	-0.0978***	0.0229	0.0765	0.6222	715.1952	733.5100
269	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D)^{\beta_2} \times (A^{-0.5})^{\beta_3}$	3.5011	0.2165***	0.4687	-0.1957***	0.0229	0.0765	0.6222	715.1952	733.5100
270	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^2)^{\beta_2} \times (TH)^{\beta_3}$	3.4063	0.2247***	0.2417	-0.0829***	0.0252	0.0561	0.6207	714.4894	732.8042
271	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^2)^{\beta_2} \times (TH^2)^{\beta_3}$	3.4063	0.2247***	0.2417	-0.0415***	0.0252	0.0561	0.6207	714.4894	732.8042
272	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^2)^{\beta_2} \times (TH^{-0.5})^{\beta_3}$	3.4063	0.2247***	0.2417	0.1659***	0.0252	0.0561	0.6207	714.4894	732.8042
273	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^2)^{\beta_2} \times (TH^{0.5})^{\beta_3}$	3.4063	0.2247***	0.2417	-0.1659***	0.0252	0.0561	0.6207	714.4894	732.8042
274	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^2)^{\beta_2} \times (Mi+1)^{\beta_3}$	3.5219	0.2279***	0.2057***	0.0943***	0.0225	0.0803	0.6224	715.3060	733.6208
275	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^{-1})^{\beta_2} \times (A^2)^{\beta_3}$	3.5011	0.2165***	-0.4687	0.0489***	0.0229	0.0765	0.6222	715.1952	733.5100
276	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^{-0.5})^{\beta_2} \times ((Mi+1)^{0.5})^{\beta_3}$	3.5219	0.2279***	-0.8226***	0.1886***	0.0225	0.0803	0.6224	715.3060	733.6208
277	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^{-0.5})^{\beta_2} \times (MS+1)^{\beta_3}$	3.5177	0.2288***	-0.8237***	0.2006***	0.0226	0.0795	0.6224	715.2838	733.5986
278	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^{-0.5})^{\beta_2} \times ((MS+1)^2)^{\beta_3}$	3.5177	0.2288***	-0.8237***	0.1003***	0.0226	0.0795	0.6224	715.2838	733.5986

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
279	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^{-0.5})^{\beta_2} \times ((MS+1)^{-1})^{\beta_3}$	3.5177	0.2288***	-0.8237	-0.2006***	0.0226	0.0795	0.6224	715.2838	733.5986
280	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (D^{-0.5})^{\beta_2} \times ((MS+1)^{-0.5})^{\beta_3}$	3.5177	0.2288***	-0.8237	-0.4012***	0.0226	0.0795	0.6224	715.2838	733.5986
281	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^2)^{\beta_2} \times (A)^{\beta_3}$	3.3753	0.2709	-1.2984	0.3592***	0.0708	0.0001	0.5917	700.1107	718.4256
282	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times (Mi+1)^{\beta_3}$	3.4359	0.2991	2.1826	0.2309***	0.0641	0.0002	0.5960	702.2752	720.5900
283	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((Mi+1)^2)^{\beta_3}$	3.4359	0.2991	2.1826	0.1154***	0.0641	0.0002	0.5960	702.2752	720.5900
284	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((Mi+1)^{-1})^{\beta_3}$	3.4359	0.2991	2.1826	-0.2309***	0.0641	0.0002	0.5960	702.2752	720.5900
285	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((Mi+1)^{-0.5})^{\beta_3}$	3.4359	0.2991	2.1826	-0.4617***	0.0641	0.0002	0.5960	702.2752	720.5900
286	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((Mi+1)^{0.5})^{\beta_3}$	3.4359	0.2991	2.1826	0.4617***	0.0641	0.0002	0.5960	702.2752	720.5900
287	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times (MS+1)^{\beta_3}$	3.4222	0.3021	2.1979	0.5011***	0.0646	0.0002	0.5956	702.0921	720.4069
288	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((MS+1)^2)^{\beta_3}$	3.4222	0.3021	2.1979	0.2506***	0.0646	0.0002	0.5956	702.0921	720.4069
289	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((MS+1)^{-1})^{\beta_3}$	3.4222	0.3021	2.1979	-0.5011***	0.0646	0.0002	0.5956	702.0921	720.4069
290	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((MS+1)^{-0.5})^{\beta_3}$	3.4222	0.3021	2.1979	-1.0022***	0.0646	0.0002	0.5956	702.0921	720.4069
291	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((MS+1)^{0.5})^{\beta_3}$	3.4222	0.3021	2.1979	1.0022***	0.0646	0.0002	0.5956	702.0921	720.4069
292	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times (W+1)^{\beta_3}$	3.6222	0.2940	2.2000	-0.2319***	0.0626	0.0003	0.5969	702.7389	721.0537
293	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((W+1)^2)^{\beta_3}$	3.6222	0.2940	2.2000	-0.1160***	0.0626	0.0003	0.5969	702.7389	721.0537
294	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((W+1)^{-1})^{\beta_3}$	3.6222	0.2940	2.2000	0.2319***	0.0626	0.0003	0.5969	702.7389	721.0537
295	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((W+1)^{-0.5})^{\beta_3}$	3.6222	0.2940	2.2000	0.4639***	0.0626	0.0003	0.5969	702.7389	721.0537
296	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times ((W+1)^{0.5})^{\beta_3}$	3.6222	0.2940	2.2000	-0.4639***	0.0626	0.0003	0.5969	702.7389	721.0537
297	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times (A)^{\beta_3}$	3.3753	0.2709	2.5967	0.3592***	0.0708	0.0001	0.5917	700.1107	718.4256
298	$AGB = \beta_0 \times (G^2)^{\beta_1} \times (R^{-1})^{\beta_2} \times (A^2)^{\beta_3}$	3.3753	0.2709	2.5967	0.1796***	0.0708	0.0001	0.5917	700.1107	718.4256

Annex 4: Model fitted for *Acacia auriculiformis* *(*** indicates p-value>0.05)*

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
1	$AGB = \exp(\beta_0 + \beta_1 TH^2)$	5.3644	-4.1514	-	-	0.1073	0.0005	0.7378	277.8661	285.6817
2	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 N^{0.5})$	7.1477	-4.2258	-0.3151	-	0.1658	0.0001	0.6961	272.7099	283.0501
3	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sh^2)$	6.7131	-4.1277	-0.1248	-	0.1697	0.0001	0.6928	272.1988	282.5390
4	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sh^{-1})$	3.2154	-4.0410	6.9505	-	0.1672	0.0001	0.6949	272.5302	282.8704
5	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sh)$	7.8752	-4.0985	-0.7675	-	0.1693	0.0001	0.6932	272.2584	282.5985
6	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sm)$	16.9614	-3.9665	-12.1873	-	0.1653	0.0001	0.6965	272.7778	283.1180
7	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sm^2)$	11.2770	-3.9718	-6.5268	-	0.1656	0.0001	0.6962	272.7349	283.0751
8	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E)$	16.1278	-3.6734	-11.3612	-	0.1541	0.0002	0.7058	274.2122	284.5524
9	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E^2)$	10.8051	-3.6752	-6.0591	-	0.1540	0.0002	0.7059	274.2263	284.5665
10	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E^{0.5})$	26.7711	-3.6725	-21.9943	-	0.1541	0.0002	0.7058	274.2061	284.5463
11	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 N^2)$	5.9042	-4.2948	-0.0005	-	0.1616	0.0001	0.6996	273.2468	283.5870
12	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 D^{-1})$	5.7929	-4.0398	-0.8047***	-	0.1143	0.0017	0.7391	279.1825	289.5227
13	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 D^{0.5})$	4.3419	-4.0357	0.7396***	-	0.1150	0.0016	0.7385	279.0981	289.4383
14	$AGB = \exp(\beta_0 + \beta_1 TH^2 + G)$	5.2864	-4.1876	0.0041***	-	0.1076	0.0025	0.7446	279.9890	290.3292
15	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 G^2)$	5.3229	-4.1952	0.0001***	-	0.1077	0.0025	0.7445	279.9784	290.3186
16	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Mi^2)$	5.3512	-4.1580	0.0288***	-	0.1075	0.0026	0.7448	280.0089	290.3491
17	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^{-0.5})$	6.1592	-4.0616	-0.3813***	-	0.1112	0.0021	0.7417	279.5594	289.8996
18	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 MS^2)$	5.2888	-4.1405	0.8267***	-	0.1165	0.0015	0.7372	278.9054	289.2455
19	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sh + \beta_3 W)$	7.9057	-4.1197	-0.7685	-0.0539***	0.1694	0.0002	0.6997	274.4360	287.2585
20	$AGB = exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sh + \beta_3 W^2)$	7.9071	-4.1417	-0.7687	-0.0898***	0.1697	0.0002	0.6995	274.4026	287.2251
21	$AGB = exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sh + \beta_3 (W+1)^{-0.5})$	7.8124	-4.1059	-0.7680	0.0783***	0.1693	0.0002	0.6998	274.4541	287.2765
22	$AGB = exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sh + \beta_3 W^{0.5})$	7.8284	-4.0868	-0.7662	0.0633***	0.1695	0.0002	0.6997	274.4320	287.2544
23	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Sh^{-1} + \beta_3 W)$	3.2433	-4.0668	6.9677	-0.0660***	0.1674	0.0003	0.7014	274.6970	287.5194

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
24	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 Sh^{-1}+\beta_3(W+1)^{-1})$	3.1903	-4.0460	6.9553	0.0347***	0.1672	0.0003	0.7016	274.7278	287.5502
25	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 Sh^{-1}+\beta_3(W+1)^{-0.5})$	3.1224	-4.0513	6.9592	0.1096***	0.1672	0.0003	0.7016	274.7221	287.5445
26	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 Sh^{-1}+\beta_3 W^{0.5})$	3.1800	-4.0303	6.9376	0.0587***	0.1673	0.0003	0.7015	274.7076	287.5301
27	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 Sh^{-1}+\beta_3 A)$	3.4091	-4.1479	6.6207	-0.0350***	0.1674	0.0003	0.7014	274.6959	287.5183
28	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 Sh^{0.5}+\beta_3 W^2)$	10.2390	-4.1292	-2.6825	-0.0944***	0.1694	0.0002	0.6998	274.4475	287.2699
29	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 Sh^2+\beta_3 W^2)$	11.3227	-4.0186	-6.5439	-0.0979***	0.1661	0.0003	0.7025	274.8691	287.6915
30	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 Sh^2+\beta_3(W+1)^{0.5})$	11.2236	-3.9783	-6.5305	0.0689***	0.1656	0.0003	0.7029	274.9316	287.7540
31	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 Sh^{-0.5}+\beta_3 W)$	-17.1691	-3.9811	22.0053	-0.0574***	0.1649	0.0003	0.7035	275.0188	287.8412
32	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 Sh^{0.5}+\beta_3 W)$	28.3990	-3.9859	-23.5858	-0.0564***	0.1653	0.0003	0.7032	274.9753	287.7977
33	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E+\beta_3 G^{0.5})$	16.4492	-3.7867	-12.4894	0.1713***	0.1599	0.0004	0.7077	275.6670	288.4894
34	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E+\beta_3 Mi)$	16.1048	-3.6857	-11.4462	0.1663***	0.1568	0.0005	0.7104	276.0720	288.8944
35	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E+\beta_3 MS^{0.5})$	15.2339	-3.6378	-10.6372	0.4251***	0.1600	0.0004	0.7076	275.6540	288.4765
36	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E+\beta_3 W)$	16.1329	-3.6795	-11.3585	-0.0153***	0.1541	0.0006	0.7126	276.4103	289.2328
37	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E+\beta_3 A^{0.5})$	15.7118	-3.8408	-10.6922***	-0.1346***	0.1546	0.0005	0.7122	276.3457	289.1682
38	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^2+\beta_3 G^{-1})$	11.7065	-3.7389	-6.6747	-6.5084***	0.1591	0.0004	0.7084	275.7684	288.5908
39	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^2+\beta_3 Mi^{0.5})$	10.5055	-3.6246	-6.1099	0.4471***	0.1652	0.0003	0.7033	274.9840	287.8064
40	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^2+\beta_3(W+1)^{-0.5})$	10.8784	-3.6669	-6.0627	-0.0852***	0.1540	0.0006	0.7127	276.4214	289.2438
41	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^2+\beta_3 W^{0.5})$	10.7428	-3.6496	-6.0852	0.1274***	0.1548	0.0005	0.7120	276.3218	289.1442
42	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^{-1}+\beta_3 G)$	-6.5357***	-3.7936	10.9221	0.0191***	0.1601	0.0004	0.7075	275.6391	288.4615
43	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^{-1}+\beta_3 G^2)$	-6.1929***	-3.8009	10.7908	0.0004***	0.1596	0.0004	0.7080	275.7038	288.5263
44	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^{-1}+\beta_3 Mi^{0.5})$	-5.5312***	-3.6227	9.9972	0.4384***	0.1651	0.0003	0.7034	275.0048	287.8272
45	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^{-1}+\beta_3 MS)$	-4.8011***	-3.6742	9.5608	0.2653***	0.1564	0.0005	0.7107	276.1241	288.9466
46	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^{-1}+\beta_3(W+1)^{-0.5})$	-5.1022***	-3.6635	9.9645	-0.0681***	0.1543	0.0006	0.7125	276.3884	289.2108
47	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^{-1}+\beta_3 A^{0.5})$	-4.3095***	-3.8401	9.3700***	-0.1366***	0.1548	0.0005	0.7120	276.3229	289.1453
48	$AGB=\exp(\beta_0+\beta_1 TH^2+\beta_2 E^{-0.5}+\beta_3 G)$	-18.1912	-3.7941***	22.5686***	0.0190	0.1601	0.0004	0.7076	275.6481	288.4705

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
49	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E^{-0.5} + \beta_3 (Mi+1)^{-1})$	-15.5161	-3.6609***	20.7000***	-0.6166	0.1609	0.0004	0.7069	275.5399	288.3623
50	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E^{-0.5} + \beta_3 Mi^{0.5})$	-16.2302	-3.6230***	20.6849***	0.4398	0.1651	0.0003	0.7034	274.9999	287.8224
51	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E^{-0.5} + \beta_3 A^{-1})$	-18.6024	-3.1247	23.4860	-0.4491***	0.1617	0.0004	0.7062	275.4371	288.2595
52	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E^{0.5} + \beta_3 (Mi+1)^{-0.5})$	27.6446	-3.6713	-22.1490	-0.9119***	0.1596	0.0004	0.7080	275.7100	288.5324
53	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E^{0.5} + \beta_3 Mi^{0.5})$	26.5567	-3.6235	-22.1251	0.4427***	0.1652	0.0003	0.7033	274.9919	287.8143
54	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 E^{0.5} + \beta_3 A^2)$	21.2750	-4.3349	-16.0430***	-0.0420***	0.1637	0.0003	0.7046	275.1827	288.0051
55	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 D + \beta_3 A^{-1})$	4.8471	-3.9388	0.2863***	-0.0883***	0.1155	0.0050	0.7452	281.2338	294.0562
56	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 D^2 + \beta_3 G)$	5.1182	-3.9964	0.0839***	-0.0036***	0.1157	0.0050	0.7449	281.2033	294.0257
57	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 D^2 + \beta_3 W^2)$	5.0749	-4.0477	0.0789***	-0.0243***	0.1156	0.0050	0.7451	281.2243	294.0467
58	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 D^2 + \beta_3 W^{0.5})$	5.7165	-4.0074	-0.8447***	0.1454***	0.1153	0.0051	0.7453	281.2545	294.0769
59	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 D^{-0.5} + \beta_3 A)$	6.5335	-4.8161	-0.7037***	-0.2503***	0.1336	0.0018	0.7299	278.9997	291.8221
60	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 D^{0.5} + \beta_3 G)$	4.3515	-4.0003	0.7784***	-0.0033***	0.1151	0.0051	0.7455	281.2775	294.1000
61	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 D^{0.5} + \beta_3 W^{0.5})$	4.2004	-4.0040	0.7719***	0.1440***	0.1160	0.0049	0.7447	281.1722	293.9946
62	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R + \beta_3 G)$	7.3007	-4.0163	-1.8518	-0.0004***	0.1498	0.0007	0.7163	276.9609	289.7833
63	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R + \beta_3 (Mi+1)^{-0.5})$	8.3975	-4.0141	-1.9742	-1.2322***	0.1595	0.0004	0.7081	275.7174	288.5398
64	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R + \beta_3 A^{-1})$	7.7082	-3.5542	-2.1008	-0.4202***	0.1564	0.0005	0.7107	276.1229	288.9453
65	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R^2 + \beta_3 G)$	6.3587	-4.0274	-0.8905	-0.0009***	0.1481	0.0008	0.7177	277.1774	289.9998
66	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R^2 + \beta_3 (Mi+1)^{-0.5})$	7.4056	-4.0305	-0.9550	-1.2541***	0.1581	0.0004	0.7092	275.8969	288.7193
67	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R^2 + \beta_3 Mi^{0.5})$	5.9957	-3.9619	-0.9892	0.5870***	0.1669	0.0003	0.7018	274.7660	287.5884
68	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R^{-1} + \beta_3 G^{0.5})$	3.3953	-4.0024	1.9260	0.0225***	0.1528	0.0006	0.7137	276.5768	289.3992
69	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R^{-1} + \beta_3 Mi)$	3.2949	-3.9963	1.9910	0.2176***	0.1572	0.0005	0.7100	276.0146	288.8371
70	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R^{-1} + \beta_3 Mi^2)$	3.4359	-3.9964	1.9497	0.0756***	0.1535	0.0006	0.7131	276.4846	289.3070
71	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R^{-0.5} + \beta_3 (W+1)^{-0.5})$	1.7588***	-3.9686	3.8582	-0.2321***	0.1523	0.0006	0.7141	276.6372	289.4596

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
72	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R^{-0.5} + \beta_3 A^{-1})$	1.2463***	-3.5161	4.3453	-0.4261***	0.1588	0.0004	0.7086	275.8065	288.6289
73	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R^{0.5} + \beta_3 G^{-0.5})$	9.3627	-4.0388	-3.7694	-0.6800***	0.1509	0.0007	0.7153	276.8243	289.6467
74	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 R^{0.5} + \beta_3 G^{0.5})$	9.1369	-4.0226	-3.7539	0.0122***	0.1506	0.0007	0.7155	276.8549	289.6773
75	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Mi^2 + \beta_3 A^{0.5})$	6.3972	-4.8379	0.0495***	-0.6526***	0.1234	0.0032	0.7385	280.2611	293.0836
76	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 Mi^2 + \beta_3 G)$	5.2330	-4.2132	0.0500***	0.0057***	0.1079	0.0076	0.7515	282.1498	294.9722
77	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 (Mi+1)^{0.5} + \beta_3 G)$	4.4331	-4.2645	0.5691***	0.0109***	0.1118	0.0062	0.7483	281.6847	294.5071
78	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 (Mi+1)^2 + \beta_3 G^2)$	4.5062	-4.2816	0.5913***	0.0003***	0.1121	0.0061	0.7480	281.6428	294.4652
79	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 MS + \beta_3 G)$	4.9352	-4.2408	0.6149***	0.0140***	0.1175	0.0045	0.7434	280.9819	293.8043
80	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 MS + \beta_3 G^2)$	5.0630	-4.2592	0.6323***	0.0004***	0.1180	0.0044	0.7430	280.9201	293.7425
81	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 MS^2 + \beta_3 G)$	5.0620	-4.2395	0.9385***	0.0113***	0.1186	0.0042	0.7426	280.8557	293.6781
82	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 MS^2 + \beta_3 G^2)$	5.1666	-4.2553	0.9551***	0.0003***	0.1190	0.0042	0.7422	280.8085	293.6310
83	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 (A+1)^{-1} + \beta_3 G^2)$	4.9662	-4.6282	1.1831***	0.0002***	0.1128	0.0058	0.7474	281.5602	294.3826
84	$AGB = exp(\beta_0 + \beta_1 TH^2 + \beta_2 (A+1)^{-0.5} + \beta_3 G^2)$	4.2796	-4.7754	1.9134***	0.0002***	0.1172	0.0046	0.7437	281.0214	293.8438
85	$AGB = exp(\beta_0 + \beta_1 TH^2 + \beta_2 S + \beta_3 Sm)$	15.8040	-3.9040	0.7724***	-11.1654***	0.1684	0.0002	0.7006	274.5761	287.3985
86	$AGB = exp(\beta_0 + \beta_1 TH^2 + \beta_2 S + \beta_3 R^{0.5})$	8.5191	-3.9070	1.1726***	-3.3712	0.1582	0.0004	0.7092	275.8856	288.7080
87	$AGB = exp(\beta_0 + \beta_1 TH^2 + \beta_2 S + \beta_3 G)$	4.7329	-4.0530	1.8445***	0.0099***	0.1270	0.0027	0.7354	279.8143	292.6368
88	$AGB = exp(\beta_0 + \beta_1 TH^2 + \beta_2 S + \beta_3 G^2)$	4.8297	-4.0622	1.8463***	0.0002***	0.1272	0.0026	0.7353	279.7953	292.6177
89	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^2 + \beta_3 D^{-0.5})$	6.0493	-3.8882	1.6957***	-1.0949***	0.1350	0.0017	0.7287	278.8219	291.6443
90	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^2 + \beta_3 D^{0.5})$	4.3610	-3.8870	1.6904***	0.6452***	0.1353	0.0017	0.7284	278.7833	291.6057
91	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^2 + \beta_3 Mi^2)$	5.2604	-3.9728	1.7793***	-0.0287***	0.1297	0.0023	0.7332	279.4861	292.3085
92	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^{-1} + \beta_3 N)$	6.1908	-4.2861	0.0360***	-0.0302	0.1657	0.0003	0.7029	274.9251	287.7475
93	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^{-1} + \beta_3 N^2)$	5.8363	-4.3102	0.0165***	-0.0005	0.1617	0.0004	0.7062	275.4333	288.2557
94	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 Sm)$	16.0348	-3.9258	0.6340***	-11.5367	0.1664	0.0003	0.7023	274.8325	287.6549
95	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 E^{0.5})$	24.8968	-3.6500	0.7104***	-20.4226	0.1555	0.0005	0.7114	276.2302	289.0526
96	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 D)$	3.9243	-3.8897	1.9660***	0.2532***	0.1275	0.0026	0.7351	279.7622	292.5846
97	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 R^{0.5})$	8.2545	-3.9191	1.2943***	-3.4518	0.1557	0.0005	0.7113	276.2119	289.0344

No.	Model	β_0	β_1	β_2	β_3	R^2	$p - value$	MSE	AIC	BIC
98	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 G)$	4.0721	-4.0667	2.2445***	0.0106***	0.1230	0.0033	0.7388	280.3115	293.1339
99	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 G^2)$	4.1734	-4.0766	2.2505***	0.0003***	0.1232	0.0033	0.7387	280.2884	293.1108
100	$AGB = \exp(\beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 Mi^2)$	4.3576	-3.9824	2.0861***	-0.0107***	0.1212	0.0037	0.7404	280.5387	293.3611
101	$AGB = \beta_0 + \beta_1 TH^2$	244.9115***	-346.2319	-	-	0.0218	0.1271	27668.4018	1415.3317	1423.1474
102	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 N^{0.5}$	659.0822	-363.5048***	-73.1782	-	0.1139	0.0017	25301.1931	1406.8062	1417.1463
103	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sh^2$	566.6381	-340.5794***	-29.7708	-	0.1256	0.0009	24969.3242	1405.3802	1415.7204
104	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sh^{-1}$	-277.7947***	-319.3735***	1690.5994	-	0.1253	0.0009	24977.9780	1405.4176	1415.7578
105	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sh^{-0.5}$	-839.2573	-322.8614***	1952.7908	-	0.1257	0.0009	24965.4399	1405.3634	1415.7035
106	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sm$	3126.9237	-300.2851***	-3028.7090	-	0.1264	0.0008	24946.8363	1405.2829	1415.6230
107	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sm^2$	1712.3475	-301.6615***	-1619.8768	-	0.1267	0.0008	24937.6125	1405.2429	1415.5831
108	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E$	3198.6344	-215.0475***	-3117.7686	-	0.1247	0.0009	24993.2952	1405.4838	1415.8240
109	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-1}$	-2642.7596	-214.1224***	2734.4879	-	0.1252	0.0009	24981.1494	1405.4313	1415.7715
110	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{0.5}$	6119.8637	-214.8000***	-6036.2291	-	0.1249	0.0009	24989.8108	1405.4688	1415.8089
111	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 D^{-1}$	378.5791	-311.4104***	-251.0465***	-	0.0415	0.1080	27369.4464	1415.2923	1425.6325
112	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 G$	246.3771	-345.5520***	-0.0764***	-	0.0218	0.3140	27931.8260	1417.4890	1427.8292
113	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 G^2$	245.0857	-346.0482***	-0.0005***	-	0.0218	0.3141	27931.9049	1417.4893	1427.8295
114	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Mi^2$	240.3250	-348.5203***	10.0192***	-	0.0222	0.3069	27919.6356	1417.4419	1427.7820
115	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^{-0.5}$	845.7403	-278.3702***	-288.2363	-	0.0858	0.0090	26106.1177	1410.1885	1420.5287
116	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 MS^2$	226.2041	-343.5372***	204.4513***	-	0.0383	0.1290	27462.5750	1415.6592	1425.9994
117	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sh + \beta_3 W^2$	820.3642***	-296.4325	-183.1843***	77.0540	0.1353	0.0017	24928.0020	1406.3677	1419.1901
118	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sh + \beta_3 (W+1)^{0.5}$	982.1257***	-317.6961	-183.1758***	-167.4709	0.1304	0.0022	25070.7042	1406.9842	1419.8066
119	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sh + \beta_3 W^{0.5}$	805.1461***	-322.9414	-183.0858***	57.6165	0.1310	0.0021	25052.2129	1406.9045	1419.7269
120	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sm^2 + \beta_3 W^2$	1677.3348***	-265.8919	-1606.7932***	74.9169	0.1354	0.0017	24926.9554	1406.3631	1419.1856
121	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sm^2 + \beta_3 (W+1)^{-0.5}$	1843.3573	-285.8721***	-1610.8471	-168.9535***	0.1310	0.0021	25052.8722	1406.9073	1419.7297
122	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sm^{-0.5} + \beta_3 W$	-5353.5909	-276.7424***	5433.1438	55.2134***	0.1311	0.0021	25050.4750	1406.8970	1419.7194

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
123	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 Sm^{0.5} + \beta_3 W$	5891.6369	-277.9778***	-5817.6302	55.4694***	0.1315	0.0021	25039.0858	1406.8479	1419.6703
124	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E + \beta_3 G^{0.5}$	3266.8399	-239.1014***	-3357.2239	36.3495***	0.1324	0.0020	25012.9101	1406.7349	1419.5573
125	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E + \beta_3 Mi$	3195.5679	-216.6864***	-3129.0943	22.1586***	0.1261	0.0028	25193.8540	1407.5134	1420.3358
126	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E + \beta_3 MS^{0.5}$	3120.1685	-211.9247	-3054.2185	37.3097***	0.1261	0.0028	25195.2146	1407.5192	1420.3416
127	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E + \beta_3 W$	3176.5819	-188.4753***	-3129.5552	65.9669***	0.1322	0.0020	25017.8664	1406.7563	1419.5787
128	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E + \beta_3 A^{0.5}$	2869.4318	-347.5634***	-2588.3924	-106.5487***	0.1342	0.0018	24959.5169	1406.5041	1419.3266
129	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^2 + \beta_3 G^{-1}$	1950.9366	-230.6456***	-1808.1156	-1539.5151***	0.1329	0.0019	24999.4113	1406.6766	1419.4990
130	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^2 + \beta_3 Mi^{0.5}$	1706.7114	-210.3382***	-1667.7519	46.2864***	0.1280	0.0025	25140.2408	1407.2833	1420.1057
131	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^2 + \beta_3 (W+1)^{-0.5}$	1917.5143	-195.0746	-1671.2015	-208.7536	0.1310	0.0021	25051.3923	1406.9009	1419.7234
132	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^2 + \beta_3 W^{0.5}$	1701.5286	-200.6813	-1677.6319	74.0819	0.1325	0.0019	25008.7810	1406.7171	1419.5395
133	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-1} + \beta_3 G$	-2929.1123	-239.7169	2933.7577	3.9581	0.1325	0.0019	25008.6661	1406.7166	1419.5390
134	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-1} + \beta_3 G^2$	-2849.0955	-240.1099	2899.3849	0.0851	0.1313	0.0021	25042.7278	1406.8636	1419.6860
135	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-1} + \beta_3 Mi^{0.5}$	-2680.4587	-209.3730	2738.0986	43.9013	0.1283	0.0025	25130.1864	1407.2401	1420.0625
136	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-1} + \beta_3 MS$	-2590.8201	-214.7133	2675.7007	38.9646	0.1265	0.0027	25183.3608	1407.4684	1420.2908
137	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-1} + \beta_3 (W+1)^{-0.5}$	-2485.3030	-194.2675	2744.5601	-204.0374	0.1315	0.0021	25039.6453	1406.8503	1419.6727
138	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-1} + \beta_3 A^{0.5}$	-1982.0394	-346.9582	2272.3941	-106.8089	0.1347	0.0017	24945.0357	1406.4415	1419.2639
139	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-0.5} + \beta_3 G$	-6059.7312	-239.8626	6061.9408	3.9406	0.1324	0.0020	25013.0550	1406.7355	1419.5580
140	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-0.5} + \beta_3 (Mi+1)^{-1}$	-5537.3734	-213.3945	5662.9819	-58.1819	0.1268	0.0027	25173.8887	1407.4278	1420.2502
141	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-0.5} + \beta_3 Mi^{0.5}$	-5607.5049	-209.5094	5662.1309	44.2942	0.1283	0.0025	25131.1641	1407.2443	1420.0667
142	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{-0.5} + \beta_3 A^{-1}$	-5814.4816	-165.5469	5911.3150	-40.1174	0.1268	0.0027	25173.7303	1407.4271	1420.2495
143	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{0.5} + \beta_3 (Mi+1)^{-0.5}$	6208.8532	-214.6815	-6051.9838	-92.8959	0.1265	0.0027	25182.5896	1407.4651	1420.2875
144	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{0.5} + \beta_3 Mi^{0.5}$	6098.0327	-209.8115	-6049.5544	45.0859	0.1282	0.0025	25133.9538	1407.2563	1420.0787
145	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 E^{0.5} + \beta_3 A^2$	4432.7325	-418.1311	-4209.3444	-12.8908	0.1511	0.0007	24473.7902	1404.3817	1417.2041
146	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 R + \beta_3 A^{-1}$	723.6945	-293.4159***	-452.8154	-19.3691	0.0928	0.0171	26154.9639	1411.5568	1424.3792
147	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 R^2 + \beta_3 G$	502.0767	-307.3570***	-212.3606	-1.2718	0.0891	0.0208	26262.0077	1411.9979	1424.8203

No.	Model	β_0	β_1	β_2	β_3	R^2	$p - value$	MSE	AIC	BIC
148	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 R^2 + \beta_3 (Mi+1)^{-0.5}$	618.7366	-318.2367***	-218.8772	-168.8910	0.0936	0.0164	26131.7067	1411.4607	1424.2831
149	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 R^2 + \beta_3 Mi^{0.5}$	430.0104	-309.2395***	-223.1559	77.0927	0.0977	0.0132	26011.7713	1410.9639	1423.7863
150	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 R^{-1} + \beta_3 G^{0.5}$	-195.7235	-301.6191***	468.8733	-3.3961***	0.1002	0.0116	25940.7769	1410.6687	1423.4911
151	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 R^{-1} + \beta_3 Mi$	-240.7768	-307.1900***	478.3689	33.7398	0.1033	0.0098	25851.5639	1410.2967	1423.1191
152	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 MS + \beta_3 G$	179.1716	-355.7289	117.6781***	1.8306	0.0324	0.3279	27894.3574	1418.5104	1431.3328
153	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^2 + \beta_3 D^{-0.5}$	430.7515	-244.9404	744.9370	-322.8977***	0.1580	0.0004	24274.2048	1403.4973	1416.3197
154	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^2 + \beta_3 D^{0.5}$	-68.7564***	-244.3977	743.2530	191.4719***	0.1590	0.0004	24246.1995	1403.3726	1416.1951
155	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^2 + \beta_3 Mi^2$	200.8237	-267.9640	773.9101	-14.9966***	0.1451	0.0009	24646.5859	1405.1415	1417.9639
156	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^{-1} + \beta_3 N$	628.1899	-330.7868	-42.1501	-6.1056***	0.1312	0.0021	25047.2128	1406.8829	1419.7053
157	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^{-1} + \beta_3 N^2$	556.9142	-335.9176***	-46.0130	-0.0988***	0.1274	0.0026	25157.8560	1407.3590	1420.1814
158	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 Mi^2$	-402.9530	-232.3624***	1042.4495	74.0316***	0.1456	0.0009	24631.4256	1405.0751	1417.8975
159	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 R^{0.5}$	494.2735	-247.2580***	920.1053	-682.5660***	0.1693	0.0002	23948.6458	1402.0390	1414.8615
160	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 G$	-362.5361	-284.9164***	1125.5250	3.2098***	0.1348	0.0017	24942.7382	1406.4315	1419.2539
161	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 G^2$	-329.5917	-286.7663	1125.1313	0.0761***	0.1349	0.0017	24941.2191	1406.4249	1419.2474
162	$AGB = \beta_0 + \beta_1 TH^2 + \beta_2 S^{0.5} + \beta_3 Mi^2$	-275.9969	-257.2589	1083.9983	-10.5567***	0.1303	0.0022	25072.5465	1406.9921	1419.8145
163	$AGB = \beta_0 \times (TH^2)^{\beta_1}$	4.4210	-0.2102	-	-	0.0522	0.0174	0.7834	284.3425	292.1581
164	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh)^{\beta_2}$	7.1706	-0.1979	-2.2938	-	0.1114	0.0020	0.7414	279.5286	289.8687
165	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm)^{\beta_2}$	3.9295	-0.1896	-11.3883	-	0.1096	0.0023	0.7429	279.7447	290.0849
166	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (E)^{\beta_2}$	3.9556	-0.1713	-11.4485	-	0.1063	0.0027	0.7458	280.1536	290.4938
167	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (D)^{\beta_2}$	4.0884	-0.2026	0.5692***	-	0.0625	0.0338	0.7823	285.3175	295.6576
168	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (R)^{\beta_2}$	4.5539	-0.1917	-1.8806	-	0.0949	0.0053	0.7552	281.5138	291.8540
169	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (G)^{\beta_2}$	4.4248	-0.2102	-0.0013***	-	0.0522	0.0600	0.7909	286.5001	296.8403
170	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (G^2)^{\beta_2}$	4.4248	-0.2102	-0.0006***	-	0.0522	0.0600	0.7909	286.5001	296.8403
171	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times ((Mi+1)^2)^{\beta_2}$	4.2256	-0.2157	0.1890***	-	0.0578	0.0439	0.7862	285.8562	296.1964
172	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh)^{\beta_2} \times (G)^{\beta_3}$	5.9574	-0.2133	-2.7728	0.5836***	0.1238	0.0032	0.7382	280.2180	293.0404

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
173	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh)^{\beta_2} \times (Mi+1)^{\beta_3}$	6.9719	-0.2024	-2.2579	0.3013***	0.1150	0.0052	0.7456	281.2943	294.1167
174	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh)^{\beta_2} \times (MS+1)^{\beta_3}$	6.9790	-0.1981	-2.2258	0.5012***	0.1159	0.0049	0.7448	281.1768	293.9992
175	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh)^{\beta_2} \times ((W+1)^{-0.5})^{\beta_3}$	7.1640	-0.1976	-2.2929	-0.0342***	0.1114	0.0063	0.7486	281.7274	294.5498
176	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh)^{\beta_2} \times ((W+1)^{0.5})^{\beta_3}$	7.1640	-0.1976	-2.2929	0.0342***	0.1114	0.0063	0.7486	281.7274	294.5498
177	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh)^{\beta_2} \times (A)^{\beta_3}$	7.8877	-0.1371	-3.1427	0.5559***	0.1283	0.0025	0.7344	279.6561	292.4785
178	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^2)^{\beta_2} \times (G)^{\beta_3}$	5.9574	-0.2133	-1.3864	0.5836***	0.1238	0.0032	0.7382	280.2180	293.0404
179	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^2)^{\beta_2} \times (Mi+1)^{\beta_3}$	6.9719	-0.2024	-1.1290	0.3013***	0.1150	0.0052	0.7456	281.2943	294.1167
180	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^2)^{\beta_2} \times (W+1)^{\beta_3}$	7.1640	-0.1976	-1.1465	0.0171***	0.1114	0.0063	0.7486	281.7274	294.5498
181	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^2)^{\beta_2} \times (A)^{\beta_3}$	7.8877	-0.1371	-1.5714	0.5559***	0.1283	0.0025	0.7344	279.6561	292.4785
182	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^2)^{\beta_2} \times (A^2)^{\beta_3}$	7.8877	-0.1371	-1.5714	0.2779***	0.1283	0.0025	0.7344	279.6561	292.4785
183	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{-1})^{\beta_2} \times (G^2)^{\beta_3}$	5.9574	-0.2133	2.7728	0.2918***	0.1238	0.0032	0.7382	280.2180	293.0404
184	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{-1})^{\beta_2} \times (Mi+1)^{\beta_3}$	6.9719	-0.2024	2.2579	0.3013***	0.1150	0.0052	0.7456	281.2943	294.1167
185	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{-1})^{\beta_2} \times (MS+1)^{\beta_3}$	6.9790	-0.1981	2.2258	0.5012***	0.1159	0.0049	0.7448	281.1768	293.9992
186	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{-1})^{\beta_2} \times ((W+1)^{0.5})^{\beta_3}$	7.1640	-0.1976	2.2929	0.0342***	0.1114	0.0063	0.7486	281.7274	294.5498
187	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{-1})^{\beta_2} \times (A^{-0.5})^{\beta_3}$	7.8877	-0.1371	3.1427	-1.1118***	0.1283	0.0025	0.7344	279.6561	292.4785
188	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{-0.5})^{\beta_2} \times (G^{-1})^{\beta_3}$	5.9574	-0.2133	5.5455	-0.5836***	0.1238	0.0032	0.7382	280.2180	293.0404
189	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{-0.5})^{\beta_2} \times ((Mi+1)^2)^{\beta_3}$	6.9719	-0.2024	4.5159	0.1506***	0.1150	0.0052	0.7456	281.2943	294.1167
190	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{-0.5})^{\beta_2} \times ((MS+1)^{0.5})^{\beta_3}$	6.9790	-0.1981	4.4517	1.0023***	0.1159	0.0049	0.7448	281.1768	293.9992
191	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{-0.5})^{\beta_2} \times (W)^{\beta_3}$	7.1640	-0.1976	4.5859	0.0171***	0.1114	0.0063	0.7486	281.7274	294.5498
192	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{-0.5})^{\beta_2} \times (A)^{\beta_3}$	7.8877	-0.1371	6.2855	0.5559***	0.1283	0.0025	0.7344	279.6561	292.4785
193	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{0.5})^{\beta_2} \times (G)^{\beta_3}$	5.9574	-0.2133	-5.5455	0.5836***	0.1238	0.0032	0.7382	280.2180	293.0404
194	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{0.5})^{\beta_2} \times ((Mi+1)^2)^{\beta_3}$	6.9719	-0.2024	-4.5159	0.1506***	0.1150	0.0052	0.7456	281.2943	294.1167
195	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{0.5})^{\beta_2} \times ((MS+1)^2)^{\beta_3}$	6.9790	-0.1981	-4.4517	0.2506***	0.1159	0.0049	0.7448	281.1768	293.9992

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
196	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{0.5})^{\beta_2} \times ((W+1)^{-0.5})^{\beta_3}$	7.1640	-0.1976	-4.5859	-0.0342***	0.1114	0.0063	0.7486	281.7274	294.5498
197	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sh^{0.5})^{\beta_2} \times (A^{0.5})^{\beta_3}$	7.8877	-0.1371	-6.2855	1.1118***	0.1283	0.0025	0.7344	279.6561	292.4785
198	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm)^{\beta_2} \times (G^{0.5})^{\beta_3}$	2.0977	-0.2028	-13.7015	1.1310***	0.1213	0.0037	0.7403	280.5231	293.3455
199	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm)^{\beta_2} \times (Mi+1)^{\beta_3}$	3.7809	-0.1943	-11.2073	0.3027***	0.1132	0.0057	0.7470	281.5074	294.3298
200	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm)^{\beta_2} \times ((MS+1)^{0.5})^{\beta_3}$	3.8477	-0.1902	-10.9887	0.9015***	0.1133	0.0057	0.7470	281.5029	294.3253
201	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm)^{\beta_2} \times (W+1)^{\beta_3}$	3.9219	-0.1892	-11.3832	0.0240***	0.1097	0.0069	0.7501	281.9426	294.7650
202	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm)^{\beta_2} \times (A^2)^{\beta_3}$	3.4888	-0.1310	-15.2057	0.2553***	0.1243	0.0031	0.7378	280.1548	292.9772
203	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (G^{0.5})^{\beta_3}$	2.0977	-0.2028	-6.8508	1.1310***	0.1213	0.0037	0.7403	280.5231	293.3455
204	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((Mi+1)^{-1})^{\beta_3}$	3.7809	-0.1943	-5.6036	-0.3027***	0.1132	0.0057	0.7470	281.5074	294.3298
205	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((MS+1)^{0.5})^{\beta_3}$	3.8477	-0.1902	-5.4944	0.9015***	0.1133	0.0057	0.7470	281.5029	294.3253
206	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (W+1)^{\beta_3}$	3.9219	-0.1892	-5.6916	0.0240***	0.1097	0.0069	0.7501	281.9426	294.7650
207	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((W+1)^2)^{\beta_3}$	3.9219	-0.1892	-5.6916	0.0120***	0.1097	0.0069	0.7501	281.9426	294.7650
208	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((W+1)^{-1})^{\beta_3}$	3.9219	-0.1892	-5.6916	-0.0240***	0.1097	0.0069	0.7501	281.9426	294.7650
209	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((W+1)^{-0.5})^{\beta_3}$	3.9219	-0.1892	-5.6916	-0.0480***	0.1097	0.0069	0.7501	281.9426	294.7650
210	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times ((W+1)^{0.5})^{\beta_3}$	3.9219	-0.1892	-5.6916	0.0480***	0.1097	0.0069	0.7501	281.9426	294.7650
211	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (A)^{\beta_3}$	3.4888	-0.1310	-7.6028	0.5105***	0.1243	0.0031	0.7378	280.1548	292.9772
212	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (A^2)^{\beta_3}$	3.4888	-0.1310	-7.6028	0.2553***	0.1243	0.0031	0.7378	280.1548	292.9772
213	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (A^{-1})^{\beta_3}$	3.4888	-0.1310	-7.6028	-0.5105***	0.1243	0.0031	0.7378	280.1548	292.9772
214	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (A^{-0.5})^{\beta_3}$	3.4888	-0.1310	-7.6028	-1.0211***	0.1243	0.0031	0.7378	280.1548	292.9772
215	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^2)^{\beta_2} \times (A^{0.5})^{\beta_3}$	3.4888	-0.1310	-7.6028	1.0211***	0.1243	0.0031	0.7378	280.1548	292.9772
216	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^{-1})^{\beta_2} \times (G)^{\beta_3}$	2.0977	-0.2028	13.7015	0.5655***	0.1213	0.0037	0.7403	280.5231	293.3455
217	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^{-1})^{\beta_2} \times ((Mi+1)^{0.5})^{\beta_3}$	3.7809	-0.1943	11.2073	0.6053***	0.1132	0.0057	0.7470	281.5074	294.3298
218	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^{-1})^{\beta_2} \times (MS+1)^{\beta_3}$	3.8477	-0.1902	10.9887	0.4508***	0.1133	0.0057	0.7470	281.5029	294.3253
219	$AGB = \beta_0 \times (TH^2)^{\beta_1} \times (Sm^{-1})^{\beta_2} \times ((W+1)^{-1})^{\beta_3}$	3.9219	-0.1892	11.3832	-0.0240***	0.1097	0.0069	0.7501	281.9426	294.7650

No.	Model	β_0	β_1	β_2	β_3	R^2	$p-value$	MSE	AIC	BIC
220	$AGB=\beta_0\times(TH^2)^{\beta_1}\times(Sm^{-1})^{\beta_2}\times(A^2)^{\beta_3}$	3.4888	-0.1310	15.2057	0.2553***	0.1243	0.0031	0.7378	280.1548	292.9772
221	$AGB=\beta_0\times(TH^2)^{\beta_1}\times(Sm^{-0.5})^{\beta_2}\times(G)^{\beta_3}$	2.0977	-0.2028	27.4031	0.5655***	0.1213	0.0037	0.7403	280.5231	293.3455
222	$AGB=\beta_0\times(TH^2)^{\beta_1}\times(Sm^{-0.5})^{\beta_2}\times((Mi+1)^2)^{\beta_3}$	3.7809	-0.1943	22.4145	0.1513***	0.1132	0.0057	0.7470	281.5074	294.3298
223	$AGB=\beta_0\times(TH^2)^{\beta_1}\times(Sm^{-0.5})^{\beta_2}\times((MS+1)^{0.5})^{\beta_3}$	3.8477	-0.1902	21.9775	0.9015***	0.1133	0.0057	0.7470	281.5029	294.3253
224	$AGB=\beta_0\times(TH^2)^{\beta_1}\times(Sm^{-0.5})^{\beta_2}\times((W+1)^{-1})^{\beta_3}$	3.9219	-0.1892	22.7665	-0.0240***	0.1097	0.0069	0.7501	281.9426	294.7650
225	$AGB=\beta_0\times(TH^2)^{\beta_1}\times(Sm^{-0.5})^{\beta_2}\times(A^2)^{\beta_3}$	3.4888	-0.1310	30.4113	0.2553***	0.1243	0.0031	0.7378	280.1548	292.9772
226	$AGB=\beta_0\times(TH^2)^{\beta_1}\times(Sm^{0.5})^{\beta_2}\times(G^{-0.5})^{\beta_3}$	2.0977	-0.2028	-27.4031	-1.1310***	0.1213	0.0037	0.7403	280.5231	293.3455

Annex 5: R-script for tree above gorund biomass and índices calcutation

```
###################################################################################
################################ MASTER THESIS ####################################
####################### DOAN THI NHAT MINH _ DATAFOREST ###########################
######################## BIOMASS & INDICES CALCULATION ############################
#----------------------------------------------------------------------------------
################## Data from Marterloscope core 43 in VNU_Vietnam #################
#----------------------------------------------------------------------------------

# Set working directory
setwd("C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/data/processed")
getwd()
# Import data of Marteloscope A43 in VNU_Vietnam
data<-read.csv("data_Marteloscope1_MSc_Minh_DATAFOREST.csv", header=TRUE)
names(data) #check data
names(data)[5]<-paste("Tree_form")
data <- subset( data, select = -c( 8 : 12 ))
names(data)
# CONTENTS of the script:
##### BIOMASS CALCULATION
# > Total Above ground biomass
# > By compartment: Stems/ Braches/ Leaves
##### CHARACTERISTICS
# > At Individual tree level
# >   -  Basal area (gi)
# >   -  Species proportion (Pi) defined in terms of basal area
# >   -  Density of the stand (Density)
# >   -  Relative density (Re_density)
# >   -  Relative density index (RDI)
# >   -  Slenderness (h/d ratio)
# >   -  Crown indices
# > At quadrant level
# >   -  Basal area (G)
# >   -  Above ground bimomass of each quadrant
# >   -  Number of tree per hectare for each quadrant (N)
##### DIVERSITY INDICES (stand level indices)
# > Simpson index (D)
# > Shannon index (H)
# > Evennes index (E)
# > Berker-Parker index (D)
##### SPATIAL POINT PATTERN ANALYZES (stand level indices)
# > L function (L)
# >   -  at whole stand level
# >   -  at quadrat level
# >   -  at species level (within and between interactions of species) within each quadrat
# > Aggregation index (R)
# >   -  at whole stand level
# >   -  at quadrat level
# >   -  at species level (within and between interactions of species) within each quadrat
##### SPECIES INTERMINGLING INDICES (tree level indices)
# > Mingling index (Mi)
# > Spatial diversity Status (MS)
# > Uniform angle index (W)
# > Segregation index (S)
##### VERTICAL SPATIAL PATTERN INDICES (stand level indices)
```

```
# > Vertical species profile (A)
# > Height differentiation index (TH)

###################################################################
####################### BIOMASS CALCULATION #######################
#------------------------------------------------------------------
# Requiring the packages
#if(!require("dplyr"))install.packages("dplyr")
# cif(!require("lattice"))install.packages("lattice")
library(dplyr)
library(lattice)
## Calculate of each species
# >   AGB =Total above ground biomass
# >   Ws = STEM biomass of different species
# >   Wl = LEAVES biomass of different species
# >   Wb = Brances biomass of different species

## 7 Species
# >   Acacia auriculiformis    #full equations
# >   Acacia mangium           #full equations
# >   Eucalyptus camaldulensis #full equations
# >   Senna siamea             #no compartments equation
# >   Litsea glutinosa         #full equations
# >   Averrhoa carambola       #no compartments equation
# >   Aporosa villosa          #no compartments equation

# Using ifelse() function to calculate AGB and biomass in compartments of each species
# ifelse(test, yes, no) where
# test: an object which can be coerced to logical mode -> defining each species
# yes: return values for true elements of test -> the equation
# no: return values for false elements of test -> Test of another specie

# defining parameters for biomass calculation
# DBH (cm), H(m), biomass(kg)
d<-data$Diameter_cm
h<-data$Total_height_m
species<-data$Specie

# AGB = Total above ground biomass of different species
data$AGB_kg <- ifelse(species == "Acacia auriculiformis", -
2.1737+0.5109*(0.1911*(d^1.9710)*(h^0.5391)), #Thanh, 2014_Vietnam
               ifelse(species == "Acacia mangium", exp(-1.073+2.081*log(d)), #Traore, 2018_Cote
d'Ivoire
               ifelse(species == "Senna siamea",exp(-3.1141+0.9719*log((d^2)*h)), #Brown, 1989_Tropical
Forest
               ifelse(species == "Eucalyptus camaldulensis",0.035*((d^2)*h)^0.953, #Ounban,
2016_Thailand
               ifelse(species == "Litsea glutinosa", 0.1142*(d^2.4451), #UN-REDD, 2012_Vietnam
               ifelse(species=="Averrhoa carambola", exp(-3.1141+0.9719*log((d^2)*h)), #Brown,
1989_Tropical Forest
               ifelse(species == "Aporosa villosa", exp(-3.1141+0.9719*log((d^2)*h)),  #Brown,
1989_Tropical Forest
               ifelse(species == "Died", exp(-3.1141+0.9719*log((d^2)*h)), NA))))))))  #Brown,
1989_Tropical Forest


# Ws = Stem biomass of different species
data$Ws_kg <- ifelse(species == "Acacia auriculiformis", -1.4322+0.5072*(0.0984*(d^1.8862)*(h^0.7628)),
#Thanh, 2014_Vietnam
              ifelse(species == "Acacia mangium", exp(-3.228+1.681*log(d)+1.056*log(h)), #Traore,
2018_Cote d'Ivoire
```

```
              ifelse(species == "Senna siamea",0, #No compartments equations
              ifelse(species == "Eucalyptus camaldulensis",0.019*((d^2)*h)^1.005, #Ounban, 
2016_Thailand
              ifelse(species == "Litsea glutinosa", 0.1274*(d^2.3655), #UN-REDD, 2012_Vietnam
              ifelse(species=="Averrhoa carambola", 0, #No compartments equations
              ifelse(species == "Aporosa villosa", 0, 0)))))))  #No compartments equations

# Wl = Leaves biomass of different species
data$Wl_kg <- ifelse(species == "Acacia auriculiformis", -0.1051+0.5135*(0.0434*(d^1.9294)*(h^0.2828)), 
#Thanh, 2014_Vietnam
              ifelse(species == "Acacia mangium", exp(-0.882+1.399*log(d)), #Traore, 2018_Cote d'Ivoire
              ifelse(species == "Senna siamea",0, #No compartments equations
              ifelse(species == "Eucalyptus camaldulensis",0.013*((d^2)*h)^0.721, #Ounban, 
2016_Thailand
              ifelse(species == "Litsea glutinosa", 0.0785*(d^1.4696), #UN-REDD, 2012_Vietnam
              ifelse(species=="Averrhoa carambola", 0, #No compartments equations
              ifelse(species == "Aporosa villosa", 0, 0)))))))  #No compartments equations

# Wb = Brances biomass of different species
data$Wb_kg <- ifelse(species == "Acacia auriculiformis", 0.0840+0.4973*((0.1911*(d^1.9710)*(h^0.5391))-
(0.0984*(d^1.8862)*(h^0.7628)+0.0434*(d^1.9294)*(h^0.2828))), #Thanh, 2014_Vietnam
              ifelse(species == "Acacia mangium", exp(-0.865+0.498*log((d^2)*h)), #Traore, 2018_Cote 
d'Ivoire
              ifelse(species == "Senna siamea",0, #No compartments equations
              ifelse(species == "Eucalyptus camaldulensis",0.015*((d^2)*h)^0.697, #Ounban, 
2016_Thailand
              ifelse(species == "Litsea glutinosa", 0.0102*(d^2.5848), #UN-REDD, 2012_Vietnam
              ifelse(species=="Averrhoa carambola", 0, #No compartments equations
              ifelse(species == "Aporosa villosa", 0, 0))))))) #No compartments equations

# View data to check result
#View(data)
sum(data$AGB_kg)
mean(data$Diameter_cm)
mean(data$Total_height_m)

# CALCULATE CARBON STOCK
data$C <- (data$AGB_kg)*0.5
data$CO2 <-(data$C)*3.666

# write csv file as the result of biomass calculation
write.csv(data, file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/Biomass_Carbon_A83.csv")

############################################################################
############################ CHARACTERISTICS ###############################
#--------------------------------------------------------------------------

#####----------------- AT INDIVIDUAL TREE LEVEL -----------------
# > At Individual tree level
# >   -  Basal area (gi)
# >   -  Species proportion (Pi) defined in terms of basal area
# >   -  Relative density (Re_density)
# >   -  Relative density index (RDI)
# >   -  Slenderness (h/d ratio)
# >   -  Crown indices
### Tree Basal area
# the cross-sectional area of a stem, usually measured at breast height
# Gi=(pi/4)*d^2
```

```
# Gi(m2) d(m)
data$Gi_m2 <- (pi/4)*(data$Diameter_cm*0.01)^2
### Species proportion (Pi) defined in terms of basal area
data$Pi <- data$Gi_m2/sum(data$Gi_m2)
### Density of the Marteloscope
D_marte<-sum(data$Gi_m2)/max(data$Gi_m2)
D_marte
### Height diameter ratio or Slenderness (h/d ratio)
# (Mitchell, 2000). The more growing space a tree is granted,
# the longer its crown and the smaller its height diameter ratio
# Slenderness = h/d where h(m), d(m)
# data$h_d_ratio_m  <- ifelse(species != "Died", (data$Total_height_m)/(data$Diameter_cm*0.01),"Died")
### Crown indices or ratios
# Crown ratio = crown length/tree height
# data$Crown_ratio <- ifelse(species != "Died", (data$Total_height_m-
data$H_to_canop_m)/(data$Total_height_m),"Died")
# Crown form index = crown length/crown width
# data$Crown_form_index <- ifelse(species != "Died", (data$Total_height_m-
data$H_to_canop_m)/((data$Canopy_W1_m+data$Canopy_W2_m)/2),"Died")
# Linear crown index
# data$Linear_crown_index <- ifelse(species != "Died",
((data$Canopy_W1_m+data$Canopy_W2_m)/2)/(data$Diameter_cm*0.01),"Died")
# Crown spread ratio
# data$Crown_spread_ratio <- ifelse(species != "Died",
((data$Canopy_W1_m+data$Canopy_W2_m)/2)/(data$Total_height_m),"Died")

#####------------------- AT QUADRANT LEVEL ---------------------
# >  Propotion of each species
# >  Basal area (G)
# >  Above ground bimomass of each quadrant
# convert name of species (column) in letter into numerical value
data$spNum <-as.numeric(data$Specie)
head(data)
# subset each quadrant separately
q1  <- subset(data, Cell==1)
q2  <- subset(data, Cell==2)
q3  <- subset(data, Cell==3)
q4  <- subset(data, Cell==4)
q5  <- subset(data, Cell==5)
q6  <- subset(data, Cell==6)
q7  <- subset(data, Cell==7)
q8  <- subset(data, Cell==8)
q9  <- subset(data, Cell==9)
q10 <- subset(data, Cell==10)
q11 <- subset(data, Cell==11)
q12 <- subset(data, Cell==12)
q13 <- subset(data, Cell==13)
q14 <- subset(data, Cell==14)
q15 <- subset(data, Cell==15)
q16 <- subset(data, Cell==16)
# create list of all the data
data.list <- list(q1,q2,q3,q4,q5,q6,q7,q8,q9,q10,q11,q12,q13,q14,q15,q16)

# function to calculate carbon stocks
C <- function(x){
  AGB <- sum(x)
  C <- AGB*0.5*3.67
  return(C)
```

```
}
# function to calculate basal area
G <- function(x){
  G  <- sum(x)/(1/16) # G=sum(gi)/S (of the quadrant
  return(G)
}
# function to calculate ABG of a quadrant
AGB<- function(x){
  AGB<- sum(x)
  return(AGB)
}
# funtion to calculate number of tree per hectare
N<- function(x){
  N<-length(x)*(10000/625) # N = no of tree in a quadrant*(1ha/S of the quadrant)
  return(N)
}
#apply all the functions for all quadrants simultineously:
Character <- lapply(data.list, function(x){
  for(i in 1:nrow(x)){
    x$TotalAGB_Kg <-AGB(x$AGB_kg)
    x$Basal_area <-G(x$Gi_m2)
    x$Treeperha <- N(x$Cell)
    x$Carbon <- C(x$AGB_kg)
  }
  x
})
#View(Character[[3]]) #to check the result of quadrant 3
# reconstruct initial dataframe back
Characteristic<- bind_rows(Character)
# Propotion of each species
# count the number of trees in each species type (n)
data1 <- Characteristic  %>%
  group_by(Cell, Specie)  %>%
  mutate(n = n())
# count the total number of trees in each quadrant (N)
Characteristic <- data1 %>%
  group_by(Cell) %>%
  mutate(N = n(),          # get total number of trees in each quadrant
         sp.prop = n/N)    # calculate proportion of each species in each quadrant

# reconstruct initial dataframe back
data <- merge(data, Characteristic, all.x = FALSE)
names(data)
#######################################################
################## DIVERISTY INDICES ##################
#-----------------------------------------------------
# >   Evennes index (E)
# >   Berker-Parker index (D)
# >   Simpson index (D)
# >   Shannon index (H)
# Requiring the packages
#if(!require("vegan"))install.packages("vegan")
#if(!require("spatstat"))install.packages("spatstat")
library(vegan)
library(spatstat)
### first thing that we need to prepare our data for the analyzes
```

```
# we already converted name of species (column) in letter into
# numerical value because of vegan requirement.
### define functions that are going to be applied for each quadrant:
# functions of some indices have already been developed in vegan package, Some are not
# we should write function for those that don't have pre-defined function.

# function for Evenness index:
E <-function(x){
  H <- diversity(x)       # shannon
  S <- specnumber(x)      # number of species, rowSums(BCI > 0) does the same...
  E <- H/log(S)           # equation of Evennes index
  return(E)
}
# function for Berger-Parker index:
D <-function(x){
  N <- length(x)           # total number of individuals in the quadrants
  n <- table(x)            # number of individuals of each species
  Nmax <-max(n)            # number of individuals in the most abundant species
  D <- Nmax/N              # equation of Berker parker index
  recip.D <- 1/D           # reciprocal of the index
  return(recip.D)
}
### apply all the functions for all quadrants simultineously:
result <- lapply(data.list, function(x){
  for(i in 1:nrow(x)){
    x$simpson <-diversity(x$spNum, "simpson") #get simmpson diversity index
    x$shannon <-diversity(x$spNum, "shannon") #get shannon index
    x$E <- E(x$spNum) #Evenness index
    x$D <- D(x$spNum) #Berger-Parker index
  }
  x  # x is argument of the function, not variable
})
#View(result[[16]]) #check if the result is okay
# reconstruct initial dataframe back
Diver <- bind_rows(result)
write.csv(Diver, file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/Diversity_Indices.csv")
# combine result into original data
data <- merge(data, Diver, all.x = FALSE)
names(data)
write.csv(data, file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/AGB_C_indices.csv")

######### SPATIAL POINT PATTERN ANALYZES (stand level indices) ########
#----------------------------------------------------------------------

#####----------------------- L function (L) --------------------------
# >   -  at whole stand level
# >   -  at quadrat level
# >   -  at species level (within and between interactions of species) within each quadrat

# L function is used to analyze spatial point pattern.
# Spatial point pattern analysis (SPP) --> used to study the distribution of discrete points,
# analyze and obtain information about spatial structure of individuals dispersed within a study area.
# The idea is to distinguish between point patterns which tend toward complete spatial randomness
(CSR),
# clumping or regularity and at which scale these characterics occur.
# Main question of our analyze here is distribution of points in our study are differs from CSR.
```

```
# Therefore, for each level:
# >   1st L function is calculated
# >   2nd randomization test (Poisson null: CSR) is used to check if points different from CSR.

##### L for a whole marteloscope ----------------
### Create spatial point pattern object from xy coordinates of the points (trees).
# Use ppp()to create spatial point pattern object.
# Syntax: name <- ppp(X, Y, rangeX, rangeY) OR name=ppp(X, Y, window=window).
# --> need find ranges of x & y (define observation window).
# create observation window from our data (xy coordinates of points) using ripras() function.
# ripras() is used to determine observation window that fit/correspond to our points.
window_marte <- ripras(data$Long, data$Lat)

# create a point-pattern object that contains both the points and the observation window.
point_patt <- ppp(data$Long, data$Lat, window= window_marte)
plot(point_patt)

# compute L function
L_marteloscope <- Lest(point_patt, correction="Ripley")
L_marteloscope
plot(L_marteloscope, main = "L-function at whole stand level")
# As we can see the result, analyzing SPP for a while plot don't provide much information for us.
# so lets analyze SPP for each quadrants.

##### L for each quadrat ---------------------
# apply L funcion for a list of datasets:
L_quadrant <- lapply(data.list, function(x) {       # apply function to a list of datasets
  window_qd <- ripras(x$Long, x$Lat)            # create observation plot that fits to points
  point_patt <- ppp(x$Long, x$Lat, window=window_qd) # create point patterns from coordinates of trees
  return( Lest(point_patt, correction="Ripley"))    # calculate L function
})

plot.anylist(L_quadrant[1:8], main="L-function for quadrants 1 to 8")
plot.anylist(L_quadrant[9:16], main="L-function for quadrants 9 to 16")
plot.anylist(L_quadrant[1])
plot.anylist(L_quadrant[9])
#export immages

##### L for each species in each quadrant -----------------
# In this section, we analyze within & between interactions of different species in each quadrants.
# Main steps for this analzye:
# 1. group species by their type with factor() function.
# 2. create observation window
# 3. create point pattern object within observation window
# 4. split each species type
# 5. compute L function
# 6. check CSR by randomisation test using envelope() function.
# Combined the steps from 1 to 5 are in a single function and applied this function to
# the list of datasets (quadrants) as below.

L_specie <- lapply(data.list, function(x) {    # apply function to a list of datasets
  group <- factor(x$Specie)            # group species that belong to the same species together
  window_sp <- ripras(x$Long, x$Lat)    # create observation window
  pp.group <- ppp(x$Long, x$Lat, window= window_sp, marks=group) # create point pattern within window
  split.group <- split(pp.group)          # split species by their group
  return(alltypes(pp.group, "L"))       # compute L function for all types of species
```

```
})

plot.anylist(L_specie[13], main="L-function for Acacia auriculiformis and Acacia mangium")
#export immages

## Explanation:
# the diagonal plots show the result of L function to examine within and between species interaction
# in quadrant 1. These indicate that there are some variation of clustering (repulsion) at
# different distances.
# the Kpois(r) line in blue is the theoretical value of L for each distance window (r) under
# a Poisson assumption of Complete Spatial Randomness (CSR). The other line is the estimated
# values of L accounting...
# wherever the value of L falls above the line, species appear to be clustered at that distance.
# Wherever the value of L is below the line, the data are dispersed. \

#####--------------------- Aggregation index (R) --------------------------
# >  at whole stand level
# >  at quadrat level
# >  at species level (within and between interactions of species) within each quadrat

##### Aggregation index measures how point objects are distributed in an area.
# Distribution could be grouped into 3 types: even (dispersed),
# random (chaotic), and aggregated (clustered) distribution.
# clarkevans.test() performs the Clark-Evans test of aggregation for a "spatial point pattern".
# This command uses the Clark and Evans (1954) aggregation index R as the basis for a
# crude test of clustering or ordering of a point pattern.
# The null hypothesis is Complete Spatial Randomness, i.e. a uniform Poisson process.

# R is a single number indix which creates one single number to characterize a certain
# structural aspect.
# IF R < 1 => clustered pp; R > 1 => regular (ordered) pp
# Syntax:
# name<-clarkevans.test(X, ...,
#                 correction = "none",
#                 clipregion = NULL,
#                 alternative = c("two.sided", "less", "greater",
#                               "clustered", "regular"),
#                 nsim = 999)
# x is point pattern object (ppp).
# clipregion is window (object of owin)
# nsim is number of Monte Carlo simulations to perform, if a Monte Carlo p-value is required.

##### R for whole marteloscope ------------------------
R_marte <- clarkevans.test(point_patt,
                           clipregion = window_marte,
                           correction = "cdf",
                           alternative = "clustered",
                           nsim = 999)
head(R_marte)

##### R for each quadrat ------------------------------
R_quadrant <- lapply(data.list, function(x) {        # apply function to a list of datasets
  window_qd <- ripras(x$Long, x$Lat)             # create observation plot that fits to points
  point_patt <- ppp(x$Long, x$Lat, window=window_qd) # create point patterns from coordinates of trees
  return(clarkevans.test(point_patt,
                         clipregion = window_qd,
```

```
                         correction = "cdf",
                         alternative = "clustered",
                         nsim=999))            # number of simulation
})
head(R_quadrant[1:4])
head(R_quadrant[5:8])
head(R_quadrant[9:12])
head(R_quadrant[13:16])

##### R for each species of each quadrat --------------
R_specie<- lapply(data.list, function(x) {  # apply function to a list of datasets
  group <- factor(x$Specie)               # group species that belong to the same species
  window_sp <- ripras(x$Long, x$Lat)       # create observation window
  pp.group <- ppp(x$Long, x$Lat, window= window_sp, marks=group) # create point pattern within window
  return(clarkevans.test(pp.group,             # calculate aggregation index (R)
                         clipregion = window_sp,
                         correction = "cdf",
                         alternative = "clustered",
                         nsim = 999))       # compute R function for all types of species
})
head(R_specie[1:4])
head(R_specie[5:8])
head(R_specie[9:12])
head(R_specie[13:16])
names(data)

#merge R in data
data$R<- ifelse(data$Cell == "1", 0.9494,
         ifelse(data$Cell == "2", 1.1597,
         ifelse(data$Cell == "3", 1.1402,
         ifelse(data$Cell == "4", 1.1244,
         ifelse(data$Cell == "5", 0.9529,
         ifelse(data$Cell == "6", 1.0935,
         ifelse(data$Cell == "7", 1.0483,
         ifelse(data$Cell == "8", 1.1466,
         ifelse(data$Cell == "9", 0.8248,
         ifelse(data$Cell == "10", 1.0243,
         ifelse(data$Cell == "11", 0.9506,
         ifelse(data$Cell == "12", 1.1714,
         ifelse(data$Cell == "13", 1.1994,
         ifelse(data$Cell == "14", 1.1326,
         ifelse(data$Cell == "15", 0.9845,
         ifelse(data$Cell == "16", 0.9166,"no"))))))))))))))))

##############################################################################################
############################ SPECIES INTERMINGLING INDICES ###################################
#---------------------------------------------------------------------------------------------
# >   Mingling index (Mi) code adapted from Irene
# >   Spatial diversity Status (MS)
# >   Uniform angle index (W)
# >   Segregation index (S)

##### ---------------Species mingling (mixture) index (Mi) -------------------
# We will use the coordinates of every tree and the basic
# equation to obtain the Euclidean distance between trees
# and then we'll select the nearest neighbour trees
```

```
##### Process
# 1/ Define the predefined number of nearest trees (neighbours [j])
# 2/ Use a loop to
# >   Calculate the distance between all the trees in the dataset (Euclidean distance)
# >   Order the results, for each tree, from the closes to the farthest tree.
# >   Keep only the predefined nearest trees (neighbours)

### Calculation of Euclidean distance:
# with the Euclidean distance equation, we will calculate distances of every trees from each
# reference tree [i}. Every trees are the reference tree which means if there are 10 trees in plot
# then distances from 1st tree to other 9 trees are calculated in pairs.
# First each tree will be numbered according to their locations in row. And then
# distances will be calculated from each tree to all other trees
### For selecting the nearest [k] trees (n.nearest) for a reference tree
# nearest neighbor trees of each tree will be selected based on distances from closest to
# farthest after distances are ordered. if we choose 3 nearest neighbour trees to each
# reference trees, then 40 distance (10 trees * 4 neigbours = 40) will be selected.
##### Calculate the distances to each neighbour ------------------------
# create a dataframe to save the result later
dist.m<-data.frame()
# defining the number of neighbours
Neareast_trees<-4
# starting the loop
for (i in 1:nrow(data)){
  # obtaining the distance from tree [i] (our target) to every tree using Euclidean equation.
  distij <- ((data$Long[i]-data$Long)^2+(data$Lat[i]-data$Lat)^2)^(1/2)
  # now we identify the tree [i] and its neighbours [j]
  temp<-data.frame(target_tree_i=data$Tree_ID[i],neighbour_j=data$Tree_ID,
                   sp_i=data$Specie[i],sp_j=data$Specie,
                   dbh_i=data$Diameter_cm[i],dbh_j=data$Diameter_cm,
                   H_i=data$Total_height_m[i],H_j=data$Total_height_m,
                   x_i=data$Long[i],x_j=data$Long,
                   y_i=data$Lat[i],y_j=data$Lat,
                   distij)
  temp<-temp[order(distij),]  # and order it from closest to farthest distance to our target tree
  temp<-temp[-1,]   # delete the first row because is our target tree i (reference tree to itself)
  neighbour<-temp[1:Neareast_trees,]  # select the neareast trees (4 trees) closest to tree i
  dist.m <- rbind(dist.m,neighbour)   # now combind the result with our original
} # close the loop
head(dist.m)  # to finish this part we check the new structure of our dataset
print(dist.m, digits = 10)

# Obtaining the spatial mingling index ---------------------------
### Define the mixture variable for each tree,
# We will use the Gadow (1993) mingling index which is an extension of the species segregation
# index by Pielou (1977) which compares pairs of points formed by the locations of an arbitrary
# plant & its nearest neighbour. For all plants in a research plot these pairs are determined.
# The tree attribute mingling describes the species variety in the nearest neighbours of a given
# reference tree and has been defined as the proportion of the n nearest neighbours that don't
# belong to the same species.

### Basic steps to achieve this is to:
# 1/ Identify whether each of the nearest 4 neighbour trees is the same species with
#      reference tree or not.
# 2/ Calculate Mi index to find out how many of the 4 are the different species than reference
```

```
#      tree. It will be expressed as proportion as mentioned right above.

# Define the mixture variable for each tree,
# >   0 if the j species is the same as i
# >   1 if not the same
dist.m$Vij <- ifelse ((dist.m$sp_i==dist.m$sp_j), 0, 1)
# write the outcome
write.csv(dist.m,file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/dist_m.csv")
head (dist.m) # check if everything is ok

# we calculate the mingling index for each target tree for the nearest neighbours
nfilas =seq(1,length(dist.m[,1]), by=Neareast_trees)
result =c()
# for each different tree
for (i in nfilas){
  vectordindices = c()
  # keep the mingling index value for each target tree
  for (j in seq(0,Neareast_trees-1)){
    vectordindices=c(vectordindices, dist.m$Vij[i+j])
  }
  # calculate the average of the mingling index (Mi) for each tree and store it
  indiceagregadoi = mean(vectordindices)
  result=c(result,rep(indiceagregadoi,Neareast_trees))
}
# add the mingling indext to our data
result <-as.matrix(result)
colnames(result)<-"Mi"
dist.m=cbind(dist.m,result)
head(dist.m) # check if everything is ok
plot(dist.m$Mi)
new <- dist.m[nfilas,]
names (new) # check the order of the columns
mixture <- new [,c(1,3,5,7,9,11,13,14,15)] #select the columns with the i tree information

# check if everything is ok
names(mixture)
names(mixture)[1]<-paste("Tree_ID")
names(mixture)[5]<-paste("Long")
# combine result into original data and clean it by deleting unesscesary column
data <- merge(data, mixture, by=c("Tree_ID","Long") , all.x = FALSE)
names(data)
data <- subset( data, select = -c( 31 : 36 ))
names(data)
names(mixture)[1]<-paste("target_tree_i")
names(mixture)[5]<-paste("x_i")
plot(data$Mi)

#------------------------- Spatial diversity status (MS) index ----------------------------
# library(dplyr)
# MS is an improvement of Mi. It describes the degree of intermingling of two species or
# species groups based on nearest-neighbor method. S considers the ratio of the observed
# probability (pij) that reference tree i and its nearest-neighbour j belong to different
# species along with the same probability for completely randomly distributed or independent
# species attributes.

# MS=Si*Mi/Nmax
```

```
# Si is the number of tree species in the neighbourhood of reference tree i (including reference tree
i)
# Nmax is the maximum number of the species in the structure unit
# Range -1 to 1. If MS > 0, it indicates toward segregation;
#                if MS < 0 => association with nn species
#                if MS near 0 => independent distribution

# To do this we will count them 4 by 4 rows. In this case, we can get
# the length of original data (507 rows). if we count them by grouping species, we will not get
names(dist.m)
Si <- dist.m %>%
  group_by(group = gl(n()/4, 4), sp_i) %>%  # generate factor level using sp.tree levels 4 by 4 rows
  summarise(count = n_distinct(sp_j)); Si  # count diff species including sp.tree (i)
# gl() is used to generate factor levels.
# Syntax: gl(n, k, labels); n=number of levels. k=the number of replications, labels is a
# vector of labels for the resulting factor levels.
# n_distinct() is to count the number Of unique values in a set Of vector
# define nmax (max number of species in the structural unit i.
nmax <- 5
# for nn = 4, nmax = 5 including reference tree itself according to reference (?).
# So in my understanding, structure unit is: structure unit = nn + reference tree.
# if nn=3, it is 4 etc
# save the result in data
data$MS <- (Si$count* data$Mi)/nmax
names(data)

#---------------------------- Uniform Angle Index (W) ------------------------------
# The uniform angle index (UAI) is used to characterize the spatial distribution of a forest
# community or of individual tree species within that community and determined as the
# proportion of the angles that are smaller than the standard angle.
# for ex: if we concern 4 neighbor trees, result will return five values,0,0.25,0.5,0.75,1,
# which means none, one, two, three, or four angles are smaller than standard angle, respectively.
# standard angle can be defined as (360/n) where n is number of neighbour tree.

### Procedures:
# >  calculate distance between ref tree & nearest neighbour trees based on Euclidean distance
# >  calculate angles between adjusting nn trees
# >  define angles less than standard angle
# >  compute w index.

##### calculate distance between tree [i] to each nearest trees [j]----------------
# this has already been done when Mi calculated
##### calculate angles between vectors of tree [i] and each nearest tree [j]------------
# Inputs:
# x1 = x coordinates of tree [i]
# y1 = y coordinates of tree [i]
# x2 = x coordinates of tree [j]
# y2 = y coordinates of tree [j]

# to calculate angles,
# 1. we need to compute length of sides (xl, yl, cl) of right rectangles.
# 2. use trigonometer to calculate angles. We use atan(yl/xl).
# 3. convert radians to degree because output of atan2() is in radians.
#    to convert radians to degree, we need to multiple radians by 180°/pi.
#    (to convert degree to radians, we need to multiply it by pi/180°)
# 4. normalise in degree
```

```
### write function to calculate angles between vectors

angle.fun <- function(x1, x2, y1, y2){
  xl <- x2-x1                 # array of vectors in X
  yl <- y2-y1                 # array of vectors in Y
  cl <- (xl^2 + yl^2)^0.5     # which is the same with "dist.m$distij"
  atang <- atan2(yl, xl)      # angle in radians
  ang.deg <- atang * 180/pi   # convert radians to degree
  ang.deg[ang.deg < 0] <- ang.deg[ang.deg < 0] + 180
  return(ang.deg)
}

# apply it on our data
dist.m$angle <- angle.fun(dist.m$x_i, dist.m$x_j, dist.m$y_i, dist.m$y_j)

##### Define angles less than standard angle ----------------------------------
st_angle <- 360/Neareast_trees     # standard angle
# if an angle is less than standard angle, then it is 1; otherwise, 0.
dist.m$Vij <- ifelse(dist.m$angle < st_angle, 1, 0)
head(dist.m)
# calculate W for each reference [i] tree
UAI_W <- dist.m %>%
  select(target_tree_i, sp_i, dbh_i, H_i, x_i, y_i, distij, Vij) %>%
  group_by(tree1 = gl(n()/4, 4), sp_i) %>%
  mutate(W = mean(Vij), dbh_i = dbh_i[1], H_i = H_i[1],
         x_i=x_i[1], y_i = y_i[1], distij = distij[1])  %>%
  slice(1); UAI_W
names(UAI_W)
names(UAI_W)[1]<-paste("Tree_ID")
names(UAI_W)[5]<-paste("Long")
# combine result into original data and clean it by deleting unesscesary column
data <- merge(data, UAI_W, by=c("Tree_ID","Long") ,all.x = FALSE)
names(data)
data <- subset( data, select = -c( 33:39))
names(data)
plot(data$W)
names(UAI_W)[1]<-paste("target_tree_i")
names(UAI_W)[5]<-paste("x_i")
write.csv(data, file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/UAI_W.csv")



#----------------------------- Segregation Index calculation (S) -------------------------------
# Main steps are:
# > 1. Distances between reference i & neighbour trees j need to be determined in order to find
#      nearest-neighbour trees to each reference tree and the distance between them
# > 2. Calculate Segregation index (S) is calculated based on the nearest neighbour distance.

# the first step has already been calculated in our previous calculation.
##### S calculation
# Segregation of species, One of the important aspect of stand structure, can be quantified by
# segregation index S by Pielou (1977). It relies on the method of the nearest neighbour and
# designed for applied to a two-species mixture. The idea is to estimate the number of mixed
# species next-neighbour pairs n-expected, which we would expect, if the two tree species would
# be distributed independently of each other. This number can be compared to the number of
# mixed species pairs observed in fact, which we call n-observed. Therefore, S is computed as
```

```
# folows:
# S=1-Pij/E(pij)
# where: pij is observed probability, E(pij) is expected probability.
# the range of values for S is -1 to 1.
# if S < 0, we observe tendency towards an association of the 2 examined species.
# If S > 0, it indicates a tendency towards a spatial segregation of the tree species.

##### Prepare datasets ----------------------------------------
# Prepare dataset for S index calculation in 2 by 2 contingency table. It
# means we will separate (subset) the 2 species pairs of data from original dataset
# because segregation index is used to analyze regularity of only 2 species.
# That is why we need to subset species 2 by 2.
# write a function to subset a pair of species based on conditions if 2 species
# after defining pairs for every species, remove the pair with all 0 observations
sub_fun <- function(data, i, j){
  subs <- subset(data, sp_i %in% c(i, j) & sp_j %in% c(i, j))
  rem <- droplevels(subs)   # remove unused levels (0) from df
  return(rem)
}
# apply this function to subset species
Aa.Am <- sub_fun(dist.m, "Acacia auriculiformis", "Acacia mangium"); table(Aa.Am$sp_i, Aa.Am$sp_j)
Aa.Se <- sub_fun(dist.m, "Acacia auriculiformis", "Senna siamea"); table(Aa.Se$sp_i, Aa.Se$sp_j)
Aa.Lg <- sub_fun(dist.m, "Acacia auriculiformis", "Litsea glutinosa"); table(Aa.Lg$sp_i, Aa.Lg$sp_j)
Aa.Eu <- sub_fun(dist.m, "Acacia auriculiformis", "Eucalyptus camaldulensis"); table(Aa.Eu$sp_i,
Aa.Eu$sp_j)
Aa.Di <- sub_fun(dist.m, "Acacia auriculiformis", "Died"); table(Aa.Di$sp_i, Aa.Di$sp_j)
Aa.Ap <- sub_fun(dist.m, "Acacia auriculiformis", "Aporosa villosa"); table(Aa.Ap$sp_i, Aa.Ap$sp_j)
Aa.Av <- sub_fun(dist.m, "Acacia auriculiformis", "Averrhoa carambola"); table(Aa.Av$sp_i, Aa.Av$sp_j)
Am.Se <- sub_fun(dist.m, "Acacia mangium", "Senna siamea"); table(Am.Se$sp_i, Am.Se$sp_j)
Am.Lg <- sub_fun(dist.m, "Acacia mangium", "Litsea glutinosa"); table(Am.Lg$sp_i, Am.Lg$sp_j)
Am.Eu <- sub_fun(dist.m, "Acacia mangium", "Eucalyptus camaldulensis"); table(Am.Eu$sp_i, Am.Eu$sp_j)
Am.Di <- sub_fun(dist.m, "Acacia mangium", "Died"); table(Am.Di$sp_i, Am.Di$sp_j)
Am.Ap <- sub_fun(dist.m, "Acacia mangium", "Aporosa villosa"); table(Am.Ap$sp_i, Am.Ap$sp_j)
Am.Av <- sub_fun(dist.m, "Acacia mangium", "Averrhoa carambola"); table(Am.Av$sp_i, Am.Av$sp_j)
Se.Lg <- sub_fun(dist.m, "Senna siamea", "Litsea glutinosa"); table(Se.Lg$sp_i, Se.Lg$sp_j)
Se.Eu <- sub_fun(dist.m, "Senna siamea", "Eucalyptus cSealdulensis"); table(Se.Eu$sp_i, Se.Eu$sp_j)
Se.Di <- sub_fun(dist.m, "Senna siamea", "Died"); table(Se.Di$sp_i, Se.Di$sp_j)
Se.Ap <- sub_fun(dist.m, "Senna siamea", "Aporosa villosa"); table(Se.Ap$sp_i, Se.Ap$sp_j)
Se.Av <- sub_fun(dist.m, "Senna siamea", "Averrhoa carSebola"); table(Se.Av$sp_i, Se.Av$sp_j)
Li.Di <- sub_fun(dist.m, "Litsea glutinosa", "Died"); table(Li.Di$sp_i, Li.Di$sp_j)
Eu.Di <- sub_fun(dist.m, "Eucalyptus camaldulensis", "Died"); table(Eu.Di$sp_i, Eu.Di$sp_j)
Eu.Ap <- sub_fun(dist.m, "Eucalyptus camaldulensis", "Aporosa villosa"); table(Eu.Ap$sp_i, Eu.Ap$sp_j)
Eu.Av <- sub_fun(dist.m, "Eucalyptus camaldulensis", "Averrhoa carEubola"); table(Eu.Av$sp_i,
Eu.Av$sp_j)
Di.Ap <- sub_fun(dist.m, "Died", "Aporosa villosa"); table(Di.Ap$sp_i, Di.Ap$sp_j)
Di.Av <- sub_fun(dist.m, "Died", "Averrhoa carDibola"); table(Di.Av$sp_i, Di.Av$sp_j)

##### Calculating S index ---------------------------------

##### Aa.Am step by step calculation of S to check if the result is right.
n <- table(Aa.Am$sp_i, Aa.Am$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Aa.Am$sp_j!=Aa.Am$sp_i))  # number of mixture species (diff sp)
N <- length(Aa.Am$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
```

```
Aa.Am$S.ind <- 1-obsProb/expProb;Saaam<-Aa.Am$S.ind[1]
# the result is ok
##### Aa.Se step by step calculation of S to check if the result is right.
n <- table(Aa.Se$sp_i, Aa.Se$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                     # for total number of reference tree by species
Ncol <- colSums(n); Ncol                     # for total number of neighbouring tree by species
Ndissim <- length(which(Aa.Se$sp_j!=Aa.Se$sp_i))  # number of mixture species (diff sp)
N <- length(Aa.Se$sp_i); N               # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb              # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Aa.Se$S.ind <- 1-obsProb/expProb;Saase<-Aa.Se$S.ind[1]
# the result is ok
##### Aa.Lg step by step calculation of S to check if the result is right.
n <- table(Aa.Lg$sp_i, Aa.Lg$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                     # for total number of reference tree by species
Ncol <- colSums(n); Ncol                     # for total number of neighbouring tree by species
Ndissim <- length(which(Aa.Lg$sp_j!=Aa.Lg$sp_i))  # number of mixture species (diff sp)
N <- length(Aa.Lg$sp_i); N               # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb              # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Aa.Lg$S.ind <- 1-obsProb/expProb;Saalg<-Aa.Lg$S.ind[1]
# the result is ok
##### Aa.Eu step by step calculation of S to check if the result is right.
n <- table(Aa.Eu$sp_i, Aa.Eu$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                     # for total number of reference tree by species
Ncol <- colSums(n); Ncol                     # for total number of neighbouring tree by species
Ndissim <- length(which(Aa.Eu$sp_j!=Aa.Eu$sp_i))  # number of mixture species (diff sp)
N <- length(Aa.Eu$sp_i); N               # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb              # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Aa.Eu$S.ind <- 1-obsProb/expProb;Saaeu<-Aa.Eu$S.ind[1]
# the result is ok
##### Aa.Di step by step calculation of S to check if the result is right.
n <- table(Aa.Di$sp_i, Aa.Di$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                     # for total number of reference tree by species
Ncol <- colSums(n); Ncol                     # for total number of neighbouring tree by species
Ndissim <- length(which(Aa.Di$sp_j!=Aa.Di$sp_i))  # number of mixture species (diff sp)
N <- length(Aa.Di$sp_i); N               # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb              # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Aa.Di$S.ind <- 1-obsProb/expProb;Saadi<-Aa.Di$S.ind[1]
# the result is ok
##### Aa.Ap step by step calculation of S to check if the result is right.
n <- table(Aa.Ap$sp_i, Aa.Ap$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                     # for total number of reference tree by species
Ncol <- colSums(n); Ncol                     # for total number of neighbouring tree by species
Ndissim <- length(which(Aa.Ap$sp_j!=Aa.Ap$sp_i))  # number of mixture species (diff sp)
N <- length(Aa.Ap$sp_i); N               # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb              # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Aa.Ap$S.ind <- 1-obsProb/expProb;Saaap<-Aa.Ap$S.ind[1]
# the result is ok
##### Aa.Av step by step calculation of S to check if the result is right.
n <- table(Aa.Av$sp_i, Aa.Av$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                     # for total number of reference tree by species
Ncol <- colSums(n); Ncol                     # for total number of neighbouring tree by species
```

```
Ndissim <- length(which(Aa.Av$sp_j!=Aa.Av$sp_i))  # number of mixture species (diff sp)
N <- length(Aa.Av$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow*Ncol+Nrow*Ncol; expProb # expected probability
Aa.Av$S.ind <- 1-obsProb/expProb;Saaav<-Aa.Av$S.ind[1]
# the result is ok
##### Am.Se step by step calculation of S to check if the result is right.
n <- table(Am.Se$sp_i, Am.Se$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Am.Se$sp_j!=Am.Se$sp_i))  # number of mixture species (diff sp)
N <- length(Am.Se$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Am.Se$S.ind <- 1-obsProb/expProb;Samse<-Am.Se$S.ind[1]
# the result is ok
##### Am.Lg step by step calculation of S to check if the result is right.
n <- table(Am.Lg$sp_i, Am.Lg$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Am.Lg$sp_j!=Am.Lg$sp_i))  # number of mixture species (diff sp)
N <- length(Am.Lg$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Am.Lg$S.ind <- 1-obsProb/expProb;Samlg<-Am.Lg$S.ind[1]
# the result is ok
##### Am.Eu step by step calculation of S to check if the result is right.
n <- table(Am.Eu$sp_i, Am.Eu$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Am.Eu$sp_j!=Am.Eu$sp_i))  # number of mixture species (diff sp)
N <- length(Am.Eu$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Am.Eu$S.ind <- 1-obsProb/expProb;Sameu<-Am.Eu$S.ind[1]
# the result is ok
##### Am.Di step by step calculation of S to check if the result is right.
n <- table(Am.Di$sp_i, Am.Di$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Am.Di$sp_j!=Am.Di$sp_i))  # number of mixture species (diff sp)
N <- length(Am.Di$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Am.Di$S.ind <- 1-obsProb/expProb;Samdi<-Am.Di$S.ind[1]
# the result is ok
##### Am.Ap step by step calculation of S to check if the result is right.
n <- table(Am.Ap$sp_i, Am.Ap$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Am.Ap$sp_j!=Am.Ap$sp_i))  # number of mixture species (diff sp)
N <- length(Am.Ap$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Am.Ap$S.ind <- 1-obsProb/expProb;Samap<-Am.Ap$S.ind[1]
# the result is ok
```

```
##### Am.Av step by step calculation of S to check if the result is right.
n <- table(Am.Av$sp_i, Am.Av$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Am.Av$sp_j!=Am.Av$sp_i))  # number of mixture species (diff sp)
N <- length(Am.Av$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow*Ncol+Nrow*Ncol; expProb # expected probability
Am.Av$S.ind <- 1-obsProb/expProb;Samav<-Am.Av$S.ind[1]
# the result is ok

##### Se.Lg step by step calculation of S to check if the result is right.
n <- table(Se.Lg$sp_i, Se.Lg$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Se.Lg$sp_j!=Se.Lg$sp_i))  # number of mixture species (diff sp)
N <- length(Se.Lg$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow*Ncol+Nrow*Ncol; expProb # expected probability
Se.Lg$S.ind <- 1-obsProb/expProb;Sselg<-Se.Lg$S.ind[1]
# the result is ok
##### Se.Eu step by step calculation of S to check if the result is right.
n <- table(Se.Eu$sp_i, Se.Eu$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Se.Eu$sp_j!=Se.Eu$sp_i))  # number of mixture species (diff sp)
N <- length(Se.Eu$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow*Ncol+Nrow*Ncol; expProb # expected probability
Se.Eu$S.ind <- 1-obsProb/expProb;Sseeu<-Se.Eu$S.ind[1]
# the result is ok
##### Se.Di step by step calculation of S to check if the result is right.
n <- table(Se.Di$sp_i, Se.Di$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Se.Di$sp_j!=Se.Di$sp_i))  # number of mixture species (diff sp)
N <- length(Se.Di$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Se.Di$S.ind <- 1-obsProb/expProb;Ssedi<-Se.Di$S.ind[1]
# the result is ok
##### Se.Ap step by step calculation of S to check if the result is right.
n <- table(Se.Ap$sp_i, Se.Ap$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Se.Ap$sp_j!=Se.Ap$sp_i))  # number of mixture species (diff sp)
N <- length(Se.Ap$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow*Ncol+Nrow*Ncol; expProb # expected probability
Se.Ap$S.ind <- 1-obsProb/expProb;Sseap<-Se.Ap$S.ind[1]
# the result is ok
##### Se.Av step by step calculation of S to check if the result is right.
n <- table(Se.Av$sp_i, Se.Av$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Se.Av$sp_j!=Se.Av$sp_i))  # number of mixture species (diff sp)
```

```
N <- length(Se.Av$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow*Ncol+Nrow*Ncol; expProb # expected probability
Se.Av$S.ind <- 1-obsProb/expProb;Sseav<-Se.Av$S.ind[1]
# the result is ok

##### Li.Di step by step calculation of S to check if the result is right.
n <- table(Li.Di$sp_i, Li.Di$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Li.Di$sp_j!=Li.Di$sp_i))  # number of mixture species (diff sp)
N <- length(Li.Di$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Li.Di$S.ind <- 1-obsProb/expProb;Slidi<-Li.Di$S.ind[1]
# the result is ok

##### Eu.Di step by step calculation of S to check if the result is right.
n <- table(Eu.Di$sp_i, Eu.Di$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Eu.Di$sp_j!=Eu.Di$sp_i))  # number of mixture species (diff sp)
N <- length(Eu.Di$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Eu.Di$S.ind <- 1-obsProb/expProb;Seudi<-Eu.Di$S.ind[1]
# the result is ok
##### Eu.Ap step by step calculation of S to check if the result is right.
n <- table(Eu.Ap$sp_i, Eu.Ap$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Eu.Ap$sp_j!=Eu.Ap$sp_i))  # number of mixture species (diff sp)
N <- length(Eu.Ap$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow[1]*Ncol[2]+Nrow[2]*Ncol[1]; expProb # expected probability
Eu.Ap$S.ind <- 1-obsProb/expProb;Seuap<-Eu.Ap$S.ind[1]
# the result is ok
##### Eu.Av step by step calculation of S to check if the result is right.
n <- table(Eu.Av$sp_i, Eu.Av$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Eu.Av$sp_j!=Eu.Av$sp_i))  # number of mixture species (diff sp)
N <- length(Eu.Av$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow*Ncol+Nrow*Ncol; expProb # expected probability
Eu.Av$S.ind <- 1-obsProb/expProb;Seuap<-Eu.Av$S.ind[1]
# the result is ok

##### Di.Ap step by step calculation of S to check if the result is right.
n <- table(Di.Ap$sp_i, Di.Ap$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Di.Ap$sp_j!=Di.Ap$sp_i))  # number of mixture species (diff sp)
N <- length(Di.Ap$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow*Ncol+Nrow*Ncol; expProb # expected probability
```

```
Di.Ap$S.ind <- 1-obsProb/expProb;Sdiap<-Di.Ap$S.ind[1]
# the result is ok
##### Di.Av step by step calculation of S to check if the result is right.
n <- table(Di.Av$sp_i, Di.Av$sp_j); n # for create contingency table by ref & neigh trees
Nrow <- rowSums(n); Nrow                      # for total number of reference tree by species
Ncol <- colSums(n); Ncol                      # for total number of neighbouring tree by species
Ndissim <- length(which(Di.Av$sp_j!=Di.Av$sp_i))  # number of mixture species (diff sp)
N <- length(Di.Av$sp_i); N                # for total number of plants in whole data
obsProb <- N * Ndissim; obsProb               # for observed probability
expProb <- Nrow*Ncol+Nrow*Ncol; expProb # expected probability
Di.Av$S.ind <- 1-obsProb/expProb;Sdiav<-Di.Av$S.ind[1]
# the result is ok

# reconstruct dataframe of dist.m using the result of S
# if_else() is very strict, so you'll need to careful match the types of true and false.
# This is most likely to bite you when you're using missing values, and you'll need to
# use a specific NA: NA_integer_, NA_real_, or NA_character_:
dist.m$Seg <- if_else(dist.m$sp_i %in% c("Acacia auriculiformis", "Acacia mangium") &
               dist.m$sp_j %in% c("Acacia auriculiformis", "Acacia mangium"), Saaam,
                   if_else(dist.m$sp_i %in% c("Acacia auriculiformis", "Senna siamea") &
                   dist.m$sp_j %in% c("Acacia auriculiformis", "Senna siamea"), Saase,
                   if_else(dist.m$sp_i %in% c("Acacia auriculiformis", "Litsea glutinosa") &
                   dist.m$sp_j %in% c("Acacia auriculiformis", "Litsea glutinosa"), Saalg,
                   if_else(dist.m$sp_i %in% c("Acacia auriculiformis", "Eucalyptus camaldulensis") &
                   dist.m$sp_j %in% c("Acacia auriculiformis", "Eucalyptus camaldulensis"), Saaeu,
                   if_else(dist.m$sp_i %in% c("Acacia auriculiformis", "Died") &
                   dist.m$sp_j %in% c("Acacia auriculiformis", "Died"), Saadi,
                   if_else(dist.m$sp_i %in% c("Acacia auriculiformis", "Aporosa villosa") &
                   dist.m$sp_j %in% c("Acacia auriculiformis", "Aporosa villosa"), Saaap,
                   if_else(dist.m$sp_i %in% c("Acacia auriculiformis", "Averrhoa carambola") &
                   dist.m$sp_j %in% c("Acacia auriculiformis", "Averrhoa carambola"), Saaav,
                   if_else(dist.m$sp_i %in% c("Acacia mangium", "Senna siamea") &
                   dist.m$sp_j %in% c("Acacia mangium", "Senna siamea"), Samse,
                   if_else(dist.m$sp_i %in% c("Acacia mangium", "Litsea glutinosa") &
                   dist.m$sp_j %in% c("Acacia mangium", "Litsea glutinosa"), Samlg,
                   if_else(dist.m$sp_i %in% c("Acacia mangium", "Eucalyptus camaldulensis") &
                   dist.m$sp_j %in% c("Acacia mangium", "Eucalyptus camaldulensis"), Sameu,
                   if_else(dist.m$sp_i %in% c("Acacia mangium", "Died") &
                   dist.m$sp_j %in% c("Acacia mangium", "Died"), Samdi,
                   if_else(dist.m$sp_i %in% c("Acacia mangium", "Aporosa villosa") &
                   dist.m$sp_j %in% c("Acacia mangium", "Aporosa villosa"), Samap,
                   if_else(dist.m$sp_i %in% c("Acacia mangium", "Averrhoa carambola") &
                   dist.m$sp_j %in% c("Acacia mangium", "Averrhoa carambola"), Samav,
                   if_else(dist.m$sp_i %in% c("Senna siamea", "Litsea glutinosa") &
                   dist.m$sp_j %in% c("Senna siamea", "Litsea glutinosa"), Sselg,
                   if_else(dist.m$sp_i %in% c("Senna siamea", "Eucalyptus camaldulensis") &
                   dist.m$sp_j %in% c("Senna siamea", "Eucalyptus camaldulensis"), Sseeu,
                   if_else(dist.m$sp_i %in% c("Senna siamea", "Died") &
                   dist.m$sp_j %in% c("Senna siamea", "Died"), Ssedi,
                   if_else(dist.m$sp_i %in% c("Senna siamea", "Aporosa villosa") &
                   dist.m$sp_j %in% c("Senna siamea", "Aporosa villosa"), Sseap,
                   if_else(dist.m$sp_i %in% c("Senna siamea", "Averrhoa carambola") &
                     dist.m$sp_j %in% c("Senna siamea", "Averrhoa carambola"), Sseav,
                     if_else(dist.m$sp_i %in% c("Litsea glutinosa", "Died") &
                     dist.m$sp_j %in% c("Litsea glutinosa", "Died"), Slidi,
                     if_else(dist.m$sp_i %in% c("Eucalyptus camaldulensis", "Died") &
```

```
                     dist.m$sp_j %in% c("Eucalyptus camaldulensis", "Died"), Seudi,
                     if_else(dist.m$sp_i %in% c("Eucalyptus camaldulensis", "Aporosa villosa") &
                     dist.m$sp_j %in% c("Eucalyptus camaldulensis", "Aporosa villosa"), Seuap,
                     if_else(dist.m$sp_i %in% c("Died", "Aporosa villosa") &
                     dist.m$sp_j %in% c("Died", "Aporosa villosa"), Sdiap,
                     if_else(dist.m$sp_i %in% c("Died", "Averrhoa carambola") &
                     dist.m$sp_j %in% c("Died", "Averrhoa carambola"),
Sdiav,NA_real_))))))))))))))))))))))

# select reference tree informations
outputS <- dist.m %>%
  select(target_tree_i, sp_i, dbh_i, H_i, x_i, y_i, distij, Seg) %>%
  group_by(tree1 = gl(n()/4, 4), sp_i) %>%
  mutate(S = mean(Seg), dbh_i = dbh_i[1], H_i = H_i[1],
         x_i = x_i[1], y_i = y_i[1], distij = distij[1])  %>%
  slice(1)
head(outputS)
### merge all outputs into one single data
names(outputS)
names(outputS)[1]<-paste("Tree_ID")
names(outputS)[5]<-paste("Long")
# combine result into original data and clean it by deleting unesscesary column
data <- merge(data, outputS, by=c("Tree_ID","Long") ,all.x = FALSE)
names(data)
data <- subset( data, select = -c( 34: 40 ))
names(data)
range(data$S)
names(outputS)[1]<-paste("target_tree_i")
names(outputS)[5]<-paste("x_i")

###################################################################################################
#################### VERTICAL SPATIAL PATTERN INDICES (stand level indices) #######################
#--------------------------------------------------------------------------------------------------
#--------------------------------- Vertical Species profile (A) -----------------------------------

packages <-c("dplyr", "vegan", "tidyverse")
lapply(packages, require, character.only=TRUE)
# A index is based on Shannon index and proposed the differentation of tree species within each
# height layer. It takes into account proportion of species and number of layers in a stand.
# Its value is greater than 0.  0 is for a single-layered pure stand. The more heterogeneous
# the vertical profile, the higher the A value.
# convert name of species (column) in letter into numerical value because of vegan requirement.
# Species types must be in numeric type for shannon indices calculation using vegan package.
# There are 2 main steps to calculate A index
# >  classify height zones
# >  compute A index

##### classify height zones:
# divide Height into 3 zones: If we assume the height of the highest tree in the stand
# to be 100%, zone I extends from 100% down to 80%, zone 2 from 80% down to 50% and zone 3 from 50%
# down to the forest ground. If the top of a tree is located in one of these zones, we
# consider the tree belonging to this zone.
# Zones:
# zone1 = 0-50% of total height
# zone2 = 50-80% of total height
# zone3 = 80-100% of total height
```

```
# write a function that divide height of the stand into 3 zones
zones.fun <- function(H){
  # determine break points that are going to be 50%, 80%, 100% values of max height
  H100 <- max(H)
  H80 <- H100 * 0.8
  H50 <- H100 * 0.5
  # divide the stand into 3 zones accordint to their height
  zones <- cut(H, breaks = c(0, H50, H80, H100),
               labels = c("zone1", "zone2", "zone3"),
               right=TRUE)
  return(zones)
}

##### A index  for a whole stand ----------------------------
data$Hzones.st <- zones.fun(data$Total_height_m)
data <- data %>%
  group_by(Hzones.st) %>%
  mutate(Atmp = diversity(spNum, "shannon"))
# Standardization of A which can be done by dividing A by max value of A. Amax=log(S*Z).
Z <- 3                                 # number of height zones in the stand
S <- length(unique(data$Specie)); S   # number of species in a stand
data$Arel <- data$Atmp/log(S*Z)
##### A index for each quadrants -----------------------------
# define zones in each quadrant
data <- data %>%
  group_by(Cell) %>%
  mutate(Hzones.qd = zones.fun(Total_height_m))
# subset each quadrant separately
q1  <- subset(data, Cell==1)
q2  <- subset(data, Cell==2)
q3  <- subset(data, Cell==3)
q4  <- subset(data, Cell==4)
q5  <- subset(data, Cell==5)
q6  <- subset(data, Cell==6)
q7  <- subset(data, Cell==7)
q8  <- subset(data, Cell==8)
q9  <- subset(data, Cell==9)
q10 <- subset(data, Cell==10)
q11 <- subset(data, Cell==11)
q12 <- subset(data, Cell==12)
q13 <- subset(data, Cell==13)
q14 <- subset(data, Cell==14)
q15 <- subset(data, Cell==15)
q16 <- subset(data, Cell==16)

# create list of all the data
data.list <- list(q1,q2,q3,q4,q5,q6,q7,q8,q9,q10,q11,q12,q13,q14,q15,q16)
# write a function to compute A for each quadrant
A.fun <- function(data, Hzones.qd, spNum) {
  data %>%
    group_by_at(Hzones.qd) %>%
    mutate(A = diversity(!! rlang::sym(spNum), "shannon"))
}
# apply it to the datalist
outA <- map(data.list, A.fun, Hzones.qd = "Hzones.qd", spNum = "spNum")
```

```
# combine data of quadrants into a single data
outA <- bind_rows(outA)
# the more heterogenious the vertical profile, A become higher.
# merge the result with data
data <- merge(data, outA, all.x = FALSE)
names(data)
data$Arel2 <- data$A/log(S*Z)
# export result as a csv file
write.csv(data, file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/Vertical_profile.csv")

#-------------------------------- Height difference index (TH) --------------------------------------
packages <- c("dplyr")
lapply(packages, require, character.only =TRUE)
# it is a single tree variable and be calulated for each pair of neighbours trees and reference/t.
# also it can be calculated at a whole stand level (subpopulation) & at species level by
# summing up TH values & divided it by the number of trees or individuals of the subpopulation.

# Formula is: Th = 1-min(Hi, Hj)/max(Hi, Hj); where Hi is height of reference tree
# Hj is height of neighbour tree. For each pair the one with min value is divided by the one
# with max value.
# 0 < TH < 1:
# if TH=1, neighbour trees have high differentiation in height,
# if TH=0, neightbour trees have equal height.
# Procedures:
# >  define nearest neighbour trees
# >  calculate TH index
# we have already calculated distances between reference tree and nearest neighbour trees.
# using that, lets calculate TH

#####  Calculate height differ index TH: ----------------------------
### compute TH for each pairs of reference tree and nearest neighbors. For example:
# if we choose 3 neihgbour trees, it will be calculated like Ti1, Ti2, Ti3 which mean that
# i is reference tree to 1st neighbour
# i reference tree to 2nd,
# i reference tree to 3rd neighbour

dist.m$THij <- 1 - (pmin(dist.m$H_i, dist.m$H_j)/pmax(dist.m$H_i, dist.m$H_j))
head(dist.m)
# pmin () and pmax() returns parallel min or max of two or more input vectors
names(dist.m)
outputTH <- dist.m %>%
  select(target_tree_i, sp_i, dbh_i, H_i, x_i, y_i, distij, THij) %>%
  group_by(tree1 = gl(n()/4, 4), sp_i) %>%
  mutate(TH = mean(THij), dbh_i = dbh_i[1], H_i = H_i[1],
         x_i=x_i[1], y_i = y_i[1], distij = distij[1])  %>%
  slice(1)


### the average of T by species
TH.sp <- outputTH  %>%
  select(sp_i, TH)  %>%
  group_by(sp_i)  %>%
  summarise(TH.sp = mean(TH)); TH.sp

### merge all outputs into one single data
#out.list <- list(data, outputS, outputTH)
```

```
#data <- Reduce(function(x, y) merge(x, y, all=TRUE), out.list)
names(outputTH)
names(outputTH)[1]<-paste("Tree_ID")
names(outputTH)[5]<-paste("Long")

# combine result into original data and clean it by deleting unesscesary column
data <- merge(data, outputTH, by=c("Tree_ID","Long") ,all.x = FALSE)
names(data)
data <- subset( data, select = -c( 41: 47 ))
names(data)
names(outputTH)[1]<-paste("target_tree_i")
names(outputTH)[5]<-paste("x_i")
write.csv(data,
file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/MSc_Minh_Calculations.csv")
```

Annex 6: R-script of Statistical annalysis for *Acacia mangium*

```
##################################################################
#####################   MODEL SELECTION  #########################
############### Doan Thi Nhat Minh _ DATAFOREST###################
####################### ACACIA MANGIDUM ##########################
#-----------------------------------------------------------------
# Install packages
setwd("C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/data/processed")
getwd()
# Load packages
packs<-c('olsrr', 'psych', 'car', 'mplot', 'caret', 'modelr', 'broom',
'MuMIn','plyr','systemfit','lattice','foreign','car','RODBC','lmtest','Matrix','zoo','reshape
2')
sapply(packs,require,character.only=TRUE)
library(broom)
# Read data
data <-
read.csv(file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/MSc_Minh_Calculations.c
sv", header=TRUE)
names(data)
names(data)[21]<-paste("G")
names(data)[22]<-paste("N_ha")
names(data)[27]<-paste("Sm")
names(data)[28]<-paste("Sh")
##### ------------ Model selection for Acacia mangium ---------------------
#--------------------------------------------------------------------------
Aca_ma  <- subset(data, Specie=="Acacia mangium")
str(Aca_ma)
names (Aca_ma)
summary(Aca_ma)
# Using pairs.panel() to look at (visualize) correlations between variables
corre <- subset(Aca_ma, select = c(AGB_kg, G, N, Sh, Sm, E, D, R, Mi,MS, W, S, A, TH))
pairs.panels(corre,
            method = "pearson", # correlation method
            hist.col = "turquoise1",
            density = TRUE,  # show density plots
            ellipses = TRUE, # show correlation ellipses
            lm=TRUE,
            pch = 20,
            stars=TRUE)
Aca_ma$logAGB<-log((Aca_ma$AGB_kg)^2)
Aca_ma$logG<-log(Aca_ma$G)
Aca_ma$logG2<-log((Aca_ma$G)^2)
Aca_ma$logG_1<-log((Aca_ma$G)^-1)
Aca_ma$logG_05<-log((Aca_ma$G)^-0.5)
Aca_ma$logG05<-log((Aca_ma$G)^0.5)
Aca_ma$logN<-log(Aca_ma$N)
Aca_ma$logN2<-log((Aca_ma$N)^2)
Aca_ma$logN_1<-log((Aca_ma$N)^-1)
Aca_ma$logN_05<-log((Aca_ma$N)^-0.5)
Aca_ma$logN05<-log((Aca_ma$N)^0.5)
Aca_ma$logSh<-log(Aca_ma$Sh)
Aca_ma$logSh2<-log((Aca_ma$Sh)^2)
Aca_ma$logSh_1<-log((Aca_ma$Sh)^-1)
Aca_ma$logSh_05<-log((Aca_ma$Sh)^-0.5)
```

```
Aca_ma$logSh05<-log((Aca_ma$Sh)^0.5)
Aca_ma$logSm<-log(Aca_ma$Sm)
Aca_ma$logSm2<-log((Aca_ma$Sm)^2)
Aca_ma$logSm_1<-log((Aca_ma$Sm)^-1)
Aca_ma$logSm_05<-log((Aca_ma$Sm)^-0.5)
Aca_ma$logSm05<-log((Aca_ma$Sm)^0.5)
Aca_ma$logE<-log(Aca_ma$E)
Aca_ma$logE2<-log((Aca_ma$E)^2)
Aca_ma$logE_1<-log((Aca_ma$E)^-1)
Aca_ma$logE_05<-log((Aca_ma$E)^-0.5)
Aca_ma$logE05<-log((Aca_ma$E)^0.5)
Aca_ma$logD<-log(Aca_ma$D)
Aca_ma$logD2<-log((Aca_ma$D)^2)
Aca_ma$logD_1<-log((Aca_ma$D)^-1)
Aca_ma$logD_05<-log((Aca_ma$D)^-0.5)
Aca_ma$logD05<-log((Aca_ma$D)^0.5)
Aca_ma$logR<-log(Aca_ma$R)
Aca_ma$logR2<-log((Aca_ma$R)^2)
Aca_ma$logR_1<-log((Aca_ma$R)^-1)
Aca_ma$logR_05<-log((Aca_ma$R)^-0.5)
Aca_ma$logR05<-log((Aca_ma$R)^0.5)
Aca_ma$logA<-log(Aca_ma$A)
Aca_ma$logA2<-log((Aca_ma$A)^2)
Aca_ma$logA_1<-log((Aca_ma$A)^-1)
Aca_ma$logA_05<-log((Aca_ma$A)^-0.5)
Aca_ma$logA05<-log((Aca_ma$A)^0.5)
Aca_ma$logTH<-log(Aca_ma$TH)
Aca_ma$logTH2<-log((Aca_ma$TH)^2)
Aca_ma$logTH_1<-log((Aca_ma$TH)^-1)
Aca_ma$logTH_05<-log((Aca_ma$TH)^-0.5)
Aca_ma$logTH05<-log((Aca_ma$TH)^0.5)
Aca_ma$logS<-log(Aca_ma$S)
Aca_ma$logS2<-log((Aca_ma$S)^2)
Aca_ma$logS_1<-log((Aca_ma$S)^-1)
Aca_ma$logS_05<-log((Aca_ma$S)^-0.5)
Aca_ma$logS05<-log((Aca_ma$S)^0.5)
Aca_ma$logMi<-log(Aca_ma$Mi+1)
Aca_ma$logMi2<-log((Aca_ma$Mi+1)^2)
Aca_ma$logMi_1<-log((Aca_ma$Mi+1)^-1)
Aca_ma$logMi_05<-log((Aca_ma$Mi+1)^-0.5)
Aca_ma$logMi05<-log((Aca_ma$Mi+1)^0.5)
Aca_ma$logMS<-log(Aca_ma$MS+1)
Aca_ma$logMS2<-log((Aca_ma$MS+1)^2)
Aca_ma$logMS_1<-log((Aca_ma$MS+1)^-1)
Aca_ma$logMS_05<-log((Aca_ma$MS+1)^-0.5)
Aca_ma$logMS05<-log((Aca_ma$MS+1)^0.5)
Aca_ma$logW<-log(Aca_ma$W+1)
Aca_ma$logW2<-log((Aca_ma$W+1)^2)
Aca_ma$logW_1<-log((Aca_ma$W+1)^-1)
Aca_ma$logW_05<-log((Aca_ma$W+1)^-0.5)
Aca_ma$logW05<-log((Aca_ma$W+1)^0.5)
##### Rank the models----------------------------------------
List<-data.frame() #creat a dataframe to store the parameters
## Selection of the best model of the significant models
# function to determine R2, SSE, RES, MSE, AIC and BIC
stats<-function(model){
```

```
  mse<-rev(anova(model)$"Mean Sq")[1]
  r2<-summary(model)$r.squared
  B0<- summary(model)$coefficients[1]
  B1<- summary(model)$coefficients[2]
  B2<- summary(model)$coefficients[3]
  B3<- summary(model)$coefficients[4]
  rse<-summary(model)$sigma
  pvalue <- glance(model)$p.value
  aic<-AICc(model)
  bic<-BIC(model)
  c(b0=B0, b1=B1, b2=B2, b3=B3, R2=r2, P=pvalue, MSE=mse, AIC=aic, BIC=bic) }
List<-data.frame(rbind(stats(MD1), stats(MD2), stats(MD3),…,stats(MD298)) #model list
presented in annex 4
#Rank the models
rankAIC <- List[order(List$AIC),] ; View(rankAIC)
rankBIC <- List[order(List$BIC),] ; View(rankBIC)
rankR2 <- List[order(-(List$R2)),] ; View(rankR2)
rankMSE <- List[order(List$MSE),] ; View(rankMSE)
write.csv(rankAIC,
file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/rankAIC_mangium.csv")


##====>>> Best model is model 9
##### ------------------------ Sensitivity analysis -----------------------------
### In this step, we will expain the relation between Sh and AGB of Acacia mangium using model
7
MD9 <- lm(log(AGB_kg) ~ I(G^2) + I(TH^2) + I(Sh^2), data=Aca_ma)
range(Aca_ma$G)

# ---> fix G at 13, 17, 21, 25
# Get intercept and coefficient from Model 7
B0<- summary(MD9)$coefficients[1];B0
B1<- summary(MD9)$coefficients[2];B1
B2<- summary(MD9)$coefficients[3];B2
B3<- summary(MD9)$coefficients[4];B3
#Define AGB when G and the cofficients is fixed to see how sensitive is AGB when Sh change --
> Biomass vs diversity
Aca_ma$AGB13<-exp(B0+(B1*(13^2))+(B2*(Aca_ma$TH)^2)+(B3*(Aca_ma$Sh)^2)) #fix G at 13
Aca_ma$AGB17<-exp(B0+(B1*(17^2))+(B2*(Aca_ma$TH)^2)+(B3*(Aca_ma$Sh)^2)) #fix G at 17
Aca_ma$AGB21<-exp(B0+(B1*(21^2))+(B2*(Aca_ma$TH)^2)+(B3*(Aca_ma$Sh)^2)) #fix G at 21
Aca_ma$AGB25<-exp(B0+(B1*(25^2))+(B2*(Aca_ma$TH)^2)+(B3*(Aca_ma$Sh)^2)) #fix G at 25
###### using package plotly to generate 3d plot
# source from https://plot.ly/r/3d-scatter-plots/
library(plotly)
p<-plot_ly(Aca_ma,  type = 'scatter3d', mode = 'markers') %>%
  add_trace(x = ~Sh, y = ~TH, z = ~AGB25, name = 'fix G at 25',
            marker = list(color="blue" , size=3)) %>%
  add_trace(x = ~Sh, y = ~TH, z = ~AGB21, name = 'fix G at 21',
            marker = list(color="green" , size=3)) %>%
  add_trace(x = ~Sh, y = ~TH, z = ~AGB17, name = 'fix G at 17',
            marker = list(color="red" , size=3)) %>%
  add_trace(x = ~Sh, y = ~TH, z = ~AGB13, name = 'fix G at 13',
            marker = list(color="orange" , size=3)) %>%
  layout(scene = list(xaxis = list(title = 'Sh index'),
                      yaxis = list(title = 'TH'),
                      zaxis = list(title = 'AGB (kg)')));p

#### export 3d grap source https://plot.ly/r/static-image-export/
```

```
## need API key
#Sys.setenv("plotly_username" = "YOUR USER NAME")
#Sys.setenv("plotly_api_key" = "YOUR API KEY")
Sys.setenv("plotly_username" = "dtnmahbu")
Sys.setenv("plotly_api_key" = "9X09RgPxK6LKLqdCZF3C")

## save image
plotly_IMAGE(p, format = "png", out_file = "output.png")
## or Create a shareable link to your chart
chart_link = api_create(p, filename="AGB_mangium")
chart_link
```

Annex 7: R-script of Statistical annalysis for *Acacia auriculiformis*

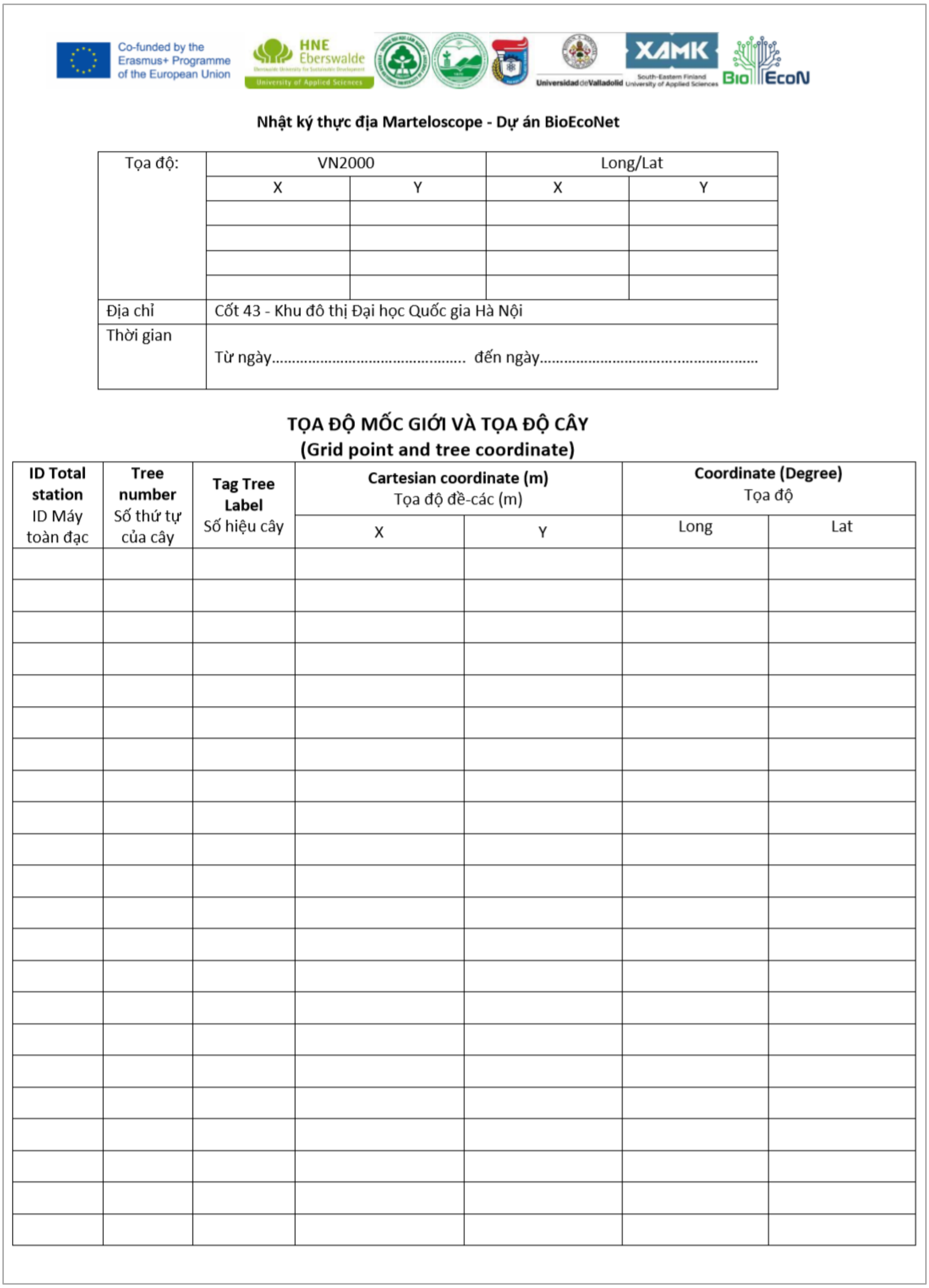
```
##################################################################
#####################   MODEL SELECTION  #########################
############### Doan Thi Nhat Minh _ DATAFOREST###################
################### ACACIA AURICULIFORMIS ########################
#-----------------------------------------------------------------
# Install packages
setwd("C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/data/processed")
getwd()
# Load packages
packs<-c('olsrr', 'psych', 'car', 'mplot', 'caret', 'modelr', 'broom',
'MuMIn','plyr','systemfit','lattice','foreign','car','RODBC','lmtest','Matrix','zoo','reshape
2')
sapply(packs,require,character.only=TRUE)
library(broom)
# Read data
data                                                                                    <-
read.csv(file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/MSc_Minh_Calculations.c
sv", header=TRUE)
names(data)
names(data)[21]<-paste("G")
names(data)[22]<-paste("N_ha")
names(data)[27]<-paste("Sm")
names(data)[28]<-paste("Sh")
##### ------------ Model selection for  Acacia mangium -------------
#-----------------------------------------------------------------------------------
Aca_au  <- subset(data, Specie=="Acacia auriculiformis")
str(Aca_au)
names (Aca_au)
summary(Aca_au)
# Using pairs.panel() to look at (visualize) correlations between variables
corre <- subset(Aca_au, select = c(AGB_kg, G, N, Sh, Sm, E, D, R, Mi,MS, W, S, A, TH))
pairs.panels(corre,
             method = "pearson", # correlation method
             hist.col = "turquoise1",
             density = TRUE,  # show density plots
             ellipses = TRUE, # show correlation ellipses
             lm=TRUE,
             pch = 20,
             stars=TRUE)
# Define parameter for the log form
Aca_au$logAGB<-log((Aca_au$AGB_kg)^2)
Aca_au$logG<-log(Aca_au$G)
Aca_au$logG2<-log((Aca_au$G)^2)
Aca_au$logG_1<-log((Aca_au$G)^-1)
Aca_au$logG_05<-log((Aca_au$G)^-0.5)
Aca_au$logG05<-log((Aca_au$G)^0.5)
Aca_au$logN<-log(Aca_au$N)
Aca_au$logN2<-log((Aca_au$N)^2)
Aca_au$logN_1<-log((Aca_au$N)^-1)
Aca_au$logN_05<-log((Aca_au$N)^-0.5)
Aca_au$logN05<-log((Aca_au$N)^0.5)
Aca_au$logSh<-log(Aca_au$Sh)
Aca_au$logSh2<-log((Aca_au$Sh)^2)
Aca_au$logSh_1<-log((Aca_au$Sh)^-1)
Aca_au$logSh_05<-log((Aca_au$Sh)^-0.5)
```

```
Aca_au$logSh05<-log((Aca_au$Sh)^0.5)
Aca_au$logSm<-log(Aca_au$Sm)
Aca_au$logSm2<-log((Aca_au$Sm)^2)
Aca_au$logSm_1<-log((Aca_au$Sm)^-1)
Aca_au$logSm_05<-log((Aca_au$Sm)^-0.5)
Aca_au$logSm05<-log((Aca_au$Sm)^0.5)
Aca_au$logE<-log(Aca_au$E)
Aca_au$logE2<-log((Aca_au$E)^2)
Aca_au$logE_1<-log((Aca_au$E)^-1)
Aca_au$logE_05<-log((Aca_au$E)^-0.5)
Aca_au$logE05<-log((Aca_au$E)^0.5)
Aca_au$logD<-log(Aca_au$D)
Aca_au$logD2<-log((Aca_au$D)^2)
Aca_au$logD_1<-log((Aca_au$D)^-1)
Aca_au$logD_05<-log((Aca_au$D)^-0.5)
Aca_au$logD05<-log((Aca_au$D)^0.5)
Aca_au$logR<-log(Aca_au$R)
Aca_au$logR2<-log((Aca_au$R)^2)
Aca_au$logR_1<-log((Aca_au$R)^-1)
Aca_au$logR_05<-log((Aca_au$R)^-0.5)
Aca_au$logR05<-log((Aca_au$R)^0.5)
Aca_au$logA<-log(Aca_au$A)
Aca_au$logA2<-log((Aca_au$A)^2)
Aca_au$logA_1<-log((Aca_au$A)^-1)
Aca_au$logA_05<-log((Aca_au$A)^-0.5)
Aca_au$logA05<-log((Aca_au$A)^0.5)
Aca_au$logTH<-log(Aca_au$TH)
Aca_au$logTH2<-log((Aca_au$TH)^2)
Aca_au$logTH_1<-log((Aca_au$TH)^-1)
Aca_au$logTH_05<-log((Aca_au$TH)^-0.5)
Aca_au$logTH05<-log((Aca_au$TH)^0.5)
Aca_au$logS<-log(Aca_au$S)
Aca_au$logS2<-log((Aca_au$S)^2)
Aca_au$logS_1<-log((Aca_au$S)^-1)
Aca_au$logS_05<-log((Aca_au$S)^-0.5)
Aca_au$logS05<-log((Aca_au$S)^0.5)
Aca_au$logMi<-log(Aca_au$Mi+1)
Aca_au$logMi2<-log((Aca_au$Mi+1)^2)
Aca_au$logMi_1<-log((Aca_au$Mi+1)^-1)
Aca_au$logMi_05<-log((Aca_au$Mi+1)^-0.5)
Aca_au$logMi05<-log((Aca_au$Mi+1)^0.5)
Aca_au$logMS<-log(Aca_au$MS+1)
Aca_au$logMS2<-log((Aca_au$MS+1)^2)
Aca_au$logMS_1<-log((Aca_au$MS+1)^-1)
Aca_au$logMS_05<-log((Aca_au$MS+1)^-0.5)
Aca_au$logMS05<-log((Aca_au$MS+1)^0.5)
Aca_au$logW<-log(Aca_au$W+1)
Aca_au$logW2<-log((Aca_au$W+1)^2)
Aca_au$logW_1<-log((Aca_au$W+1)^-1)
Aca_au$logW_05<-log((Aca_au$W+1)^-0.5)
Aca_au$logW05<-log((Aca_au$W+1)^0.5)

##### Defining models----------------------------------------
## Model list presented in annex 3
##### Rank the models----------------------------------------
List<-data.frame() #creat a dataframe to store the parameters
```

```
## Selection of the best model of the significant models
# function to determine R2, SSE, RES, MSE, AIC and BIC
stats<-function(model){
  mse<-rev(anova(model)$"Mean Sq")[1]
  r2<-summary(model)$r.squared
  B0<- summary(model)$coefficients[1]
  B1<- summary(model)$coefficients[2]
  B2<- summary(model)$coefficients[3]
  B3<- summary(model)$coefficients[4]
  rse<-summary(model)$sigma
  pvalue <- glance(model)$p.value
  aic<-AICc(model)
  bic<-BIC(model)
  c(b0=B0, b1=B1, b2=B2, b3=B3, R2=r2, P=pvalue, MSE=mse, AIC=aic, BIC=bic) }

List<-data.frame(rbind(stats(MD1),   stats(MD2),   stats(MD3),…,stats(MD226))   #model   list
presented in annex 4
#Rank the models
rankAIC <- List[order(List$AIC),] ; View(rankAIC)
rankBIC <- List[order(List$BIC),] ; View(rankBIC)
rankR2 <- List[order(-(List$R2)),] ; View(rankR2)
rankMSE <- List[order(List$MSE),] ; View(rankMSE)
write.csv(rankAIC,
file="C:/Users/DELL/Desktop/MScThesis_DATAFOREST_UVa/outputs/rankAIC_auri.csv")
##====>>> Best model is model 3
##### ------------------------ Sensitivity analysis -----------------------------
### In this step, we will explain the relation between Sh and AGB of Acacia auriculiformis
using the optimum model
MD3 <- lm(log(AGB_kg) ~ I(TH^2) + I(Sh^2),data=Aca_au)
summary(MD3)
B0<- summary(MD3)$coefficients[1];B0
B1<- summary(MD3)$coefficients[2];B1
B2<- summary(MD3)$coefficients[3];B2
##### Fix TH at 0.05 0.15 0.25 0.35 0.45 0.55
Aca_au$AGB.TH05<-exp(B0 + B1*(0.05)^2 + B2*(Aca_au$Sh)^2)
Aca_au$AGB.TH15<-exp(B0 + B1*(0.15)^2 + B2*(Aca_au$Sh)^2)
Aca_au$AGB.TH25<-exp(B0 + B1*(0.25)^2 + B2*(Aca_au$Sh)^2)
Aca_au$AGB.TH35<-exp(B0 + B1*(0.35)^2 + B2*(Aca_au$Sh)^2)
Aca_au$AGB.TH45<-exp(B0 + B1*(0.45)^2 + B2*(Aca_au$Sh)^2)
Aca_au$AGB.TH55<-exp(B0 + B1*(0.55)^2 + B2*(Aca_au$Sh)^2)
f <- list(
  family = "Arial",
  size = 18,
  color = "#ffffff")
a1 <- list(
a2 <- list(
  title = "Shannon index",
  titlefont = f,
  showline = TRUE,
  linewidth = 1)
b2 <- list(
  title = "AGB (kg)",
  titlefont = f,
  showline = TRUE,
  linewidth = 1)
p <- plot_ly(Aca_au, x = ~Sh) %>%
  add_trace(y = ~AGB.TH05, type='scatter', name = 'fix TH at 0.05', mode = 'markers') %>%
```

```
  add_trace(y = ~AGB.TH15, type='scatter', name = 'fix TH at 0.15', mode = 'markers') %>%
  add_trace(y = ~AGB.TH25, type='scatter', name = 'fix TH at 0.25', mode = 'markers') %>%
  add_trace(y = ~AGB.TH35, type='scatter', name = 'fix TH at 0.35', mode = 'markers') %>%
  add_trace(y = ~AGB.TH45, type='scatter', name = 'fix TH at 0.45', mode = 'markers') %>%
  add_trace(y = ~AGB.TH55, type='scatter', name = 'fix TH at 0.55', mode = 'markers') %>%
  layout(xaxis = a2, yaxis = b2, showlegend = TRUE);p
#Sys.setenv("plotly_username" = "YOUR USER NAME")
#Sys.setenv("plotly_api_key" = "YOUR API KEY")
Sys.setenv("plotly_username" = "dtnmahbu")
Sys.setenv("plotly_api_key" = "9X09RgPxK6LKLqdCZF3C")
## save image
plotly_IMAGE(p, format = "png", out_file = "AGB_auri.png")
```

Annex 8: Forms for data collection



Co-funded by the Erasmus+ Programme of the European Union

HNE Eberswalde University of Applied Sciences

Universidad de Valladolid

XAMK South-Eastern Finland University of Applied Sciences

BioEcoN

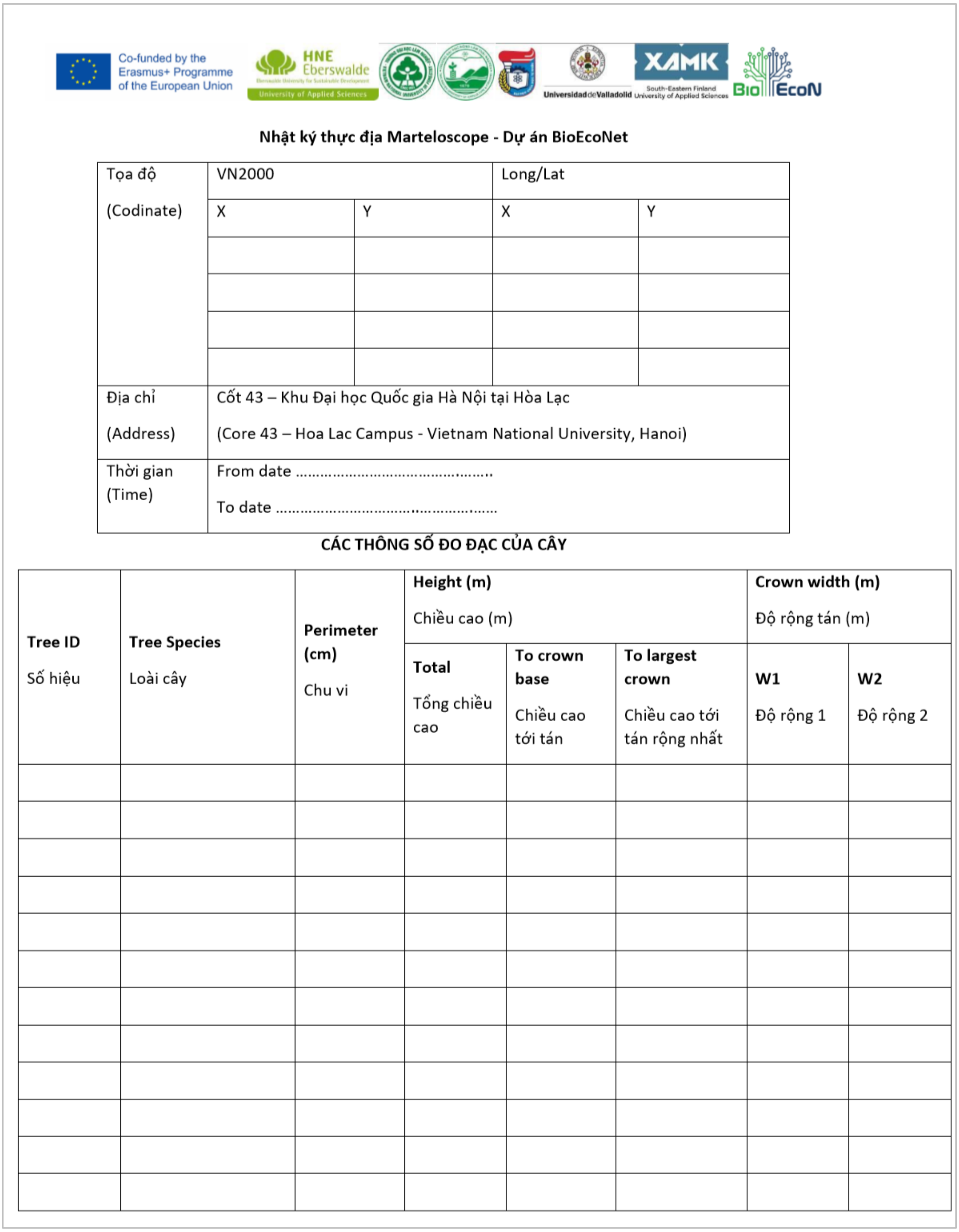
Nhật ký thực địa Marteloscope - Dự án BioEcoNet

Tọa độ:	VN2000		Long/Lat	
	X	Y	X	Y
Địa chỉ	Cốt 43 - Khu đô thị Đại học Quốc gia Hà Nội			
Thời gian	Từ ngày... đến ngày...			

TỌA ĐỘ MỐC GIỚI VÀ TỌA ĐỘ CÂY

(Grid point and tree coordinate)

ID Total station ID Máy toàn đạc	**Tree number** Số thứ tự của cây	**Tag Tree Label** Số hiệu cây	**Cartesian coordinate (m)** Tọa độ đề-các (m)		**Coordinate (Degree)** Tọa độ	
			X	Y	Long	Lat



Co-funded by the Erasmus+ Programme of the European Union

Nhật ký thực địa Marteloscope - Dự án BioEcoNet

Tọa độ (Codinate)	VN2000		Long/Lat	
	X	Y	X	Y
Địa chỉ (Address)	Cốt 43 – Khu Đại học Quốc gia Hà Nội tại Hòa Lạc (Core 43 – Hoa Lac Campus - Vietnam National University, Hanoi)			
Thời gian (Time)	From date …………………………………….. To date ……………………………………….……			

CÁC THÔNG SỐ ĐO ĐẠC CỦA CÂY

Tree ID Số hiệu	**Tree Species** Loài cây	**Perimeter (cm)** Chu vi	**Height (m)** Chiều cao (m)			**Crown width (m)** Độ rộng tán (m)	
			Total Tổng chiều cao	**To crown base** Chiều cao tới tán	**To largest crown** Chiều cao tới tán rộng nhất	**W1** Độ rộng 1	**W2** Độ rộng 2

Annex 9: Picture from field measurements

Determining the coordinates of each tree

Setting up the grid line

Trees measuring

Measuring tree height

Discussion before the field work

Tree lable