



Universidad de Valladolid
Campus de Palencia

**ESCUELA TÉCNICA SUPERIOR
DE INGENIERÍAS AGRARIAS**

Titulación
**MASTER EN CONSERVACIÓN Y USOS SOSTENIBLES DE
SISTEMAS FORESTALES**

Título del Trabajo

**TERRESTRIAL LASER SCANNING DATA
PROCESSING: DEVELOPMENT OF A NEW
METHODOLOGY APPLIED TO MIXED
FORESTS.**

Alumna: SARA UZQUIANO PÉREZ

Tutor: FELIPE BRAVO OVIEDO

Septiembre de 2016

MEMORY

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RESUMEN

El poder conocer variables dendrométricas para los inventarios forestales de forma rápida y con el mínimo error posible es hoy en día posible gracias al uso de Láser Escáner Terrestre (TLS) con el que se obtienen nubes de puntos 3D con gran cantidad de detalle de la que podemos extraer prácticamente cualquier variable del árbol. Sin embargo, el procesado de los datos es largo y en muchos de los casos, complicado. El objetivo de este estudio ha sido desarrollar una metodología combinando varios programas informáticos (*Polyworks*, *CompuTree* y *Photoshop*) que nos permita obtener datos de una manera semiautomática, y de forma objetiva en una masa mixta de *Pinus sylvestris* y *Quercus pyrenaica* del norte de España. Nuestros datos han sido evaluados en 15 árboles de cada especie ajustando modelos predictivos básicos de variables de volumen de copa, diámetro normal, ratio del tronco y altura a la máxima anchura de copa y modelos expandidos para evaluar el efecto de la mezcla sobre las variables dendrométricas. Los resultados muestran que a través de la metodología seguida se pueden obtener buenas estimaciones de variables dendrométricas estudiadas (a excepción del ratio de copa) pero no así en los modelos expandidos, posiblemente debido al escaso número de datos. De forma adicional, se compararon las medidas de diámetro normal extraídas de las nubes de puntos con las obtenidas con forcípula a través de una regresión lineal simple cuyos resultados demostraron que no existen diferencias significativas entre ambas formas de medir. Gracias a este trabajo hemos podido familiarizarnos con nuevos programas utilizados en el proceso de los datos TLS, lo que nos permitirá realizar futuros estudios sobre esta misma masa mixta y profundizar así en el entendimiento de la dinámica de crecimiento de masas mixtas.

ABSTRACT

The knowledge of dendrometric variables for forest inventories with the minimal error and fast is nowadays possible thanks to 3D point clouds reconstruction through Terrestrial Laser Scanner (TLS), a device able to provide great amount of detailed data from which, almost any tree variables can be extracted. However the data processing is long and in many cases, difficult. The aim of this study is to develop a methodology combining several computer programs (*Polyworks*, *CompuTree* and *Photoshop*) that allows us to obtain data in a semi-automatic manner and objectively in a mixed stand of *Pinus sylvestris* and *Quercus pyrenaica* in northern Spain. Our data have been evaluated on 15 trees of each species adjusting basic predictive models of variable (Crown volume, Diameter at Breast Height (DBH), Height to crown base and height to the largest crown width) and expanded models to evaluate the effect of the mixture on the each dendrometric variables. The results show that the applied methodology good estimates of dendrometric studied variables (except the crown ratio) can be obtained. But not for the expanded models, possibly due to the small number of data. In addition, DBH TLS data were compared with caliper data by doing a simple linear regression, where non significance differences between them were found. Thanks to this work we have become familiar with new programs used in the data processing, which will allow us to conduct future studies on this mixed stand and thus, and go deeper in the understanding of the growth dynamics of mixed forests.

1. INTRODUCTION

Forest inventory information are important to assess the potential of forests (Moskal and Zhen, 2011, Pretzsch *et al.*, 2016) and for the sustainable management of their resources (Hauglin *et al.*, 2014). For these reasons forest inventory automation has become a major issue in forestry (Piboule *et al.*, 2015). The single-tree information and future costs for data acquisition need to be increased (Hauglin *et al.*, 2014) thus, detailed information about 3D stand structure in forest science is a good tool for analyzing the space-time development of plants as well as precise harvest forecasting in forest industry (Schilling and Maas, 2014).

Forest structure is described by various attributes associated with spatiotemporal properties of forest stands, including height, canopy closure, understory cover, Diameter at Breast Height (DBH), and volume of standing and lying trees (Moskal and Zhen, 2011; Latifiet *al.*, 2015). These attributes are easier obtainable in monocultures than in mixed stands and that is why they have been long studied but, currently mixed-species stands are receiving a lot of interest (Puettmann *et al.*, 2012) since they can have higher structural heterogeneity (Verga *et al.*, 2005; Ríó *et al.*, 2016) and positive effects on various ecosystems services (Gamfeldt *et al.*, 2013). Nevertheless, there is lack in the canopy and crowns structure knowledge due to the difficulty of obtaining those variables, but to understand the inner working of it, it is important for the feedback between structures within stand environment since they influence the local environmental conditions within the stand (Pretzsch *et al.*, 2016).

The major productivity mixed forests seems to have are making that managing them become more prevalent and this seems to be worldwide trend (Zhao, 2004). Although many studies have often addressed that forests composed of mixed stands can be more productive compared to those with pure stands (Ríó *et al.*, 2016; Morin *et al.*, 2011; Paquette and Messier, 2011), this fact is rarely quantified (Pretzsch *et al.*, 2016). This is due to the mixtures of trees species with their different ecological requirements and great variation in the size of trees complicate modeling of mixed stands (Lähdeet *al.*, 1999 in Kuuluvainen, 2002). Nevertheless, greater knowledge of mixed forest dynamics is needed (Ríó *et al.*, 2016) after this kind of forests has been identified as an adaptation strategy in forest management to cope with climate change (Bravo-Oviedo *et al.*, 2014; Kolström *et al.*, 2011). This change from pure single species stand management to mixed species stand management stresses the need for tools to support management decision making in such stands. Specifically, reliable growth

models for mixed species stands are required for managing these complex stands (Zhao, 2011).

Usually, as point out by Vanclay (1994), data available for developing models for mixed forests do not contain sufficient observations to allow reliable relationships to be established for all species (Zhao, 2011). With regard to this concept, Light Detection And Ranging (LiDAR) systems provide accurate data for describing forest structure because of their ability to measure the inherent three-dimensional structure of stands via discrete return or full waveform measurements (Latifi, 2012). The assets of LiDAR data have been discussed based on cases studied on a wide variety of forest ecosystems worldwide, ranging from boreal (Hyypä *et al.*, 2008) to temperate (Latifi *et al.*, 2012 and Tsui *et al.*, 2013) and tropical (Drake *et al.*, 2002 and Treuhaft *et al.*, 2010) ecosystems. Terrestrial Laser Scanning (TLS) is a device belonging to this technology and it has become, in recent years, an important focus in forestry area (Othmani *et al.*, 2011) since, it offers the potential to study forest ecosystems by providing spatially and temporally distributed information on key biophysical and biochemical variables (Schneider *et al.*, 2014).

The application of TLS in forest inventories is becoming more effective (Bauwens *et al.*, 2016, Othmani *et al.*, 2011) and popular due to the degree of detail this technology is able to provide and so, its capacity to solve current limitations in traditional inventory methods. Thus, it has being wide studied and there exist already several studies about its use to provide more accurate measurements of the trees (latifi *et al.*, 2015; Bayer *et al.*, 2013; Béland *et al.*, 2011; Côté *et al.*, 2011; Dassot *et al.*, 2012; Seidel *et al.*, 2011^a). However, the challenge remains on extracting pertinent and correctly estimated forest inventory parameters from TLS raw data. There already exist several methodologies trying to automate the extraction of information from TLS and the study of the structure of stands are becoming more affordable (Othmani *et al.*, 2011). Nevertheless, the occlusion effect is still limiting the processing efficiency to extract forest attributes (Bauwens *et al.*, 2016). An existing ground forest inventory can act as a basis for subsequent LiDAR forest inventory systems by providing not only essential reference data for the model building process, but also an additional source of a priori knowledge when designing an improved field survey (Latifi *et al.*, 2015). There still exists a long way to go on the operational use of this technology and the understanding of mixed forest structure.

The aim of the present study was to assess a new methodology to improve TLS data processing and assess its value fitting predictive models in a single-tree forest inventory. To that, we propose a procedure of single-tree variables using training data with 3D TLS point clouds values. An independently developed TLS-based model was used to obtain the ground reference data, and automated single-tree segmentation combining different software (*Polyworks*, *CompuTree* and *Photoshop*). Finally, to test our proposed procedure TLS data in forest inventory, we estimated single-tree Diameter at Breast Height (DBH), Total tree height (HT), Height to the largest crown width (HLCW), height to crown base (HCB) and crown volume (CV) of *Pinus sylvestris* and *Quercus pyrenaica* in a mixed stand in northern Spain. Furthermore, DBH measurements obtained with TLS were compared with measurements made by a caliper.

2. OBJECTIVE

The main objective of the present study is to validate a methodology using TLS data in mixed forests, which will help to obtain reliable tree structures faster and without bias. Once the methodology has been developed and used in mixed stands, in order to test the validity of our results, the following steps have been carried out:

1. Fit basic models for different tree form and size a) Crown Volume (CV), b) Total tree Height (HT), c) Height at Crown Base (HCB) regarding HT d) Height at Largest Crown Width (HLCW) without taking into account the effect of the mix within the stands.
2. Determine the mixture degree through the relative importance of pines on basal area and trees per ha.
3. Expand the parameters of the basic models by including a linear relationship with the mixture degree and fit these new expanded models.

3. MATERIAL AND METHODS

3.1. STUDY AREA

A permanent plot of about two ha of a mixed forest set up by *Pinus sylvestris* planting stand and natural *Quercus pyrenaica* stand, located at the long-term experimental site of "Palacio de Valdellorma" (León) in North-West central Spain, at an altitude of 1000m has been used to measure the relevant variables. The plantation is located on a terraced slope, where the mean rainfall is 936 mm and mean temperature is 9 °C. In this place, split-plot design was performed: one single block divided in nine plots 50x40m. Within these plots, three forest thinning effects have been carried out regarding

their Basal Area (BA) during summer 2015: plots A1, Z1 and B2 have 50% intensity of cutting, Z2, D1 and E2 25%. Finally, plots A2, B1 and D2 are control plots, so none cutting was made on them (Annex 1). Thus, we can observe how these species react to different thinning percentage and how it affects to their productivity. For our study, we have scanned only three of the nine plots, each one with different harvest intensity (A1, A2 and Z2).

3.2. DATA COLLECTION

TLS data were acquired during the winter 2016. The existing inventory (stem UTM coordinates and DBH and species identification) was used as auxiliary information in the interpretation process.

- **Georeferencing**

Data scan are metric, that is to say, we can make used data to obtain dendrometric and mensuration data but these data are not oriented, neither referenced nor locally or globally (UTM coordinates). For this reason, georeferencing was needed, so we could compare our point clouds data with other previous studies where every tree belonging to the plots have been already identified with their UTM coordinates by a Total Station. Thus, before starting scanning process a sub-metric GPS Leica model SR20 single frequency equipment with external antenna reception AT501 was used for georeferencing our point clouds data to UTM coordinates, this equipment has an error margin of centimeters. We selected 5 specific points connecting the three studied plots (Figure 1) and we let the GPS for 30 minutes in each station, so that, error was minimized.

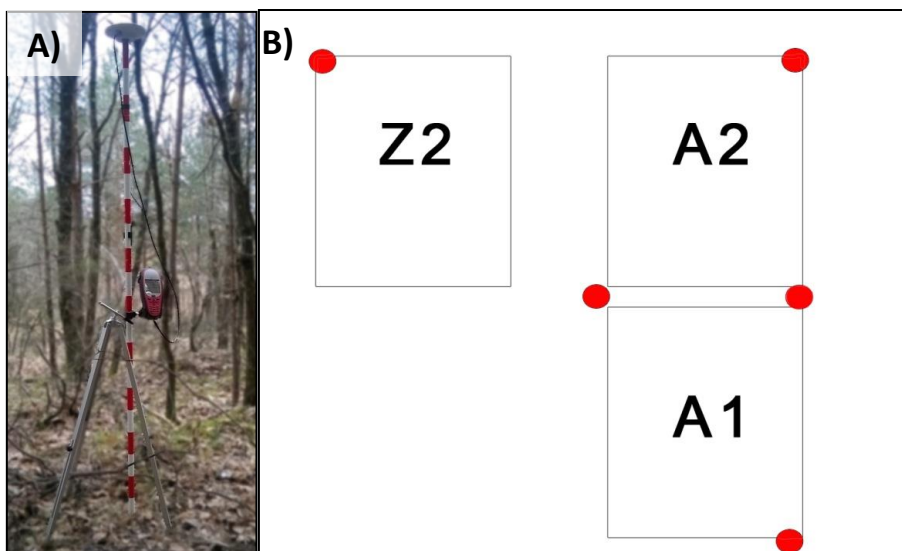


Figure 1. A) Sub-metric GPS Leica model SR20. B) Sketch of the studied plots. Red circles represent the station points GPS was placed around the plots.

The perfect identification of these points is very important afterwards in deskwork, thus, after each GPS station, exact place was marked with one white sphere over a wooden pole (needed for scanning process) and perfectly distinguish from the rest of white spheres (Figure 2). These spheres were not moved at all during the full scanning process, as the other spheres did.



Figure 2. The five georeferencing points were marked by using White spheres needed for later 3D reconstruction and in order to distinguish them from other they were marked as in this case with a luggage.

- **Scanning process**

Terrestrial LiDAR data were captured by a Faro Focus 3D device. Panoramic spherical scans were captured, containing a horizontal angle from 0° to 360° and vertical angle from -60° to 90°. Each scan size was 8190x3414 points, that is to say 28.0 millions of points per capture and spatial resolution of 7.670 mm in 10 m. Each scan took about one minute and a half. In order we could relate data obtained from all scans positions properly, we used 15 white plastic spheres, 18 cm diameter, which work like reference points. They were winded on one-meter high wooden poles (Figure 3) which we were going changing their positions time to time in each scan position, so at least 3 of them were seen from every scan position, crucial for post processing data. Total scanning time was depending on plot density: in plots A2 and Z2 (harvest intensity 0% and 25% respectively) 48 scans were needed. This took an average of 5 hours each plot. However scanning number needed in plot A1 (50% harvest intensity) were 24 scans, which took a total of 2 hours.



Figure 3. One scan station taking care enough white spheres were well visible to be captured by TLS.

3.3. PROCESSING DATA

The great amount of data (pictures and point-clouds) to be processed, oblige to use powerful equipment. In this study processing data were carried out by a Workstation Intel CORE i7-5280K. Hard disk SSD 256 GB Samsung 950 PPRO M. S2. Hard disk SATA 4TB. WD Blank CPU INTEL 1022 CORE i7-5820K 3'3G. 6 CORE 6 CACHE. 4 memories DIMM 8 GB DDR4. As follows, data processing is described in detail and Diagram 1 was made to help the understanding of this process.

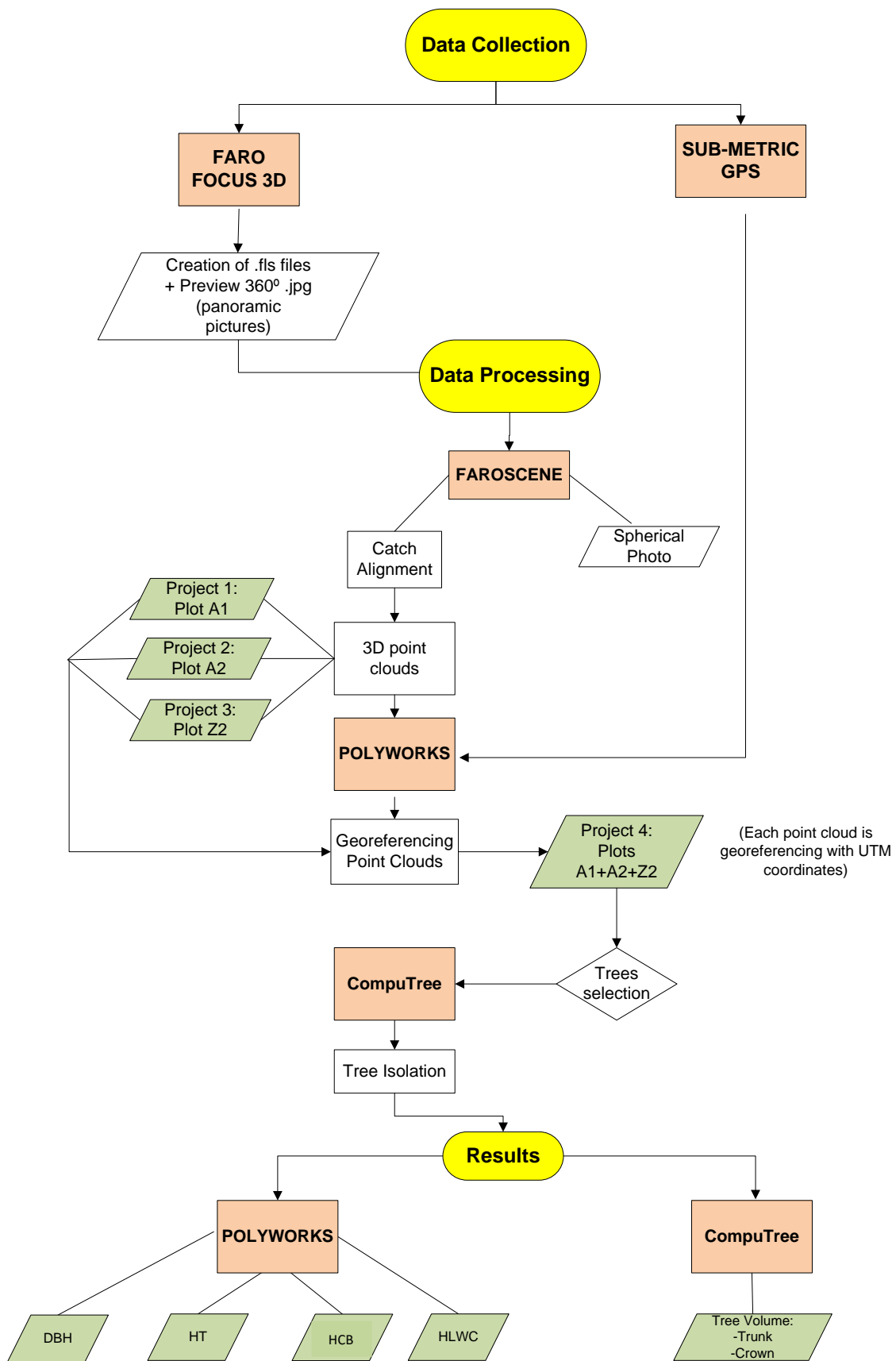


Diagram 1. Flowchart of TLS data from its collection on field until obtaining trees measures. From *Polyworks*: Diameter at breast Height (DBH), Total height (HT), Height to Crown Base (HCB) and Height to the Largest Crown Width (HLCW). From *CompuTree*: the tree timber volume (from the trunk and the crown).

- Faroscene

The first step is to convert the panoramic pictures (2D), obtained by Faro Focus 3D, into 3D point clouds. This process was performed by *FaroScene* software (version 5.2) and is called “Catch alignment”, where every picture belonging to each plot are matched by the recognition of white spheres with enough resolution (mentioned above). This process is automatic and once is finished 3D reconstruction is made and saved in files “.fls” extension (These files can also be opened by Arcview). This procedure was made each time with each plot. As follows, point clouds edition was performed by using two software: *Polyworks* version 12.1.3 (64 bits) and *CompuTree*.

- Polyworks

Since our study was focus in 30 specific trees, from which we knew their UTM coordinates from previous studies. Their identification within point clouds were able by georeferencing the plots. For this process we used *IM Inspect* module of *Polyworks*. Coordinates taken from sub-metric GPS were import as .txt file. As follows, we imported each plot within the same project as “Point clouds”. Once plots were charged in the program, we overlapped plots point clouds over georeferenced points. This process was done thanks to the characterization made during field work, which let us know, which ones were the georeferenced points to be overlapped on the coordinates (Figure 4).

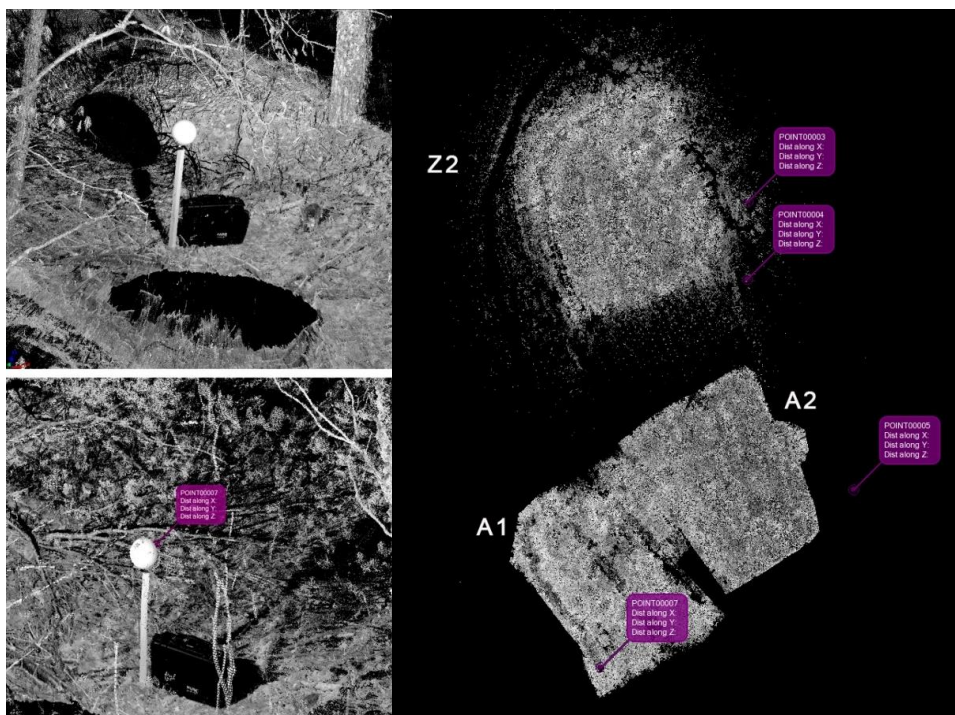


Figure 4. Placing of the three studied plots within one project. Purple squares represent point stations made by sub-metric GPS.

Finally, we imported as text file (.txt format) UTM coordinates of each selected tree. Since the project was already georeferenced, these points were overlapped on their right position (Figure 5).

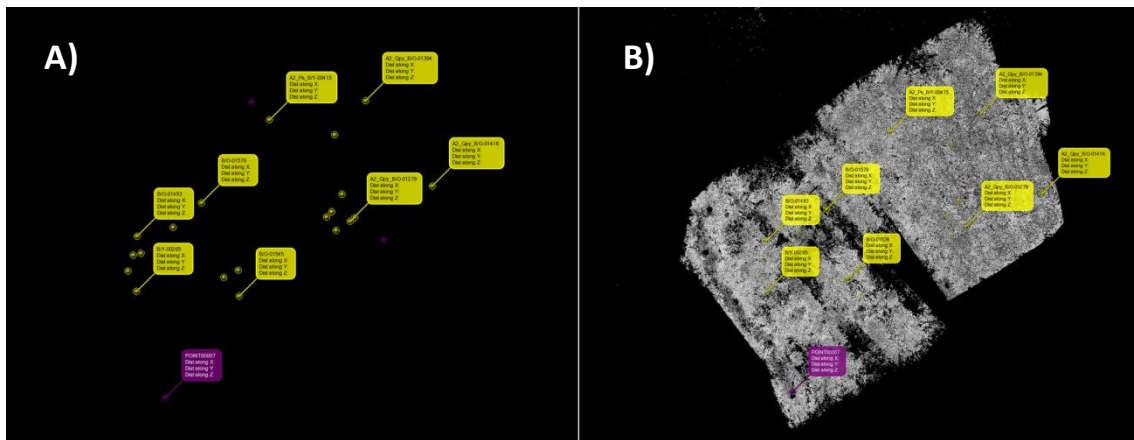


Figure 5. A) Importation of coordinates from selected trees to *Polyworks* software (yellow squares). B) Overlapping of point clouds plots and coordinates from selected trees.

- CompuTree

Plots density, ground step and rugged made difficult the isolation of each tree in *Polyworks*. For that reason and in order to avoid bias data from trees isolation, this process was performed by the free software *CompuTree* version 3.418. We used a script developed by LerFob- INRA (Nancy-France) (Annex 2.a) which identifies, by colors, each foot from point clouds and isolate automatically the selected tree (Figure 6). Finally, isolated tree was export like ASCII file.

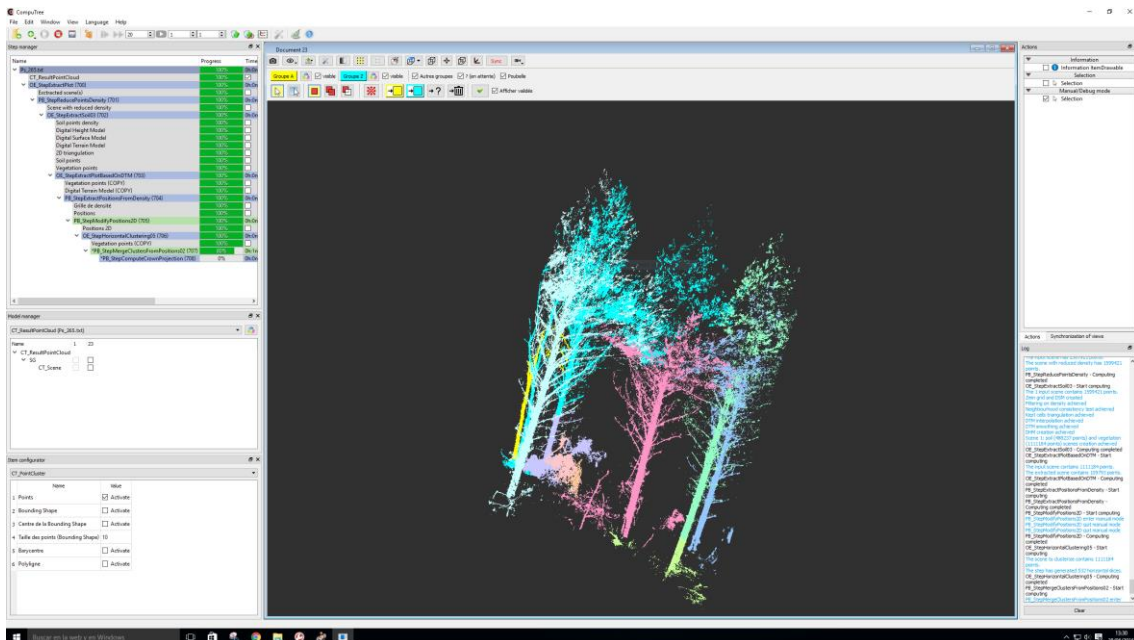


Figure 6. Screenshot of *CompuTree* software running the script and identifying each tree by colors.

3.4. OBTAINING TREE MEASURES

Both, *Polyworks* and *Computree* were used to obtain tree-level variables. On one hand, *Polyworks* was used to obtain: Total height (HT), Height to Crown Base (HCB), Height to the Largest Crown Width (HLCW) and Diameter at Breast Height (DBH) (Figure 7). On the other hand, another given script (Annex 2.b) was given to be applied on *CompuTree* software to create envelopes around each tree every 10 cm (Figure 8); these data were exported as a spreadsheet file where the area enveloping each section was defined. Thanks to this, we could defined the timber volume of each tree.

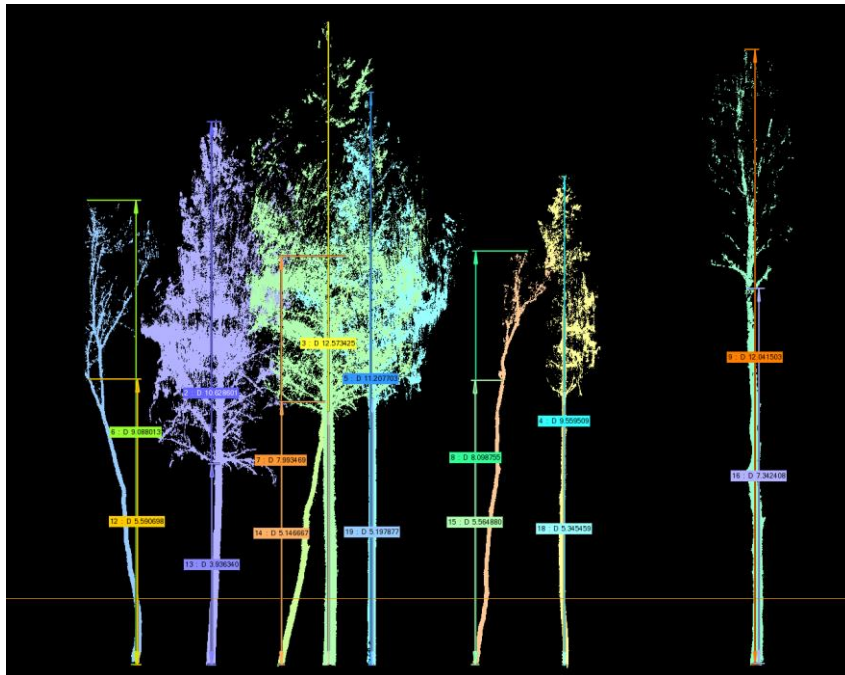


Figure 7. Screenshot from *Polyworks* with the isolated trees from one of the studied plots. Horizontal line represents the high at 1.3 m to extract Diameter at Breast Height (DBH). Vertical arrows gave us the measure of the height of each tree, both total height (HT), height to Crown Base (HCB) and Height to the Largest Crown Width (HLCW).

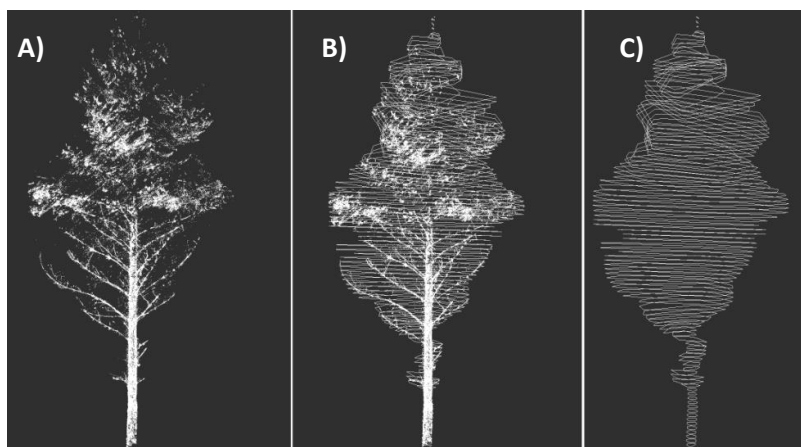


Figure 8. **A)** Performing of the tree on *Computree*. **B)** Envelopes created around the tree every 10cm. **C)** Detail of envelopes, which surround the tree.

Finally the mixture effects on trees allometry from mixed forests has been studied by creating circular subplots 5 m radius (White *et al.*, 2013) around each selected tree in *Polyworks* software (Figure 9). Every sub-plot was imported in *CompuTree*, where soil was separated from trees by using the same script for isolate trees but avoiding the last 2 steps. Finally, sub-plots without the ground were imported once more to *Polyworks* where DBH of each tree belonging to subplots were measured.

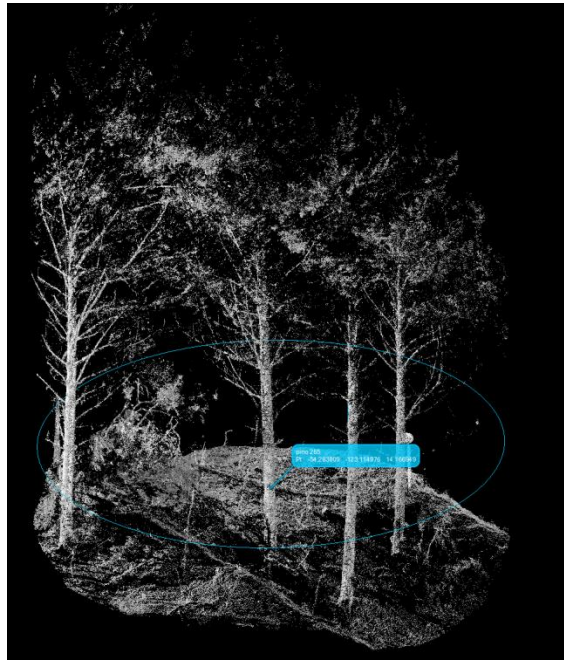


Figure 9. Circular plot 5m radius marked out by the blue circle. In the middle the studied tree marked by the blue square.

To automate the collection of DBH from each sub-plot we applied the same methodology we developed in a previous study (Uzquiano, 2014). We created a square frame around each tree to export DBH images with the same zoom (Figure 10), thus DBH measures were collected automatically by using the program *Adobe Photoshop* CS version 8.0.1. Since this program allows one to create actions, that can be applied to a whole share. This consisted on cutting out the images until the external edge of figures (tree parts) and according to the frame that surrounds every image, scaling them in order 1 pixel represent 1 millimeter in reality. Finally, this action was applied to the share of all images exported from *Polyworks*. Thanks to this, we were able to gather all measurements in few minutes. The program *XNView* was used to export images' properties (pixel size information) in .txt format and then to an *Excel* table.

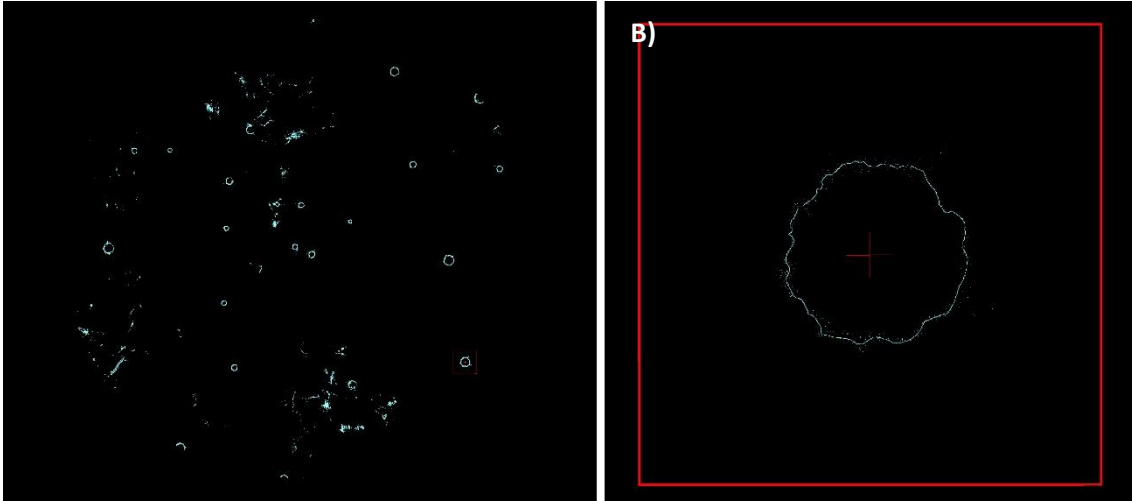


Figure 10. A) Clip view at 1.3 m of each tree belonging to one subplot 5m radius. **B)** Detail of one tree within the frame 50x50cm created in order to export every image with the same zoom.

3.5. DATA ANALYSIS

Since we count with trees DBH measures taken with caliper, simple linear regression comparing both LiDAR DBH and traditional DBH measures were performed for each species (*Pinus sylvestris* and *Quercus pyrenaica*) by using the program SAS 9.2.

$$Y = \beta_0 + \beta_1 * X + \xi$$

Where, Y=measurements obtained by traditional methods. β_0 = independent parameter, which must be 0. And β_1 is the slope, which must be 1. The control measurements by both traditional and alternative methods are the same. X= measurements obtained by TLS and, ξ = Model error parameter, it verifies residuals are normal, average 0, constant and independent variance. Script is shown in Annex 3.a.

On the other hand, we used equations to fit basic models for volume, total tree height, HCB and HLCW, which were performed by using R statistic programs (R core team, 2016). The models applied were:

- $\text{Log VC} = \beta_0 + \beta_1 * \text{Log (DBH)}$
- $\text{Log HT} = \beta_0 + \beta_1 * \text{Log (DBH)} + \beta_2 * \text{Log(G)}$
- $1 - (\text{HCB/HT}) = \beta_0 + \beta_1 * (\text{HT/DBH})$
- $\text{HLCW} = \beta_0 + \beta_1 * \text{HT} + \beta_2 * \text{HT}^2$

Where, VC = Crown volume; DBH= Diameter at Breast Height; HT= Total Height of the tree; G= quadratic mean diameter; HCB= Height to Crown Base; HLCW= Height to the Largest Crown Width. Finally, β_0 , β_1 and β_2 are the parameter to be specified for each case.

In order to study the mixture effects on trees allometry from mixed forests on the significant variables obtained in the basic models, the parameters were expanded by replacing them with a linear relationship with mixture proportion. So each β_i were replaced by $\beta_{i0} + \beta_{i1} * \text{MIXTURE}$. Where MIXTURE were represented by the proportion of pines in term of trees per ha or basal area over the total for the stand.

In this study, R2 values above 50% were considered enough to be recognized as good statistical adjustments. Estimator of parameter indicates straight bias, and its p-value, if these biases are significant or not. Scripts are shown in Annex 3.b.

4. RESULTS

4.1. TLS RESULTS

3D point clouds offer us reliable 3D representation, both trees and surface (Figure 1), as well as supply an exact trees georeferencing as good or better as the one we can obtain from a total station, but in shorter time.

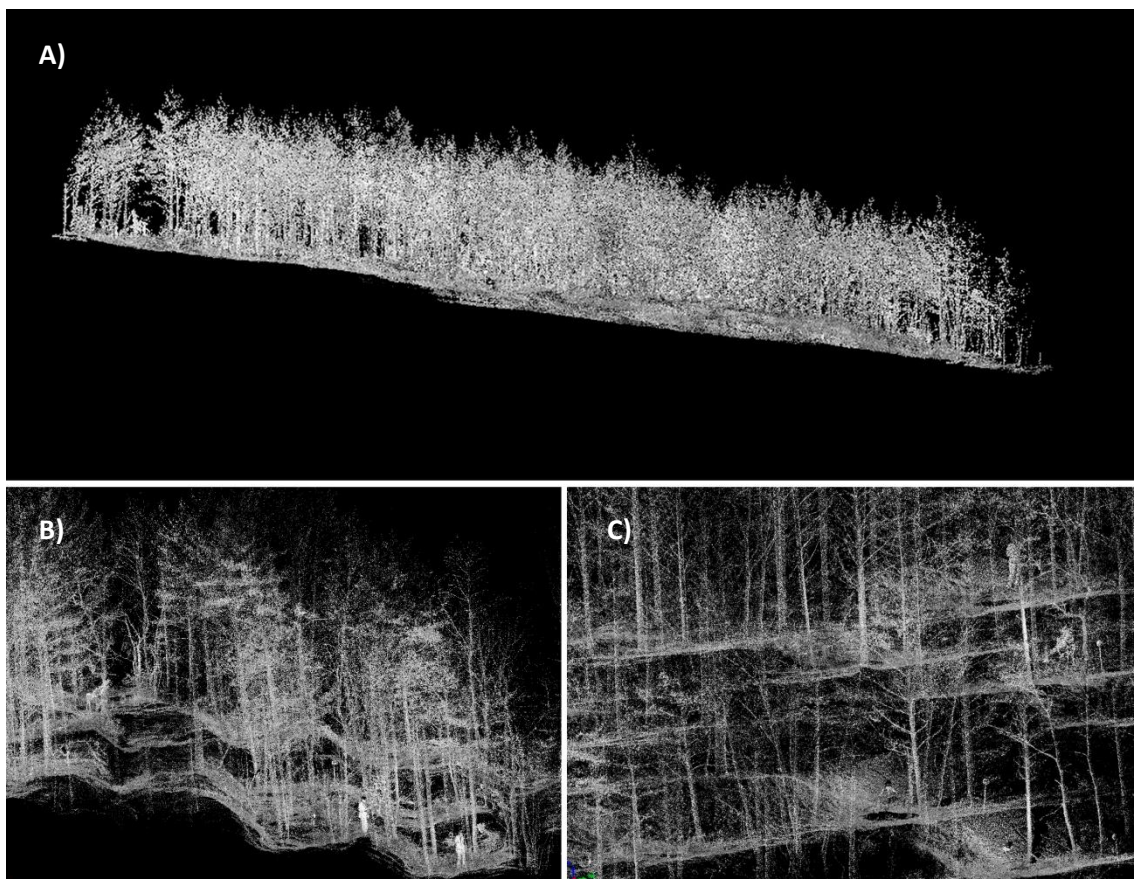


Figure 11. **A)** Side view of one of the entire plots. **B)** Detail of side view where rugged terrain is well appreciated. **C)** Detail of a frontal view of the plot.

4.2. STATISTICS ANALYSIS

Descriptive statistics summary of variables for each species were extracted and measured from individual trees are shown in Table 1. DBH, HT, HCB and HLCW were measured in *Polyworks* and Volume variables were extracted from *CompuTree*.

Table 1. Descriptive statistics of the variables measured through 3D point clouds. Table shows: Number of measured trees (n), mean (\bar{x}), maximum (max), minimum (min) and standard deviation (σ). Where HC is the height of the crown. V. Trunk is the volume of the trunk, V. Crown, the volume of the crown and Vt is the Total Volume.

Pine								
	DBH (cm)	Ht (m)	HCB (m)	HC (m)	HLCW (m)	V. Stem(m ³)	V. Crown(m ³)	Vt (m ³)
n	15	15	15	15	15	15	15	15
\bar{x}	16.78	10.51	4.13	6.39	6.88	0.22	26.42	26.60
Max	21.38	12.50	5.80	9.40	8.70	0.57	64.30	64.46
min	9.38	7.30	2.00	4.30	3.10	0.11	2.33	2.39
σ	3.41	1.48	1.07	1.28	1.75	0.14	18.25	18.29
Oak								
	DBH (cm)	Ht (m)	HCB (m)	HC (m)	HLCW (m)	V. trunk(m ³)	V. Crown(m ³)	Vt (m ³)
n	15	15	15	15	15	15	15	15
\bar{x}	11.88	9.02	5.17	3.85	7.45	0.35	4.95	5.30
Max	17.93	12.00	7.30	5.90	9.90	1.90	19.19	19.64
min	7.10	5.90	2.70	2.50	3.40	0.04	0.34	0.38
σ	2.82	1.51	1.21	1.08	1.61	0.54	4.73	4.96

DBH was measured for every tree belonging to each subplot 5m radius created around trees under study. Thanks to that mensuration variables were measured (Basal Area, stems per ha, Subplot Basal Area, Quadratic mean diameter and Reineke index) which have provided us a good information about current state of each plot after thinning. Descriptive statistics summary is shown in Table 2.

Reineke index was calculated by using the formula:

$$S = N * \left(\frac{Dg}{25.4}\right)^r$$

N= stem per hectare

Dg= Quadratic mean diameter

r= 1,605 (Reineke, 1933)

Table 2. Descriptive statistics of the variables measured through 3D point clouds for each plot (A1, A2 and Z2) and per species (pine and oak). Table shows, on the rows: Number of measured trees (n), mean (\bar{x}), maximum (max), minimum (min) and standard deviation (σ). And on the columns: mensuration variables: Basal Area (BA), number of stems per hectare (N), Subplot Basal Area (G), Quadratic mean diameter (Dg) and Reineke index (S).

A1	Pine					
		BA (m²)	N (stem/ha)	G (m²/ha)	Dg	S
	n	28	28	28	28	28
	\bar{x}	0.11	713.01	13.50	15.65	322.20
	max.	0.13	891.27	16.10	17.95	366.81
	min.	0.07	509.30	8.90	13.34	226.47
	σ	0.02	170.82	2.86	2.09	63.28
	Oak					
		BA (m²)	N (stem/ha)	G (m²/ha)	Dg	S
	n	26	26	26	26	26
	\bar{x}	0.08	662.08	9.89	13.45	247.34
	max.	0.12	763.94	15.45	16.05	365.57
	min.	0.02	254.65	2.83	11.90	75.45
σ	0.04	227.76	4.82	1.86	110.88	
A2	Pine					
		BA (m²)	N (stem/ha)	G (m²/ha)	Dg	S
	n	146	146	146	146	146
	\bar{x}	0.28	3717.86	35.94	11.25	981.27
	max.	0.32	4838.31	40.78	12.77	1062.01
	min.	0.20	2291.83	25.52	9.86	679.44
	σ	0.05	991.98	5.99	1.12	168.80
	Oak					
		BA (m²)	N (stem/ha)	G (m²/ha)	Dg	S
	n	172	172	172	172	172
	\bar{x}	0.30	4405.41	38.02	10.77	1061.22
	max.	0.38	6111.55	47.93	13.15	1318.93
	min.	0.22	2037.18	27.66	9.62	707.93
σ	0.07	1553.14	8.78	1.41	267.25	

Table 2. (Cont.) Descriptive statistics of the variables measured through 3D point clouds for each plot (A1, A2 and Z2) and per species (pine and oak). Table shows, on the rows: Number of measured trees (n), mean (\bar{x}), maximum (max), minimum (min) and standard deviation (σ). And on the columns: mensuration variables: Basal Area (BA), number of stems per hectare (N), Subplot Basal Area (G), Quadratic mean diameter (Dg) and Reineke index (S).

Z2	Pine					
		BA (m ²)	N (stem/ha)	G (m ² /ha)	Dg	S
	n	89	89	89	89	89
	\bar{x}	0.24	2266.37	31.00	13.21	791.85
	max.	0.28	2546.48	35.23	13.99	895.77
	min.	0.20	1782.54	25.47	12.34	645.40
	σ	0.03	290.34	4.19	0.61	101.52
	Oak					
		BA (m ²)	N (stem/ha)	G (m ² /ha)	Dg	S
	n	115	115	115	115	115
	\bar{x}	0.28	2928.45	35.42	12.48	926.49
	max.	0.30	3310.42	38.30	13.42	1011.86
	min.	0.26	2419.16	33.14	11.29	868.52
	σ	0.02	422.29	2.02	0.86	58.02

In order to observe in detail the values trend obtained by TLS comparing with those obtained with caliper, a simple linear regression was made. This analysis was made only for DBH measured because is the only measure we had with both, conventional (caliper) and TLS methods. Table 3 shows the relevant results and complete results are shown in Annex 4.

Table 3. DBH summary of statistical model results most characteristic for pine and oak. The rows specify the significance of models, the estimated parameters and their significance, set test on the parameters and individual test on the slope and finally test Kolmogorov-Smirnov normality on the residuals model

	DBH	
	Pine	Oak
Linear Regression model		
Pr > t 	<.0001	<.0001
F-Value	55	81.49
R² (%)	80.88	86.24
Estimator of Parameter		
Independent Variable	0.67382	-1.35623
Slope	0.89589	1.00299
Pr > t of the estimator of parameter		
Independent Variable	0.6549	0.4824
Slope	<.0001	<.0001
Test H₀: a=0		
p_value	0.6549	0.4824
Test H₀: b=1		
p-value	0.4044	0.9789
Kolmogorov-Smirnov: Normality test		
Statistics D	0.165824	0.165824
Pr > t 	>0.1500	>0.1500

For both species, we obtained a good linear regression model for DBH variable, with R2 value equal to 80.88% and 86.24% for *Pinus sylvestris* and *Quercus pyrenaica* respectively. The test H₀: a=0 reveals independent term is not significant different from zero, and test H₀ b=1 reveals slope (dependent term i.e. TLS point clouds) does not differ significantly from one. Finally, Kolmogorov-Smirnov test shows our data follows a normal distribution. Thus, we can conclude DBH data obtained by TLS point clouds are as good as those obtained by caliper, there are not significant differences.

4.3. MODELS

Final results of our adjustment data for *Pinus sylvestris* and *Quercus pyrenaica* are shown in Table 4. In general, we have found good adjustments for every model and species by doing some modifications showing in Table 4. Only for *Quercus pyrenaica* crown ratio model significant difference in the parameter “intercept” were found, so we removed it for the following studies.

Table 4. Equations tested for each species

Model	Species	Equation
Crown Volume	Pine	$Log CV = \beta_0 + \beta_1 * \log(DBH)$
	Oak	
Total Height	Pine	$\log HT = \beta_0 + \beta_1 * \log(DBH) + \beta_2 * \log(G)$
	Oak	$\log HT = \beta_0 + \beta_1 * DBH^2 + \log(G)$
Crown ratio	Pine	$1 - \left(\frac{HCB}{HT}\right) = \beta_0 + \beta_1 \left(\frac{HT}{DBH}\right)$
	Oak	--
HLCW	Pine	$HLCW = \beta_0 + \beta_1 + HT + \sqrt{HT}$
	Oak	$HLCW = \beta_0 + \beta_1 + HT + \beta_2 * HT^2$

In general, it is observed linear models proposed for each dendrometric variable (*intercept*) studied have significant adjustments, i.e. there exists a relationship between the studied variable and the dependent one for each fit model. Depending on the case this level of significance is greater or less (Table 5). Furthermore, this dependency ratio is significant in all cases except for *Quercus pyrenaica* crown ratio with respect to the HT and DBH relationship, whose significance level is greater than 0.01 so, relationships between these variables, cannot be established.

Table 5. Estimated parameters for each basic model, their bias (error), their t value, p value (pr (<|t|)) and finally their significance level (sig.) Significance codes: 0 '***'; 0.001 '**'; 0.01 '*'; 0.05 '.'.

Model	Species	Variables	Coefficients				
			Estimate Std.	Error	t value	pr (< t)	Sig.
Crwon Volume	Pine	Intercept	-5.4506	1.8344	-2.971	0.010819	*
		Log (DBH)	3.0247	0.6568	4.606	0.000493	***
	Oak	Intercept	-5.7219	2.2994	-2.488	0.02717	*
		Log (DBH)	2.8165	0.9348	3.013	0.00999	**
Total Height	Pine	Intercept	-3.74353	0.99936	-3.746	0.003233	**
		log (DBH)	0.30383	0.06627	4.585	0.000784	***
		log (G)	1.51668	0.28677	5.289	0.000257	***
	Oak	Intercept	-4.9846789	1.9247282	-2.59	0.02367	*
		(DBH ²)	0.0009317	0.0004211	2.212	0.04707	*
		log (G)	2.031847	0.56448	3.634	0.00342	**
Crown Ratio	Pine	Intercept	0,86579	0,08529	10,151	1,51E-07	***
		(Htotal/DBH)	-0,39104	0,12834	-3,047	0,00936	**
	Oak	Intercept	0,5205	0,1152	4,52	0,000576	***
		(Htotal/DBH)	-0,1179	0,1427	0,1427	0,423609	
HLCW	Pine	Intercept	-13.528	3.651	-3.705	0.00264	**
		\sqrt{HT}	6.278	1.132	5.545	9.46E-05	***
	Oak	Intercept	-9.74624	3.83995	-2.538	0.02603	*
		HT	2.86556	0.85729	3.343	0.00586	**
		\sqrt{HT}	-0.10365	0.04723	-2.195	0.0486	*

After obtaining the parameters that adjust the proposed models, we studied how these variables are affected by the proportion of mixture within the sub-plot 5 m radius created around each goal tree (Table 6), except for the variable “crown ratio” since; as we said before, none good adjustment was found to its model equation. Results are shown in Table 7. It is generally observed that the proportion of mixture do not affect the relation between the dendrometric variables for each case and model.

Table 6. Equations tested for each species applying mixture interaction.

Model	Species	Equation
Crown Volume	Pine	$Log CV = \beta_{00} * Mix.prop + \beta_{01} * (\log(DBH)) * Mix.prop.$
	Oak	
Total Height	Pine	$\log HT = \beta_{00} * Mix.prop + \beta_{01} * (\log(DBH)) * Mix.prop + \beta_{02} * \log(G)$
	Oak	$\log HT = \beta_{00} * Mix.prop + (\beta_{01} * DBH^2 * Mix.prop) + \log(G)$
HLCW	Pine	$HLCW = \beta_{00} + \beta_{01} + HT * (Mix.prop) + \sqrt{HT}$
	Oak	$HLCW = \beta_0 + \beta_1 + HT * (Mix.prop) + \beta_2 * HT^2$

Table 7. Estimated parameters for each expanded model, their bias (error), their t value, p value (pr (<|t|) and finally their significance level (sig.) Significance codes: 0 '***'; 0.001 '**'; 0.01 '*'; 0.05 '.'.

Model	Species	Variables	Coefficients				
			Estimate Std.	Error	t value	pr (< t)	Sig.
Crown Volume	Pine	Intercept	-24.44	28.76	-0.85	0.413	
		Mix prop.	29.16	44.36	0.657	0.524	
		Log (DBH)	10.08	10.4	0.969	0.353	
		Mix prop: Log(DBH)	-10.81	15.99	-0.676	0.513	
	Oak	Intercept	-34.115	22.873	-1.492	0.164	
		Mix prop.	77.488	61.958	1.251	0.237	
		Log (DBH)	14.878	9.333	1.594	0.139	
		Mix prop: Log(DBH)	-33.093	25.333	-1.306	0.218	
Total Height	Pine	Intercept	-0.2377	2.7994	-0.085	0.9342	
		log (DBH)	-0.5376	0.912	-0.59	0.56999	
		Mix prop.	-4.3632	3.8976	-1.119	0.29192	
		log (G)	1.2947	0.291	4.447	0.00161	**
		Mix prop: log(DBH):	1.3539	1.4052	0.963	0.36047	

Table 7. (Cont.). Estimated parameters for each expanded model, their bias (error), their t value, p value (pr (<|t|)) and finally their significance level (sig.) Significance codes: 0 '***'; 0.001 '**'; 0.01 '*'; 0.05 '.'.

Model	Species	Variables	Coefficients				
			Estimate Std.	Error	t value	pr (< t)	Sig.
	Oak	Intercept	-5.321768	2.078197	-2.561	0.02834	*
		DBH ²	-2.404562	1.922596	-1.251	0.23925	
		Mix prop.	-0.004012	0.004287	-0.936	0.37146	
		log (G)	2.379233	0.659332	3.609	0.00478	**
		Mix prop: DBH ²	0.013494	0.011657	1.158	0.27391	
HLCW	Pine	Intercept	55.581	92.326	0.602	0.561	
		HT	-3.195	4.415	-0.724	0.486	
		Mix prop	-78.698	72.007	-1.093	0.300	
		sqrt(HT)	-2.835	33.668	-0.084	0.935	
		Mix Prop: HT	6.641	6.759	0.983	0.349	
	Oak	Intercept	-12.93863	6.52195	-1.984	0.07539	.
		Mix prop.	15.4941	31.60973	0.49	0.63459	
		HT	2.80988	0.78373	3.585	0.00497	**
		sqrt(HT)	-0.08357	0.07615	-1.097	0.29817	
		Mix Prop: HT	-1.04057	3.58729	-0.29	0.77769	

5. DISCUSSION

Our results prove the accuracy of TLS method for tree structure assessment on standing trees. In this research we have combine several software, which have helped us to automate measurements through tree point clouds avoiding bias in the extraction of measures. On one hand, as many other authors e.g. Hopkinson *et al.*, 2004; Dassot *et al.*, 2012, Uzquiano 2014; we have tested the use of retro-engineering *Polyworks* software for processing point clouds. Furthermore, we have complement point clouds edition with *CompuTree* software.

The speed and objectivity of data collection with TLS device are desirable attributes (Hopkinson, 2004) and data processing is time consuming (Uzquiano *et al.*, 2014; Xu *et al.*, 2013). The methodology we describe here needs still to be adjusted but compare with a previous study we carried out (Uzquiano, 2014) we could see, the incorporation of *CompuTree* software reduces data processing time. We lasted around 30 minutes to isolate each tree from the plot, while with *CompuTree* it took us only 10 minutes to get

each tree completely isolate. However, external problems such as get familiar with every software needed for the processing, licenses required for point clouds edition (FaroScene and *Polyworks*) together with the great amount of weight data occupies makes necessary to have a powerful computer, which might be not yet within reach of all and is still not functional in real forest inventories.

- **TLS**

Like Dassot *et al.* (2012) research, as a pre-processing step we designed FARO FOCUS scanner positions within the plots. We found out scanning time is quite depending on terrain and trees density. We spent 5 hours in plots A2 and Z2 where density was high, and only 2 hours in plot A1 where density was low. Our research agrees with Hauglin *et al.* (2014) The use of TLS in forestry has not become operational to the same degree as the use of Arial Laser Scanning (ALS), but several applications, such as the estimation of tree position and DBH, offer us detailed registrations of features that are practically unobtainable through conventional field measurements.

- **CompuTree**

As in Othmani *et al.*, 2011 study, we found *CompuTree* is a good tool for isolate trees automatically without bias but the principal inconvenience of this program is that is not able to process data bigger than 44 million point clouds i.e. not bigger than 2Gb. In spite of that, we can conclude tree isolation was fast and accurate (Figure 1.A) for the most of cases. Only in plot A2 where the density was the highest one, we found problems isolating trees since crowns where too joined, thus the program identified all crowns together as a part of one single tree (Figure 1.B). During this process, the classical personal estimation data are removed and we can obtain a lot of information for each tree like have shown in this study (Volume, DBH, Tree high, etc.) in only few minutes and minimizing errors. Nevertheless this process is not still applicable to isolate all trees belonging to the same whole stand because the isolation process with *CompuTree* is still time-consuming since the script we used to isolate tree cannot be performed to more than one tree in the same step. That is to say, the program identifies every tree, but then only one tree can be selected to be isolating from the plot. Thus, get all measures from the full trees belonging to the same plot is still unthinkable.

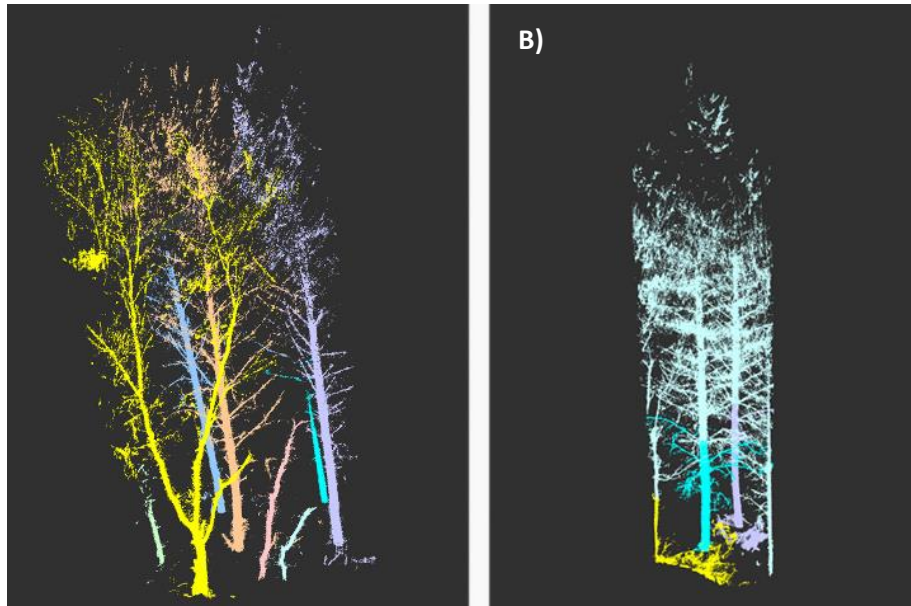


Figure 12. *Computree* software identifies each tree by colors. Figure **A)** shows good tree isolation from plot A1 where stem density was low. Figure **B)** shows problem identification due to extreme crown overlapping in plot A2 where stem density was too high.

One of the great advantages *CompuTree* provides us is data can be export in numerous formats (e.g.: csv; Points XYB; Points ASCII; polygons 2D, etc.) and thus, they can be imported once again to *Polyworks* but as individual files without the noise of ground or surrounded trees, i.e. a file per tree. This allowed us to locate every tree at will and facilitate DBH collection by locating trees at the same level (Figure 2) eliminating slope problem and the cutting waste on the ground we had originally, which made almost impossible to obtain the DBH measures precisely.

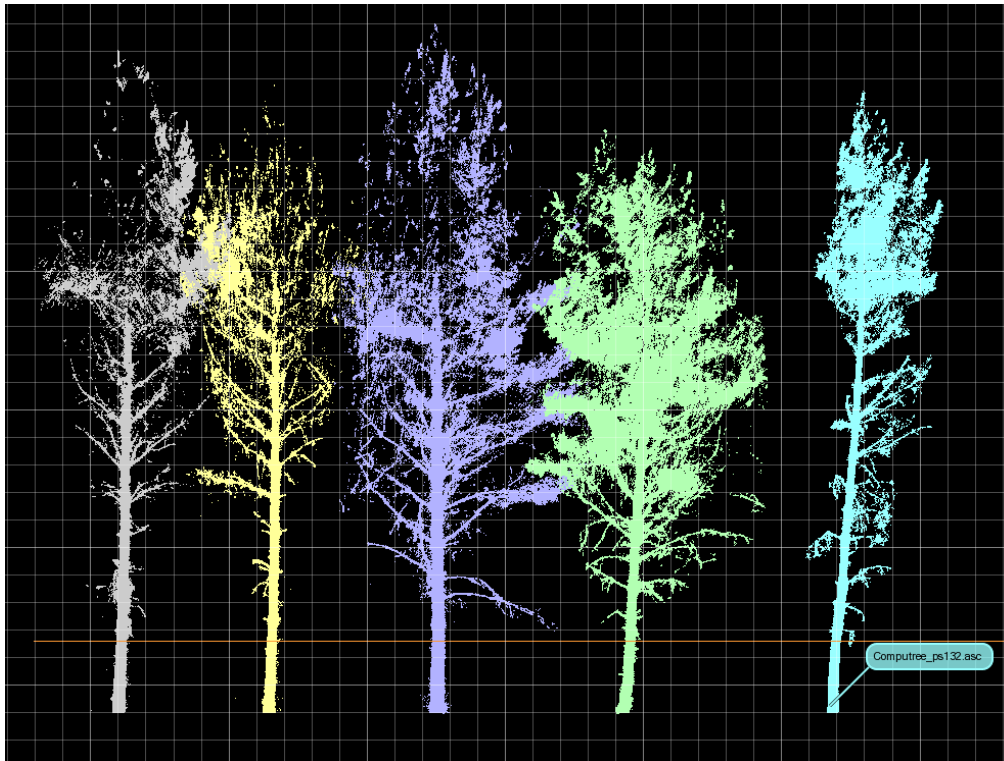


Figure 13. Once we have isolated trees in *CompuTree*, these were imported again in *Polyworks* as different files per tree, so we could locate each tree at the same level and measure DBH by creating one only plane at 1.3m high.

The spreadsheet file *CompuTree* is able to export showing the area enclosed by each enveloping, in this case, each 10cm has provided the volume of trees in very short time. However, volume script needs to be improved. Due to the enveloping beyond the branches are not able to fit to every branch but around the whole crown thus, over-estimation can be create errors in models.

One of the biggest problems we had was the extraction of BA for each subplot since the terrain was steep and rugged, apart from the cutting waste, which made hard to identify where stem base was for each tree. This problem was solved thanks to *CompuTree*, which is able to extract and separate the soil from the trees. Othmani *et al.*, 2011 explain in his study they found problems to separate soil and trees within the plots that had a lot of regeneration since seedlings masked the ground and hinder the process. In this study, the same problem was found but with the great amount of cutting waste which covered the ground (Figure 3). Nevertheless, this process can be considered as a good starting point in the study of accelerate stand data since one of the most time-consuming facts are the isolation of ground from trees.

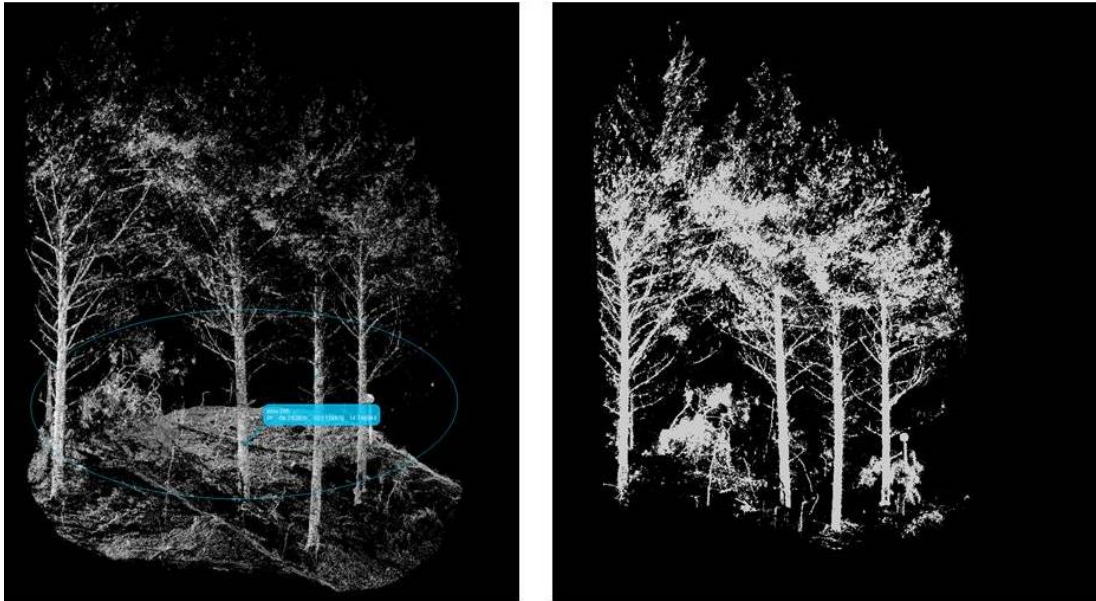


Figure 14. Ground isolation. A) subplot with ground. B) Same subplot after isolate ground in *CompuTree*

- TLS data and modeling results

DBH is the only variable which has been compared with traditional measures (caliper). In the same way previous studies observed (Hopkinson, 2004; Watt, 2005), we found good agreement between 3D point clouds and field measures.

Regarding fitting models, Dassot *et al.* (2012) studied 17 Sessile oaks, Hauglin *et al.* (2014) studied 60 trees of Norway Spruce, Raumonen *et al.* (2015) 27 eucalyptus and 15 oaks to validate their models from TLS data. So we have considered our estimation with 15 trees of each species studied as a good number to obtain significant results. However, in any of them, mixing effect was studied. Therefore, we have no reference to compare with our data but we believe results were no significant due to: (1) low number of observations; (2) all observations came from plots belonging to the same place. Modelling growth of one species in a mixed stand has to consider that this species only occupies a portion of the stand's growing space. Consequently, to compare its growth with its corresponding growth in pure stands, it is necessary to correct the growth with the species proportion. Otherwise growth will be correlated with species proportion (Sterba *et al.*, 2014); (3) Environmental and the degree of mixing differences are low and, (4) Research species proportion was measured by basal area since is the most common way to define species proportion (Légaré *et al.*, 2004; Perot and Picard, 2012; Groot *et al.*, 2014 in Bravo-Oviedo *et al.*, 2014) and due to the very small period of time that cutting was made (Summer 2015) we decided to model the mixing effect of each species as non-cut was made, because we considered less than one year is not time enough so trees structure have changed. After all these

consideration, further studies with more individuals are necessary to be able to more reliable results. Nevertheless this has been a first attempt in our way on dynamic mixed forest understanding.

6. CONCLUSION

As we found in our previous research (Uzquiano, 2014) and in line with e.g. Raumonon *et al.*, 2015; Dassot *et al.*, 2012 automatic tree extraction is still a big bottleneck for reconstruction methods for estimating tree structure and so, largescale use of TLS. In addition, in most cases, getting familiar with the use of necessary software slows down the processes. Nevertheless the results have demonstrated the process worth since thanks to this technology we could extract more robust and accurate data unthinkable with traditional methods taken on field. TLS data has provided us a very important back-up of our stands that can be compared after few years with new scans to see allometry changes over time and how it reacts to different silviculture and The mixture effects on trees allometry from mixed forests.

As a result, an important step forward has been made to increase our knowledge of mixed forest dynamic. Now we have got familiar with all software, isolation of more trees will be possible, and further research will be able to be carried out.

ACKNOWLEDGEMENTS

The project FORMIXING (Ref: AGL2014-51964-C2-1-R) financed by the Spanish Ministry of Economy and Competitiveness and FEDER fund, thanks to which, expenses for all field trips and the use of TLS have been covered. To the program COST Action FP1206 which gave me the opportunity to meet Dr. Ignacio Barbetiro and Dr. Mahieu Dassot who have introduced me to the knowledge of *CompuTree* software developed by Alexandre Piboule from the ONF.

Thanks to the Laboratory of Architectural Photogrammetry belonging to the School of Architecture (University of Valladolid), especially to José Martínez, Luis García and David Marcos who have helped me in every question I had in TLS use and methodology design.

Thanks to Sustainable Forest Management Research Institute UVa-INIA, to Felipe Bravo who gave me once more the chance to develop this research and all my friends and colleagues who have collaborated somehow in this project: Cristóbal, Ana, Jorge, Nico, María, Irene, David, Guille, Sara, Alicia, Mónica and Artzai. Thanks to my friend

Dani who has helped me in all my mathematic and statistics questions and most particularly to my colleague and friend Jose Guillermo who has supported and gave me so much time of his summer, words are not enough to show my gratitude to you.

And last but not least, I want to thanks Jorge and my family who always are there for me. This study is especially dedicated to my uncle Salvador and my grandfather José who taught me to keep going no matter what and so, this one is for you both.

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ANNEXES

1. Location plan

2. CompuTree Software

2.a. Tree Isolation Script

2.b. Tree Volumen Script

3. Statistics

3.a. SAS scripts

3.b. R Script

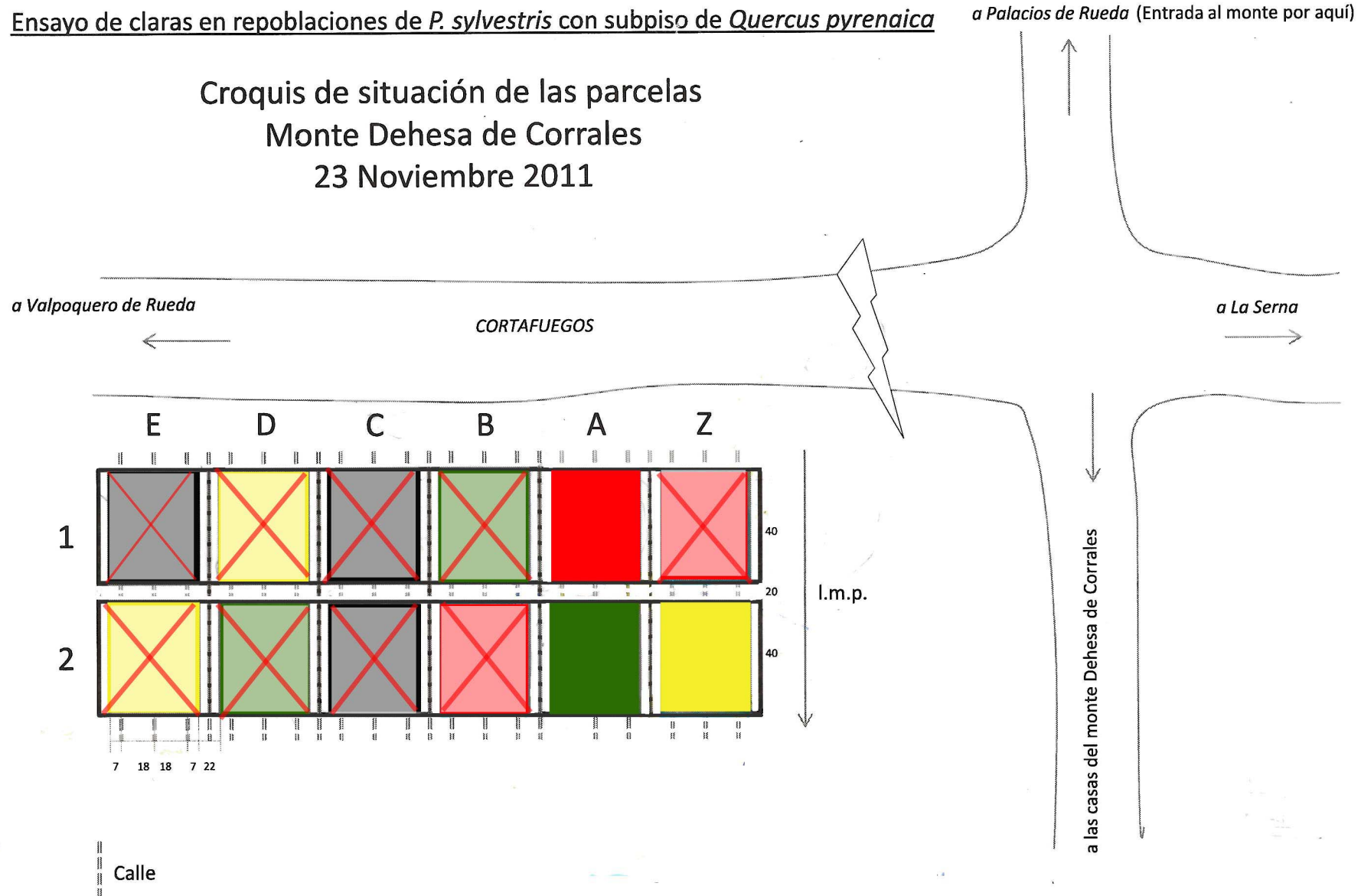
4. Statistics result: DBH comparison

ANNEX 1

Location plan

Ensayo de claras en repoblaciones de *P. sylvestris* con subpiso de *Quercus pyrenaica*

Croquis de situación de las parcelas
 Monte Dehesa de Corrales
 23 Noviembre 2011



||| Calle

Unidades en metros, no está a escala
 l.m.p.: línea de máxima pendiente

- Parcelas no utilizadas
- Intensidad de corta 50%
- Intensidad de corta 25%
- Intensidad de corta 0%
- ⊠ Parcelas no utilizadas en el presente estudio



ANNEX 2

2.a. Tree Isolation Script

2.b. Tree Volume Script

ANNEX 2.a. Tree Isolation Script

A1_ps265.txt	100%	0h:0m:0s:190ms	<input type="checkbox"/>
CT_ResultPointCloud	100%		<input type="checkbox"/>
▼ OE_StepExtractPlot (579)	100%	0h:0m:0s:18ms	<input type="checkbox"/>
Exctracted scene(s)	100%		<input type="checkbox"/>
▼ PB_StepReducePointsDensity (580)	100%	0h:0m:0s:83ms	<input type="checkbox"/>
Scene with reduced density	100%		<input type="checkbox"/>
▼ OE_StepExtractSoil03 (581)	100%	0h:0m:0s:78ms	<input type="checkbox"/>
Soil points density	100%		<input type="checkbox"/>
Digital Height Model	100%		<input type="checkbox"/>
Digital Surface Model	100%		<input type="checkbox"/>
Digital Terrain Model	100%		<input type="checkbox"/>
2D triangulation	100%		<input type="checkbox"/>
Soil points	100%		<input type="checkbox"/>
Vegetation points	100%		<input type="checkbox"/>
▼ OE_StepExtractPlotBasedOnDTM (582)	100%	0h:0m:0s:9ms	<input type="checkbox"/>
Vegetation points (COPY)	100%		<input type="checkbox"/>
Digital Terrain Model (COPY)	100%		<input type="checkbox"/>
▼ PB_StepExtractPositionsFromDensity (583)	100%	0h:0m:0s:1ms	<input type="checkbox"/>
Grille de densité	100%		<input type="checkbox"/>
Positions	100%		<input type="checkbox"/>
▼ PB_StepModifyPositions2D (584)	100%	0h:0m:7s:620ms	<input type="checkbox"/>
Positions 2D	100%		<input type="checkbox"/>
▼ OE_StepHorizontalClustering05 (585)	100%	0h:0m:0s:197ms	<input type="checkbox"/>
Vegetation points (COPY)	100%		<input type="checkbox"/>
▼ PB_StepMergeClustersFromPositions02 (586)	100%	0h:0m:6s:790ms	<input type="checkbox"/>
Positions 2D (COPY)	100%		<input type="checkbox"/>
▼ PB_StepComputeCrownProjection (587)	100%	0h:0m:0s:71ms	<input type="checkbox"/>
Positions 2D (COPY)	100%		<input type="checkbox"/>
Points, ASCII(X,Y,Z,R,G,B,NX,NY,NZ)	100%	0h:0m:0s:0ms	<input type="checkbox"/>

ANNEX 2.b. Tree Volume Script

Name	Progress	Time / Show	Debug
▼ A1_ps265.txt	100%	0h:0m:0s:154ms	<input type="checkbox"/>
CT_ResultPointCloud	100%		<input type="checkbox"/>
▼ PB_StepComputeCrownProjection (592)	100%	0h:0m:0s:358ms	<input type="checkbox"/>
CT_ResultPointCloud (COPY)	100%		<input type="checkbox"/>
Export d'attributs (csv)	100%	0h:0m:0s:33ms	<input type="checkbox"/>

ANNEX 3

3.a. SAS script

3.b. R Script

ANNEX 3.a. SAS Script

```
libname DBH'G:\TFM CUSF\Datos';

/* parcelas*/

PROC IMPORT OUT= WORK.LIDAR
            DATAFILE= "G:\TFM CUSF\Datos\dbh_sas.xlsx"
            DBMS=EXCEL REPLACE;
    RANGE="dbh$";
    GETNAMES=YES;
    MIXED=YES;
    SCANTEXT=YES;
    USEDATE=YES;
    SCANTIME=YES;
RUN;
proc print data=work.lidar;
run;

Data work.pino;
set work.lidar;
if Especie="Pino";
run;
proc print data=work.pino;
run;

Data work.roble;
set work.lidar;
if Especie="Roble";
run;
proc print data=work.roble;
run;

ods graphics on;
PROC REG DATA=work.roble outest=reg01 tableout;
MODEL DBH_conv=DBH_Lidar;
output out=error p=predicho r=error rstudent=t;
test intercept=0;
test DBH_Lidar=1;
RUN;
ods graphics off;

ods graphics on;
proc univariate data=error normal plot;
var error;
run;
ods graphics off;

ods graphics on;
PROC REG DATA=work.pino outest=reg01 tableout;
MODEL DBH_conv=DBH_Lidar;
output out=error p=predicho r=error rstudent=t;
test intercept=0;
test DBH_Lidar=1;
RUN;
ods graphics off;
```

```
ods graphics on;  
proc univariate data=error normal plot;  
var error;  
run;  
ods graphics off;
```

```
data error2;  
set error;  
if t>3 or t<-3;  
run;
```

```
proc print data=error2;  
run;
```

```
proc gplot data=error;  
plot t*predicho=1;  
symbol1 v=circle c=blue;  
run;  
quit;
```

ANNEX 3.b. R Script

```

#carpeta de trabajo y librerias
setwd("L:/TFM CUSF/Datos")
install.packages('ggplot2')
require(ggplot2)
require(plyr)

packs<-c("plyr","ggplot2")#paquetes que se necesitan
sapply(packs,require,character.only=TRUE)

#Preparar datos-----
#tabla de datos LIDAR
dir()
data<-read.csv('Datos_modelos.csv',sep=';',dec='.', header = T)
head(data,15)
summary(data)
names(data)
data['code_tree']<-with(data,paste(Plot,Arbol,sep=''))

#Inv.1 = inventario previo a la clara (medidas tomadas con forcipula)
dir()
Inv.1<-read.csv('Cistierna_dbh_forcipula.csv',sep=';',dec='.', header = T)
head(Inv.1)
summary(Inv.1,10)
names(Inv.1)
Inv.1$BA<-(pi*(Inv.1$DBHm/100)^2)/4#area basal por arbol en m2

Inv.1['Especie']<-with(Inv.1,ifelse(Tipo=='Ps','Pino',
                                   ifelse(Tipo=='Qpy','Roble',Tipo)))
#calcular G por especie
G.sp<-ddply(Inv.1, c('Plot','Especie'),summarise, g.sp=sum(BA,na.rm=T)*5)

#incluir g por sp en df data
data<-merge(data,G.sp, by=c('Plot','Especie'))
#calcular proporcion de mezcla
data['propmezcla']<-with(data, g.sp/G)

#calculamos area basimetrica por parcela. G=SBA
G_plots<-ddply(Inv.1, c('Plot'),summarise, G=sum((pi*(DBHm/100)^2)/4,na.rm=T))
G_plots$G<-G_plots$G*10000/2000

#incluimos en tabla de datos (data frame =df). es decir, juntamos las tablas de un csv con otro.
data<-merge(data,G_plots,by='Plot')

#calculamos el BAL

tmp<-subset(Inv.1,Plot=='A1')#subset para probar funcion
summary(tmp)
head(tmp)

#funcion para calcular BAL-----
f.BAL <- function(tmp){
  ltmy <- list()
  for(i in 1:nrow(tmp))
    ltmy[[i]] <- subset(tmp,BA>tmp$BA[i])
  names(ltmy) <- tmp$lbl
  BAL <- list()
  for(i in 1:nrow(tmp))
    BAL[[i]] <- sum(ltmy[[i]][,'BA']*5)
  names(BAL) <- tmp$lbl
  return(BAL)
}

head(as.data.frame((unlist(f.BAL(tmp)))))#probar funcion

tmps <- split(Inv.1,Inv.1$Plot)#listas por plot
head(tmps[[1]])

#aplicar funcion
BAL.tmp<-as.data.frame((unlist(
  lapply(tmps,function(x)f.BAL(x)) #aplicar funcion a listas por plot
)))

#organizar df BAL para unir con data
head(BAL.tmp)
names(BAL.tmp)<-c('BAL')
BAL.tmp$code_tree<-rownames(BAL.tmp)
BAL.tmp$code_tree<-lapply(strsplit(as.character(BAL.tmp$code_tree),"\\."),"[",2)

#incluir BAL en Inv.1,unir por lbl
Inv.1<-merge(Inv.1,BAL.tmp, by.x="lbl",by.y="code_tree")
head(Inv.1[c(26,30,31)])

data<-merge(data,Inv.1[c(26,30,31)],BAL.tmp, by.x=c('Especie','Arbol'),
            by.y=c('Especie','IDNew'),all.x = TRUE)

```



```

#datos de arboles replicados robles#1224,1274,1279
#mismo numero diferente color de chapa en df Inv.1
#seleccionamos de acuerdo al DBH m?s parecido
subset(Inv.1,IDNew%in% c(1224,1274,1279))
subset(data,Arbol%in% c(1224,1274,1279))

data<- (data[-c(16,18,21),])#eliminar filas

#robles q no coinciden con las etiquetas
subset(Inv.1,Punto%in% c(1897,1901,1904,1919,2026))
#incluir los datos a mano, nada elegante pero paso de cambiar mas cosas...
fix(data)
subset(data,Arbol%in% c(1897,1901,1904,1919,2026))

#ajustamos el modelo de volumen de copa-----
ggplot(data,aes(x=prop_mezcla,y=log(Vol_copa_m3)))+geom_point()+theme_bw()+facet_grid(.~Especie)
model_vol<-lm(data,log(Vol_copa_m3)~log(DBH))#modelo con ambas sp
summary(model_vol)
AIC(model_vol)
#modelo para Pino
model_vol.P<-lm(data,subset=Especie=='Pino',formula= log(Vol_copa_m3)~log(DBH))#modelo de pino
AIC(model_vol.P)
summary(model_vol.P)
plot(model_vol.P)
#modelo para pino considerando la mezcla- extendido
model_vol.P1<-lm(data,subset=Especie=='Pino',
formula= log(Vol_copa_m3)~(prop_mezcla)+log(DBH)+(prop_mezcla*log(DBH))
)#modelo de pino
summary(model_vol.P1)

#modelo para roble
model_vol.R<-lm(data,subset=Especie=='Roble',formula= log(Vol_copa_m3)~log(DBH))#modelo de roble
summary(model_vol.R)
plot(model_vol.R)
AIC(model_vol.R)
#modelo para roble considerando la mezcla
model_vol.Rmix<-lm(data,subset=Especie=='Roble',
formula= log(Vol_copa_m3)~(prop_mezcla)+log(DBH)+(prop_mezcla*log(DBH))
)#modelo de roble
summary(model_vol.Rmix)

#ajustamos el modelo de altura total-----
ggplot(data,aes(y=(H_total_m),x=(G),colour=Especie))+geom_point()+theme_bw()+facet_grid(.~Especie)
ggplot(data,aes(y=(H_total_m),x=G))+geom_point()+theme_bw()+facet_grid(.~Especie)
model_HT<-lm(data=data, log(H_total_m)~log(DBH)+log(G))
summary(model_HT)
plot(model_HT)
AIC(model_HT)

#modelo para pino
model_HT.P<-lm(data=data,subset=c(Especie=='Pino'&!Arbol==306),formula=log(H_total_m)~log(DBH)+log(G))
summary(model_HT.P)
plot(model_HT.P)
AIC(model_HT.P)

#modelo para pino considerando la mezcla
model_HT.Pmix<-lm(data=data,subset=c(Especie=='Pino'&!Arbol==306),
formula=log(H_total_m)~(prop_mezcla)+log(DBH)*(prop_mezcla)+log(G))
summary(model_HT.Pmix)

#modelo para roble
model_HT.R<-lm(data=data,subset=Especie=='Roble',
formula=log(H_total_m)~I(DBH^2)+log(G))
summary(model_HT.R)
plot(model_HT.R)
AIC(model_HT.R)

#modelo para roble considerando mezcla
model_HT.Rmix<-lm(data=data,subset=Especie=='Roble',
formula=log(H_total_m)~(prop_mezcla)*I(DBH^2)+log(G))
summary(model_HT.Rmix)

#ajustamos el modelo de ratio de tronco-----
ggplot(data,aes(y=(H_Copa_m/H_total_m),x=(H_total_m/DBH)))+geom_point()+theme_bw()+facet_grid(.~Especie)
model_RT<-lm(data=data, 1-(H_baseCopa_m/H_total_m)~I(H_total_m/DBH))
summary(model_RT)
plot(model_RT)

#modelo para el pino rtio del tronco
model_RT.P<-lm(data=data,subset=Especie=="Pino", (H_Copa_m/H_total_m)~I(H_total_m/DBH))
summary(model_RT.P)
plot(model_RT.P)

#modelo para pino considerando mezcla
model_RT.Pmix<-lm(data=data,subset=Especie=="Pino",
formula= 1-(H_Copa_m/H_total_m)~(prop_mezcla)+((prop_mezcla)*I(H_total_m/DBH)))
summary(model_RT.Pmix)

```

```

summary(model_RT.Pmix)

#modelo para el roble del ratio del tronco
model_RT.R<-lm(data=data,subset=Especie=="Roble", formula= (H_Copa_m/H_total_m)~I((H_total_m/DBH)))
summary(model_RT.R)
plot(model_RT.R)

#ajustamos el modelo de Altura de la Maxima Amplitud de copa (HMAC)-----
ggplot(data,aes(y=(H_maxAmpCopa_m),x=(H_total_sqrt)))+geom_point()+theme_bw()+facet_grid(.~Especie)
data$H_total_sqrt<-(data$H_total_m)^2
model_HMAC<-lm(data=data, (H_maxAmpCopa_m)~H_total_m+H_total_sqrt)
summary(model_HMAC)
plot(model_HMAC)

#modelo para pino
data$H_total_sqrt<-(data$H_total_m)^2
model_HMAC.P<-lm(data=data,subset=Especie=="Pino", formula= (H_maxAmpCopa_m)~sqrt(H_total_m))
summary(model_HMAC.P)
plot(model_HMAC.P)

#modelo para pino considerando mezcla
model_HMAC.Pmix<-lm(data=data,subset=Especie=="Pino",
                    formula= (H_maxAmpCopa_m)~ H_total_m*propmezcla+sqrt(H_total_m))
summary(model_HMAC.Pmix)

#modelo para roble
model_HMAC.R<-lm(data=data,subset=Especie=="Roble", formula= (H_maxAmpCopa_m)~H_total_m+H_total_sqrt)
summary(model_HMAC.R)
plot(model_HMAC.R)
#modelo para roble considerando mezcla
model_HMAC.Rmix<-lm(data=data,subset=Especie=="Roble",
                    formula= (H_maxAmpCopa_m)~propmezcla*H_total_m+H_total_sqrt)
summary(model_HMAC.Rmix)

```

ANNEX 4

4. Statistics results: DBH comparison

ANNEX 4. Statistics results: DBH comparison

Obs	Arbol	DBH_conv	DBH_Lidar	Especie	F5
1	A1_ps265.png	17.8	19.950	Pino	
2	A1_ps267.png	19.0	20.375	Pino	
3	A1_ps282.png	11.2	12.900	Pino	
4	A1_ps306.png	14.6	18.575	Pino	
5	A1_ps316.png	12.6	13.350	Pino	
6	A1_qpy1484.png	9.5	10.575	Roble	
7	A1_qpy1493.png	11.1	12.125	Roble	
8	A1_qpy1538.png	8.5	11.950	Roble	
9	A1_qpy1574.png	11.5	9.725	Roble	
10	A1_qpy1579.png	12.4	12.850	Roble	
11	A2_ps372.png	19.4	21.375	Pino	
12	A2_ps375.png	12.7	14.300	Pino	
13	A2_ps415.png	15.2	16.400	Pino	
14	A2_ps429.png	8.1	9.375	Pino	
15	A2_ps503.png	12.8	14.525	Pino	
16	A2_qpy1224.png	8.1	8.800	Roble	
17	A2_qpy1274.png	11.0	10.375	Roble	
18	A2_qpy1279.png	7.8	7.100	Roble	
19	A2_qpy1394.png	18.0	17.925	Roble	
20	A2_qpy1416.png	14.1	13.925	Roble	
21	Z2_ps22.png	19.2	18.050	Pino	
22	Z2_ps48.png	16.3	16.025	Pino	
23	Z2_ps57.png	21.6	21.225	Pino	
24	Z2_ps60.png	12.5	15.950	Pino	
25	Z2_ps132.png	15.7	15.925	Pino	
26	Z2_qpy1897.png	9.1	11.350	Roble	
27	Z2_qpy1901.png	15.0	16.525	Roble	
28	Z2_qpy1904.png	12.8	13.525	Roble	
29	Z2_qpy1919.png	11.1	11.700	Roble	
30	Z2_qpy2026.png	9.8	9.800	Roble	
31		.	.		

Obs	Arbol	DBH_conv	DBH_Lidar	Especie	F5
-----	-------	----------	-----------	---------	----

Obs	Arbol	DBH_conv	DBH_Lidar	Especie	F5
1	A1_ps265.png	17.8	19.950	Pino	
2	A1_ps267.png	19.0	20.375	Pino	
3	A1_ps282.png	11.2	12.900	Pino	
4	A1_ps306.png	14.6	18.575	Pino	
5	A1_ps316.png	12.6	13.350	Pino	
6	A2_ps372.png	19.4	21.375	Pino	
7	A2_ps375.png	12.7	14.300	Pino	
8	A2_ps415.png	15.2	16.400	Pino	
9	A2_ps429.png	8.1	9.375	Pino	
10	A2_ps503.png	12.8	14.525	Pino	
11	Z2_ps22.png	19.2	18.050	Pino	
12	Z2_ps48.png	16.3	16.025	Pino	
13	Z2_ps57.png	21.6	21.225	Pino	
14	Z2_ps60.png	12.5	15.950	Pino	
15	Z2_ps132.png	15.7	15.925	Pino	

Obs	Arbol	DBH_conv	DBH_Lidar	Especie	F5
1	A1_qpy1484.png	9.5	10.575	Roble	
2	A1_qpy1493.png	11.1	12.125	Roble	
3	A1_qpy1538.png	8.5	11.950	Roble	
4	A1_qpy1574.png	11.5	9.725	Roble	
5	A1_qpy1579.png	12.4	12.850	Roble	
6	A2_qpy1224.png	8.1	8.800	Roble	
7	A2_qpy1274.png	11.0	10.375	Roble	
8	A2_qpy1279.png	7.8	7.100	Roble	
9	A2_qpy1394.png	18.0	17.925	Roble	
10	A2_qpy1416.png	14.1	13.925	Roble	
11	Z2_qpy1897.png	9.1	11.350	Roble	
12	Z2_qpy1901.png	15.0	16.525	Roble	
13	Z2_qpy1904.png	12.8	13.525	Roble	
14	Z2_qpy1919.png	11.1	11.700	Roble	
15	Z2_qpy2026.png	9.8	9.800	Roble	

PINE:

Procedimiento REG

Modelo: MODEL1

Variable dependiente: DBH_conv DBH_conv

Número de observaciones leídas	15
Número de observaciones usadas	15

Análisis de la varianza					
Fuente	DF	Suma de cuadrados	Cuadrado de la media	F-Valor	Pr > F
Modelo	1	89.57123	89.57123	55.00	<.0001
Error	13	21.17277	1.62867		
Total corregido	14	110.74400			

Raíz MSE	1.27620	R-cuadrado	0.8088
Media dependiente	11.32000	Adj R-Sq	0.7941
Coeff Var	11.27381		

Estimadores de parámetros						
Variable	Etiqueta	DF	Estimador del parámetro	Error estándar	Valor t	Pr > t
Intercept	Intercept	1	0.67382	1.47291	0.46	0.6549
DBH_Lidar	DBH_Lidar	1	0.89589	0.12081	7.42	<.0001

Procedimiento REG

Modelo: MODEL1

Resultados 1 de test para variable dependiente DBH_conv				
Fuente	DF	Cuadrado de la media	F-Valor	Pr > F
Numerador	1	0.34086	0.21	0.6549
Denominador	13	1.62867		

Procedimiento REG

Modelo: MODEL1

Resultados 2 de test para variable dependiente DBH_conv				
Fuente	DF	Cuadrado de la media	F-Valor	Pr > F
Numerador	1	1.20957	0.74	0.4044
Denominador	13	1.62867		

Procedimiento UNIVARIATE

Variable: error (Residual)

Momentos			
N	15	Sumar pesos	15
Media	0	Observ suma	0
Desviación std	1.22977252	Varianza	1.51234045
Asimetría	-0.6999619	Curtosis	1.18617705
SC no corregida	21.1727663	SC corregida	21.1727663
Coef. variación	.	Media error std	0.3175259

Medidas estadísticas básicas			
Ubicación		Variabilidad	
Media	0.000000	Desviación std	1.22977
Mediana	0.009245	Varianza	1.51234
Moda	.	Rango	4.99336
		Rango intercuantil	1.42932

Tests para posición: $\mu_0=0$			
Test	Estadístico	P-valor	
T de Student	t	0	Pr > t 1.0000
Signo	M	0.5	Pr >= M 1.0000
Puntuación con signo	S	4	Pr >= S 0.8469

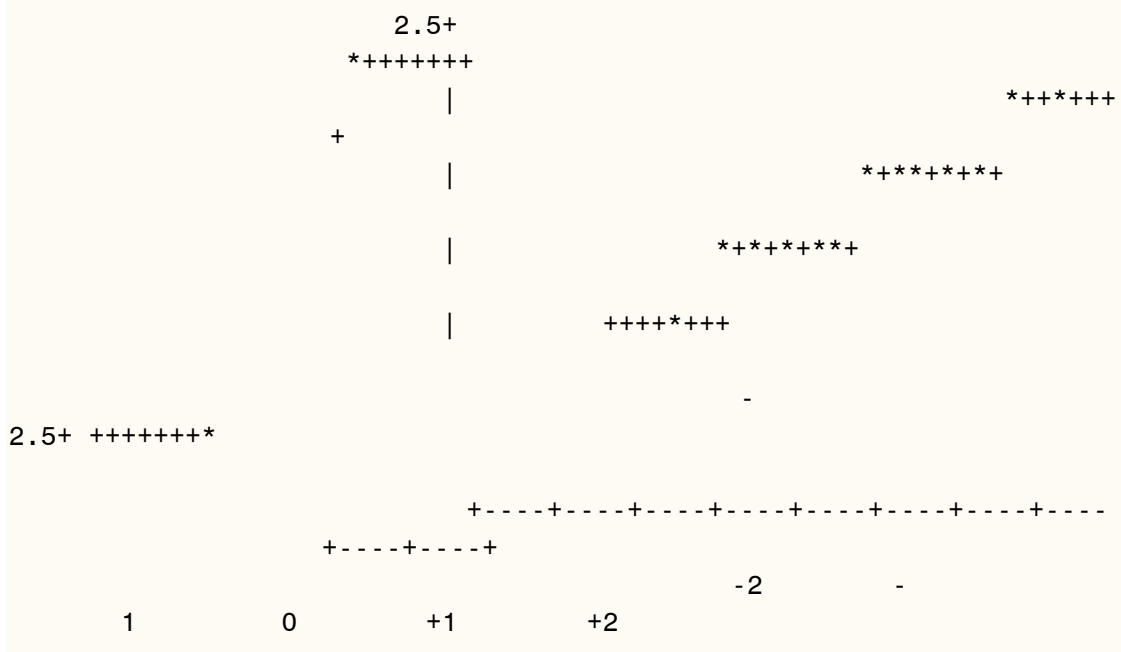
Tests para normalidad			
Test	Estadístico	P-valor	
Shapiro-Wilk	W	0.956584	Pr < W 0.6333
Kolmogorov-Smirnov	D	0.165824	Pr > D >0.1500
Cramer-von Mises	W-Sq	0.048538	Pr > W-Sq >0.2500
Anderson-Darling	A-Sq	0.318534	Pr > A-Sq >0.2500

Cuantiles (Definición 5)	
Cuantil	Estimador
100% Máx	2.11363252
99%	2.11363252
95%	2.11363252
90%	1.26732209
75% Q3	0.95088816
50% Mediana	0.00924476
25% Q1	-0.47842979
10%	-1.74219119
5%	-2.87972610
1%	-2.87972610
0% Mín	-2.87972610

Observaciones extremas			
Inferior		Superior	
Valor	Observación	Valor	Observación
-2.879726	3	0.765348	8
-1.742191	11	0.950888	10
-0.647875	1	1.031303	7
-0.478430	12	1.267322	9
-0.457668	6	2.113633	4

	Stem Hoja	#
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	1 003	3
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	0 0238	4
	--+-	
		-
0 65541		+-----
	5	
	+	
1 7	1	
		-
2 9	1	0
		-----+-----+-----+-----
+		

Trazado de probabilidad normal



OAK:

Procedimiento REG

Modelo: MODEL1

Variable dependiente: DBH_conv DBH_conv

Número de observaciones leídas	15
Número de observaciones usadas	15

Análisis de la varianza					
Fuente	DF	Suma de cuadrados	Cuadrado de la media	F-Valor	Pr > F
Modelo	1	163.90946	163.90946	81.49	<.0001
Error	13	26.14787	2.01137		
Total corregido	14	190.05733			

Raíz MSE	1.41823	R-cuadrado	0.8624
Media dependiente	15.24667	Adj R-Sq	0.8518
Coeff Var	9.30190		

Estimadores de parámetros						
Variable	Etiqueta	DF	Estimador del parámetro	Error estándar	Valor t	Pr > t
Intercept	Intercept	1	-1.35623	1.87530	-0.72	0.4824
DBH_Lidar	DBH_Lidar	1	1.00299	0.11111	9.03	<.0001

Procedimiento REG

Modelo: MODEL1

Variable dependiente: DBH_conv DBH_conv

Procedimiento REG

Modelo: MODEL1

Resultados 1 de test para variable dependiente DBH_conv				
Fuente	DF	Cuadrado de la media	F-Valor	Pr > F
Numerador	1	1.05201	0.52	0.4824
Denominador	13	2.01137		

Procedimiento REG

Modelo: MODEL1

Resultados 2 de test para variable dependiente DBH_conv				
Fuente	DF	Cuadrado de la media	F-Valor	Pr > F
Numerador	1	0.00146	0.00	0.9789
Denominador	13	2.01137		

Procedimiento UNIVARIATE

Variable: error (Residual)

Momentos			
N	15	Sumar pesos	15
Media	0	Observ suma	0
Desviación std	1.22977252	Varianza	1.51234045
Asimetría	-0.6999619	Curtosis	1.18617705
SC no corregida	21.1727663	SC corregida	21.1727663
Coef. variación	.	Media error std	0.3175259

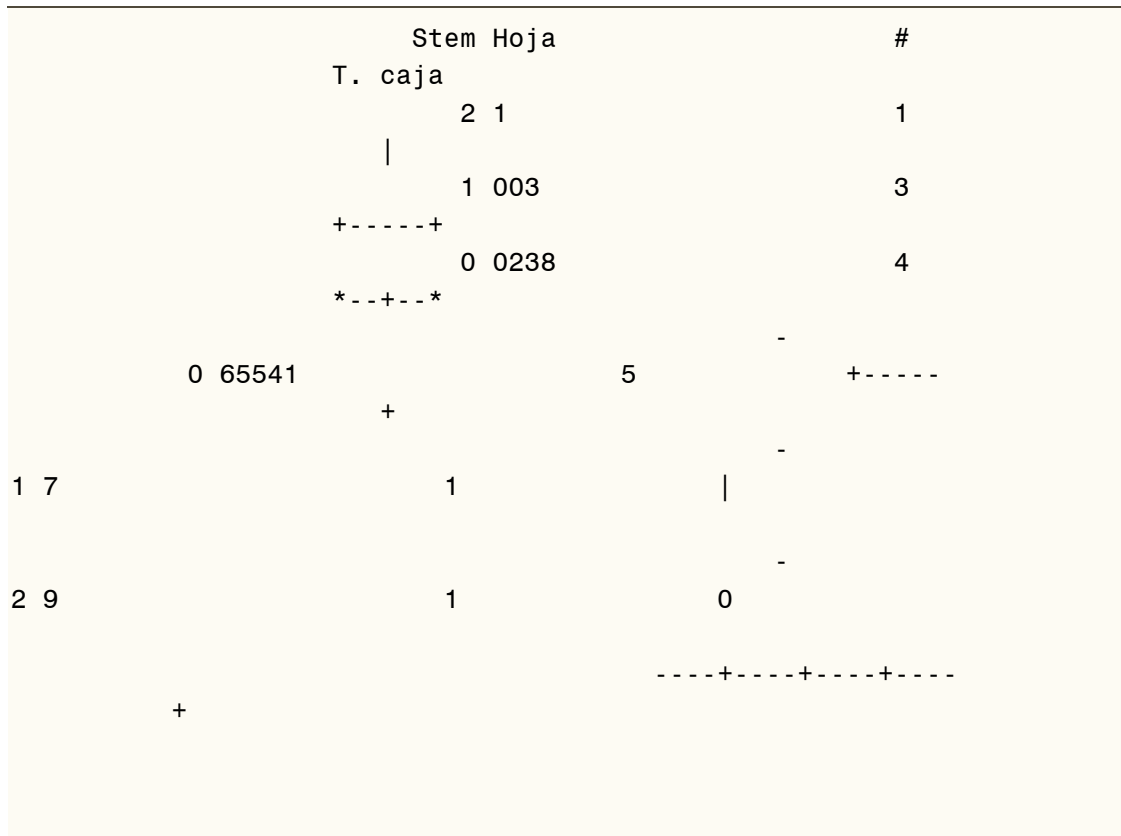
Medidas estadísticas básicas			
Ubicación		Variabilidad	
Media	0.000000	Desviación std	1.22977
Mediana	0.009245	Varianza	1.51234
Moda	.	Rango	4.99336
		Rango intercuantil	1.42932

Tests para posición: $\mu_0=0$			
Test	Estadístico	P-valor	
T de Student	t	0	Pr > t 1.0000
Signo	M	0.5	Pr >= M 1.0000
Puntuación con signo	S	4	Pr >= S 0.8469

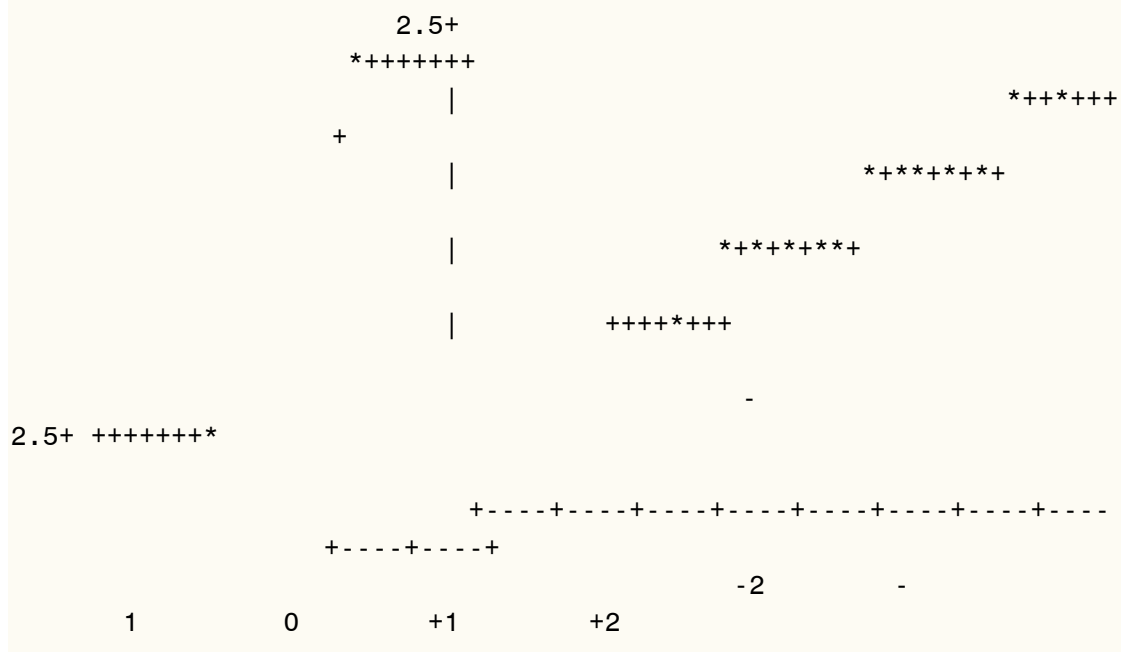
Tests para normalidad			
Test	Estadístico	P-valor	
Shapiro-Wilk	W	0.956584	Pr < W 0.6333
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Inferior		Superior	
Valor	Observación	Valor	Observación
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-0.647875	1	1.031303	7
-0.478430	12	1.267322	9
-0.457668	6	2.113633	4



Trazado de probabilidad normal



Residual estudentizado sin obs actuales

