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Universidad de Valladolid

Climate impact on early growth of *Pinus pinuster* Ait.

Muha Abdullah Al Pavel

A dissertation to obtain the degree of Master in Mediterranean Forestry and Natural Resources Management (MEDfOR)

Palencia, July 2017

Supervisor: Dr. Felipe Bravo Oviedo

Co-supervisor: Ing. Cristóbal Ordóñez Alonso

Education and Culture

Erasmus Mundus

MEDfOR

Universidad de Valladolid

School of Agriculture, Food Technology and Forestry

Sustainable Forest Management Research Institute

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Acknowledgement

I would like to voice my earnest thank to my supervisor Professor Dr. Felipe Bravo Oviedo for his sustained guidance, suggestions, inspiration, and constructive criticism to complete my thesis work.

I place on record, my sincere gratitude to Ing. Cristóbal Ordóñez Alonso for their logistic support and guidance, encouragement to complete my dissertation.

I am also grateful especially to Professor Carlos del Peso Taranco for their logistic support and encouragement to complete my dissertation.

I am particularly acknowledge for this Erasmus Mundus MEDfOR Master program funded by the European Union (EU).

I would like to give special thanks to all my colleagues: Ana Martín Ariza, Wilson Lara Henao, José Riofrío Salazar, Encarna Rodríguez-García,Sara Uzquiano Pérez, Irene Ruano Benito, Brenda Itzel Morales Rodríguez, Sara De Paula Peláez, Jorge Aldea Mallo, Guillermo Jové Alcalde, Nicolás Cattaneo, María Felicidad López Sáinz, Diana Becerra and Diego Rodríguez de Prado who helped me during the research work. My thanks also go to all my MEDfOR fellows with whom I shared these two extraordinary years. At finally yet importantly I must utter my gratefulness to all of my friends from University of Padova, Italy and Univsersity of Valladolid, Spain for their continuous support and contribution.

I am always grateful and pleased to my family members, relatives and well-wishers who supported to me to complete this dissertation successfully.

My attempts would be successful, if this thesis work would assist for someone for further study and forest manager to adapt their forest system in this context even to a little extent.

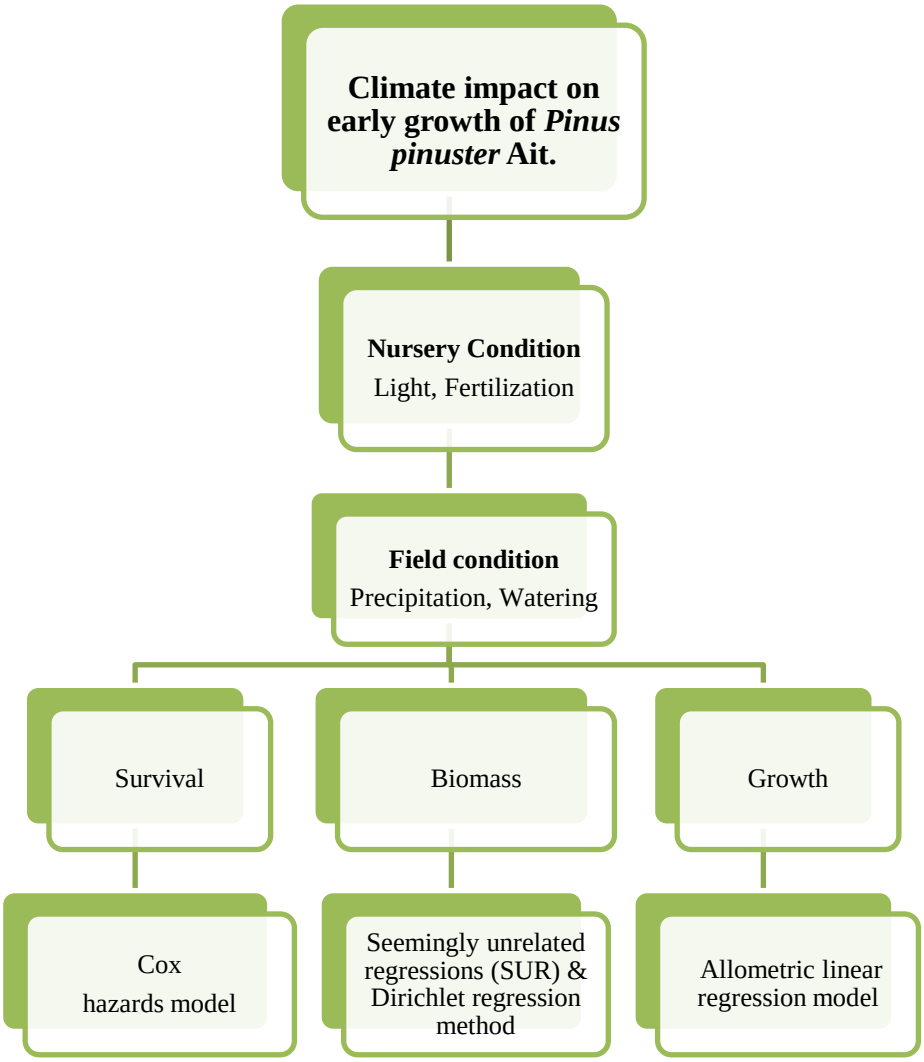


Figure: A diagram of the thesis.

Resumen

El pino negral (*Pinus pinaster* Ait.) tiene una gran importancia económica, ecológica y paisajística. En el presente trabajo se ha estudiado la supervivencia, el reparto de las fracciones de biomasa en el árbol y el crecimiento en diámetro basal de plántulas de esta conífera mediterránea. El experimento se instaló a partir de plántulas que fueron cultivadas en vivero bajo diferentes condiciones, y posteriormente plantadas en una masa natural en el centro de España. Tras once años los árboles fueron cosechados. Los objetivos principales fueron: identificar los factores más importantes que afectan la supervivencia de las plántulas; Analizar el efecto de los factores climáticos en el reparto por fracciones de la biomasa y la cantidad de biomasa total; y analizar el efecto de los factores climáticos sobre el crecimiento anual en diámetro basal de las plántulas en masas naturales. Se realizaron cuatro inventarios para medir variables biométricas y registrar la supervivencia entre mayo de 2007 y febrero de 2017. Se eligió una muestra aleatoria de 36 árboles, con tres repeticiones de cada tratamiento, para la asignación de la biomasa y el análisis del crecimiento del diámetro basal. Los métodos utilizados para cada análisis fueron los siguientes: (i) el modelo de Cox para el análisis de supervivencia; (ii) análisis de regresión *SUR* (seemingly unrelated regression) para predecir el contenido en biomasa de cada fracción y la biomasa total, para lo que se testaron trece ecuaciones alométricas lineales y no lineales, y se ajustó el mejor; (iii) regresión de *Dirichlet* para predecir la proporción de biomasa en cada fracción; y (iv) regresión lineal para el análisis del crecimiento anual en diámetro basal. Los resultados obtenidos muestran que el agua junto con la luz son buenos predictores para la supervivencia. Por otra parte la exposición total al sol durante la fase de vivero y la disponibilidad de agua tienen una fuerte influencia en la asignación de las distintas fracciones de biomasa. El método *SUR* presentó mejores resultados que el método de *Dirichlet*, con valores de *RMSE* muy pequeños y menores sesgos para la estimación de la distribuciónde biomasa por fracciones delasplántulas. Además, el crecimiento anual en diámetro basal está fuertemente influenciado por la disponibilidad de agua en verano y la exposición total al sol en la fase de vivero. El estudio global indicó que la deriva ontogenética (pendiente $\neq 1$) en las tasas de crecimiento y la asignación del reparto de biomasa depende de qué recursos son más limitantes, de acuerdo con la teoría de la partición óptima. La principal conclusión de este estudio es que la luz junto a la disponibilidad de agua en verano muestra un mayor impacto en la supervivencia, la asignación de las fracciones de biomasa y el crecimiento del diámetro basal durante las primeras etapas de crecimiento del pino negral.

Palabras clave: *Asignación de biomasa, supervivencia, modelo de Cox riesgos; Regresión de Dirichlet.*

Abstract

Maritime pine (*Pinus pinaster* Ait.) has a great economic, ecological and aesthetic importance among Mediterranean tree species. Survival probability, biomass fractions and basal diameter growth of the Mediterranean conifer sapling of *P. pinaster* Ait. was studied. To generate the experiment material, seedling were grown in different conditions in nursery, and planted in a natural forest stand in central Spain. Eleven years later saplings were harvested. Main objectives of this study were: to identify the most important factors affecting sapling survival; to analyse the effect of climate factors on biomass partitioning and estimating sapling biomass; to analyse the effect of climate factors on annual basal diameter growth of sapling operating at natural stand of *P. pinaster* Ait. Four inventories were conducted in order to measure biometric variable and survival counted of sapling during consecutive years (May 2007 to February 2017). A total of 36-sample trees (maximum three replicates) were randomly harvested from each treatment for biomass allocation and basal diameter growth analysis. The Cox model was used for survival analysis. Thirteen linear and non-linear allometric equations were tested to predict biomass contents of each component, and the best model were fitted with non-linear system of seemingly unrelated regression (*SUR*) method. The *Dirichlet* regression was applied in order to predict the proportion of biomass in each compartment. In addition, linear model was applied to analysis of annual basal diameter growth of sapling. The result revealed that water is associated with light good predictive for survival. Moreover, biomass allocation has a strongly influenced with completely sun exposition. The *SUR* method was superior to *Dirichlet* methods due to less bias and smaller *RMSE* values for biomass estimation of sapling. Moreover, annual basal diameter growth has a strong influence with summer water availability and completely sun exposition. The overall study indicated ontogenetic drift (slope≠1) in growth rates and biomass allocation depended upon which resources was more limiting, according to optimal partitioning theory. The main conclusion of this study is that summer water availability shows a higher impact in respect to survival, biomass allocation and basal diameter growth in the early stages of Mediterranean Maritime pine.

Key words: *Biomass, Survival, Cox hazards model, Dirichlet regression, dendroecology, Spain Northern Plateau.*

1. Introduction

Maritime pine (*Pinus pinaster* Ait.) is a Mediterranean species of great economic, ecological and aesthetic importance (Ruano et al., 2009; Ruano et al., 2015a and 2015b). It is a forest species that grows naturally in the western part of the Mediterranean, but that has been planted in many countries around the world (CAB-International, 2002). It covers also over four million hectares among Spain, Portugal, France and Italy (Ribeiro et al., 2001). In Spain, it covers over a million hectares, of which more than half correspond to plantations (DGCN, 1998). This is also especially true for the Castilian Plateau in central Spain, where this species covers more than 114,000 ha, which represents about 7.5% of the species' European distribution (Ruano et al., 2015b).

Maritime pine has been widely used for dunes stabilization (Farjon, 2010), and protecting agricultural crops against salt spray along the western coast of the Iberian Peninsula (Pereira, 2002). Furthermore, its uses include soil conservation, protection of slopes against erosion, and shade tree in parks. The wood is the major product, which has a broad range of final products such as construction wood, furniture, poles and posts (Praciak et al., 2013). Resin is the most important of the non-wood products, and is used, directly or indirectly after distillation, to make turpentine (volatile oil distilled from pine resin) and rosin (the solid material left behind after distillation), both used in a wide range of products: oils, varnishes, adhesives, waxes, soaps and medicines (Farjon, 2010). It barks also produce tar, or is chipped and composted to produce a low-weight substrate for nursery containers (Praciak et al., 2013; Farjon, 2010). Moreover, its stands are also an ideal ecosystem for the development of edible fungi, such as mushrooms of genus *Boletus* (porcini) and *Lactarius* (milk-caps) (Pereira, 2002).

Natural establishment of the Maritime pine in forest communities is a very complex process in the Iberian Peninsula (Rodríguez-García et al., 2011), in which multiple factors that

condition future stand development intervene, with the sapling phases recognized as the most critical and least stress-tolerant (Houle, 1996). It is also a key process for stand persistence in slow-growing Mediterranean species. The key factors influencing Maritime pine survival, biomass allocation and growth are those of climate (i.e. water availability, light intensity and temperature), although other factors can interact such as, specific plasticity or genetic origin (Bogino and Bravo, 2008). There is a new situation with different conditions for forest, as droughts (Castro et al., 2004) will be increasingly longer and more intense and climate irregularity will dominate (IPCC, 2007) in Iberian Peninsula. For these reasons, knowing the response of the species to this change is crucial for predicting the future stand development and conditions. There is very little information on intra-specific variation in survival, morphology, annual growth and biomass allocation as a mechanism involved in shade avoidance (Rodríguez-García and Bravo, 2013) at the sapling phase, and the influence of site factor. Understanding how saplings respond to resource variations is very important for predicting sapling establishment and growth of future stands structure (Jose et al., 2003), and evaluating the success of sapling establishment (Rodríguez-García and Bravo, 2013) from nursery seedling to natural stands.

Phenotypic plasticity can be defined as the ability of a single genotype to express different morphological, anatomical, physiological and/or behavioural traits in response to environmental variation (Chapin et al., 1987). New biomass is allocated to organs with the most limiting resources according to the optimal partitioning theory, (*OPT*) or balanced-growth hypothesis (Chapin et al., 1987). A different approach is the allometric biomass partitioning theory (*APT*) model, based on allometric theory that examines how organism attributes change with body size (Müller et al., 2000; Moriuchi and Winn, 2005; McCarthy and Enquist, 2007; Poorter et al., 2012), and which proportionally more biomass is allocated to leaves than to roots as plants grow (Shipley and Meziane, 2002). Nonetheless, if allocation

changes with size, any factor that influences size should thereby change allocation (Müller et al., 2000). Then, If the variation in biomass distribution demonstrates (*OPT*), plants should invest more in roots if water and nutrients become limiting; while biomass allocation should favour leaves and/or stem if light becomes more limiting or there is surplus of Nitrogen (Rodríguez-García and Bravo, 2013).

Light has been the focus of most research on forests dynamics, and the sapling stage have been associated with a range of shade tolerant physiologies (Catovsky and Bazzaz, 2002) and competitive abilities related to differences in responsiveness to light (Valladares and Niinemets, 2008; Monnier et al., 2013). Pioneer, fast growing, tall plants are commonly shade avoiders which characterise early to intermediate succession stages (Grime, 1979), and that maximise vertical growth (to suppress neighbours) and light interception through plastic crown adjustments (Monnier et al., 2013). Nevertheless, the magnitude of sapling response to light quantity and quality also depends on nutrient requirements of species and on nutrient availability, specially of N availability (Dehlin et al., 2004;Sardans et al., 2006). Then, structural and physiological plasticity may depend on the species shade tolerance (Portsmuth and Niinemets, 2007) and may vary along soil fertility and seasonal drought gradients (Coomes and Grubb, 2000). These plastic shade and nutrient-induced adjustments may procure an important adaptive advantage to successional species sapling by higher niche pre-emption and occupation in natural forest (Monnier et al., 2013). *P. pinaster* grows in a great range of soils conditions varying from Mediterranean to Temperate-Oceanic climates (Gandullo and Sánchez-Palomares, 1994). The species is considered as a main colonising species after disturbance with high light regime for growth (Gil et al., 1990) but that can take advantage of microenvironmental amelioration imposed by shelter's shade (tree over storey, understory or both) at sapling stage (Rodríguez-García et al., 2011). Soil fertility and chemistry properties (e.g. pH) have been shown to affect early establishment of *P. pinaster*

(Rodríguez-García et al., 2011). Additionally, *P. pinaster* shows elevated levels of genetic variability (González-Martínez et al., 2002) and many different populations can be found due to an important genotype by environmental interaction that has enabled local adaptation to ecological conditions (Gandullo and Sánchez-Palomares, 1994). This is important because soil fertility, geographical location and climate may influence on the response to light variation, and therefore, populations located in different ranges may present different coping strategies to light and soil fertility variation.

Light availability was an important factor controlling seedling growth and morphological structure of *P. pinaster* (Rodríguez-García and Bravo, 2013). However, differences between productivity environments were observed, especially in full sunlight and medium light condition. This also mentioned that light are needed for the expression of N effects on *P. pinaster* seedling growth. Moreover, Ruano et al., (2009) explained that water availability influenced on growth and biomass of *P. pinaster* seedlings more than light. Therefore, our study are likely comparable in field trial from nursery products. Our objectives were to know: (1) to identify the most important factors affecting sapling survival, (2) to analyse the effect of climate factors on biomass partitioning and estimate sapling biomass (3) to analyse the effect of climate factors on annual basal diameter growth of sapling operating at natural stand of *P. pinaster*. To accomplish this objective, seeds were sown to grow seedling under three different levels of shade coverage combine two different of fertilization in nursery on January, 2006 (Rodríguez-García and Bravo, 2013), then these were planted with two different watering regimes in the experimental site of *Mata de Cuéllar* (central Spain) on May, 2007 (Figure 1). The information obtained will serve to understand the impact of climate irregularity on regeneration in nursery and consequently define the most appropriate forest management strategy to ensure long-term persistence in order to establish certain sapling in natural forest stand.

2. Material and Method

2.1 Study area

The experiment was carried out in natural *P. pinaster* stand at long-term experimental site of *Mata de Cuéllar*, Segovia, central Spain (41°22′N, 4°29′W; Figure. 2; Ruano et al., 2015b). The experiment was designed to take advantage of the experimental site carried out in 2004, where an integrated analysis of Maritime pine regeneration is started, setting out 10 plots of 70 m ×70 m (Ruano et al., 2009). Sixteen months old of *P. pinaster* Ait. were planted in plot, and eleven years old sapling were harvested in order to take advantage of the experimental site to integrated analysis of Maritime pine sapling of stand dynamics (Figure 1). The site is located in a flat, sandy region characterized by a semi-arid Mediterranean climate, with a strong summer drought and a period of potential frost of at least 3 months. Mean annual precipitation is 610 mm, and mean annual temperature is 11.2 °C. The floristic community within the stand is composed of continental Mediterranean annual species typical of central Spain, i.e., *Micropyrum tenellum* (L.) Link, *Sedum amplexicaule* D C., *Vulpia myuros* (L.) C.C.Gmel., and *Lupinus angustifolius* L., with patches of shrubs, *Lavandula pedunculata* (Mill.) Cav. and *Helichrysum italicum* (Roth) G. Don, and isolated Stone pine trees (*P. pinea* L.). Silviculture in the area is traditionally based on natural regeneration following a seed-tree system adapted to resin production, leading to low stand densities (Ruano et al., 2015b).

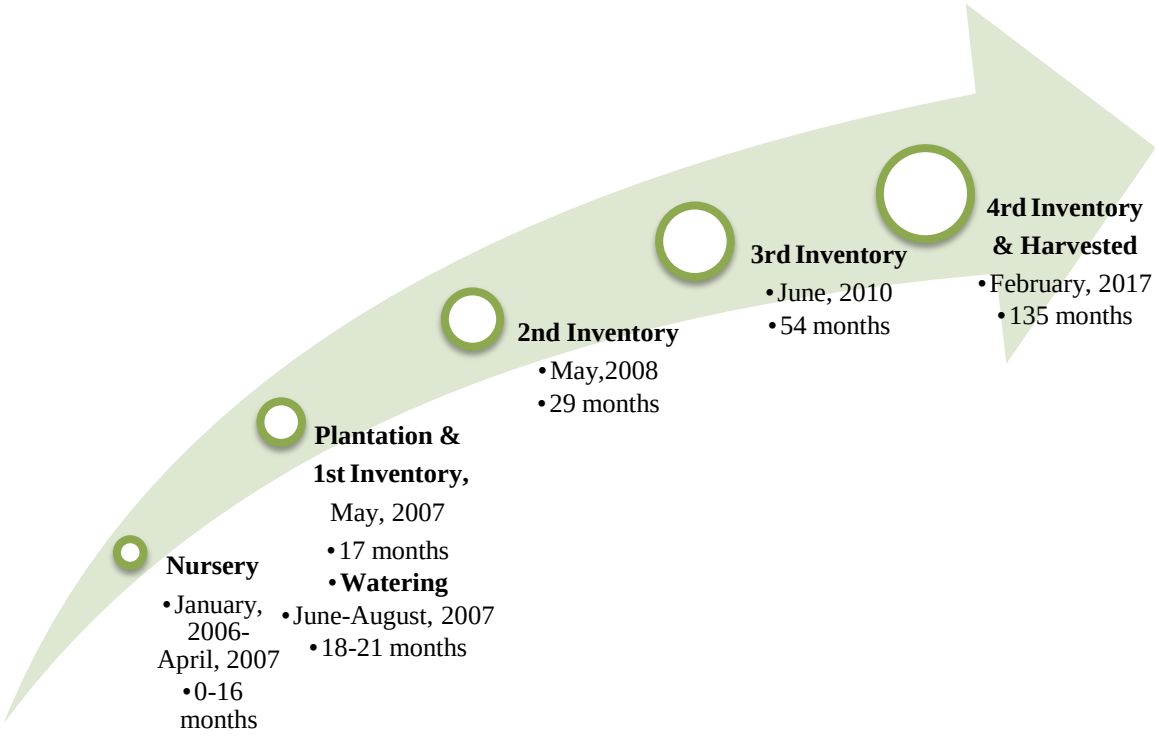


Figure 1: Sapling life cycle, watering and inventory for biometric data collection of *Pinus pinaster* Ait. experiment plot.

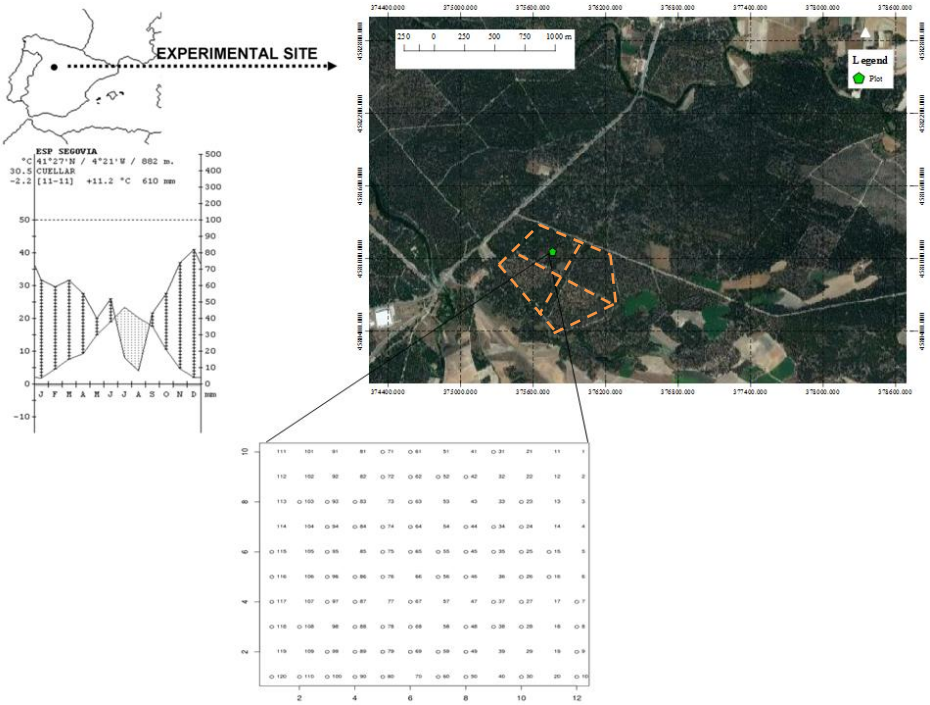


Figure 2: Location of the experimental plot and a climodiagram in *Mata de Cuéllar* (Central Spain), and position of all saplings in the experimental plot.

2.2 Plant materials and experimental design

2.2.1 Seedling production

According to Rodríguez-García and Bravo, (2013) seedling production was conducted on a plot of land neighbouring a greenhouse located at the Universidad de Valladolid in Palencia, Spain (42^0 01′N- $4^0$32′W, 739 masl). Organizations of seedling production with different operations are showed in Figure 3. Commercial seeds of *Pinus pinaster* Ait from different seed provenances were received in January 2006 from the Centro Nacional de Mejora Forestal (INIA. Madrid, Spain). Following germination and initial growth, seedlings were transferred (April 2006) to Arnabat@ 48 cavity forest trays (308 cm^3). Seedlings planted in the 24 central cavities of the trays were used for the experiment; seedlings planted in the border cavities were excluded from the measurements. Each cavity was 18 cm^2 with vertical anti-spiralling ribs along the inside walls. The trays were filled with a 3:1 (v:v) unfertile peat-vermiculite mixture, to which 3.5 kg/m^3 of NPK (14-8-15) slow release fertiliser (*SRF*) was added, following commercial indications (Plantacote@) of dose for a normal nutrition state of culture of conifers longer than 6 months in tray. A blocked, split-plot experiment with a factorial combination of light (three levels) population origin (ten levels) and nutrient availability (two levels) was designed to test for main effects and interactions on seedling morphology and biomass traits. Three blocks were defined to central local different experiment. A light gradient consisting of three light environments (main plots) was randomly established per block: light (A), completely sun exposition; light (B), 30% sun exposition; and light (C), 11-12% sun exposition. Twenty forest trays, consisting of two trays for each of the 10 populations were randomly placed within each light plot. A two-level nutrient treatment (low-N and high-N) was implemented in the split-plot design and randomly assigned to half the trays, one per population, in each light plot. Control or low-N treatment was established by the amount of *SRF* added to the substrate when the trays were

filled. The average volume of compacted substrate per cavity was of 453.3 mL. So, on average, each cavity received 222 mg N, 127 mg P and 238 mg K. The high-N (twofold N than low-N) treatment was obtained by adding N to the control substrate in a concentrated NH^4NO^3 solution (32%; 1.3 g/mL) divided into 18 equal weekly doses (June to mid November 2006) and administered to the other half of the trays, one per population. Total N administered was 222 mg per control (low-N) seedling and 444 mg per (high-N) seedling.

2.2.2 Experimental plantation

The experimental design was developed to test the effects of light condition, nutrient and watering on survival, biomass allocation and early plant growth on *Pinus pinaster* Ait. from one provenance (Meseta Castellana) in the nursery, after that, seedling was planted at 1.5 meter distance from each sapling in naturals stand of *Mata de Cuéllar* (Central Spain). There were total 120 plants and each combination has 10 plants with 6 treatments from nursery; in each treatment were design with 3 light conditions× 2 fertilization. To simulate different summer water regimes, the plots were water in the hottest months (from 15th June to 9th September). During the summer of 2007, half of the experimental units were watered (60 plants); half of the experimental units were not watered (60 plants). Each irrigated experimental unit was watered with 2 litres of water in every 15 days during the period indicated (Ruano et al., 2009). This amount based on the study of the summer storm rainfall in the study area, adding 100% to compensate for greater evapotranspiration as the temperatures were higher than those that correspond to stormy years. Summer rainfall in 2007 was 63.7 mm. On the other hand, in summer 2007, mean temperature was 19.85ºC, mean minimum temperature was 0.726ºC and mean maximum temperature was 27.53ºC. This allowed analysing the influence of light and drought on Maritime pine early development (Ruano et al., 2009).

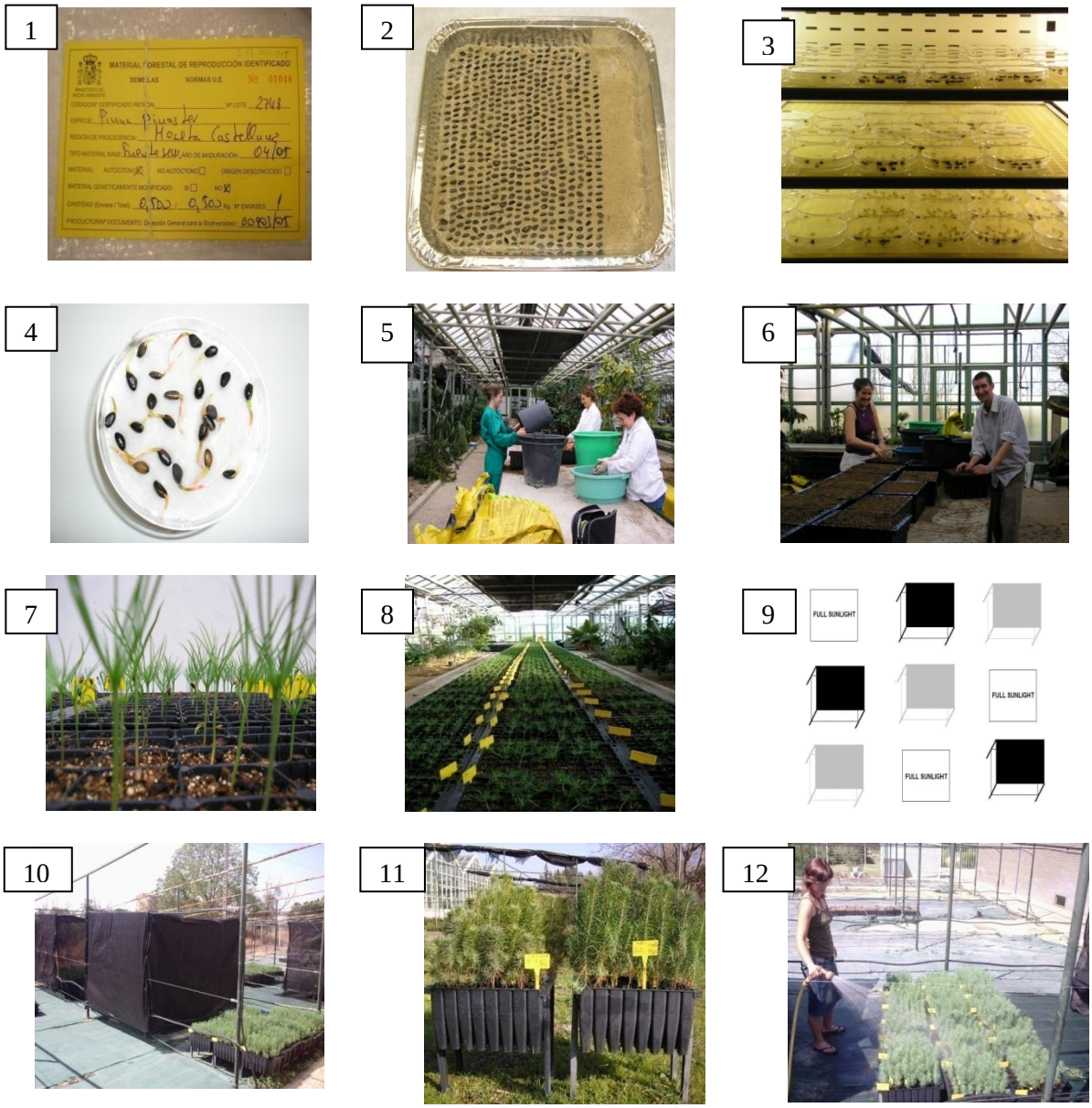


Figure 3: Organization of seedling production with different operations. (1) certified of *Pinus pinaster* Ait. seeds; (2), seeds scarification with sterile sand; (3), seed germination in chamber; (4) seed germination in Petri dish; (5) preparation of substrate; (6), filling the trails; (7), transplanting germinated seeds to trails with substrate; (8), seedlings growing in the greenhouse (just for one week while preparing the light houses); (9), diagram of light-houses; (10), installation of trails inside the light-houses (11) two trails of sapling with different treatment of nitrogen (12) watering and harvesting when plants were ready for plantation (Photo Credit: Rodríguez-García, E. 2005).

2.3 Data gathering

Firstly, saplings have been tagged with their previous number and position in the *Pinus pinaster* Ait. experiment plot. Four inventories were conducted (Figure 1) in order to measure biometric variable of sapling and counting of dead and alive sapling of the *Pinus pinaster* Ait. experiment plantation plot from May, 2007 to February, 2017 (Figure 1). Sample saplings were selected randomly for harvesting from the experiment plantation plot. Total 36 sample plants (maximum three replicate) were harvest from each treatment in the *Pinus pinaster* Ait. experiment plantation plot for biomass calculation and basal diameter growth analysis.

2.3.1 Survival

For survival analysis, three inventories' data were used only about counting dead or alive sapling in the *Pinus pinaster* Ait. experiment plantation plot from May 2007 to June, 2010. Cumulative summer watering was used for survival analysis from June 2007 to August, 2007. Moreover, cumulative only summer rainfall data was used in order to survival analysis consider the hottest months (from 1 June, 2007 to 15 September, 2010) (Figure 1) (Ruano et al., 2009).

2.3.2 Biomass

Organization of a biomass measurement is presented in Figure 5. In the field, total height (*ht; m*), maximum crown wide (*MCW; m*), height of maximum crown wide (*HMCW; m*) two collar diameter at base and two diameter at breast height (1.30 m) (*dbh; cm*) were measured (one perpendicular to the other of trunk for each sample sapling) using callipers. Firstly, branch was stripping from sapling sample using big scissor. Then, sapling was cross cut at breast height (1.30 m) in order to fell plant in the ground. The biomass components considered were: stem with bark, thick branches (diameter > 7 cm), medium branches

(diameter 2-7 cm), thin branches (diameter < 2 cm) and needles with cones (Figure 6; Breu et al., 2012). The sample biomass data are showed in Table 3.

The sapling biomass component (e.g. stem, branch, needle, cones) were totally stripping from the trunk after felling of each sapling sample. Moreover, needles were totally stripping from branch because of sapling sample were small. After that, each component was measured of total fresh weight and a representative subset sample of each of them was measured again

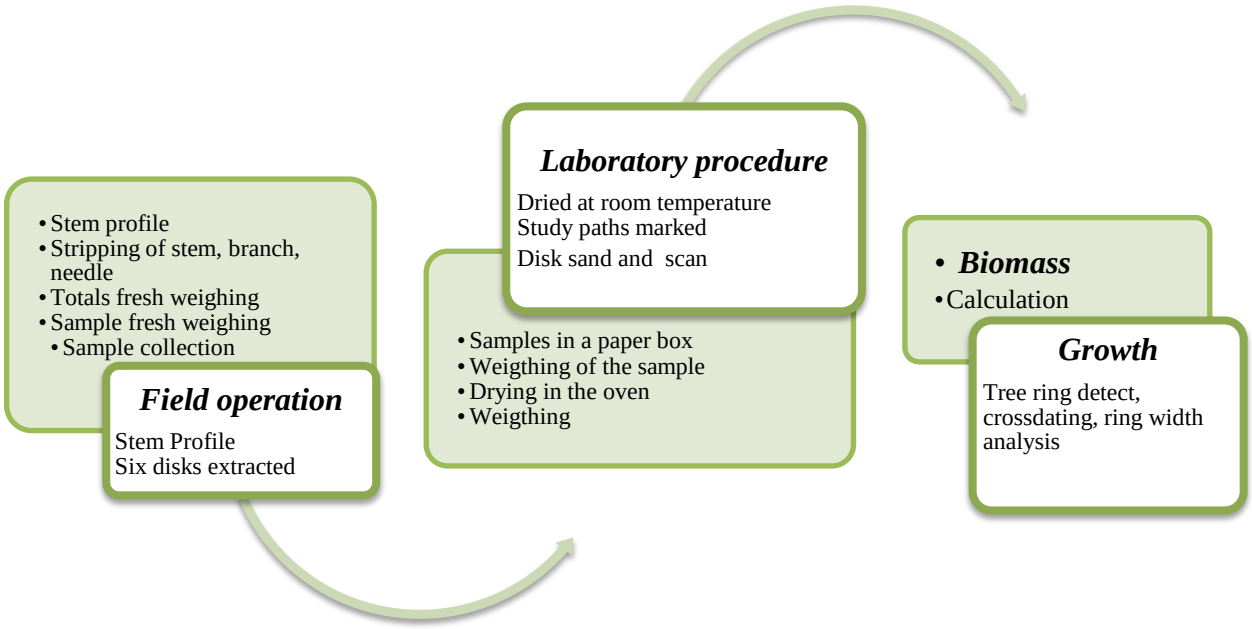


Figure 4: Cycle of biomass and growth measurement process from operation field to laboratory.

of sample fresh weight in the field, which is carried to laboratory in airtight polythene bags (Figure 5). In the laboratory, samples were kept in tagged boxes tagging (Figure 7). Then, a sample fresh weight of each component was measured to obtain fresh weight (precision of 0.01g) using 'GRAM precision series SV' immediately on arrival at laboratory. Sample of each component was kept in 'Serie DRY-BIG' heater for oven dry. A temperature of 80°C was used for biomass determinations for all categories of sample compartment. Two-control

Figure 5: Organization of measurement and sample collection process in experiment plot with different operations. (1), sapling sample in the plot; (2), measurement of (*HMCW; m*); (3), stripping branch from stem; (4) sapling cross-cutting at 1.3 m; (5), measurement of diameter (cm) at breast height (1.30 m); (6), measurement of total height (*ht; m*); (7), cross-cutting into stem and disks; (8),disk samples; (9), stripping of needles from branches; (10), weighting totals fresh mass of stem, branch, and needle; (11),weighting sample; (12), collected samples under tree to avoid moisture content loss in the field (Photo Credit: Pavel, M.A.A., Sara. U. P, Cristóbal, O. A. and Brenda, I. M. R.).

weight was measured in every days for sample compartment until a constant weight was reached. In this way, the stem dry weight was expended average about 21 days to become; diameter (2-7 cm) branch in average about 11 days; diameter smaller than (2 cm) branch in average about 9 days; and needle in average about 7 days. It is noted that woody sample (e.g. stem, branch) was dried depending on the sample size. It is also mentioned that diameter (> 7 cm) was not found because sample tree was sapling.

To obtain the biomass, in each sample of sapling compartment (e.g. stem, branch and needle) was calculated the moisture content: Total dry weight (kg) = Total fresh weight× (Sample dry weight/ Sample fresh weight).

Leaves & cones: total and sample fresh weight; sample taken for moisture content

Branches: (dbh > 7 cm; dbh 2 to 7 cm; dbh< 2 cm): total and sample fresh weight; sample taken of cross cuts for moisture content

Stem: total and sample fresh weight; sample taken of cross cuts for moisture content

Disks: Six disks extracted; the first at (1.30 m), second at base and four distributed at 20% proportion uniformly along the tree stem

Figure 6: Sapling compartmentalization for biomass and basal diameter growth analysis.

Figure 7: Weighting and dry procedure for samples on arrival at the laboratory, (1), fresh sample of stem, branch in a paper box; (2), fresh sample of needle in a paper box; (3), fresh sample weighting; (4), drying in the oven; (5), dry sample of stem, branch and needle for weighting again; (6),weighting of the dry needle sample; (7), weighting of the dry branch (2-7cm) sample; (8), weighting of the dry branch (2cm) sample; (9), weighting of the dry stem sample; (10), again sample put in the oven for drying; (12), keep out the final dry sample from oven (Photo Credit: Pavel, M.A.A. and Cristóbal, O. A.).

2.3.3 Basal diameter growth

In the field, six disks were extracted from total 36 sample plants (maximum three replicates) from each treatment in the *Pinus pinaster* Ait. experiment plantation plot; the first from at breast height (1.30 m), second at the base and the remaining four from points distributed at 20% proportion uniformly along the sapling trunk (Figure 5 and 6). Disks of each saplings sample were collected separately in airtight polythene bags for laboratory.

In the laboratory, samples of disks identified with tags in the paper box and dried at room temperature during at least a week for further processing. The study paths were marked in each disks sample in order to help the sapling ring detection and ring width analysis of sapling rings in the scanner. That is, the path (straight-line segment from the pith to the bark) whose radius is equal to the radius calculated from the perimeter of the disk. Firstly, a belt sander was used for sanding (120-180 grit) of each disk sample. At this point, those paths only focus using sandpaper grits from the coarse grain to the finer (>240-320-400 and intermediates) with verify under a magnifying glass those narrow sections. Sometimes sand paper was to repeat a previous grit, or to use an intermediate grit to facilitate the detection of those sapling rings on the disks (Figure 8). The disks were scanned for sapling ring identification using an EPSON EXPRESSION 1640XL scanner, with a resolution of 800 dots/in. Annual growth and basal diameter data in each year were obtained considering over bark diameter and tree ring widths from the basal disk of each sapling sampling. Moreover, rings were counted to know the age of the saplings. Sapling were found about 11 years old (date of first ring 2006) (Ruano et al., 2013). Sapling rings were detected, crossdated as well as sapling ring widths analysis were conducted in R version 3.3.3 (R Core Team, 2015) with package *'MeasuRing'* (Lara et al., 2015). Total 12 sub-set sample plants among a total of 36 sample plants were crossdated from each treatment (maximum four replicates) in the *Pinus pinaster* Ait. experiment plantation plot for basal diameter growth analysis. Recursive

processing (mapping) of both images was conduct for ring counting and ring widths analysis with *multidetect* and *map* functions. Again, ring widths analysis rechecked on specific problematic sample previously set of ring widths of sample.

Crossdating was performed to maintain fundamental principle of dendroecology as it looks at the correlation between each sapling ring series (Ariza et al., 2016). These correlations were calculated overlapping consecutive segments (R-core team, 2015) with the package *'dplR'* (Bunn, 2010). The *crossRings* function (Lara et al., 2015) was used to allow the evaluation of the synchrony among sapling-ring series, thus detecting possible dating errors.

2.3.4 Climate data

Climatic data were obtained from a nearby meteorological station (SG01-Gomezserracín; Segovia) managed by the Instituto Tecnológico Agrario de Castilla y León, located approximately 20 km from the experimental site (www.inforiego.org, accessed 20th March 2017).

2.4 Selected treatment for analysis

The multifactor analysis of variance (*GLMs*) test were conducted in order to investigate and identify the influence of different light conditions and fertilization treatments on specific objectives affecting survival, biomass partitioning and annual growth of sapling operating at natural stand of *P. pinaster*. First inventory, biometric data (diameter and total height) and treatments were considered for multifactor analysis of variances (*GLMs*) test.

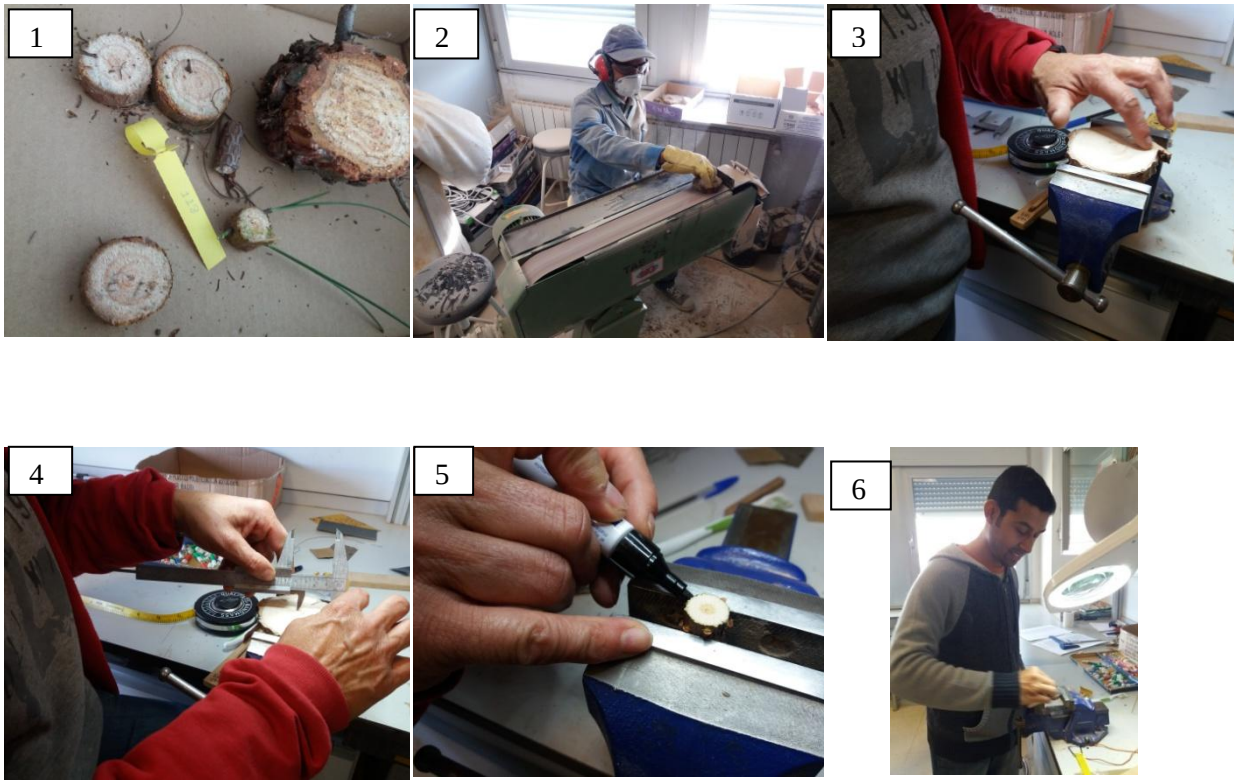


Figure 8: Dendroecological procedure for samples process at the laboratory. (1), sample dried at room temperature in a paper box; (2), sanding disk using belt sander (120-180 grit) (3), finding the study path; (4) define the study path using callipers; (5) study paths marked; (6), sanding only focus paths using sand paper on disk, (7) Scanning disk by scanner, (8) Scan image of disk (Photo Credit: Pavel M.A.A., Cristóbal, O. A. and Brenda, I. M. R.).

2.5 Data analysis

2.5.1 Survival analysis

Survival analysis corresponds to a set of statistical approaches used to investigate the time it takes for an event of interest to occur. Two related probabilities are use to describe survival data: the survival probability and the hazard probability. The survival probability, also known as the survivor function *S(t)*, is the probability that an individual survives from the time origin to a specified future

The Kaplan-Meier (*KM*) method is a non-parametric method used to estimate the survival probability from observed survival times (Kaplan and Meier, 1958). The survival probability at time t_i, $S(t_i)$, is calculated as follow:

(1) $S(t_i)=S(t_{i-1})(1-d_i/n_i)$

where, $S(t_{i-1})$ = the probability of being alive sapling at t_{i-1}; n_i = the number of alive sapling just before t_i; d_i = the number of events (stand inventory) at t_i.

The Cox proportional-hazards model (Cox, 1972) is essentially a regression model commonly used statistical in survival research for investigating the association between the survival time of subject and one or more predictor variables. The Cox model is expressed by the hazard function denoted by *h(t)*. Briefly, the hazard function can be interpreted as the risk of dying at time *t*. It can be estimated as follows:

(2) $h(t)=h_0(t)exp(b_1x_1+b_2x_2+...+b_px_p)$

where, *t* represents the survival time; *h(t)* is the hazard function determined by a set of *p* covariates $(x_1,x_2,..., x_p)$; the coefficients $(b_1,b_2,... ,b_p)$ measure the impact *(i.e., the effect size)* of covariates; h_0 is the baseline hazard. The point is to compare the hazard rates of individuals who have different covariates

(3) $HR = \frac{h1(t)}{h2(t)} = \frac{h0(t)exp\,(b1x1+b2x2+...+bpxp)}{h0(t)exp\,(b2x2+b2x2+...+bpxp)}$

The quantities *exp* (b_i) are called hazard ratios (*HR*). It does not depend on value of *X*, similar to odds ratio in logistic regression. A value of b_i greater than zero, or equivalently a hazard ratio greater than one, indicates that as the value of the i^{th} covariate increases, the event hazard increases and thus the length of survival decreases. The survival analysis was performed in R version 3.3.3 (R Core Team, 2015) with function *coxph* in package *survival* (Therneau, 2015).

2.5.2 Biomass analysis

2.5.2.1Estimating aboveground biomass

Initial exploratory graphical analyses were carried out to assess the relationships between the explanatory variables (*dbh* and *ht*) and the dependent variables, in order to identify outliers that might alter the modelling results. Thirteen linear and non-linear allometric equations were tested to predict biomass contents of each component (Riofrío et al., 2015) (Table 1). The equations included diameter (*dbh*) and total sapling height (*ht)* as independent variables, based on their potential to produce models for large-scale applications and because explains most of the variability in observed sapling biomass. Only the models were considered in which all parameters significant ($p < 0.05$). Mainly, stem, branch (diameter; 2-7 cm and < 2 cm), and needle with cones were considered for biomass compartment in order to select the best model. In this way, the best model was selected according to the results of several statistics: particularly, the Akaike Information Criterion (*AIC*), the root mean squared error (*RMSE*), the proportion of variance explained by the model (R^2). Selected models for each biomass component were fitted simultaneously using seemingly unrelated regressions (*SUR*) in a system of biomass equations. The selected best model structure for each component and total biomass in the *SUR* method are showed in Table 2. When a system of equations is fitted simultaneously, the residuals are correlated, because the component biomasses come from the

same sapling. Therefore, the *SUR* method that allows the inclusion of dependencies among the error terms of the component biomass equations is commonly used to estimate component and total aboveground biomass (e.g., Parresol, 1999; Lambert et al., 2005; Ritchie et al., 2013). The *SUR* models can be constrained such that the prediction of component equations sum to the prediction of total sapling regression. The *SUR* model was performed in R version 3.3.3 (R Core Team, 2015) with function *nlsystemfit* in package *systemfit* (Henningsen and Hamann, 2007).

Table 1: Biomass models tested for different sapling component.

No	Model
1	$W=b1*dbh*ht$
2	$W=b1*dbh^2*ht$
3	$W=b1*dbh+ b2*dbh^2$
4	$W=b1*dbh+ b2*dbh^2+ b3*dbh^2*ht$
5	$W=b1*dbh+ b2*ht$
6	$W=b1*dbh^2+b2*dbh^2*ht$
7	$W=b1*dbh^2+b2*ht$
8	$W=b1*dbh^2+b2*ht+b3*dbh^2*ht$
9	$W=b1*dbh^2+b2*dbh*ht$
10	$W=b1*dbh^2*ht+b2*dbh*ht$
11	$W=b1*dbh^{b2}*ht^{b3}$
12	$W=b1*dbh^{b2}$
13	$W=b1*(dbh*ht)^{b2}$

Note:W- biomass component (kg); dbh-diameter at breast height (cm); ht-total height (m); b1, b2 and b3- model parameters.

Table 2: Selected best biomass model fitted with *SUR* method for different compartment of *Pinus pinaster* Ait. in all treatment.

Component	Biomass equation
Stem	$W_s = b1*dbh^2+ b2*dbh*ht$
Branch	$W_b = b3*dbh^2+ b4*dbh^2*ht$
Needle	$W_n= b5*dbh^2*ht$
AGB	$W_{total}=b1*dbh^2+b2*dbh*ht+b3*dbh^2+b4*dbh^2*ht+b5*dbh^2*ht$

Note:AGB-total above ground biomass, W_s-stem biomass component (kg); W_b-branch biomass component (kg); W_n-needle biomass component (kg); W_{total}-total biomass component (kg); dbh: diameter at breast height (cm); ht-total height (m); b1, b2, b3,b4 and b5-model parameters.

Table 3: Summary statistics for sapling data (n=36) sampled.

Variable	Minimum	Mean (sd)	Maximum
Stem (kg)	0.65	6.82(5.63)	28.42
Branch (kg)	0.49	5.16(5.65)	33.18
Needle (kg)	0.67	5.81(5.55)	30.19
Total biomass(kg)	2.09	17.79(14.42)	76.31
DBH(cm)	1.20	7.35(3.16)	15.18
Height (m)	1.82	4.30 (1.12)	6.70

Note: DBH-diameter at breast hight(cm); sd-standard deviation

2.5.2.2 Estimating component proportions

The component biomass can be estimated as the proportions of total aboveground biomass. A proportion is bounded between 0 and 1, and therefore, the effect of explanatory variables tends to be nonlinear and the variance tends to decrease when the mean get closer to one of the boundaries (Poudel & Temesgen, 2016). *Dirichlet* regression was used for estimating proportions in this study. The *Dirichlet* distribution is a multivariate generalization of the beta distribution (Poudel & Temesgen, 2016) and takes the following form:

(5) $f(y;\alpha)= 1/B(\alpha)\prod_{c=1}^{C} y_c^{(\alpha_c-1)}$

Where, α_c are shape parameters for each variable, $\alpha_c>0$ for all c (component ID, ranges from 1 to C), $y_c \in (0,1)$, $\sum_c^C y_c = 1$ for all c and C is the number of variables. $B(\alpha_c) = [\prod_c^C y_c \, r(\alpha_c)) / r(\sum_{c=1}^{C} \alpha_c)]$ is the multinomial beta function. If C=2, then the *Dirichlet* distribution reduces to the beta distribution. (Maier, 2014a) used the generalization of Ferrari and Cribari-Neto (2004) and reparameterized the *Dirichlet* distribution with mean and precision parameters $\mu_c = (\alpha_c/\phi)$ and $\phi = \alpha_o = (\sum_{c=1}^{C} \alpha_c)$, respectively. Then, the *Dirichlet* density has the following form:

(6) $f(y;\alpha) = 1/B(\alpha)\prod_{c=1}^{C} y_c^{(\mu_c \phi-1)}$ where $0 < \mu < 1$ and $\phi > 0$.

The *Dirichlet* regression is useful for modelling data that represent the components as percentage of the total. With the usual parameterization, the regression model can be formulated a

$$(7) \quad g(\alpha_c) = \eta_c = X^{[c]}\,\beta^{[c]}$$

Where g(·) is the link function, which is log (·) for the model withusual parameterization (Maier, 2014a), the superscript [c] represents the predicted proportion of component c. The predicted values are obtained as $\mu_c = \exp(\eta_c)$. The *Dirichlet* regression was performed in R version 3.3.3 (R Core Team, 2015) with function '*DirichReg'* in package '*DirichletReg'* (Maier, 2014b). The explanatory variables were used in various combinations to predict proportion of aboveground biomass present in different components. The predictor variables used in *Dirichlet* regression were also *DBH* and total sapling height (*ht*) for species.

2.5.2.3 Comparison estimates biomass between SUR and Dirichlet method

The seemingly unrelated regressions (*SUR*) and *Dirichlet* regression method was compared by mean bias (mean error) and square root of the mean square error (*RMSE*) of fitted biomass model for each compartment of *Pinus pinaster* Ait. sapling. The precision of the equations was quantified using the square root of the mean square error (*RMSE*) using Eq. (8) (Forrester et al., 2017) calculated.

$$(8) \quad RMSE = \sqrt{\{\sum_{i=1}^{n}(Pi - Oi)\text{^}2\}/n}$$

Where, O are the observed values and P are the predicted values.

The bias was quantified using Eq. (9) (Forrester et al., 2017)

$$(9)\ Bias\ (\%) = \quad 100/n\ \{\sum_{i=1}^{n}(Pi - Oi)/Oi\}$$

2.5.2 Basal diameter growth analysis

Basal diameter growth analysis was conducted to estimate annual growth (Ruano et al., 2013) of sapling by treatment effect in the *Pinus pinaster* Ait. experiment plot. Two co-variables were considered for this analysis: growth after nursery treatment in the natural stand of *Pinus pinaster* Ait. experiment plot and total annual precipitation during the hydrological year from plantation to harvested (Figure 1). An initial exploratory graphical analysis was carried out to

assess the relationships between the dependent variables (cumulative basal diameter and annual basal radial growth) and the independent three factor variables (e.g. light, watering with summer rainfall, fertilizer), in order to identify outliers that might alter the modelling results. Sapling annual radial growth was studied (Ruano et al., 2013). An analysis of covariance (*ANCOVA*) was applied to create models which describe the effect of variation in predictor variables on the response variable to all sapling in the experiment plot using two factors variables (e.g. light and fertilizer) with one covariate as watering with summer rainfall. Then, allometric relationships (Rodríguez-García and Bravo, 2013) between plant annual basal diameter and age were looked, that is, linear annual basal diameter regression models were constructed. The common allometrical relationship between the annual basal diameter of Y and age of X is $Y = a \cdot X^b$. We used logarithmic-transformed values of X and Y to make relationships linear (Lenssen et al., 2003). We obtained plots and linear regression equations. All equations fits were checked by model's adjustment parameters. Changes in linear regression slopes were investigated according to the methodology described by (Coleman et al., 1994; McConnaughay and Coleman, 1999). If b is equal to 1 a gives the ratio between Y and X; but if b significantly differs from 1, the ratio of Y and X changes with size (McCarthy and Enquist, 2007). When there were signs of ontogenetic drift and significant effects of light, or water with summer rainfall on basal diameter growth, the analysis of covariance (*ANOVA*) was tested with combination in each treatment effect as a function to parameter on basal diameter growth for sapling (Coleman et al., 1994; Lenssen et al., 2003).

3. Results

3.1 Light, fertilization and their interaction effects

Light availability is an important controlling factor on sapling biomass allocation and morphological structure of *Pinus pinaster* Ait. (Table 4). The multifactor of analysis of variances (*GLMs*) test revealed that the morphological traits are impacted by fertilization and light treatment, but their interaction has not any influenced on sapling traits. On the other hand, the multifactor of analysis of variances (*GLMs*) test showed that the sapling biomass of *Pinus pinaster* Ait. was impacted by light (C), also interaction between fertilization and light (A and B) has impact on biomass.

Table 4: Significance for fertilization, light and their interactions effects (error term are not included) on the biomass and sapling traits of *Pinus pinaster* Ait.

No	Variables	Fertilization	Light (C)	Light (A&B)	Light(C) ×Light (A&B)	Fertilization ×Light (A&B)	Fertilization ×Light (C)
1		ns	***	ns	×	×	×
2	hd^2	.	ns	ns	×	**	ns
3		ns	***	ns	ns	×	×
1		**	***	***	×	×	×
2	h/d	**	***	***	ns	×	×

*Note: light (A)-completely sun exposition; light (B)-30% sun exposition; light (C)-11-12% sun exposition; biomass (hd^2); slenderness(h/d); (×)-not us for model; Fertilization-low N and high N availability; Akaike Information of Criteria (AIC); ns not significant (p>0.05); (***)p<0.001;(**)p<0.01;(*)p<0.05,(.)p<0.1.*

3.2 Survival

3.2.1 Multivariate survival regression analysis

The candidate model three is the best model on the basis of Akaike Information of Criteria (*AIC*) and all covariates are significant ($p \leq 0.05$) except one covariate ($p=0.1$), even though the entire models are significance. In the multivariate survival model, the covariates treatment of light (C; 11-12% sun exposition) and watering with summer rainfall ($p \leq 0.05$) are

significant, although the covariate light (A; completely sun exposition) and light (B; 30% sun exposition) are not significant ($p=0.1$). The hazard ratio (HR) = $e^{(0.02949)}$ = 0.97 ($p < 0.05$), indicating a strong relationship between watering with summer rainfall and sapling survival; decreased risk of sapling mortality. It indicates that sapling mortality rate goes down by (1-0.97) = 3% with one unit change in summer water availability (mm). Similarly, the hazard ratio (HR) = $e^{(0.795067)}$ =2.22 ($p=0.05$), indicating a strong relationship between light (C) and sapling; increased risk of sapling mortality. It noticed that a higher value of hazard ratio for light (C) is associated with a poor survival of sapling. By contrast, the hazard ratio (HR) = $e^{(0.673907)}$= 1.96 ($p=0.1$), indicating a weak relationship between light (A) and light (B) and sapling survival; which is not significantly contribution to increased risk of sapling mortality. The adjusted survival curves also estimates proportional hazards for light (A, B and C) and watering with summer rainfall (Annex; Figure S1). Therefore, more light is the necessary for survival of saplings. Holding the other covariates (light; A, B and C) are constant, watering with summer rainfall reduces the hazard by a factor of 0.97, or 3%. It concludes that summer water availability (mm) is associated with light good predictive for survival of sapling (Table 5).

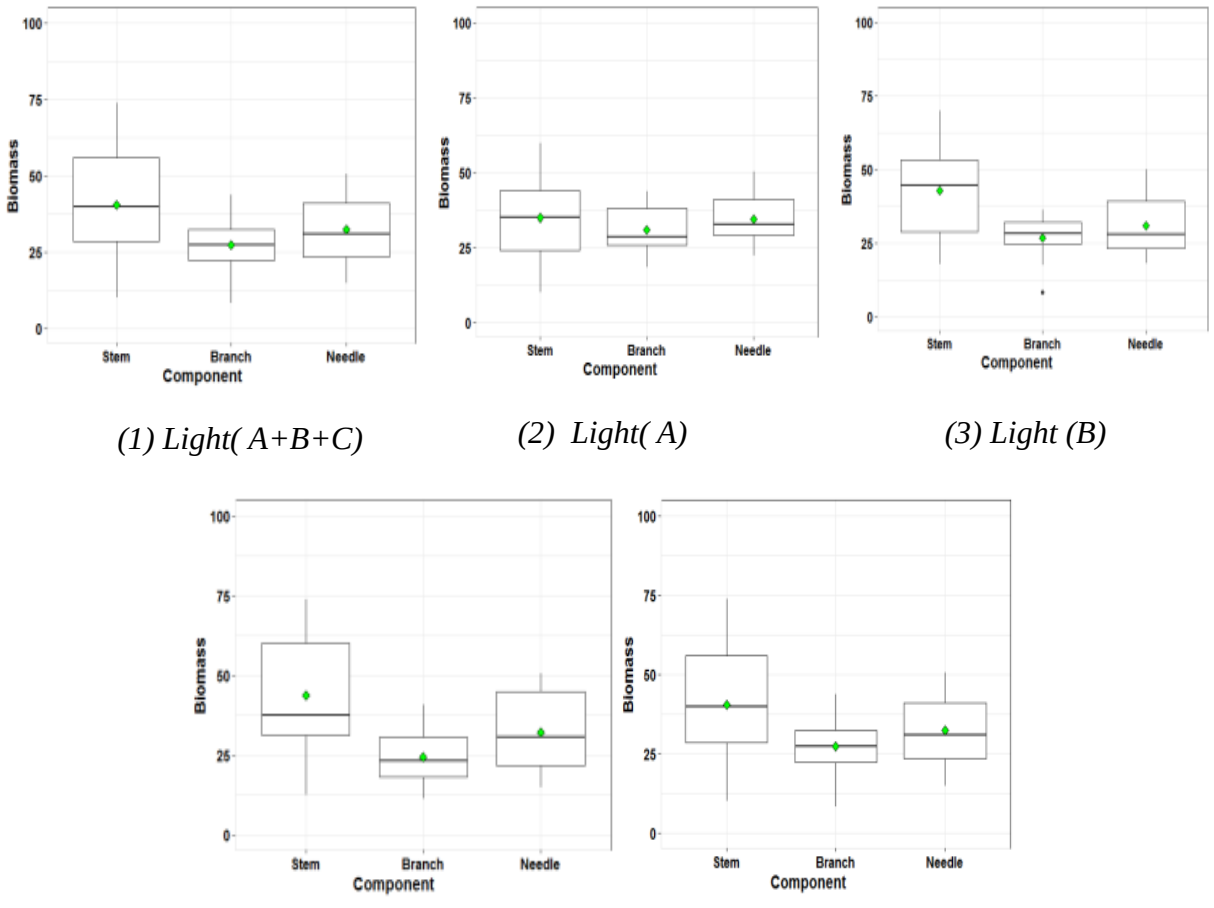
Table 5: Significance and goodness-of-fit of statistics of *Coxph* models for survival probability of *Pinus pinaster* Ait. during the summer time in the experiment plot.

Model	Fertilization (B_1)	Light (C) (B_2)	Light (A&B) (B_3)	Watering+Summer rainfall (B_4)	Biomass (B_5)	Slenderness (B_6)	R^2	AIC
1	0.399761 (ns)	0.823157 (*)	0.763272 (.)	-0.02978 (***)	×	×	0.667	347.743
2	×	×	×	0.040894 (***)	0.000906 (ns)	-0.02989 (ns)	0.654	350.387
3	**×**	***0.795067 (*)***	***0.673907 (.)***	***-0.02949 (***)***	**×**	**×**	***0.662***	***347.553***
4	0.306912 (ns)	×	×	-0.02995 (***)	×	×	0.652	348.997
5	×	0.3709 (ns)	×	-0.02951 (***)	×	×	0.654	348.492
6	×	×	0.17188 (ns)	-0.02992 (***)	×	×	0.650	349.785
7	0.29218 (ns)	0.36075 (ns)	×	-0.02963 (***)	×	×	0.657	349.452
8	0.360474 (ns)	×	0.246799 (ns)	-0.03014 (***)	×	×	0.654	350.311
9	0.068737 (ns)	0.434766 (*)	0.991544 (.)	0.73782 (***)	-0.03001 (ns)	×	0.670	348.589
10	0.023976 (ns)	×	×	0.320014 (***)	-0.03008 (ns)	×	0.653	350.819
11	×	0.060447 (*)	0.928273 (ns)	0.651131 (***)	-0.02962 (ns)	×	0.664	348.687
12	-0.00021 (ns)	0.386596 (.)	0.902671 (.)	-0.02978 (***)	×	0.814353 (ns)	0.667	349.696
13	×	-0.00045 (.)	0.965841 (.)	0.788439 (***)	×	-0.02947 (ns)	0.663	349.323
14	×	0.000413 (ns)	×	0.270528 (***)	×	-0.02954 (ns)	0.654	350.224
15	×	×	0.000742 (ns)	0.144799 (***)	×	-0.02981 (ns)	0.653	350.587
16	×	×	×	0.000759 (***)	×	-0.02973 (ns)	0.653	348.837
17	×	×	×	0.01818 (***)	-0.02992 (ns)	×	0.649	350.039

Note: light (A)-completely sun exposition; light (B)-30% sun exposition; light (C)-11-12% sun exposition; B1, B2, B3,B4 and B5-model parameters; biomass (hd^2); slenderness(h/d); (×)- not use for model; Akaike information of criteria (AIC); ns not significant (p>0.05); (***)p<0.001; (**)p<0.01; (*)p<0.05; (.)p<0.1.

3.3 Biomass

The mean biomass proportion of stem with respect to the total above ground biomass (*AGB*) was approximate 37.5%, whereas branch approx. 27% and needle approx. 30%. Mean biomass proportion of stem in treatment of light (A) was approx. 33%, whereas branch and needle represent approx. 27% and 30%, respectively. Mean biomass proportion of stem in light (B) approx. 40%, whereas branch and needle was approx. 27%. Mean biomass proportion of stem in light (C) was approx. 35%, whereas branch was approx. 24% but needle was approx. 30%. Mean biomass proportion of stem in light (B) and light (C) was approx. 37.5%, whereas branch was approx. 27% and needle was approx. 30% (Figure 9).



(1) Light(A+B+C) *(2) Light(A)* *(3) Light (B)*

(4) Light (C) *(5) Light(B+C)*

Figure 9: Aboveground biomass total (%) distribution in sapling component.

3.3.1 Aboveground biomass estimation using SUR method

The correlation of diameter (*dbh*) and total height (*ht*) with the total aboveground biomass (*AGB)* was high (R^2 >0.70) (Table 6) and showed very significant values in all component of treatment sapling (Annex; Table S1). All biomass components models fitted, and selected for all each treatment explained more than 78% observed biomass, only model for stem biomass explained relatively lower R^2 value. The component models associated with crown (needles and branch) explained greater R^2 values for the coefficient of determination (0.87-0.90) than stem (0.31) for overall treatment. The models fitted the *AGB* data well with the model R^2 values (0.93) for light (A) treatment. The component models associated with (needles and branch) explained greater R^2 values for the coefficient of determination (0.90-0.95) than stem (0.63). The models fitted the *AGB* data well with R^2 (0.74) for light (B) treatment. The component models associated with (needles and branch) explained greater R^2 values for the coefficient of determination (0.78-0.80) than stem (0.23). The models fitted the *AGB* data well with R^2 (0.72) for light (C) treatment. The component models associated with (needles and branch) explained greater R^2 values for the coefficient of determination (0.85-0.88) than stem (0.32). The models fitted the *AGB* data well with R^2 (0.70) for light (B) and (C) treatment. The component models associated with (needles and branch) explained greater R^2 values for the coefficient of determination (0.81-0.82) than stem (0.27).

Table 6: Biomass equation systems simultaneously fitted (*SUR*) and goodness-of-fit of statistics for studied sapling component.

Treatment	Component	Biomass equation	*RMSE*	R^2
A+B+C	*Stem*	$W_s = -0.139413159*dbh^2+0.449992086*dbh*ht$	*4.74*	*0.311*
	Branch	$W_b = -0.008863034*dbh^2+0.017698661*dbh^2*ht$	*2.09*	*0.867*
	Needle	$W_n=0.017469480*dbh^2*ht$	*1.78*	*0.898*
	AGB		*6.16*	*0.829*
A	*Stem*	$W_s = -0.14639762*dbh^2+0.43671867*dbh*ht$	*2.86*	*0.626*
	Branch	$W_b = -0.01018928*dbh^2+0.01936938*dbh^2*ht$	*2.70*	*0.905*
	Needle	$W_n=0.01835939*dbh^2*ht$	*1.69*	*0.949*

	AGB		*5.69*	*0.924*
B	*Stem*	$W_s = 0.038168564*dbh^2+0.110189222*dbh*ht$	*3.39*	*0.229*
	Branch	$W_b = 0.004190713*dbh^2+0.014285156*dbh^2*ht$	*1.68*	*0.798*
	Needle	$W_n=0.016175219*dbh^2*ht$	*2.06*	*0.775*
	AGB		*5.92*	*0.738*
C	*Stem*	$W_s = -0.26810818*dbh^2+0.75731672*dbh*ht$	*7.08*	*0.318*
	Branch	$W_b = -0.01571221*dbh^2+0.01608178*dbh^2*ht$	*1.15*	*0.879*
	Needle	$W_n=0.01574017 *dbh^2*ht$	*1.45*	*0.845*
	AGB		*7.57*	*0.718*
B+C	*Stem*	$W_s = -0.12510369*dbh^2+0.44410015*dbh*ht$	*5.43*	*0.271*
	Branch	$W_b = -0.01107733*dbh^2+0.01593271*dbh^2*ht$	*1.44*	*0.818*
	Needle	$W_n=0.01598849*dbh^2*ht$	*1.75*	*0.803*
	AGB		*6.65*	*0.693*

Note: RMSE- the root mean squared error; dbh-diameter at breast height (cm); ht- total height (m); light (A)-completely sun exposition; light (B)-30% sun exposition, and light (C)-11-12% sun exposition; AGB- total above ground biomass; W_s-stem biomass component (kg); W_b-branch biomass component (kg); W_n-needle biomass component (kg).

3.3.2 Estimation biomass component proportions using Dirichlet method

The *Dirichlet* regressions provided the predicted proportions of each component biomass. The different combination of diameter (*dbh*) and total height (*ht*) with the predicted proportions of each component biomass was highly variance (Table 7). A system of biomass equations was fitted by *Dirichlet* methodology with the component ratio for selected models for each all treatment. Most of all parameter were considered significant at the 95% confidence level (Annex; Table S2). From the coefficients (*b1, b2, b3* and *b4*) for all treatment showed that, with increasing diameter (*dbh)* and total tree height (*ht),* all (*b0*) increase, but branch and needle more than stem biomass, which means that branch and needle occupied more biomass than stem. The increasing values of all (*b0*) also mean that the precision of coefficients (*b1, b2, b3* and *b4*) gets higher as diameter (*dbh)* and total tree height (*ht)* increases. From the coefficients (*b1* and *b2*) for treatment light (A) showed that, with increasing diameter (*dbh)* and total tree height (*ht),* all (*b0*) decrease, but stem more than branch and needle biomass, which means that stem occupied more biomass than branch and needle. The decreasing values of all (*b0*) also mean that the precision of coefficients (*b1, b2, b3* and *b4*) gets higher as diameter (*dbh)* and total tree height (*ht)* increases. Similarly, the

coefficients (*b1*, *b2*, *b3* and *b4*) for treatment light (B) showed that, same trend as treatment light (A) showed. The treatment both together light (A) and light (C) same as light (A). But the treatment light (C) showed that the same nature showed for all treatment.

Table 7: *Dirichlet* regression biomass fitted best models and goodness-of-fit of statistics for studied sapling component biomass proportion.

Treatment	Component	Biomass equation	Log-likelihood
A+B+C	*Stem*	$W_s = -5.535894 +1.247571*dbh+3.233171*ht+0.004055*(dbh * ht)^2 -0.634618 *dbh*ht$	*75.77*
	Branch	$W_b = -7.361286 +1.906751 *dbh+3.370068 *ht+00.004675 *(dbh * ht)^2-0.778159 *dbh*ht$	
	Needle	$W_n=-5.535894 -1.247571*dbh+3.233171*ht+0.004055*(dbh * ht)^2-0.634618 dbh*ht$	
A	*Stem*	$W_s = -11.1478 -0.3421 *dbh+3.5704 *ht$	*37.43*
	Branch	$W_b = -10.55521 +0.06512 *dbh+2.68585 *ht$	
	Needle	$W_n=-10.229385 -0.009877 *dbh+2.794153 *ht$	
B	*Stem*	$W_s = 6.231908 -1.112362 *dbh-2.418731 *ht-0.002507*(dbh * ht)^2+0.479202*dbh*ht$	*27.18*
	Branch	$W_b = 0.091878 -0.067554 *dbh-0.256485 *ht-0.000443 *(dbh * ht)^2+0.061257 *dbh*ht$	
	Needle	*Reference category 3*	
C	*Stem*	$W_s = 0.4762 -2.1006 *dbh-0.7038 *ht -0.2981 *dbh*ht$	*24.51*
	Branch	$W_b = 1.2496 +3.1455 *dbh-2.1760 *ht -0.3710 *dbh*ht$	
	Needle	$W_n= 1.8846 + 3.3146 *dbh-2.4311 *ht -0.3891 *dbh*ht$	
B+C	*Stem*	$W_s = 1.95677 - 0.01795 *dbh$	*41.1*
	Branch	$W_b = 0.93623 + 0.07423 *dbh$	
	Needle	$W_n= 1.27072 +0.04987 *dbh$	

Note: dbh-diameter at breast height (cm); ht- total height (m); Category 3 is used as baseline category for "alternative" model, light (A)-completely sun exposition; light (B)-30% sun exposition; light (C)-11-12% sun exposition;W_s-stem biomass component (kg); W_b-branch biomass component (kg); W_n-needle biomass component (kg).

3.3.3 Comparison estimate biomass using SUR and Dirichlet method

The *RMSE* for total aboveground biomass is increased by using the *SUR* method in treatment of light (A) followed by light (B) and light (C). The *RMSE* was decreased for stem, branch biomass, as well as increased for needle biomass in treatment of light (A) followed by light (B); again it decreased by light (C) and (B), in opposite for stem. For the *Dirichlet* method, the *RMSE* was decreased for stem, branch and needle in treatment of light (A) followed by

light (B) and light (C); except light (C) for stem biomass. Both of these method were produced lower *RMSE,* but *SUR* method compared to the *Dirichlet* method for component biomass of all treatment. The *Dirichlet* method increased *RMSEs* by 27%, 149.93% and 164.43% for stem, branch and needle of all treatment, respectively compared to the *SUR* models. Similarly, the *Dirichlet* regression increased *RMSE*s by 98.25%, 172.96% and 319.56% for stem, branch and needle in treatment of light (A), respectively. The *Dirichlet* regression increased *RMSE*s by 59.57%, 128.33% and 84.71% for stem, branch and needle in treatment of light (B), respectively. The *Dirichlet* regression increased *RMSEs* by 188.47% and 151.15 % for branch and needle, opposite in stem (22.83%) in treatment of light (C), respectively. In treatment of light (B and C), the *Dirichlet* regression increased *RMSEs* by 26.89% and 6.26% for branch and needle, opposite in stem (46.58%), respectively (Table 8; Figure 10).

Table 8: Mean bias (%) and *RMSE* for component and total aboveground biomass produced by *SUR* and *Dirichlet* method.

Treatment	***SUR* model approaches (kg)**							
	Bias				***RMSE***			
	Stem	**Branch**	**Needle**	**Total**	**Stem**	**Branch**	**Needle**	**Total**
A+B+C	*-1.529*	*0.128*	*0.224*	*2.865*	*3.296*	*1.424*	*1.428*	*6.147*
A	*-2.978*	*-1.928*	*-1.287*	*9.512*	*2.349*	*1.801*	*1.222*	*5.371*
B	*0.297*	*1.823*	*1.906*	*6.173*	*2.335*	*1.338*	*1.746*	*5.419*
C	*-13.238*	*2.194*	*2.124*	*10.459*	*4.975*	*0.885*	*1.171*	*7.031*
B+C	*-2.754*	*1.089*	*1.002*	*3.972*	*7.696*	*2.209*	*2.921*	*12.826*
	***Dirichlet* regression approaches (kg)**							
A+B+C	*1.686*	*2.015*	*1.856*		*4.186*	*3.559*	*3.776*	
A	*5.581*	*5.778*	*5.309*		*4.657*	*4.916*	*5.127*	
B	*4.926*	*6.017*	*5.725*		*3.726*	*3.055*	*3.225*	
C	*4.538*	*6.271*	*5.859*		*3.839*	*2.553*	*2.941*	
B+C	*2.456*	*3.041*	*2.836*		*4.111*	*2.803*	*3.104*	

Note: RMSE- the root mean squared error; light (A)-completely sun exposition; light (B)-30% sun exposition, and light (C)-11-12% sun exposition.

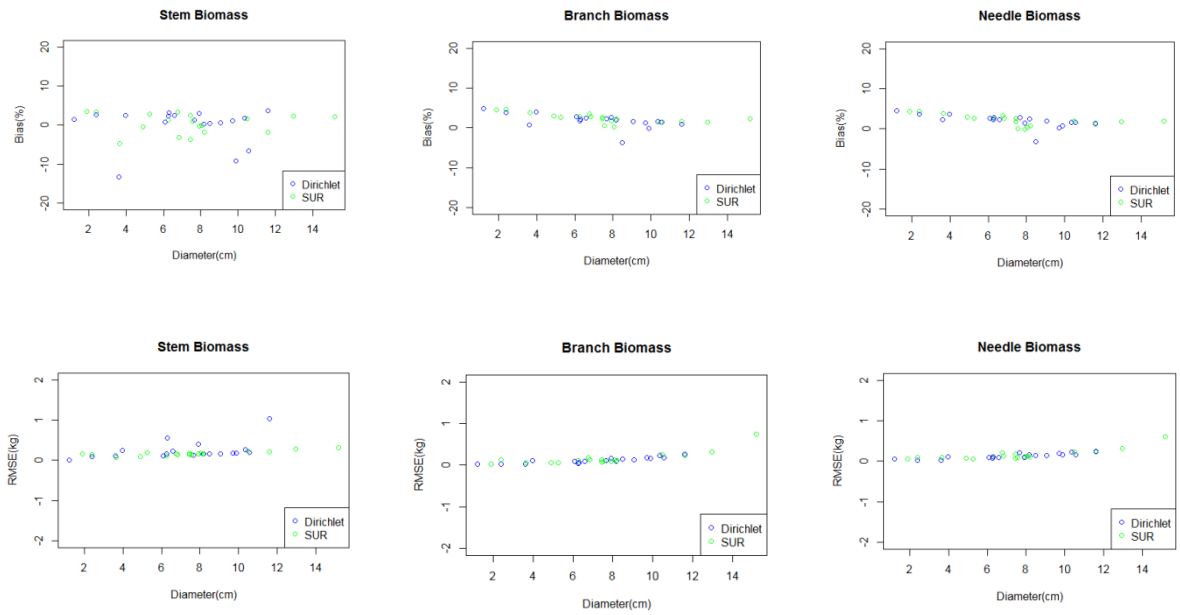


Figure 10: Bias (%) and *RMSE* distributed on diameter (cm) between (*SUR*) and *Dirichelet* regression models for biomass estimation in sapling component in all treatment.

3.4 Basal diameter growth

An initial exploratory graphical analysis is presented (Figure 13 and 14), the relationships between the dependent variables (cumulative basal diameter and annual radial growth) and the independent three factor variables (e.g. light, watering with summer rainfall, fertilizer); it showed that cumulative basal diameter is larger due to light (A) followed by light (C) and light (B). In addition, it showed that cumulative basal diameter is larger due to water with summer rainfall followed by "No" watering treatment. In addition, it showed that cumulative basal diameter is larger due to "high" fertilizer followed by "low" fertilizer treatment. Similarly, it showed that cumulative annual basal radial growth is larger due to light (A) followed by light (B) and light (C). Moreover, it showed that cumulative annual basal radial growth is larger due to water with summer rainfall followed by "No" watering with summer rainfall treatment. In addition, it showed that cumulative annual basal radial growth is larger

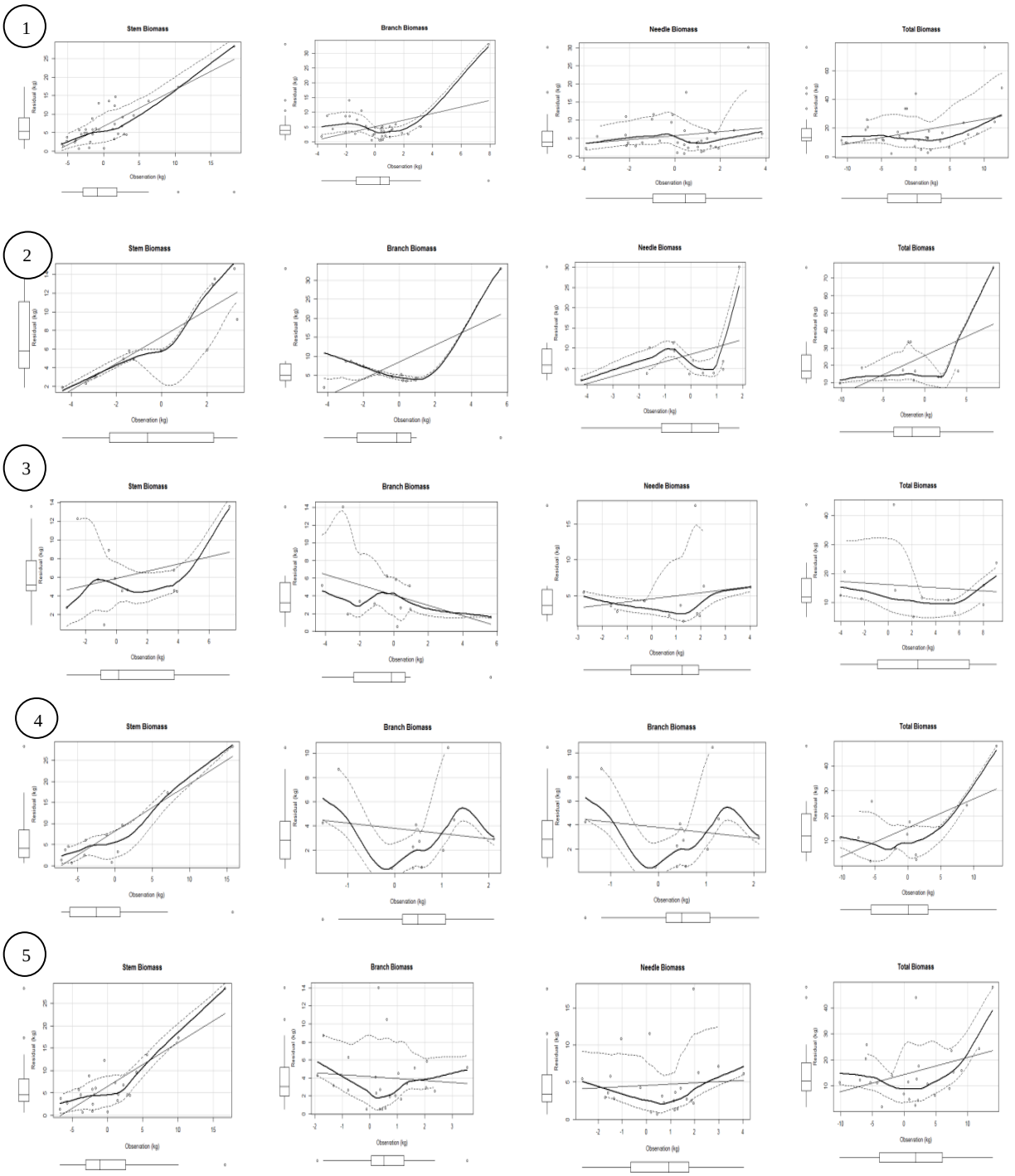


Figure 11: Residuals versus observed for the (*SUR*) models for biomass estimation in sapling component in (1), all treatment; (2), light (A); (3), light (B); (4), light (C); (5), light (B) and light (C).

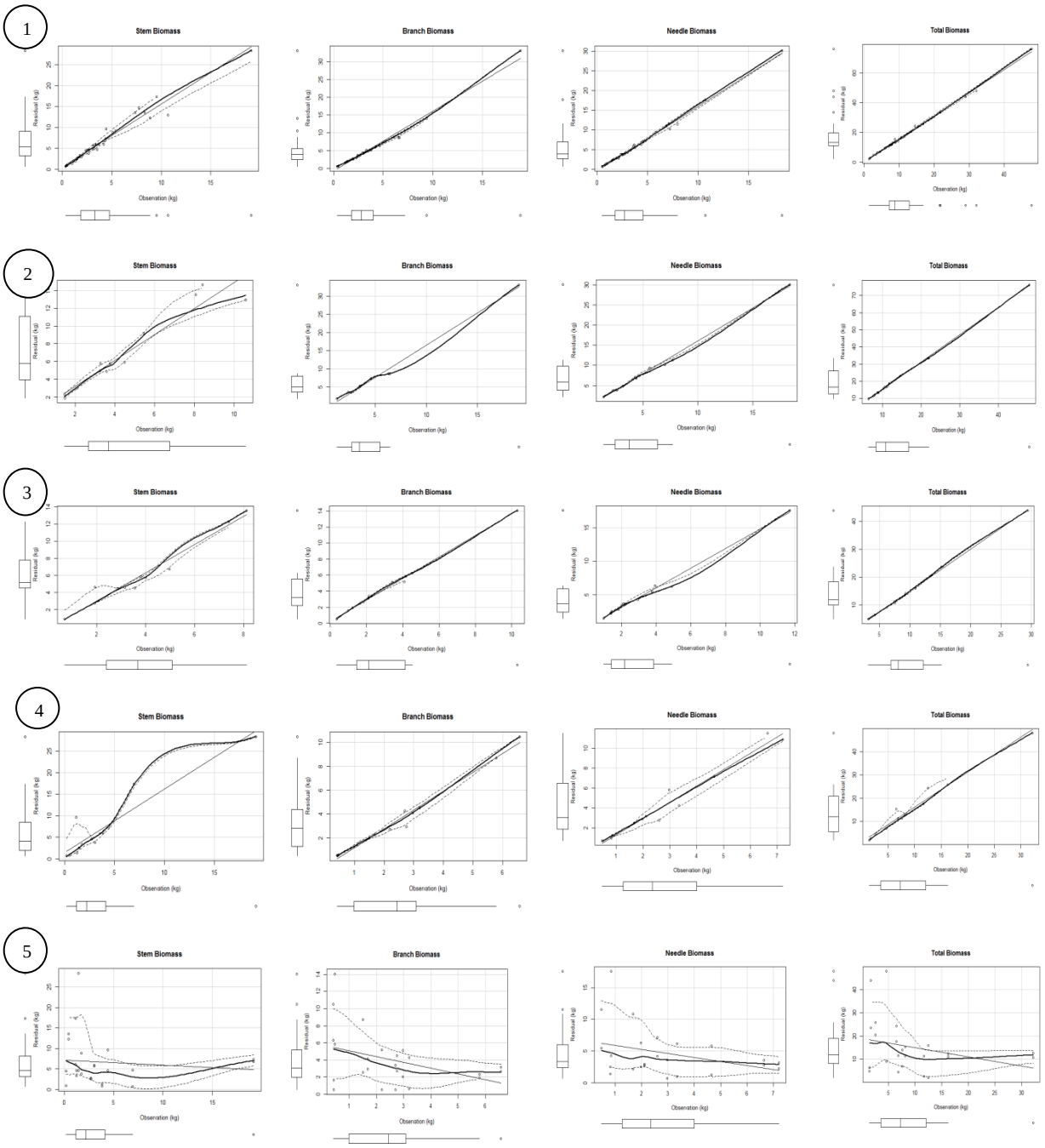


Figure 12: Residuals versus observed for the *Dirichlet* regression models for biomass estimation in sapling component in (1), all treatment; (2), light (A); (3), light (B); (4), light (C) (5), light (B) and light (C).

due to “low” fertilizer followed by “high” fertilizer treatment. An analysis of covariance (*ANCOVA*) result are described the effect of variation in predictor variable (fertilizer) were not significance on the response variable to all sapling in the experiment plot (Table 9). Then, different linear models were constructed for each treatment effect on annual basal diameter growth. The model estimates parameter, their approximate standard errors, and p-values of the treatment effect on basal diameter growth for sapling are presented in (Table S3). It showed that basal diameter radial growth is larger due to combination of watering with summer rainfall and light (A) treatment followed by “No” watering with summer rainfall with light (B) and “No” watering with summer rainfall with light (C) differ from the total basal diameter radial growth model. Again, it showed that basal diameter radial growth is smaller due to combination of “No” watering with summer rainfall with light (C) treatment followed by watering with summer rainfall with light (B) and watering with summer rainfall with light (C) from the total basal diameter radial growth model (Figure 15). The significance of analysis of covariance (*ANOVA*) test result showed that there are no significance ($p>0.05$) difference on the parameter (b1) for sapling basal diameter growth. In addition, the result revealed that there are difference on the parameter (b0), but no significance ($p>0.05$) for sapling basal diameter growth (Table 10). Therefore, there was no significant differences among treatments in annual basal diameter growth were detected, but allometric relationships indicated that differences in growth rates were due to ontogenetic drift (slopes; $b0 \neq 1$) or environmental factors (i.e. summer water availability).

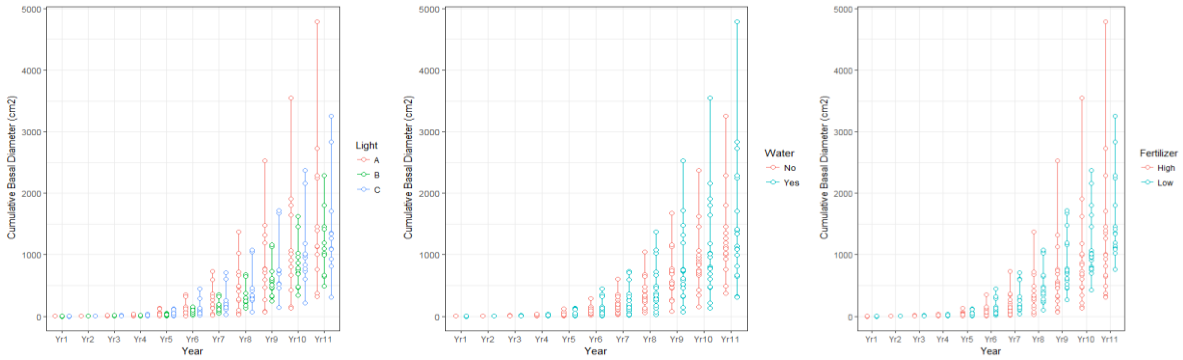


Figure 13: Standard error of the mean and 95% confidence interval of size variable of all sapling of the plot depending on years and cumulative basal diameter (cm^2).

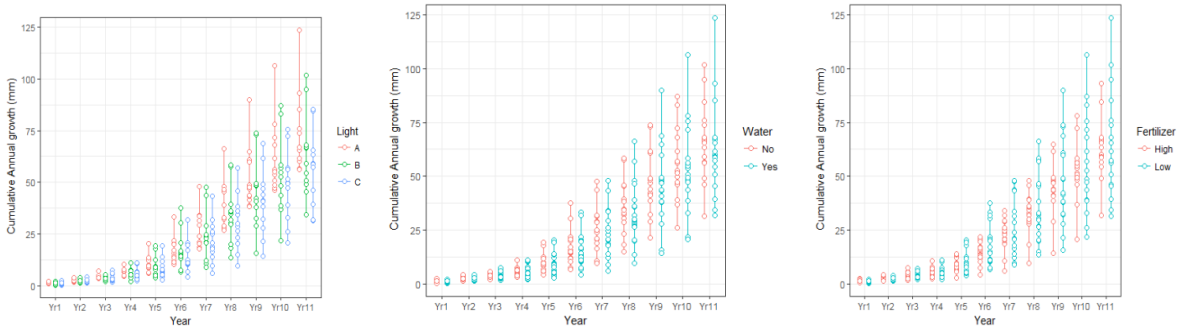


Figure 14: Standard error of the mean and 95% confidence interval of size variable of all sapling of the plot depending on years and cumulative annual radial growth (mm).

Table 9: Significance of analysis of covariance (*ANCOVA*) test for fertilization, light, watering with summer rainfall and their interactions effects on the basal diameter growth of *Pinus pinaster* Ait.

No	Variables	Light	Fertilization	Water	Light × Water	Fertilization × Water
1	Annual radial growth (mm)	ns	ns	ns	×	×
2		×	ns	ns	×	ns
3		*	ns	ns	*	×

Note: (×)- not use for model; ns not significant (p>0.05); (***)p<0.001; (**)p<0.01; (*)p<0.05; (˙)p<0.1.

Table 10: Significance of analysis of variance (*ANOVA*) test for parameter and p-values of the treatment effect on basal diameter growth for sapling.

Parameter	Treatments	SS	MS	Pr > |t|
b0	*Light*	*0.03023*	*0.015117*	*0.513*
	Water	*0.00435*	*0.004349*	*0.653*
	Residuals	*0.03180*	*0.015898*	
b1	*Light*	*0.002642*	*0.0013209*	*0.278*
	Water	*0.000001*	*0.0000010*	*0.969*
	Residuals	*0.001016*	*0.0005078*	

Note- Intercept-b0; Cofficient-b1; sum of squares (SS); Mean square (MS); (p>0.05); (***)p<0.001; (**)p<0.01; (*)p<0.05; (˙)p<0.1.

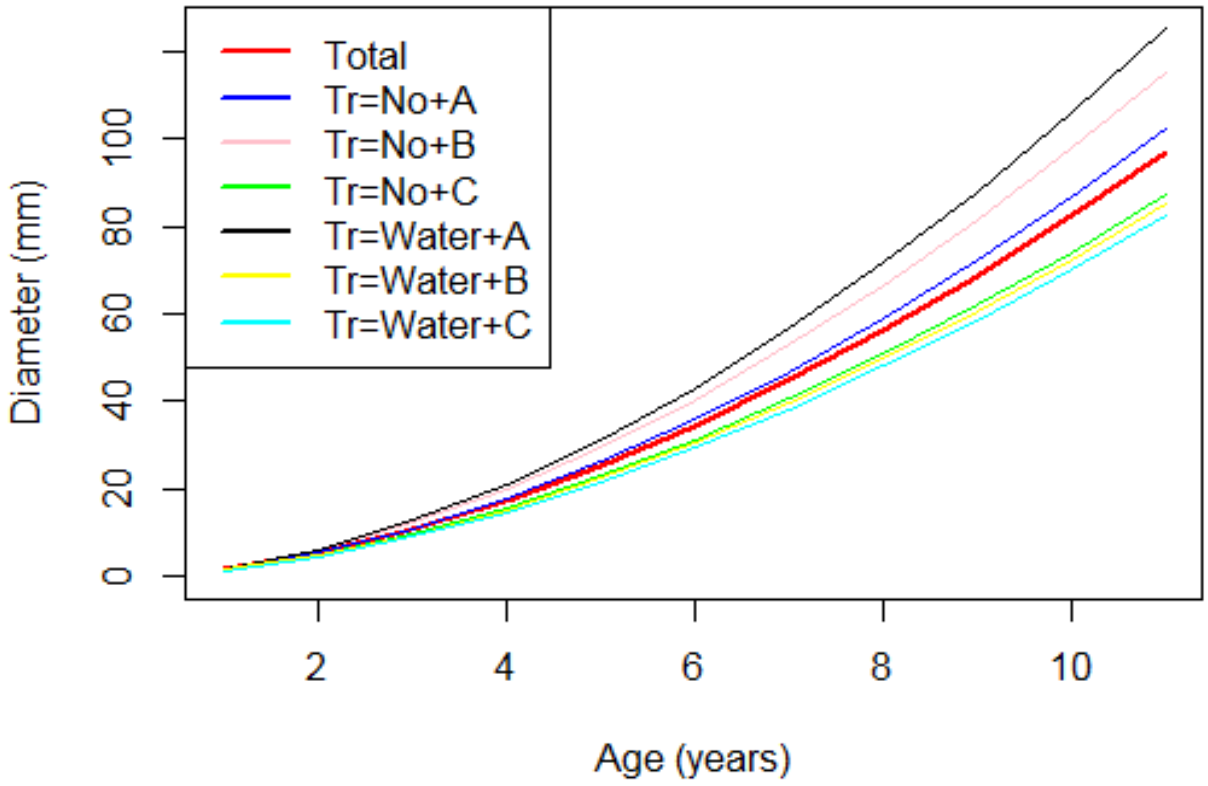


Figure 15: Treatments effect on the basal diameter growth of *Pinus pinaster* Ait.

4. Discussion

The results obtained support that summer water availability have a significant influenced on early development of *P. pinaster* Ait. from nursery product to field. There are several studies on survival and growth in various situations of shade and water stress for Mediterranean species, such as *Quercus coccifera* or *Arbutus unedo* (Sanchez-Gomez et al., 2006a,b,c), for calcicole species (Matesanz et al., 2008), bushy communities (Dato et al., 2006) and for pines (Fernandez et al., 1999; Chambel et al., 2007). However, all these studies were carried out controlling not only the light and water available, but also the temperature, soil composition, etc. In addition, most of these studies lasted less than a year (Ruano et al., 2009). It should be pointed out that our study was performed totally under field conditions from nursery treatments product (Figure 3; Rodríguez-García and Bravo, 2013) and lasted 118 months (Figure 1).

Our result of light availability is an important factor for controlling sapling biomass allocation and morphological structure of *Pinus pinaster*. Ruano et al., (2009) reported similar result explained with *Pinus pinaster* Ait. seedling. The study result strongly indicated that sapling mortality increased risk due to treatment of light (C). It is also noticed that light (C) is associated with a poor survival of sapling. By contrast, treatment of light (A) and light (B) weakly indicated, which contribution to increased risk of sapling mortality is not significantly (Table 5). The findings of Awada et al., (2003) strongly support same result that Maritime pine is a high light demanding species in the Mediterranean climate condition. Similarly, Ruano et al., (2009) study showed that light intensity influences survival of Maritime pine seedling. In contrast, Sanchez-Gomez et al., (2006a) found no differences in survival among the four light intensities they considered. The only differences found on survival were inter-specific. In addition, no interactions between light and water availability were observed in the current study, while Sanchez-Gomez et al., (2006b,c) found that drought

affected survival more in situations of strong light than in those of deep shade, from tissue drying. As for water availability, they observed that light did not influence survival in most of the studied species, as happens in the Pinus species (Ruano et al., 2009). There are some other examples of greater seedling densities in open canopy sites than in closed canopy sites (Fernández et al., 2001; Rodríguez et al., 2008), which confirmed the shade-intolerant nature of this species. Holding with other covariates e.g. light (A), light (B) and light (C) were constant, the result explored that sapling mortality rate goes down by 3% with one unit change in summer water availability (mm) in the experiment plot. Therefore, more light is the necessary for survival of saplings. It concludes that summer water availability is associated with sapling survival of Maritime pine stand. This result strongly supported by Fernández et al., (1999) findings that survival of the species was greater than 97% when there was sufficient water. Although our study covered only the Castilian Plateau provenance, these survival levels were not reached under any other situation. Perhaps the simulation of the stormy year was not as strong in the current study as in the previously mentioned study because ours was under field conditions with longer time while the others were in a nursery. In addition, Chambel et al., (2007) analyzed the response of *P. pinaster* with two water regimes that their result similar to those obtained in this study, given that water stress influences the species studied significantly. Moreover, the result confirm those obtained by Matesanz et al., (2008), who studied the effect of water stress on species of semi-arid calcicole ecosystems. Besides, the study has very weak point that this did not consider about sapling size (diameter and total height) and basal area due to limited of consistency of forest inventory data from the experiment plot for sapling survival analysis,.

Available estimates of biomass and carbon in the forestry has become important for potential in climate change mitigation and adaptation strategies (Riofrío et al., 2015). The estimation of

forest carbon stocks from forest requires the use of accurate and unbiased biomass models (Ruiz-Peinado et al., 2011). In this study, all the model fitted were either linear and non linear equations, with an allometric expression including diameter (cm) and/or total tree height (m) appearing by themselves with different parameters or together in various different combinations. This was provide an operational method for obtaining accurate *AGB* estimation for individual species of Maritime pine, which seedling stage was developed in the nursery with different treatment, and planted in natural forest stand. Belowground biomass is not considered in our studies because of the high-cost, even though it makes up a significant part of the total sapling biomass. Biomass additives has been recognized as a desirable characteristic of a system of equations for predicting component as well as total tree biomass (Bi et al., 2004). The use of nonlinear seemingly unrelated regressions (*SUR*) method to fit the system of equations guarantees this property and reducing confidence and prediction intervals of the biomass estimations (Kozak, 1970) and using the power function to directly fit the original biomass data scale can also provide model fitting as well as the log-transformed models (Parresol, 1999; Parresol, 2001). Similarly, our study result (Table 6) showed high goodness of fit in all components for all treatment equation systems fitted with *SUR* methodology. In all models, coefficients related to both together diameter (*dbh*) and total tree height (*ht*) were positive for components and *AGB.* In contrast, coefficients were negative that included only diameter (*dbh*) independent variables, especially for stem and branch component biomass in all treatment except light (B). This indicated that coefficients of component biomass increased with increasing interaction between diameter and total tree height of sapling, and the negative sign associated with only diameter. Similarly, Lambert et al., (2005) interpreted as an indirect expression of the competitive environment of the sapling, which involves interaction between species shade tolerance and site factors (i.e. summer water availability). The findings of (Riofrío et al., 2015) explained that the differences in

proportional biomass distribution among components reflect morphological and ecological species traits. However, branch and needle biomass are naturally more variable than stem component (Table 6 and Figure 11) since they are influenced largely by nursery treatment to stand growth by site factor (i.e. summer water availability). Similarly, the output of (Cole and Ewel, 2006; Bi et al., 2004) strongly supported our result. The allometric relationships were only observed within the range of values used to fit the models, which represents of the ontogeny of this species (Table 6). The result of (Riofrío et al., 2015) that strongly suported this result as well.

The knowledge of biomass distributions in different tree components is essential to determine which portion of the tree can provide what amount of biomass for different purposes. The proportion of component biomass can be predicted using the *Dirichlet* regressions (Poudel and Temesgen, 2016). One desired property in the component biomass estimation is the property of additivity, which can be attained by simultaneous fitting of component proportions in the *Dirichlet* regression (Poudel and Temesgen, 2016). In practice, it is unreasonable to assume that information on actual or measured total *AGB* would be available. In that case, the *AGB* should be replaced with $\hat{AGB}$, i.e., the predicted total aboveground biomass (Poudel and Temesgen, 2016). The model given in (Table 2) can be used to obtain $\hat{AGB}$. The predicted proportions were then applied to observed total aboveground biomass to obtain predicted biomass estimates in different components ($\hat{B_c}$), i.e., $\hat{B_c} = \hat{p}\hat{AGB}$, where $\hat{p}$ and *AGB* are predicted proportions and observed total aboveground biomass (kg), respectively (Poudel and Temesgen, 2016).

Our study revealed that the coefficients for all treatment showed that, with increasing diameter (*dbh*) and total tree height (*ht),* all (*b0*) increase, but branch and needle more than stem biomass, which means that branch and needle occupied more biomass than stem. The

coefficients for treatment of light (A) showed that, with increasing diameter (*dbh*) and total tree height (*ht)*, all (*b0*) decrease, but stem more than branch and needle biomass, which means that stem occupied more biomass than branch and needle. Similarly, the coefficients for treatment light (B) showed that, same trend as treatment light (A) showed. The treatment both together light (A) and light (C) same as light (A). But the treatment light (C) showed that the same nature showed for all treatment (Table 7 and Table S2).

Both of these methods were produced lower *RMSE* and bias (%), but *SUR* compared to the *Dirichlet* methods for component biomass of all treatment (Table 8 and Figure 10). In contrast, the finding of (Poudel and Temesgen, 2016) explained that the *Dirichlet* regression produced a smaller *RMSE* and bias (%) compared with the *SUR* methods for component biomass.

The both method explained that the higher biomass production was observed in light (A) followed by light (B) and light (C). Specially, biomass allocation was observed higher in needle rather than stem and branch in light (A). In contrast, more growth and biomass allocation was observed in stem than branch and needle in both treatment of light (B) and light (C). This variation due to ontogenetically (slopes, $b0 \neq 1$), which coincides with other findings (Muller et al., 2000; Shipley and Meziane, 2002; Poorter et al., 2012). The results suggested from (Xie et al., 2012) that the environmental factors governed the biomass allocation to roots and leaves, and ontogenetic drift (slopes, $b0 \neq 1$) governed the biomass allocation to stems. The results also demonstrated from (Xie et al., 2012) that biomass allocation to metabolically active organs (e.g., roots and leaves) was mainly governed by environmental factors, and that biomass allocation to metabolically non-active organs (e.g., stems) was mainly governed by ontogenetic drift. The most remarkable difference between treatments was that saplings with light (A) treatments allocated proportionately more biomass

to needle and lower to stem, as plant grew larger, even though our study did not consider for root biomass; while light (B) and light (C) saplings showed the opposite trend. These results agree with the results of Muller et al., (2000), who observed preferential allocation to leaves over roots as plant grew larger. When light, soil fertility, and summer water availability effects were assessed in same age of saplings, the saplings growth and biomass allocation did not occur uniformly in stem and branch with the different treatment. The relative allocation of resources to stem versus branch depended upon which resource (light or water) was more limiting (Cronin et al., 2003), which agrees with optimal partitioning theory (*OPT*). Many studies have concluded that ontogenetic drift caused biomass allocation patterns (McConnaughay and Coleman,1999), but they have overlooked the response of biomass allocation pattern to environmental factors, and thus missed mechanisms rather than ontogenetic drift. It is easily understandable that in resource-poor site, plants develop higher root/shoot ratio than those in resource-rich site (Shipley and Meziane, 2002; Moriuchi, and Winn, 2005). However, in some cases, delayed plant development may also result in this phenomenon (Moriuchi and Winn, 2005). Some even concluded that this is exclusively a consequence of ontogenetic drift (McConnaughay and Coleman,1999; Coleman et Al., 1994). Our results differed from those conclusions. As pointed out by Moriuchi and Winn, (2005) that the biomass allocation of plants in a resource-poor treatment could not be simply due to delayed development.

With increasing low fertility condition, saplings responded with stem elongation and higher relative allocation of biomass to leaves and branch, but at expense of lower inversion to the stem system. This indicates that the *P. pinaster* sapling was not severely stressed by the shade. These results agree with the results of (Rodríguez-García and Bravo, 2013), who observed the *P. pinaster* seedling were not severely stressed by the shade. Higher soil fertility affected to allocation to leaves (increasing it), and especially allocation to stem (decreasing

it), in completely sun exposition and 30% sun exposition; while it did not affect to biomass allocation to stem and stem height elongation in deep shade. Lack of growth response to fertilization is consistent with other fertilization studies in pines (Kishchuk et al., 2002). According to Bogino and Bravo, (2008), rainfall before and during the growth period is directly related to growth for *P. pinaster*. Intra-specific responses to water and light variation have been observed previously in *P. pinaster* at seedling stage (Fernández et al., 1999; Awada et al., 2003; Chambel et al., 2007). In our study, a species-specific variation in growth response to increased shade and N availability was observed at same-age sapling stage, which may reflects *P. pinaster* intra-specific differences in nutrient and light (gaps) requirements for growth and establishment.

5. Conclusion

The main conclusion of this study is that summer water availability shows a higher impact in respect to survival, biomass allocation and basal diameter growth in the early stages of Mediterranean Maritime pine. The summer water availability is associated with sapling survival of *P.pinaster* Ait. in the site. Moreover, biomass allocation has a strong influence with completely sun exposition. The allometric based on seemingly unrelated regression (*SUR*) and *Dirichlet* methods was provided accurate biomass estimation that guarantee additivity among biomass component for *P.pinaster* Ait. The *SUR* method were superior to *Dirichlet* methods due to less bias and smaller *RMSE* values for biomass estimation of sapling. Moreover, annual basal diameter growth has a strong influence with summer water availability and completely sun exposition. The findings explained that the differences in proportional biomass distribution among components and basal diameter growth variation reflect morphological and ecological species traits of *P.pinaster* Ait. Ontogenetic drift (slope, $b0 \neq 1$) was observed in growth rates and biomass allocation depended upon which resources was more limiting, according to (*OPT*). Therefore, different light exposition in the nursery stage of sapling associated with summer water availability appeared the most important environmental factor to determining survival, biomass allocation and basal diameter growth of *P.pinaster* Ait. in the site. The information obtained will serve to understand the impact of climate irregularity on regeneration in nursery and consequently define the most appropriate adaptive forest management strategy to ensure long-term persistence in order to establish certain forest management goals.

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Annex

1. Supplementary figure

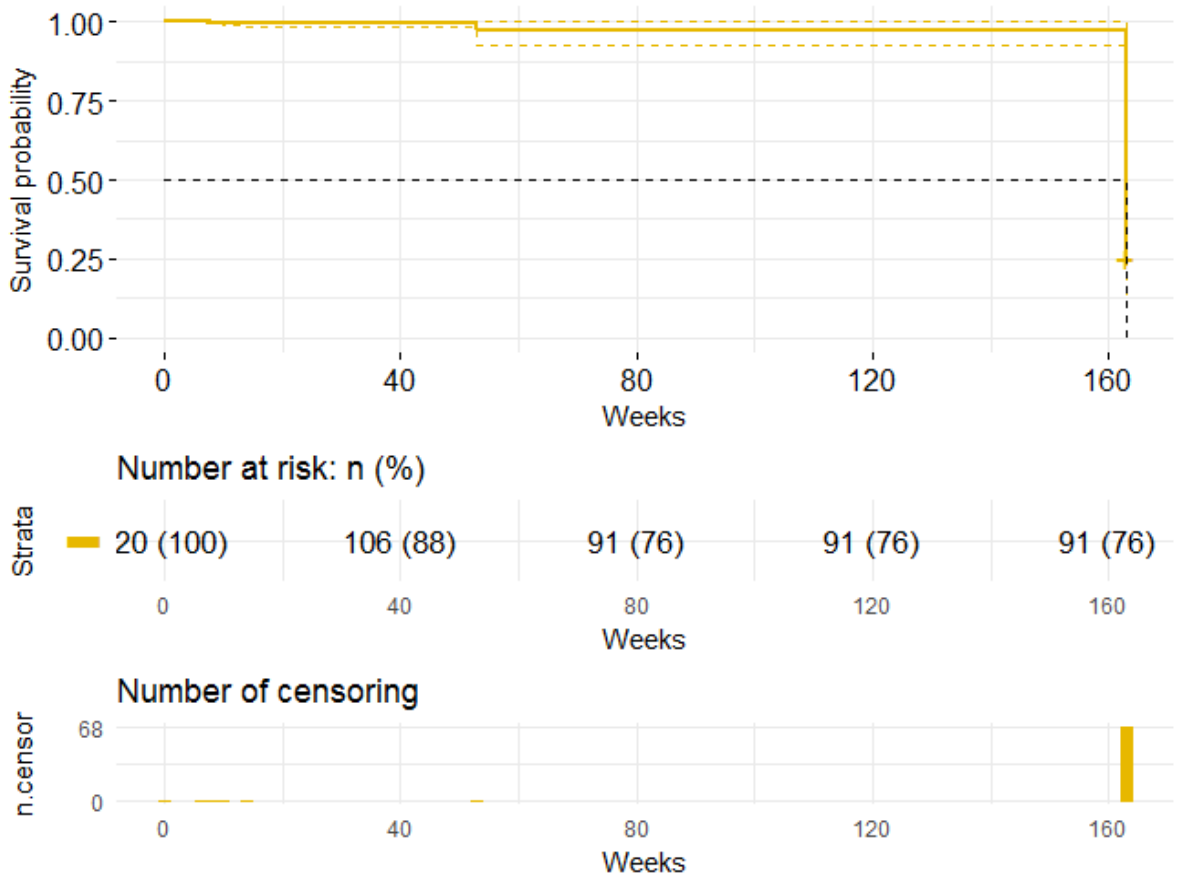

Figure S1: Adjusted survival probability of sapling at the mean values of covariates

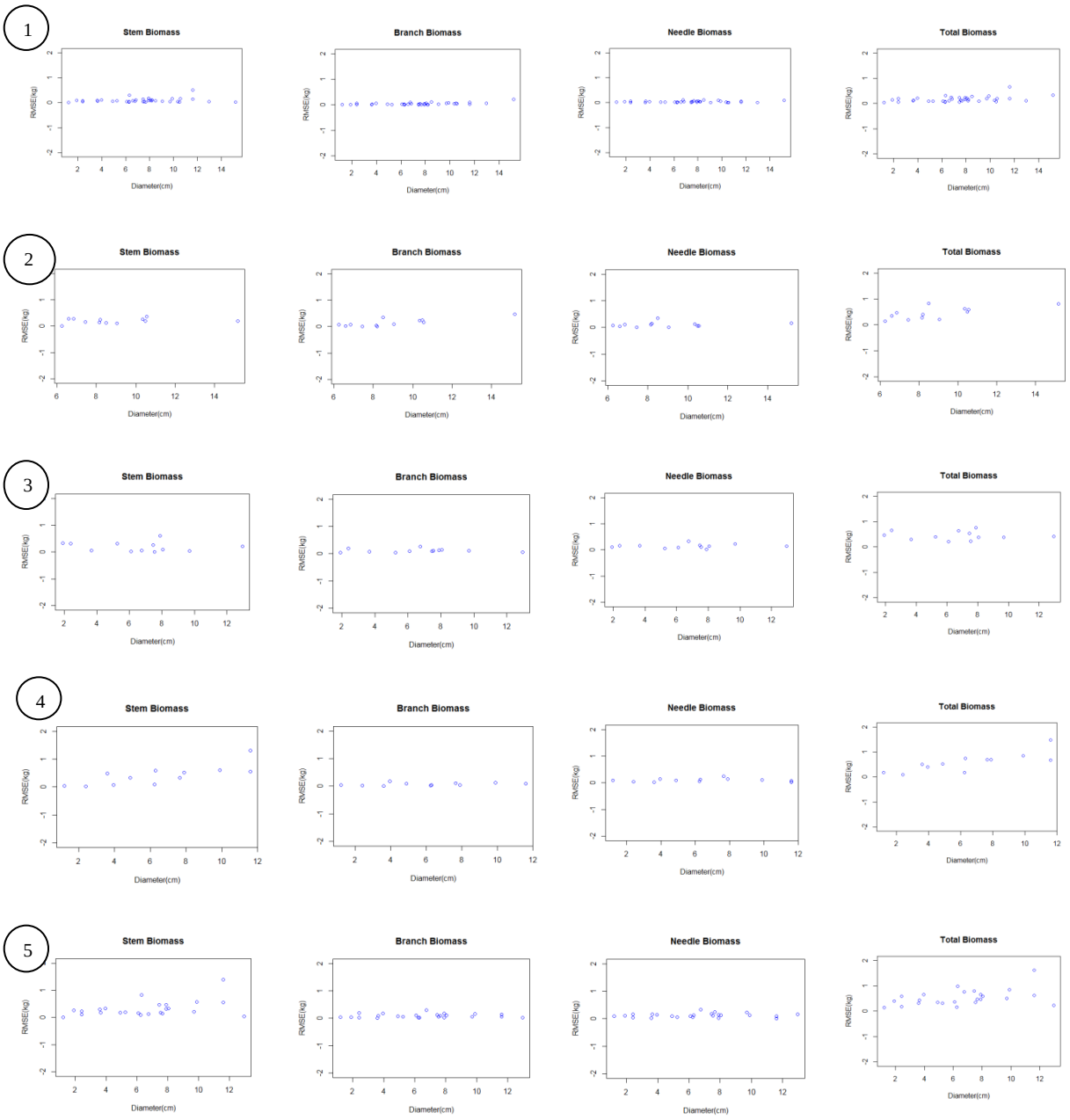

Figure S2: *RMSE* distributed on diameter (cm) using (*SUR*) regression models for biomass estimation in sapling component in (1), all treatment; (2), light (A); (3), light (B); (4), light (C); (5), light (B) and light (C).

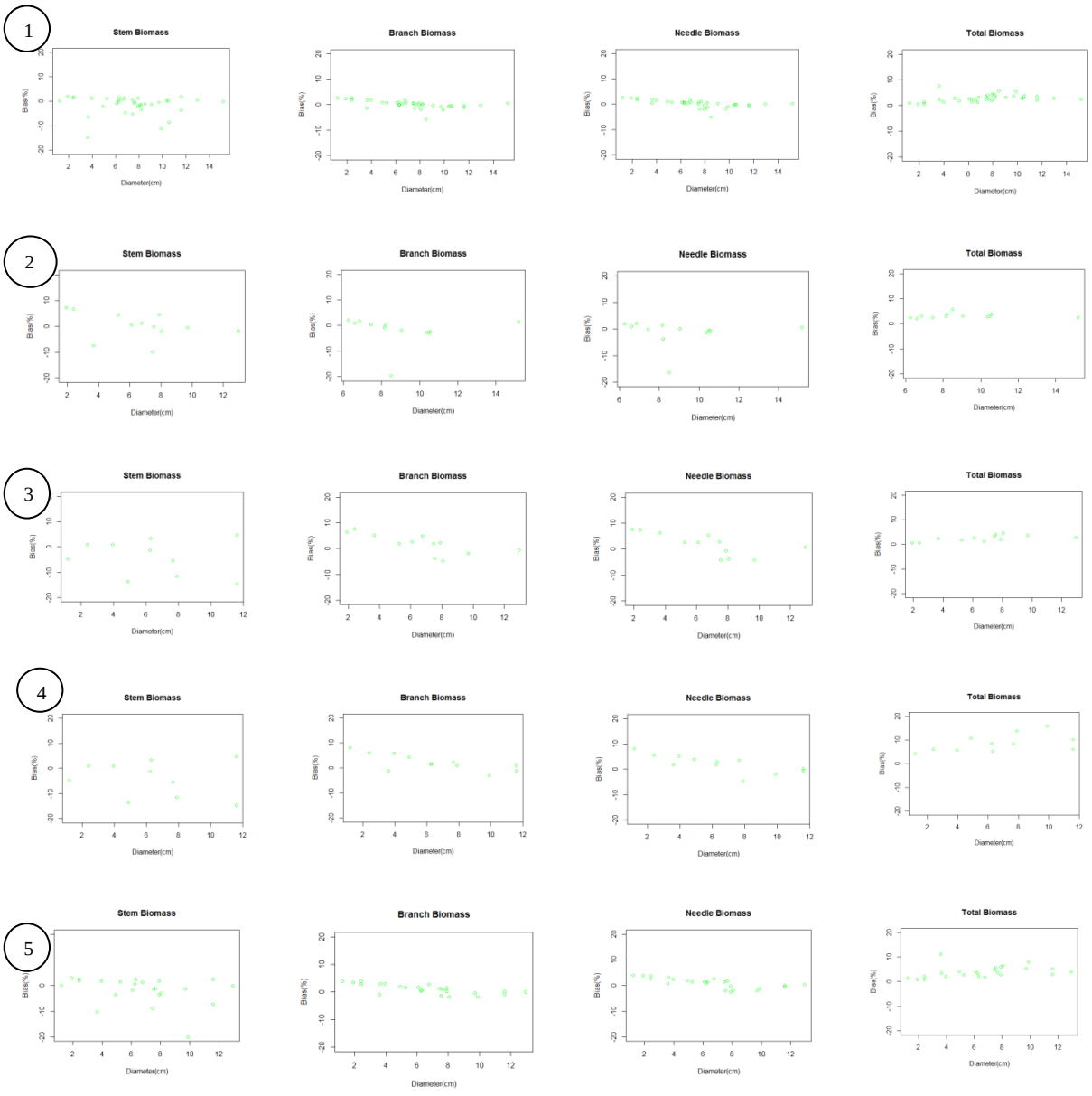

Figure S3: Bias (%) distributed on diameter (cm) using (*SUR*) regression models for biomass estimation in sapling component in (1), all treatment; (2), light (A); (3), light (B); (4), light (C); (5), light (B) and light (C).

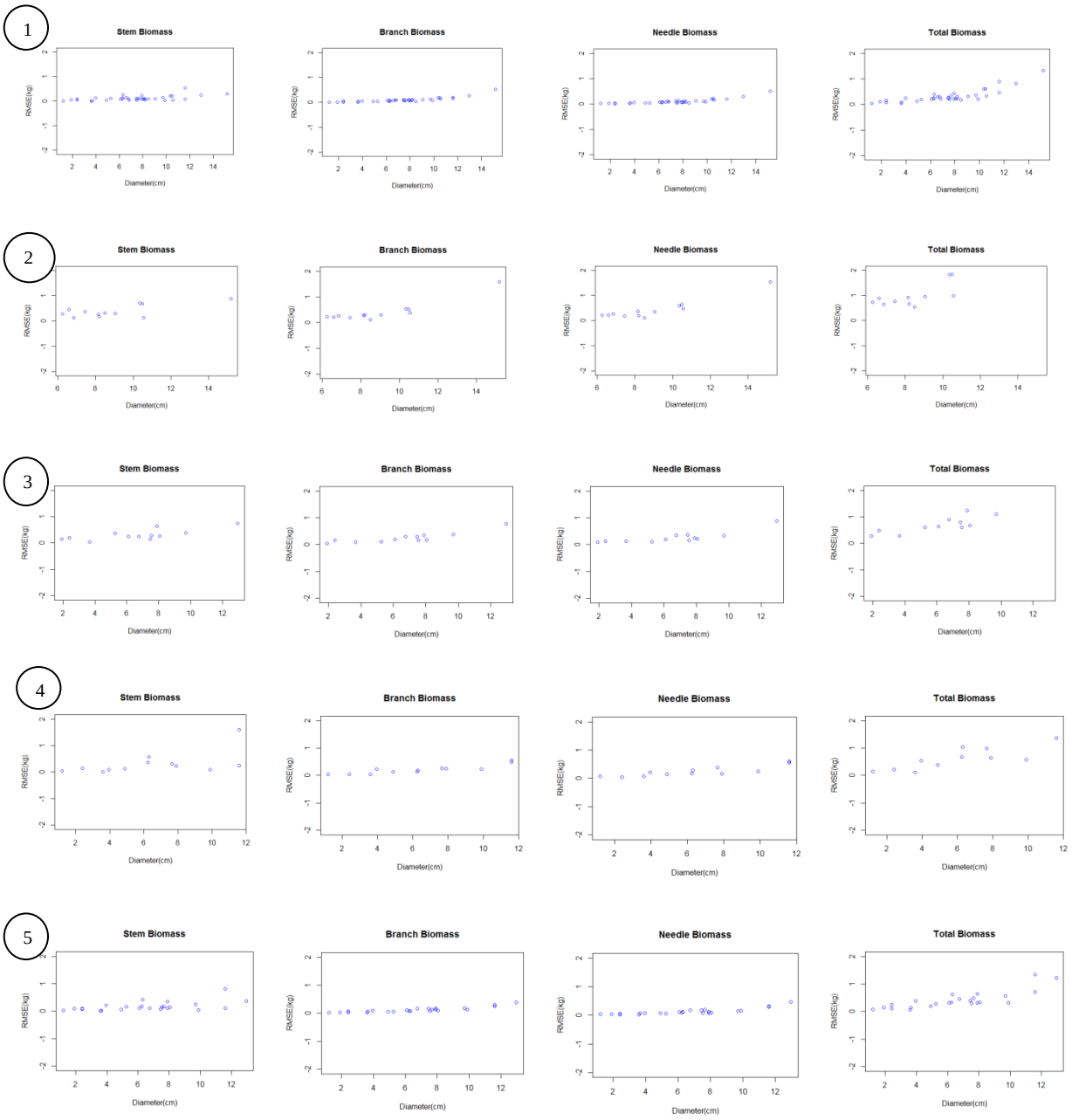

Figure S4: *RMSE* distributed on diameter (cm) using *Dirichlet* regression models for biomass estimation in sapling component in (1), all treatment; (2), light (A); (3), light (B); (4), light (C) (5), light (B) and light (C).

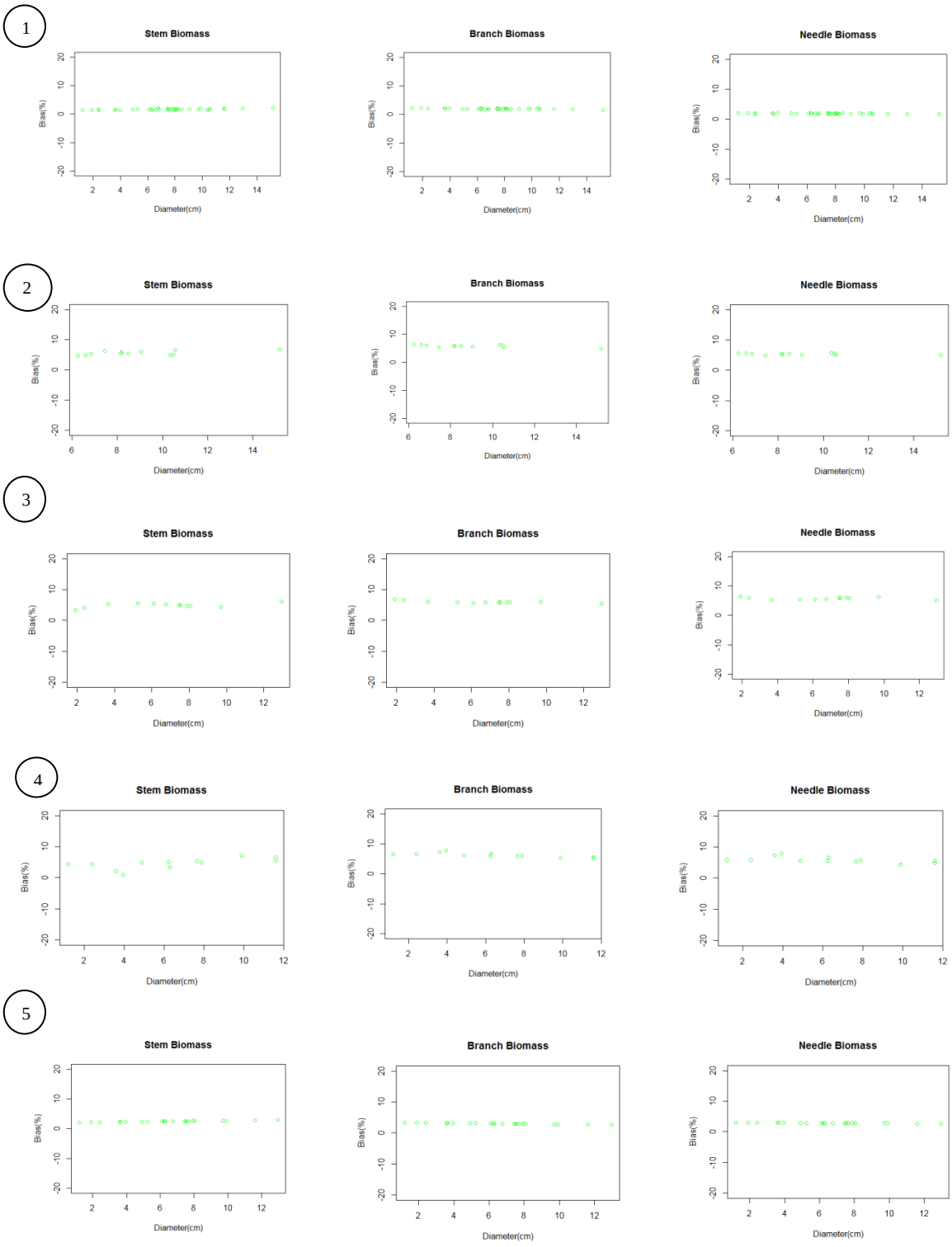

Figure S5: Bias (%) distributed on diameter (cm) using *Dirichlet* regression models for biomass estimation in sapling component in (1), all treatment; (2), light (A); (3), light (B); (4), light (C); (5), light (B) and light (C).

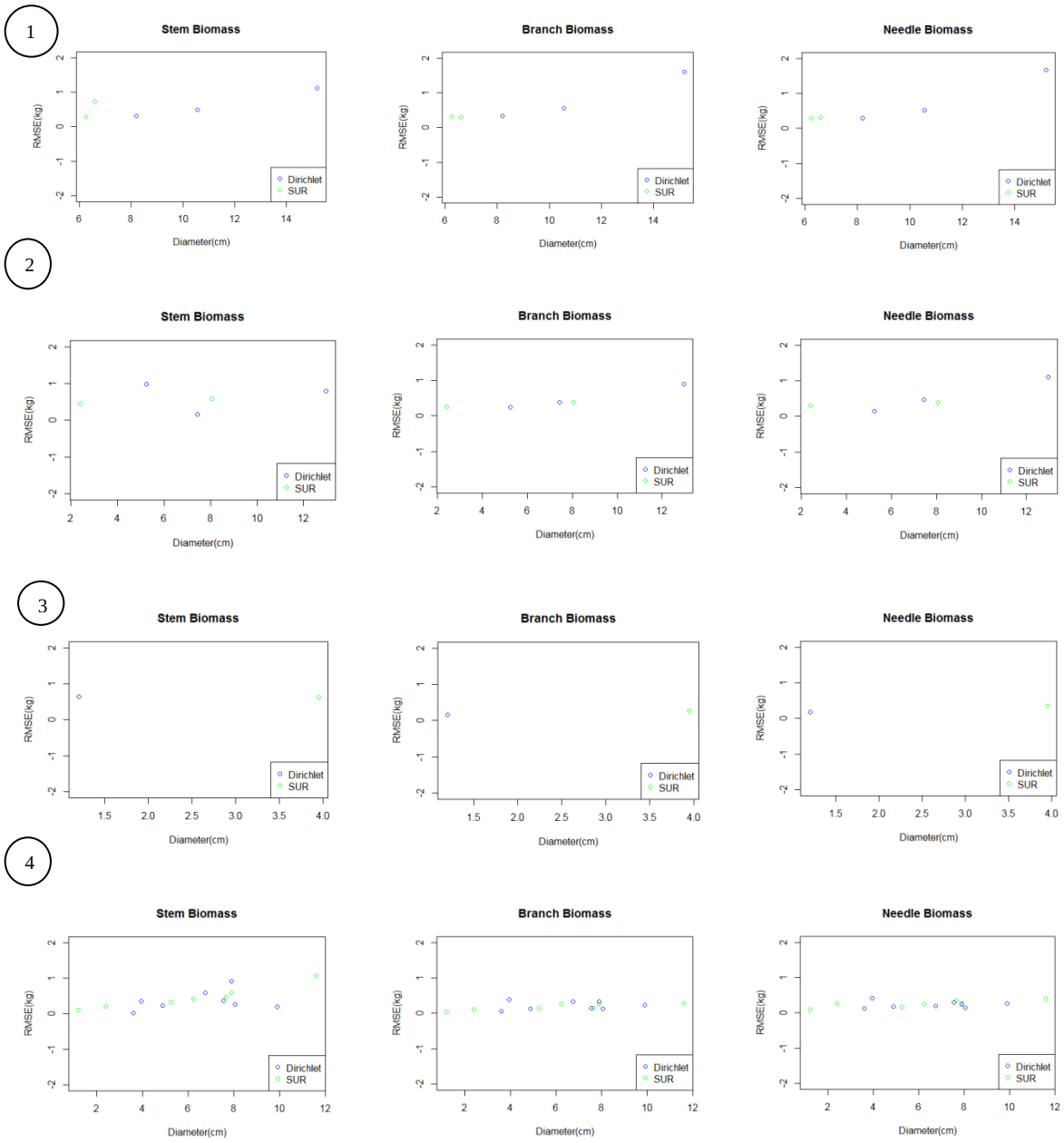

Figure S6: *RMSE* distributed on diameter (cm) between (*SUR*) and *Dirichlet* regression models for biomass estimation in sapling component in (1) light (A); (2) light (B); (3) light (C) (4) light (B) and light (C).

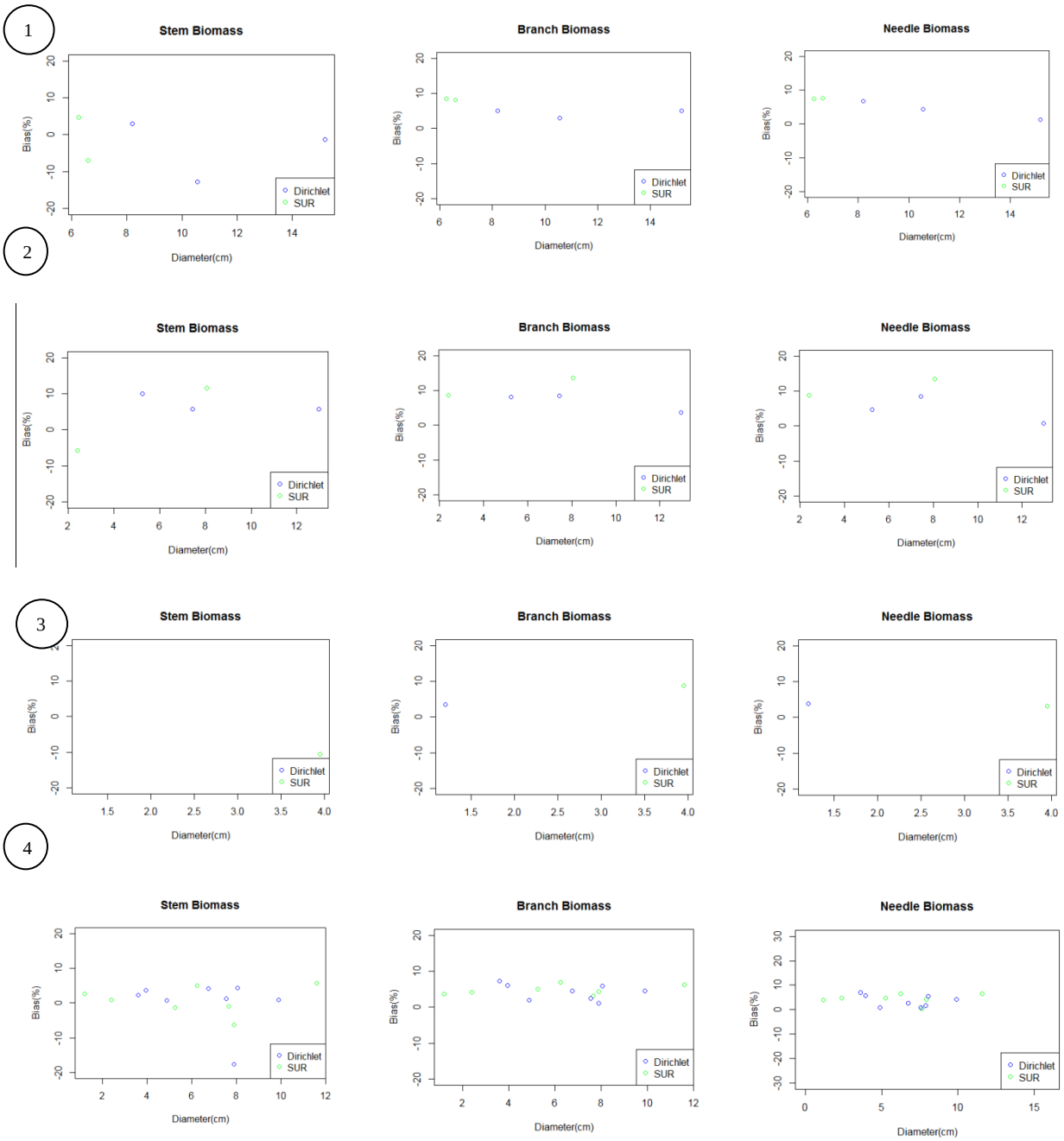

Figure S7: Bias (%) distributed on diameter (cm) between (*SUR*) and *Dirichlet* regression models for biomass estimation in sapling component in (1) light (A); (2) light (B); (3) light (C) (4) light (B) and light (C).

2. Supplementary table

Table S1: Parameter estimates, their approximate standard errors, and p-values of the (*SUR*) biomass models for different sapling compartment.

Treatment	Parameter	Estimate	Standard Error	*Pr* > |*t*|
A+B+C	*b1*	*-0.139413159*	*0.0593*	*0.02*
	b2	*0.449992086*	*0.1157*	*0.001*
	b3	*-0.008863034*	*0.0028*	*0.002*
	b4	*0.017698661*	*0.0007*	*0.00*
	b5	*0.017469480*	*0.0007*	*0.00*
A	*b1*	*-0.14639762*	*0.0639*	*0.03*
	b2	*0.43671867*	*0.1273*	*0.01*
	b3	*-0.01018928*	*0.0055*	*0.07*
	b4	*0.01936938*	*0.0011*	*0.00*
	b5	*0.01835939*	*0.0009*	*0.00*
B	*b1*	*0.038168564*	*0.0689*	*0.06*
	b2	*0.110189222*	*0.1299*	*0.04*
	b3	*0.004190713*	*0.0069*	*0.06*
	b4	*0.014285156*	*0.0019*	*0.00*
	b5	*0.016175219*	*0.0016*	*0.00*
C	*b1*	*-0.29892167*	*0.0754*	*0.0001*
	b2	*0.81782494*	*0.1311*	*0.00*
	b3	*-0.01326037*	*0.0051*	*0.001*
	b4	*0.01568697*	*0.0014*	*0.00*
	b5	*0.01566080*	*0.0012*	*0.00*
B+C	*b1*	*-0.12510369*	*0.0264*	*0.00*
	b2	*0.44410015*	*0.0359*	*0.00*
	b3	*-0.01107733*	*0.0034*	*0.09*
	b4	*0.01593271*	*0.0011*	*0.00*
	b5	*0.01598849*	*0.0009*	*0.00*

Note: light (A)-completely sun exposition; light (B)-30% sun exposition and light (C)-11-12% sun exposition;); b1, b2, b3,b4 and b5: model parameters.

Table S2: Parameter estimates, their approximate standard errors, and p-values of the *Dirichlet* regression biomass models for different treatment sapling compartment.

Treatment &Compartment		Parameter	Estimate	Standard Error	Pr > |t|
A+B+C	*Stem*	*b0*	*-5.535894*	*3.417655*	*0.11*
		b1	*1.247571*	*0.877589*	*0.16*
		b2	*3.233171*	*1.160903*	*0.01*
		b3	*0.004055*	*0.001560*	*0.01*
		b4	*-0.634618*	*0.292112*	*0.03*
	Branch	*b0*	*-7.361286*	*3.140183*	*0.02*
		b1	*1.906751*	*0.868215*	*0.03*
		b2	*3.370068*	*1.091798*	*0.01*
		b3	*0.004675*	*0.001581*	*0.01*
		b4	*-0.778159*	*0.290872*	*0.01*
	Needle	*b0*	*-5.945282*	*3.055292*	*0.05*
		b1	*1.688325*	*0.857275*	*0.05*
		b2	*2.988557*	*1.067757*	*0.01*
		b3	*0.004389*	*0.001559*	*0.01*
		b4	*-0.706207*	*0.286532*	*0.02*
A	*Stem*	*b0*	*-11.1478*	*3.1157*	*0.01*
		b1	*-0.3421*	*0.4132*	*0.41*
		b2	*3.5704*	*0.9411*	*0.00*
	Branch	*b0*	*-10.55521*	*3.12592*	*0.00*
		b1	*0.06512*	*0.42556*	*0.88*
		b2	*2.68585*	*1.00916*	*0.01*
	Needle	*b0*	*-10.229385*	*2.990065*	*0.01*
		b1	*-0.009877*	*0.429752*	*0.98*
		b2	*2.794153*	*1.015549*	*0.01*
B	*Stem*	*b0*	*6.231908*	*2.614618*	*0.02*
		b1	*-1.112362*	*0.447654*	*0.02*
		b2	*-2.418731*	*1.163781*	*0.04*
		b3	*-0.002507*	*0.001084*	*0.02*
		b4	*0.479202*	*0.203980*	*0.02*
	Branch	*b0*	*0.091878*	*2.851189*	*0.98*
		b1	*-0.067554*	*0.484723*	*0.89*
		b2	*-0.256485*	*1.259250*	*0.84*
		b3	*-0.000443*	*0.001158*	*0.71*
		b4	*0.061257*	*0.219256*	*0.78*
	Needle	*Reference category 3*			
C	*Stem*	*b0*	*0.4762*	*2.2324*	*0.83*
		b1	*2.1006*	*0.8381*	*0.02*
		b2	*-0.7038*	*0.8311*	*0.39*
		b3	*-0.2981*	*0.1275*	*0.02*
	Branch	*b0*	*1.2496*	*2.2820*	*0.59*
		b1	*3.1455*	*0.8384*	*0.00*
		b2	*-2.1760*	*0.9607*	*0.03*
		b3	*-0.3710*	*0.1158*	*0.00*
	Needle	*b0*	*1.8846*	*2.3861*	*0.43*

		b1	*3.3146*	*0.8632*	*0.00*
		b2	*-2.4311*	*0.9754*	*0.01*
		b3	*-0.3891*	*0.1213*	*0.00*
	Stem	*b0*	*1.95677*	*0.45330*	*0.00*
B+C		*b1*	*-0.01795*	*0.06135*	*0.77*
	Branch	*b0*	*0.93623*	*0.45394*	*0.03*
		b1	*0.07423*	*0.06183*	*0.23*
	Needle	*b0*	*1.27072*	*0.49051*	*0.03*
		b1	*0.04987*	*0.06760*	*0.46*

Note- Category 3 is used as baseline category for "alternative" model, light (A)-completely sun exposition; light (B)-30% sun exposition and light (C)-11-12% sun exposition; Intercept-b0; Cofficient-b1, b2, b3, b4.

Table S3: Parameter estimates, their approximate standard errors, and p-values of the treatment effect on basal diameter growth for sapling.

Treatments	**Parameter**	**Estimate**	**Standard Error**	**Pr > |t|**
A+B+C	*b0*	*0.48372*	*0.05812*	*1.43e-15*
	b1	*1.70591*	*0.03336*	*< 2e-16*
No watering+A	*b0*	*0.48158*	*0.10039*	*1e-05*
	b1	*1.72944*	*0.05761*	*<2e-16*
No watering+B	*b0*	*0.60676*	*0.13484*	*2.94e-05*
	b1	*1.72697*	*0.07738*	*< 2e-16*
No watering+C	*b0*	*0.41183*	*0.14332*	*0.0055*
	b1	*1.69098*	*0.08225*	*<2e-16*
Watering+A	*b0*	*0.61303*	*0.12114*	*3.77e-06*
	b1	*1.75923*	*0.06952*	*< 2e-16*
Watering+B	*b0*	*0.38251*	*0.15120*	*0.0139*
	b1	*1.69365*	*0.08677*	*<2e-16*
Watering+C	*b0*	*0.34309*	*0.16912*	*0.0467*
	b1	*1.69694*	*0.09706*	*<2e-16*

Note- light (A)-completely sun exposition; light (B)-30% sun exposition and light (C)-11-12% sun exposition; Intercept-b0; Cofficient-b1.

3. R script

3.1 R Script for selected treatment for survival, biomass and basal diameter growth analysis

```
##Program for multifactor of analysis of variances (GLMs) test
##Created by MAA Pavel
##date 14.03.2017
##setting working directory
Run;
setwd("C:/cuellar")
## Loading ".RData)
load('cuellar-plantation.RData')
##############################################
##Create dammy varaibles
##fertilization
#0 (2) (F) -> fertilization with Low Nitrogen
#1 (1) (N) -> fertilization with High Nitrogen

## light conditions
##(0,0)A - nursery conditions with completely sun exposition
##(0,1)B - nursery conditions with 30% sun exposition
##(1,0)C - nursery conditions with 11-12% sun exposition
##light1=li1(0,1,0)
##light=li2(0,0,1)
Run;
treesDaso1$light1=with(treesDaso1,ifelse(light=='C',1,0))
treesDaso1$light2=with(treesDaso1,ifelse(light=='B',1,0))
#Create variable of Biomass(hd2) and Slemderness(h_d)
Run;
treesDaso1$hd2=with(treesDaso1,ht*diameter1*diameter2/100)
treesDaso1$h_d=with(treesDaso1,ht/((diameter1+diameter2)/200))
##Multifactor of analysis of variances (GLMs) Anova test
Run;
m1<-glm(treesDaso1$hd2~treesDaso1$fer+treesDaso1$li1+treesDaso1$li2)
summary(m1)
m2<-glm(treesDaso1$hd2~treesDaso1$fer+treesDaso1$li1+treesDaso1$li2+
       treesDaso1$fer*treesDaso1$li1+treesDaso1$fer*treesDaso1$li2)
summary(m2)
m3<-glm(treesDaso1$hd2~treesDaso1$fer+treesDaso1$li1*treesDaso1$li2)
summary(m3)

m4<-glm(treesDaso1$h_d~treesDaso1$fer+treesDaso1$li1+treesDaso1$li2)
summary(m4)
m5<-glm(treesDaso1$h_d~treesDaso1$fer+treesDaso1$li1*treesDaso1$li2)
summary(m5)
q ()
######end#######
```

3.2 R Script for survival analysis

```
##Program for simple cox proportional hazard model
##for Pinus pinater survival analysis
##Created by MAA Pavel
##date 14.03.2017

##setting working directory
Run;
setwd("C:/cuellar")
## Loading ".RData)
Run;
load('cuellar-plantation.RData')
##installing require packages
install.packages("survival")
install.packages("survminer")
## Loading library
library("survival")
library("survminer")
##Create dammy varaibles
##fertilization
#0 (2) (F) -> fertilization with (Low) Nitrogen
#1 (1) (N) -> fertilization with (High) Nitrogen
## light conditions
##(0,0)A - nursery conditions with completely sun exposition
##(0,1)B - nursery conditions with 30% sun exposition
##(1,0)C - nursery conditions with 11-12% sun exposition
##light1=li1(0,1,0)
##light=li2(0,0,1)

###Coxp model run before organize and created dammy variables in

##"mortality" data set
Run;
mortality$fer=with(mortality,ifelse(fertilization=='F',0,1))
mortality$light1=with(mortality,ifelse(light=='C',1,0))
mortality$light2=with(mortality,ifelse(light=='B',1,0))

## "mortality" data set merge with "trees"  and "treesDaso1" dataset
Run;
survival=merge(mortality,trees,by="nroTree")
survival=merge(survival,treesDaso1,by="nroTree")
#Die varaible define;dead=True=1; alive=False=0
Run;
survival$die.0<-with(survival, ifelse(die,1,0))
cut.points<-unique(survival$time[survival$die.0==1])
str(survival)
#Organize event time variables
Run;
plantation<-as.Date("2007.05.01","%Y.%m.%d")
cut<-c("2007.06.15","2007.06.29","2007.07.13","2007.08.09",
       "2008.05.08","2010.06.14")
cut.points<-as.Date(cut,"%Y.%m.%d")
survival$date.x[is.na(survival$date.x)] <-"2010.06.14"
survival$date.x=as.Date(survival$date.x,"%Y.%m.%d")
survival$time=with(survival,difftime(date.x,plantation,units = "weeks"))
survival$time=round(survival$time,0)
survival$time=as.numeric(survival$time)

##Create water and rainfall variables from rainfall data set
##Indicate week period in every inventory and watering
##(from 15.06.2007 to 14.06.2010)
Run;
time<-c(6, 8, 10,14,53,163)
```

```
##cumulative summer watering (15.06.2007 to 09.08.2007)
Run;
water<-c(16,32,48,80,0,0)

##Cumulative summer rainfall consider date (from 01.06.2007 to 14.09.2010)
##Cumulative rain fall consider only in inventory date
Run;
rainfall<-c(25,48,62,76,105,322)

##Merge water and rainfall variable in "survival" data set
Run;
waterreceived <- data.frame (time,water, rainfall)
survival=merge(survival,waterreceived,by="time")
survival$Watering=with(survival,water+rainfall)
str(survival)

##Create variable of Biomass(hd2) and Slemderness(h_d)in "survival" data set
Run;
survival$hd2=with(survival,ht*diameter1*diameter2/100)
survival$h_d=with(survival,ht/((diameter1+diameter2)/200))
summary(survival)

#######Fitting simple cox proportional hazard of candidate model#######
 Run;
model.1 <-coxph(Surv(time,die.0)~fer+light1+light2+Watering,data= survival)
summary(model.1)
model.2 <-coxph(Surv(time,die.0)~ hd2+h_d+Watering,data=survival)
summary(model.2)
model.3 <-coxph(Surv(time,die.0) ~  light1+light2+Watering,data = survival)
summary(model.3)
model.4 <- coxph(Surv(time,die.0)~fer+Watering, data = survival)
summary(model.4)
model.5 <- coxph(Surv(time,die.0)~ light1+Watering, data = survival)
summary(model.5)
model.6 <- coxph(Surv(time,die.0)~light2+Watering, data = survival)
summary(model.6)
model.7 <- coxph(Surv(time,die.0)~fer + light1+Watering, data = survival)
summary(model.7)
model.8 <- coxph(Surv(time,die.0)~fer + light2+Watering, data = survival)
summary(model.8)
model.9   <-coxph(Surv(time,die.0)~   hd2   +   fer+light1+light2+Watering,   data   =
    survival)
summary(model.9)
model.10 <-coxph(Surv(time,die.0)~ hd2 + fer+Watering, data = survival)
summary(model.10)
model.11 <-coxph(Surv(time,die.0)~ hd2 +light1+light2+Watering, data = survival)
summary(model.11)
model.12<-coxph(Surv(time,die.0)~h_d+fer+light1+light2+Watering, data = survival)
summary(model.12)
model.13 <-coxph(Surv(time,die.0)~ h_d+light1+light2+Watering, data = survival)
summary(model.13)
model.14 <-coxph(Surv(time, die.0)~h_d+light1+Watering, data = survival)
summary(model.14)
model.15 <- coxph(Surv(time, die.0)~h_d+light2+Watering, data = survival)
summary(model.15)
model.16 <-coxph(Surv(time, die.0)~h_d +Watering, data = survival)
summary(model.16)
model.17 <-coxph(Surv(time, die.0)~ hd2 +Watering, data = survival)
summary(model.17)

###Selection  of  best  model  (among  significatives);lowest  value  of  AIC&BIC;  is
    indicate the best
Run;
anova(model.1,model.2,model.3,model.4,model.5,model.6,model.7,model.8,model.9,model
    .10,model.11,model.12,model.13,model.14,model.15,model.16,model.1)
AIC(model.1,model.2,model.3,model.4,model.5,model.6,model.7,model.8,model.9,model.1
```

```
    0,model.11,model.12,model.13,model.14,model.15,model.16,model.17)
BIC(model.1,model.2,model.3,model.4,model.5,model.6,model.7,model.8,model.9,model.1
    0,model.11,model.12,model.13,model.14,model.15,model.16,model.17)

###Selected best model
Run;
model.3 <-coxph(Surv(time, die.0) ~  light1+light2+Watering,data = survival)
summary(model.3)
predict(model.3)
survfit(model.3)
residuals(model.3)

#####Graph 1
#To visualize the predicted survival proportion at any given point in time, by
    default at the mean values of covariates.
Run;
ggsurvplot(survfit(model.3), data=survival,pval = TRUE,
           conf.int = TRUE,conf.int.style = "step",
           xlab="Weeks",break.time.by =40,
           risk.table = "abs_pct",risk.table.y.text.col = T,
           risk.table.y.text = FALSE,
           surv.median.line = "hv",
           ncensor.plot = TRUE,
           color = "#E7B800",#"#2E9FDF"
           ggtheme = theme_minimal())
q ()

######end#######
```

3.3R Script for biomass analysis

```
#Program for Biomass estimation
#Script developed by MAA Pavel
#date:07.04.2017

#Clean behind run history
rm(list=ls())

#Loaded working directory
setwd("C:/cuellar")

#install libraries
install.packages('plyr')
install.packages('systemfit')
install.packages('lattice')
install.packages('RODBC')

#loaded libraries
packs<-
    c('plyr','lattice','car','RODBC','lmtest','Matrix','zoo','reshape2','systemfit'
    )
sapply(packs,require,character.only=TRUE)

#Read data
datos<-read.csv("C:/cuellar/Cuellar_biomas.csv")

#Variable introduce by "kg" (unit) from "gram"
datos$biomastotal=with(datos,TTB/1000)
datos$stem=with(datos,TDSt/1000)
datos$Br27=with(datos,TDBr27/1000)
datos$Br2=with(datos,TDBr2/1000)
datos$needle=with(datos,TDN/1000)

#Variable created by dbh from DBH1 and DBH2
datos$dbh=with(datos,(DBH1+DBH2)/2)
```

```
datos$d=with(datos,(diameter1+diameter2)/2)

#Sum of thick and thin branch
datos$Br=with(datos,(Br2+Br27))

#Sum of thin and needle
datos$BrN=with(datos,(Br2+needle))

## check data set
str(datos)
View(datos)
summary(datos)


####Boxplot for component biomass with mean values

##install and loaded libraries for boxplot
install.packages("devtools")
library(devtools)
install_github("easyGgplot2", "kassambara")
library(easyGgplot2)

#Created variable use to make mean boxplot for component biomass

#Biomass (%) in tree component in "datos" data set
datos$Stem=with(datos,(stem/biomastotal)*100)
datos$Branch=with(datos,(Br/biomastotal)*100)
datos$Needle=with(datos,(needle/biomastotal)*100)
datosal <-datos[,c(2,43,44,45)]
head(datos)


#####Boxplot for whole data sub set datos
P_biomas<-melt(datosal,id.vars=c("nroTree"),
               measure.vars=c("Stem","Branch","Needle"),
               variable.name="Component",value.name="Biomass")
head(P_biomas)

ggplot2.boxplot(data=P_biomas, xName='Component',yName='Biomass',ylim=c(0,100),
                addMean=TRUE, meanPointShape=23, meanPointSize=2.5,
                meanPointColor="black",backgroundColor="white",
    meanPointFill="green")

####light A treatment data sub set
datos1 <- datos[c(1,2,5,6,12,17,19,20,24,31,33,34),]


#biomass (%) in tree component in "datos1" dataset
datos1$Stem=with(datos1,(stem/biomastotal)*100)
datos1$Branch=with(datos1,(Br/biomastotal)*100)
datos1$Needle=with(datos1,(needle/biomastotal)*100)
datosal1 <-datos1[,c(2,43,44,45)]
head(datosal1)

# Boxplot for light A treatment data sub set "datos1"
P_biomas<-melt(datosal1,id.vars=c("nroTree"),
               measure.vars=c("Stem","Branch","Needle"),
               variable.name="Component",value.name="Biomass")
head(P_biomas)

ggplot2.boxplot(data=P_biomas, xName='Component',yName='Biomass',ylim=c(0,100),
                addMean=TRUE, meanPointShape=23, meanPointSize=2.5,
                meanPointColor="black",backgroundColor="white",
    meanPointFill="green")
```

```
####light B treatment data sub set
datos2 <- datos[c(3,9,4,10,11,14,16,18,28,30,32,36),]

#biomass (%) in tree component in "datos2" dataset
datos2$Stem=with(datos2,(stem/biomastotal)*100)
datos2$Branch=with(datos2,(Br/biomastotal)*100)
datos2$Needle=with(datos2,(needle/biomastotal)*100)
datosal2 <-datos2[,c(2,43,44,45)]
head(datosal2)

#Boxplot for light B treatment data sub set "datos2"
P_biomas<-melt(datosal2,id.vars=c("nroTree"),
               measure.vars=c("Stem","Branch","Needle"),
               variable.name="Component",value.name="Biomass")
head(P_biomas)

ggplot2.boxplot(data=P_biomas, xName='Component',yName='Biomass',ylim=c(0,100),
                addMean=TRUE, meanPointShape=23, meanPointSize=2.5,
                meanPointColor="black",backgroundColor="white",
    meanPointFill="green")

#light C treatment data sub set
datos3 <- datos[c(7,8,13,15,21,22,23,25,26,27,29,35),]

#biomass (%) in tree component in "datos3" dataset
datos3$Stem=with(datos3,(stem/biomastotal)*100)
datos3$Branch=with(datos3,(Br/biomastotal)*100)
datos3$Needle=with(datos3,(needle/biomastotal)*100)
datosal3 <-datos3[,c(2,43,44,45)]
head(datosal3)

#Boxplot for light C treatment data sub set "datos3"
P_biomas<-melt(datosal3,id.vars=c("nroTree"),
               measure.vars=c("Stem","Branch","Needle"),
               variable.name="Component",value.name="Biomass")
head(P_biomas)

ggplot2.boxplot(data=P_biomas, xName='Component',yName='Biomass',ylim=c(0,100),
                addMean=TRUE, meanPointShape=23, meanPointSize=2.5,
                meanPointColor="black",backgroundColor="white",
    meanPointFill="green")


#light B and C treatment data sub set
datos4                          <-                          datos[c(3,4,7,8,9,10,11,13,
    14,15,16,18,21,22,23,25,26,27,28,29,30,32,35,36),]

#biomass (%) in tree component in "datos4" dataset
datos4$Stem=with(datos4,(stem/biomastotal)*100)
datos4$Branch=with(datos4,(Br/biomastotal)*100)
datos4$Needle=with(datos4,(needle/biomastotal)*100)
datosal4 <-datos[,c(2,43,44,45)]
head(datosal4)

# Boxplot for light B+C treatment data sub set "datos4"
P_biomas<-melt(datosal4,id.vars=c("nroTree"),
               measure.vars=c("Stem","Branch","Needle"),
               variable.name="Component",value.name="Biomass")
head(P_biomas)

ggplot2.boxplot(data=P_biomas, xName='Component',yName='Biomass',ylim=c(0,100),
                addMean=TRUE, meanPointShape=23, meanPointSize=2.5,
                meanPointColor="black",backgroundColor="white",
    meanPointFill="green")
```

```
##############################################################################
     ###########

#loaded library
require('lattice')

#Graphical analysis of "datos" data set
plot(datos$DBH1,datos$DBH2,col="red",main="Graph of the two
     Diameters collected in the sampling",
     ylab="DBH2(cm)", xlab="DBH1(cm)",type="p")

boxplot(dbh~ht,datos, ylab = "ht (m)", xlab= "dbh(cm)")

scatter.smooth(datos$dbh, datos$ht, ylab = "ht (m)",
               xlab= "dbh (cm)", col="red")

histogram(~ht |dbh, datos)
pairs(~dbh+ht+d+HMCW,datos, main="Matrix of Scatterplots")


#Exploratory data analysis


#Install and load the required libraries
install.packages('ggplot2')
install.packages('reshape2')
install.packages('lattice')
install.packages('plyr')
require('ggplot2')
require('reshape2')
require('lattice')
require('plyr')


##Split data from "datos"
datosc <-datos[,c(2,6,39,34,35,36,37,38)]
head(datosc)
summary(datosc)


#Analysis of correlation of explanatory variables
xyplot(biomastotal~dbh,data=datosc,xlab="dbh(cm)",
       ylab="Biomass total(kg)",pch=20,cex=1,col="black")
xyplot(biomastotal~ht,data=datosc,xlab="ht(m)",
       ylab="Biomass total(kg)",pch=20,cex=1,col="black")


# Matrix of correlation of the "datosc"
datosc$nroTree =as.numeric(datosc$nroTree)


# Check data set
str(datosc)
cor(datosc)

# Matrix of scatterplots
pairs(~ht+dbh+biomastotal+stem+Br27+Br2+needle,datosc,        main="Matrix        of
     scatterplots")


##############################################################################
# Program for system fit Biomass equation by SUR method                      #
#                                                                            #
##############################################################################
```

```
######fit model for stem

# models definition
modelo01 <- stem ~ b1*dbh*ht
modelo02 <- stem ~ b1*dbh^2*ht
modelo03 <- stem ~ (b1*dbh)+ (b2*dbh^2)
modelo04 <- stem ~ (b1*dbh)+ (b2*dbh^2)+ (b3*dbh^2*ht)
modelo05 <- stem ~ (b1*dbh)+ (b2*ht)
modelo06 <- stem ~ (b1*dbh^2)+(b2*dbh^2*ht)
modelo07 <- stem ~ (b1*dbh^2)+(b2*ht)
modelo08 <- stem ~ (b1*dbh^2)+(b2*ht)+(b3*dbh^2*ht)
modelo09 <- stem ~ (b1*dbh^2)+(b2*dbh*ht)
modelo10 <- stem ~ (b1*dbh^2*ht)+(b2*dbh*ht)
modelo11 <- stem ~ (b1*dbh^b2*ht^b3)
modelo12 <- stem ~ (b1*dbh^b2)
modelo13 <- stem ~ (b1*(dbh*ht)^b2)

## Models fitting (nonlinear regresion)
## You should change start values from previous linear regression
MS.01 <- nls (modelo01, datos, start=list(b1=1))
MS.02 <- nls (modelo02, datos, start=list(b1=1))
MS.03 <- nls (modelo03, datos, start=list(b1=1, b2=1))
MS.04 <- nls (modelo04, datos, start=list(b1=1, b2=1,b3=1))
MS.05 <- nls (modelo05, datos, start=list(b1=1, b2=1))
MS.06 <- nls (modelo06, datos, start=list(b1=1, b2=1))
MS.07 <- nls (modelo07, datos, start=list(b1=1, b2=1))
MS.08 <- nls (modelo08, datos, start=list(b1=1, b2=1,b3=1))
MS.09 <- nls (modelo09, datos, start=list(b1=1, b2=1))
MS.10 <- nls (modelo10, datos, start=list(b1=0.06, b2=0.3), control=list(msMaxIter
    = 200))
MS.11   <-   nls   (modelo11,   datos,   start=list(b1=0.07,   b2=2.8,   b3=-0.84),
    control=list(msMaxIter = 200))
MS.12 <- nls (modelo12, datos, start=list(b1=0.07, b2=2.45), control=list(msMaxIter
    = 200))
MS.13    <-    nls    (modelo13,    datos,    start=list(b1=0.007,    b2=1.88    ),
    control=list(msMaxIter = 200))

## Selecting models: regarding parameter significativity
summary(MS.01)
summary(MS.02)
summary(MS.03)
summary(MS.04)
summary(MS.05)
summary(MS.06)
summary(MS.07)
summary(MS.08)
summary(MS.09)
summary(MS.10)
summary(MS.11)
summary(MS.12)
summary(MS.13)

## Selection of best model (among significatives)
## anonimous function for determining r^2, sse, res, AICs Y BICs
stats <- function(model){
    var.<-all.vars(as.formula(model))[1]
    sse<-sum(residuals(model)^2)
    set<-eval(model$call$data)
    fr2<-function(model){#funcion de r^2
        datos<-eval(model$call$data)
        datos$MS<-datos[,var.]-mean(datos[,var.])
        datos$MS2<-datos$MS^2
        SST<-sum(datos$MS2)
        1-(sse/SST)}
    rse<-summary(model)$sigma
    aic<-AIC(model)
```

```
    bic<-BIC(model)
    c(r2=fr2(model), sse=sse,rse=rse,AIC=aic,BIC=bic) }

##  parameter calculation
parameters <- rbind(stats(MS.01), stats(MS.02), stats(MS.04), stats(MS.09))
parameters


                              #######fit model for Br27

# models definition
modelo01 <- Br27 ~ b1*dbh*ht
modelo02 <- Br27 ~ b1*dbh^2*ht
modelo03 <- Br27 ~ (b1*dbh)+ (b2*dbh^2)
modelo04 <- Br27 ~ (b1*dbh)+ (b2*dbh^2)+ (b3*dbh^2*ht)
modelo05 <- Br27 ~ (b1*dbh)+ (b2*ht)
modelo06 <- Br27 ~ (b1*dbh^2)+(b2*dbh^2*ht)
modelo07 <- Br27 ~ (b1*dbh^2)+(b2*ht)
modelo08 <- Br27 ~ (b1*dbh^2)+(b2*ht)+(b3*dbh^2*ht)
modelo09 <- Br27 ~ (b1*dbh^2)+(b2*dbh*ht)
modelo10 <- Br27 ~ (b1*dbh^2*ht)+(b2*dbh*ht)
modelo11 <- Br27 ~ (b1*dbh^b2*ht^b3)
modelo12 <- Br27 ~ (b1*dbh^b2)
modelo13 <- Br27 ~ (b1*(dbh*ht)^b2)

## Models fitting (nonlinear regresion)
## You should change start values from previous linear regression
MB.01 <- nls (modelo01, datos, start=list(b1=1))
MB.02 <- nls (modelo02, datos, start=list(b1=1))
MB.03 <- nls (modelo03, datos, start=list(b1=1, b2=1))
MB.04 <- nls (modelo04, datos, start=list(b1=1, b2=1,b3=1))
MB.05 <- nls (modelo05, datos, start=list(b1=1, b2=1))
MB.06 <- nls (modelo06, datos, start=list(b1=1, b2=1))
MB.07 <- nls (modelo07, datos, start=list(b1=1, b2=1))
MB.08 <- nls (modelo08, datos, start=list(b1=1, b2=1,b3=1))
MB.09 <- nls (modelo09, datos, start=list(b1=1, b2=1))
MB.10 <- nls (modelo10, datos, start=list(b1=0.06, b2=0.3), control=list(msMaxIter
    = 200))
MB.11   <-   nls   (modelo11,   datos,   start=list(b1=0.07,   b2=2.8,   b3=-0.84),
    control=list(msMaxIter = 200))
MB.12 <- nls (modelo12, datos, start=list(b1=0.07, b2=2.45), control=list(msMaxIter
    = 200))
MB.13    <-    nls    (modelo13,    datos,    start=list(b1=0.007,    b2=1.88    ),
    control=list(msMaxIter = 200))

## Selecting models: regarding parameter significativity
summary(MB.01)
summary(MB.02)
summary(MB.03)
summary(MB.04)
summary(MB.05)
summary(MB.06)
summary(MB.07)
summary(MB.08)
summary(MB.09)
summary(MB.10)
summary(MB.11)
summary(MB.12)
summary(MB.13)

## Selection of best model (among significatives)
## anonimous function for determining r^2, sse, res, AICs Y BICs
stats <- function(model){
  var.<-all.vars(as.formula(model))[1]
  sse<-sum(residuals(model)^2)
  set<-eval(model$call$data)
```

```
  fr2<-function(model){#funcion de r^2
    datos<-eval(model$call$data)
    datos$MB<-datos[,var.]-mean(datos[,var.])
    datos$MB2<-datos$MB^2
    SST<-sum(datos$MB2)
    1-(sse/SST)}
  rse<-summary(model)$sigma
  aic<-AIC(model)
  bic<-BIC(model)
  c(r2=fr2(model), sse=sse,rse=rse,AIC=aic,BIC=bic) }

##  parameter calculation
parameters <- rbind(stats(MB.01), stats(MB.02),stats(MB.06),stats(MB.07))
parameters


                          #######fit model for Br2

# models definition
modelo01 <- Br2 ~ b1*dbh*ht
modelo02 <- Br2 ~ b1*dbh^2*ht
modelo03 <- Br2 ~ (b1*dbh)+ (b2*dbh^2)
modelo04 <- Br2 ~ (b1*dbh)+ (b2*dbh^2)+ (b3*dbh^2*ht)
modelo05 <- Br2 ~ (b1*dbh)+ (b2*ht)
modelo06 <- Br2 ~ (b1*dbh^2)+(b2*dbh^2*ht)
modelo07 <- Br2 ~ (b1*dbh^2)+(b2*ht)
modelo08 <- Br2 ~ (b1*dbh^2)+(b2*ht)+(b3*dbh^2*ht)
modelo09 <- Br2 ~ (b1*dbh^2)+(b2*dbh*ht)
modelo10 <- Br2 ~ (b1*dbh^2*ht)+(b2*dbh*ht)
modelo11 <- Br2 ~ (b1*dbh^b2*ht^b3)
modelo12 <- Br2 ~ (b1*dbh^b2)
modelo13 <- Br2 ~ (b1*(dbh*ht)^b2)

## Models fitting (nonlinear regresion)
## You should change start values from previous linear regression
Mb.01 <- nls (modelo01, datos, start=list(b1=1))
Mb.02 <- nls (modelo02, datos, start=list(b1=1))
Mb.03 <- nls (modelo03, datos, start=list(b1=1, b2=1))
Mb.04 <- nls (modelo04, datos, start=list(b1=1, b2=1,b3=1))
Mb.05 <- nls (modelo05, datos, start=list(b1=1, b2=1))
Mb.06 <- nls (modelo06, datos, start=list(b1=1, b2=1))
Mb.07 <- nls (modelo07, datos, start=list(b1=1, b2=1))
Mb.08 <- nls (modelo08, datos, start=list(b1=1, b2=1,b3=1))
Mb.09 <- nls (modelo09, datos, start=list(b1=1, b2=1))
Mb.10 <- nls (modelo10, datos, start=list(b1=0.06, b2=0.3), control=list(msMaxIter
    = 200))
Mb.11   <-   nls   (modelo11,   datos,   start=list(b1=0.07,   b2=2.8,   b3=-0.84),
    control=list(msMaxIter = 200))
Mb.12 <- nls (modelo12, datos, start=list(b1=0.07, b2=2.45), control=list(msMaxIter
    = 200))
Mb.13    <-    nls    (modelo13,    datos,    start=list(b1=0.007,    b2=1.88    ),
    control=list(msMaxIter = 200))

## Selecting models: regarding parameter significativity
summary(Mb.01)
summary(Mb.02)
summary(Mb.03)
summary(Mb.04)
summary(Mb.05)
summary(Mb.06)
summary(Mb.07)
summary(Mb.08)
summary(Mb.09)
summary(Mb.10)
summary(Mb.11)
summary(Mb.12)
```

```
summary(Mb.13)

## Selection of best model (among significatives)
## anonimous function for determining r^2, sse, res, AICs Y BICs
stats <- function(model){
  var.<-all.vars(as.formula(model))[1]
  sse<-sum(residuals(model)^2)
  set<-eval(model$call$data)
  fr2<-function(model){#funcion de r^2
    datos<-eval(model$call$data)
    datos$Mb<-datos[,var.]-mean(datos[,var.])
    datos$Mb2<-datos$Mb^2
    SST<-sum(datos$Mb2)
    1-(sse/SST)}
  rse<-summary(model)$sigma
  aic<-AIC(model)
  bic<-BIC(model)
  c(r2=fr2(model), sse=sse,rse=rse,AIC=aic,BIC=bic) }

##  parameter calculation
parameters     <-     rbind(stats(Mb.01),     stats(Mb.02),stats(Mb.04),stats(Mb.05),
     stats(Mb.12), stats(Mb.13))
parameters


                          #######fit model for Br=Br2+Br27

# models definition
modelo01 <- Br ~ b1*dbh*ht
modelo02 <- Br ~ b1*dbh^2*ht
modelo03 <- Br ~ (b1*dbh)+ (b2*dbh^2)
modelo04 <- Br ~ (b1*dbh)+ (b2*dbh^2)+ (b3*dbh^2*ht)
modelo05 <- Br ~ (b1*dbh)+ (b2*ht)
modelo06 <- Br ~ (b1*dbh^2)+(b2*dbh^2*ht)
modelo07 <- Br ~ (b1*dbh^2)+(b2*ht)
modelo08 <- Br ~ (b1*dbh^2)+(b2*ht)+(b3*dbh^2*ht)
modelo09 <- Br ~ (b1*dbh^2)+(b2*dbh*ht)
modelo10 <- Br ~ (b1*dbh^2*ht)+(b2*dbh*ht)
modelo11 <- Br ~ (b1*dbh^b2*ht^b3)
modelo12 <- Br ~ (b1*dbh^b2)
modelo13 <- Br ~ (b1*(dbh*ht)^b2)

## Models fitting (nonlinear regresion)
## You should change start values from previous linear regression
MBb.01 <- nls (modelo01, datos, start=list(b1=1))
MBb.02 <- nls (modelo02, datos, start=list(b1=1))
MBb.03 <- nls (modelo03, datos, start=list(b1=1, b2=1))
MBb.04 <- nls (modelo04, datos, start=list(b1=1, b2=1,b3=1))
MBb.05 <- nls (modelo05, datos, start=list(b1=1, b2=1))
MBb.06 <- nls (modelo06, datos, start=list(b1=1, b2=1))
MBb.07 <- nls (modelo07, datos, start=list(b1=1, b2=1))
MBb.08 <- nls (modelo08, datos, start=list(b1=1, b2=1,b3=1))
MBb.09 <- nls (modelo09, datos, start=list(b1=1, b2=1))
MBb.10 <- nls (modelo10, datos, start=list(b1=0.06, b2=0.3), control=list(msMaxIter
     = 200))
MBb.11   <-   nls   (modelo11,   datos,   start=list(b1=0.07,   b2=2.8,   b3=-0.84),
     control=list(msMaxIter = 200))
MBb.12     <-     nls     (modelo12,     datos,     start=list(b1=0.07,     b2=2.45),
     control=list(msMaxIter = 200))
MBb.13    <-    nls    (modelo13,    datos,    start=list(b1=0.007,    b2=1.88    ),
     control=list(msMaxIter = 200))

## Selecting models: regarding parameter significativity
summary(MBb.01)
summary(MBb.02)
summary(MBb.03)
```

```
summary(MBb.04)
summary(MBb.05)
summary(MBb.06)
summary(MBb.07)
summary(MBb.08)
summary(MBb.09)
summary(MBb.10)
summary(MBb.11)
summary(MBb.12)
summary(MBb.13)

## Selection of best model (among significatives)
## anonimous function for determining r^2, sse, res, AICs Y BICs
stats <- function(model){
  var.<-all.vars(as.formula(model))[1]
  sse<-sum(residuals(model)^2)
  set<-eval(model$call$data)
  fr2<-function(model){#funcion de r^2
    datos<-eval(model$call$data)
    datos$MBb<-datos[,var.]-mean(datos[,var.])
    datos$MBb2<-datos$Mb^2
    SST<-sum(datos$MBb2)
    1-(sse/SST)}
  rse<-summary(model)$sigma
  aic<-AIC(model)
  bic<-BIC(model)
  c(r2=fr2(model), sse=sse,rse=rse,AIC=aic,BIC=bic) }

##  parameter calculation
parameters                                                                    <-
    rbind(stats(MBb.01),stats(MBb.02),stats(MBb.05),stats(MBb.06),stats(MBb.07),sta
    ts(MBb.09), stats(MBb.10))
parameters


                                ########fit model for needle

# models definition
modelo01 <- needle ~ b1*dbh*ht
modelo02 <- needle ~ b1*dbh^2*ht
modelo03 <- needle ~ (b1*dbh)+ (b2*dbh^2)
modelo04 <- needle ~ (b1*dbh)+ (b2*dbh^2)+ (b3*dbh^2*ht)
modelo05 <- needle ~ (b1*dbh)+ (b2*ht)
modelo06 <- needle ~ (b1*dbh^2)+(b2*dbh^2*ht)
modelo07 <- needle ~ (b1*dbh^2)+(b2*ht)
modelo08 <- needle ~ (b1*dbh^2)+(b2*ht)+(b3*dbh^2*ht)
modelo09 <- needle ~ (b1*dbh^2)+(b2*dbh*ht)
modelo10 <- needle ~ (b1*dbh^2*ht)+(b2*dbh*ht)
modelo11 <- needle ~ (b1*dbh^b2*ht^b3)
modelo12 <- needle ~ (b1*dbh^b2)
modelo13 <- needle ~ (b1*(dbh*ht)^b2)

## Models fitting (nonlinear regresion)
## You should change start values from previous linear regression
MN.01 <- nls (modelo01, datos, start=list(b1=1))
MN.02 <- nls (modelo02, datos, start=list(b1=1))
MN.03 <- nls (modelo03, datos, start=list(b1=1, b2=1))
MN.04 <- nls (modelo04, datos, start=list(b1=1, b2=1,b3=1))
MN.05 <- nls (modelo05, datos, start=list(b1=1, b2=1))
MN.06 <- nls (modelo06, datos, start=list(b1=1, b2=1))
MN.07 <- nls (modelo07, datos, start=list(b1=1, b2=1))
MN.08 <- nls (modelo08, datos, start=list(b1=1, b2=1,b3=1))
MN.09 <- nls (modelo09, datos, start=list(b1=1, b2=1))
MN.10 <- nls (modelo10, datos, start=list(b1=0.06, b2=0.3), control=list(msMaxIter
    = 200))
MN.11   <-   nls   (modelo11,   datos,   start=list(b1=0.07,   b2=2.8,   b3=-0.84),
```

```
    control=list(msMaxIter = 200))
MN.12 <- nls (modelo12, datos, start=list(b1=0.07, b2=2.45), control=list(msMaxIter
    = 200))
MN.13    <-    nls    (modelo13,    datos,    start=list(b1=0.007,    b2=1.88    ),
    control=list(msMaxIter = 200))

## Selecting models: regarding parameter significativity
summary(MN.01)
summary(MN.02)
summary(MN.03)
summary(MN.04)
summary(MN.05)
summary(MN.06)
summary(MN.07)
summary(MN.08)
summary(MN.09)
summary(MN.10)
summary(MN.11)
summary(MN.12)
summary(MN.13)

## Selection of best model (among significatives)
## anonimous function for determining r^2, sse, res, AICs Y BICs
stats <- function(model){
  var.<-all.vars(as.formula(model))[1]
  sse<-sum(residuals(model)^2)
  set<-eval(model$call$data)
  fr2<-function(model){#funcion de r^2
    datos<-eval(model$call$data)
    datos$MN<-datos[,var.]-mean(datos[,var.])
    datos$MN2<-datos$MN^2
    SST<-sum(datos$MN2)
    1-(sse/SST)}
  rse<-summary(model)$sigma
  aic<-AIC(model)
  bic<-BIC(model)
  c(r2=fr2(model), sse=sse,rse=rse,AIC=aic,BIC=bic) }

##  parameter calculation
parameters   <-   rbind(stats(MN.01),   stats(MN.02),   stats(MN.06),   stats(MN.09),
    stats(MN.10), stats(MN.12),stats(MN.13))
parameters


                                ########fit model for BrN=Br2+needle

# models definition
modelo01 <- BrN ~ b1*dbh*ht
modelo02 <- BrN ~ b1*dbh^2*ht
modelo03 <- BrN ~ (b1*dbh)+ (b2*dbh^2)
modelo04 <- BrN ~ (b1*dbh)+ (b2*dbh^2)+ (b3*dbh^2*ht)
modelo05 <- BrN ~ (b1*dbh)+ (b2*ht)
modelo06 <- BrN ~ (b1*dbh^2)+(b2*dbh^2*ht)
modelo07 <- BrN ~ (b1*dbh^2)+(b2*ht)
modelo08 <- BrN ~ (b1*dbh^2)+(b2*ht)+(b3*dbh^2*ht)
modelo09 <- BrN ~ (b1*dbh^2)+(b2*dbh*ht)
modelo10 <- BrN ~ (b1*dbh^2*ht)+(b2*dbh*ht)
modelo11 <- BrN ~ (b1*dbh^b2*ht^b3)
modelo12 <- BrN ~ (b1*dbh^b2)
modelo13 <- BrN ~ (b1*(dbh*ht)^b2)

## Models fitting (nonlinear regresion)
## You should change start values from previous linear regression
MBN.01 <- nls (modelo01, datos, start=list(b1=1))
MBN.02 <- nls (modelo02, datos, start=list(b1=1))
MBN.03 <- nls (modelo03, datos, start=list(b1=1, b2=1))
```

```
MBN.04 <- nls (modelo04, datos, start=list(b1=1, b2=1,b3=1))
MBN.05 <- nls (modelo05, datos, start=list(b1=1, b2=1))
MBN.06 <- nls (modelo06, datos, start=list(b1=1, b2=1))
MBN.07 <- nls (modelo07, datos, start=list(b1=1, b2=1))
MBN.08 <- nls (modelo08, datos, start=list(b1=1, b2=1,b3=1))
MBN.09 <- nls (modelo09, datos, start=list(b1=1, b2=1))
MBN.10 <- nls (modelo10, datos, start=list(b1=0.06, b2=0.3), control=list(msMaxIter
    = 200))
MBN.11   <-   nls   (modelo11,   datos,   start=list(b1=0.07,   b2=2.8,   b3=-0.84),
    control=list(msMaxIter = 200))
MBN.12    <-    nls    (modelo12,    datos,    start=list(b1=0.07,    b2=2.45),
    control=list(msMaxIter = 200))
MBN.13    <-    nls    (modelo13,    datos,    start=list(b1=0.007,    b2=1.88    ),
    control=list(msMaxIter = 200))

## Selecting models: regarding parameter significativity
summary(MBN.01)
summary(MBN.02)
summary(MBN.03)
summary(MBN.04)
summary(MBN.05)
summary(MBN.06)
summary(MBN.07)
summary(MBN.08)
summary(MBN.09)
summary(MBN.10)
summary(MBN.11)
summary(MBN.12)
summary(MBN.13)

## Selection of best model (among significatives)
## anonimous function for determining r^2, sse, res, AICs Y BICs
stats <- function(model){
  var.<-all.vars(as.formula(model))[1]
  sse<-sum(residuals(model)^2)
  set<-eval(model$call$data)
  fr2<-function(model){#funcion de r^2
    datos<-eval(model$call$data)
    datos$MBN<-datos[,var.]-mean(datos[,var.])
    datos$MBN2<-datos$MBN^2
    SST<-sum(datos$MBN2)
    1-(sse/SST)}
  rse<-summary(model)$sigma
  aic<-AIC(model)
  bic<-BIC(model)
  c(r2=fr2(model), sse=sse,rse=rse,AIC=aic,BIC=bic) }

##  parameter calculation
parameters   <-   rbind(stats(MBN.01),   stats(MBN.02),   stats(MBN.04),stats(MBN.05),
    stats(MBN.12),stats(MBN.13))
parameters


#Selected best biomass component equation
summary(MS.09)
summary(MBb.06)
summary(MN.02)


####Simultaneus fitting equations at SUR

##Model definition for each fraction
MS <- stem ~ (b1*dbh^2)+(b2*dbh*ht)
MBb <- Br ~ (b3*dbh^2)+(b4*dbh^2*ht)
MN <- needle ~ b5*dbh^2*ht
```

```
## additive model for total biomass
MBT <- biomastotal ~ ((b1*dbh^2)+(b2*dbh*ht)+(b3*dbh^2)+(b4*dbh^2*ht)+b5*dbh^2*ht)

##Simultaneus fitting
labels        <- list("Stem","Br","Needle","Biomastotal") # label for each model
start.values  <- c(b1=-0.14772 ,b2=0.46673,b3=-0.058035 ,b4=0.026637 ,b5=0.0174218)
system.biomas <- list(MS,MBb, MN, MBT) # sistema de ecuaciones - modelos

modelBIOM   <-   nlsystemfit("SUR",   system.biomas,   start.values,   data=datos,
     eqnlabels=labels)

## nlsystemfit= non-linear equation system
## SUR = method, system.biomas = equations system, coeff values,
## information from fitted model
## Summary

print(modelBIOM)
head(datos)

## fitted equation [[x]]
modelBIOM$eq[[1]]

## coeficients
modelBIOM$b

##Standard Error
modelBIOM$se

##  p-values
modelBIOM$p

## R2 of the adjusted models
sapply(modelBIOM$eq, function(x){(x)$adjr2}) #adjr2


## extract fitted and residuals from SUR model
fit_SUR <- data.frame(sapply(modelBIOM$eq,function(x){(x)$predicted}))
names(fit_SUR) <- c('fit_MS', 'fit_MBb','fit_N','fit_BT')
res_SUR <- data.frame(sapply(modelBIOM$eq,function(x){(x)$res}))
names(res_SUR) <- c('res_MS','res_MBb','res_N','res_BT')
X <- seq(1:36)
SUR_R <- cbind(X,fit_SUR,res_SUR)


#Check data set
View(SUR_R)
summary(SUR_R)


# Merge two data set
datos<- merge(datos, SUR_R, by="X")
head(datos)


# Compute mean bias of component biomass
datos$stembias=with(datos,((100/36)*(stem-fit_MS)/stem))
mean(datos$stembias)
datos$Brbias=with(datos,((100/36)*(Br-fit_MBb)/Br))
mean(datos$Brbias)
datos$needlebias=with(datos,((100/36)*(needle-fit_N)/needle))
mean(datos$needlebias)
datos$totalbias=with(datos,((100/36)*(fit_BT)/biomastotal))
mean(datos$totalbias)


# Compute mean RMSE of component biomass
```

```
datos$stemrmse<-with(datos,sqrt((stem-fit_MS)^2)/36)
sum(datos$stemrmse)
datos$Brrmse<-with(datos,sqrt((Br-fit_MBb)^2)/36)
sum(datos$Brrmse)
datos$needlermse<-with(datos,sqrt((needle-fit_N)^2)/36)
sum(datos$needlermse)
datos$totalrmse<-with(datos,(stemrmse+Brrmse+needlermse))
sum(datos$totalrmse)

#save data
save(datos, file="datos.RData")
load("datos.RData")
save.image("datos.RData")

str(datos)


##Graph-1

par(mfrow=c(2, 2))

#loaded library for graph
library(car)


## to visualized residual versus observed biomass
scatterplot(datos$stem~datos$res_MS,col="Black",main="Stem Biomass",
     ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos$Br~datos$res_MBb,col="Black",main="Branch Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos$needle~datos$res_N,col="Black",main="Needle Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos$biomastotal~datos$res_BT,col="Black",main="Total Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")


##Graph-2
## to visualized RMSE versus dbh class

plot(datos$dbh,datos$stemrmse,ylim=c(-2,2),col=c("blue"),main="Stem Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos$dbh,datos$Brrmse,ylim=c(-2,2),col=c("blue"),main="Branch Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos$dbh,datos$needlermse,ylim=c(-2,2),col=c("blue"),main="Needle Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos$dbh,datos$totalrmse,ylim=c(-2,2),col=c("blue"),main="Total Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")


##Graph-3
## to visualized Bias(%) versus dbh class

plot(datos$dbh,datos$stembias,ylim=c(-20,20),col=c("green"),main="Stem Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos$dbh,datos$Brbias,),ylim=c(-20,20),col=c("green"),main="Branch Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos$dbh,datos$needlebias,ylim=c(-20,20),col=c("green"),          main="Needle
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos$dbh,datos$totalbias,ylim=c(-20,20),col=c("green"),main="Total Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
```

```
##############Treatment A-SUR###########################################

###split treatment A data from "datos"


datos1 <- datos[c(1,2,5,6,12,17,19,20,24,31,33,34),]


##Simultaneus fitting

modelBIOM1   <-   nlsystemfit("SUR",   system.biomas,   start.values,   data=datos1,
     eqnlabels=labels)

## nlsystemfit= non-linear equation system
## SUR = method, system.biomas = equations system, coeff values,
## information from fitted model
## Summary
print(modelBIOM1)

## fitted equation [[x]]
modelBIOM1$eq[[4]]


## coeficients
modelBIOM1$b

##Standard Error
modelBIOM1$se

##  p-values
modelBIOM1$p

## R2 of the adjusted models
sapply(modelBIOM1$eq, function(x){(x)$adjr2}) #adjr2


## extract fitted and residuals from SUR model
fit_SUR <- data.frame(sapply(modelBIOM1$eq,function(x){(x)$predicted}))
names(fit_SUR) <- c('fit_MS', 'fit_MBb','fit_N','fit_BT')
res_SUR <- data.frame(sapply(modelBIOM1$eq,function(x){(x)$res}))
names(res_SUR) <- c('res_MS','res_MBb','res_N','res_BT')
X <- c(1,2,5,6,12,17,19,20,24,31,33,34)
SUR_R <- cbind(X,fit_SUR,res_SUR)

# Merge two data set
datos1<- merge(datos1, SUR_R, by="X")


# Check data set
View(SUR_R)
head(datos1)


# Compute mean bias of component biomass
datos1$stembias=with(datos1,((100/12)*(stem-fit_MS)/stem))
mean(datos1$stembias)
datos1$Brbias=with(datos1,((100/12)*(Br-fit_MBb)/Br))
mean(datos1$Brbias)
datos1$needlebias=with(datos1,((100/12)*(needle-fit_N)/needle))
mean(datos1$needlebias)
datos1$biomastotalbias=with(datos1,((100/12)*(fit_BT)/biomastotal))
mean(datos1$biomastotalbias)

head(res_SUR)
summary(SUR_R)
```

```
# Compute mean RMSE of component biomass
datos1$stemrmse<-with(datos1,sqrt((stem-fit_MS)^2)/12)
sum(datos1$stemrmse)
datos1$Brrmse<-with(datos1,sqrt((Br-fit_MBb)^2)/12)
sum(datos1$Brrmse)
datos1$needlermse<-with(datos1,sqrt((needle-fit_N)^2)/12)
sum(datos1$needlermse)
datos1$totalrmse<-with(datos1,(stemrmse+Brrmse+needlermse))
sum(datos1$totalrmse)


# save data
save(datos1, file="datos1.RData")
str(datos1)
load("datos1.RData")
save.image("datos1.RData")

##Graph-1
par(mfrow=c(2, 2))
library(car)


 ## to visulized residual versus observed biomass
scatterplot(datos1$stem~datos1$res_MS,col="Black",main="Stem Biomass",
     ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos1$Br~datos1$res_MBb,col="Black",main="Branch Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos1$needle~datos1$res_N,col="Black",main="Needle Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos1$biomastotal~datos1$res_BT,col="Black",main="Total Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")


##Graph-2
## to visulized RMSE versus dbh class

plot(datos1$dbh,datos1$stemrmse,ylim=c(-2,2),col=c("blue"),main="Stem Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos1$dbh,datos1$Brrmse,ylim=c(-2,2),col=c("blue"),main="Branch Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos1$dbh,datos1$needlermse,ylim=c(-2,2),col=c("blue"),main="Needle Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos1$dbh,datos1$totalrmse,ylim=c(-2,2),col=c("blue"),main="Total Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")

##Graph-3
## to visulized Bias(%) versus dbh class

plot(datos1$dbh,datos1$stembias,ylim=c(-20,20),col=c("green"),main="Stem Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos1$dbh,datos1$Brbias,ylim=c(-20,20),col=c("green"),main="Branch Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos1$dbh,datos1$needlebias,ylim=c(-20,20),col=c("green"),main="Needle
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos1$dbh,datos1$totalbias,ylim=c(-
    20,20),col=c("red","green","blue"),main="Total Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
```

```
################################Treatment B- SUR#####################################

#light B treatment data sub set
datos2 <- datos[c(3,9,4,10,11,14,16,18,28,30,32,36),]


##Simultaneus fitting
modelBIOM2   <-   nlsystemfit("SUR",   system.biomas,   start.values,   data=datos2,
     eqnlabels=labels)

## nlsystemfit= non-linear equation system
## SUR = method, system.biomas = equations system, coeff values,
## information from fitted model
## Summary
print(modelBIOM2)

## fitted equation [[x]]
modelBIOM2$eq[[4]]

## coeficients
modelBIOM2$b
##Standard Error
modelBIOM2$se

##  p-values
modelBIOM2$p

## R2 of the adjusted models
sapply(modelBIOM2$eq, function(x){(x)$adjr2}) #adjr2

## extract fitted and residuals from SUR model
fit_SUR <- data.frame(sapply(modelBIOM2$eq,function(x){(x)$predicted}))
names(fit_SUR) <- c('fit_MS', 'fit_MBb','fit_N','fit_BT')
res_SUR <- data.frame(sapply(modelBIOM2$eq,function(x){(x)$res}))
names(res_SUR) <- c('res_MS','res_MBb','res_N','res_BT')
X <- c(3,9,4,10,11,14,16,18,28,30,32,36)
SUR_R <- cbind(X,fit_SUR,res_SUR)

# merge two data set
datos2<- merge(datos2, SUR_R, by="X")
head(datos2)

# Compute mean bias of component biomass
datos2$stembias=with(datos2,((100/12)*(stem-fit_MS)/stem))
mean(datos2$stembias)
datos2$Brbias=with(datos2,((100/12)*(Br-fit_MBb)/Br))
mean(datos2$Brbias)
datos2$needlebias=with(datos2,((100/12)*(needle-fit_N)/needle))
mean(datos2$needlebias)
datos2$biomastotalbias=with(datos2,((100/12)*(fit_BT)/biomastotal))
mean(datos2$biomastotalbias)


# Compute mean RMSE of component biomass
datos2$stemrmse<-with(datos2,sqrt((stem-fit_MS)^2)/12)
sum(datos2$stemrmse)
datos2$Brrmse<-with(datos2,sqrt((Br-fit_MBb)^2)/12)
sum(datos2$Brrmse)
datos2$needlermse<-with(datos2,sqrt((needle-fit_N)^2)/12)
sum(datos2$needlermse)
datos2$totalrmse<-with(datos2,(stemrmse+Brrmse+needlermse))
sum(datos2$totalrmse)

## save data
save(datos2, file="datos2.RData")
load("datos2.RData")
```

```
save.image("datos2.RData")
str(datos2)


##Graph-1
par(mfrow=c(2, 2))
library(car)


 ## to visulized residual versus observed biomass
scatterplot(datos2$stem~datos2$res_MS,col="Black",main="Stem Biomass",
     ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos2$Br~datos2$res_MBb,col="Black",main="Branch Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos2$needle~datos2$res_N,col="Black",main="Needle Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos2$biomastotal~datos2$res_BT,col="Black",main="Total Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")


##Graph-2
## to visulized RMSE versus dbh class

plot(datos2$dbh,datos2$stemrmse,ylim=c(-2,2),col=c("blue"),main="Stem Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos2$dbh,datos2$Brrmse,ylim=c(-2,2),col=c("blue"),main="Branch Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos2$dbh,datos2$needlermse,ylim=c(-2,2),col=c("blue"),main="Needle Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos2$dbh,datos2$totalrmse,ylim=c(-2,2),col=c("blue"),main="Total Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")


##Graph-3
## to visulized Bias(%) versus dbh class

plot(datos2$dbh,datos2$stembias,,ylim=c(-20,20),col=c("green"),main="Stem Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos2$dbh,datos2$Brbias,ylim=c(-20,20),col=c("green"),main="Branch Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos2$dbh,datos2$needlebias,ylim=c(-20,20),col=c("green"),main="Needle
     Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos2$dbh,datos2$totalbias,ylim=c(-20,20),col=c("green"),main="Total
     Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")


 ##############################Treatment-C-SUR)###################################


 #light C treatment data sub set
datos3 <- datos[c(7,8,13,15,21,22,23,25,26,27,29,35),]


##Simultaneus fitting
modelBIOM3   <-   nlsystemfit("SUR",   system.biomas,   start.values,   data=datos3,
     eqnlabels=labels)

## nlsystemfit= non-linear equation system
## SUR = method, system.biomas = equations system, coeff values,
## information from fitted model
## Summary
print(modelBIOM3)

## fitted equation [[x]]
```

```
modelBIOM3$eq[[4]]

## coeficients
modelBIOM3$b

##Standard Error
modelBIOM3$se

##  p-values
modelBIOM3$p

## R2 of the adjusted models
sapply(modelBIOM3$eq, function(x){(x)$adjr2}) #adjr2

## extract fitted and residuals from SUR model
fit_SUR <- data.frame(sapply(modelBIOM3$eq,function(x){(x)$predicted}))
names(fit_SUR) <- c('fit_MS', 'fit_MBb','fit_N','fit_BT')
res_SUR <- data.frame(sapply(modelBIOM3$eq,function(x){(x)$res}))
names(res_SUR) <- c('res_MS','res_MBb','res_N','res_BT')
X <- c(7,8,13,15,21,22,23,25,26,27,29,35)
SUR_R <- cbind(X,fit_SUR,res_SUR)


# Merge two data set
datos3<- merge(datos3, SUR_R, by="X")

head(datos3)

# Compute mean bias of component biomass
datos3$stembias=with(datos3,((100/12)*(stem-fit_MS)/stem))
mean(datos3$stembias)
datos3$Brbias=with(datos3,((100/12)*(Br-fit_MBb)/Br))
mean(datos3$Brbias)
datos3$needlebias=with(datos3,((100/12)*(needle-fit_N)/needle))
mean(datos3$needlebias)
datos3$biomastotalbias=with(datos3,((100/12)*(fit_BT)/biomastotal))
mean(datos3$biomastotalbias)


#Check data set
View(SUR_R)
View(datos3)
head(res_SUR)
summary(SUR_R)


# Compute mean RMSE of component biomass
datos3$stemrmse<-with(datos3,sqrt((stem-fit_MS)^2)/12)
sum(datos3$stemrmse)
datos3$Brrmse<-with(datos3,sqrt((Br-fit_MBb)^2)/12)
sum(datos3$Brrmse)
datos3$needlermse<-with(datos3,sqrt((needle-fit_N)^2)/12)
sum(datos3$needlermse)
datos3$totalrmse<-with(datos3,(stemrmse+Brrmse+needlermse))
sum(datos3$totalrmse)

#save data
save(datos3, file="datos3.RData")

load("datos3.RData")

str(datos3)
save.image("datos3.RData")

#Graph-1
par(mfrow=c(1, 3))
```

```
#loaded library for graph
library(car)

##to visualized residual versus observed biomass
scatterplot(datos3$stem~datos3$res_MS,col="Black",main="Stem Biomass",
     ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos3$Br~datos3$res_MBb,col="Black",main="Branch Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos3$needle~datos3$res_N,col="Black",main="Needle Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos3$biomastotal~datos3$res_BT,col="Black",main="Total Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")


##Graph-2
## to visualized RMSE versus dbh class

plot(datos3$dbh,datos3$stemrmse,ylim=c(-2,2),col=c("blue"),main="Stem Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos3$dbh,datos3$Brrmse,ylim=c(-2,2),col=c("blue"),main="Branch Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos3$dbh,datos3$needlermse,ylim=c(-2,2),col=c("blue"),main="Needle Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos3$dbh,datos3$totalrmse,ylim=c(-2,2),col=c("blue"),main="Total Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")

##Graph-3

## to visualized Bias(%) versus dbh class

plot(datos3$dbh,datos3$stembias,ylim=c(-20,20),col=c("green"),main="Stem Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos3$dbh,datos3$Brbias,ylim=c(-20,20),col=c("green"),main="Branch Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos3$dbh,datos3$needlebias,ylim=c(-20,20),col=c("green"),main="Needle
     Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos3$dbh,datos3$   biomastotalbias,ylim=c(-20,20),col=c("green"),main="Total
     Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")



###################Treatment B and C-SUR#################################


#light B and C treatment data sub set
datos4                          <-                          datos[c(3,4,7,8,9,10,11,13,
     14,15,16,18,21,22,23,25,26,27,28,29,30,32,35,36),]

###Simultaneus fitting
modelBIOM4   <-   nlsystemfit("SUR",   system.biomas,   start.values,   data=datos4,
     eqnlabels=labels)

## nlsystemfit= non-linear equation system
## SUR = method, system.biomas = equations system, coeff values,
## information from fitted model
## Resumen
print(modelBIOM1)

## fitted equation [[x]]
modelBIOM4$eq[[4]]

## coeficients
modelBIOM4$b
```

```
##Standard Error
modelBIOM4$se

##  p-values
modelBIOM4$p

##  p-values
modelBIOM4$rmse

## R2 of the adjusted models
sapply(modelBIOM4$eq, function(x){(x)$adjr2}) #adjr2

## extract fitted and residuals from SUR model
fit_SUR <- data.frame(sapply(modelBIOM4$eq,function(x){(x)$predicted}))
names(fit_SUR) <- c('fit_MS', 'fit_MBb','fit_N','fit_BT')
res_SUR <- data.frame(sapply(modelBIOM4$eq,function(x){(x)$res}))
names(res_SUR) <- c('res_MS','res_MBb','res_N','res_BT')
X <- c(3,4,7,8,9,10,11,13, 14,15,16,18,21,22,23,25,26,27,28,29,30,32,35,36)
SUR_R <- cbind(X,fit_SUR,res_SUR)


##Merge two dataset
datos4<- merge(datos4, SUR_R, by="X")


# Compute mean bias of component biomass
datos4$stembias=with(datos4,((100/24)*(stem-fit_MS)/stem))
mean(datos4$stembias)
datos4$Brbias=with(datos4,((100/24)*(Br-fit_MBb)/Br))
mean(datos4$Brbias)
datos4$needlebias=with(datos4,((100/24)*(needle-fit_N)/needle))
mean(datos4$needlebias)

datos4$biomastotalbias=with(datos4,((100/24)*(fit_BT)/biomastotal))
mean(datos4$biomastotalbias)


# Compute mean RMSE of component biomass
datos4$stemrmse<-with(datos4,sqrt((stem-fit_MS)^2)/12)
sum(datos4$stemrmse)
datos4$Brrmse<-with(datos4,sqrt((Br-fit_MBb)^2)/12)
sum(datos4$Brrmse)
datos4$needlermse<-with(datos4,sqrt((needle-fit_N)^2)/12)
sum(datos4$needlermse)
datos4$totalrmse<-with(datos4,(stemrmse+Brrmse+needlermse))
sum(datos4$totalrmse)

#save data
save(datos4, file="datos4.RData")
load("datos4.RData")
str(datos4)
save.image("datos4.RData")

#Check data set
View(datos4)
head(datos4)
view(SUR_R)
head(res_SUR)
summary(SUR_R)

#Graph-1
par(mfrow=c(1, 3))

# loaded library for graph
library(car)
```

```
## to visualized residual versus observed biomass
scatterplot(datos4$stem~datos4$res_MS,col="Black",main="Stem Biomass",
     ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos4$Br~datos4$res_MBb,col="Black",main="Branch Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos4$needle~datos4$res_N,col="Black",main="Needle Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datos4$biomastotal~datos4$res_BT,col="Black",main="Total Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")



##Graph-2
## to visualized RMSE versus dbh class

plot(datos4$dbh,datos4$stemrmse,ylim=c(-2,2),col=c("blue"),main="Stem Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos4$dbh,datos4$Brrmse,ylim=c(-2,2),col=c("blue"),main="Branch Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos4$dbh,datos4$needlermse,ylim=c(-2,2),col=c("blue"),main="Needle Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datos4$dbh,datos4$totalrmse,ylim=c(-2,2),col=c("blue"),main="Total Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")


##Graph-3
## to visualized Bias(%) versus dbh class

plot(datos4$dbh,datos4$stembias,ylim=c(-20,20),col=c("green"),main="Stem Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos4$dbh,datos4$Brbias,ylim=c(-20,20),col=c("green"),main="Branch Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos4$dbh,datos4$needlebias,ylim=c(-20,20),col=c("green"),main="Needle
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datos4$dbh,datos4$biomastotalbias,ylim=c(-20,20),col=c("green"),main="Total
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")

###################################end for SUR #######



#############################################################################
#                                                                           #
#  Dirichelet regression modelling program for estimate biomass proportion  #
#############################################################################


#Clean behind run history
rm(list=ls())

#Loaded working directory
setwd("C:/cuellar")

# Read data
datosd<-read.csv("C:/cuellar/Cuellar_biomas.csv")


#variable introduce by "kg" (unit) from "gram"
datosd$biomastotal=with(datosd,TTB/1000)
datosd$stem=with(datosd,TDSt/1000)
datosd$Br27=with(datosd,TDBr27/1000)
datosd$Br2=with(datosd,TDBr2/1000)
datosd$needle=with(datosd,TDN/1000
```

```
#variables introduce by dbh from DBH1
datosd$dbh=with(datosd,(DBH1+DBH2)/2)
datosd$d=with(datosd,(diameter1+diameter2)/2)
datosd$Br=with(datosd,(Br2+Br27))
datosd$BrN=with(datosd,(Br2+needle))


##loaded library
packs<-c('Formula', 'rgl', 'DirichletReg')
sapply(packs,require,character.only=TRUE)


#introduce mean of biomass(dependent) variable by biomasstotal (to calculate
    precision parameter)
datosd$stemp=with(datosd,(stem/biomastotal))
datosd$Brp=with(datosd,(Br/biomastotal))
datosd$Br27p=with(datosd,(Br27/biomastotal))
datosd$Br2p=with(datosd,(Br2/biomastotal))
datosd$needlep=with(datosd,(needle/biomastotal))
head(datosd)


## Split data for using in Dirichilet regression
datosal <-datosd[,c(6,39,34,35,36,37,38,41,43,44,47,45,46)]
head(datosal)

# Make format data for Dirichilet's Regression
# Assumes that your components are in column 9 - 11
biomastotalp<-DR_data(datosal[, 9:11], trafo = TRUE)


#null model
model<- DirichReg(biomastotalp ~ 1, datosal)
coef(model)
summary(model)

#Different combination between dbd and ht for fitting model "common"
model1 <- DirichReg(biomastotalp ~ dbh, datosal)
coef(model1)
summary(model1)

model2 <- DirichReg(biomastotalp ~ dbh+((dbh)^2), datosal)
coef(model2)
summary(model2)
model3 <- DirichReg(biomastotalp ~ dbh+I((dbh)^2), datosal)
coef(model3)
summary(model3)

model4 <- DirichReg(biomastotalp ~ ((dbh)^2), datosal)
coef(model4)
summary(model4)

model5 <- DirichReg(biomastotalp ~ ((dbh)^2)+I((dbh)^2), datosal)
coef(model5)
summary(model5)

model6 <- DirichReg(biomastotalp ~ ht, datosal)
coef(model6)
summary(model6)

model7 <- DirichReg(biomastotalp ~ ht+I((ht)^2), datosal)
coef(model7)
summary(model7)

model8 <- DirichReg(biomastotalp ~ dbh+ht, datosal)
```

```
coef(model8)
summary(model8)

model9 <- DirichReg(biomastotalp ~ dbh*ht, datosal)
summary(model9)

model10 <- DirichReg(biomastotalp ~ dbh^2*ht, datosal)
summary(model10)


# fit quadratic Dirichlet regression models ("common")
model11 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2), data = datosal)
summary(model11)

model12 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2)+I((dbh+ht)^2), data =
    datosal)
summary(model12)

model13 <- DirichReg(biomastotalp ~ dbh^2*ht + I((dbh^2*ht)), data = datosal)
summary(model13)

model14 <- DirichReg(biomastotalp ~ dbh*ht + I((dbh*ht)^2), data = datosal)
coef(model3)
summary(model14)


# fit a Dirichlet regression with quadratic predictor for the mean and
# a linear predictor for precision ("alternative")

model15 <- DirichReg(biomastotalp ~ dbh+ht, datosal, model = "alternative",base =
    2)
summary(model15)

model16<- DirichReg(biomastotalp ~ dbh*ht, datosal, model = "alternative",base = 2)
summary(model16)

model17 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2), data = datosal,model =
    "alternative", base = 2)
summary(model17)

model18 <- DirichReg(biomastotalp ~ dbh*ht + I((dbh*ht)^2), data = datosal,model =
    "alternative", base = 2)
summary(model18)

model19<- DirichReg(biomastotalp ~ dbh*ht|dbh+ht, datosal, model =
    "alternative",base = 2)
summary(model19)

anova(model1,model2, model3, model4,model5,model6, model7,model8, model9,
    model10,model11, model12,model13,
      model14, model15, model16,model17,model18,model19)


## information from fitted model
## Summary
fitted(model14)

predict(model14, newdata = data.frame("dbh*ht" = seq(10, 100, 1000)))

residuals(model14, type = c("standardized"))

head(predict(model14))

confint(model14)
confint(model14, exp = TRUE)
```

```
logLik(model14)
round(vcov(model4), 5)


#Compute predicted(fitted) percentages of component biomas
datosal$stempp <- (fitted(model14)[,"stemp"])
datosal$Brpp <- (fitted(model14)[,"Brp"])
datosal$needlepp <- (fitted(model14)[,"needlep"])


#Compute predicted(fitted) of component biomas
datosal$pstem<-with(datosal,(stempp*stem))
datosal$pBr<-with(datosal,(Brpp*Br))
datosal$pneedle<-with(datosal,(needlepp*needle))
datosal$pbiomastotal<-with(datosal,(pstem+pBr+pneedle))


#Compute mean bias of component biomass
datosal$stembias=with(datosal,((100/36)*(stem-pstem)/stem))
mean(datosal$stembias)
datosal$Brbias=with(datosal,((100/36)*(Br-pBr)/Br))
mean(datosal$Brbias)
datosal$needlebias=with(datosal,((100/36)*(needle-pneedle)/needle))
mean(datosal$needlebias)
datosal$totalbias<-with(datosal,(stembias+Brbias+needlebias))
mean(datosal$totalbias)


#Compute mean RMSE of component biomass
datosal$stemrmse<-with(datosal,sqrt((stem-pstem)^2)/36)
sum(datosal$stemrmse)
datosal$Brrmse<-with(datosal,sqrt((Br-pBr)^2)/36)
sum(datosal$Brrmse)
datosal$needlermse<-with(datosal,sqrt((needle-pneedle)^2)/36)
sum(datosal$needlermse)
datosal$totalrmse<-with(datosal,(stemrmse+Brrmse+needlermse))
sum(datosal$totalrmse)


#Compute residual of component biomass
datosal$rstem<-with(datosal,(stem-pstem))
datosal$rBr<-with(datosal,(Br-pBr))
datosal$rneedle<-with(datosal,(needle-pneedle))
datosal$rbiomastotal<-with(datosal,(biomastotal-pbiomastotal))


#save data
save(datosal, file="datosal.RData")
save.image("datosal.RData")
str (datosal)
###Graph-1

par(mfrow=c(1, 4))

#Loaded library for graph
library(car)


## to visualized observed versus residual values
scatterplot(datosal$stem~datosal$rstem,col="Black",main="Stem Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal$Br~datosal$rBr,col="Black",main="Branch Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal$needle~datosal$rneedle,col="Black",main="Needle Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal$biomastotal~datosal$rbiomastotal,col="Black",main="Total
```

```
    Biomass",
           ylab="Residual (kg)", xlab="Observation (kg)")


##Graph-2


## to visualized RMSE versus dbh class
library(lattice)

plot(datosal$dbh,datosal$stemrmse,ylim=c(-2,2),col=c("blue"), main="Stem Biomass",
           ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal$dbh,datosal$Brrmse,ylim=c(-2,2),col=c("blue"), main="Branch Biomass",
           ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal$dbh,datosal$needlermse,ylim=c(-2,2),col=c("blue"),        main="Needle
    Biomass",
           ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal$dbh,datosal$totalrmse,ylim=c(-2,2),col=c("blue"),          main="Total
    Biomass",
           ylab="RMSE(kg)", xlab="Diameter(cm)")

##Graph-3


## to visualizedlized Bias(%) versus dbh class

plot(datosal$dbh,datosal$stembias,ylim=c(-20,20),col=c("green"),main="Stem
    Biomass",
           ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal$dbh,datosal$Brbias,ylim=c(-20,20),col=c("green"),main="Branch
    Biomass",
           ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal$dbh,datosal$needlebias,ylim=c(-20,20),col=c("green"),main="Needle
    Biomass",
           ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal$dbh,datosal$totalbias,ylim=c(-20,20),col=c("green"),main="Total
    Biomass",
           ylab="Bias(%)", xlab="Diameter(cm)")

head(datosal)


###################Treatment A-Dirichelet regression modelling####################

#light A treatment data sub set
##Split data for using in Dirichilet regression
datosd1 <- datosd[c(1,2,5,6,12,17,19,20,24,31,33,34),]
datosal1 <-datosd1[,c(6,39,34,35,36,37,38,41,43,44,47,45,46)]
head(datosal1)


# Make format data for Dirichilet's Regression
# Assumes that your components are in column 9 - 11
biomastotalp<-DR_data(datosal1[, 9:11], trafo = TRUE)

#null model
model<- DirichReg(biomastotalp ~ 1, datosal1)
coef(model)
summary(model)

#fitting model
model1 <- DirichReg(biomastotalp ~ dbh, datosal1)
coef(model1)
summary(model1)

model2 <- DirichReg(biomastotalp ~ dbh+((dbh)^2), datosal1)
```

```
coef(model2)
summary(model2)
model3 <- DirichReg(biomastotalp ~ dbh+I((dbh)^2), datosal1)
coef(model3)
summary(model3)

model4 <- DirichReg(biomastotalp ~ ((dbh)^2), datosal1)
coef(model4)
summary(model4)

model5 <- DirichReg(biomastotalp ~ ((dbh)^2)+I((dbh)^2), datosal1)
coef(model5)
summary(model5)

model6 <- DirichReg(biomastotalp ~ ht, datosal1)
coef(model6)
summary(model6)

model7 <- DirichReg(biomastotalp ~ ht+I((ht)^2), datosal1)
coef(model7)
summary(model7)

model8 <- DirichReg(biomastotalp ~ dbh+ht, datosal1)
coef(model8)
summary(model8)

model9 <- DirichReg(biomastotalp ~ dbh*ht, datosal1)
summary(model9)

model10 <- DirichReg(biomastotalp ~ dbh^2*ht, datosal1)
summary(model10)

# fit a quadratic Dirichlet regression models ("common")
model11 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2), data = datosal1)
summary(model11)

model12 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2)+I((dbh+ht)^2), data =
    datosal1)
summary(model12)

model13 <- DirichReg(biomastotalp ~ dbh^2*ht + I((dbh^2*ht)), data = datosal1)
summary(model13)

model14 <- DirichReg(biomastotalp ~ dbh*ht + I((dbh*ht)^2), data = datosal1)
summary(model14)


# fit a Dirichlet regression with quadratic predictor for the mean and
# a linear predictor for precision ("alternative")

model15 <- DirichReg(biomastotalp ~ dbh+ht, datosal1, model = "alternative",base =
    2)
summary(model15)

model16<- DirichReg(biomastotalp ~ dbh*ht, datosal1, model = "alternative",base =
    2)
summary(model16)

model17 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2), data = datosal1,model =
    "alternative", base = 2)
summary(model17)

model18 <- DirichReg(biomastotalp ~ dbh*ht + I((dbh*ht)^2), data = datosal1,model =
    "alternative", base = 2)
summary(model18)
```

```
model19<-    DirichReg(biomastotalp    ~    dbh*ht|dbh+ht,    datosal1,    model    =
     "alternative",base = 2)
summary(model19)

anova(model1,model2, model3, model4,model5,model6, model7,model8, model9, model10,
model11, model12,model13, model14, model15, model16,model17,model18,model19)


## information from fitted model
## Summary
fitted(model8)

predict(model18, newdata = data.frame("ht" = seq(10, 100, 1000)))

residuals(model8, type = c("standardized"))

head(residuals(model8))

confint(model8)

confint(model8, exp = TRUE)

logLik(model8)

round(vcov(model8), 5)


# Compute predicted(fitted) percentages of component biomas
datosal1$stempp <- (fitted(model8)[,"stemp"])
datosal1$Brpp <- (fitted(model8)[,"Brp"])
datosal1$needlepp <- (fitted(model8)[,"needlep"])


# Compute predicted(fitted) of component biomas
datosal1$pstem<-with(datosal1,(stempp*stem))
datosal1$pBr<-with(datosal1,(Brpp*Br))
datosal1$pneedle<-with(datosal1,(needlepp*needle))
datosal1$pbiomastotal<-with(datosal1,(pstem+pBr+pneedle))


# Compute mean bias of component biomass
datosal1$stembias=with(datosal1,((100/12)*(stem-pstem)/stem))
mean(datosal1$stembias)
datosal1$Brbias=with(datosal1,((100/12)*(Br-pBr)/Br))
mean(datosal1$Brbias)
datosal1$needlebias=with(datosal1,((100/12)*(needle-pneedle)/needle))
mean(datosal1$needlebias)
datosal1$totalbias<-with(datosal1,(stembias+Brbias+needlebias))
mean(datosal1$totalbias)


# Compute mean RMSE of component biomass
datosal1$stemrmse<-with(datosal1,sqrt((stem-pstem)^2)/12)
sum(datosal1$stemrmse)
datosal1$Brrmse<-with(datosal1,sqrt((Br-pBr)^2)/12)
sum(datosal1$Brrmse)
datosal1$needlermse<-with(datosal1,sqrt((needle-pneedle)^2)/12)
sum(datosal1$needlermse)
datosal1$totalrmse<-with(datosal1,(stemrmse+Brrmse+needlermse))

str(datosal1)


# Compute residual of component biomas
datosal1$rstem<-with(datosal1,(stem-pstem))
datosal1$rBr<-with(datosal1,(Br-pBr))
```

```
datosal1$rneedle<-with(datosal1,(needle-pneedle))
datosal1$rbiomastotal<-with(datosal1,(biomastotal-pbiomastotal))


#save data
save(datosal1, file="datosal1.RData")
load("datosal1.RData")
save.image("datosal1.RData")
str(datosal1)


###Graph-1

par(mfrow=c(1, 4))


## loaded library for graph
library(car)

scatterplot(datosal1$stem~datosal1$rstem,col="Black",main="Stem Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal1$Br~datosal1$rBr,col="Black",main="Branch Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal1$needle~datosal1$rneedle,col="Black",main="Needle Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal1$biomastotal~datosal1$rbiomastotal,col="Black",main="Total
    Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")


##Graph-2


## to visualized RMSE versus dbh class
library(lattice)

plot(datosal1$dbh,datosal1$stemrmse,ylim=c(-2,2),col=c("blue"),          main="Stem
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal1$dbh,datosal1$Brrmse,ylim=c(-2,2),col=c("blue"),          main="Branch
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal1$dbh,datosal1$needlermse,ylim=c(-2,2),col=c("blue"),      main="Needle
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal1$dbh,datosal1$totalrmse,ylim=c(-2,2),col=c("blue"),        main="Total
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")

##Graph-3


## to visualizedlized Bias(%) versus dbh class

plot(datosal1$dbh,datosal1$stembias,ylim=c(-20,20),col=c("green"),main="Stem
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal1$dbh,datosal1$Brbias,ylim=c(-20,20),col=c("green"),main="Branch
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal1$dbh,datosal1$needlebias,ylim=c(-20,20),col=c("green"),main="Needle
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal1$dbh,datosal1$totalbias,ylim=c(-20,20),col=c("green"),main="Total
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
```

```
#########################Treatment B-Dirichelet regression modelling#############

##Split data for using in Dirichilet regression
#light B treatment data sub set
datosd2 <- datosd[c(3,9,4,10,11,14,16,18,28,30,32,36),]
datosal2 <-datosd2[,c(6,39,34,35,36,37,38,41,43,44,47,45,46)]
head(datosal2)

# Make format data for Dirichilet's Regression
# Assumes that your components are in column 9 - 11
biomastotalp<-DR_data(datosal2[, 9:11], trafo = TRUE)

#null model
model<- DirichReg(biomastotalp ~ 1, datosal)
coef(model)
summary(model)
#fitting model
model1 <- DirichReg(biomastotalp ~ dbh, datosal2)
coef(model1)
summary(model1)

model2 <- DirichReg(biomastotalp ~ dbh+((dbh)^2), datosal2)
coef(model2)
summary(model2)
model3 <- DirichReg(biomastotalp ~ dbh+I((dbh)^2), datosal2)
coef(model3)
summary(model3)

model4 <- DirichReg(biomastotalp ~ ((dbh)^2), datosal2)
coef(model4)
summary(model4)

model5 <- DirichReg(biomastotalp ~ ((dbh)^2)+I((dbh)^2), datosal2)
coef(model5)
summary(model5)

model6 <- DirichReg(biomastotalp ~ ht, datosal2)
coef(model6)
summary(model6)

model7 <- DirichReg(biomastotalp ~ ht+I((ht)^2), datosal2)
coef(model7)
summary(model7)

model8 <- DirichReg(biomastotalp ~ dbh+ht, datosal2)
coef(model8)
summary(model8)

model9 <- DirichReg(biomastotalp ~ dbh*ht, datosal2)
summary(model9)

model10 <- DirichReg(biomastotalp ~ dbh^2*ht, datosal2)
summary(model10)

# fit a quadratic Dirichlet regression models ("common")
model11 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2), data = datosal2)
summary(model11)

model12 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2)+I((dbh+ht)^2), data =
    datosal2)
summary(model12)

model13 <- DirichReg(biomastotalp ~ dbh^2*ht + I((dbh^2*ht)), data = datosal2)
summary(model13)
```

```
model14 <- DirichReg(biomastotalp ~ dbh*ht + I((dbh*ht)^2), data = datosal2)
summary(model14)


# fit a Dirichlet regression with quadratic predictor for the mean and
# a linear predictor for precision ("alternative")

model15 <- DirichReg(biomastotalp ~ dbh+ht, datosal2, model = "alternative",base =
    2)
summary(model15)

model16<- DirichReg(biomastotalp ~ dbh*ht, datosal2, model = "alternative",base =
    2)
summary(model16)

model17 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2), data = datosal2,model =
    "alternative", base = 2)
summary(model17)

model18 <- DirichReg(biomastotalp ~ dbh*ht + I((dbh*ht)^2), data = datosal2,model =
    "alternative", base = 3)
summary(model18)

model19<-   DirichReg(biomastotalp   ~   dbh*ht|dbh+ht,   datosal2,   model   =
    "alternative",base = 2)
summary(model19)

anova(model1,model2, model3, model4,model5,model6, model7,model8, model9, model10,
model11, model12,model13, model14, model15, model16,model17,model18,model19)


## information from fitted model
## Summary
fitted(model18)
print(model18)

predict(model18, newdata = data.frame("ht" = seq(10, 100, 1000)))

residuals(model18, type = c("standardized"))


head(residuals(model18))

confint(model18)
confint(model18, exp = TRUE)

logLik(model18)
round(vcov(model18), 5)

# Compute predicted(fitted) percentages of component biomas
datosal2$stempp <- (fitted(model18)[,"stemp"])
datosal2$Brpp <- (fitted(model18)[,"Brp"])
datosal2$needlepp <- (fitted(model18)[,"needlep"])
datosal2$biomastotalpp<-with(datosal2,(stempp+Brpp+needlepp))


# Compute predicted(fitted) of component biomas
datosal2$pstem<-with(datosal2,(stempp*stem))
datosal2$pBr<-with(datosal2,(Brpp*Br))
datosal2$pneedle<-with(datosal2,(needlepp*needle))
datosal2$pbiomastotal<-with(datosal2,(pstem+pBr+pneedle))


# Compute mean bias of component biomass
datosal2$stembias=with(datosal2,((100/12)*(stem-pstem)/stem))
mean(datosal2$stembias)
```

```
datosal2$Brbias=with(datosal2,((100/12)*(Br-pBr)/Br))
mean(datosal2$Brbias)
datosal2$needlebias=with(datosal2,((100/12)*(needle-pneedle)/needle))
mean(datosal2$needlebias)
datosal2$totalbias<-with(datosal2,(stembias+Brbias+needlebias))
mean(datosal2$totalbias)


# Compute mean RMSE of component biomass
datosal2$stemrmse<-with(datosal2,sqrt((stem-pstem)^2)/12)
sum(datosal2$stemrmse)
datosal2$Brrmse<-with(datosal2,sqrt((Br-pBr)^2)/12)
sum(datosal2$Brrmse)
datosal2$needlermse<-with(datosal2,sqrt((needle-pneedle)^2)/12)
sum(datosal2$needlermse)
datosal2$totalrmse<-with(datosal2,(stemrmse+Brrmse+needlermse))

head(datosal2)


# Compute residual of component biomas
datosal2$rstem<-with(datosal2,(stem-pstem))
datosal2$rBr<-with(datosal2,(Br-pBr))
datosal2$rneedle<-with(datosal2,(needle-pneedle))
datosal2$rbiomastotal<-with(datosal2,(biomastotal-pbiomastotal))


#save data
save(datosal2, file="datosal2.RData")
load("datosal2.RData")
save.image("datosal2.RData")
str(datosal2)

###Graph-1

par(mfrow=c(1, 4))


##loaded library for graph
library(car)

scatterplot(datosal2$stem~datosal2$rstem,col="Black",main="Stem Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal2$Br~datosal2$rBr,col="Black",main="Branch Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal2$needle~datosal2$rneedle,col="Black",main="Needle Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal2$biomastotal~datosal2$rbiomastotal,col="Black",main="Total
    Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")


##Graph-2


## to visualized RMSE versus dbh class
library(lattice)

plot(datosal2$dbh,datosal2$stemrmse,ylim=c(-2,2),col=c("blue"),          main="Stem
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal2$dbh,datosal2$Brrmse,ylim=c(-2,2),col=c("blue"),          main="Branch
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal2$dbh,datosal2$needlermse,ylim=c(-2,2),col=c("blue"),      main="Needle
    Biomass",
```

```
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal2$dbh,datosal2$totalrmse,ylim=c(-2,2),col=c("blue"),         main="Total
     Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")

##Graph-3


## to visualizedlized Bias(%) versus dbh class

plot(datosal2$dbh,datosal2$stembias,ylim=c(-20,20),col=c("green"),main="Stem
     Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal2$dbh,datosal2$Brbias,ylim=c(-20,20),col=c("green"),main="Branch
     Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal2$dbh,datosal2$needlebias,ylim=c(-20,20),col=c("green"),main="Needle
     Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal2$dbh,datosal2$totalbias,ylim=c(-20,20),col=c("green"),main="Total
     Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")



########################Treatment C-Dirichelet regression modelling###############

#light C treatment data sub set
##Split data for using in Dirichilet regression
datosd3 <- datosd[c(7,8,13,15,21,22,23,25,26,27,29,35),]
datosal3 <-datosd3[,c(6,39,34,35,36,37,38,41,43,44,47,45,46)]
head(datosal3)

# Make format data for Dirichilet's Regression
# Assumes that your components are in column 9 - 11
biomastotalp<-DR_data(datosal3[, 9:11], trafo = TRUE)

#null model
model<- DirichReg(biomastotalp ~ 1, datosal3)
coef(model)
summary(model)

#fitting model
model1 <- DirichReg(biomastotalp ~ dbh, datosal3)
coef(model1)
summary(model1)

model2 <- DirichReg(biomastotalp ~ dbh+((dbh)^2), datosal3)
coef(model2)
summary(model2)
model3 <- DirichReg(biomastotalp ~ dbh+I((dbh)^2), datosal3)
coef(model3)
summary(model3)

model4 <- DirichReg(biomastotalp ~ ((dbh)^2), datosal3)
coef(model4)
summary(model4)

model5 <- DirichReg(biomastotalp ~ ((dbh)^2)+I((dbh)^2), datosal3)
coef(model5)
summary(model5)

model6 <- DirichReg(biomastotalp ~ ht, datosal3)
coef(model6)
summary(model6)
```

```
model7 <- DirichReg(biomastotalp ~ ht+I((ht)^2), datosal3)
coef(model7)
summary(model7)

model8 <- DirichReg(biomastotalp ~ dbh+ht, datosal3)
coef(model8)
summary(model8)

model9 <- DirichReg(biomastotalp ~ dbh*ht, datosal3)
summary(model9)

model10 <- DirichReg(biomastotalp ~ dbh^2*ht, datosal3)
summary(model10)

# fit a quadratic Dirichlet regression models ("common")
model11 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2), data = datosal3)
summary(model11)

model12 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2)+I((dbh+ht)^2), data =
    datosal3)
summary(model12)

model13 <- DirichReg(biomastotalp ~ dbh^2*ht + I((dbh^2*ht)), data = datosal3)
summary(model13)

model14 <- DirichReg(biomastotalp ~ dbh*ht + I((dbh*ht)^2), data = datosal3)
summary(model14)


# fit a Dirichlet regression with quadratic predictor for the mean and
# a linear predictor for precision ("alternative")

model15 <- DirichReg(biomastotalp ~ dbh+ht, datosal2, model = "alternative",base =
    2)
summary(model15)

model16<- DirichReg(biomastotalp ~ dbh*ht, datosal2, model = "alternative",base =
    2)
summary(model16)

model17 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2), data = datosal3,model =
    "alternative", base = 2)
summary(model17)

model18 <- DirichReg(biomastotalp ~ dbh*ht + I((dbh*ht)^2), data = datosal3,model =
    "alternative", base = 3)
summary(model18)

model19<- DirichReg(biomastotalp ~ dbh*ht|dbh+ht, datosal3, model =
    "alternative",base = 2)
summary(model19)

anova(model1,model2, model3, model4,model5,model6, model7,model8, model9,
    model10,model11,
model12,model13, model14, model15, model16,model17,model18,model19)


## information from fitted model
## summary
fitted(model9)

predict(model9, newdata = data.frame("ht" = seq(10, 100, 1000)))

residuals(model9, type = c("standardized"))
```

```
head(residuals(model9))

confint(model9)
confint(model9, exp = TRUE)

logLik(model9)
round(vcov(model9), 5)


# Compute predicted(fitted) percentages of component biomas
datosal3$stempp <- (fitted(model9)[,"stemp"])
datosal3$Brpp <- (fitted(model9)[,"Brp"])
datosal3$needlepp <- (fitted(model9)[,"needlep"])
datosal3$biomastotalpp<-with(datosal3,(stempp+Brpp+needlepp))


# Compute predicted(fitted) of component biomas
datosal3$pstem<-with(datosal3,(stempp*stem))
datosal3$pBr<-with(datosal3,(Brpp*Br))
datosal3$pneedle<-with(datosal3,(needlepp*needle))
datosal3$pbiomastotal<-with(datosal3,(pstem+pBr+pneedle))


# Compute mean bias of component biomass
datosal3$stembias=with(datosal3,((100/12)*(stem-pstem)/stem))
mean(datosal3$stembias)
datosal3$Brbias=with(datosal3,((100/12)*(Br-pBr)/Br))
mean(datosal3$Brbias)
datosal3$needlebias=with(datosal3,((100/12)*(needle-pneedle)/needle))
mean(datosal3$needlebias)
datosal3$biomastotalbias<-with(datosal3,(stembias+Brbias+needlebias))
mean(datosal3$totalbias)


# Compute mean RMSE of component biomass
datosal3$stemrmse<-with(datosal3,sqrt((stem-pstem)^2)/12)
sum(datosal3$stemrmse)
datosal3$Brrmse<-with(datosal3,sqrt((Br-pBr)^2)/12)
sum(datosal3$Brrmse)
datosal3$needlermse<-with(datosal3,sqrt((needle-pneedle)^2)/12)
sum(datosal3$needlermse)
datosal3$totalrmse<-with(datosal3,(stemrmse+Brrmse+needlermse))


head(datosal3)


# Compute residual of component biomas
datosal3$rstem<-with(datosal3,(stem-pstem))
datosal3$rBr<-with(datosal3,(Br-pBr))
datosal3$rneedle<-with(datosal3,(needle-pneedle))
datosal3$rbiomastotal<-with(datosal3,(biomastotal-pbiomastotal))

## save data
save(datosal3, file="datosal3.RData")
load("datosal3.RData")
save.image("datosal3.RData")
str(datosal3)

###Graph-1

par(mfrow=c(1, 4))


##loaded library for graph
library(car)
```

```
scatterplot(datosal3$stem~datosal3$rstem,col="Black",main="Stem Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal3$Br~datosal3$rBr,col="Black",main="Branch Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal3$needle~datosal3$rneedle,col="Black",main="Needle Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal3$biomastotal~datosal3$rbiomastotal,col="Black",main="Total
    Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")



##Graph-2


## to visualized RMSE versus dbh class
library(lattice)

plot(datosal3$dbh,datosal3$stemrmse,ylim=c(-2,2),col=c("blue"),          main="Stem
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal3$dbh,datosal3$Brrmse,ylim=c(-2,2),col=c("blue"),          main="Branch
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal3$dbh,datosal3$needlermse,ylim=c(-2,2),col=c("blue"),      main="Needle
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal3$dbh,datosal3$totalrmse,ylim=c(-2,2),col=c("blue"),        main="Total
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")

##Graph-3


## to visualizedlized Bias(%) versus dbh class

plot(datosal3$dbh,datosal3$stembias,ylim=c(-20,20),col=c("green"),main="Stem
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal3$dbh,datosal3$Brbias,ylim=c(-20,20),col=c("green"),main="Branch
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal3$dbh,datosal3$needlebias,ylim=c(-20,20),col=c("green"),main="Needle
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal3$dbh,datosal3$totalbias,ylim=c(-20,20),col=c("green"),main="Total
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")


########################Treatment B and C-Dirichelet regression modelling##########

#light C treatment data sub set
##Split data for using in Dirichilet regression
datosd4                        <-                        datosd[c(3,4,7,8,9,10,11,13,
    14,15,16,18,21,22,23,25,26,27,28,29,30,32,35,36),]
datosal4 <-datosd4[,c(6,39,34,35,36,37,38,41,43,44,47,45,46)]
head(datosal4)

# Format data for Dirichilet's Regression
# Assumes that your components are in column 9 - 11
biomastotalp<-DR_data(datosal4[, 9:11], trafo = TRUE)

#null model
model<- DirichReg(biomastotalp ~ 1, datosal4)
```

```
coef(model)
summary(model)

#fitting model
model1 <- DirichReg(biomastotalp ~ dbh, datosal4)
coef(model1)
summary(model1)

model2 <- DirichReg(biomastotalp ~ dbh+((dbh)^2), datosal4)
coef(model2)
summary(model2)
model3 <- DirichReg(biomastotalp ~ dbh+I((dbh)^2), datosal4)
coef(model3)
summary(model3)

model4 <- DirichReg(biomastotalp ~ ((dbh)^2), datosal4)
coef(model4)
summary(model4)

model5 <- DirichReg(biomastotalp ~ ((dbh)^2)+I((dbh)^2), datosal4)
coef(model5)
summary(model5)

model6 <- DirichReg(biomastotalp ~ ht, datosal4)
coef(model6)
summary(model6)

model7 <- DirichReg(biomastotalp ~ ht+I((ht)^2), datosal4)
coef(model7)
summary(model7)

model8 <- DirichReg(biomastotalp ~ dbh+ht, datosal2)
coef(model8)
summary(model8)

model9 <- DirichReg(biomastotalp ~ dbh*ht, datosal4)
summary(model9)

model10 <- DirichReg(biomastotalp ~ dbh^2*ht, datosal4)
summary(model10)


# fit a quadratic Dirichlet regression models ("common")
model11 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2), data = datosal4)
summary(model11)

model12 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2)+I((dbh+ht)^2), data =
    datosal4)
summary(model12)

model13 <- DirichReg(biomastotalp ~ dbh^2*ht + I((dbh^2*ht)), data = datosal4)
summary(model13)

model14 <- DirichReg(biomastotalp ~ dbh*ht + I((dbh*ht)^2), data = datosal4)
summary(model14)


# fit a Dirichlet regression with quadratic predictor for the mean and
# a linear predictor for precision ("alternative")

model15 <- DirichReg(biomastotalp ~ dbh+ht, datosal4, model = "alternative",base =
    2)
summary(model15)

model16<- DirichReg(biomastotalp ~ dbh*ht, datosal4, model = "alternative",base =
    2)
```

```
summary(model16)

model17 <- DirichReg(biomastotalp ~ dbh+ht + I((dbh+ht)^2), data = datosal4,model =
    "alternative", base = 2)
summary(model17)

model18 <- DirichReg(biomastotalp ~ dbh*ht + I((dbh*ht)^2), data = datosal4,model =
    "alternative", base = 3)
summary(model18)

model19<-    DirichReg(biomastotalp    ~    dbh*ht|dbh+ht,    datosal4,    model    =
    "alternative",base = 2)
summary(model19)

anova(model1,model2,    model3,    model4,model5,model6,    model7,model8,    model9,
    model10,model11,          model12,model13,          model14,          model15,
    model16,model17,model18,model19)


## information from fitted model
## summary
fitted(model4)

str(summary(model4))

predict(model4, newdata = data.frame("ht" = seq(10, 100, 1000)))


residuals(model4, type = c("standardized"))

head(residuals(model4))

confint(model4)
confint(model4, exp = TRUE)

logLik(model4)
round(vcov(model4), 5)


# Compute predicted(fitted) percentages of component biomas
datosal4$stempp <- (fitted(model4)[,"stemp"])
datosal4$Brpp <- (fitted(model4)[,"Brp"])
datosal4$needlepp <- (fitted(model4)[,"needlep"])
datosal4$biomastotalpp<-with(datosal4,(stempp+Brpp+needlepp))


# Compute predicted(fitted) of component biomas
datosal4$pstem<-with(datosal4,(stempp*stem))
datosal4$pBr<-with(datosal4,(Brpp*Br))
datosal4$pneedle<-with(datosal4,(needlepp*needle))
datosal4$pbiomastotal<-with(datosal4,(pstem+pBr+pneedle))


# Compute mean bias of component biomass
datosal4$stembias=with(datosal4,((100/24)*(stem-pstem)/stem))
mean(datosal4$stembias)
datosal4$Brbias=with(datosal4,((100/24)*(Br-pBr)/Br))
mean(datosal4$Brbias)
datosal4$needlebias=with(datosal4,((100/24)*(needle-pneedle)/needle))
mean(datosal4$needlebias)
datosal4$totalbias<-with(datosal4,(stembias+Brbias+needlebias))
mean(datosal4$totalbias)


# Compute mean RMSE of component biomass
datosal4$stemrmse<-with(datosal4,sqrt((stem-pstem)^2)/24)
```

```
sum(datosal4$stemrmse)
datosal4$Brrmse<-with(datosal4,sqrt((Br-pBr)^2)/24)
sum(datosal4$Brrmse)
datosal4$needlermse<-with(datosal4,sqrt((needle-pneedle)^2)/24)
sum(datosal4$needlermse)
datosal4$totalrmse<-with(datosal4,(stemrmse+Brrmse+needlermse))

head(datosal4)


# Compute residual of component biomas
datosal4$rstem<-with(datosal4,(stem-pstem))
datosal4$rBr<-with(datosal4,(Br-pBr))
datosal4$rneedle<-with(datosal4,(needle-pneedle))
datosal4$rbiomastotal<-with(datosal4,(biomastotal-pbiomastotal))


#save data
save(datosal4, file="datosal4.RData")
load("datosal4.RData")
str(datosal4)
save.image("datosal4.RData")


###Graph-1

par(mfrow=c(1, 4))

##loaded library for graph
library(car)

scatterplot(datosal4$stem~datosal4$rstem,col="Black",main="Stem Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal4$Br~datosal4$rBr,col="Black",main="Branch Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal4$needle~datosal4$rneedle,col="Black",main="Needle Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")
scatterplot(datosal4$biomastotal~datosal4$rbiomastotal,col="Black",main="Total
    Biomass",
            ylab="Residual (kg)", xlab="Observation (kg)")


##Graph-2


## to visualized RMSE versus dbh class
library(lattice)

plot(datosal4$dbh,datosal4$stemrmse,ylim=c(-2,2),col=c("blue"),          main="Stem
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal4$dbh,datosal4$Brrmse,ylim=c(-2,2),col=c("blue"),          main="Branch
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal4$dbh,datosal4$needlermse,ylim=c(-2,2),col=c("blue"),      main="Needle
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
plot(datosal4$dbh,datosal4$totalrmse,ylim=c(-2,2),col=c("blue"),        main="Total
    Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")

##Graph-3


## to visualizedlized Bias(%) versus dbh class
```

```
plot(datosal4$dbh,datosal4$stembias,ylim=c(-20,20),col=c("green"),main="Stem
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal4$dbh,datosal4$Brbias,ylim=c(-20,20),col=c("green"),main="Branch
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal4$dbh,datosal4$needlebias,ylim=c(-20,20),col=c("green"),main="Needle
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")
plot(datosal4$dbh,datosal4$totalbias,ylim=c(-20,20),col=c("green"),main="Total
    Biomass",
            ylab="Bias(%)", xlab="Diameter(cm)")

q()

###################################end for Dirichlet regresion###################



####to make comparison graph for estimate biomass both using SUR and Dirichlet
    method

##data extracted from Dirichlet regression method
datocomd<-datosal[c(2,21:28)]
X <- seq(1:36)
datocom<- cbind(X,datocomd)


##data extracted from SUR regression method
datocoms<-datos[c(1, 51:58)]

## merge to data set
datocomd<-merge(datocom, datocoms, by="X")

head(datocomd)

##save and load data in ".RData)
save(datocomd, file="allRMSEbias.RData")
load("allRMSEbias.RData")

save.image("allRMSEbias.RData")

## loaded library
library(lattice)
par(mfrow=c(2, 2))
dim(datocomd$dbh)

datocomd

##to visualized RMSE distributted along dbh
plot(datocomd$dbh, datocomd$stemrmse.x+datocomd$stemrmse.y, pch=c(21,21), ylim=c(-
    2,2), col=c("blue", "green"), main="Stem Biomass",
            ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocomd$dbh, datocomd$Brrmse.x+datocomd$Brrmse.y, pch=c(21,21), ylim=c(-2,2),
    col=c("blue", "green"), main="Branch Biomass",
     ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocomd$dbh,    datocomd$needlermse.x+datocomd$needlermse.y,    pch=c(21,21),
    ylim=c(-2,2), col=c("blue", "green"), main="Needle Biomass",
     ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocomd$dbh,     datocomd$totalrmse.x+datocomd$totalrmse.y,     pch=c(21,21),
```

```
     ylim=c(-2,2), col=c("blue", "green"), main="Total Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))



##to visualized Bias distributted along dbh
plot(datocomd$dbh,datocomd$stembias.x+datocomd$stembias.y,  pch=c(21,21),  ylim=c(-
     20,20), col=c("blue", "green"), main="Stem Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocomd$dbh,    datocomd$Brbias.x+datocomd$Brbias.y,pch=c(21,21),    ylim=c(-
     20,20), col=c("blue", "green"), main="Branch Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocomd$dbh,         datocomd$needlebias.x+datocomd$needlebias.y,pch=c(21,21),
     ylim=c(-20,20), col=c("blue", "green"), main="Needle Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocomd$dbh, datocomd$totalbias.x+datocomd$totalbias.y,pch=c(21,21), ylim=c(-
     20,20), col=c("blue", "green"), main="Total Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))


####light A treatment data sub set

##data extracted from Dirichlet regression method
datocomd1<-datosal1[c(2,21:28)]
X <- seq(1:12)
datocom1<- cbind(X,datocomd1)


##data extracted from SUR regression method
datocoms1<-datos1[c(1, 51:58)]

# two merge two data set
datocom1<-merge(datocom1, datocoms1, by="X")

head(datocom1)

##save and load data in ".RData)
save(datocom1, file="ARMSEbias.RData")
load("ARMSEbias.RData")
save.image()

#loaded library
library(lattice)
par(mfrow=c(2, 2))


##to visualized RMSE distributted along dbh
plot(datocom1$dbh,  datocom1$stemrmse.x+datocom1$stemrmse.y,  pch=c(21,21),  ylim=c(-
     2,2), col=c("blue", "green"), main="Stem Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom1$dbh, datocom1$Brrmse.x+datocom1$Brrmse.y, pch=c(21,21), ylim=c(-2,2),
     col=c("blue", "green"), main="Branch Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom1$dbh,    datocom1$needlermse.x+datocom1$needlermse.y,    pch=c(21,21),
```

```
     ylim=c(-2,2), col=c("blue", "green"), main="Needle Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom1$dbh,      datocom1$totalrmse.x+datocom1$totalrmse.y,      pch=c(21,21),
     ylim=c(-2,2), col=c("blue", "green"), main="Total Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))



##to visualized Bias distributted along dbh
plot(datocom1$dbh, datocom1$stembias.x+datocom1$stembias.y,  pch=c(21,21), ylim=c(-
     20,20), col=c("blue", "green"), main="Stem Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom1$dbh,  datocom1$Brbias.x+datocom1$Brbias.y,    pch=c(21,21),  ylim=c(-
     20,20), col=c("blue", "green"), main="Branch Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom1$dbh,   datocom1$needlebias.x+datocom1$needlebias.y,      pch=c(21,21),
     ylim=c(-20,20), col=c("blue", "green"), main="Needle Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom1$dbh,    datocom1$totalbias.x+datocom1$totalbias.y,       pch=c(21,21),
     ylim=c(-20,20), col=c("blue", "green"), main="Total Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))



####light B treatment data sub set

head (datosal2)
##data extracted from Dirichlet regression method
datocomd2<-datosal2[c(2,21:28)]
X <- seq(1:12)
datocom2<- cbind(X,datocomd2)


##data extracted from SUR regression method
datocoms2<-datos2[c(1, 51:58)]

### two merge two data set
datocom2<-merge(datocom2, datocoms2, by="X")

head(datocom2)

##save and load data in ".RData)
save(datocom2, file="ARMSEbias.RData")
save.image()

library(lattice)
par(mfrow=c(2, 2))


##to visualized RMSE distributted along dbh
plot(datocom2$dbh,  datocom2$stemrmse.x+datocom2$stemrmse.y,  pch=c(21,21),  ylim=c(-
     2,2), col=c("blue", "green"), main="Stem Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom2$dbh, datocom2$Brrmse.x+datocom2$Brrmse.y, pch=c(21,21), ylim=c(-2,2),
```

```
     col=c("blue", "green"), main="Branch Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom2$dbh,     datocom2$needlermse.x+datocom2$needlermse.y,     pch=c(21,21),
     ylim=c(-2,2), col=c("blue", "green"), main="Needle Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom2$dbh,      datocom2$totalrmse.x+datocom2$totalrmse.y,      pch=c(21,21),
     ylim=c(-2,2), col=c("blue", "green"), main="Total Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))


##to visualized Bias distributted along dbh
plot(datocom2$dbh,  datocom2$stembias.x+datocom2$stembias.y,  pch=c(21,21),  ylim=c(-
     20,20), col=c("blue", "green"), main="Stem Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom2$dbh,   datocom2$Brbias.x+datocom2$Brbias.y,   pch=c(21,21),   ylim=c(-
     20,20), col=c("blue", "green"), main="Branch Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom2$dbh,datocom2$needlebias.x+datocom2$needlebias.y,         pch=c(21,21),
     ylim=c(-20,20), col=c("blue", "green"), main="Needle Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom2$dbh,datocom2$totalbias.x+datocom2$totalbias.y, pch=c(21,21), ylim=c(-
     20,20), col=c("blue", "green"), main="Total Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))



####light C treatment data sub set


head(datosal3)

##data extracted from Dirichlet regression method
datocomd3<-datosal3[c(2,22:29)]
X <- seq(1:12)
datocom3<- cbind(X,datocomd3)



##data extracted from SUR regression method
datocoms3<-datos3[c(1, 51:58)]

##merge two data set
datocom3<-merge(datocom3, datocoms3, by="X")

head(datocom3)


## save data
save(datocom3, file="ARMSEbias.RData")
save.image("ARMSEbias.RData")


#loaded library
library(lattice)
```

```
##make window for seveal graph
par(mfrow=c(2, 2))


##to visualized RMSE distributted along dbh
plot(datocom3$dbh,datocom3$stemrmse.x+datocom3$stemrmse.y,  pch=c(21,21),  ylim=c(-
     2,2), col=c("blue", "green"), main="Stem Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom3$dbh, datocom3$Brrmse.x+datocom3$Brrmse.y, pch=c(21,21), ylim=c(-2,2),
     col=c("blue", "green"), main="Branch Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom3$dbh,    datocom3$needlermse.x+datocom3$needlermse.y,    pch=c(21,21),
     ylim=c(-2,2), col=c("blue", "green"), main="Needle Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom3$dbh,     datocom3$totalrmse.x+datocom3$totalrmse.y,     pch=c(21,21),
     ylim=c(-2,2), col=c("blue", "green"), main="Total Biomass",
      ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))


##to visualized Bias distributted along dbh
plot(datocom3$dbh,datocom3$stembias.x+datocom3$stembias.y,  pch=c(21,21),  ylim=c(-
     20,20), col=c("blue", "green"), main="Stem Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom3$dbh,datocom3$Brbias.x+datocom3$Brbias.y,    pch=c(21,21),    ylim=c(-
     20,20), col=c("blue", "green"), main="Branch Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom3$dbh,datocom3$needlebias.x+datocom3$needlebias.y,        pch=c(21,21),
     ylim=c(-20,20), col=c("blue", "green"), main="Needle Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom3$dbh,datocom3$totalbias.x+datocom3$totalbias.y, pch=c(21,21), ylim=c(-
     20,20), col=c("blue", "green"), main="Total Biomass",
      ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))



####light B  and C treatment data sub set

head(datosal4)
##data extracted from Dirichlet regression method
datocomd4<-datosal4[c(2,22:29)]
X <- seq(1:24)
datocom4<- cbind(X,datocomd4)



##data extracted from SUR regression method
datocoms4<-datos4[c(1, 51:58)]


##merge two data set
datocom4<-merge(datocom4, datocoms4, by="X")
```

```
head(datocom4)


##save  data
save(datocom4, file="ARMSEbias.RData")
save.image()

#loaded library
library(lattice)

## make window for several graph
par(mfrow=c(2, 2))

##to visualized RMSE distributted along dbh
plot(datocom4$dbh,datocom4$stemrmse.x+datocom4$stemrmse.y,  pch=c(21,21),  ylim=c(-
     2,2), col=c("blue", "green"), main="Stem Biomass",
     ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom4$dbh,datocom4$Brrmse.x+datocom4$Brrmse.y,  pch=c(21,21),  ylim=c(-2,2),
     col=c("blue", "green"), main="Branch Biomass",
     ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom4$dbh,datocom4$needlermse.x+datocom4$needlermse.y,         pch=c(21,21),
     ylim=c(-2,2), col=c("blue", "green"), main="Needle Biomass",
     ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom4$dbh,datocom4$totalrmse.x+datocom4$totalrmse.y, pch=c(21,21), ylim=c(-
     2,2), col=c("blue", "green"), main="Total Biomass",
     ylab="RMSE(kg)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))


##to visualized Bias distributted along dbh
plot(datocom4$dbh,datocom4$stembias.x+datocom4$stembias.y,  pch=c(21,21),  ylim=c(-
     20,20), col=c("blue", "green"), main="Stem Biomass",
     ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom4$dbh,datocom4$Brbias.x+datocom4$Brbias.y,    pch=c(21,21),    ylim=c(-
     20,20), col=c("blue", "green"), main="Branch Biomass",
     ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom4$dbh,datocom4$needlebias.x+datocom4$needlebias.y,xlim=c(0,16),
     pch=c(21,21), ylim=c(-30,30), col=c("blue", "green"), main="Needle Biomass",
     ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

plot(datocom4$dbh,datocom4$totalbias.x+datocom4$totalbias.y, pch=c(21,21), ylim=c(-
     20,20), col=c("blue", "green"), main="Total Biomass",
     ylab="Bias(%)", xlab="Diameter(cm)")
legend("bottomright", legend=c("Dirichlet", "SUR"),pch=21, col=c("blue","green"))

#save the datos in RData format
save(datos,datos1,datos2,datos3,datos4,datosal,datosal1,datosal2,datosal3,datosal4,
     datocomd,datocom1,datocom2,datocom3,datocom4, file="Biomass.RData")

ls()
save.image("Biomass.RData")
load("Biomass.RData")
q()

########end#######
```

3.4 R Script for counting tree rings, crossdating, tree ring widths and basal diameter growth analysis

```
##Program for tree ring counting, ring widths analysis, crossdating and basal
    diameter growth analysis
##Developed by MAA Pavel
##Adopted from measuRing mannual
##date: 09.06.2017
rm(list=ls())

##loaded library
library('measuRing')

##working directory
setwd('C:/dendro')

##loaded and instal library
install.packages("measuRing")
packs<-c('gmp','stringi','measuRing','dplR','reshape2','ggplot2')
sapply(packs,require,character.only=TRUE)

#loaded ".RData"
load('ring.RData')

###### trw counting process #####

## list of tif files
path. <- list.files(path=getwd(),pattern='.tif')

## two images from path.
alltf <- gsub('.tif','',path.)

## Recursive processing (mapping) of both images with multidetect function
ring <- Map(function(x)multiDetect(x, auto.det = FALSE,
             last.yr = 2016, plot = TRUE,
             segs = 1,
             rgb = c(0.1,0.1,0.8),
             origin=-0.02,
             darker = FALSE,
             marker = 5),alltf)

#save object
save(ring,file='ring.RData')
save.image ('ring.RData')

##check list of variable
ls()
str(ring)

## Put "ring.RData" workspace in image-file path
setwd('C:/dendro')

## make a new working list
allcounts4 <- ring

## Put name of the processed image here:
tocmp. <- "C025H0093A" # specafic sample for recheck

## copy the gray-column matrix:
inclu.dats <- allcounts4[[tocmp.]][['colNames']]

##Again recheck trw on specefic problematic sample (remember previously set your
    wd)
ctmp <- multiDetect(tocmp.,
```

```
                    auto.det = FALSE,
                    last.yr = 2016,
                    plot = TRUE,
                    segs = 1,
                    inclu.dat = inclu.dats,
                    rgb = c(0.1, 0.1, 0.8),
                    origin = -0.02,
                    darker = FALSE,
                    marker = 5)

## make a backup
allcounts4_back <- allcounts4
## allcounts4 <- allcounts4_back

## update the ring list
allcounts4[[tocmp.]] <- ctmp
allcounts4 <- allcounts4[order(names(allcounts4))]
## str(allcounts4[tocmp.])
## str(ctmp)
#names(allcounts4)

##fun for to visulization or plot
fun. <- 'spag'
fun. <- 'corr'
fun. <- 'ccf'

###Crossdating
crossRings(allcounts4,
           tocmp = tocmp.,
           from.to = c(1:8,27:34,49:56),## selected sample for crossdating
           fun = fun.,
           seg.length = 4,
           bin.floor = 0,
           lag.max = 2, pcrit = 0.3) #pcrit=p value


save(allcounts4, file="cross.RData")

## uncomment below lines whether aim to save crossdating
## diagnostic plots;

#image or pdf or tif or any format save in Desktop

#plotDesk <- T
#plotDesk <- F

tofi <- 'C:/Users/Pavel/Desktop/corr.pdf'
if(plotDesk){
dev.copy(pdf,tofi)
dev.off()
graphics.off()}

##reduceList transformlist in data.frame object

Df<-reduceList(ring)

##save data
save(Df,file="Df.RData")
save.image("Df.RData")

#write csv file
write.csv (Df, 'file.csv')

#loaded libraries
packs<-
    c('plyr','lattice','car','RODBC','lmtest','Matrix','zoo','reshape2','systemfit'
```

```
    )
sapply(packs,require,character.only=TRUE)

#Read data
datas<-read.csv("C:/dendro/basaldata.csv")

View(datas)
str(datas)

#loaded library for from wide to long formats data
library(tidyr)

# Make sure the subject column is a factor
datas$nroTree <- factor(datas$nroTree)

head(datas)

#From wide to long format
data_long <- gather(datas, Year, Basaldiameter, Yr1:Yr11, factor_key=TRUE)
View(data_long)

# loaded library
library(plyr)

#  Run the functions length, mean, and sd on the value of "change" for each
    treatment,
# broken down by water+light+Fertilizer+ year

cdata_long<- ddply(data_long,
              c("Water","Light" ,"Fertilizer","Year","Basaldiameter"), summarise,
               N    = sum(!is.na(Basaldiameter)),
               mean = mean(Basaldiameter, na.rm=TRUE),
               sd   = sd(Basaldiameter, na.rm=TRUE),
               se   = sd / sqrt(N))

#loaded library
install.packages("ggplot2")
library(ggplot2)


# Standard error of the mean
ggplot(cdata_long, aes(x=Year, y=Basaldiameter, colour=Light)) +
  geom_errorbar(aes(ymin=Basaldiameter-se, ymax=Basaldiameter+se), width=.1) +
  geom_line() +
  geom_point()+
  theme_bw()

# The errorbars overlapped, so use position_dodge to move them horizontally
pd <- position_dodge(0.8) # move them .05 to the left and right

#for light treatment
ggplot(cdata_long, aes(x=Year, y=Basaldiameter, colour=Light)) +
  geom_errorbar(aes(ymin=Basaldiameter-se,ymax=Basaldiameter+se),width=.1,
    position=pd) +
  geom_line(position=pd) +
  geom_point(position=pd,size=2, shape=21,fill="white")+
  theme_bw() +
  xlab("Year") +
  ylab(" Cumulative Basal Diameter (cm2)")

#for water treatment
ggplot(cdata_long, aes(x=Year, y=Basaldiameter, colour=Water)) +
  geom_errorbar(aes(ymin=Basaldiameter-se,ymax=Basaldiameter+se),width=.1,
    position=pd) +
  geom_line(position=pd) +
  geom_point(position=pd,size=2, shape=21,fill="white")+
```

```
  theme_bw() +
  xlab("Year") +
  ylab(" Cumulative Basal Diameter (cm2)")

#for fertilizer treatment
ggplot(cdata_long, aes(x=Year, y=Basaldiameter, colour=Fertilizer)) +
  geom_errorbar(aes(ymin=Basaldiameter-se,ymax=Basaldiameter+se),width=.1,
     position=pd) +
  geom_line(position=pd) +
  geom_point(position=pd,size=2, shape=21,fill="white")+
  theme_bw() +
  xlab("Year") +
  ylab(" Cumulative Basal Diameter (cm2)")


library(lattice)

#for annalysis annual growth
#Read data
gdata<-read.csv("C:/dendro/annualgrowth.csv")

#split data for combination of each treatment
gdata1 <- gdata[c(2,5,19, 20,24,31),]
gdata2 <- gdata[c(4,9,11,14,28,36),]
gdata3 <- gdata[c(8,13,21,22,25,27),]
gdata4 <- gdata[c(1,6,12,17,33,34),]
gdata5 <- gdata[c(27,10,16,18,30,3),]
gdata6 <- gdata[c(7,15,23,26,29,35),]

#loaded library for from wide to long formats data
library(tidyr)

# Make sure the subject column is a factor
gdata$nroTree <- factor(gdata$nroTree)
gdata1$nroTree <- factor(gdata1$nroTree)
gdata2$nroTree <- factor(gdata2$nroTree)
gdata3$nroTree <- factor(gdata3$nroTree)
gdata4$nroTree <- factor(gdata4$nroTree)
gdata5$nroTree <- factor(gdata5$nroTree)
gdata6$nroTree <- factor(gdata6$nroTree)

#From wide to long format
gdata_long <- gather(gdata, Year, Annualgrowth, Yr1:Yr11, factor_key=TRUE)
gdata_long1 <- gather(gdata1, Year, Annualgrowth, Yr1:Yr11, factor_key=TRUE)
gdata_long2 <- gather(gdata2, Year, Annualgrowth, Yr1:Yr11, factor_key=TRUE)
gdata_long3 <- gather(gdata3, Year, Annualgrowth, Yr1:Yr11, factor_key=TRUE)
gdata_long4 <- gather(gdata4, Year, Annualgrowth, Yr1:Yr11, factor_key=TRUE)
gdata_long5 <- gather(gdata5, Year, Annualgrowth, Yr1:Yr11, factor_key=TRUE)
gdata_long6 <- gather(gdata6, Year, Annualgrowth, Yr1:Yr11, factor_key=TRUE)


# loaded library
library(plyr)

#  Run the functions length, mean, and sd on the value of "change" for each
    treatment,
# broken down by water+light+Fertilizer+ year

ggdata_long<- ddply(gdata_long,
                 c("Water","Light" ,"Fertilizer","Year","Annualgrowth"), summarise,
                   N    = sum(!is.na(Annualgrowth)),
                   mean = mean(Annualgrowth, na.rm=TRUE),
                   sd   = sd(Annualgrowth, na.rm=TRUE),
                   se   = sd / sqrt(N))

#loaded library
```

```
install.packages("ggplot2")
library(ggplot2)

# Standard error of the mean
ggplot(ggdata_long, aes(x=Year, y=Annualgrowth, colour=Light)) +
  geom_errorbar(aes(ymin=Annualgrowth-se, ymax=Annualgrowth+se), width=.1) +
  geom_line() +
  geom_point()+
  theme_bw()

# The errorbars overlapped, so use position_dodge to move them horizontally
pd <- position_dodge(0.8) # move them .05 to the left and right

#for light treatment
ggplot(ggdata_long, aes(x=Year, y=Annualgrowth, colour=Light)) +
  geom_errorbar(aes(ymin=Annualgrowth-se,ymax=Annualgrowth+se),width=.1,
    position=pd) +
  geom_line(position=pd) +
  geom_point(position=pd,size=2, shape=21,fill="white")+
  theme_bw() +
  xlab("Year") +
  ylab(" Cumulative Annual growth (mm)")

#for water treatment
ggplot(ggdata_long, aes(x=Year, y=Annualgrowth, colour=Water)) +
  geom_errorbar(aes(ymin=Annualgrowth-se,ymax=Annualgrowth+se),width=.1,
    position=pd) +
  geom_line(position=pd) +
  geom_point(position=pd,size=2, shape=21,fill="white")+
  theme_bw() +
  xlab("Year") +
  ylab(" Cumulative Annual growth (mm)")

#for water fertilizer treatment
ggplot(ggdata_long, aes(x=Year, y=Annualgrowth, colour=Fertilizer)) +
  geom_errorbar(aes(ymin=Annualgrowth-se,ymax=Annualgrowth+se),width=.1,
    position=pd) +
  geom_line(position=pd) +
  geom_point(position=pd,size=2, shape=21,fill="white")+
  theme_bw() +
  xlab("Year") +
  ylab(" Cumulative Annual growth (mm)")

#Basal diameter growth analysis by ANCOVA
#annual growth dependent variable

#install libraries
install.packages('car')
install.packages('compute.es')
install.packages('effects')
install.packages('ggplot2')
install.packages('multcomp')
install.packages('pastecs')
install.packages('WRS')

#loaded libraries
packs<-c('car','compute.es','effects','ggplot2','multcomp','pastecs','WRS')
sapply(packs,require,character.only=TRUE)

#set the contrasts using the "contrasts" function before doing ANCOVA

contrasts(gdata_long$Light)=contr.poly # of levels, i.e. 3
contrasts(gdata_long$Fertilizer)=contr.poly # of levels, i.e. 3

model.1=aov(Annualgrowth~Wrainfall+Light+Fertilizer, data=gdata_long)
summary.lm(model.1)
```

```
model.2=aov(Annualgrowth~Wrainfall+Light, data=gdata_long)
summary.lm(model.2)

model.3=aov(Annualgrowth~Wrainfall+Fertilizer, data=gdata_long)
summary.lm(model.3)

model.4=aov(Annualgrowth~Wrainfall*Fertilizer, data=gdata_long)
summary.lm(model.4)

model.5=aov(Annualgrowth~Wrainfall*Light, data=gdata_long)
summary.lm(model.5)

model.6=aov(Annualgrowth~Wrainfall+Light+Fertilizer+Wrainfall*Light+Wrainfall*Ferti
    lizer, data=gdata_long)
summary.lm(model.6)

model.7=aov(Annualgrowth~Wrainfall+Light*Fertilizer, data=gdata_long)
summary.lm(model.7)


##Multifactor of analysis of variances (GLMs) for Anova test

m1<-glm(Annualgrowth~Wrainfall+Light+Fertilizer, data=gdata_long)
summary(m1)

m2<-glm(Annualgrowth~Wrainfall+Light, data=gdata_long)
summary(m2)

m3<-glm(Annualgrowth~Wrainfall+Fertilizer, data=gdata_long)
summary(m3)

m4<-glm(Annualgrowth~Wrainfall*Fertilizer, data=gdata_long)
summary(m4)

m5<-glm(Annualgrowth~Wrainfall*Light, data=gdata_long)
summary(m5)

m6<-
    glm(Annualgrowth~Wrainfall+Light+Fertilizer+Wrainfall*Light+Wrainfall*Fertilize
    r, data=gdata_long)
summary(m6)

m7=glm(Annualgrowth~Wrainfall+Light*Fertilizer, data=gdata_long)
summary.lm(m7)


#radius convert to diamter
gdata_long$D<-with(gdata_long, Annualgrowth*2)
gdata_long1$D<-with(gdata_long1, Annualgrowth*2)
gdata_long2$D<-with(gdata_long2, Annualgrowth*2)
gdata_long3$D<-with(gdata_long3, Annualgrowth*2)
gdata_long4$D<-with(gdata_long4, Annualgrowth*2)
gdata_long5$D<-with(gdata_long5, Annualgrowth*2)
gdata_long6$D<-with(gdata_long6, Annualgrowth*2)

##convert "Yr1" in year
gdata_long$yr[gdata_long$Year=='Yr1']<-1
gdata_long$yr[gdata_long$Year=='Yr2']<-2
gdata_long$yr[gdata_long$Year=='Yr3']<-3
gdata_long$yr[gdata_long$Year=='Yr4']<-4
gdata_long$yr[gdata_long$Year=='Yr5']<-5
gdata_long$yr[gdata_long$Year=='Yr6']<-6
gdata_long$yr[gdata_long$Year=='Yr7']<-7
gdata_long$yr[gdata_long$Year=='Yr8']<-8
gdata_long$yr[gdata_long$Year=='Yr9']<-9
```

```
gdata_long$yr[gdata_long$Year=='Yr10']<-10
gdata_long$yr[gdata_long$Year=='Yr11']<-11

#combination light(A) with "NO" watering
gdata_long1$yr[gdata_long1$Year=='Yr1']<-1
gdata_long1$yr[gdata_long1$Year=='Yr2']<-2
gdata_long1$yr[gdata_long1$Year=='Yr3']<-3
gdata_long1$yr[gdata_long1$Year=='Yr4']<-4
gdata_long1$yr[gdata_long1$Year=='Yr5']<-5
gdata_long1$yr[gdata_long1$Year=='Yr6']<-6
gdata_long1$yr[gdata_long1$Year=='Yr7']<-7
gdata_long1$yr[gdata_long1$Year=='Yr8']<-8
gdata_long1$yr[gdata_long1$Year=='Yr9']<-9
gdata_long1$yr[gdata_long1$Year=='Yr10']<-10
gdata_long1$yr[gdata_long1$Year=='Yr11']<-11

#combination light(B) with "NO" watering
gdata_long2$yr[gdata_long2$Year=='Yr1']<-1
gdata_long2$yr[gdata_long2$Year=='Yr2']<-2
gdata_long2$yr[gdata_long2$Year=='Yr3']<-3
gdata_long2$yr[gdata_long2$Year=='Yr4']<-4
gdata_long2$yr[gdata_long2$Year=='Yr5']<-5
gdata_long2$yr[gdata_long2$Year=='Yr6']<-6
gdata_long2$yr[gdata_long2$Year=='Yr7']<-7
gdata_long2$yr[gdata_long2$Year=='Yr8']<-8
gdata_long2$yr[gdata_long2$Year=='Yr9']<-9
gdata_long2$yr[gdata_long2$Year=='Yr10']<-10
gdata_long2$yr[gdata_long2$Year=='Yr11']<-11

#combination light(C) with "NO" watering
gdata_long3$yr[gdata_long3$Year=='Yr1']<-1
gdata_long3$yr[gdata_long3$Year=='Yr2']<-2
gdata_long3$yr[gdata_long3$Year=='Yr3']<-3
gdata_long3$yr[gdata_long3$Year=='Yr4']<-4
gdata_long3$yr[gdata_long3$Year=='Yr5']<-5
gdata_long3$yr[gdata_long3$Year=='Yr6']<-6
gdata_long3$yr[gdata_long3$Year=='Yr7']<-7
gdata_long3$yr[gdata_long3$Year=='Yr8']<-8
gdata_long3$yr[gdata_long3$Year=='Yr9']<-9
gdata_long3$yr[gdata_long3$Year=='Yr10']<-10
gdata_long3$yr[gdata_long3$Year=='Yr11']<-11

#combination light(A) with "yes" watering
gdata_long4$yr[gdata_long4$Year=='Yr1']<-1
gdata_long4$yr[gdata_long4$Year=='Yr2']<-2
gdata_long4$yr[gdata_long4$Year=='Yr3']<-3
gdata_long4$yr[gdata_long4$Year=='Yr4']<-4
gdata_long4$yr[gdata_long4$Year=='Yr5']<-5
gdata_long4$yr[gdata_long4$Year=='Yr6']<-6
gdata_long4$yr[gdata_long4$Year=='Yr7']<-7
gdata_long4$yr[gdata_long4$Year=='Yr8']<-8
gdata_long4$yr[gdata_long4$Year=='Yr9']<-9
gdata_long4$yr[gdata_long4$Year=='Yr10']<-10
gdata_long4$yr[gdata_long4$Year=='Yr11']<-11

#combination light(B) with "yes" watering
gdata_long5$yr[gdata_long5$Year=='Yr1']<-1
gdata_long5$yr[gdata_long5$Year=='Yr2']<-2
gdata_long5$yr[gdata_long5$Year=='Yr3']<-3
gdata_long5$yr[gdata_long5$Year=='Yr4']<-4
gdata_long5$yr[gdata_long5$Year=='Yr5']<-5
gdata_long5$yr[gdata_long5$Year=='Yr6']<-6
gdata_long5$yr[gdata_long5$Year=='Yr7']<-7
gdata_long5$yr[gdata_long5$Year=='Yr8']<-8
gdata_long5$yr[gdata_long5$Year=='Yr9']<-9
gdata_long5$yr[gdata_long5$Year=='Yr10']<-10
```

```
gdata_long5$yr[gdata_long5$Year=='Yr11']<-11

#combination light(C) with "yes" watering
gdata_long6$yr[gdata_long6$Year=='Yr1']<-1
gdata_long6$yr[gdata_long6$Year=='Yr2']<-2
gdata_long6$yr[gdata_long6$Year=='Yr3']<-3
gdata_long6$yr[gdata_long6$Year=='Yr4']<-4
gdata_long6$yr[gdata_long6$Year=='Yr5']<-5
gdata_long6$yr[gdata_long6$Year=='Yr6']<-6
gdata_long6$yr[gdata_long6$Year=='Yr7']<-7
gdata_long6$yr[gdata_long6$Year=='Yr8']<-8
gdata_long6$yr[gdata_long6$Year=='Yr9']<-9
gdata_long6$yr[gdata_long6$Year=='Yr10']<-10
gdata_long6$yr[gdata_long6$Year=='Yr11']<-11

##data transform in log format
gdata_long$lnD<-with(gdata_long,log(D))
gdata_long$lnyr<-with(gdata_long, log(yr))

#combination light(A) with "NO" watering
gdata_long1$lnD<-with(gdata_long1,log(D))
gdata_long1$lnyr<-with(gdata_long1, log(yr))

#combination light(B) with "NO" watering
gdata_long2$lnD<-with(gdata_long2,log(D))
gdata_long2$lnyr<-with(gdata_long2, log(yr))

#combination light(C) with "NO" watering
gdata_long3$lnD<-with(gdata_long3,log(D))
gdata_long3$lnyr<-with(gdata_long3, log(yr))

#combination light(A) with "Yes" watering
gdata_long4$lnD<-with(gdata_long4,log(D))
gdata_long4$lnyr<-with(gdata_long4, log(yr))

#combination light(B) with "Yes" watering
gdata_long5$lnD<-with(gdata_long5,log(D))
gdata_long5$lnyr<-with(gdata_long5, log(yr))

#combination light(C) with "Yes" watering
gdata_long6$lnD<-with(gdata_long6,log(D))
gdata_long6$lnyr<-with(gdata_long6, log(yr))


# Growth model
# Shows the result of the linear fit for each treatment
M0 <- lm(lnD ~ lnyr, data=gdata_long)
M1 <- lm(lnD ~ lnyr, data=gdata_long1)
M2 <- lm(lnD ~ lnyr, data=gdata_long2)
M3 <- lm(lnD ~ lnyr, data=gdata_long3)
M4 <- lm(lnD ~ lnyr, data=gdata_long4)
M5 <- lm(lnD ~ lnyr, data=gdata_long5)
M6 <- lm(lnD ~ lnyr, data=gdata_long6)

summary(M6)

## a and b values to obtain linear model
#a1=0.48158#, a2=0.60676, a3= 0.41183, a4=0.61303, a5=0.38251,a6=0.34309
#b1=1.72944#, b2=1.72697, b3=1.69098,b4=1.75923, b5=1.69365, b6=1.69694

#to make data frame for Anova test

b0<-c(0.48158,0.60676,0.41183,0.61303,0.38251,0.34309)
b1<-c(1.72944,1.72697,1.69098,1.75923, 1.69365,1.69694)
light<-c('A','B','C','A','B','C')
water<-c('No','No','No','Yes','Yes','Yes')
```

```
coeff<-data.frame(b0,b1,light,water)

#Anova test for parameter
aov0 <- aov(b0 ~ light+water,data=coeff)
aov1 <- aov(b1 ~ light+water, data=coeff)
summary(aov0)
summary(aov1)

#Graph for basal diameter growth model

library(lattice)

xT<-c(1:11)
D0<-
  c(exp(0.48372)*xT^1.70591)
D1<-
  c(exp(0.48158)*xT^1.72944)
D2<-
  c(exp(0.60676)*xT^1.72697)
D3<-
  c(exp(0.41183)*xT^1.69098)
D4<-
  c(exp(0.61303)*xT^1.75923)
D5<-
  c(exp(0.38251)*xT^1.69365)
D6<-
  c(exp(0.34309)*xT^1.69694)
plot   (xT,D0,lwd=2,   type="l",ylim=c(0,125),   col   =   "red",   lty=1,   ljoin=10,
    main="Basal diameter growth",
      ylab="Diameter (mm)", xlab = "Age (years)")
lines(xT,D1,lwd=1, col = "blue")
lines(xT,D2,lwd=1, col = "pink")
lines(xT,D3,lwd=1, col = "green")
lines(xT,D4,lwd=1, col = "black")
lines(xT,D5,lwd=1, col = "yellow")
lines(xT,D6,lwd=1, col = "cyan")
legend("topleft",  legend=c("Total",  "Tr=No+A","Tr=No+B",  "Tr=No+C",  "Tr=Water+A",
    "Tr=Water+B","Tr=Water+C"),
       lty=c("solid","solid", "solid", "solid","solid" ),
       lwd=c(2,2,2,2,2),
       col=c("red", "blue", "pink","green", "black", "yellow", "cyan"))

#save the gdata_long in RData format
save(gdata_long,gdata_long1,gdata_long2,gdata_long3,gdata_long4,gdata_long5,gdata_l
    ong6, file="gdata_long.RData")
ls()
save.image("gdata_long.RData")
load("gdata_long.RData")


q ()

#########end############
```