Exploring Stand Structural Complexity's Drivers: A Cerrado (São Paulo State, Brazil) Case Using Stand Structural Complexity Index (SSCI)

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Abstract

Developing and understanding full potential of new tools for large scale reforestation programs has become essential nowadays. In this framework, stand structural complexity (SSC) has been identified as essential driver for multiple ecosystem services. Using terrestrial laser scanner (TLS) with light detection and ranging (LiDAR), I measured stand structural complexity index (SSCI) among four experimental reforestation sites in early development stage (three to eighteen years old) to identify impact of five potential SSC drivers: (1) water availability, (2) species diversity, (3) functional diversity, (4) tree density and (5) treatment applied on reforested sites. I find that (1) increased water availability enhances SSC as well as species diversity on lower level (up to six species) and (3) functional diversity. Contrastingly, no effect on SSC was observed for (2) high species diversity (twenty to one hundred fourteen species), (4) tree density and (5) treatment. SSC is likely to be enhanced by (1) water availability by promoting shade tolerant species abundance, and niche complementarity can explain positive impact on SSC by both (2) species and (3) functional diversity. On the other hand, competition for resources is likely to explain the limited impact on SSC by (4) increased tree density and (5) treatment. Finally, niche complementarity saturation is likely to explain saturating SSC on high species diversity plots. I conclude that (1) water availability plays a crucial role for improving stand structural complexity, being its main driver, (2) species diversity and (3) functional diversity (on lower level) improves it, but high tree density and species diversity as well as increased treatment play a neglectable role for enhancing stand structural complexity on forest's early stage. Those results put forward the importance of species mixtures with various functional traits in reforestation programs, and the unnecessity of increasing tree density and treatments (resulting in additional costs) for enhancing stand structural complexity.

Keywords: Stand structural complexity, stand structural complexity index, terrestrial laser scanner, reforestation programs, water availability, species diversity, functional diversity, tree density, treatment

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1. Introduction

Forests are some of the most complex and diverse ecosystems on our planet, providing numerous benefits to humans and wildlife alike. They are critical for regulating the Earth's climate, conserving biodiversity, providing ecosystem services, and supporting human livelihoods (Jenkins & Schaap 2018). Despite their importance, the cover of forests continues reducing nowadays. From 2000 to 2012, 1.5 Mha of forests got destroyed (Hansen & al. 2013) at a time when it is becoming increasingly important to recover its lost territories (Hakimovich & Alishovich, 2023; Silver & al. 2004; Locatelli & al. 2015; Egginton & al. 2014). However, increasing number of reforestations programs exist nowadays in order to fight this problem. For instance, the *Bonn Challenge* aims to reforest 168 Mha of degraded and deforested land in mainly tropical and subtropical area (IUCN 2020). Given the importance and the scale of this kind of program, efficiency becomes a key factor in order to achieve it. Improving knowledge and developing tool applicable on large scale is thus a priority to achieve expected goals.

In this framework, Stand Structural Complexity (SSC) appears as a powerful tool, as it has been suggested as an essential biodiversity variable (EBV) (Pereira & al. 2013; Reddy & al. 2021) as well as an indicator of ecosystem structure that is related to ecosystem services such as productivity (Dănescu et al. 2016; Juchheim et al. 2017; Gough & al. 2019; Stark & al. 2012), ecosystem resilience (Neill and Puettmann 2013), biodiversity (Lindenmayer et al. 2000; Zemp & al. 2019), habitat provision (Eichhorn et al. 2017) and functional richness (Lian & al. 2022). Among several definitions, it is, in the framework of this research, defined as “a measure of the number of different attributes present and the relative abundance of each of these attributes” (McElhinny et al. 2005). Its advantage lies in its ease and speed of measurement. Indeed, a recently developed index, the Stand Structural Complexity Index (SSCI) (Ehbrecht & al. 2017), may be a solution to the challenge of large-scale monitoring. Using a Terrestrial Laser Scanner (TLS) with LiDAR (Light Detection And Ranging) technology, SSCI can be locally measured in a few minutes only. Its second advantage is its application on very diverse forest type (Ehbrecht & al. 2021). It could thus become a strong tool to assess forests restauration needs and success. However, because of its recentness, we still lack of knowledge about its potential applications. As Stand Structural Complexity is likely to vary due to environmental factors, it is needed to collect new data on all the world forests, and moreover to understand which factors have an influence on it.

In this experiment, 5 factors have been selected to assess their impact on SSCI: (1) water availability, (2) tree species diversity, (3) trees functional diversity, (4) tree density and (5) treatment applied on reforested area. Those factors were selected because of their importance on reforestation process, as they are likely to impact forest ecosystem services (2,3) (Derhé & al. 2018; Quijas & al. 2019; Cheesman & al. 2018), establishment cost (4,5) (Brancalion & al. 2019) as well as productivity (1) (Gholz & al. 1990), thus reforestation program success. Moreover, preliminary tests were made in order to clarify on-field SSCI application, possible comparisons on experimental plots and to better understand effect of scanner’s parameter settings on SSCI.

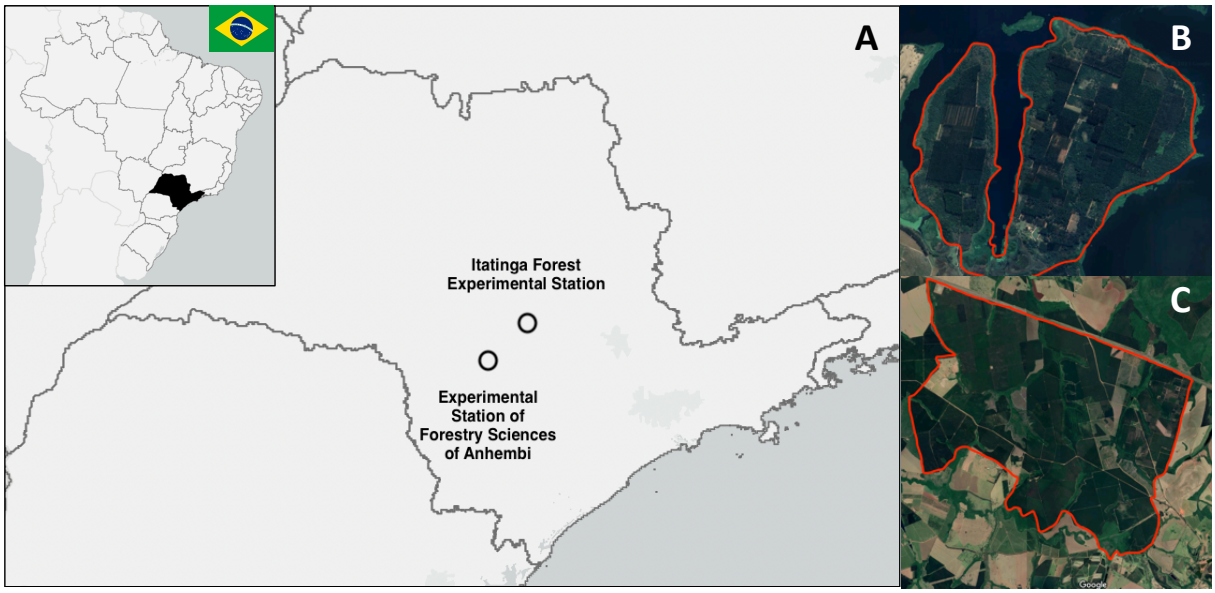
I hypothesized that, based on previous studies (Ehbrecht & al. 2021; Ali & al. 2019), (1) water availability has a strong positive impact on SSCI as it allows better tree survival and growth. (2) Tree species diversity is also expected to have a positive effect on SSCI by increasing vertical stratification and crown spatial complementarity (Xu & al. 2022). (3) Tree functional diversity is expected to have a positive effect on SSCI as well. Mix between fast and slow growing species should also create more vertical layer and crown complementarity that is expected to increase SSCI. (4) Tree density is once again expected to have a positive effect on SSCI. Indeed, increased density for same composition forest is expected to increase the forest’s complexity by providing more occupied space in a given area, but can be saturating in highest

density due to competition for resources acquisition. Finally, (5) increased treatments on reforested area are expected to increase SSCI by providing more nutrient and decreasing competition between trees, resulting in taller, denser and healthier, thus more complex forests.

2. Material and Method

2.1. Study sites

Both study sites are located in the state of São Paulo, Brazil (**Map.1**). The study focuses on four established experiments located in two experimental stations. All experience dry and moderately cold winters and rainy hot summers and located in the Cerrado biome (Appendix, **Map. A**). Measurements were made from September to December 2022 in-between the end of the dry season and the beginning of the rainy season in the early stage of leaf-fall season (Jackson, 1978). Main characteristics of each experimental site are summarized in **Tab. 1** and detailed below.



Map. 1. Experimental Stations map. (A) Experimental stations' location **(**São Paulo State, Brazil), background map from https://cepe-geo.maps.arcgis.com/apps/View/index.html?appid=d1c91fe2ccad4c79bb0fca5c216bbc16. (B) Experimental Station of Forestry Sciences of Anhembi, satellite view (https://www.google.com/maps)**. (**C) Itatinga Forest Experimental Station, satellite view (https://www.google.com/maps).

	Biodiversidade	**Carbono-Petrobras**	**Gradient**	**MataDiv**
Experimental Station	Anhembi	Anhembi	Itatinga	Itatinga
Forest Type	Plantation	Plantation	Natural Regeneration	Plantation
Year of Establishment	2006	2004	2007	2019
Factors Studied	Species diversity Density	Treatment Density	Humidity	Species Diversity Functional Diversity

Tab. 1. Experimental site summary. Headers correspond to experimental site's name.

2.1.1. Experimental stations

Experimental Station of Forestry Sciences of Anhembi

The first station is the Experimental Station of Forestry Sciences of Anhembi, at 22°40′ S latitude and 48°10′ W longitude and at an altitude of 455m, dominated by deep, sandy soil (Stape & al. 2006). The climate is classified as mesothermal Cwa (Köppen). The annual average rainfall is 1100 mm, with 20 mm of annual water deficit in the dry months (April to September) and the mean temperature is around 23,0°C (Dias Junior & al. 2021). Soil is characterized as acid (pH 4.0), Yellow Distrophic Latossols (Embrapa 2006), with low nutrient content (organic matter: 20 g/dm3; P: 7 mg/dm3; K: 1.1 mmolc/dm3; Ca: 7.0 mmolc/dm3; Mg: 4.0 mmolc/dm3; cation exchange capacity: 38.1 mmolc/dm3) and sandy texture (5% silt, 13% clay, and 82% sand) (Brancalion & al. 2019). Before the station's establishment, the area was covered by pastures of exotic grasses with no regeneration of native tree species (Duarte & al. 2021).

Itatinga Forest Experimental Station

The second station is the Itatinga Forest Experimental Station, at 23°02' S latitude and 48°38' W longitude and at an altitude of 830m. The climate is classified as humid subtropical Cfa (Köppen). Soils of the area vary from sandy to clayey (from altered sandstones) and are very deep (Lima & al. 1996). The average annual precipitation is about 1635 mm without significant water annual deficit, and mean annual temperature is around 19.4° C (Lima & al. 1996). Before the station was established, the land was used for eucalyptus plantation.

2.1.2. Experiments

MataDiv Experiment

Established in 2019 inside the Itatinga Forest Experimental Station, MataDiv is a tree plantation experiment on species and functional diversity gradient. It consists in 48 plots (20m x 23m, 100 trees per plot), in a randomized split-plot block design (Messier & al. 2022). Each of the 4 blocks is divided into 12 plots. Plots composition vary in number of species (1, 3, 6 and 20 species) as well as functional diversity (Monocultures (1 sp.), low (3 sp.), high (3 sp.), Maximum (6 sp.) and reference (20 sp.). Difference between low and high plots for functional diversity consist in variation of species with specific functional traits: slow- and fast-growing. Each plot composition is described in appendix (**Fig. H**).

Carbono-Petrobras Experiment

The *Carbono-Petrobras* project is located inside the Experimental Station of Forestry Sciences of Anhembi. Established in 2004, if focuses on tree plantation density, treatment (soil fertilization and weeding gradient) and abundance of pioneer species (Brancalion & al. 2019) effects on carbon storage. Each of them is compared by two different level, resulting in eight contrasted treatments. The experiment is implemented in a randomized block design with four replicates, resulting in 32 plots (42x30m per plot). As previous study (Brancalion & al. 2019) showed no impact on aboveground woody biomass between pioneer species proportions, focus is thus made here on density and treatment.

Density is measured by the distance between each tree planted in line (1m (high density) and 2m (low density)) and the distance between lines (3m), resulting in 1666 trees/ha for low density and 3333 trees/ha for high density plots.

Treatment corresponds to fertilizer and weed control application. Low treatment is considered as usual application for reforestation programs on abandoned pastures in the São Paulo region. It consists in repeated weeding use in a 50 cm width strip in planting rows and mechanized chopping between rows at 6, 12, 18, and 24 months after planting. Additionally, fertilization is made with 27 kg N, 21 kg P, 11 kg K, and 24 kg Ca per hectare, distributed as one single basal fertilization and two broadcasting fertilizations in the second and third year with NPK 18-06-24 (Brancalion & al. 2019). On the other hand, intensive treatment corresponds to use of 5 L/ha of glyphosate to control weeds across the entire plot every 3 months until canopy closure (first 2 yr), and fertilizers are tripled (81 kg N, 62 kg P, 33 kg K, 452 kg Ca, and 180 kg Mg per hectare) and used similarly as for low treatment (Campoe et al. 2010).

Biodiversidade Experiment

Located inside the Experimental Station of Forestry Sciences of Anhembi, the Biodiversidade experiment was established in 2006 on previously degraded area of pastures with exotic grasses (Duarte & al. 2021). It consists in a biodiversity gradient experiment of native species, divided into 3 categories (20 sp., 58sp. and 114sp.), as well as a fourth category that studies impact of density (114 sp.). The smaller species pools were subsets of the larger ones. It was implemented in a completely randomized design with 4 replicates, with sixteen 45x48m plots in total. Trees are spaced 1.5m apart in lines, and each line is 3m apart in less dense plots (20 sp., 58sp. and 114sp.; 2'500 trees/ha) and 1.5m in denser plots (114 sp.; 5'000 trees/ha).

Gradient Experiment

This experiment takes place inside the Itatinga Forest Experimental Station. In particular, I analyzed 3 locations split into three replicate plots (30m x 30m) next to each other. Plots consists in forest naturally regenerated for 15 years, after the cutting of an eucalyptus plantation. (1) The first location (plot type: Humid) is close to a water body at lower elevation (788m) characterized by denser vegetation with trees with lower diameter (average DBH 14 cm) with species such as *Casearia sylvestris* and *Eugenia dodonaeifolia* typical of riverine forest (Texeira & al. 2008). (2) The second location (plot type: Dry) is at higher elevation (815m), further from the water body, is characterized by sparse vegetation with larger tree diameters (average DBH 16 cm). Finally, (3) the third location (plot type: intermediate) is located at intermediate elevation (811m) and at intermediate proximity with water source.

This small elevation gradient results in differences in water availability, particularly in these sandy soils (~ 85% sand) with high water drainage, that influence the vegetation structure (Texeira & al. 2008, Elias & al. 2019). Since the preceding Eucalyptus plantation was managed uniformly, the regenerated forest on the selected plots has the same management history. As plots were newly established, no publication, thus no precise data on water availability, was available. Rather, this experiment focuses on a more general water availability gradient, with three categories: dry, intermediate and humid.

2.2. Scanner Measurement Settings

2.2.1. Scanner and Specific Parameters

All measurements have been processed using a Terrestrial Laser Scanner (TLS), the Faro Focus M70 (Faro Technologies Inc., Lake Mary, USA). It was placed on a tripod at breast height (1.3m) in vertical position. The field of view was set to 300° vertically and 360° horizontally with a step width of 0.035°. As no experiment exist to my knowledge to evaluate

impact of resolution and quality (specific parameter settings) on SSCI measurement, preliminary tests were made to assess optimal parameter settings (**Appendix Fig. B**). Based on those results and following Ehbrech & al. experiments (Ehbrecht & al. 2017, Zemp & al. 2019, Ehbrecht & al. 2021), intermediate scanning parameter have been chosen for resolution (1/4) and quality (x2), resulting in 43.7 mio. pixel scans. Those parameters allow significant time gain (scanning takes no longer than 6 min) without losing too much precision.

2.2.2. On-plot Measurement

As diverse forests were scanned in this experiment, two scanner position settings were chosen depending on plots size. On smaller plots (< 20m on smallest side), a single scan was performed by placing the scanner in the plot center. For plots larger than 20m side, three scans were made by placing the scanner around the plot center (distance between scans: 2-5m) in order to limit impact on SSCI of possible big obstacles (trunks or big leaves) close to the plot center. The mean of those 3 scans was then calculated to obtain a single SSCI value per plot.

Then, different parameter restrictions distances have been applied in post analysis to avoid any points scanned outside plots. They are determined by the plot size minus a 1-to-3-meter margin. In consequence, no comparison is possible between different-sized plots were parameter restriction smaller than 20m (radius) is applied. Indeed, preliminary tests were made (**Appendix, Fig. A**) to assess the impact of parameter restriction on SSCI and showed no significant difference on it for parameter restriction larger than 20m. Finally, in young reforestation plots with no or very few vegetation higher than 1.3m, any data experiencing negative MeanFRAC (see below) values were removed as no SSCI can be calculated in those condition.

2.3. Stand Structural Complexity Index

The Stand Structural Complexity Index was developed by Ehbrecht & al. (2017) in order to allow stand structural complexity measurement and comparison on very diverse forest type. It is calculated from two concepts: (1) MeanFRAC and (2) the Effective Number of Layer (ENL), following Ehbrecht & al. (2017) procedure. It is calculated as followed:

$$SSCI = MeanFrac^{\ln(ENL)}$$

(1) MeanFRAC is a measure of the forest's fractal dimension. To calculate it, scanned points are first turned into three-dimensional point clouds. Then, if needed, a parameter restriction is applied by excluding all points further from a given distance around the scanner position. Resulting point clouds are then cut into 1'280 vertical cross sections (based on scanner parameter divided by 4 to limit processing time). For each cross section, a polygon is created by sorting points by angle and linking them together. The ratio between the polygon's perimeter and area gives a fractal dimension's measure of the cross section. Finally, the mean of all cross-section's fractal dimension gives the MeanFRAC. Fractal dimension in calculated as followed, P corresponding to the polygon perimeter and A to its area:

$$FRAC = \frac{2*\ln(0.25*P)}{\ln(A)}$$

On the other hand, (2) ENL is a measure of the heterogeneity of vegetation in forest's horizontal layers that also takes stand height into account. As MeanFRAC is scale-dependent, ENL is used to scale it in order to enable SSCI measurement on very diverse forests. To calculate ENL, point clouds are cut into 1m horizontal layers. Then, the number of points per layer and the number of layers is measured to calculate the amount of vegetation per layer.

Finally, matter distribution's homogeneity is measured using the inversed Simpson's index. To summarize, ENL increases SSCI values in higher and more homogenous forests. It is calculated as followed:

$$ENL = 1/\sum_{i=1}^{N_{top}} p_i^2$$

SSCI, MeanFRAC and ENL were computed using RStudio (Version 2022.12.0+353) with packages *data.table*, *sphereplot*, *pracma*, *plot3D*, *rgl*, *sp*, *spacialEco*, *animation*, *rgeos* and *raster*. Script (v1.3) was made by Ehbrecht & al. (2017) and is available on https://github.com/ehbrechtetal/Stand-structural-complexity-index---SSCI. A code for perimeter restriction was added to the main script.

2.4. Canopy Cover

Canopy cover was calculated from scans by selecting a 60° opening angle above scanner. The amount of non-filled voxels on a two-dimensional picture was calculated and turned into a percentage using Ehbrecht & al. (2017) code, resulting in a measure of canopy openness. Canopy cover was finally calculated by subtracting canopy openness to 100% in order to facilitate understanding of results.

2.5. Statistical Analysis

All statistical computation were made using the software environment R, version 4.2.1 (R Development Core Team, 2016). A linear model was built to analyze comparisons for factors measured in the *Gradient* and the *Biodiversidade* experiments. SSCI, MeanFRAC, ENL and canopy cover were chosen as response variable and factors studied, corresponding to plot types (*Biodiversidade*: species diversity and density; *Gradient*: water availability), as explanatory variable. In the *MataDiv* and *Carbono-Petrobras* experiments, a linear mixed effect model was built with similar variables previously described (plot types focusing here on: *MataDiv*: species and functional diversity; *Carbono-Petrobras*: density and treatment), including blocks as random effect. Blocks in the *MataDiv* experiment are likely to vary because of the slope variation between block, and in the Carbono-Petrobras experiment because of the potential impact of neighboring plantation being different between blocks. Statistical significance was determined using an analysis of variance (ANOVA) and a Tukey test were then processed in post analysis to assess differences between groups. In order to identify which variable (MeanFRAC, ENL or canopy openness) was more likely to explain SSCI variations, a principal component analysis (PCA) was also applied for each factor in each experiment. Packages *multcomp* (Hothorn & al. 2008) *lme* (Pinheiro & al. 2007), and *corrr* (Kuhn & al. 2022) were used for statistical analysis.

3. Results

3.1. Data Visualization

All SSCI values are reported in the following plot (**Fig. 1**) in order to better understand SSCI variation and potential values. Values are ranged between 0,183 and 9.543. Statistical significances for MeanFRAC, ENL, canopy cover and SSCI are reported in **Tab. 2**.

	Stat Mod	Df	Sum Sq	Mean Sq	*F*-value	*p*-value
MeanFrac						
Biodiversidade – Sp. Div.	lm	2	0.03493	0.017467	1.769	0.225
Biodiversidade - Density	lm	1	0.05129	0.05129	9.457	0.0218 *
Gradient - Humidity	lm	2	1.1276	0.5638	27.54	0.000948 ***
MataDiv – Sp. Div.	lme	3	0.17293	0.057642	0.0659	0.9776
MataDiv – Fun. Div.	lme	4	0.70617	0.17654	0.2004	0.9365
Carbono-Petrobras - Treatment	lme	1	0.02353	0.02353	0.9466	0.3491
Carbono-Petrobras - Density	lme	1	0.014776	0.014776	0.5797	0.4606
ENL						
Biodiversidade – Sp. Div.	lm	2	4.397	2.1983	3.48	0.076
Biodiversidade - Density	lm	1	5.711	5.711	11.5	0.0147 *
Gradient - Humidity	lm	2	0.0948	0.0474	0.106	0.901
MataDiv – Sp. Div.	lme	3	13.958	4.6526	12.191	1.058e-05 ***
MataDiv – Fun. Div.	lme	4	14.108	3.527	9.0802	3.504e-05 ***
Carbono-Petrobras - Treatment	lme	1	8.7399	8.7399	5.8662	0.03268 *
Carbono-Petrobras - Density	lme	1	10.83	10.83	5.947	0.02866 *
Canopy Cover						
Biodiversidade – Sp. Div.	lm	2	7.688	3.844	2.189	0.168
Biodiversidade - Density	lm	1	17.11	17.11	10.06	0.0193 *
Gradient - Humidity	lm	2	4164	2082.1	20.95	0.00196 **
MataDiv – Sp. Div.	lme	3	778.83	259.61	1.2528	0.3048
MataDiv – Fun. Div.	lme	4	958.34	239.59	1.1556	0.3467
Carbono-Petrobras - Treatment	lme	1	18.289	18.289	0.6485	0.4341
Carbono-Petrobras - Density	lme	1	14.628	14.628	0.5139	0.4852
SSCI						
Biodiversidade – Sp. Div.	lm	2	2.194	1.0971	1.684	0.239
Biodiversidade - Density	lm	1	0.6526	0.6526	1.28	0.301
Gradient - Humidity	lm	2	30.4956	15.248	24.428	0.00131**
MataDiv – Sp. Div.	lme	3	4.0979	1.366	3.2676	0.03212 *
MataDiv – Fun. Div.	lme	4	5.0258	1.2564	3.1336	0.02634 *
Carbono-Petrobras - Treatment	lme	1	0.012416	0.012416	0.0125	0.9127
Carbono-Petrobras - Density	lme	1	0.02492	0.02492	0.0249	0.8771

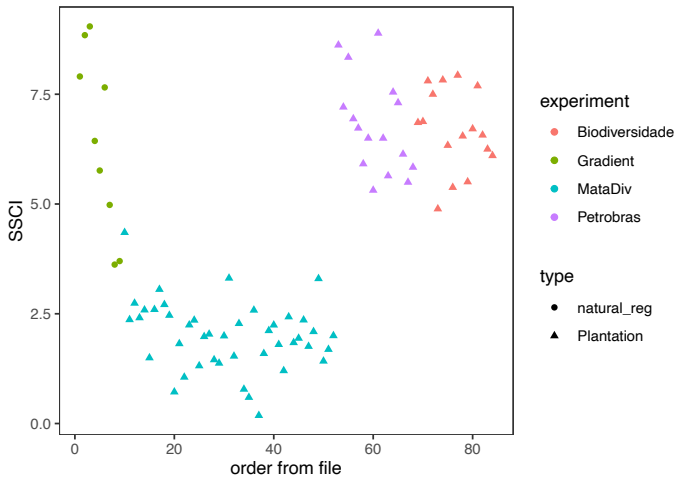


Fig. 1. Data presentation (Right). X axis corresponds to data order as the appear in data file, Y axis corresponds to SSCI values and colors and shapes represent experiments and forest types (natural regeneration and plantation).

Tab. 2. ANOVA results of the mean fractal dimensions (MeanFRAC), effective number of layer (ENL), canopy cover and stand structural complexity index (SSCI) (Left). *Note*: Stat Mod: statistical model, lm: linear model, lme: linear mixed-effect model, Df: degree of freedom, Sq: square, Sp. Div.: species diversity, Fun. Div.: functional diversity. Statistical significances are indicated: *p*-value <0.001 '***', <0.01 '**', <0.05 '*'.

3.2. SSCI Drivers

3.2.1. Humidity

Humidity has a significant impact on SSCI (Df = 2, Sum Sq = 30.4956, Mean Sq = 15.248, *F*-value = 24.428, *p*-value = 0.001308). In the Gradient experiment, each plot type was significantly different from others (Tukey test: Intermediate – Dry: p-value = 0.0186440; Intermediate – Humid: p-value = 0.0499265; Dry – Humid: p-value = 0.0010547), with higher SSCI values in plots experimenting higher humidity gradient (**Fig. 3**). PCA indicates that SSCI is strongly linked with canopy cover and MeanFRAC, but not with ENL (**Fig. 3**).

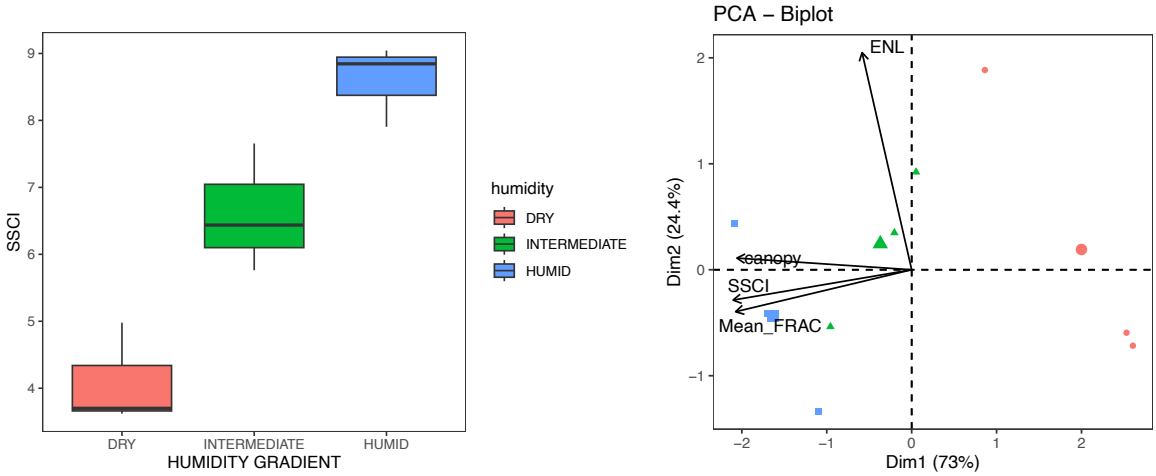


Fig. 3. Effect of humidity gradient on SSCI (*Gradient* experiment). (A)Evolution of SSCI depending on humidity gradient. Humidity is split into 3 categories: dry, intermediate and humid. (B) Output of principal component analysis (PCA) of the different components of structural complexity: mean fractal dimensions (MeanFRAC), effective number of layers (ENL) and SSCI. Measures about canopy openness (canopy) are also included. All variables were scaled to unit variance and centered around zero. The proportion of variance explained by the two principal components (Dim1 and Dim2) are indicated in the axes. Colors associated for each group match in both figures.

3.2.2. Species Diversity

In the *MataDiv* experiment, species diversity has a significant impact on SSCI (Df = 3, Sum Sq = 4.0979, Mean Sq = 1.366, *F*-value = 3.2676, *p*-value = 0.03212). However, no significant differences were observed between plot types, 1-6 species plots being the most different (Tukey test [1-6 Species]: p-value = 0.0908300). An increasing SSCI mean can be observed from 1 to 6 species plots, but 20 species plots had a lower mean than 6 species ones (Tukey test for SSCI: mean 6sp. = 2.88 vs. mean 20 sp. = 2.40). PCA results suggest a contrasted impact on SSCI from all influencing factors, MeanFRAC having the greater one (**Fig. 4**).

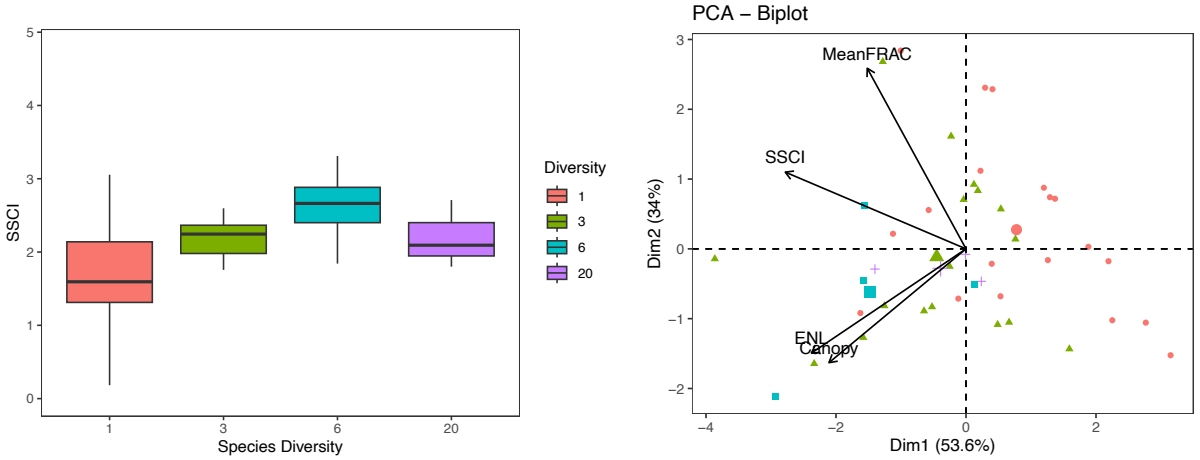


Fig. 4. Effect of species diversity on SSCI (*MataDiv* experiment). Species diversity is split into 4 categories: mono-species, 3, 6 and 20 species per plot. **Left**: Boxplot of SSCI values depending on species diversity. **Right**: Output of principal component analysis (PCA) of the different components of structural complexity: mean fractal dimensions (MeanFRAC), effective number of layers (ENL) and SSCI. Measures about canopy openness (canopy) are also included. All variables were scaled to unit variance and centered around zero. The proportion of variance explained by the two principal components (Dim1 and Dim2) are indicated in the axes. Colors associated for each group works for both figures.

On the other hand, SSCI in the *Biodiversidade* experiment didn't show any significant difference among plots (Df = 2, Sum Sq = 2.194, Mean Sq = 1.0971, *F*-value = 1.684, *p*-value = 0.239). Rather, it decreased for intermediate diversity (58 sp.: mean = 5.84) and was almost equivalent for lower (20 sp.) and higher diversity (114 sp.) plots (mean 20 sp. = 6.54 vs. mean 114 sp. = 6.87) (**Fig. 5**). No plot type was significantly different from others (Tukey test: 20-58 sp.: p-value = 0.4718670; 58-114sp.: p-value = 0.2246405; 20-114sp.: p-value = 0.8350488). PCA results suggest a main effect on SSCI from MeanFRAC, rather than canopy cover or ENL, being inversely correlated (**Fig. 5**).

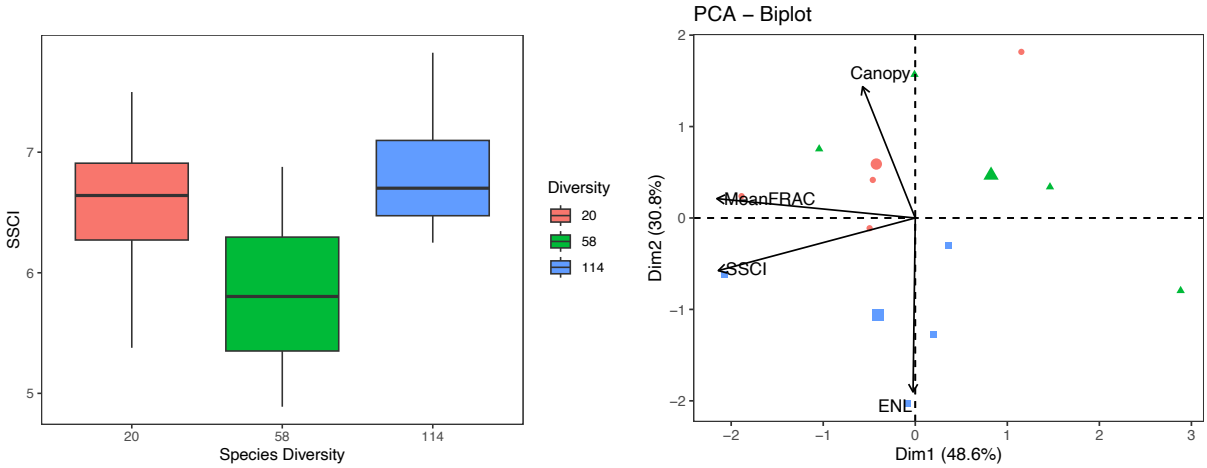


Fig. 5. Effect of species diversity on SSCI (*Biodiversidade* experiment). Left: Boxplot of SSCI values depending on species diversity. Numbers on the x axis correspond to the number of tree species per plot. **Right**: Output of principal component analysis (PCA) of the different components of structural complexity: mean fractal dimensions (MeanFRAC), effective number of layers (ENL) and SSCI. Measures about canopy openness (canopy) are also included. All variables were scaled to unit variance and centered around zero. The proportion of variance explained by the two principal components (Dim1 and Dim2) are indicated in the axes. Colors associated for each group match in both figures.

3.2.3. Functional Diversity

Functional diversity in the *MataDiv* experiment shows a significant impact on SSCI (Df = 4, Sum Sq = 5.0258, Mean Sq = 1.2564, *F*-value = 3.1336, *p*-value = 0.02634). No plot type was significantly from each other, but monocultures had the smallest mean (Tukey test [Monoculture]: mean = 1.65) and 6 species plots (Maximum) had the highest one (Tukey test [Maximum]: mean = 2.62) (**Fig. 6**). Although non-significant, SSCI shows an increasing trend when functional diversity increases as well, but decreases on high diversity plots (Reference). PCA results are showed in **Fig. 6**.

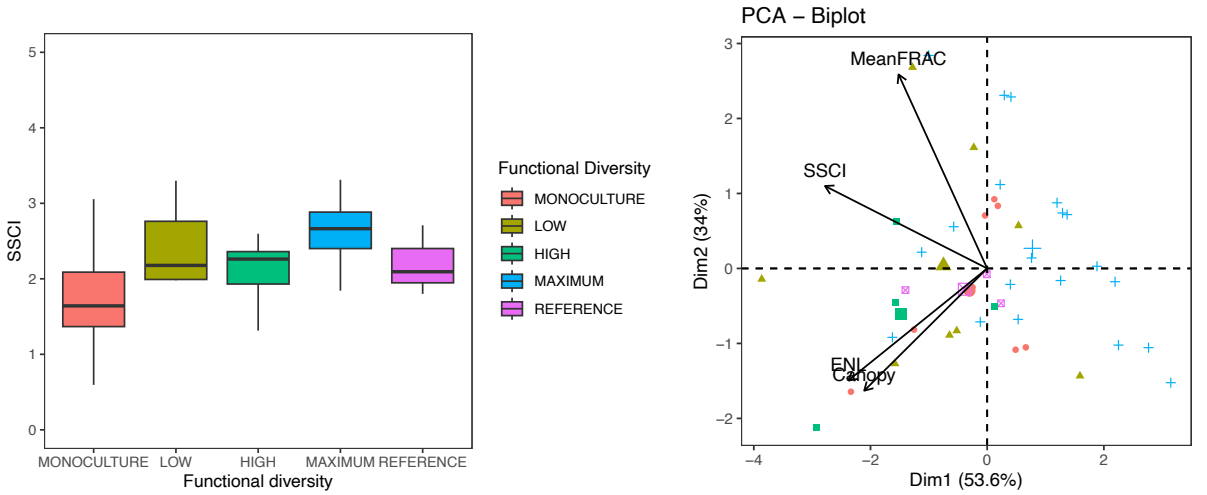


Fig. 6. Effect of functional diversity on SSCI (*MataDiv* experiment). Left: Boxplot of SSCI values depending on functional diversity. MONOCULTURE corepond to 1 species plots, LOW corresponds to no mix between slow- and fast-growing species (n. sp.= 3), HIGH corresponds to a mix between slow- and fast-growing species (n. sp.= 3), MAXIMUM corresponds to all 6 species combined and REFERENCE corresponds to a 20 species reference including 6 pervious species. **Right**: Output of principal component analysis (PCA) of the different components of structural complexity: mean fractal dimensions (MeanFRAC), effective number of layers (ENL) and SSCI. Measures about canopy openness (canopy) are also included. All variables were scaled to unit variance

and centered around zero. The proportion of variance explained by the two principal components (Dim1 and Dim2) are indicated in the axes. Colors associated for each group works for both figures.

3.2.4. Tree Density

In the *Carbono-Petrobras* experiment, no significant differences were observed between low- and high-density plantation for SSCI (Df = 1, Sum Sq = 0.2492, Mean Sq = 0.2492, *F*-value = 0.0249, *p*-value = 0.8771). However, SSCI mean is slightly higher in denser plots (Tukey test: mean high-density = 6.92 vs. mean low-density = 6.69). PCA results suggest a main effect on SSCI from MeanFRAC, rather than ENL (**Fig. 7**). Canopy cover had few impacts on SSCI.

Similar results were obtained in the *Biodiversidade* experiment. No significant difference between low- and high-density plantation were observed for SSCI (Df = 1, Sum Sq = 0.06526, Mean Sq = 0.6526, *F*-value = 1.28, *p*-value = 0.301). As for the *Carbono-Petrobras* experiment, high-density plantations were however slightly more complex (Tukey test: mean high-density = 7.44 vs. mean low-density = 6.87). PCA results suggest a main effect on SSCI from MeanFRAC rather than ENL (**Fig. 8**). Canopy cover had fewer impact on SSCI.

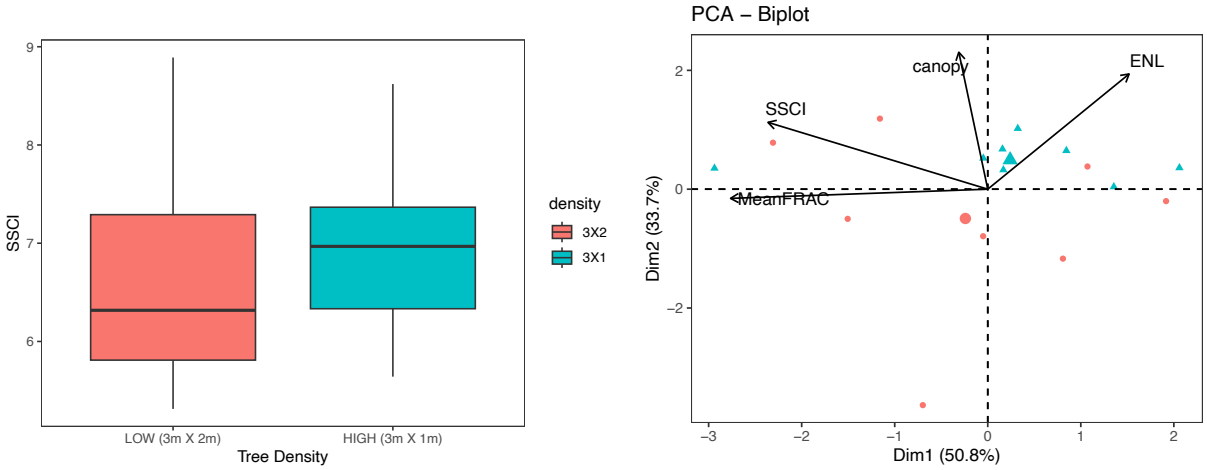


Fig. 7. Effect of tree density on SSCI (*Carbono-Petrobras* experiment). Density is determined by space between trees in a line (1m or 2m) and space between lines (3m). **Left**: Boxplot of SSCI values depending on tree density. **Right**: Output of principal component analysis (PCA) of the different components of structural complexity: mean fractal dimensions (MeanFRAC), effective number of layers (ENL) and SSCI. Measures about canopy openness (canopy) are also included. All variables were scaled to unit variance and centered around zero. The proportion of variance explained by the two principal components (Dim1 and Dim2) are indicated in the axes. Colors associated for each group match in both figures.

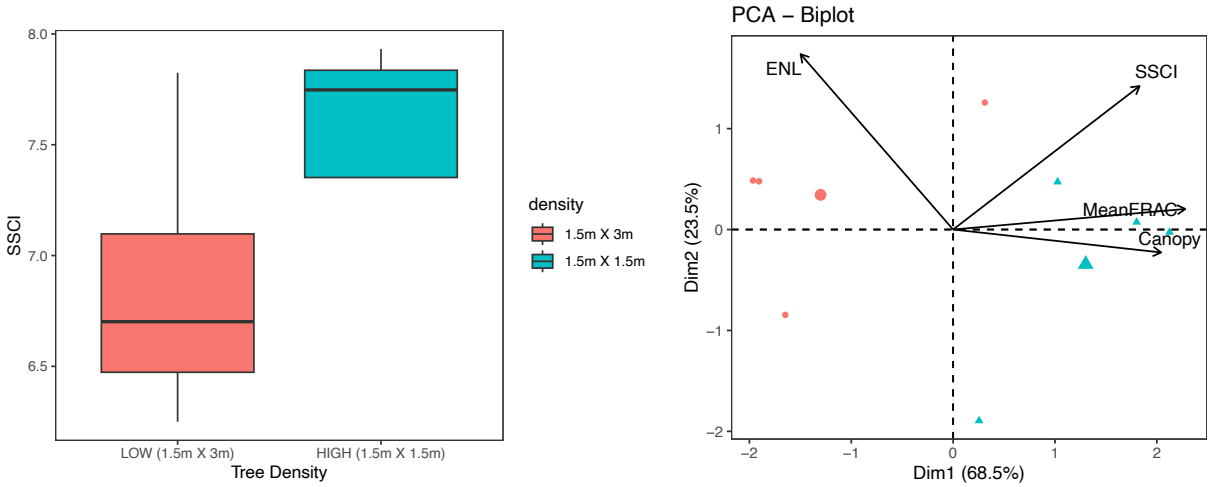


Fig. 8. Effect of tree density on SSCI (*Biodiversidade* experiment). Density is determined by space between trees planted in lines (1.5m) and space between lines (1.5m or 3m). **Left**: Boxplot of SSCI values depending on tree density. **Right**: Output of principal component analysis (PCA) of the different components of structural complexity: mean fractal dimensions (MeanFRAC), effective number of layers (ENL) and SSCI. Measures about canopy openness (Canopy) are also included. All variables were scaled to unit variance and centered around zero. The proportion of variance explained by the two principal components (Dim1 and Dim2) are indicated in the axes. Colors associated for each group match in both figures.

3.2.5. Treatment

Tripling fertilizers and applying chemical weed control showed no significant difference on SSCI in the *Carbono-Petrobras* experiment (Df = 1, Sum Sq = 0.012416, Mean Sq = 0.012416, *F*-value = 0.0125, *p*-value = 0.9127). Mean SSCI measured on intensive treatment plots was even slightly lower (Tukey test: mean usual = 6.86 vs. mean intensive = 6.75). PCA shows a main effect on SSCI from MeanFRAC and canopy cover rather than ENL (**Fig. 9**)

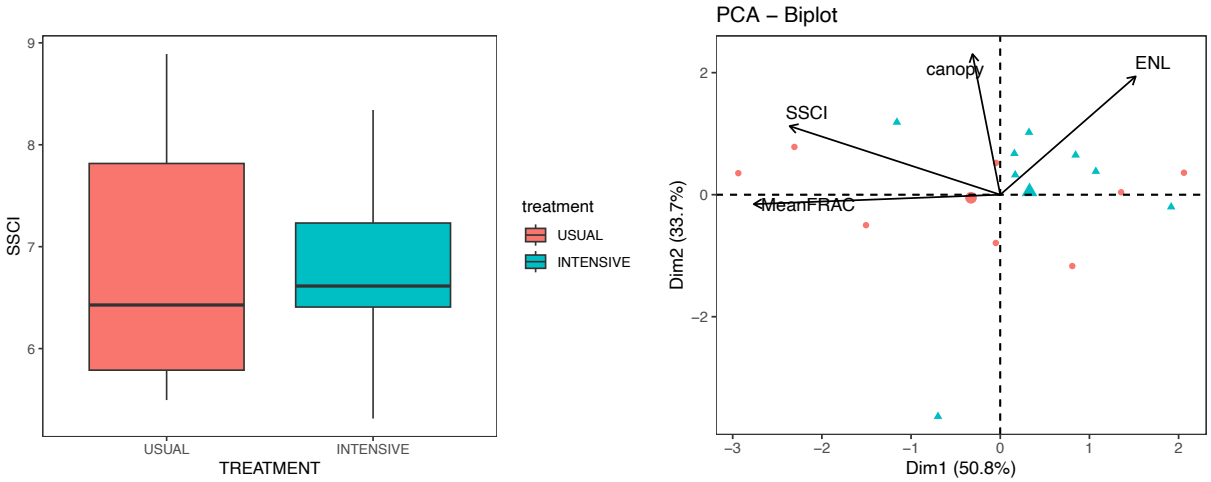


Fig. 9. Effect of treatment on SSCI (*Carbono-Petrobras* experiment). Usual corresponds to normal fertilization (27 kg N, 21 kg P, 11 kg K, and 24 kg Ca per hectare) and mechanical weed control (6, 12, 18, and 24 months after planting) and Intensive corresponds to a tripled amount of fertilizer (81 kg N, 62 kg P, 33 kg K, 452 kg Ca, and 180 kg Mg per hectare) and weed control using glyphosate (5 L/ha). **Left**: Boxplot of SSCI values depending on applied treatment. **Right**: Output of principal component analysis (PCA) of the different components of structural complexity: mean fractal dimensions (Mean_FRAC), effective number of layers (ENL) and SSCI. Measures about canopy openness (canopy) are also included. All variables were scaled to unit variance and centered around zero. The proportion of variance explained by the two principal components (PC1 and PC2) are indicated in the axes. Colors associated for each group match in both figures.

4. Discussion

4.1. SSCI Drivers

4.1.1. Humidity

Results on humidity gradient are the most significant obtained of all experiments (**Tab. 2**). According to PCA results (**Fig. 3**), differences in SSCI were mainly due to MeanFRAC and canopy openness variations rather than ENL. The density variation among plot types was visually observable (**Appendix 6.5.1**) with denser vegetation in more humid plots and more opened one in dryer plots.

As canopy cover was significantly correlated with the water gradient (**Tab. 2**), one can consider the Physiological Tolerance Hypothesis (Currie & al. 2004) as an explanatory theory. It justifies the density variation by the inability of specific plant groups to spread and survive because of specific climatic factors. Shade tolerant plants, for instance, are indeed less likely to survive in dryer conditions (Valladares & Niinemets, 2008). This group's lack of abundance is likely to have an impact on stand structural complexity as it can represent an important part of the under-canopy layers (Mestre, 2017). Additionally, because of its diversity in height and shapes, this group is likely to increase vertical stratification and complementarity in canopy cover (Ehbrecht & al. 2021). In consequences, forests become less occupied on low and intermediate layers which results in a lower density and fractal dimension, as supported by MeanFRAC results (**Appendix Fig. C**). The combination of lack of vegetation on under-canopy layer and the lack of canopy closure results in loss of structural complexity on every layer, which is likely to explain the highly significant impact of water availability on SSCI.

However, other parameters have been put forward as complementary hypotheses in similar studies (Ehbrecht & al. 2021), like the impact of water availability on trees dimensions (height and canopy tree dimensional crown structure) (Ryan & al. 2006; Klein & al. 2015) but have not been tested in this experiment. Knowledge about full mechanisms involved in stand structural complexity-water availability relationship remain scarce as water availability impacts several other factors (functional diversity, physiological tolerance) that can affect stand structural complexity. It is likely that a combination of all factors involving water would result in a more accurate overview of its impact on stand structural complexity.

4.1.2. Species Diversity

On low diversity experiment (*MataDiv*), species diversity had a significant impact on SSCI. However, the relationship didn't follow a linear trend, as maximal diversity plots (20sp. (Reference)) had smaller SSCI than 3 and 6 species plots. It is likely that the plantation's youth (3 y.o.) doesn't allows to observe a clear linear effect as young trees are not fully developed, thus full potential structural complexity isn't achieved yet. This trend has been observed in similar study (Perles-Garcia & al. 2021) with a negative correlation between tree species richness and SSCI in the same stage of trees growth (3-4 y.o.) that inversed on later stages (10 y.o.).

It is also possible that species added to high diversity plots (20sp.) can negatively impact SSCI. Slow-growing or less structurally complex species would decrease SSCI and decrease in relative abundance of the 6 remaining species couldn't counterbalance this effect. As 14 complementary species aren't named in the original experimental protocol, no analyze is possible here. Further research about species-specific effects for the added species on reference plots (20sp.) should be thus made to clarify this point. Note that no significant species-specific effect on SSCI for the 6 main species have been found in this experiment (**Appendix Fig. F**).

It is also likely that the season where measurement were made could have impacted SSCI results, as not all trees had their full leaves developed (**Appendix 6.5.2**), which could have result in neglected effect of crucial species for enhancing SSCI.

Additionally, it could also be possible that tree species richness-SSC relationship reaches a threshold for a given tree diversity. Coverdale & Davies (2023) showed in an overview study that the relation between SSC and tree species richness saturated when reaching a given richness level. This would here suggest a threshold between 6 and 20 species. However, this limit is likely to vary depending on location, climate and trees age (Perles-Garcia & al. 2021).

Although contrasted by the 20 species plots SSCI's values, those results are consistent with previous studies on the subject (Perles-Garcia & al. 2021; Ehbrecht & al. 2017; Juchheim & al. 2019; Zemp & al. 2019). As well as adding new evidences of the link between stand structural complexity and tree species richness, they especially underline this trend on very young forest stage, supporting the importance of stand structural complexity on reforestation programs.

On the other hand, SSCI showed no linear relation to species diversity on high diversity experiment (*Biodiversidade*). Even if maximal diversity plots (sp. = 114) had highest SSCI values, 58 species plots experienced smaller stand structural complexity than 20 species plots. Although different than results obtained in the low diversity experiment, these results seem to point the existence of a threshold in species diversity-SSC relationship, as showed by Coverdale & Davies (2023), that could fit with the threshold theory previously discussed. MeanFRAC followed similar pattern than SSCI (**Appendix Fig. C**) with lower values for 58 species plots, which supports the structural complexity's saturation. However, ENL followed a linear trend, although insignificant (p-value = 0.076), being maximal on maximal diversity plots. Variations once the limit reached could be due to differences in crown complementarity depending on the species mixture (Ammer, 2018), that could explain and ENL increase without SSCI's increase. Increase in tree species diversity could thus result in more stratified forests rather than more complex ones. Nevertheless, as vertical stratification has been proven as a driver for vertebrates and invertebrates' diversity (Basham & al. 2023; Oliveira & Scheffers, 2019; Plewa & al. 2017; de Souza Amorim & al. 2022) as well as productivity (Lin & al. 2018; Dănescu & al. 2016), these results still support the impact of plant diversity on forest 3D-structure and its importance arising from it although saturating on Stand Structural Complexity.

4.1.3. Functional Diversity

Results obtained for functional diversity were very similar to the ones for species diversity. Knowing that species diversity affects ecosystem functioning via functional diversity (Hooper & al. 2005), this similarity was expected. Species were selected for their variance in functional traits and the low number of selected traits (growth speed) and the low differences between species number (6) and the functional traits selected (3: low, intermediate and fast growing), was expected to give similar results. More contrasted results would have been expected if species number was higher for the same trait selected (growth rate).

Although no significant difference was observed among three species mixtures, we still can observe a significant increasing trend (p-value = 0.02634), with minimal SSCI values on monoculture plots and maximal SSCI on maximal diversity plots (6 sp.), reference plots (20 sp.) being once again less complex than the latter. Analyses on species-specific effect have showed a significant difference on ENL and canopy cover (**Appendix Fig. F**) between plots containing Jeriva (*Syagrus romanzoffiana*) (slow-growing) and Embauba (*Cecropia pachystachya*) (fast-growing) trees, the latter having higher values. Unfortunately, both trees were present in both low- and high-functional diversity groups, which is likely to explain the

lack of difference obtained in those groups. SSCI mean on low functional diversity plots (mean = 2.42) was even higher than on high ones (mean = 2.08).

The niche complementarity hypothesis (Tilman 1999), namely the enhanced ecosystem functioning by an increase of niche complementarity induced by variation in species of functional diversity (Ali et al., 2018, Zhang et al., 2012), is likely to explain increasing SSCI trend when functional diversity increases induced by species diversity increase. Variation in tree growth, thus height, enhances available 3D space which allows better leaves development and, by extension, light acquisition, as supported by both ENL and canopy cover results.

On the other hand, the selection effect (Loreau & Hector 2001) (in opposition to the niche complementarity effect), namely a higher impact on ecosystem functioning by few productive and high functioning species in the community (Ali, 2019), can better explain the lack of difference among 3 species mixture plots. As Embauba (*Cecropia pachystachya*) trees, being the high functioning species in this case, were present in both low- and high-functional diversity plots, the selection effect could have overpassed the complementarity effect, preventing expected complementarity in high-functional diversity plots. Other study put forward impact on SSCI from single highly-complex individuals (Seidel & al. 2019) rather that a mixed community. It is also possible that functional traits haven't fully emerged, which would suggest a clearer effect on latter plantation development stages. Selection effect could also explain lower SSCI values in 20 species plots than in 6 species plots. If Embauba trees indeed act as a high functioning species, its relative abundance's decrease in 20 species plots could justify lower SSCI values. Complementary study should be made to identify other potential high functioning species in reference plots (20 sp.) to confirm this hypothesis. Nevertheless, those explanation are likely to evolve over time, as the plantation's stage is probably unlikely to show expected results because of its youth. Actual results however remain strong argument of the importance of species mixtures for enhancing stand structural complexity even on very young plantation's stage.

4.1.4. Tree Density

Impact of tree density on SSCI showed contrasted results. When results in the *Carbono-Petrobras* experiment only showed significant difference ENL, being higher in denser plots, results in the *Biodiversidade* experiment were significantly different for MeanFRAC, ENL and canopy cover. Surprisingly in this latter, ENL was lower in denser plots, whereas MeanFRAC and canopy cover had higher values.

Results obtained in the *Carbono-Petrobras* experiment can be explained by the competition for resources, light in this case, which is likely to explain higher ENL (**Appendix Fig. D**) in denser plots. Previous studies (Stape & Binkley, 2010; Pretzsch, 2009; Gonçalves & al. 2004) put forward similar results, namely thinner and higher stems in denser forests. Difference in height could justify similar MeanFRAC results as both plot types had same fertilizer inputs and, as increased density results in less available space, which is likely to prevents horizontal growth in denser plots. Once again, results for canopy cover match with this theory as both plot types obtained values close to 100% (**Appendix Fig. E**), which underlines the importance of light acquisition. Moreover, Brancalion & al. (2019) put forward the increased proportion of colonizing species in plots with lower density, that could have induced a bias in effective density in those plots, which could also justify the lack of differences in both plot types.

Contrastingly, MeanFRAC and canopy cover were significantly higher in denser plots in the *Biodiversidade* experiment, but ENL was significantly lower in those plots, which justifies the similarity obtained in SSCI values. It is possible that higher density in this experiment (2'500 and 5'000 trees/ha vs. (Carbono-Petrobras) 1'666 and 3'333 trees/ha) has results in over-exploited plots, that could have results in smaller trees in high density plots. This would suggest

additional limiting factor, such as soil nutrients, that would have prevented higher trees in denser plots (Duan & al. 2019; John & al. 2007) as suggested before. Indeed, high density plots with intensive treatment (**Appendix Fig. G**) had highest SSCI means, although unsignificant. In this situation, MeanFRAC difference would be justified only by the difference in density, resulting in more occupied space, rather than by modification in trees dimensions induced by density (Ledermann & Stage, 2001). It would thus result in higher and more open forests in less dense plots, and lower and denser forests in denser plots. Canopy cover, although significantly different, is not likely to explain SSCI values, as both were close to 100% (**Appendix Fig. E**). It could, as for the *Carbono-Petrobras* experiment, only justify a competition for resources effect. Further researches should be made about tree height and soil composition differences to confirm those theories.

No effect of density was observed in this experiment. When a saturating effect was expected in denser plots, it appeared in lower density and an increasing (although unsignificant) SSCI was observed in highest density, invalidating hypothesis 4. Rather, those results suggest a negligible effect of tree density on SSCI due to competition for resources acquisition. However, an effect remains possible for lower densities, which should be further explored.

4.1.5. Treatment

Tripling the amount of fertilizer and using chemical weed control had no effect on SSCI. Similarly, none of ENL, MeanFRAC, or canopy cover showed any significant differences. The only slight SSCI increase observed was for high density plots with intensive treatment (**Appendix Fig. G**) for reasons described in the density discussion (4.1.4), namely a better tolerance to competition due to fertilizer increase.

Brancalion & al. (2019) put forward that three-quarter of all regenerating species on plots where not planted but colonizing species. Moreover, 74 % of all individuals were *Senegalia polyphylla* (DC.), a legume tree producing many leaves. It is thus likely that resulting differences in species compositions between plot types, as well as a high proportion of *Senegalia polyphylla* in all plots that is likely to have a strong impact on SSCI measurement due to its high leaves content, would have counterbalance the effect of fertilizer and chemical weed control on stand structural complexity. Additionally, as fertilization and weed control were only made in the two first years of establishment, it is possible that the effect of treatment has fade away over time. This study was made 7 years after the last study (Brancalion & al. 2019) on the experiment site. Even though this latter and the two previous studies (Campoe & al. 2010; Ferez & al. 2015) on this experiment showed a significant effect of intensive treatment on above ground biomass, it is possible that differences between plot types were reduced due to a higher competition between individuals in more developed plots that would have slowed plot total growth. Less developed plots, being less impacted by this constraint, would thus have a higher growth rate in the meantime. Further researches are needed to clarify this point by assessing this evolution on a longer time range. Finally, it is also possible that increasing fertilizer makes no difference in the framework of stand structural complexity. Low treatments correspond to ones usually used in reforestation programs in the region (Brancalion & al. 2019), which should already have been selected for its efficiency. Although other studies (Looney & Zhang 2022; Lindgren & Sullivan 2013; Edenius & al. 2011) showed a clear increase in stand structural complexity in fertilized stands compared to unfertilized ones, no study to my knowledge explored impact of increased fertilization on stand structural complexity. Those results thus suggest a maximal fertilizer input threshold for enhancing stand structural complexity, although not clearly defined in this study.

4.2. Limitations and Further Researches

One main limitation in this study is the forests and plantations' age range limitation. As already mentioned, all obtained results are likely to evolve over latter forests development. Unfortunately, no older experiment was available in the region to prove this point. Impact of species and functional diversity on stand structural complexity could be studied by comparing natural forest with variation in those parameters. Density could also be compared by comparing logged and unlogged natural forests. It remains however likely that resulting results would lack of strength because of additional variables dues to natural conditions, compared to controlled established experiments. It results from this point an essential factor, but not measured in this experiment: age. Although intuitively crucial, precise evolutional trend of stand structural complexity over forest's development remain unstudied to my knowledge. It seems obvious that SSC strongly increases in first development stages, but its evolution on later stage (+50 y.o.) is likely to be more contrasted. Primary forest has been showed to be most complex stage (Donato & al 2012), but most study on the subject were in the framework of stopping forest management, rather that pure natural evolution.

Another potential bias in this study is the line planting design in experimental sites. It results in open lines that could influence SSCI measurement, especially MeanFRAC. This design is likely to increase plots heterogeneity compared to a random planting design, more coherent with natural forest's composition. An experiment could be established with various planting design and the same tree composition in each to assess the potential impact of it on stand structural complexity.

4.3. Conclusion

Over all drivers tested in the framework of this study, water availability was by far the most decisive one for enhancing stand structural complexity, by impacting forests' fractal dimension (MeanFRAC) and canopy cover. Those results are consistent with the ones obtained in Ehbrecht & al. (2021) study, namely that stand structural complexity is climate-dependent, thus maximal valued cannot be expected to be the same depending on biomes concerned. However, water inputs in reforestation programs remains crucial for achieving full potential stand structural complexity.

Results on species diversity showed an increasing impact on SSCI at low diversity (up to 6 species) and a saturating one for higher species diversity (20 – 114 species), supporting analyses made in Coverdale & Davies (2023) overview paper. Those results put forward the effect of species diversity on very early forest development's stage (3 y.o.), especially by enhancing effective number of layers (ENL). The saturating trend, although consistent with previously named study, was also observed in relatively young forest's stage (16 y.o.). It remains likely that this trend can evolve over time, a supported in Stiers & al. (2018) study.

Functional diversity, strongly linked with species diversity, failed to show significant relationship with SSCI. Although an increasing trend was observed when species number in plots increased (1 – 6 species), thus functional diversity because of the chosen species in this experiment, due to the niche complementarity effect, variation in functional traits among 3 species mixtures failed to show significant differences, probably due to the selection effect induced by Embauba (*Cecropia pachystachya*) trees present in both plot types (low- and high-functional diversity plots). Additionally, further analyses on species-specific effect are needed to better understand SSCI decrease in 20 species plots (for functional and species diversity).

SSCI wasn't significantly different on low- and high-density plots. It is likely that limiting factors, such as light acquisition in lower density experiment (*Carbono-Petrobras*: 1'666 and 3'333 trees/ha) and light as well as soil nutrients in higher density experiment (*Biodiversidade*:

2’500 and 5’000 trees/ha) have constrained tree development, in addition to higher number of colonizing species in less dense plots, creating a bias of effective tree density.

Finally, increased fertilization and chemical weed control made no differences on stand structural complexity, although previous studies on the same experiment site showed strong correlation between increased treatment and aboveground biomass. It is likely that colonizing species producing many leaves (*Senegalia polyphylla* especially) present in both plot types have induced a bias for SSCI measurement. It is also possible that specific treatment only made in the two first years of experiment’s establishment have fade away over time, resulting in equally complex plots.

4.4. Reforestation Guidelines

This study mainly puts forward the unnecessity to increase tree density or fertilizer inputs in order to improve stand structural complexity. As reforestations programs can be costly, especially on large scale, results obtained suggest the possibility to avoid unnecessary expenses for similar results. Fertilizer in early stages remains essential for quick forest development and to limit negative effect of competition for resources, but increasing usual doses would only results in increased cost. Exact amount needed is of course site depending, and become more important in poor soil conditions (Günter & al. 2009). Decreased density put forward the better possibility for colonizing species to develop in reforested areas due to decreased competition for resources, such as light acquisition. If those species are expected (depending on reforestation purposes), they can settle through natural processes at zero cost. This is especially relevant in the framework of natural forest restauration.

Then, although results on both species and functional diversity failed to show benefits for stand structural complexity on higher diversity (more than 6 species), it remains important to specify that this study focuses on very early stages of forest’s development (3 – 18 y.o.). Those results cannot thus be interpreted as a limitation for increasing species diversity in restoration programs because of the likely evolution on later development stages. Moreover, all results on those factors clearly put forward the decreased structural complexity in monoculture plots, supporting the importance of species mixtures.

Finally, water availability appears in this study as an indicator for potential stand structural complexity, rather than a recommendation for project management. Water needs for vegetation growth in of course not new, but as suggested in Ehbrecht & al. (2021) study, maximal potential stand structural complexity in natural forests depends on climatic condition, especially on water availability.

Acknowledgment

I thank the Biology Conservation laboratory of University of Neuchâtel, especially Clara Zemp and Vannesa Montoya-Sánchez for supervising my Master thesis, providing the (expensive) scanner and making this study possible. I also thank the LasTrop team from the Escola Superior de Agricultura "Luiz de Queiroz"/University of São Paulo (ESALQ/USP), under the direction of Pedro H.S. Brancalion, for allowing this study on their experiment sites. A Special thanks to Martin Ehbrecht for kindly helping on SSCI specificitie. Additionally, I thank Rildo Moreira e Moreira, the Itatinga Forest Experimental Station’s manager for driving me among plots and pushing me to practice Portuguese. Finally, a huge thank to Greta Formaglio for supervising my research on field, proposing additional experiments, helping me for data collection, helping me to install in Piracicaba (Brazil), in short, without whom this paper would never have existed.

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6. Appendix

6.1. Parameter Tests

To ensure a coherent data sampling, two parameter tests have to be done. The reason of it is that (1) measured plots (especially on experiment and plantations) can be smaller than the scanner's range, thus leading to unwanted points measured. Additionally, (2) the number of points measured by the scanner is settings dependent, thus it is very likely to have an impact on SSCI calculation. Two tests have thus been performed to assess if both of those factors have to be taken into account and if a transformation is possible to adapt the experiment method to any plot of scanner.

1. Restriction Distance

The first test consists in normal scans (settings: resolution= ¼; quality = x2) where several perimeter restrictions are applied. Plots showing a relative homogeneity (tree height, density, plantation type) as well as differences in structure between each other (both based on visual determination) were chosen to ensure a coherent perimeter restriction evolution and a sufficient SSCI range to understand its evolution on different environments. 5 plots have been chosen and 7 distance restrictions applied (70m; 30m; 20m; 15m; 10m; 7m; 5m). Finally, the 5 plots' mean evolutions have been measured to obtain a reference evolution. This mean was then transformed by dividing each value by the 70m value to obtain a reference for max values of 1 and the rest depending on it.

2. Settings

The second test consists in testing different resolution and quality settings to understand their impact on SSCI. To assess this evolution, eight settings have been chosen, including Resolution (re) and Quality (qu): re = 1/4 ; 1/8 ; 1/16 and qu = 2x ; 3x ; 4x. Resolution impacts the number of points measured and Quality is a complementary setting to improve Resolution quality. Three tests have been performed in low, middle and high complexity environment (visually determined). The scanner was placed in the middle of measured plots and remained untouched during measurement. Measurement was made under (almost) no wind condition to avoid any bias due to leaf movement. All possibilities proposed by the scanner have been tested (tot = 8) (1/16; 2x doesn't exists). Note that more settings exist but imply time consuming or too low-resolution scans. Then, SSCI was measured on a given Quality to understand Resolution impact and vice-versa.

Results

1. Restriction distance

Perimeter restriction has a significant impact on SSCI (df = 6; Sum Sq = 0.15184; Mean Sq = 0.025307; F value 13.16; p-value= 9.69e-08). All values under 20m showed a significant difference (p-value [70m-15m] = 0.0404171) compared to the reference (70m) (**Fig. A**). Restriction for all plots seems to follow a similar trend (**Fig. A**) by experiencing SSCI decrease under 20 m. However, this trend isn't homogenous. In some case, SSCI can slightly increase close to 20m's restriction.

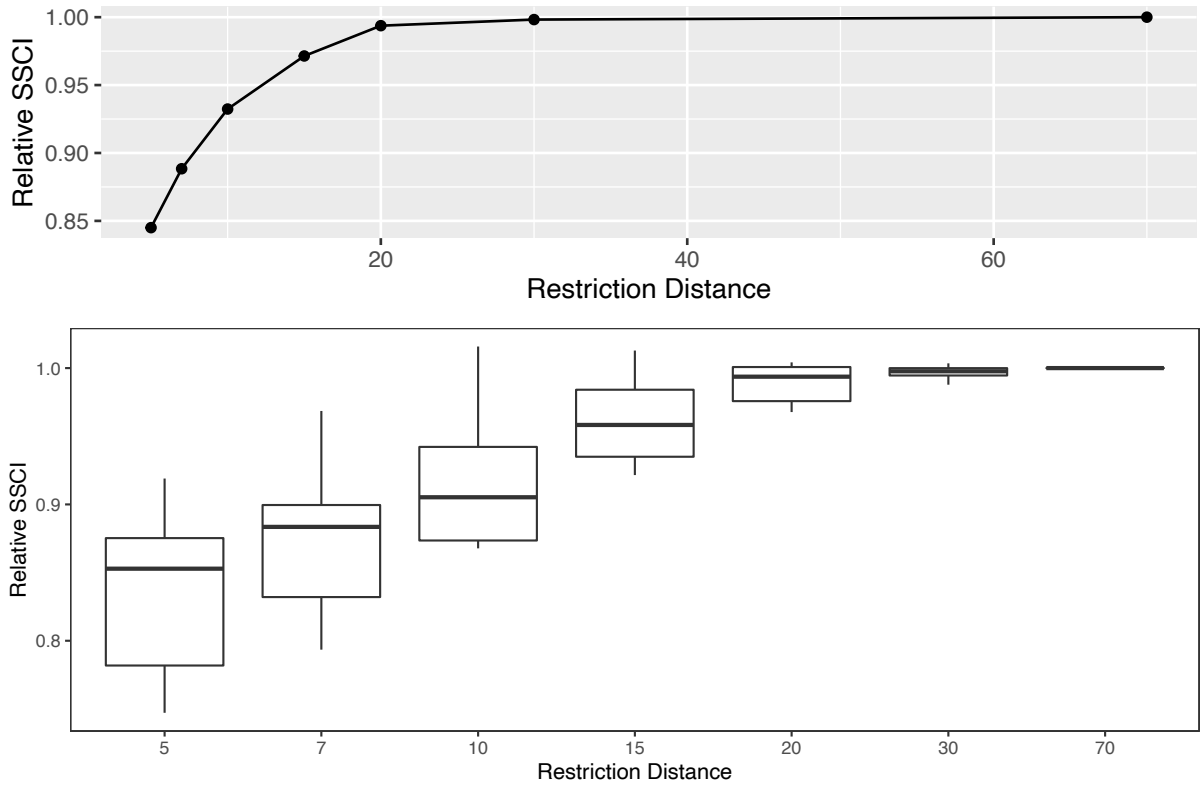


Fig. A. Top: **Mean relative SSCI depending on applied restriction distance,** SSCI for maximum distance being scaled to 1. Bottom: **Relative SSCI values depending on applied restriction distance,** SSSCI for maximum distance being scaled to 1.

2. Settings

Resolution has a significant impact on SSCI (Df = 2; Sum Sq=47.07; Mean Sq = 23.522; F value = 6.093; p value = 0.0108). SSCI systematically decreases when scanner's Resolution decreases. On the other hand, Quality has no significant impact on SSCI (Df = 2; Sum Sq=0.03; Mean Sq = 0.014; F value = 0.004; p value = 0.9964). A slight increase can be observed when quality increases (**Fig. B**), but not enough to be a decisive variable.

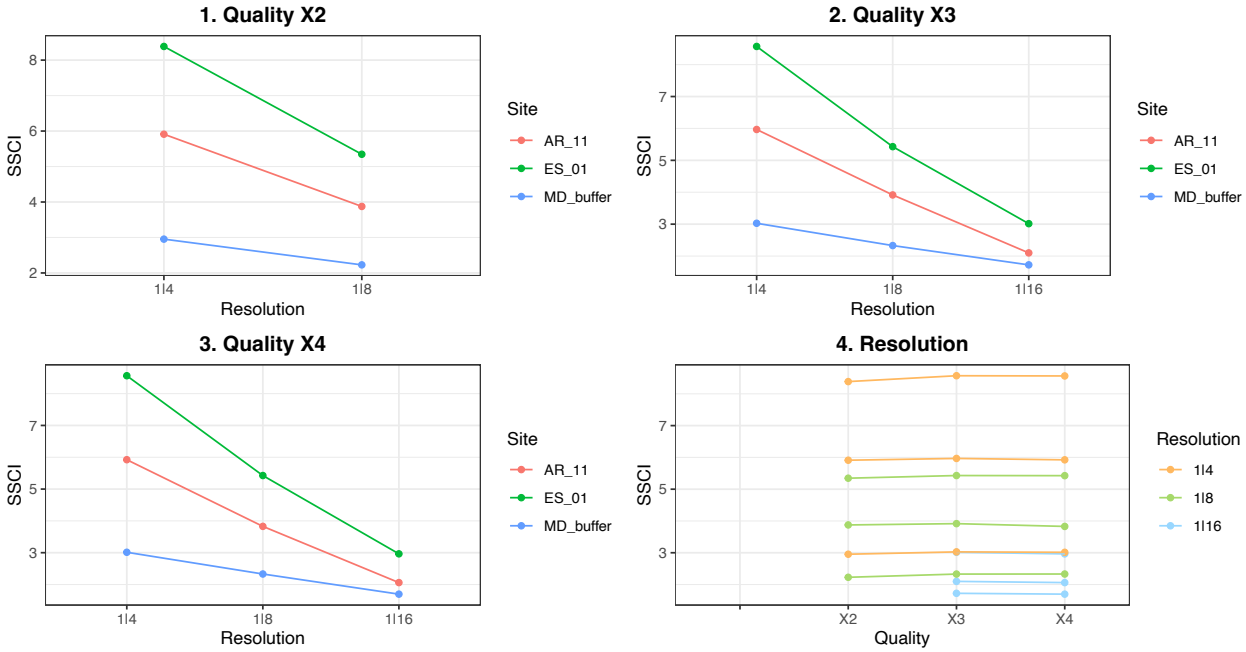


Fig. B. SSCI evolution depending on settings. The three first graphs show the evolution of SSCI in function of Resolution for a given Quality (X2; X3; X4). Colors correspond to measured sites. The last graph (4.) shows the evolution of SSCI in function of the chosen quality. Colors correspond to Resolution settings.

Conclusion

Applying a perimeter restriction to scans leads, in general, to decrease SSCI values. However, this trend isn't homogenous. Trying to apply a transformation function to SSCI results isn't thus desirable as it would result in an increase of the error margin depending on the type of forest measured. As SSCI evolution under 20m is significantly different than without any restriction, it has been chosen to avoid any comparative analysis between plots smaller than 40m wide (20m radius). Smaller plots measurement stays possible, but can only be compared when the same perimeter restriction is applied.

Quality settings shows no significant difference on SSCI values. As it has an impact on scanning time (higher quality means more time), it is desirable to use the lowest quality available for each Resolution. On the other hand, Resolution showed a strong effect on SSCI. More measured points imply an increase of SSCI values. As the scanner measures more points, the laser beam is more likely to pass through small gaps in the canopy, leading to an increase of polygons' perimeter used to measure MeanFRAC. In those conditions, it would be best to choose the highest resolution possible, but it would imply a way longer scanning time (Faro Technologies Inc., Lake Mary, USA). Resolution ¼ and Quality X2 has thus been chosen as the best compromise between accuracy and time saving. Those settings have also been chosen in Ehbrecht & al. (2017), Zemp & al. (2019) and Perles-Garcia & al. (2021) studies.

6.2 Complementary Boxplots

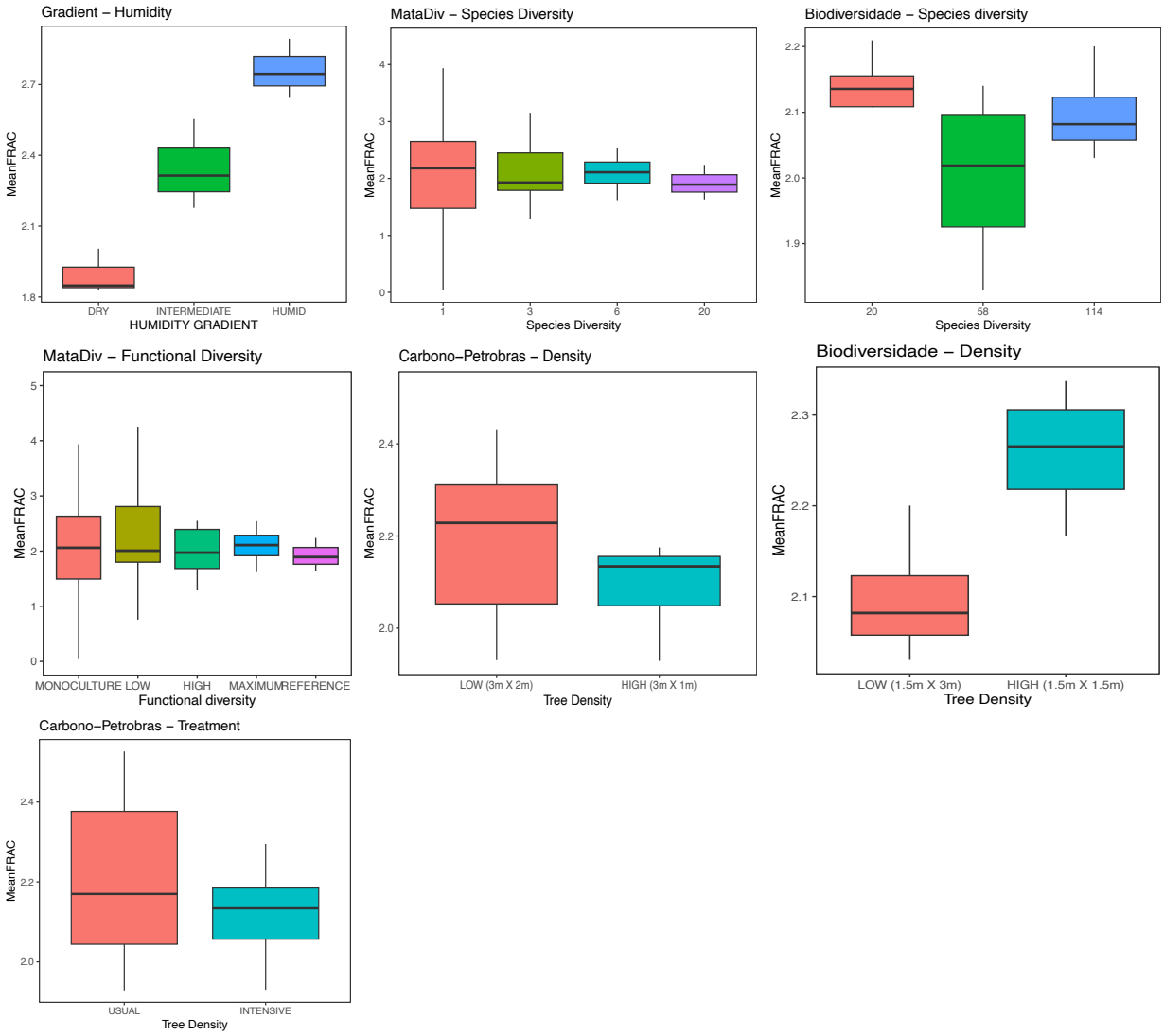


Fig. C. Mean fractal dimension (MeanFRAC) boxplots. X axis in each plot corresponds to the parameter tested in each experiment. Y axis corresponds to MeanFRAC values. Each boxplot color is the same than for SSCI results for the same experiment.

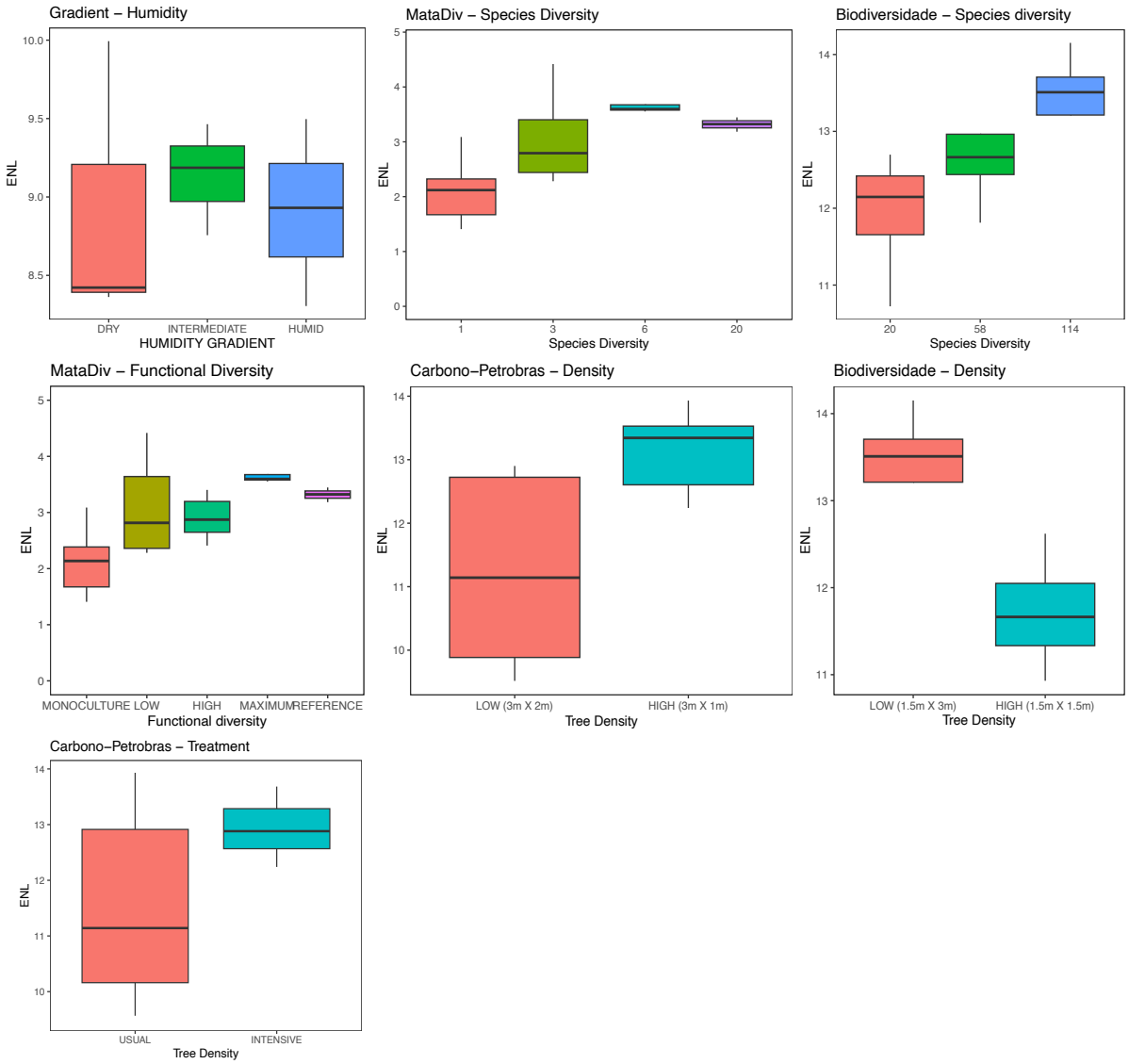


Fig. D. Effectve Number of Layers (ENL) boxplots. X axis in each plot corresponds to the parameter tested in each experiment. Y axis corresponds to ENL values. Each boxplot color is the same than for SSCI results for the same experiment.

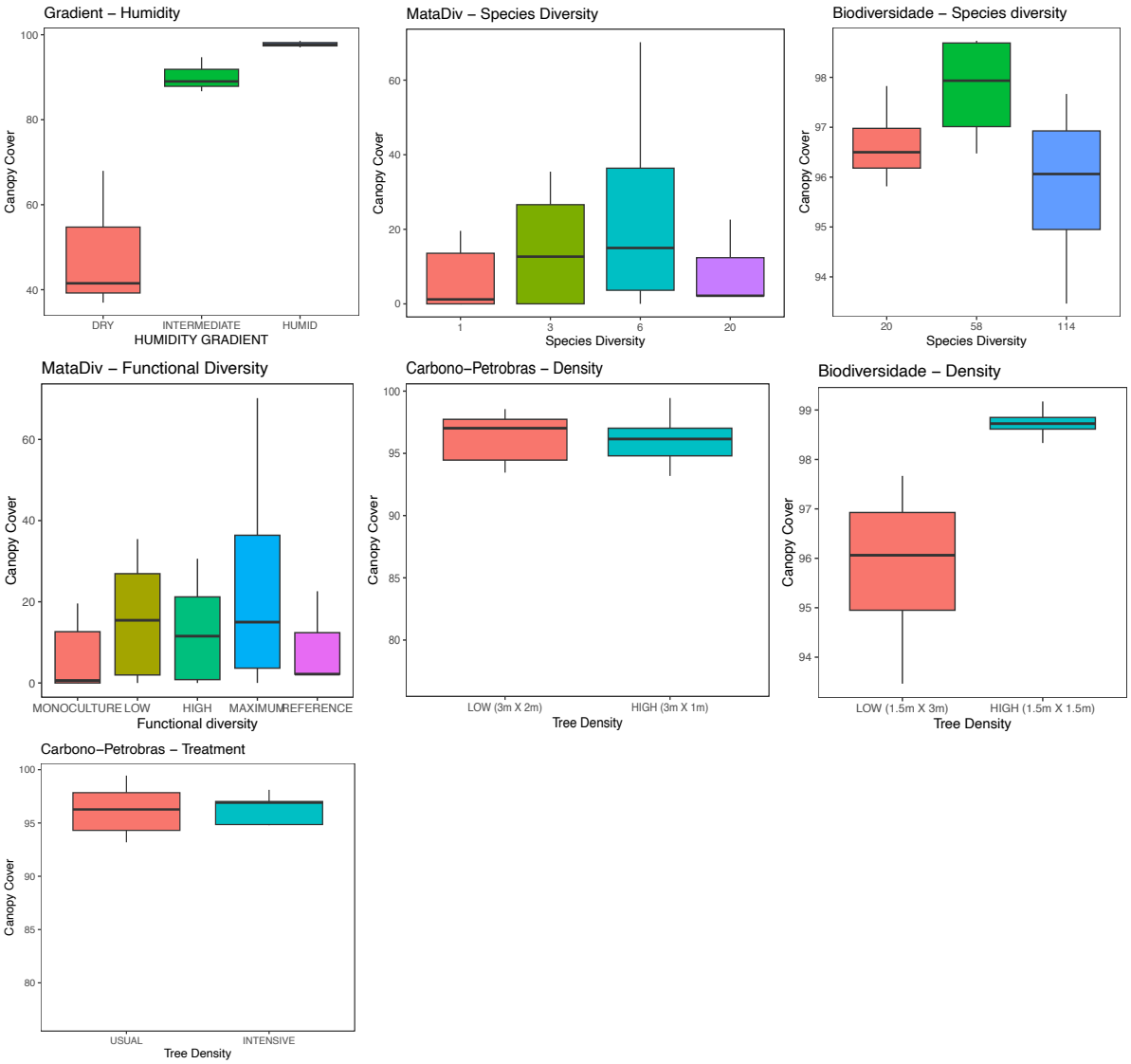


Fig. E. Canopy Cover boxplots. X axis in each plot corresponds to the parameter tested in each experiment. Y axis corresponds to canopy cover values (in %). Each boxplot color is the same than for SSCI results for the same experiment.

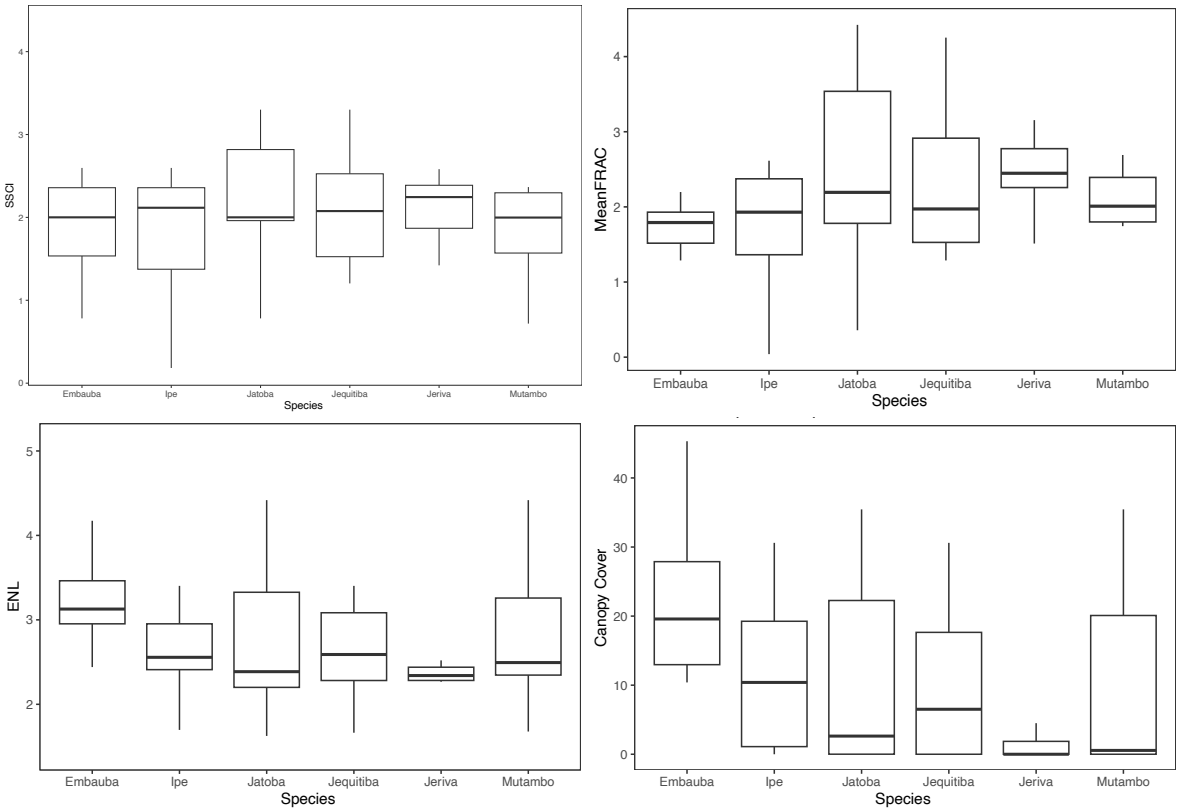


Fig. F. Species-specific effect results (*MataDiv* experiment). X axis correspond to each species in the 6 main species from the experiment (Jatoba *(Hymenaea courbaril*), Mutambo (*Guazuma ulmifolia*), Embauba (*Cecropia pachystachya*), Jequitiba branco (*Cariniana estrellensis*)**,** Ipe roxo (*Handroanthus impetiginosus*), Jeriva (*Syagrus romanzoffiana*)). Y axis correspond to the parameters measured (SSCI, mean fractal dimension (MeanFRAC), effective number of layer (ENL) and canopy cover).

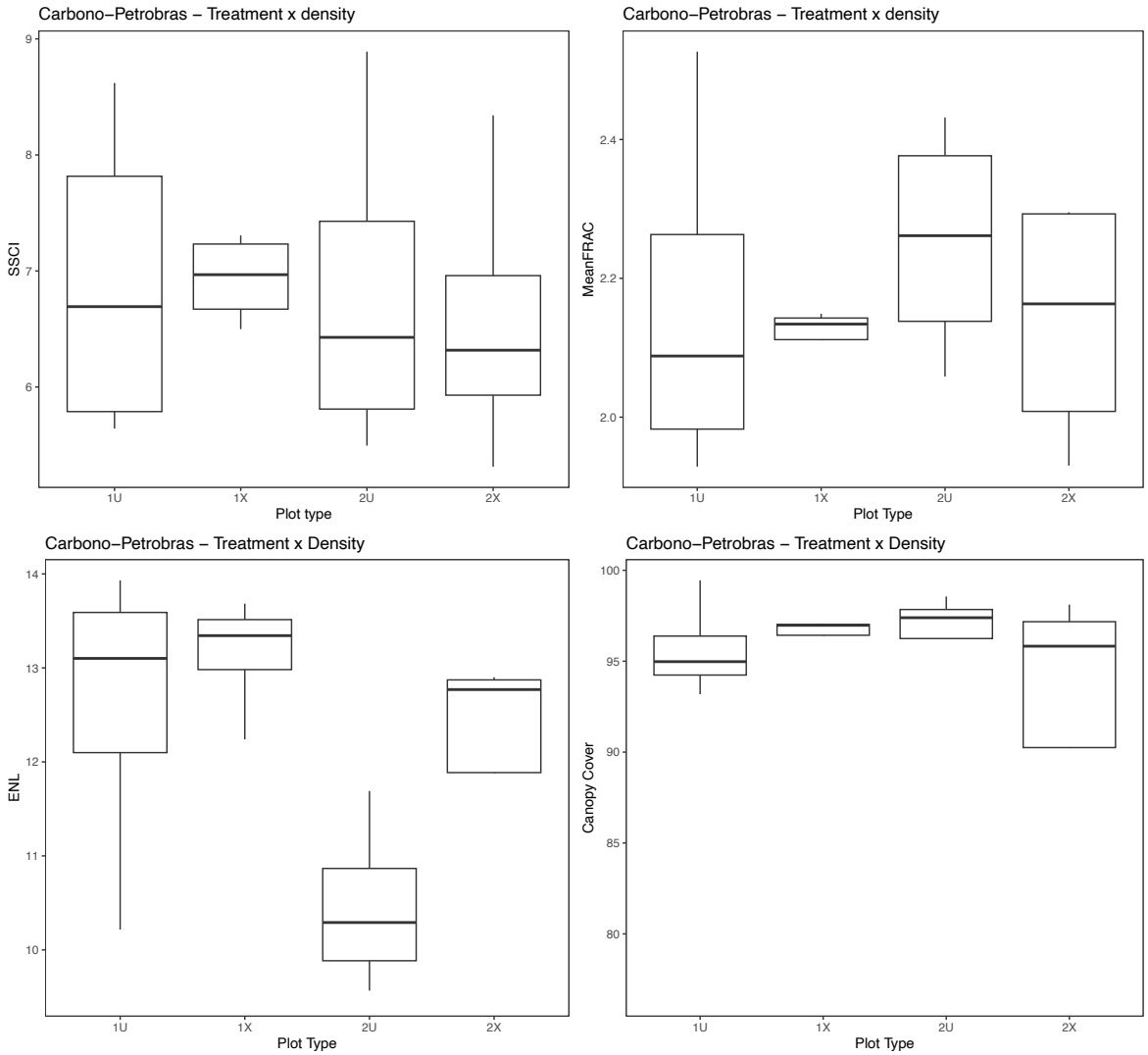
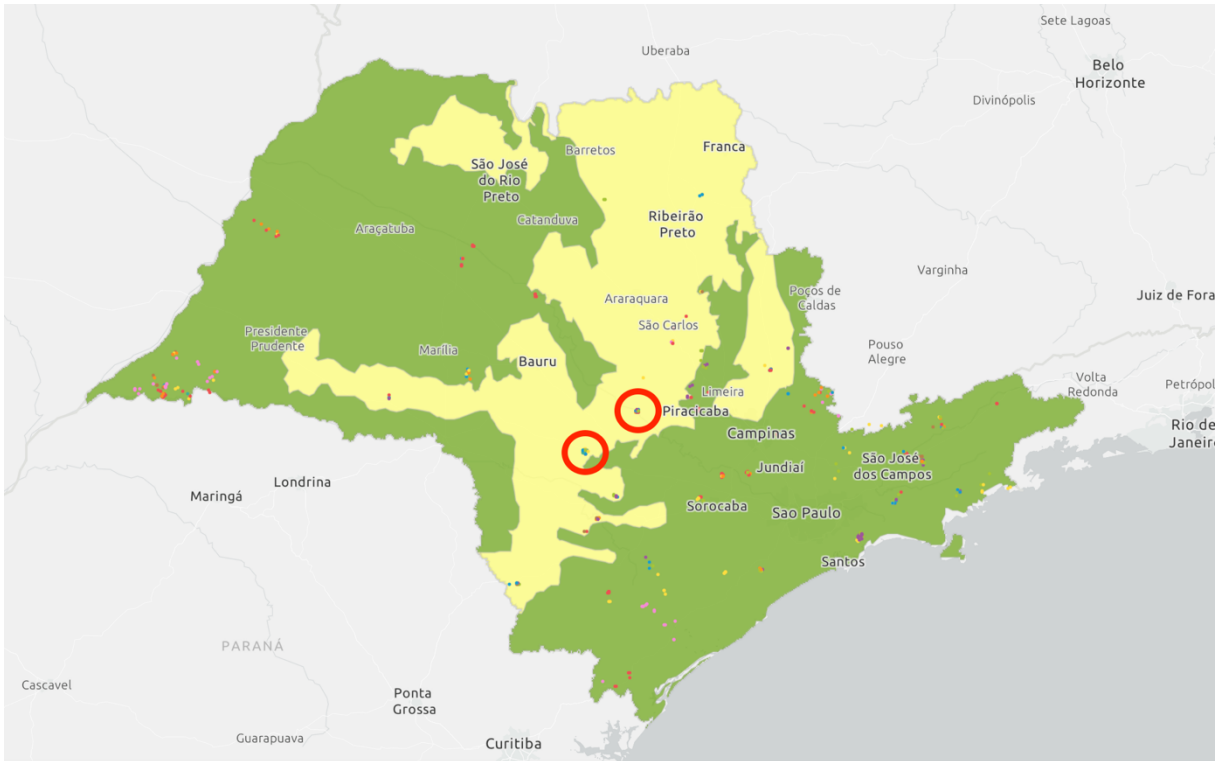


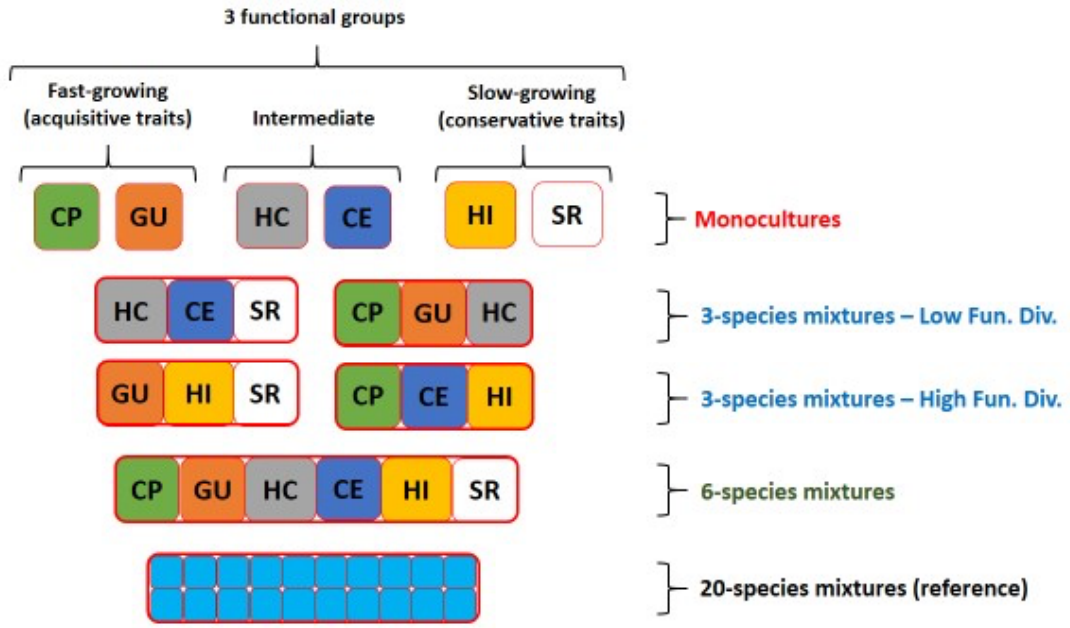
Fig. G. Plot type effect (*Carbono-Petrobras* experiment). X axis: 1 corresponds to high density plots (3x1m space between trees), 2 corresponds to low density plots (3x2m space between trees), U corresponds to usual treatments and X corresponds to intensive treatments. Y axis corresponds to the parameters selected (SSCI, mean fractal dimension (MeanFRAC), effective number of layer (ENL) and canopy cover).

6.3 Complementary Maps



Map. A. Biomes inside São Paulo State (Brazil). Green areas correspond to Mata Altlantica biome (Atlantic Forest) and yellow areas corresponds to Cerrado Biome. Red dots correspond to experimental stations location (top-right: Itatinga Forest Experimental Station; Bottom-left: Experimental Station of Forestry Sciences of Anhembi). Background Map: https://cepe-geo.maps.arcgis.com/apps/View/index.html?appid=d1c91fe2ccad4c79bb0fca5c216bbc16

6.4 MataDiv Plots Composition



1- Cecropia pachystachya (*Urticacaea*)
Embauba
C P

2- Guazuma ulmifolia (Malvaceae)
Mutambo
G U

3- Hymenaea courbaril (*Fabaceae*)
Jatoba
H C

4- Cariniana estrellensis (*Lecythidaceae*)
Jequitiba branco
C E

5- Handroanthus impetiginosus
(*Bignoniaceae*) *Ipe roxo*
H I

6- Syagrus romanzoffiana (Arecaceae)
Jeriva
S R

Fig. H. MataDiv plot composition. Top: plot composition (6 monocultures, 4 three species mixtures, 1 six species mixtures and 1 twenty species mixtures. **Bottom**: Species name.

6.5. Code (R.) - Boxplots and Analyses

Gradient Experiment :

```
### Gradient code

#install.packages("car")
#install.packages("nlme")
#install.packages("lme4")
#install.packages("emmeans")
#install.packages("plotrix")
#install.packages("tidyverse")
#install.packages("dplyr")

require(car)
require(nlme)
require(lme4)
require(emmeans)
require(plotrix)
require(tidyverse)
require(ggplot2)
require(scales)
library(datasets)
library(ggplot2)
library(multcompView)
library(dplyr)

library(cowplot)
library(magick)
library(sp)
library(raster)
library(ggfortify)
library(cluster)
library(factoextra)
library(devtools)
library(FactoMineR)
library(ggcorrplot)
library(corrr)

setwd("~/Desktop/")
data <- read.csv("gradient_final.csv", sep=";")
data
data$humidity <- as.factor(data$humidity)
data$plot <- as.factor(data$plot)
data$ENL <- as.numeric(data$ENL)
data$canopy <- 100 - data$canopy
data$humidity <- factor(data$humidity, levels = c("DRY",
"INTERMEDIATE", "HUMID"))
data



# Humidity - Boxplots-----------------------------------------------------
-------------------------


#SSCI
```

```
ggplot(data, aes(x =humidity,y = SSCI, fill = humidity)) +
  geom_boxplot() +
  labs(x="HUMIDITY GRADIENT", y="SSCI") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())


#meanfrac

ggplot(data, aes(x = humidity,y = Mean_FRAC, fill=humidity)) +
  geom_boxplot() +
  labs(x="HUMIDITY GRADIENT", y="MeanFRAC") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("Gradient - Humidity")


#ENL

ggplot(data, aes(x = humidity,y = ENL, fill=humidity)) +
  geom_boxplot() +
  labs(x="HUMIDITY GRADIENT", y="ENL") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("Gradient - Humidity")


# canopy

ggplot(data, aes(x = humidity,y = canopy , fill = humidity)) +
  geom_boxplot() +
  labs(x="HUMIDITY GRADIENT", y="Canopy Cover") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("Gradient - Humidity")







# Humidity - statistic analysis----------------------------------------
--------------------

# SSCI

l1 <- aov(SSCI ~ humidity, data = data)
qqPlot(resid(l1))
summary(l1)
TukeyHSD(l1)

tukey <- TukeyHSD(l1)
```

```
print(tukey)

Tk <- group_by(data, humidity) %>%
  summarise(mean=mean(SSCI), quant = quantile(SSCI, probs = 0.75, na.rm
= T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$humidity)
Tk$cld <- cld$Letters

print(Tk)



# ENL

l1 <- aov(ENL ~ humidity, data = data)
qqPlot(resid(l1))
summary(l1)
TukeyHSD(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, humidity) %>%
  summarise(mean=mean(ENL), quant = quantile(ENL, probs = 0.75, na.rm =
T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$humidity)
Tk$cld <- cld$Letters

print(Tk)



#MeanFRAC

l1 <- aov(Mean_FRAC ~ humidity, data = data)
qqPlot(resid(l1))
summary(l1)
TukeyHSD(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, humidity) %>%
  summarise(mean=mean(Mean_FRAC), quant = quantile(Mean_FRAC, probs =
0.75, na.rm = T)) %>%
  arrange(desc(mean))
```

```
cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$humidity)
Tk$cld <- cld$Letters

print(Tk)



# Canopy Cover

l1 <- aov(canopy ~ humidity, data = data)
qqPlot(resid(l1))
summary(l1)
TukeyHSD(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, humidity) %>%
  summarise(mean=mean(canopy), quant = quantile(canopy, probs = 0.75,
na.rm = T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$humidity)
Tk$cld <- cld$Letters

print(Tk)






#PCA analysis------------------------------------------------------------
--


data <- read.csv("gradient_final.csv", sep=";")
data
data$humidity <- as.factor(data$humidity)
data$canopy <- 100 - data$canopy
data$humidity <- factor(data$humidity, levels = c("DRY",
"INTERMEDIATE", "HUMID"))
df <- data[,3:6]
pca_res <- prcomp(df, scale. = TRUE)

pca <- autoplot(pca_res, data = data, colour = 'humidity',
                loadings = TRUE,loadings.colour = 'black',
                loadings.label = TRUE, loadings.label.size = 3,
loadings.label.colour = "black"+ theme(panel.grid.major =
element_blank(), panel.grid.minor = element_blank())  )
```

```
pca

fviz_pca_biplot(pca_res,
                col.ind = data$humidity,
                addEllipses = FALSE, label = "var",
                col.var = "black", repel = T,
                legend.title = "Species") + theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())
```

MataDiv experiment :

```
### MataDiv script

#install.packages("car")
#install.packages("nlme")
#install.packages("lme4")
#install.packages("emmeans")
#install.packages("plotrix")
#install.packages("scales")
#install.packages("multcompView")
#install.packages(("lmerTest"))
#install.packages("devtools")
install.packages("ggbiplot")
install.packages(c("FactoMineR", "factoextra"))

require(car)
require(nlme)
require(lme4)
require(emmeans)
require(plotrix)
require(tidyverse)
require(ggplot2)
require(scales)
library(datasets)
library(ggplot2)
library(multcompView)
library(dplyr)
library(lmerTest)
library(devtools)
library(ggbiplot)
library(FactoMineR)
library(factoextra)

setwd("~/Desktop/")
data <- read.csv("MataDiv_final.csv", sep=";")
data
data$plot_type <- as.factor(data$plot_type)
data$fun_div <- as.factor(data$fun_div)
data$diversity <- as.factor(data$diversity) ## !!! only for graphs
data$Canopy <- 100- data$Canopy
data$fun_div <- factor(data$fun_div, levels = c("MONOCULTURE", "LOW",
"HIGH", "MAXIMUM", "REFERENCE"))
data

datas <- read.csv("matadiv_species.csv", sep=";")
datas

## Species Diversity - Boxplots and analysis--------------------------
--------------------------------

# SSCI

ggplot(data, aes(x=diversity,y= SSCI, fill= diversity)) +
  geom_boxplot(outlier.shape = NA) +
  coord_cartesian(ylim = c(0, 4.8))+
```

```
  labs(x="Species Diversity", y="SSCI") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  scale_fill_discrete(name = "Diversity")



l1 <- aov(SSCI ~ diversity, data = data)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, diversity) %>%
  summarise(mean=mean(SSCI), quant = quantile(SSCI, probs = 0.75, na.rm
= T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$diversity)
Tk$cld <- cld$Letters

print(Tk)


mixed1 <- lmer(SSCI ~ diversity + (1|Block) , data=data)
summary(mixed1)
anova(mixed1)







# ENL

ggplot(data, aes(x=diversity,y= Effective.number.of.layers..ENL., fill=
diversity)) +
  geom_boxplot(outlier.shape = NA) +
  #coord_cartesian(ylim = c(0, 4.8))+
  labs(x="Species Diversity", y="ENL") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("MataDiv - Species Diversity")

l1 <- aov(Effective.number.of.layers..ENL. ~ diversity, data = data)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
```

```
print(tukey)

Tk <- group_by(data, diversity) %>%
  summarise(mean=mean(Effective.number.of.layers..ENL.), quant =
quantile(dEffective.number.of.layers..ENL., probs = 0.75, na.rm = T))
%>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$diversity)
Tk$cld <- cld$Letters

print(Tk)


mixed1 <- lmer(data$Effective.number.of.layers..ENL. ~ diversity +
(1|Block) , data=data)
summary(mixed1)
anova(mixed1)

#MeanFrac

ggplot(data, aes(x=diversity,y= Mean.fractal.dimension..MeanFrac.,
fill= diversity)) +
  geom_boxplot(outlier.shape = NA) +
  #coord_cartesian(ylim = c(0, 4.8))+
  labs(x="Species Diversity", y="MeanFRAC") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("MataDiv - Species Diversity")


l1 <- aov(Mean.fractal.dimension..MeanFrac. ~ diversity, data = data)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, diversity) %>%
  summarise(mean=mean(Mean.fractal.dimension..MeanFrac.), quant =
quantile(Mean.fractal.dimension..MeanFrac., probs = 0.75, na.rm = T))
%>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$diversity)
Tk$cld <- cld$Letters

print(Tk)
```

```
mixed1 <- lmer(Mean.fractal.dimension..MeanFrac. ~ diversity +
(1|Block) , data=data)
summary(mixed1)
anova(mixed1)


# canopy cover

ggplot(data, aes(x=diversity,y= Canopy, fill= diversity)) +
  geom_boxplot(outlier.shape = NA) +
  #coord_cartesian(ylim = c(0, 4.8))+
  labs(x="Species Diversity", y="Canopy Cover") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("MataDiv - Species Diversity")



l1 <- aov(Canopy ~ diversity, data = data)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, diversity) %>%
  summarise(mean=mean(Canopy), quant = quantile(Canopy, probs = 0.75,
na.rm = T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$diversity)
Tk$cld <- cld$Letters

print(Tk)


mixed1 <- lmer(Canopy ~ diversity + (1|Block) , data=data)
summary(mixed1)
anova(mixed1)


## Functional diversity - boxplot and analysis-------------------------
--------------------------------------

# SSCI

ggplot(data, aes(x=fun_div, y=SSCI, fill= fun_div)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Functional diversity", y="SSCI") +
  theme_bw() +
  coord_cartesian(ylim = c(0, 5))+
```

```
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  scale_fill_discrete(name = "Functional Diversity")



l1 <- aov(SSCI ~ fun_div, data = data)
qqPlot(resid(l1))
summary(l1)

tukey <- TukeyHSD(l1)
print(tukey)


Tk <- group_by(data, fun_div) %>%
  summarise(mean=mean(SSCI), quant = quantile(SSCI, probs = 0.75, na.rm
= T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$fun_div)
Tk$cld <- cld$Letters

print(Tk)


mixed1 <- lmer(SSCI ~ fun_div + (1|Block) , data=data)
summary(mixed1)
anova(mixed1)

# MeanFrac

ggplot(data, aes(x=fun_div, y=Mean.fractal.dimension..MeanFrac., fill =
fun_div)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Functional diversity", y="MeanFRAC") +
  theme_bw() +
  coord_cartesian(ylim = c(0, 5))+
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  #scale_fill_discrete(name = "pas besoin heheheeeee")+
  ggtitle("MataDiv - Functional Diversity")


l1 <- aov(Mean.fractal.dimension..MeanFrac. ~ fun_div, data = data)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, fun_div) %>%
  summarise(mean=mean(Mean.fractal.dimension..MeanFrac.), quant =
quantile(Mean.fractal.dimension..MeanFrac., probs = 0.75, na.rm = T))
%>%
```

```
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$fun_div)
Tk$cld <- cld$Letters

print(Tk)

mixed1 <- lmer(Mean.fractal.dimension..MeanFrac. ~ fun_div + (1|Block)
, data=data)
summary(mixed1)
anova(mixed1)


# ENL

ggplot(data, aes(x=fun_div, y=Effective.number.of.layers..ENL., fill =
fun_div)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Functional diversity", y="ENL") +
  theme_bw() +
  coord_cartesian(ylim = c(0, 5))+
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  scale_fill_discrete(name = "pas besoin heheheeeee")+
  ggtitle("MataDiv - Functional Diversity")


l1 <- aov(Effective.number.of.layers..ENL. ~ fun_div, data = data)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, fun_div) %>%
  summarise(mean=mean(Effective.number.of.layers..ENL.), quant =
quantile(Effective.number.of.layers..ENL., probs = 0.75, na.rm = T))
%>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$fun_div)
Tk$cld <- cld$Letters

print(Tk)


mixed1 <- lmer(Effective.number.of.layers..ENL. ~ fun_div + (1|Block) ,
data=data)
summary(mixed1)
anova(mixed1)
```

```
#Canopy Cover

ggplot(data, aes(x=fun_div, y=data$Canopy, fill = fun_div)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Functional diversity", y="Canopy Cover") +
  theme_bw() +
  #coord_cartesian(ylim = c(0, 5))+
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  scale_fill_discrete(name = "pas besoin heheheeeee")+
  ggtitle("MataDiv - Functional Diversity")



l1 <- aov(Canopy~ fun_div, data = data)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, fun_div) %>%
  summarise(mean=mean(Canopy), quant = quantile(Canopy, probs = 0.75,
na.rm = T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$fun_div)
Tk$cld <- cld$Letters

print(Tk)



mixed1 <- lmer(Canopy ~ fun_div + (1|Block) , data=data)
summary(mixed1)
anova(mixed1)

# Species-specific effect - Boxplots and analysis----------------------
---------


# SSCI

boxplot(data$SSCI ~ data$Species)
ggplot(datas, aes(x=Species,y= SSCI)) +
  geom_boxplot(outlier.shape = NA) +
  #coord_cartesian(ylim = c(0, 4.8))+
  labs(x="Species ", y="SSCI") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("MataDiv - Species-Specific Effect")

l1 <- aov(SSCI ~ Species , data = datas)
```

```
qqPlot(resid(l1))
summary(l1)

tukey <- TukeyHSD(l1)
print(tukey)


Tk <- group_by(datas, Species) %>%
  summarise(mean=mean(SSCI), quant = quantile(SSCI, probs = 0.75, na.rm
= T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$Species)
Tk$cld <- cld$Letters

print(Tk)


# MeanFRAC

boxplot(data$MeanFRAC ~ data$Species)

ggplot(datas, aes(x=Species,y= MeanFRAC)) +
  geom_boxplot(outlier.shape = NA) +
  #coord_cartesian(ylim = c(0, 4.8))+
  labs(x="Species ", y="MeanFRAC") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("MataDiv - Species-Specific Effect")


l1 <- aov(MeanFRAC ~ Species , data = datas)
qqPlot(resid(l1))
summary(l1)

tukey <- TukeyHSD(l1)
print(tukey)


Tk <- group_by(datas, Species) %>%
  summarise(mean=mean(MeanFRAC), quant = quantile(MeanFRAC, probs =
0.75, na.rm = T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$Species)
Tk$cld <- cld$Letters

print(Tk)
```

```
#ENL

boxplot(data$ENL ~ data$Species)

ggplot(datas, aes(x=Species,y= ENL)) +
  geom_boxplot(outlier.shape = NA) +
  #coord_cartesian(ylim = c(0, 4.8))+
  labs(x="Species ", y="ENL") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("MataDiv - Species-Specific Effect")



l1 <- aov(ENL ~ Species , data = datas)
qqPlot(resid(l1))
summary(l1)

tukey <- TukeyHSD(l1)
print(tukey)


Tk <- group_by(datas, Species) %>%
  summarise(mean=mean(ENL), quant = quantile(ENL, probs = 0.75, na.rm =
T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$Species)
Tk$cld <- cld$Letters

print(Tk)



# Canopy

ggplot(datas, aes(x=Species,y= Canopy)) +
  geom_boxplot(outlier.shape = NA) +
  #coord_cartesian(ylim = c(0, 4.8))+
  labs(x="Species ", y="Canopy Cover") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("MataDiv - Species-Specific Effect")



l1 <- aov(Canopy ~ Species , data = datas)
qqPlot(resid(l1))
summary(l1)

tukey <- TukeyHSD(l1)
```

```
print(tukey)


Tk <- group_by(datas, Species) %>%
  summarise(mean=mean(Canopy), quant = quantile(Canopy, probs = 0.75,
na.rm = T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$Species)
Tk$cld <- cld$Letters

print(Tk)




## PCA analyses ------------------------------------------------------
---------

# Species Diversity

data <- read.csv("MataDiv_pca_final.csv", sep=";")
data
data$diversity <- as.factor(data$diversity)
data$fun_div <- as.factor(data$fun_div)
data$Canopy <- 100 - data$Canopy
df <- data[,3:6]
pca_res <- prcomp(df, scale. = TRUE)

pca <- autoplot(pca_res, data = data, colour = 'diversity',
                loadings = TRUE,loadings.colour = 'black',
                loadings.label = TRUE, loadings.label.size = 3,
loadings.label.colour = "black" )

pca


fviz_pca_biplot(pca_res,
                col.ind = data$diversity,
                addEllipses = FALSE, label = "var",
                col.var = "black", repel = F,
                legend.title = "Species") + theme_bw() +
                theme(panel.grid.major = element_blank(),
panel.grid.minor = element_blank())

## Functional diversity


data <- read.csv("MataDiv_pca_final.csv", sep=";")
data
data$diversity <- as.factor(data$diversity)
data$fun_div <- as.factor(data$fun_div)
data$Canopy <- 100 - data$Canopy
df <- data[,3:6]
```

```
pca_res <- prcomp(df, scale. = TRUE)

pca <- autoplot(pca_res, data = data, colour = 'fun_div',
                loadings = TRUE,loadings.colour = 'black',
                loadings.label = TRUE, loadings.label.size = 3,
loadings.label.colour = "black" )

pca


fviz_pca_biplot(pca_res,
                col.ind = data$fun_div,
                addEllipses = FALSE, label = "var",
                col.var = "black", repel = F,
                legend.title = "Species") + theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())
```

Biodiversidade Experiment:

```
### BioDiversitade code

#install.packages("car")
#install.packages("nlme")
#install.packages("lme4")
#install.packages("emmeans")
#install.packages("plotrix")
#install.packages("tidyverse")
#install.packages("dplyr")

require(car)
require(nlme)
require(lme4)
require(emmeans)
require(plotrix)
require(tidyverse)
require(ggplot2)
require(scales)
library(datasets)
library(ggplot2)
library(multcompView)
library(dplyr)


setwd("~/Desktop/")
data <- read.csv("biodiversitade_corr.csv", sep=";")
data
data$TYPE <- as.factor(data$TYPE)
data$REPETITION <- as.factor(data$REPETITION)
data$SSCI <- as.numeric(data$SSCI)
data$canopy <- 100 - data$canopy
data$density <- as.factor(data$density)
datacut <- subset(data, density == "1.5m X 3m") # sans densit√© x2
datadens<- subset(data, TYPE == 3 | TYPE== 4) # avec densit√© x2
datacut$Diversity <- as.factor(datacut$Diversity)
datadens$density <- factor(datadens$density, levels = c("1.5m X
3m","1.5m X 1.5m"))

data




## Species diversity - Boxplots and analyses----------------------------
-------------------------


#SSCI

ggplot(datacut, aes(group= Diversity, x =Diversity,y = SSCI, fill=
Diversity)) +
  geom_boxplot() +
  labs(x="Species Diversity", y="SSCI") +
  theme_bw() +
```

```
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())



l1 <- aov(SSCI ~ Diversity, data = datacut)
qqPlot(resid(l1))
summary(l1)

tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(datacut, Diversity) %>%
  summarise(mean=mean(SSCI), quant = quantile(SSCI, probs = 0.75, na.rm
= T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$Diversity)
Tk$cld <- cld$Letters

print(Tk)



#ENL

ggplot(datacut, aes(x=Diversity, y=ENL, fill = Diversity)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Species Diversity", y="ENL") +
  theme_bw() +
  #coord_cartesian(ylim = c(0, 5))+
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  scale_fill_discrete(name = "pas besoin heheheeeee")+
  ggtitle("Biodiversidade - Species diversity")



l1 <- aov(ENL ~ Diversity, data = datacut)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(datacut, Diversity) %>%
  summarise(mean=mean(ENL), quant = quantile(ENL, probs = 0.75, na.rm =
T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$Diversity)
```

```
Tk$cld <- cld$Letters

print(Tk)



#Mean_FRAC

ggplot(datacut, aes(x=Diversity, y= Mean_FRAC, fill = Diversity)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Species Diversity", y="MeanFRAC") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  ggtitle("Biodiversidade - Species diversity")



l1 <- aov(Mean_FRAC ~ Diversity, data = datacut)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(datacut, Diversity) %>%
  summarise(mean=mean(Mean_FRAC), quant = quantile(Mean_FRAC, probs =
0.75, na.rm = T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$Diversity)
Tk$cld <- cld$Letters

print(Tk)




# canopy

ggplot(datacut, aes(x=Diversity, y= canopy, fill = Diversity)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Species Diversity", y="Canopy Cover") +
  theme_bw() +
  #coord_cartesian(ylim = c(0, 5))+
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  scale_fill_discrete(name = "pas besoin heheheeeee")+
  ggtitle("Biodiversidade - Species diversity")


l1 <- aov(canopy ~ Diversity, data = datacut)
qqPlot(resid(l1))
summary(l1)
```

```
tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(datacut, Diversity) %>%
  summarise(mean=mean(canopy), quant = quantile(canopy, probs = 0.75,
na.rm = T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$Diversity)
Tk$cld <- cld$Letters

print(Tk)



#### tree density analyse-----------------------------------------------
-------------


# SSCI

ggplot(datadens, aes(group= density,x =density,y = SSCI, fill =
density)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="SSCI") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  scale_x_discrete(labels = c("1.5m X 3m" = "LOW (1.5m X 3m)","1.5m X
1.5m" = "HIGH (1.5m X 1.5m)"))


l1 <- aov(SSCI ~ density, data = datadens)
qqPlot(resid(l1))
summary(l1)

tukey <- TukeyHSD(l1)
print(tukey)


Tk <- group_by(datadens, density) %>%
  summarise(mean=mean(SSCI), quant = quantile(SSCI, probs = 0.75, na.rm
= T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

# extracting the compact letter display and adding to the Tk table
cld <- as.data.frame.list(cld$density)
Tk$cld <- cld$Letters
```

```
print(Tk)



#ENL

ggplot(datadens, aes(group = density, x=density, y=ENL, fill =
density)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="ENL") +
  theme_bw() +
  #coord_cartesian(ylim = c(0, 5))+
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  scale_fill_discrete(name = "pas besoin heheheeeee")+
  scale_x_discrete(labels = c("1.5m X 3m" = "LOW (1.5m X 3m)","1.5m X
1.5m" = "HIGH (1.5m X 1.5m)"))+
  ggtitle("Biodiversidade - Density")



l1 <- aov(ENL ~ density, data = datadens)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(datadens, density) %>%
  summarise(mean=mean(ENL), quant = quantile(ENL, probs = 0.75, na.rm =
T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$density)
Tk$cld <- cld$Letters

print(Tk)



#Mean_FRAC

ggplot(datadens, aes(group = density, x=density, y=Mean_FRAC, fill =
density)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="MeanFRAC") +
  theme_bw() +
  #coord_cartesian(ylim = c(0, 5))+
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
```

```
  scale_fill_discrete(name = "pas besoin heheheeeee")+
  scale_x_discrete(labels = c("1.5m X 3m" = "LOW (1.5m X 3m)","1.5m X
1.5m" = "HIGH (1.5m X 1.5m)"))+
  ggtitle("Biodiversidade - Density")



l1 <- aov(Mean_FRAC~ density, data = datadens)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(datacut, density) %>%
  summarise(mean=mean(Mean_FRAC), quant = quantile(MeanFRAC, probs =
0.75, na.rm = T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$density)
Tk$cld <- cld$Letters

print(Tk)




# canopy

ggplot(datadens, aes(group = density, x=density, y=canopy, fill =
density)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="Canopy Cover") +
  theme_bw() +
  #coord_cartesian(ylim = c(0, 5))+
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank()) +
  scale_fill_discrete(name = "pas besoin heheheeeee")+
  scale_x_discrete(labels = c("1.5m X 3m" = "LOW (1.5m X 3m)","1.5m X
1.5m" = "HIGH (1.5m X 1.5m)"))+
  ggtitle("Biodiversidade - Density")



l1 <- aov(canopy~ density, data = datadens)
qqPlot(resid(l1))
summary(l1)


tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(datadens, Diversity) %>%
```

```
  summarise(mean=mean(canopy), quant = quantile(canopy, probs = 0.75,
na.rm = T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$Diversity)
Tk$cld <- cld$Letters

print(Tk)




### PCA analysis ----------------------------------------------------
---------


library(cowplot)
library(magick)
library(sp)
library(raster)
library(ggfortify)
library(cluster)
library(factoextra)
library(devtools)
library(FactoMineR)
library(ggcorrplot)
library(corrr)



# Species Diversity

data <- read.csv("Biodiversidade_pca.csv", sep=";")
data
data$Diversity <- as.factor(data$Diversity)
data$density <- as.factor(data$density)
data$Canopy <- 100 - data$Canopy
data
datacut <- subset(data, density == "1.5m X 3m") # sans densit√© x2
df <- datacut[,3:6]
pca_res <- prcomp(df, scale. = TRUE)

pca <- autoplot(pca_res, data = datacut, colour = 'Diversity',
                loadings = TRUE,loadings.colour = 'black',
                loadings.label = TRUE, loadings.label.size = 3,
loadings.label.colour = "black" )

pca

fviz_pca_biplot(pca_res,
                col.ind = datacut$Diversity,
                addEllipses = FALSE, label = "var",
                col.var = "black", repel = T,
```

```
                legend.title = "Species") + theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())


# Tree Density

data <- read.csv("Biodiversidade_pca.csv", sep=";")
data
data$density <- factor(data$density, levels = c("1.5m X 3m","1.5m X
1.5m"))
data$Diversity <- as.factor(data$Diversity)
data$density <- as.factor(data$density)
data$Canopy <- 100 - data$Canopy
datadens<- subset(data, Diversity == 114 | Diversity== 118) # avec
densit√© x2
df <- datadens[,3:6]
pca_res <- prcomp(df, scale. = TRUE)

pca <- autoplot(pca_res, data = datadens, colour = 'density',
                loadings = TRUE,loadings.colour = 'black',
                loadings.label = TRUE, loadings.label.size = 3,
loadings.label.colour = "black" )

pca

fviz_pca_biplot(pca_res,
                col.ind = datadens$density,
                addEllipses = FALSE, label = "var",
                col.var = "black", repel = T,
                legend.title = "Species") + theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())
```

Carbono-Petrobras Experiment :

```
### Petrobras code

#install.packages("car")
#install.packages("nlme")
#install.packages("lme4")
#install.packages("emmeans")
#install.packages("plotrix")
#install.packages("tidyverse")
#install.packages("dplyr")

require(car)
require(nlme)
require(lme4)
require(emmeans)
require(plotrix)
require(tidyverse)
require(ggplot2)
require(scales)
library(datasets)
library(ggplot2)
library(multcompView)
library(dplyr)
library(lmerTest)

setwd("~/Desktop/")
data <- read.csv("Petrobras.csv", sep=";")
data
data$treatment <- as.factor(data$treatment)
data$density <- as.factor(data$density)
data$Canopy <- 100 - data$Canopy
data$density <- factor(data$density, levels = c("3X2","3X1"))
data$treatment <- factor(data$treatment, levels =
c("USUAL","INTENSIVE"))
data


## density analyse and plots-----------------------------------------
---------

#SSCI

ggplot(data, aes(group= density,x =density,y = SSCI, fill= density)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="SSCI") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH (3m
X 1m)"))


l1 <- aov(SSCI ~ density, data = data)
qqPlot(resid(l1))
summary(l1)
```

```
tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, density) %>%
  summarise(mean=mean(SSCI), quant = quantile(SSCI, probs = 0.75, na.rm
= T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$density)
Tk$cld <- cld$Letters

print(Tk)


mixed1 <- lmer(SSCI ~ density + (1|Block) , data=data)
summary(mixed1)
anova(mixed1)

# meanfrac

l1 <- aov(Mean.fractal.dimension..MeanFrac. ~ density, data = data)
qqPlot(resid(l1))
summary(l1)

ggplot(data, aes(group= density,x =density,y =
Mean.fractal.dimension..MeanFrac., fill= density)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="MeanFRAC") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH (3m
X 1m)")) +
  ggtitle("Carbono-Petrobras - Density")


mixed1 <- lmer(Mean.fractal.dimension..MeanFrac. ~ density + (1|Block)
, data=data)
summary(mixed1)
anova(mixed1)

#enl

l1 <- aov(Effective.number.of.layers..ENL. ~ density, data = data)
qqPlot(resid(l1))
summary(l1)

ggplot(data, aes(group= density,x =density,y =
Effective.number.of.layers..ENL., fill= density)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="ENL") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
```

```
  scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH (3m
X 1m)")) +
  ggtitle("Carbono-Petrobras - Density")


mixed1 <- lmer(Effective.number.of.layers..ENL.~ density + (1|Block) ,
data=data)
summary(mixed1)
anova(mixed1)


# canopy

l1 <- aov(Canopy ~ density, data = data)
qqPlot(resid(l1))
summary(l1)

ggplot(data, aes(group= density,x =density,y = Canopy, fill= density))
+
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="Canopy Cover") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH (3m
X 1m)")) +
  ggtitle("Carbono-Petrobras - Density")



mixed1 <- lmer(Canopy ~ density + (1|Block) , data=data)
summary(mixed1)
anova(mixed1)




## treatmnent analyse and plots-----------------------------------------
---------

#SSCI
ggplot(data, aes(group= treatment,x =treatment,y = SSCI, fill =
treatment)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="TREATMENT", y="SSCI") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  scale_x_discrete(labels = c("MAX" = "INTENSIVE", "NORMAL" = "USUAL"))



l1 <- aov(SSCI ~ treatment, data = data)
qqPlot(resid(l1))
summary(l1)

tukey <- TukeyHSD(l1)
print(tukey)
```

```
Tk <- group_by(data, treatment) %>%
  summarise(mean=mean(SSCI), quant = quantile(SSCI, probs = 0.75, na.rm
= T)) %>%
  arrange(desc(mean))

cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$treatment)
Tk$cld <- cld$Letters

print(Tk)

mixed1 <- lmer(SSCI ~ treatment + (1|Block) , data=data)
summary(mixed1)
anova(mixed1)


#meanfrac

l1 <- aov(Mean.fractal.dimension..MeanFrac. ~ treatment, data = data)
qqPlot(resid(l1))
summary(l1)

ggplot(data, aes(x =treatment,y = Mean.fractal.dimension..MeanFrac.,
fill = treatment)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="MeanFRAC") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH (3m
X 1m)")) +
  ggtitle("Carbono-Petrobras - Treatment")


mixed1 <- lmer(Mean.fractal.dimension..MeanFrac. ~ treatment +
(1|Block) , data=data)
summary(mixed1)
anova(mixed1)

#ENL

l1 <- aov(Effective.number.of.layers..ENL. ~ treatment, data = data)
qqPlot(resid(l1))
summary(l1)

ggplot(data, aes(x =treatment,y = Effective.number.of.layers..ENL.,
fill = treatment)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="ENL") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH (3m
X 1m)")) +
  ggtitle("Carbono-Petrobras - Treatment")
```

```
mixed1 <- lmer(Effective.number.of.layers..ENL. ~ treatment + (1|Block)
, data=data)
summary(mixed1)
anova(mixed1)

# canopy

l1 <- aov(data$Canopy ~ treatment, data = data)
qqPlot(resid(l1))
summary(l1)

ggplot(data, aes(x =treatment,y = Canopy, fill = treatment)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Tree Density", y="Canopy Cover") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH (3m
X 1m)")) +
  ggtitle("Carbono-Petrobras - Treatment")


mixed1 <- lmer(Canopy ~ treatment + (1|Block) , data=data)
summary(mixed1)
anova(mixed1)


### plot type effect-----------------------------------------------------
---------

# SSCI

boxplot(data$SSCI ~ data$plot_no)
ggplot(data, aes(x =plot_no,y = SSCI)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Plot Type", y="SSCI") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  #scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH
(3m X 1m)")) +
  ggtitle("Carbono-Petrobras - Treatment x density")


l1 <- aov(SSCI ~ plot_no, data = data)
qqPlot(resid(l1))
summary(l1)

tukey <- TukeyHSD(l1)
print(tukey)

Tk <- group_by(data, plot_no) %>%
  summarise(mean=mean(SSCI), quant = quantile(SSCI, probs = 0.75, na.rm
= T)) %>%
  arrange(desc(mean))
```

```
cld <- multcompLetters4(l1, tukey)
print(cld)

cld <- as.data.frame.list(cld$plot_no)
Tk$cld <- cld$Letters

print(Tk)

# MeanFRAC

ggplot(data, aes(x =plot_no,y = Mean.fractal.dimension..MeanFrac.)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Plot Type", y="MeanFRAC") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  #scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH
(3m X 1m)")) +
  ggtitle("Carbono-Petrobras - Treatment x density")

l1 <- aov(Mean.fractal.dimension..MeanFrac. ~ treatment, data = data)
qqPlot(resid(l1))
summary(l1)

# ENL

ggplot(data, aes(x =plot_no,y = Effective.number.of.layers..ENL.)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Plot Type", y="ENL") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH (3m
X 1m)")) +
  ggtitle("Carbono-Petrobras - Treatment x Density")


l1 <- aov(Effective.number.of.layers..ENL. ~ treatment, data = data)
qqPlot(resid(l1))
summary(l1)


# canopy cover

ggplot(data, aes(x =plot_no,y = Canopy)) +
  geom_boxplot(outlier.shape = NA) +
  labs(x="Plot Type", y="Canopy Cover") +
  theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())+
  #scale_x_discrete(labels = c("3X2" = "LOW (3m X 2m)","3X1" = "HIGH
(3m X 1m)")) +
  ggtitle("Carbono-Petrobras - Treatment x Density")


l1 <- aov(Canopy ~ treatment, data = data)
qqPlot(resid(l1))
summary(l1)
```

```
# height

boxplot(data$Top.height..m. ~ data$treatment)

l1 <- aov(Top.height..m. ~ treatment, data = data)
qqPlot(resid(l1))
summary(l1)


### PCA analysis-----------------------------------------------------
---------


library(cowplot)
library(magick)
library(sp)
library(raster)
library(ggfortify)
library(cluster)
library(factoextra)
library(devtools)
library(FactoMineR)
library(ggcorrplot)
library(corrr)


# treatment

data <- read.csv("Petrobras_pca.csv", sep=";")
data
data$treatment <- as.factor(data$treatment)
data$treatment <- factor(data$treatment, levels = c("NORMAL","MAX"))
data$density <- as.factor(data$density)
data$canopy <- 100 - data$canopy
df <- data[,3:6]
pca_res <- prcomp(df, scale. = TRUE)

pca <- autoplot(pca_res, data = data, colour = 'treatment',
                loadings = TRUE,loadings.colour = 'black',
                loadings.label = TRUE, loadings.label.size = 3,
loadings.label.colour = "black" )

pca

fviz_pca_biplot(pca_res,
                col.ind = data$treatment,
                addEllipses = FALSE, label = "var",
                col.var = "black", repel = T,
                legend.title = "Species") + theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())


# density

data <- read.csv("Petrobras_pca.csv", sep=";")
data
```

```
data$density <- factor(data$density, levels = c("3X2","3X1"))
data$treatment <- as.factor(data$treatment)
data$density <- as.factor(data$density)
data$canopy <- 100 - data$canopy
df <- data[,3:6]
pca_res <- prcomp(df, scale. = TRUE)

pca <- autoplot(pca_res, data = data, colour = 'density',
                loadings = TRUE,loadings.colour = 'black',
                loadings.label = TRUE, loadings.label.size = 3,
loadings.label.colour = "black" )

pca

fviz_pca_biplot(pca_res,
                col.ind = data$density,
                addEllipses = FALSE, label = "var",
                col.var = "black", repel = T,
                legend.title = "Species") + theme_bw() +
  theme(panel.grid.major = element_blank(), panel.grid.minor =
element_blank())
```

6.6. Faro Focus M70 manual (French)

FARO FOCUS M70

MANUEL D'UTILISATION

Université de Neuchâtel

Louis Fontaine

TABLE DES MATIERES

1. Présentation Et Détails Techniques

1. Fiche technique

- Terrestrial laser scanner (TLS)
- Mesures par Light Detection And Ranging (LiDAR)
- Mesure simple (1 scan)
- Distance max. : 70m
- Résolution max. : ~50 millons de pixels
- Durée batterie : ~3-5h suivant utilisation (2 batteries)
- Temps d'un scan : 5-7 min
- Volume d'un scan : 150-300 Mo

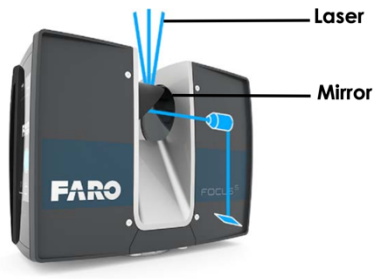
2. Principe de fonctionnement

Le **FARO FOCUS M70** permet d'effectuer des scans à 360° dans une grande diversité de milieu. Il utilise le principe de mesure LiDAR, c'est-à-dire qu'il envoie un faisceau lumineux (laser) qui va rebondir sur un objet et revenir au scanner. Le scanner est en mesure de calculer la distancer parcoure par le faisceau lumineux et donc de déterminer la distance de l'objet par rapport à ce premier. Chaque scan est finalement composé de l'ensemble de ces points mesurés et forme une image finale.

Le scanner est muni d'un miroir rotatif et est capable de faire une rotation complète sur son support. Il peut donc faire un scan presque complet de l'environnement, à l'exception d'une section située sous le scanner (60°).

Rotation du laser

Rotation du scanner



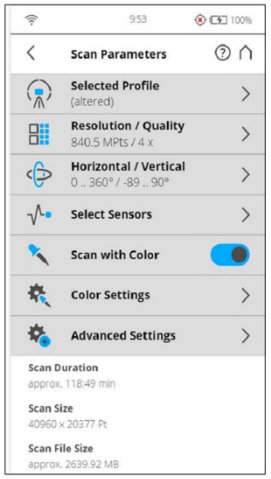
Laser interne

2. Allumage Et Calibrage

1. Écran d'accueil

Avant de vous lancer dans la prise de scans, plusieurs précautions sont à prendre impérativement si vous voulez ensuite pouvoir les analyser sans problème.

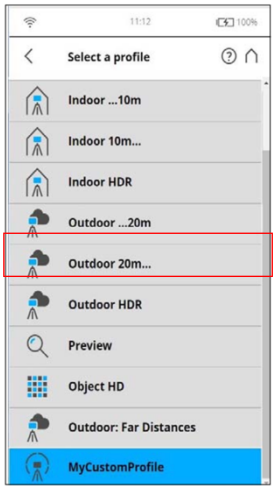
Tout d'abord vérifiez que la **carte SD** est en place et que la **batterie** est suffisante (des problèmes surviennent lorsque qu'elle descend en dessous de **15%**).



2. Paramètres

Ensuite, accédez aux paramètres. Les paramètres choisis impacteront la transformation des scans. Une modification des paramètres impliquera la modification du code ou l'impossibilité de transformer les scans. Il est donc impératif de les choisir correctement.

- Profile

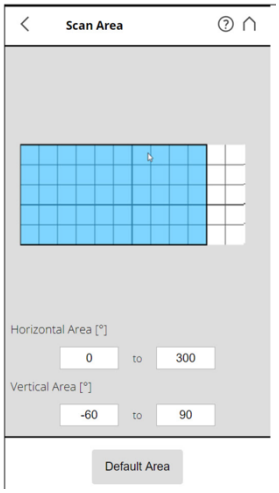


Le profil n'a que peu d'impact sur les résultats. Cependant, il est recommandé d'utiliser le « Outdoor 20m… » qui correspond à une mesure optimale d'objets en extérieur entre 20m et 70m, le plus approprié dans le cas de scans en forêt naturelle. Le paramètre « Outdoor …20m » peut également être utilisé en cas de mesure de petites parcelles jusqu'à 20m. Il est cependant conseillé de choisir un réglage avant de procéder aux mesures et de le conserver tout au long de l'expérience.

- Resolution/Quality

La résolution est un paramètre ayant un grand impact sur le calcul du SSCI et sa modification en implique d'autre dans le code de transformation des scans. Elle correspond au nombre de pixels mesuré par le scanner. La qualité, elle, est complémentaire à la résolution en apportant un niveau de détail supplémentaire. Elle est cependant négligeable par rapport à la résolution.

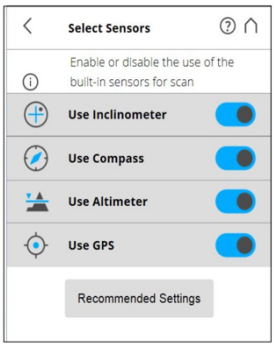
Le grand avantage de ce scanner est sa rapidité et sa précision. Les deux étant inversement proportionnels, une résolution intermédiaire est le compromis pour conserver une haute qualité sans perdre trop de temps. Il est donc conseillé d'utiliser la **résolution ¼** et la **qualité 2x** pour une durée de scan d'environ **5min.**



- **Horizontal / Vertical**

Ce paramètre calibre l'angle de scan désiré. Pour le calcul du SSCI, il est impératif de choisir les angles les plus larges, soit de **0° à 360°** pour l'angle horizontal, et de **-60° à 90°** pour l'angle vertical.

- **Select Sensors**



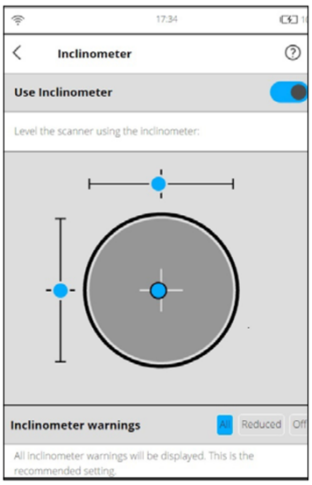
Un mauvais choix de ces paramètres peut résulter en l'incapacité d'analyser les scans, il est donc impératif de vérifier le bon paramétrage à **chaque** utilisation du scanner. L'**inclinomètre** permet de vérifier que le scanner est placé verticalement, il doit donc être activé. Le **compas** permet de calibrer les scans entre eux par rapport aux points cardinaux. Il n'a pas d'impact sur l'analyse donc il est conseillé de le désactiver. L'**altimètre** mesure l'altitude du scanner et des points mesurés. Il doit être désactivé pour éviter d'ajouter l'altitude initial à la mesure de hauteur d'arbre. Notons qu'il est possible d'enlever l'altitude à posteriori, bien que couteux en temps. Notons également que l'altitude 0 devient le centre du scanner et non le sol, il est donc impératif de rajouter cette différence pour une mesure correcte de hauteur d'arbre. Finalement, le **GPS** enregistrera les coordonnées GPS des points du premier scan effectué et calibrera tous les autres par rapport à ce premier. Il est absolument impératif de le désactiver, car il est impossible d'analyser les scans avec cette configuration.

- **Autres Paramètres**

Les derniers paramètres n'ont aucun impact sur la mesure du SSCI. Il reste donc conseillé de ne pas y toucher.

3. Scanner

1. <u>Avant de scanner</u>



Avant de procéder aux scans, plusieurs facteurs doivent être pris en compte. Tout d'abord le scanner doit être placé au centre de la parcelle/forêt à mesurer. Il doit être placé verticalement à l'aide de l'inclinomètre. Notons qu'un raccourci existe en haut à gauche de l'écran d'accueil pour y accéder.

Ensuite, le centre du scanner (miroir) doit être positionné à 1,3m du sol approximativement. Cela est dû au fait que les points mesurés sous la hauteur du scanner seront ensuite supprimés pour éviter de prendre en compte la couche du sol qui pourrait avoir des effets négatifs sur le calcul du SSCI.

Enfin, il faut faire attention à ne pas placer le scanner à proximité d'un objet volumineux comme une feuille ou un tronc car cela impactera une fois encore le SSCI. Il est donc conseillé de se placer à 1m au moins d'un gros tronc ou 50 cm de plus petits objets (feuille, branche).

2. Pendant le scan

Le scanner est correctement positionné, tous les paramètres sont corrects, vous êtres donc prêts à scanner. Appuyez sur le bouton sur l'écran principal. A partir de ce moment, il est impératif de ne jamais intercepter le laser du scanner, et surtout ne jamais regarder le laser qui peut vous abimer les yeux ! Pour cela, vous devez toujours être positionné sur le côté du scanner et de vous éloigner le temps du scan. Comme le scanner tourne sur lui-même, vous devrez également tourner en même temps, et les pas à proximité du scanner – surtout sur un sol meuble – peuvent faire bouger le scanner et dégrader le scan. La meilleure solution est de se cacher derrière un gros tronc le temps du scan. Si aucun objet volumineux n'est disponible, il est conseillé de s'éloigner d'au moins 20m et de s'assoir, dos au scanner, derrière le plus gros objet disponible. Cela limitera votre présence sur le scan. Attention, un buisson n'est pas un gros objet car le laser est susceptible de passer dans les trous entre les feuilles, il faut donc favoriser les troncs !

Le scanner fera un bruit au moment où il aura terminé son scan. Cependant, si vous êtes loin du scan, il est possible que vous ne l'entendiez pas. Il est donc conseillé de noter le temps nécessaire au scan (le temps du scan dépend de la résolution choisie) et de calculer le temps par vos propres moyens. Vous pouvez ensuite vous rapprocher du scan. La photo de votre scan s'affichera à l'écran et sera enregistrée automatiquement. Vous pouvez ensuite procéder au scan suivant.

4. Analyse Des Scans

Dans un premier temps, les scans bruts doivent être transformés au format « .xyz » pour être utilisables. Cela va attribuer à chaque point du scan une position tridimensionnelle par rapport au centre du scanner. Le nombre d'angle horizontaux est également réduit pour faciliter cette transformation. Cette étape se fait dans le logiciel SCENE de FARO (logiciel d'essais gratuit pendant 30 jours). Un Powerpoint détaillant chaque étape est disponible en annexe de ce manuel.

Lien pour télécharger SCENE :
https://knowledge.faro.com/Software/FARO_SCENE/SCENE/Software_Download_Installation_and_Release_Notes_for_SCENE

Ensuite, il est possible de visualiser le nuage de point créé via le logiciel CloudCompare. Notons que la première étape est également possible via ce logiciel, mais ne sera pas détaillée ici.

Lien pour télécharger CloudCompare :
https://www.danielgm.net/cc/release/

Une fois les scans transformés, nous pouvons calculer le SSCI. Son calcul se fait sur RStudio. Il est possible d'ajouter au code une correction de pente si les scans sont faits dans des environnements ou la pente varie, ce qui peut avoir un impact sur le résultat final. L'ensemble des codes sont disponible en annexe de ce manuel. Le résultat final est la valeur du SSCI, l'ENL, le MeanFRAC et d'autre mesures comme la hauteur max, etc.

5. Stand Structural Complexity Index

1. Définition

La complexité structurelle a de nombreuses définitions différentes. Cependant, la définition de McElhinny & al. (2005) s'applique bien à notre cas d'étude. Ils définissent la complexité structurelle comme « une mesure du nombre d'attributs différents présents et leur abondance relative ». Plusieurs indexes existent pour tenter de la calculer en utilisant différents paramètres pour la calculer comme la rugosité ou la dispersion par exemple. Martin Ehbrecht a proposé en 2017 une nouvelle façon de la mesuré décrite au paragraphe suivant.

2. Construction

Le SSCI est construit à partir de deux concepts distincts. Le principal est une mesure de la dimension fractale du milieu, mise à l'échelle par le nombre effectif de couche du milieu.

La dimension fractale (**FRAC**) est calculée par la création de polygones obtenus à partir des scans. Les points mesurés par le scanner sont liés à un angle donné lors de la rotation du scanner. L'ensemble des points d'un angle donné sont reliés ensemble pour former un polygone. Le rapport entre l'aire et le périmètre calculé par l'équation suivante donne la dimension fractale d'un angle spécifique. La dimension fractale du milieu est ensuite calculée par la moyenne arithmétique de l'ensemble des polygones crées (**MeanFrac**).

Exemple de polygone
(Ehbrecht & al. 2017)

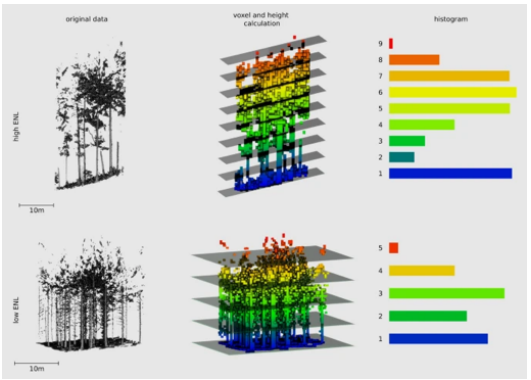
$$FRAC = \frac{2*\ln(0.25*P)}{\ln(A)}$$

Équation de la dimension fractale. P= périmètre ; A=aire
(Ehbrecht & al. 2017)

Ensuite, la dimension fractale est mise à l'échelle par le nombre effectif de couche (**ENL**). Le nombre effectif de couche est calculé en divisant le milieu en couche de 1m de haut, et l'occupation (quantité de matière présente dans la couche) de chaque couche est mesurée. Enfin l'hétérogénéité de de la répartition de la matière dans les couches est calculé en utilisant l'index de Simpson inversé.

$$ENL = 1/\sum_{i=1}^{N_{top}} p_i^2$$

Équation du nombre effectif de couches
(Ehbrecht & al. 2017)



Visualisation du calcul de ENL
(Ehbrecht & al. 2017)

Finalement, le SSCI est calculé avec l'équation suivante :

$$SSCI = MeanFrac^{\ln(ENL)}$$

(Ehbrecht & al. 2017)

Ce calcul de la complexité structurelle nous donne donc au final une valeur unique, permettant une comparaison simple d'une grande diversité de milieu. Comme les scans contiennent une grande quantité de polynômes, l'ensemble des calcules est fait informatiquement grâce au code suivant (Ehbrecht, 2022), disponible en libre accès :

https://github.com/ehbrechtetal/Stand-structural-complexity-index---SSCI/blob/main/Ehbrecht%20et%20al_Stand%20Structural%20Complexity%20Index_Code_v1.3.R

3. Utilisation / Potentiel

Cet index s'inscrit dans la recherche de nouveaux outils pour évaluer l'état d'une ou plusieurs forêts de façon rapide. Il peut servir de proxy pour mesurer certaines caractéristiques de cette dernière comme le stockage de Carbon (au-dessus du sol), la productivité, la résilience ou encore la biodiversité. L'avantage de l'utilisation de cet index est un gain de précision et rapidité, et par extension de coût. Un travail équivalent peut être fait par une personne en quelque heures, alors qu'il faudrait une équipe entière pendant une semaine avec des méthodes manuelles.

Cependant, l'utilisation de cet index est récente et les limites de son potentiel ne sont pas encore clairement définies. Son utilisation comme proxy n'est pas la plus exacte qui soit. Il ne faut donc pas la considérer comme l'unique méthode existante pour la mesure des proxy décrits, mais plutôt comme un nouvel outil particulièrement efficace pour la récolte de données à moyenne et large échelle.

6. Bibliographie

Ehbrecht, M., Schall, P., Ammer, C., Seidel, D., 2017. Quantifying stand structural complexity and its relationship with forest management, tree species diversity and microclimate. Agricultural and Forest Meteorology 242, 1–9. https://doi.org/10.1016/j.agrformet.2017.04.012

McElhinny, C., Gibbons, P., Brack, C., Bauhus, J., 2005. Forest and woodland stand structural complexity: Its definition and measurement. Forest Ecology and Management 218, 1–24. https://doi.org/10.1016/j.foreco.2005.08.034

L'ensemble des images non référencées proviennent du manuel d'utilisation du FARO FOCUS M70 :

https://fr-knowledge.faro.com/Hardware/Focus/Focus/User_Manuals_and_Quick_Start_Guides_for_the_Focus_Laser_Scanner