4PMI Data Analysis

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2024-06-09

Set the right working directory.

```
setwd("C:/Users/elise/Documents/Mémoire/Main/Data/Templates/4PMI")
```

Data importation

Import the data sets extracted from the Data Preparation R Markdown.

```
list.files()
```

```
## [1] "endpoint.txt"   "plant_info.txt"
```

```
plant_info <- read.table("plant_info.txt", header = TRUE, sep = "\t")
endpoint <- read.table("endpoint.txt", header = TRUE, sep = "\t")
```

Convert the columns to factor and date formats.

```
# plant_info
plant_info <- lapply(plant_info, factor)

# endpoint
matching_cols <- intersect(names(endpoint), names(plant_info))
endpoint[, matching_cols] <- lapply(endpoint[, matching_cols], factor)
endpoint$Date <- date(endpoint$Date)
endpoint$Timestamp <- NA
```

Collect the variables of every data template and print the names of the variables. This serves as a double check.

```
platform <- "4PMI"

# endpoint
df <- endpoint[,colSums(is.na(endpoint))<nrow(endpoint)]
genotype_index <- which(colnames(df) == "Genotype")
variables <- colnames(df[, c(3:(genotype_index - 1))]) # We remove the 3 first columns
that are "Unit.ID" and "Date" etc

print(paste(platform, ": The variables for endpoint are", paste(variables, collapse =
", "), sep = " "))
```

```
## [1] "4PMI : The variables for endpoint are DW_shoot_g, DW_root_g, Leaf_number, DW_se
ed_g"
```

Add a column Plant_type with three levels, H L and T. This variable is useful to test for heterosis effects.

```
endpoint$Plant_type <- substr(endpoint$Genotype, nchar(as.character(endpoint$Genotyp
e)), nchar(as.character(endpoint$Genotype)))
```

1. Endpoint dataframe

A. Exploration of data

Exploration tables using the rstatix, janitor and skimr packages

```
endpoint %>%
  count(Genotype)
```

```
##     Genotype  n
## 1        10H 10
## 2        10L 10
## 3        11H 10
## 4        11L 10
## 5        12H 10
## 6        12L 10
## 7        13H 10
## 8        13L 10
## 9        14H 10
## 10       14L 10
## 11       15H 10
## 12       15L 10
## 13        1H 10
## 14        1L 10
## 15       20T 10
## 16       23T 10
## 17       24T 10
## 18        2H 10
## 19        2L 10
## 20        3H 10
## 21        3L 10
## 22        4H 10
## 23        4L 10
## 24        5H 10
## 25        5L 10
## 26        6H 10
## 27        6L 10
## 28        7H 10
## 29        7L 10
## 30        8H 10
## 31        8L 10
## 32        9H 10
## 33        9L 10
```

```
endpoint %>%
  tabyl(Genotype, Column) %>%
  adorn_totals("row") %>%
  adorn_percentages("row") %>%
  adorn_pct_formatting() %>%
  adorn_ns() %>%
  adorn_title("combined")
```

```
## Genotype/Column        8            9           10           11           12
##           10H 10.0%  (1)   0.0%  (0) 10.0%  (1)   0.0%  (0) 10.0%  (1)
##           10L 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1)   0.0%  (0)
##           11H 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1)
##           11L 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1)   0.0%  (0)
##           12H 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1)   0.0%  (0)
##           12L 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1)   0.0%  (0)
##           13H 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1)
##           13L 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1)
##           14H 10.0%  (1)   0.0%  (0) 10.0%  (1)   0.0%  (0) 10.0%  (1)
##           14L  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1) 10.0%  (1)
##           15H 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1)   0.0%  (0)
##           15L  0.0%  (0) 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1)
##            1H 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1)   0.0%  (0)
##            1L  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1) 10.0%  (1)
##           20T  0.0%  (0) 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1)
##           23T  0.0%  (0) 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1)
##           24T 10.0%  (1) 10.0%  (1)   0.0%  (0)   0.0%  (0) 10.0%  (1)
##            2H 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1)
##            2L  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1) 10.0%  (1)
##            3H 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1)   0.0%  (0)
##            3L 10.0%  (1)   0.0%  (0) 10.0%  (1)   0.0%  (0) 10.0%  (1)
##            4H  0.0%  (0) 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1)
##            4L 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1)   0.0%  (0)
##            5H  0.0%  (0) 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1)
##            5L 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1)   0.0%  (0)
##            6H  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1) 10.0%  (1)
##            6L 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1)
##            7H 10.0%  (1) 10.0%  (1)   0.0%  (0)   0.0%  (0) 10.0%  (1)
##            7L  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1)   0.0%  (0)
##            8H 10.0%  (1) 10.0%  (1)   0.0%  (0) 10.0%  (1)   0.0%  (0)
##            8L  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1) 10.0%  (1)
##            9H 10.0%  (1)   0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1)
##            9L 10.0%  (1) 10.0%  (1)   0.0%  (0)   0.0%  (0) 10.0%  (1)
##         Total  6.7% (22)  6.7% (22)  6.7% (22)  6.7% (22)  6.7% (22)
##          13           14           15           16           17           18           19
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##  6.7% (22)  6.7% (22)  6.7% (22)  6.7% (22)  6.7% (22)  6.7% (22)  6.7% (22)
##            20         21         22
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## 10.0%  (1)  0.0%  (0) 10.0%  (1)
##  6.7% (22)  6.7% (22)  6.7% (22)
```

```
endpoint %>%
  tabyl(Genotype, Row) %>%
  adorn_totals("row") %>%
  adorn_percentages("row") %>%
  adorn_pct_formatting() %>%
  adorn_ns() %>%
  adorn_title("combined")
```

```
endpoint %>%
  tabyl(Genotype, Row) %>%
  adorn_totals("row") %>%
  adorn_percentages("row") %>%
  adorn_pct_formatting() %>%
  adorn_ns() %>%
  adorn_title("combined")
```

```
## Genotype/Row        1           2           3           4           5           6
##            10H  0.0%  (0)  0.0%  (0)  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1)
##            10L  0.0%  (0)  0.0%  (0) 10.0%  (1)  0.0%  (0) 10.0%  (1) 10.0%  (1)
##            11H  0.0%  (0)  0.0%  (0) 10.0%  (1) 10.0%  (1)  0.0%  (0)  0.0%  (0)
##            11L 10.0%  (1) 10.0%  (1)  0.0%  (0) 10.0%  (1)  0.0%  (0) 10.0%  (1)
##            12H  0.0%  (0)  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1)  0.0%  (0)
##            12L  0.0%  (0) 10.0%  (1)  0.0%  (0)  0.0%  (0)  0.0%  (0)  0.0%  (0)
##            13H 10.0%  (1) 10.0%  (1)  0.0%  (0)  0.0%  (0)  0.0%  (0) 10.0%  (1)
##            13L 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1) 10.0%  (1)  0.0%  (0)
##            14H 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1)  0.0%  (0) 10.0%  (1)
##            14L  0.0%  (0) 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1) 10.0%  (1)
##            15H  0.0%  (0)  0.0%  (0) 10.0%  (1) 10.0%  (1)  0.0%  (0) 10.0%  (1)
##            15L  0.0%  (0) 10.0%  (1) 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1)
##             1H 10.0%  (1)  0.0%  (0) 10.0%  (1)  0.0%  (0)  0.0%  (0)  0.0%  (0)
##             1L  0.0%  (0)  0.0%  (0)  0.0%  (0) 10.0%  (1)  0.0%  (0)  0.0%  (0)
##            20T 10.0%  (1) 10.0%  (1)  0.0%  (0)  0.0%  (0)  0.0%  (0) 10.0%  (1)
##            23T  0.0%  (0) 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1)  0.0%  (0)
##            24T 10.0%  (1)  0.0%  (0)  0.0%  (0)  0.0%  (0) 10.0%  (1)  0.0%  (0)
##             2H  0.0%  (0)  0.0%  (0) 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1)
##             2L 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1)  0.0%  (0) 10.0%  (1)
##             3H 10.0%  (1)  0.0%  (0)  0.0%  (0)  0.0%  (0)  0.0%  (0) 10.0%  (1)
##             3L  0.0%  (0)  0.0%  (0) 10.0%  (1)  0.0%  (0) 10.0%  (1) 10.0%  (1)
##             4H 10.0%  (1)  0.0%  (0) 10.0%  (1)  0.0%  (0)  0.0%  (0)  0.0%  (0)
##             4L 10.0%  (1)  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1)  0.0%  (0)
##             5H  0.0%  (0) 10.0%  (1)  0.0%  (0) 10.0%  (1)  0.0%  (0) 10.0%  (1)
##             5L  0.0%  (0) 10.0%  (1) 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1)
##             6H  0.0%  (0) 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1)  0.0%  (0)
##             6L 10.0%  (1) 10.0%  (1) 10.0%  (1)  0.0%  (0)  0.0%  (0)  0.0%  (0)
##             7H  0.0%  (0) 10.0%  (1)  0.0%  (0) 10.0%  (1)  0.0%  (0)  0.0%  (0)
##             7L 10.0%  (1) 10.0%  (1)  0.0%  (0) 10.0%  (1) 10.0%  (1)  0.0%  (0)
##             8H 10.0%  (1) 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1)  0.0%  (0)
##             8L  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1) 10.0%  (1)  0.0%  (0)
##             9H  0.0%  (0)  0.0%  (0) 10.0%  (1) 10.0%  (1) 10.0%  (1)  0.0%  (0)
##             9L 10.0%  (1)  0.0%  (0) 10.0%  (1)  0.0%  (0) 10.0%  (1)  0.0%  (0)
##          Total  4.5% (15)  4.5% (15)  4.5% (15)  4.5% (15)  4.5% (15)  4.5% (15)
##            7           8           9          10          11          12          13
##   0.0%  (0)  0.0%  (0)  0.0%  (0) 10.0%  (1) 10.0%  (1)  0.0%  (0) 10.0%  (1)
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##  10.0%  (1)  0.0%  (0) 10.0%  (1) 10.0%  (1)  0.0%  (0)  0.0%  (0) 10.0%  (1)
##   0.0%  (0)  0.0%  (0)  0.0%  (0)  0.0%  (0) 10.0%  (1) 10.0%  (1)  0.0%  (0)
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```

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##            14          15          16          17          18          19          20
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##            21          22
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```

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## 10.0%  (1) 10.0%  (1)
##   0.0%  (0) 10.0%  (1)
##   4.5% (15)  4.5% (15)
```

```
get_summary_stats(data = endpoint,
                  variables,
                  type = "common")
```

```
## Warning: Using an external vector in selections was deprecated in tidyselect 1.1.0.
## ℹ Please use `all_of()` or `any_of()` instead.
##   # Was:
##   data %>% select(variables)
##
##   # Now:
##   data %>% select(all_of(variables))
##
## See <https://tidyselect.r-lib.org/reference/faq-external-vector.html>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## # A tibble: 4 × 10
##   variable       n   min   max median   iqr  mean    sd    se    ci
##   <fct>      <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 DW_shoot_g   325 0.006 0.638  0.224 0.153 0.241 0.121 0.007 0.013
## 2 DW_root_g    324 0.005 0.431  0.173 0.11  0.179 0.086 0.005 0.009
## 3 Leaf_number  319 1     6      4     1     4.33  0.692 0.039 0.076
## 4 DW_seed_g    330 0.01  0.222  0.036 0.027 0.043 0.027 0.002 0.003
```

```
skim(endpoint[variables])
```

Data summary

Name	endpoint[variables]
Number of rows	330
Number of columns	4
_____	
Column type frequency:	
numeric	4
_____	
Group variables	None

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
DW_shoot_g	5	0.98	0.24	0.12	0.01	0.16	0.22	0.31	0.64	▁▇▇▃▁
DW_root_g	6	0.98	0.18	0.09	0.01	0.12	0.17	0.23	0.43	▃▇▇▂▁
Leaf_number	11	0.97	4.33	0.69	1.00	4.00	4.00	5.00	6.00	▁▁▇▅▁
DW_seed_g	0	1.00	0.04	0.03	0.01	0.02	0.04	0.05	0.22	▇▃▁▁▁

Data visualization

Using several functions that are located in the functions.R script

Boxplots

```
create_boxplots(endpoint, variables, "Genotype")
```

```
## Warning: `aes_string()` was deprecated in ggplot2 3.0.0.
## ℹ Please use tidy evaluation idioms with `aes()`.
## ℹ See also `vignette("ggplot2-in-packages")` for more information.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning: Removed 5 rows containing non-finite values (`stat_boxplot()`).
```

```
## Warning: Removed 6 rows containing non-finite values (`stat_boxplot()`).
```

```
## Warning: Removed 11 rows containing non-finite values (`stat_boxplot()`).
```
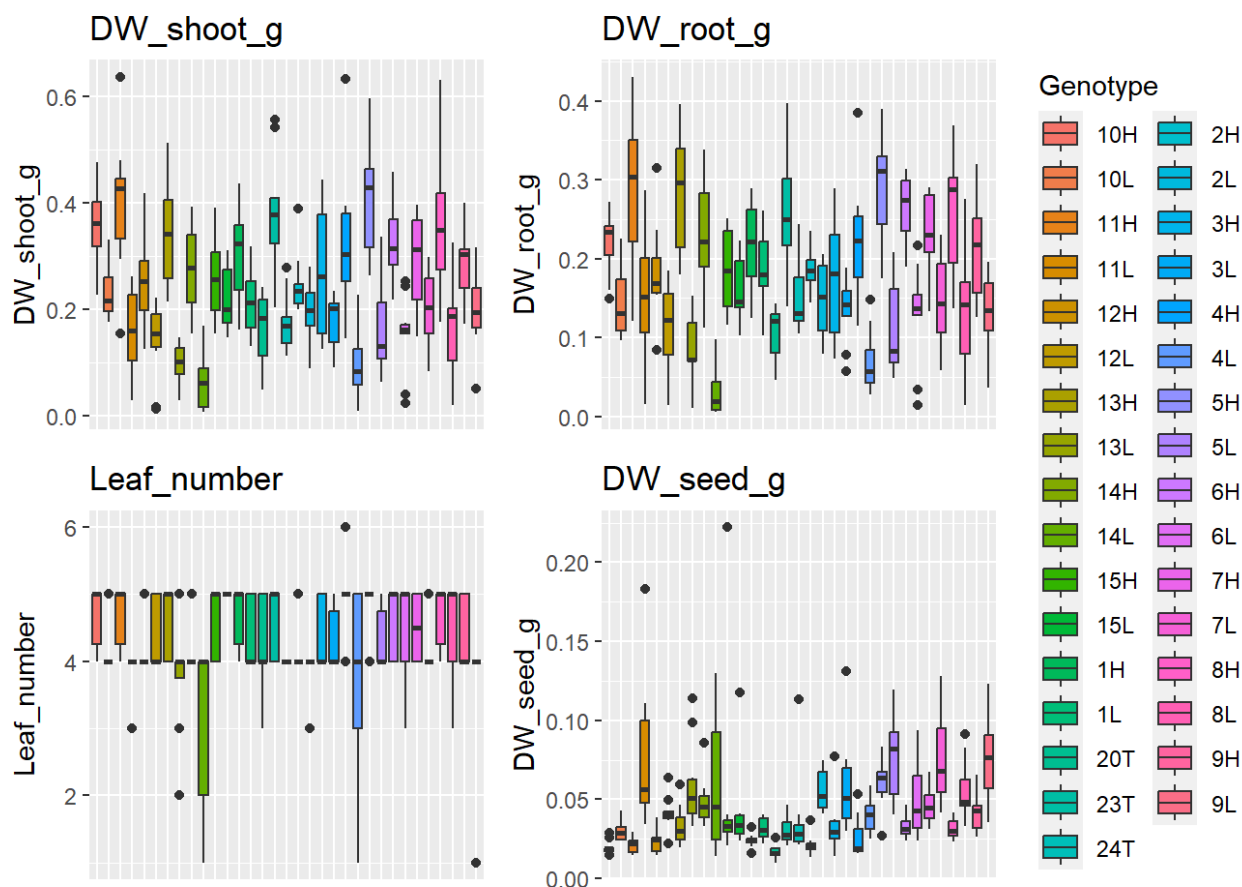


```
create_boxplots(endpoint, variables, "Plant_type")
```

```
## Warning: Removed 5 rows containing non-finite values (`stat_boxplot()`).
```

```
## Warning: Removed 6 rows containing non-finite values (`stat_boxplot()`).
```

```
## Warning: Removed 11 rows containing non-finite values (`stat_boxplot()`).
```
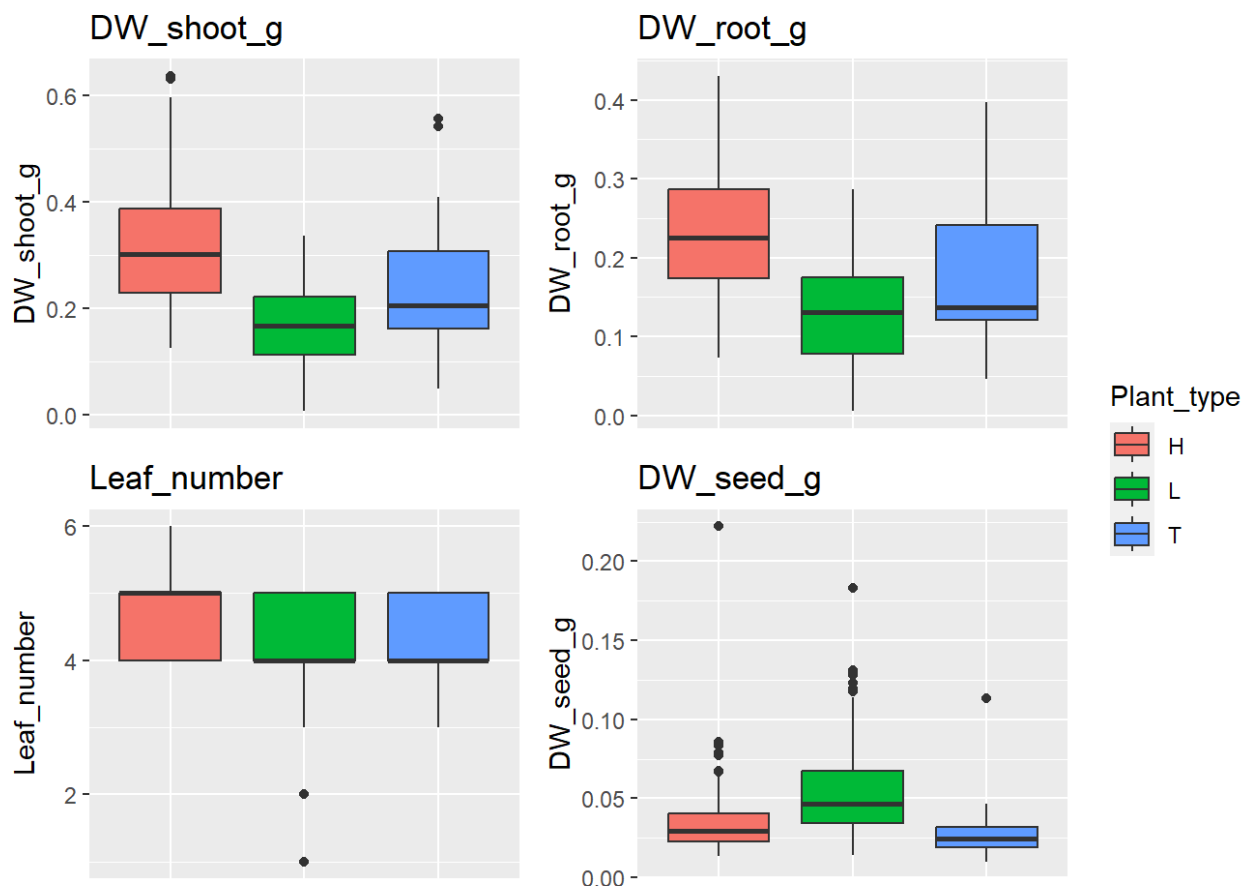
Correlation plots

```r
for (i in 1:(length(variables) - 1)) {
  for (j in (i + 1):length(variables)) {
    calculate_correlation_plot(endpoint, variables[i], variables[j])
  }
}
```
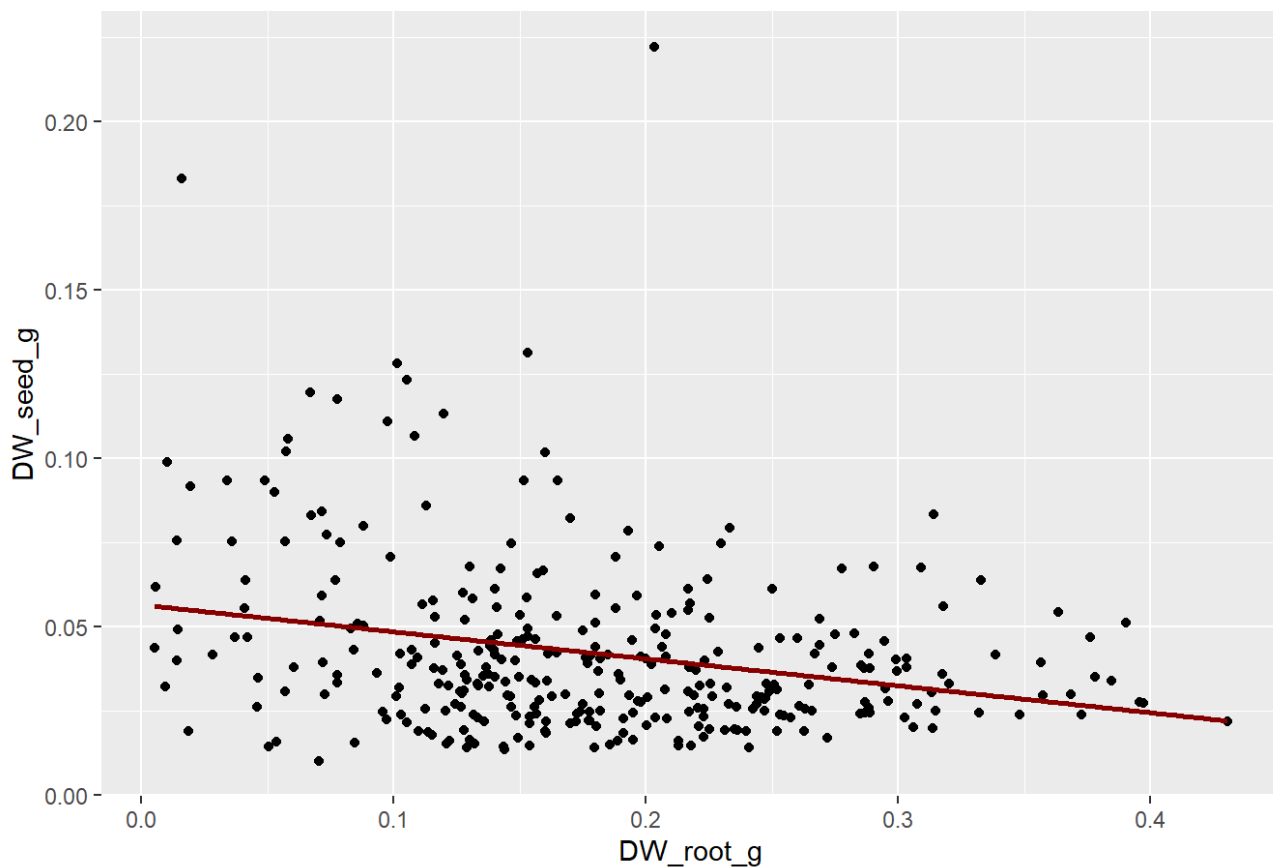
```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 6 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 6 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 330 rows containing missing values (`geom_text()`).
```

Correlation Plot between DW_shoot_g and DW_root_g
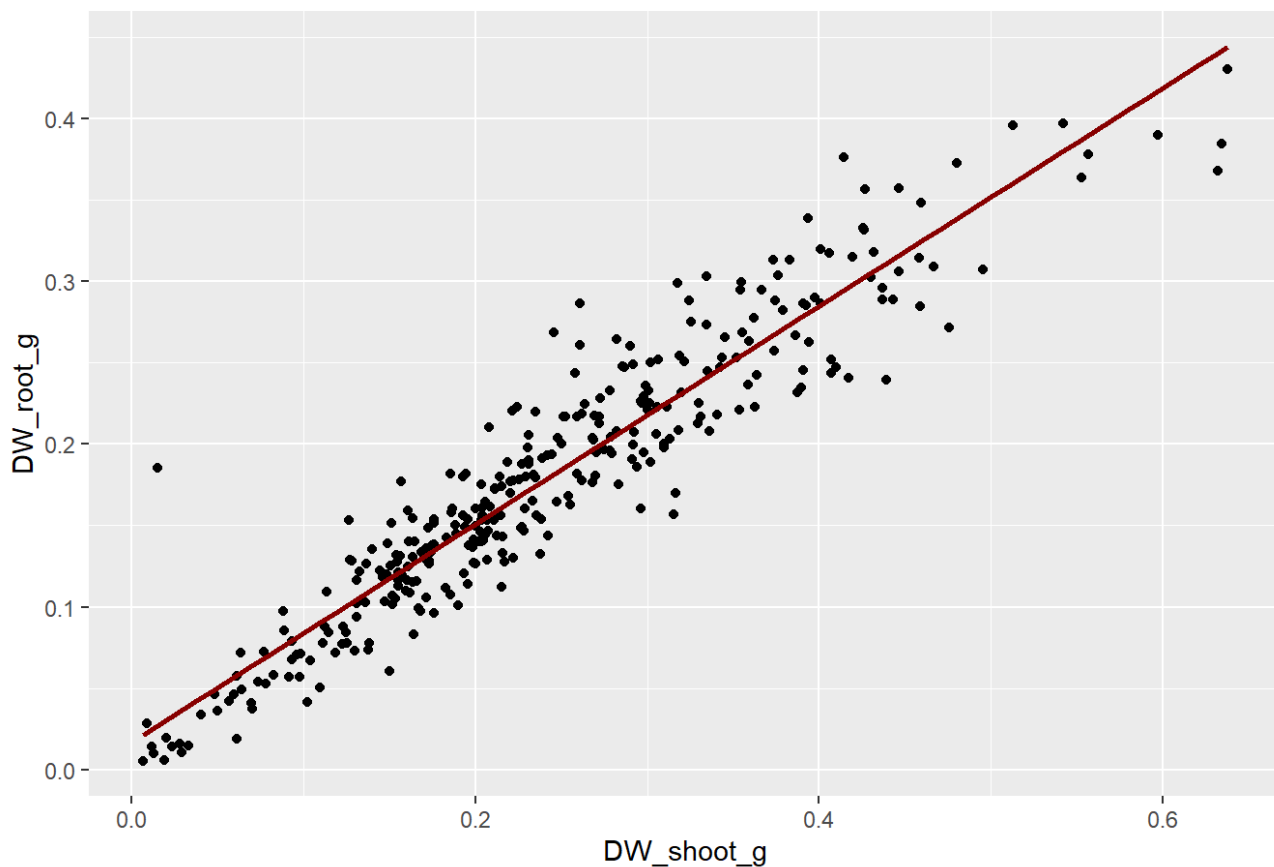

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 11 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 11 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 330 rows containing missing values (`geom_text()`).
```

Correlation Plot between DW_shoot_g and Leaf_number
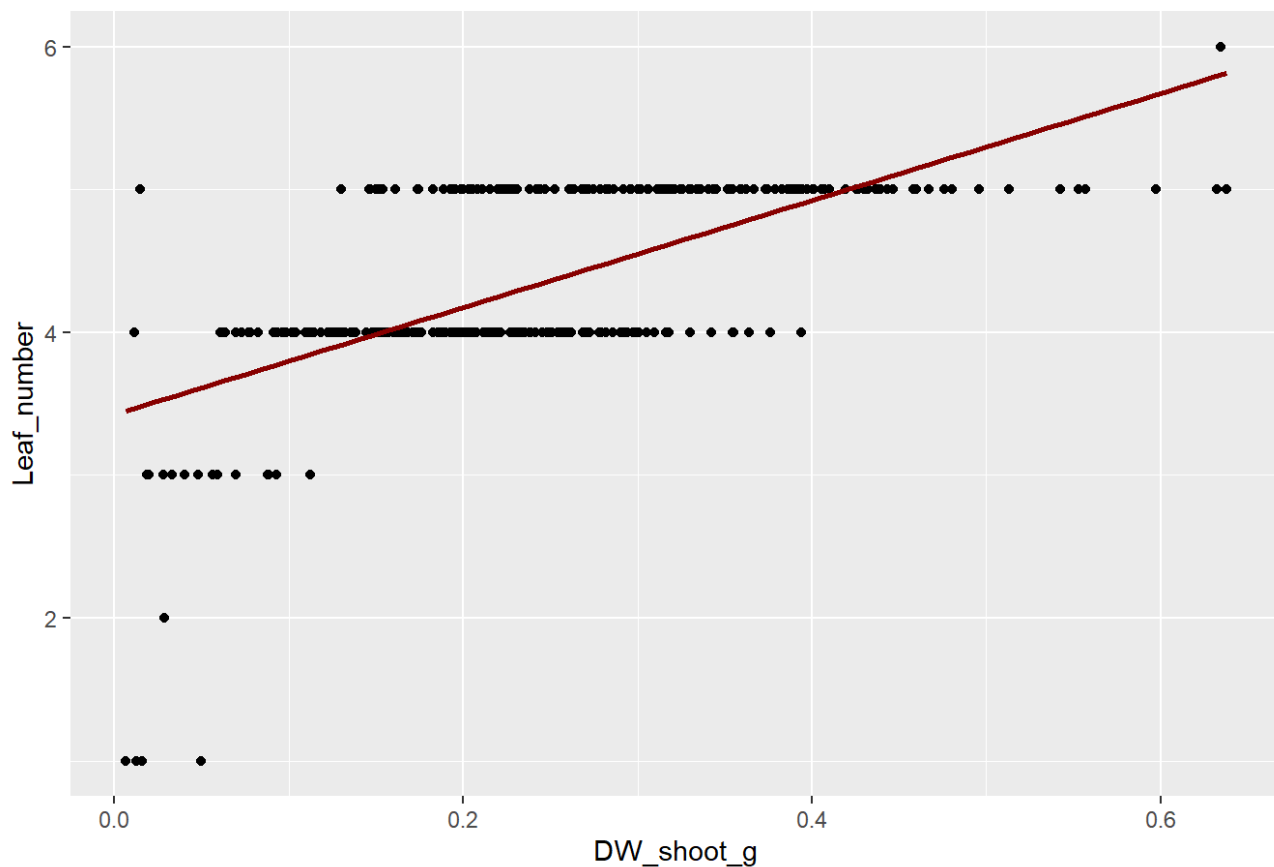

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 5 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 5 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 330 rows containing missing values (`geom_text()`).
```

Correlation Plot between DW_shoot_g and DW_seed_g


```
## `geom_smooth()` using formula = 'y ~ x'
```
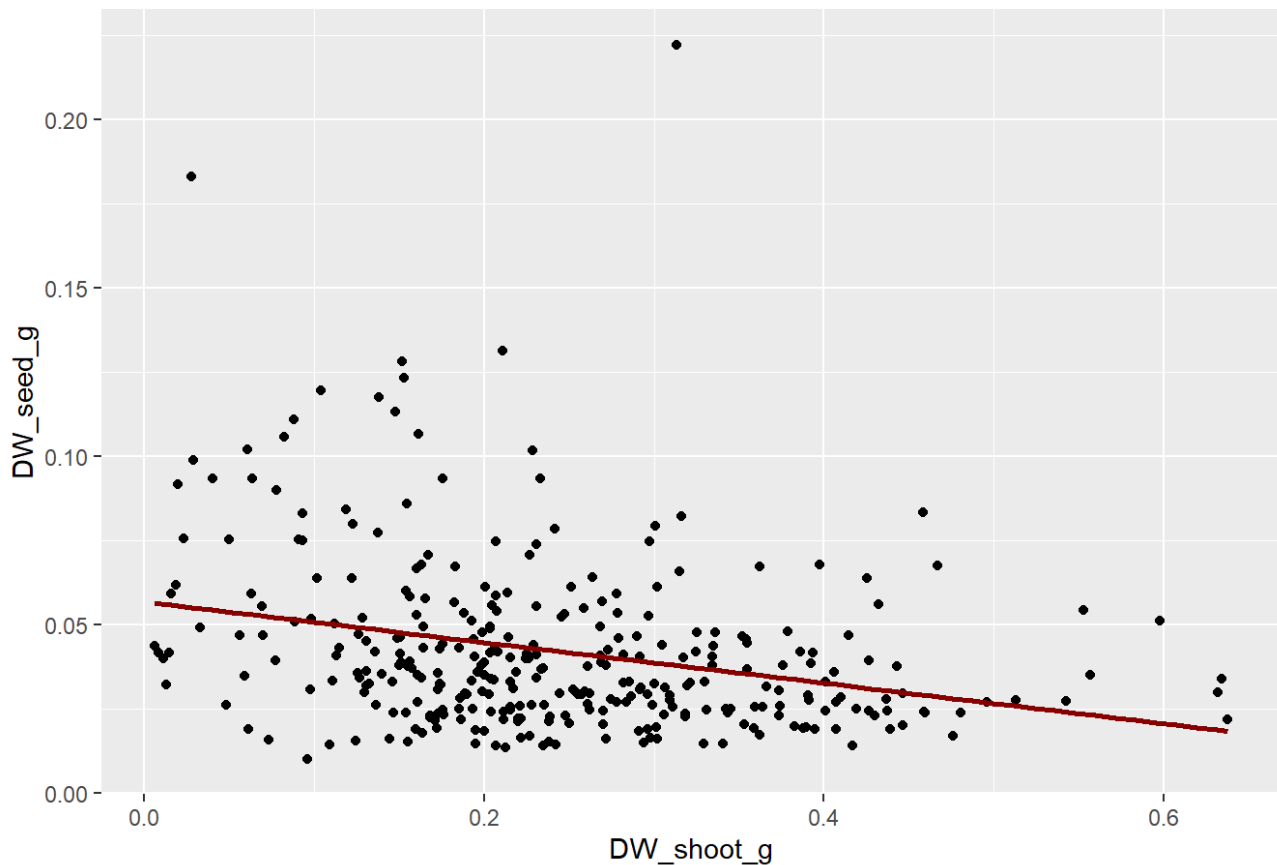
```
## Warning: Removed 12 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 12 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 330 rows containing missing values (`geom_text()`).
```

Correlation Plot between DW_root_g and Leaf_number
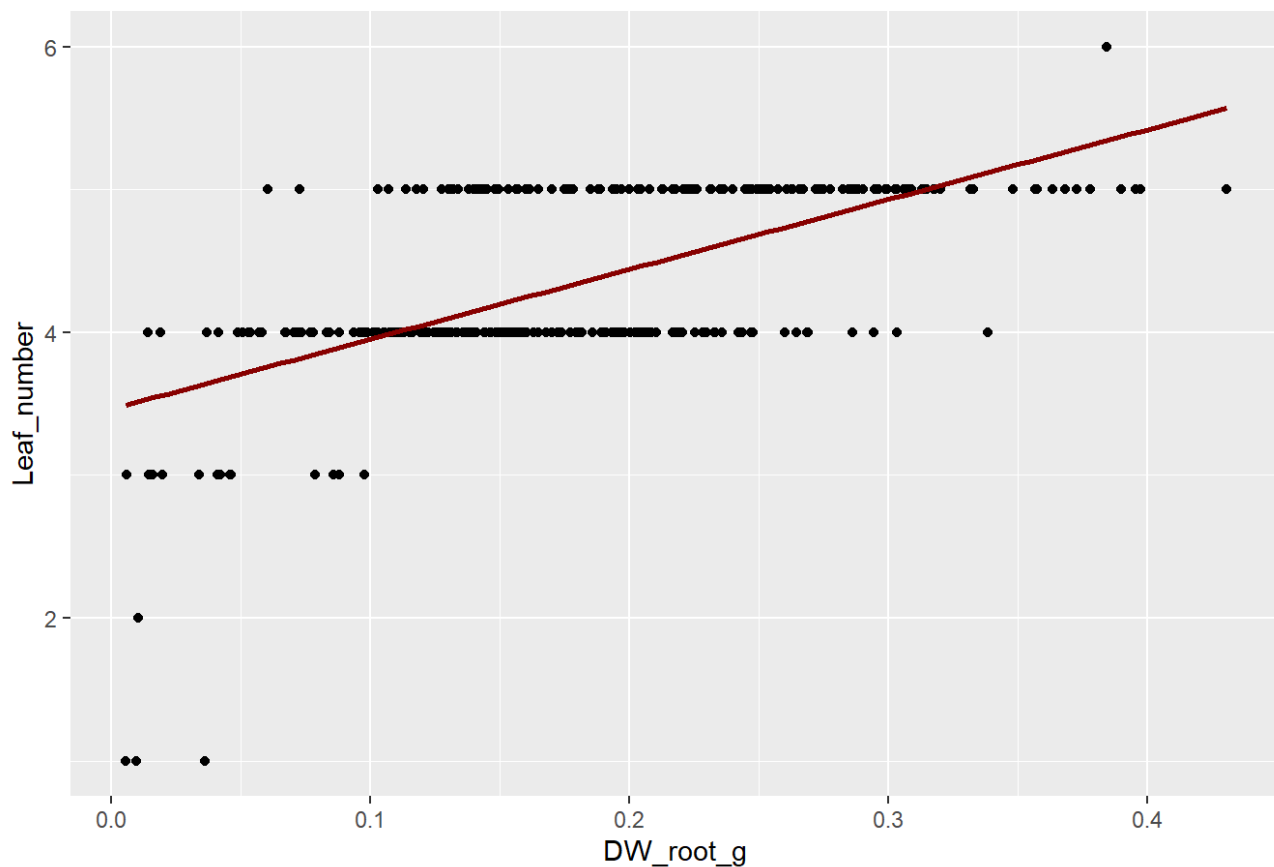

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 6 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 6 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 330 rows containing missing values (`geom_text()`).
```

Correlation Plot between DW_root_g and DW_seed_g


```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 11 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 11 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 330 rows containing missing values (`geom_text()`).
```

Correlation Plot between Leaf_number and DW_seed_g
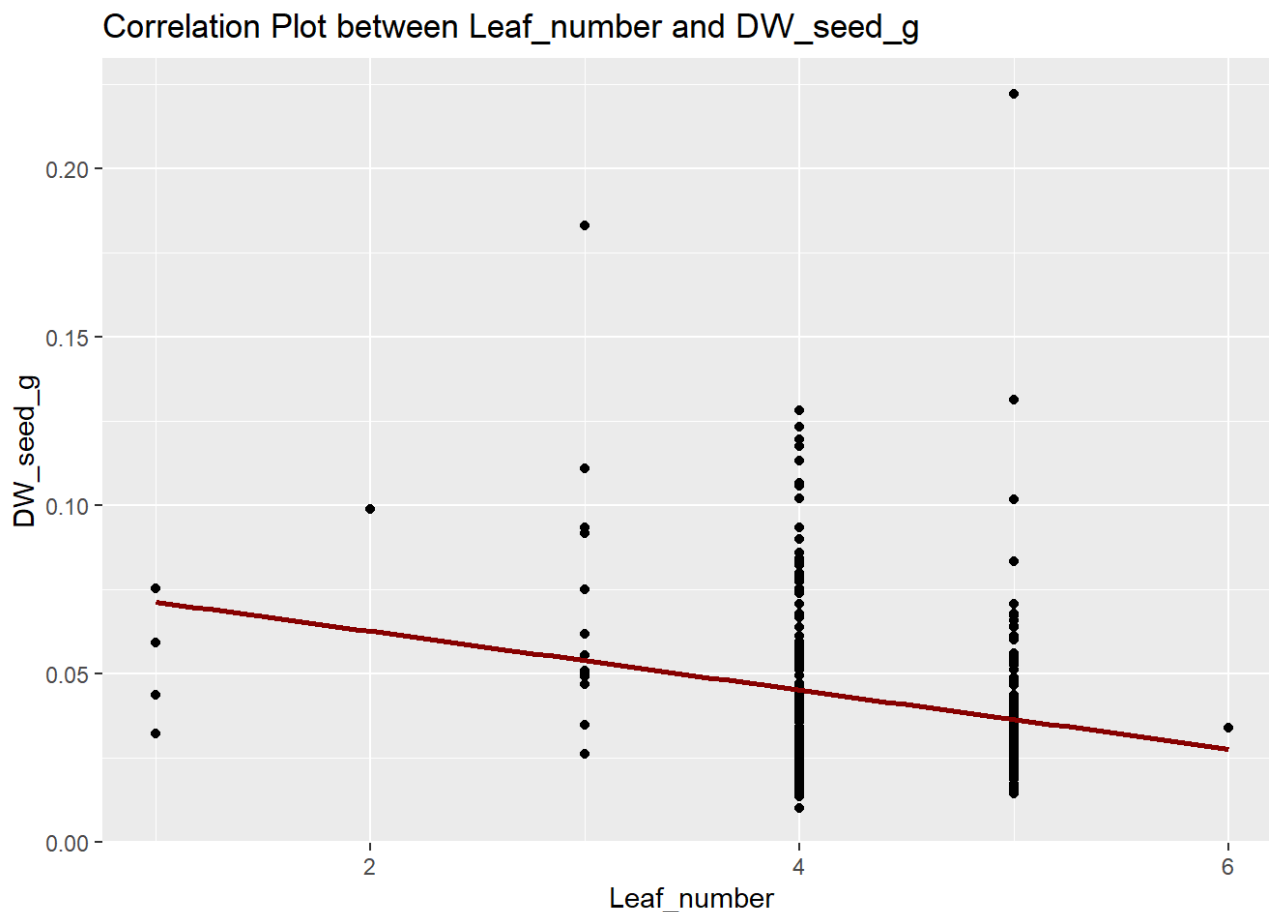
B. Normality hypothesis and outlier detection

Test for normality hypothesis and plot density histogram. The red curve is the normal distribution, the blue dotted curve is the data density curve.

```
normality_results <- normality_test_histogram(endpoint)
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

QQ Plot of DW_shoot_g
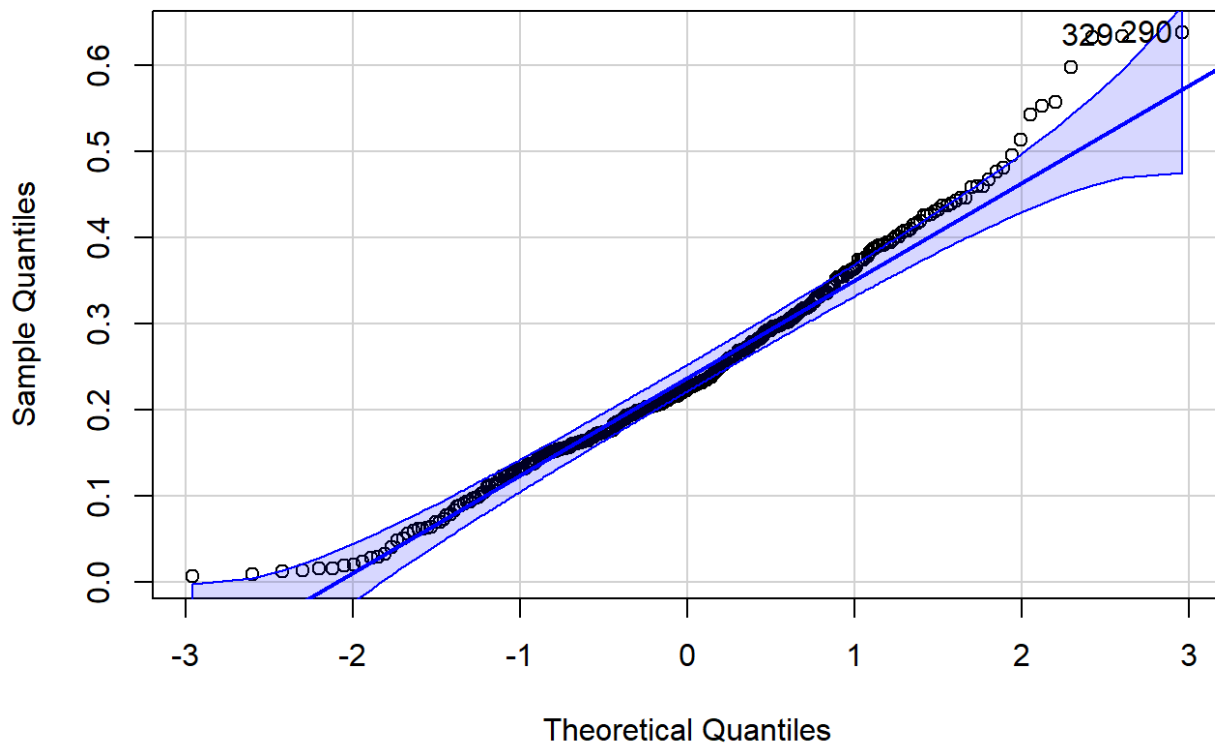

```
## Warning: The dot-dot notation (`..density..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(density)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```
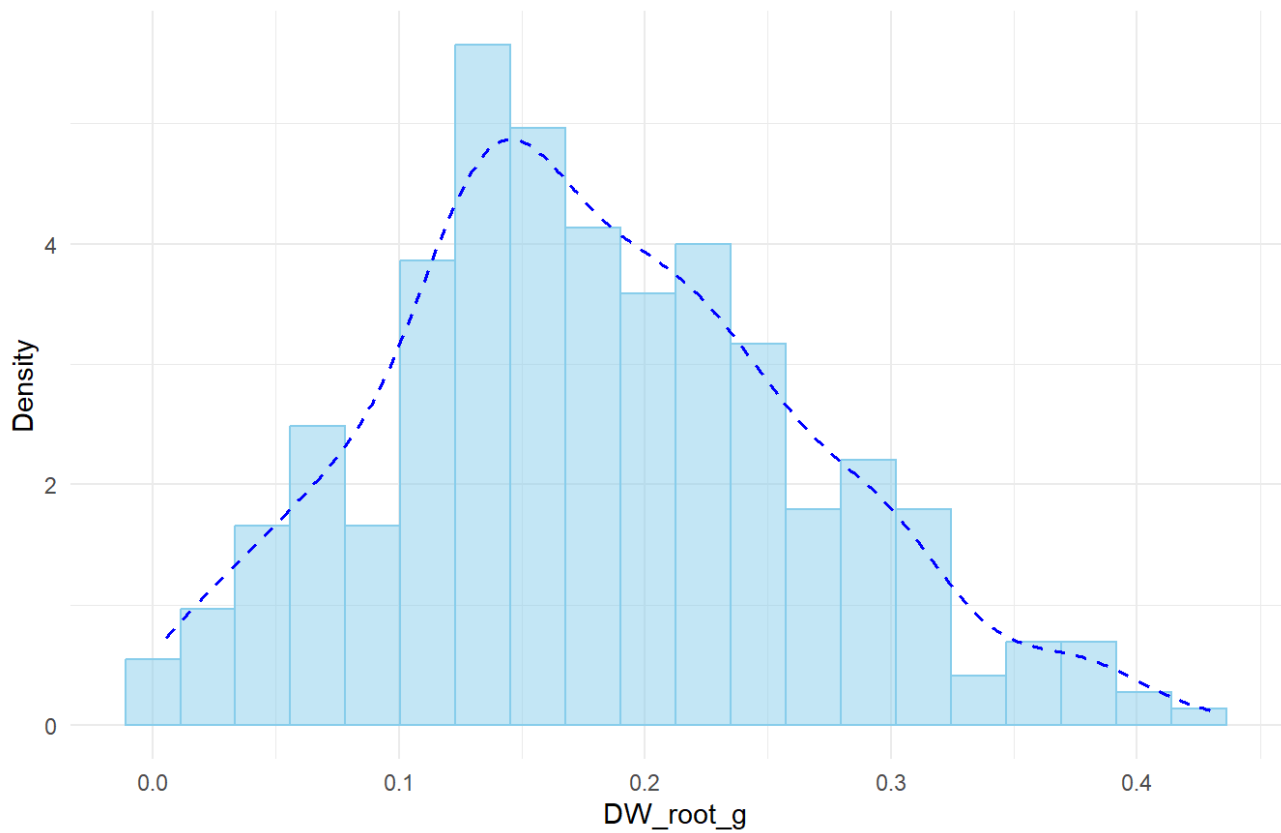
```
## Warning: Removed 5 rows containing non-finite values (`stat_bin()`).
```

```
## Warning: Removed 5 rows containing non-finite values (`stat_density()`).
```
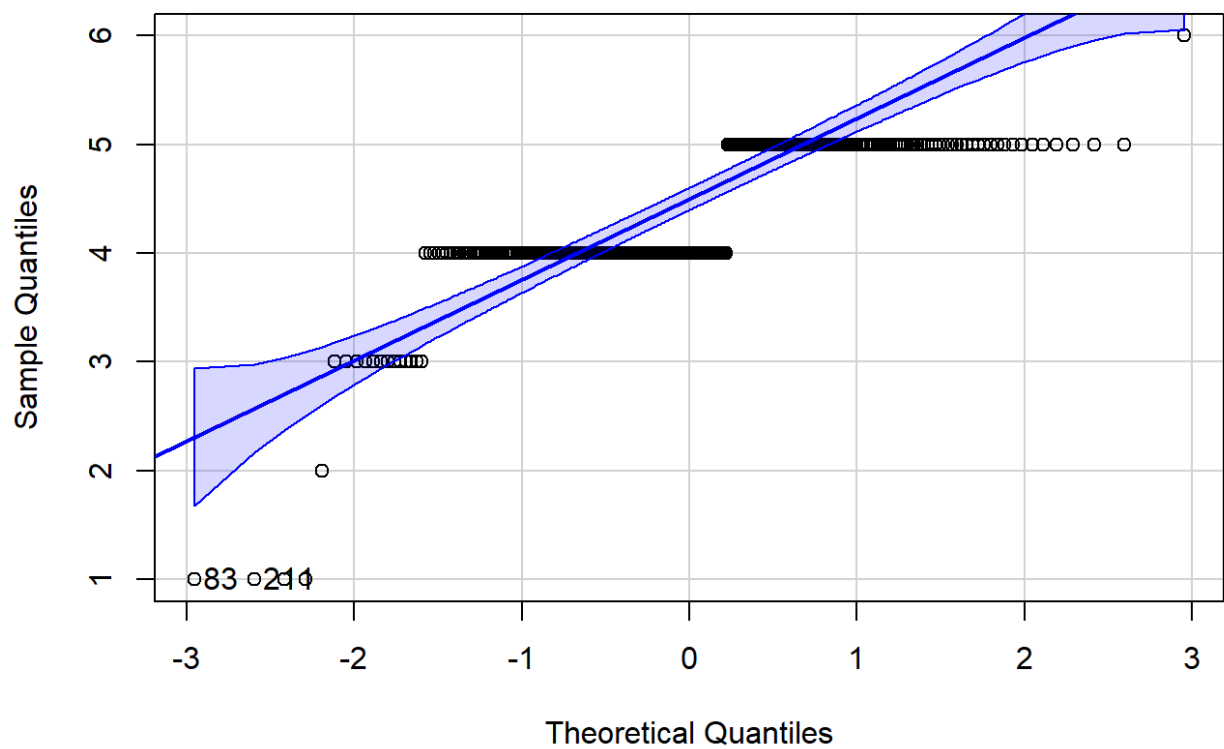
```
## Warning: Removed 101 rows containing missing values (`geom_function()`).
```

Histogram of DW_shoot_g
Normality Test: p = 1e-04
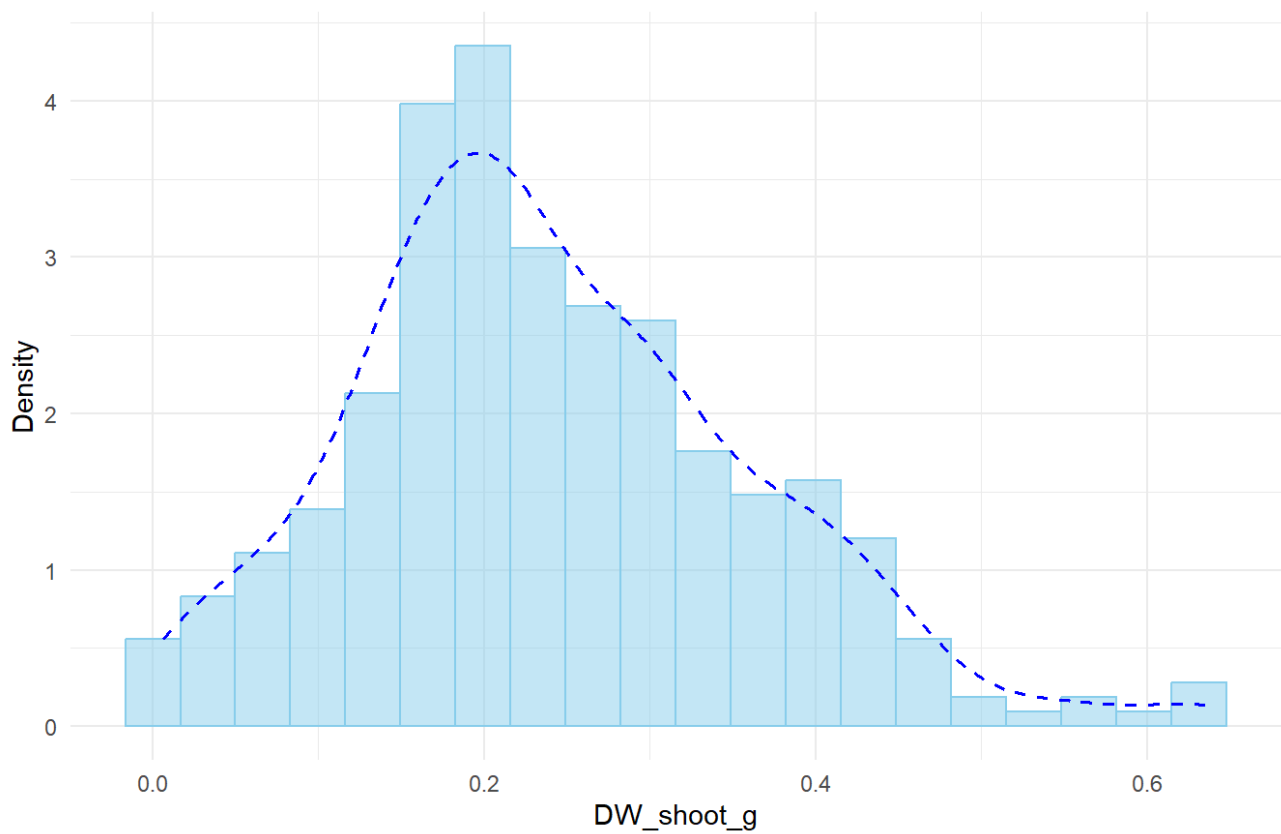

```
## [1] 290 329
```

QQ Plot of DW_root_g
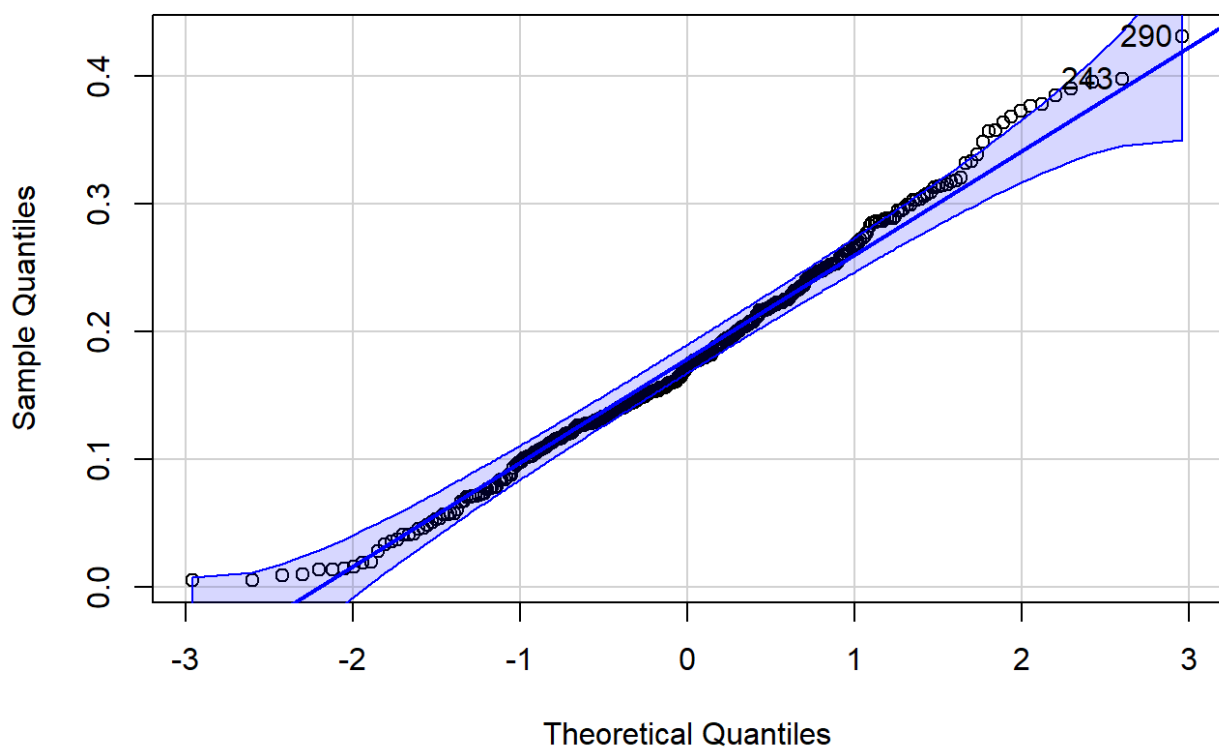

```
## Warning: Removed 6 rows containing non-finite values (`stat_bin()`).
```

```
## Warning: Removed 6 rows containing non-finite values (`stat_density()`).
```

```
## Warning: Removed 101 rows containing missing values (`geom_function()`).
```

Histogram of DW_root_g
Normality Test: p = 0.0106
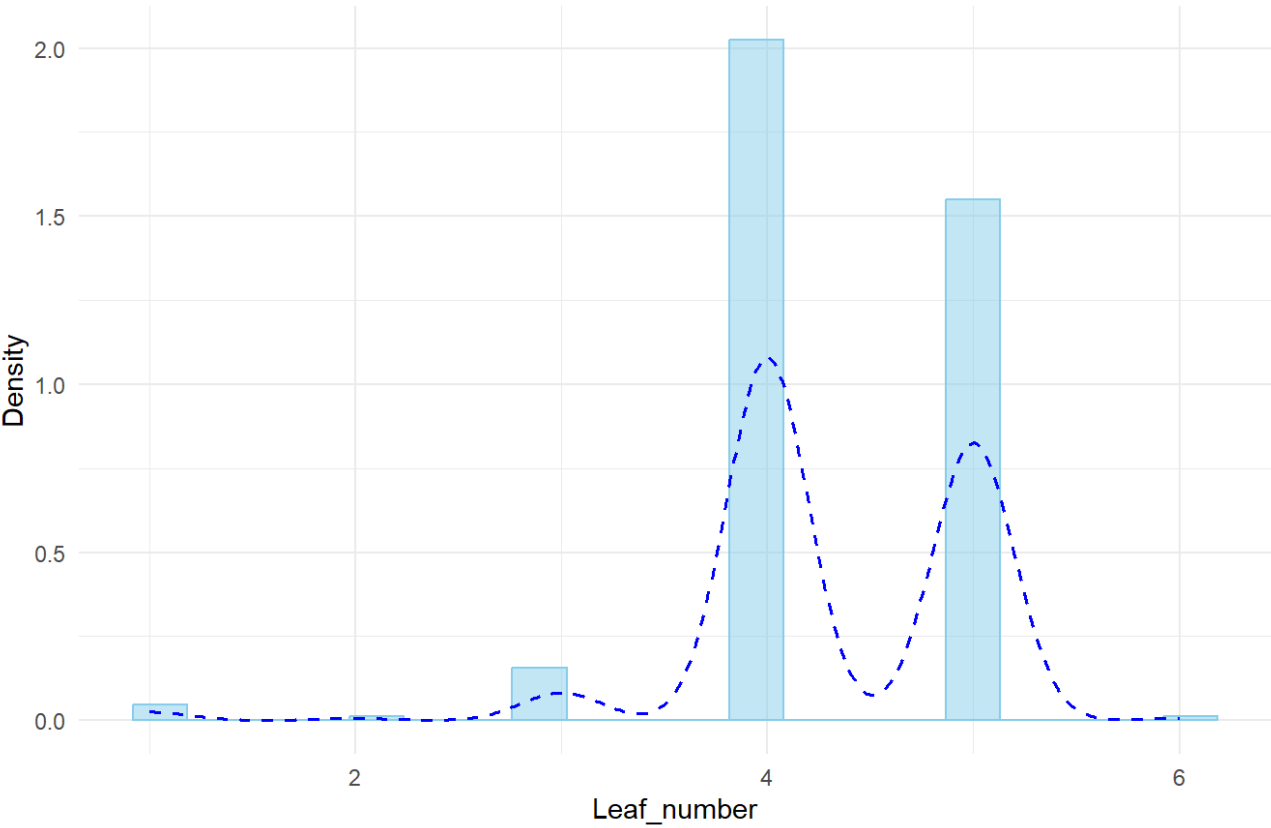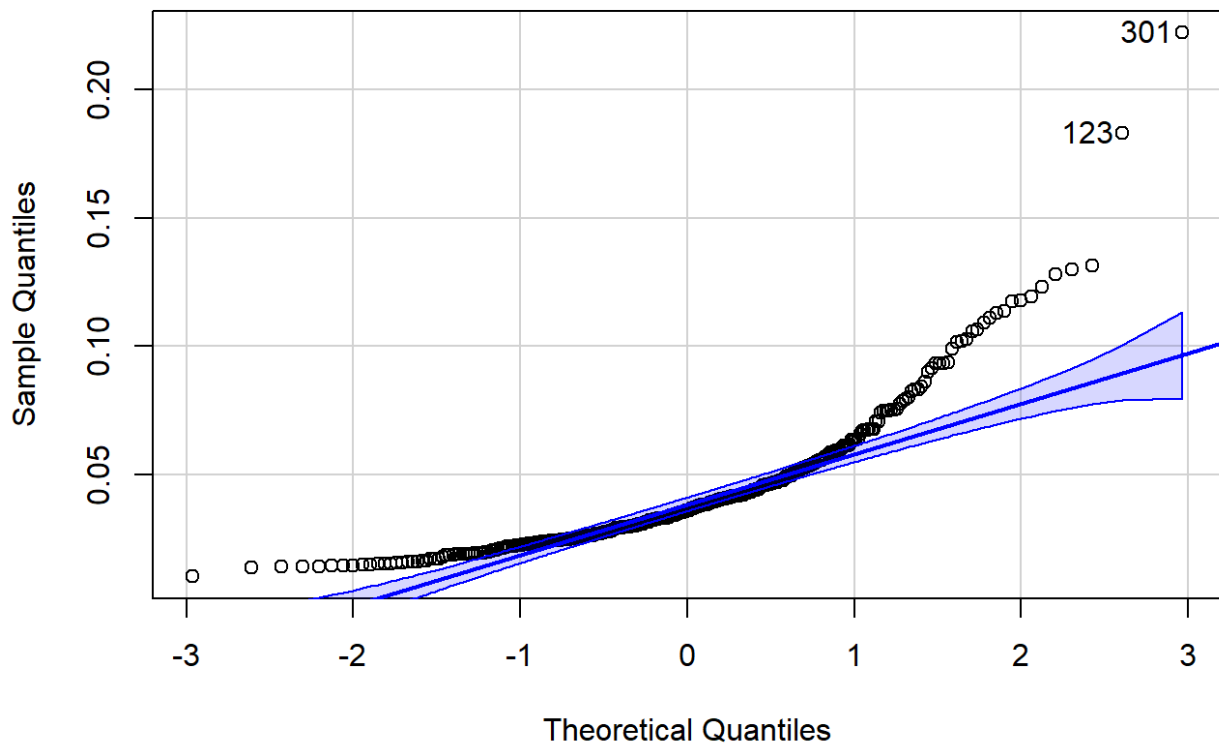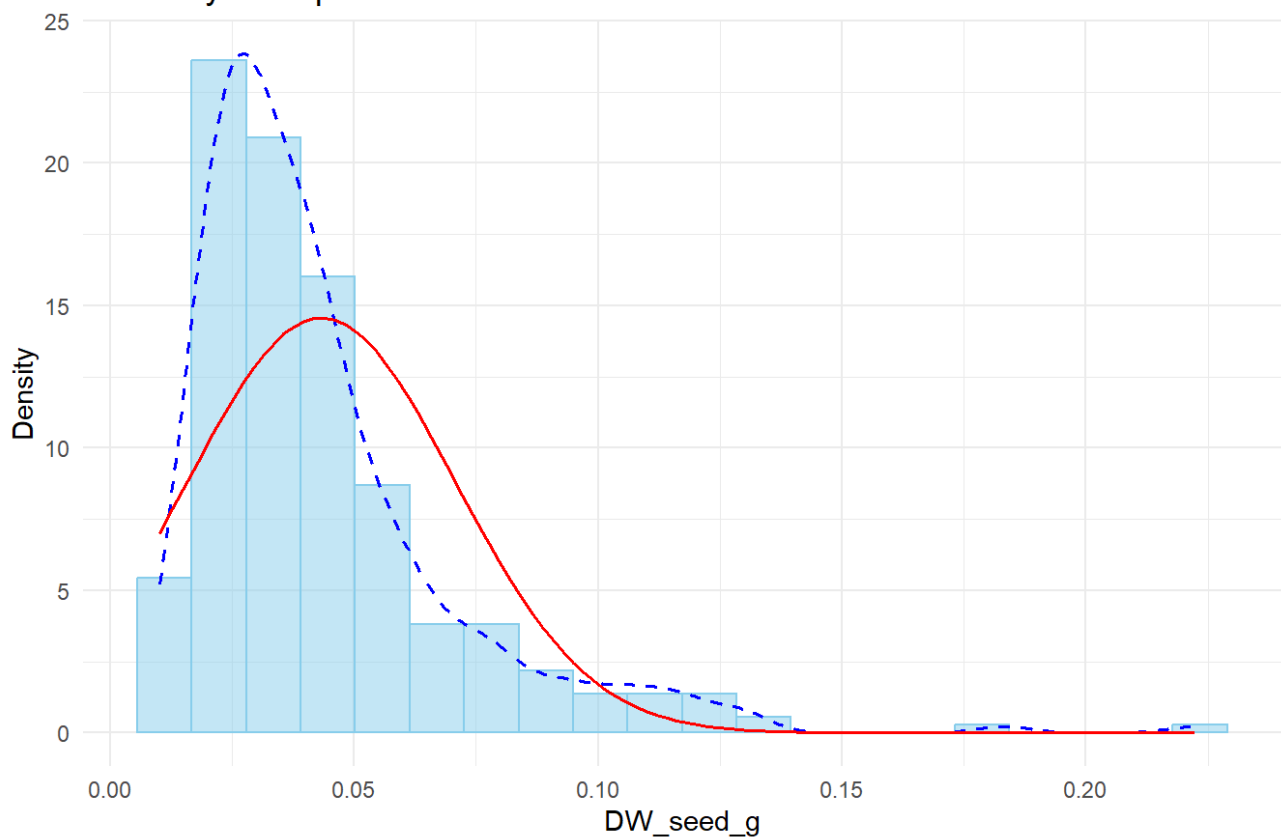


```
## [1] 290 243
```

QQ Plot of Leaf_number


```
## Warning: Removed 11 rows containing non-finite values (`stat_bin()`).
```

```
## Warning: Removed 11 rows containing non-finite values (`stat_density()`).
```

```
## Warning: Removed 101 rows containing missing values (`geom_function()`).
```

Histogram of Leaf_number
Normality Test: p = 0


```
## [1]  83 211
```

QQ Plot of DW_seed_g

Histogram of DW_seed_g
Normality Test: p = 0


```
## [1] 301 123
```

Remove the outliers, replacing them with NULL values and normality visual verification.

The function detect_replace_ouliers_by_genotype checks for outlying values, using the Tukey method.

Then run the function on all variables of the dataset.

```
endpoint_clean <- endpoint
# Run the function on the dataset for all the variables
endpoint_clean <- detect_replace_outliers_by_genotype(endpoint_clean)
```
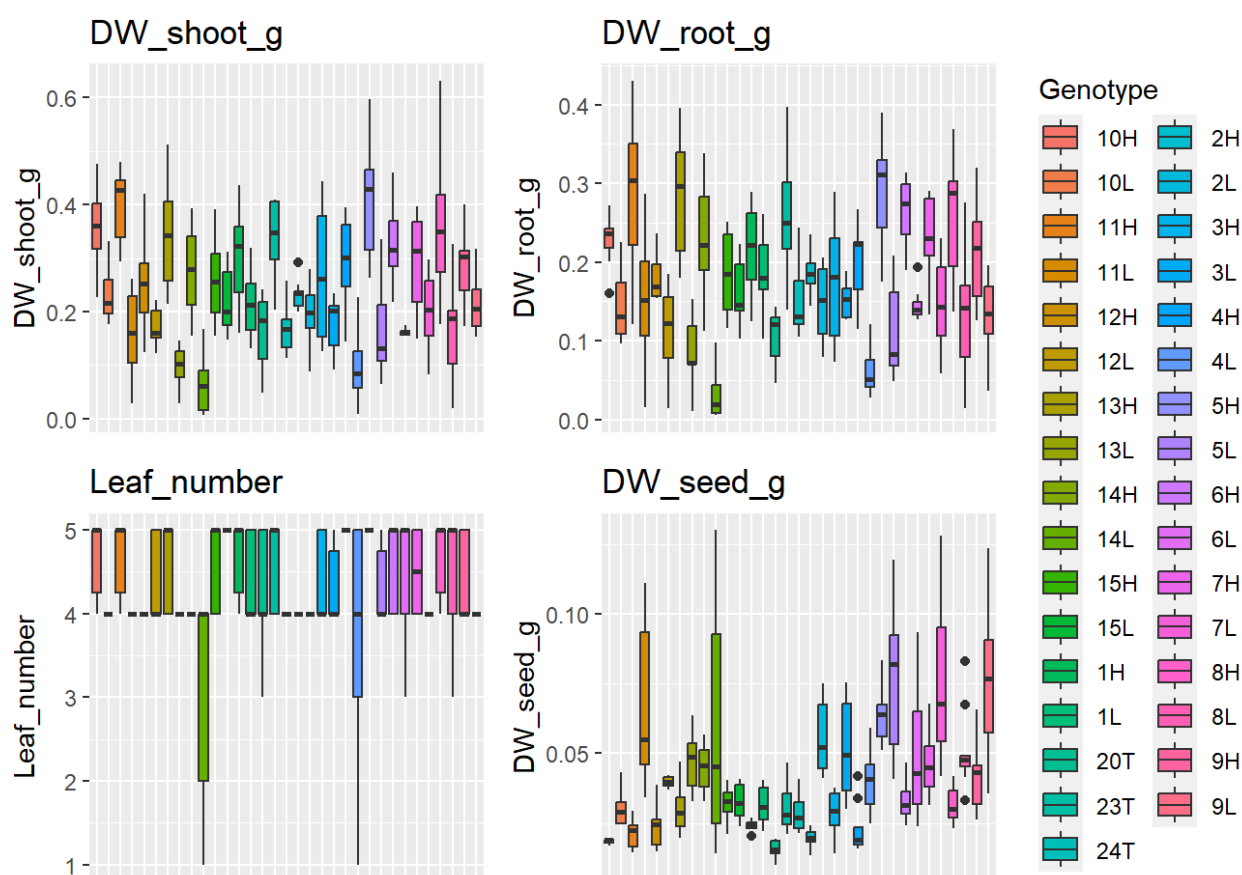
Boxplots after outlier detection

```
create_boxplots(endpoint_clean, variables, "Genotype")
```

```
## Warning: Removed 19 rows containing non-finite values (`stat_boxplot()`).
```

```
## Warning: Removed 16 rows containing non-finite values (`stat_boxplot()`).
```

```
## Warning: Removed 30 rows containing non-finite values (`stat_boxplot()`).
```

```
## Warning: Removed 23 rows containing non-finite values (`stat_boxplot()`).
```
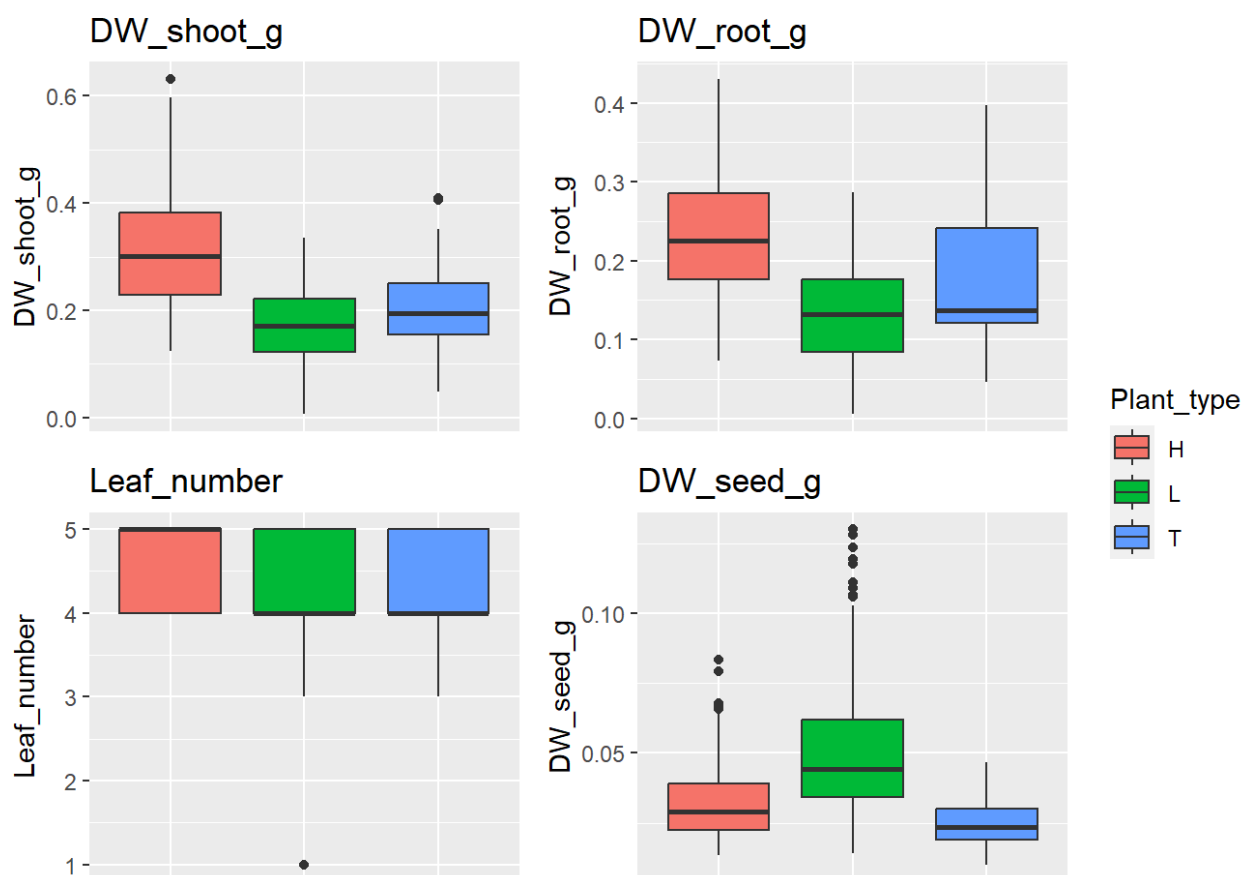


```
create_boxplots(endpoint_clean, variables, "Plant_type")
```

```
## Warning: Removed 19 rows containing non-finite values (`stat_boxplot()`).
```

```
## Warning: Removed 16 rows containing non-finite values (`stat_boxplot()`).
```

```
## Warning: Removed 30 rows containing non-finite values (`stat_boxplot()`).
```

```
## Warning: Removed 23 rows containing non-finite values (`stat_boxplot()`).
```


Violin and sina plots after outlier detection

```
create_violin_plots(endpoint_clean, variables, "Genotype")
```

```
## Warning: The `size` argument of `element_line()` is deprecated as of ggplot2 3.4.0.
## ℹ Please use the `linewidth` argument instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

```
## Warning: Removed 19 rows containing non-finite values (`stat_ydensity()`).
```

```
## Warning: Removed 19 rows containing non-finite values (`stat_sina()`).
```

```
## Warning: Removed 16 rows containing non-finite values (`stat_ydensity()`).
```
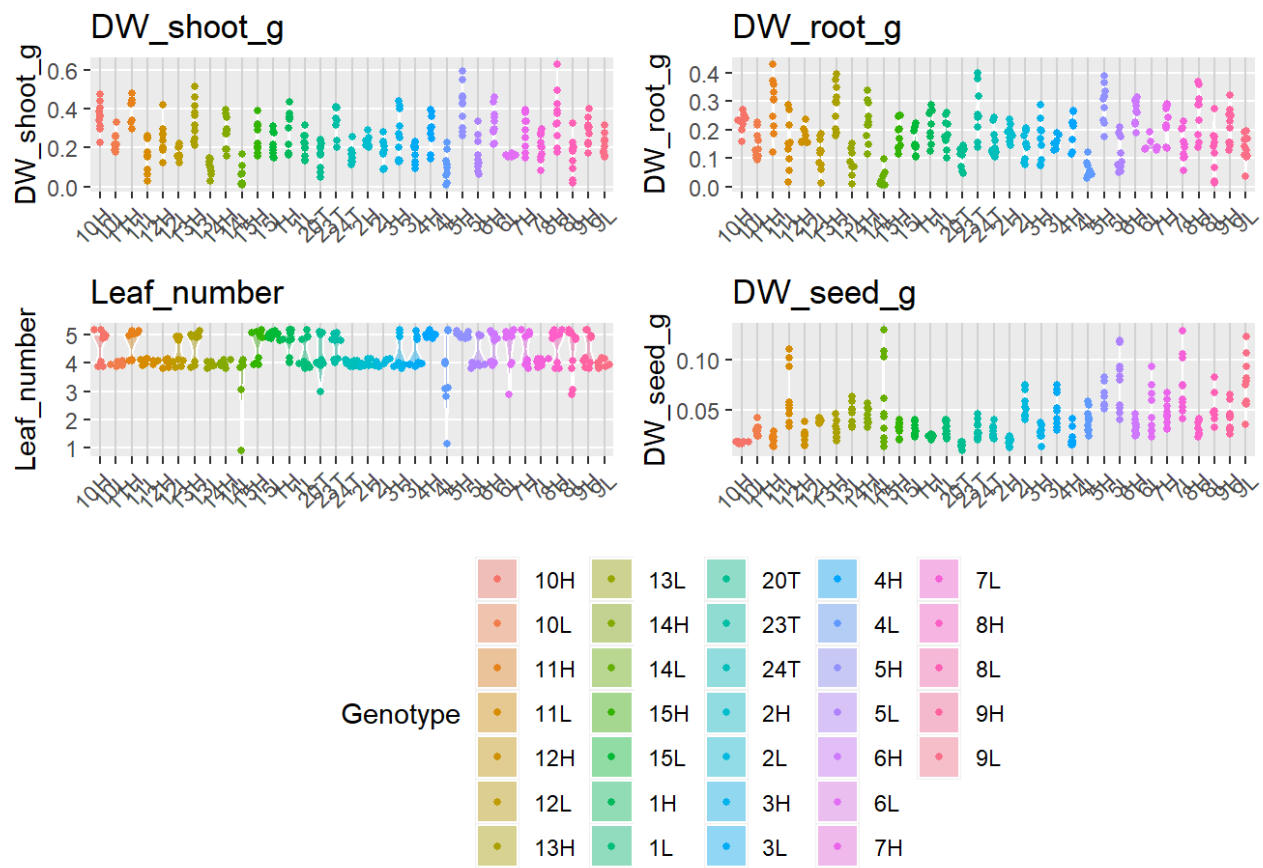
```
## Warning: Removed 16 rows containing non-finite values (`stat_sina()`).
```

```
## Warning: Removed 30 rows containing non-finite values (`stat_ydensity()`).
```

```
## Warning: Removed 30 rows containing non-finite values (`stat_sina()`).
```

```
## Warning: Removed 23 rows containing non-finite values (`stat_ydensity()`).
```

```
## Warning: Removed 23 rows containing non-finite values (`stat_sina()`).
```



```
create_violin_plots(endpoint_clean, variables, "Plant_type")
```

```
## Warning: Removed 19 rows containing non-finite values (`stat_ydensity()`).
```

```
## Warning: Removed 19 rows containing non-finite values (`stat_sina()`).
```

```
## Warning: Removed 16 rows containing non-finite values (`stat_ydensity()`).
```

```
## Warning: Removed 16 rows containing non-finite values (`stat_sina()`).
```

```
## Warning: Removed 30 rows containing non-finite values (`stat_ydensity()`).
```

```
## Warning: Removed 30 rows containing non-finite values (`stat_sina()`).
```

```
## Warning: Removed 23 rows containing non-finite values (`stat_ydensity()`).
```

```
## Warning: Removed 23 rows containing non-finite values (`stat_sina()`).
```


Exploration statistics for the variables after outlier detection

```
skim(endpoint_clean[variables])
```

Data summary

Name	endpoint_clean[variables]
Number of rows	330
Number of columns	4
Column type frequency:	
numeric	4
Group variables	None

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
DW_shoot_g	19	0.94	0.24	0.11	0.01	0.16	0.22	0.31	0.63	▃▇▃▁
DW_root_g	16	0.95	0.18	0.08	0.01	0.13	0.17	0.23	0.43	▃▇▅▁

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
Leaf_number	30	0.91	4.35	0.63	1.00	4.00	4.00	5.00	5.00	▁▁▁█▇
DW_seed_g	23	0.93	0.04	0.02	0.01	0.02	0.04	0.05	0.13	█▇▅▁▁

```r
for (var in variables) {
  cat("\nSummary for:", var, "\n")
  endpoint_clean %>%
    group_by(Genotype) %>%
    summarize(mean    = mean(get(var), na.rm = TRUE),
              std.dev = sd(get(var), na.rm = TRUE),
              n_missing  = sum(is.na(get(var)))) %>%
    arrange(desc(mean)) %>%
    print(n = Inf)
}
```

```
##
## Summary for: DW_shoot_g
## # A tibble: 33 × 4
##    Genotype   mean std.dev n_missing
##    <fct>     <dbl>   <dbl>     <int>
##  1 5H        0.414  0.112          0
##  2 11H       0.399  0.0675         2
##  3 10H       0.361  0.0726         0
##  4 8H        0.360  0.138          0
##  5 13H       0.343  0.101          0
##  6 23T       0.335  0.0785         2
##  7 6H        0.327  0.0814         0
##  8 1H        0.302  0.0915         0
##  9 7H        0.291  0.0916         0
## 10 9H        0.287  0.0678         0
## 11 4H        0.286  0.0901         1
## 12 14H       0.279  0.0809         0
## 13 3H        0.269  0.121          0
## 14 15H       0.256  0.0768         0
## 15 12H       0.250  0.0811         0
## 16 10L       0.238  0.0562         0
## 17 2H        0.232  0.0278         1
## 18 15L       0.216  0.0597         1
## 19 9L        0.216  0.0558         1
## 20 1L        0.211  0.0599         0
## 21 7L        0.202  0.0689         0
## 22 2L        0.189  0.0610         0
## 23 3L        0.178  0.0509         0
## 24 12L       0.172  0.0340         2
## 25 24T       0.166  0.0433         1
## 26 20T       0.165  0.0700         0
## 27 5L        0.162  0.0884         0
## 28 6L        0.161  0.00741        4
## 29 8L        0.161  0.0929         0
## 30 11L       0.159  0.0817         0
## 31 13L       0.0993 0.0379         1
## 32 4L        0.0972 0.0712         0
## 33 14L       0.0638 0.0591         3
##
## Summary for: DW_root_g
## # A tibble: 33 × 4
##    Genotype   mean std.dev n_missing
##    <fct>     <dbl>   <dbl>     <int>
##  1 5H        0.294  0.0664         0
##  2 11H       0.287  0.0945         0
##  3 13H       0.285  0.0773         0
##  4 6H        0.266  0.0416         0
##  5 8H        0.260  0.0810         0
##  6 23T       0.259  0.0849         0
##  7 14H       0.229  0.0706         0
##  8 7H        0.228  0.0580         0
##  9 10H       0.228  0.0324         1
## 10 1H        0.215  0.0549         0
## 11 9H        0.211  0.0632         0
## 12 4H        0.202  0.0556         1
```

```
## 13 1L      0.188   0.0516        0
## 14 2H      0.187   0.0272        0
## 15 15H     0.185   0.0516        0
## 16 12H     0.180   0.0296        2
## 17 3H      0.177   0.0802        0
## 18 15L     0.157   0.0428        1
## 19 24T     0.154   0.0502        0
## 20 11L     0.153   0.0861        0
## 21 3L      0.153   0.0235        2
## 22 2L      0.148   0.0473        0
## 23 6L      0.147   0.0231        3
## 24 7L      0.146   0.0542        0
## 25 10L     0.146   0.0475        0
## 26 9L      0.135   0.0487        0
## 27 8L      0.129   0.0788        0
## 28 12L     0.113   0.0550        0
## 29 5L      0.110   0.0596        0
## 30 20T     0.106   0.0356        0
## 31 13L     0.0846  0.0452        1
## 32 4L      0.0615  0.0299        2
## 33 14L     0.0321  0.0334        3
## 
## Summary for: Leaf_number
## # A tibble: 33 × 4
##    Genotype  mean std.dev n_missing
##    <fct>     <dbl>  <dbl>    <int>
##  1 15L        5     0          1
##  2 4H         5     0          3
##  3 5H         5     0          1
##  4 10H        4.7   0.483      0
##  5 11H        4.7   0.483      0
##  6 1H         4.7   0.483      0
##  7 8H         4.7   0.483      0
##  8 13H        4.67  0.5        1
##  9 23T        4.67  0.5        1
## 10 15H        4.6   0.516      0
## 11 6H         4.6   0.516      0
## 12 6L         4.56  0.726      1
## 13 7H         4.5   0.527      0
## 14 12L        4.4   0.516      0
## 15 1L         4.4   0.516      0
## 16 8L         4.4   0.843      0
## 17 9H         4.4   0.516      0
## 18 3H         4.33  0.5        1
## 19 20T        4.3   0.675      0
## 20 3L         4.3   0.483      0
## 21 5L         4.3   0.483      0
## 22 10L        4     0          2
## 23 11L        4     0          2
## 24 12H        4     0          1
## 25 13L        4     0          5
## 26 14H        4     0          1
## 27 24T        4     0          0
## 28 2H         4     0          1
## 29 2L         4     0          2
## 30 7L         4     0          2
```

```
## 31 9L          4        0                1
## 32 4L          3.67    1.32             1
## 33 14L         3        1.41             3
##
## Summary for: DW_seed_g
## # A tibble: 33 × 4
##    Genotype   mean std.dev n_missing
##    <fct>     <dbl>  <dbl>     <int>
##  1 5L       0.0781 0.0282        0
##  2 9L       0.0766 0.0263        0
##  3 7L       0.0748 0.0283        0
##  4 11L      0.0655 0.0288        1
##  5 5H       0.0651 0.0108        1
##  6 14L      0.0581 0.0416        0
##  7 2L       0.0558 0.0130        0
##  8 8L       0.0514 0.0148        1
##  9 3L       0.0507 0.0170        1
## 10 6L       0.0500 0.0229        0
## 11 13L      0.0474 0.0110        2
## 12 7H       0.0460 0.0120        0
## 13 14H      0.0447 0.00784       1
## 14 9H       0.0425 0.0131        0
## 15 4L       0.0406 0.0110        0
## 16 12L      0.0398 0.00204       3
## 17 6H       0.0330 0.00698       0
## 18 15L      0.0326 0.00645       1
## 19 8H       0.0315 0.00627       0
## 20 15H      0.0314 0.00665       1
## 21 1L       0.0312 0.00687       0
## 22 23T      0.0309 0.00855       0
## 23 13H      0.0306 0.00873       1
## 24 10L      0.0298 0.00576       0
## 25 3H       0.0287 0.00737       1
## 26 24T      0.0283 0.00651       1
## 27 1H       0.0241 0.00194       2
## 28 12H      0.0234 0.00722       0
## 29 4H       0.0227 0.00914       1
## 30 11H      0.0212 0.00498       0
## 31 2H       0.0192 0.00365       1
## 32 10H      0.0184 0.00102       3
## 33 20T      0.0158 0.00291       1
```

2. Exploration of the timeseries data

In this part, we look at the timeseries, S_timeseries and T_timeseries datasets, also using several functions, located in the functions.R script.

Number of data observations per day for the traits of the timeseries datasets

```
print(paste0("No data for", platform))
```

```
## [1] "No data for4PMI"
```

A. Exploration of the timeseries dataframe

Scatter plots by Genotype

```
print(paste0("No data for", platform))
```

```
## [1] "No data for4PMI"
```

Scatterplots for all genotypes by Plant type (Hybride, Line, EPPN20_T) with smooth line.

```
print(paste0("No data for", platform))
```

```
## [1] "No data for4PMI"
```

Scatter plots for all genotypes by water treatment

```
print(paste0("No data for", platform))
```

```
## [1] "No data for4PMI"
```

B. Exploration of the S_timeseries dataframe

Scatter plots by Genotype

```
print(paste0("No data for", platform))
```

```
## [1] "No data for4PMI"
```

Scatterplots for all genotypes by Plant type (Hybride, Line, EPPN20_T) with smooth line.

```
print(paste0("No data for", platform))
```

```
## [1] "No data for4PMI"
```

Scatter plots for all genotypes by water treatment

```
print(paste0("No data for", platform))
```

```
## [1] "No data for4PMI"
```

C. Exploration of the T_timeseries dataframe

Scatter plots by Genotype

```
print(paste0("No data for", platform))
```

```
## [1] "No data for4PMI"
```

Scatterplots for all genotypes by Plant type (Hybride, Line, EPPN20_T) with smooth line.

```
print(paste0("No data for", platform))
```

```
## [1] "No data for4PMI"
```

Scatter plots for all genotypes by water treatment

```
print(paste0("No data for", platform))
```

```
## [1] "No data for4PMI"
```