# Architecture_analysis

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# 1    Requierements

## 1.1    Packages install

```
install.packages("plyr")
install.packages("ggplot2")
install.packages("gtable")
install.packages("grid")
install.packages("cowplot")
install.packages("reshape2")
install.packages("scales")
install.packages("knitr")
```

```r
install.packages("tinytex")
install.packages("dplyr")
install.packages("lmtest")
install.packages("agricolae")
install.packages("PMCMR")
install.packages("gtools")
install.packages("RVAideMemoire")
#install.packages("RCurl")
```

## 1.2   Packages loading

```r
library(plyr)
library(ggplot2)
library(gtable)
library(grid)
library(cowplot)
library(reshape2)
library(scales)
library(knitr)
library(tinytex)
library(dplyr)
#library(RCurl)
library(rmarkdown)
library(lmtest)
library(agricolae)
library(PMCMR)
library(gtools)
library(RVAideMemoire)
```

## 1.3   Functions importing

```r
source(file = "c:/Users/mlabadie/Documents/GitHub/strawberry/Rscript/Functions.R")
```

# 2   Import and transformation of dataset

## 2.1   Import dataset

**INDEX_PARAMETER :** TIME # vertex_id

**15 VARIABLES:**

- VARIABLE 1 : INT # nb_visible_leaves. No. elongated leaves (F)
- VARIABLE 2 : INT # nb_foliar_primordia No. primordia (f)
- VARIABLE 3 : INT # nb_total_leaves. Total no. leaves (F+f)
- VARIABLE 4 : INT # nb_open_flowers. No. open flowers
- VARIABLE 5 : INT # nb_aborted_flowers No. aborted flowers
- VARIABLE 6 : INT # nb_total_flowers Total no. flowers
- VARIABLE 7 : INT # vegetative_bud. No. vegetative buds (axillary vegetative bud)
- VARIABLE 8 : INT # Initiated_bud. No. initiated bud (axillary initiated bud)
- VARIABLE 9 : INT # floral_bud. No. floral buds (axillary floral bud)
- VARIABLE 10 : INT # stolons No. stolons

- VARIABLE 11 : INT # type_of_crown. Type of crown (1: primary crown, 2: extention crowns, 3: branch crown)
- VARIABLE 12 : INT # Crown_status (1: Terminal Vegetative bud (bt, stage 17, 18, 19, None), 2:Terminal bud initiated (bt, stage A), 3: Terminal floral bud(ht), 4: Inflorescence(HT), -1: rotten or aborded)
- VARIABLE 13 : INT # genotype (1: Gariguette, 2: Ciflorette, 3: Clery, 4: Capriss, 5:Darselect, 6: Cir107)
- VARIABLE 14 : INT # date (1: mid December, 2: early Junuary, 3: mid February, 4: early March, 5: early April, 6: end May/early June)
- VARIABLE 15 : INT # plant. plant index

```
DataSet <- read.csv(file = "c:/Users/mlabadie/Documents/GitHub/strawberry/Rscript/Dataset.csv",
  sep=";",
  na.strings = "-1")

colstart<-1
colend<-dim(DataSet)[2]-2

data<-DataSet[,c(colstart:colend)]
```

## 2.2   Dataset Class Object

```
str(object = data)
```

```
## 'data.frame':    1796 obs. of  16 variables:
##  $ Index            : Factor w/ 17 levels "0","0-1","0-1-2",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ nb_visible_leaves  : int  8 8 11 8 6 7 7 6 7 11 ...
##  $ nb_foliar_primordia: int  4 4 3 3 4 4 4 3 3 8 ...
##  $ nb_total_leaves    : int  12 12 14 11 10 11 11 9 10 19 ...
##  $ nb_open_flowers    : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ nb_aborted_flowers : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ nb_total_flowers   : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ vegetative_bud     : int  1 4 3 6 5 3 7 1 4 3 ...
##  $ Initiated_bud      : int  3 3 1 0 2 2 1 3 0 2 ...
##  $ floral_bud         : int  7 4 8 5 2 5 2 4 5 10 ...
##  $ stolons            : int  1 1 2 0 1 1 1 1 1 1 ...
##  $ type_of_crown      : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ Crown_status       : int  3 3 3 3 3 3 3 3 3 3 ...
##  $ genotype           : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ date               : int  1 1 1 1 1 1 1 1 1 2 ...
##  $ plant              : int  1 2 3 4 5 6 7 8 9 1 ...
```

## 2.3   Transformation of Class object

```
data$genotype<- as.factor(data$genotype)
data$date<- as.factor(DataSet$date)
data$Crown_status<- as.factor(DataSet$Crown_status)
data$type_of_crown<- as.factor(DataSet$type_of_crown)
```

## 2.4   Conversion of dataset

```
# Convert numerical categorical ordered value in factor values with their properties

data$genotype<- factor(x = data$genotype,
                    levels = levels(x = data$genotype),
```

```r
                            labels = c("Gariguette","Ciflorette","Clery","Capriss","Darselect","Cir107")
                            )

data$date<- factor(x = data$date,
                   levels = levels(x = data$date),
                   labels = c("Mid-December","Early-Junuary","Mid-February","Early-March","Early-April","Ea
                   )

data$type_of_crown<- factor(x = DataSet$type_of_crown,
                           levels = levels(x = data$type_of_crown),
                           labels = c("Primary_Crown","Extention_Crown","Branch_Crown")
                           )
data$Crown_status<- factor(x = data$Crown_status,
                          levels = levels(x = data$Crown_status),
                          labels = c("Terminal_Vegetative_bud","Terminal_initiated_bud","Terminal_Flora
```

```r
#convert index sequence analysis in index for R analysis
dat<-data[2:colend]
for (i in 1:nrow(data)){
  if (data[i,'Index']=="0"){
    dat[i,"Index"]<- 0
  }else if (data[i,'Index']=="0-1"){
    dat[i,"Index"]<- 1
  }else if (data[i,'Index']=="0-1-2"){
    dat[i,"Index"]<- 2
  }else if (data[i,'Index']=="0-1-2-3"){
    dat[i,"Index"]<- 3
  }else if (data[i,'Index']=="0-1-2-3-4"){
    dat[i,"Index"]<- 4
  }else if (data[i,'Index']=="0-1-2-3-4-5"){
    dat[i,"Index"]<- 5
  }else if (data[i,'Index']=="1"){
    dat[i,"Index"]<- 1
  }else if (data[i,'Index']=="1-2"){
    dat[i,"Index"]<- 2
  }else if (data[i,'Index']=="1-2-3"){
    dat[i,"Index"]<- 3
  }else if (data[i,'Index']=="1-2-3-4"){
    dat[i,"Index"]<- 4
  }else if (data[i,'Index']=="1-2-3-4-5"){
    dat[i,"Index"]<- 5
  }else if (data[i,'Index']=="2"){
    dat[i,"Index"]<- 2
  }else if (data[i,'Index']=="2-3"){
    dat[i,"Index"]<- 3
  }else if (data[i,'Index']=="2-3-4"){
    dat[i,"Index"]<- 4
  }else if (data[i,'Index']=="3"){
    dat[i,"Index"]<- 3
  }else if (data[i,'Index']=="3-4"){
    dat[i,"Index"]<- 4
  }else if (data[i,'Index']=="4"){
    dat[i,"Index"]<- 4
  }
}
```

```
dat$Index<-as.factor(x = dat$Index)

#Remplacer les valeurs 0 dans la colone total flowers par NA
dat$nb_total_flowers[dat$nb_total_flowers==0]<-NA

#kable(x = dat,digits = 2,caption = "Data extract from MTG")
```

# 3 Exploratory analysis

## 3.1 At plant scale

## 3.2 At module scale

### 3.2.1 Extraction of data at module scale

```
data_at_module_scale<-ddply(.data = dat,
                            .variables = c("genotype","Index"),
                            summarise,
                            MeanTotalLeave= mean(x = nb_total_leaves,
                                                 na.rm = T),
                            SdTotalLeave= sd(x = nb_total_leaves,
                                             na.rm = T),
                            MeanTotalFlower= mean(x = nb_total_flowers,
                                                  na.rm = T),
                            SdTotalFlower= sd(x = nb_total_flowers,
                                              na.rm = T),
                            MeanStolon= mean(x = stolons,
                                             na.rm = T),
                            SdStolon= sd(x = stolons,
                                         na.rm = T),
                            N=length(nb_total_leaves))

kable(x = data_at_module_scale,
      digits = 2,
      caption = " Data at module scale")
```

Table 1: Data at module scale

| genotype | Index | MeanTotalLeave | SdTotalLeave | MeanTotalFlower | SdTotalFlower | MeanStolon | SdStolon | N |
|----------|-------|----------------|--------------|-----------------|---------------|------------|----------|-----|
| Gariguette | 0 | 10.43 | 2.35 | 18.71 | 3.70 | 0.67 | 0.75 | 54 |
| Gariguette | 1 | 3.28 | 1.28 | 8.20 | 3.25 | 0.00 | 0.00 | 94 |
| Gariguette | 2 | 3.66 | 1.55 | 6.85 | 2.41 | 0.10 | 0.65 | 62 |
| Gariguette | 3 | 2.81 | 0.51 | 6.08 | 1.61 | 0.29 | 0.56 | 21 |
| Gariguette | 4 | 2.78 | 0.44 | 5.11 | 1.17 | 1.11 | 0.78 | 9 |
| Gariguette | 5 | 3.00 | NA | 7.00 | NA | 2.00 | NA | 1 |
| Ciflorette | 0 | 7.63 | 2.57 | 10.95 | 2.76 | 1.09 | 0.96 | 54 |
| Ciflorette | 1 | 3.33 | 0.90 | 6.66 | 2.06 | 0.00 | 0.00 | 115 |
| Ciflorette | 2 | 3.60 | 1.01 | 5.95 | 1.64 | 0.00 | 0.00 | 78 |
| Ciflorette | 3 | 2.94 | 0.63 | 5.89 | 1.85 | 0.87 | 0.85 | 31 |
| Ciflorette | 4 | 3.59 | 1.54 | 6.54 | 1.20 | 1.88 | 0.78 | 17 |
| Ciflorette | 5 | 4.67 | 2.31 | 9.00 | NA | 1.33 | 0.58 | 3 |
| Clery | 0 | 8.33 | 2.97 | 13.71 | 3.34 | 1.65 | 1.25 | 54 |
| Clery | 1 | 3.09 | 1.04 | 6.34 | 2.13 | 0.01 | 0.10 | 98 |

| genotype | Index | MeanTotalLeave | SdTotalLeave | MeanTotalFlower | SdTotalFlower | MeanStolon | SdStolon | N |
|---|---|---|---|---|---|---|---|---|
| Clery | 2 | 3.46 | 0.78 | 4.24 | 1.46 | 0.10 | 0.35 | 63 |
| Clery | 3 | 2.94 | 0.65 | 4.35 | 1.30 | 0.38 | 0.70 | 34 |
| Clery | 4 | 2.86 | 0.77 | 3.89 | 1.17 | 0.79 | 0.70 | 14 |
| Capriss | 0 | 10.35 | 1.82 | 11.92 | 2.87 | 1.96 | 0.97 | 54 |
| Capriss | 1 | 3.43 | 1.04 | 4.28 | 1.28 | 0.00 | 0.00 | 190 |
| Capriss | 2 | 3.86 | 0.94 | 3.71 | 1.23 | 0.01 | 0.10 | 102 |
| Capriss | 3 | 2.97 | 0.71 | 3.45 | 0.74 | 0.19 | 0.40 | 31 |
| Capriss | 4 | 2.50 | 1.00 | 2.00 | 0.00 | 0.25 | 0.50 | 4 |
| Darselect | 0 | 6.11 | 2.29 | 10.50 | 4.77 | 0.94 | 1.11 | 54 |
| Darselect | 1 | 3.34 | 1.08 | 7.69 | 3.03 | 0.01 | 0.11 | 87 |
| Darselect | 2 | 2.84 | 0.96 | 5.09 | 1.27 | 0.09 | 0.34 | 57 |
| Darselect | 3 | 2.56 | 0.68 | 5.00 | 0.79 | 0.23 | 0.48 | 39 |
| Darselect | 4 | 3.00 | 2.07 | 4.33 | 0.82 | 0.62 | 1.06 | 8 |
| Darselect | 5 | 2.00 | NA | 5.00 | NA | 1.00 | NA | 1 |
| Cir107 | 0 | 9.63 | 3.29 | 16.00 | 4.20 | 1.83 | 1.33 | 54 |
| Cir107 | 1 | 3.75 | 1.61 | 8.98 | 3.46 | 0.03 | 0.25 | 154 |
| Cir107 | 2 | 3.02 | 0.94 | 6.90 | 1.90 | 0.00 | 0.00 | 110 |
| Cir107 | 3 | 3.27 | 0.71 | 5.44 | 1.50 | 0.29 | 0.56 | 41 |
| Cir107 | 4 | 3.88 | 2.10 | 5.17 | 0.98 | 1.00 | 0.76 | 8 |

### 3.2.2 Number of Module for successive orders

```
tab1<- fc_dist_module_by_order(data = dat,
                         index = "Index")


kable(x = tab1,
     caption = "No. Module by varieties for successive orders "
     )
```

Table 2: No. Module by varieties for successive orders

| | 0 | 1 | 2 | 3 | 4 | 5 | Frequency |
|---|---|---|---|---|---|---|---|
| Gariguette | 54 | 94 | 62 | 21 | 9 | 1 | 241 |
| Ciflorette | 54 | 115 | 78 | 31 | 17 | 3 | 298 |
| Clery | 54 | 98 | 63 | 34 | 14 | 0 | 263 |
| Capriss | 54 | 190 | 102 | 31 | 4 | 0 | 381 |
| Darselect | 54 | 87 | 57 | 39 | 8 | 1 | 246 |
| Cir107 | 54 | 154 | 110 | 41 | 8 | 0 | 367 |
| Frequency | 324 | 738 | 472 | 197 | 60 | 5 | 1796 |

### 3.2.3 Occurence of the higher order along time

- **Table of distribution of higher order along time**

```
tab2<- fc_dist_order_by_date(data = dat,
                         genotype = "Gariguette",
                         prob = "cumulative")
kable(x = tab2,
     digits = 2,
     caption = "Module order frequency distribution for successive date")
```
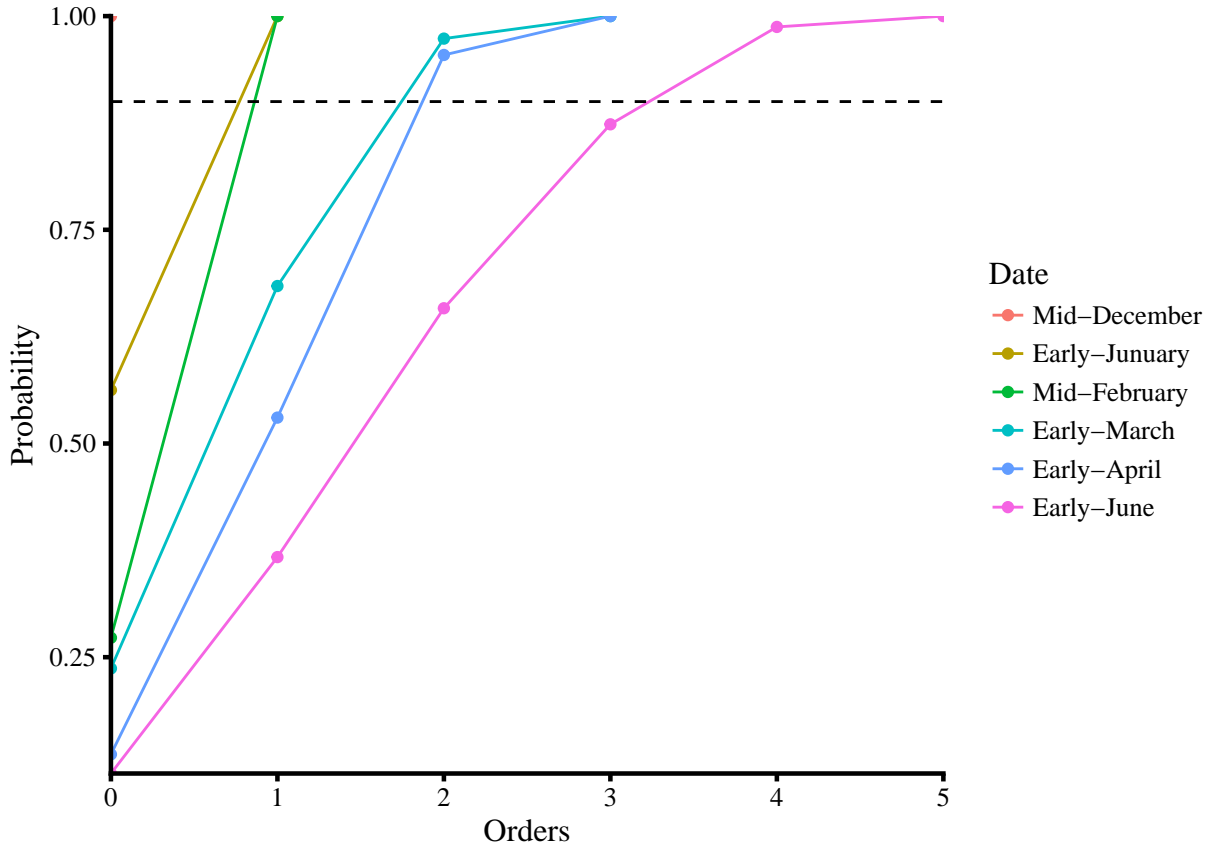
Figure 1: Module order frequency distribution for successive date

Table 3: Module order frequency distribution for successive date

|   | Mid-December | Early-Junuary | Mid-February | Early-March | Early-April | Early-June |
|---|---|---|---|---|---|---|
| 0 | 1 | 0.56 | 0.27 | 0.24 | 0.14 | 0.11 |
| 1 | NA | 1.00 | 1.00 | 0.68 | 0.53 | 0.37 |
| 2 | NA | NA | NA | 0.97 | 0.95 | 0.66 |
| 3 | NA | NA | NA | 1.00 | 1.00 | 0.87 |
| 4 | NA | NA | NA | NA | NA | 0.99 |
| 5 | NA | NA | NA | NA | NA | 1.00 |

- **Plot visualization of distribution of higher order along time**

```
fc_dist_order_by_date.plot(data=tab2)+
  geom_hline(yintercept = 0.9,
             linetype="dashed")
```

### 3.2.4 Analysis of quantitative variable function of successive orders

In the following architectural analyses, we chose to group the highest-order modules because of the small sample size (cf. tables 1: No. Module by varieties for successive orders).

For this, we used a recursive pooling of samples from the highest order downward if sample size =< 8

- **Build data according group**

```r
dat_group<-data[2:colend]

for (i in 1:nrow(data)){
  if( dat_group[i,"genotype"]=="Capriss"){
    if (data[i,'Index']=="0"){
      dat_group[i,"Index"]<- 0
      }else if (data[i,'Index']=="0-1"){
      dat_group[i,"Index"]<- 1
      }else if (data[i,'Index']=="0-1-2"){
        dat_group[i,"Index"]<- 2
      }else if (data[i,'Index']=="0-1-2-3"){
        dat_group[i,"Index"]<- 3
      }else if (data[i,'Index']=="0-1-2-3-4"){
        dat_group[i,"Index"]<- 3
      }else if (data[i,'Index']=="0-1-2-3-4-5"){
        dat_group[i,"Index"]<- 3
      }else if (data[i,'Index']=="1"){
        dat_group[i,"Index"]<- 1
      }else if (data[i,'Index']=="1-2"){
        dat_group[i,"Index"]<- 2
      }else if (data[i,'Index']=="1-2-3"){
        dat_group[i,"Index"]<- 3
      }else if (data[i,'Index']=="1-2-3-4"){
        dat_group[i,"Index"]<- 3
      }else if (data[i,'Index']=="1-2-3-4-5"){
        dat_group[i,"Index"]<- 3
      }else if (data[i,'Index']=="2"){
        dat_group[i,"Index"]<- 2
      }else if (data[i,'Index']=="2-3"){
        dat_group[i,"Index"]<- 3
      }else if (data[i,'Index']=="2-3-4"){
        dat_group[i,"Index"]<- 3
      }else if (data[i,'Index']=="3"){
        dat_group[i,"Index"]<- 3
      }else if (data[i,'Index']=="3-4"){
        dat_group[i,"Index"]<- 3
      }else if (data[i,'Index']=="4"){
        dat_group[i,"Index"]<- 3
      }
    }else
  if (data[i,'Index']=="0"){
    dat_group[i,"Index"]<- 0
  }else if (data[i,'Index']=="0-1"){
    dat_group[i,"Index"]<- 1
  }else if (data[i,'Index']=="0-1-2"){
    dat_group[i,"Index"]<- 2
  }else if (data[i,'Index']=="0-1-2-3"){
    dat_group[i,"Index"]<- 3
  }else if (data[i,'Index']=="0-1-2-3-4"){
    dat_group[i,"Index"]<- 4
  }else if (data[i,'Index']=="0-1-2-3-4-5"){
    dat_group[i,"Index"]<- 4
  }else if (data[i,'Index']=="1"){
    dat_group[i,"Index"]<- 1
  }else if (data[i,'Index']=="1-2"){
    dat_group[i,"Index"]<- 2
```

```r
  }else if (data[i,'Index']=="1-2-3"){
    dat_group[i,"Index"]<- 3
  }else if (data[i,'Index']=="1-2-3-4"){
    dat_group[i,"Index"]<- 4
  }else if (data[i,'Index']=="1-2-3-4-5"){
    dat_group[i,"Index"]<- 4
  }else if (data[i,'Index']=="2"){
    dat_group[i,"Index"]<- 2
  }else if (data[i,'Index']=="2-3"){
    dat_group[i,"Index"]<- 3
  }else if (data[i,'Index']=="2-3-4"){
    dat_group[i,"Index"]<- 4
  }else if (data[i,'Index']=="3"){
    dat_group[i,"Index"]<- 3
  }else if (data[i,'Index']=="3-4"){
    dat_group[i,"Index"]<- 4
  }else if (data[i,'Index']=="4"){
    dat_group[i,"Index"]<- 4
  }
}

#Remplacer les valeurs 0 dans la colone total flowers par NA
dat_group$nb_total_flowers[dat_group$nb_total_flowers==0]<-NA

dat_group$Index<-as.factor(dat_group$Index)
```

- **check that the modules have been well grouped**

```r
tab3<- fc_dist_module_by_order(data = dat_group,
                               index = "Index")

kable(x = tab3,
      caption = "Number of modules for each successive orders after grouping for each varieties")
```

Table 4: Number of modules for each successive orders after grouping for each varieties

|  | 0 | 1 | 2 | 3 | 4 | Frequency |
|---|---|---|---|---|---|---|
| Gariguette | 54 | 94 | 62 | 21 | 10 | 241 |
| Ciflorette | 54 | 115 | 78 | 31 | 20 | 298 |
| Clery | 54 | 98 | 63 | 34 | 14 | 263 |
| Capriss | 54 | 190 | 102 | 35 | 0 | 381 |
| Darselect | 54 | 87 | 57 | 39 | 9 | 246 |
| Cir107 | 54 | 154 | 110 | 41 | 8 | 367 |
| Frequency | 324 | 738 | 472 | 201 | 61 | 1796 |

**Hint:** Compare tab4 with tab1

### 3.2.4.1 Data at module scale after grouping

```r
data_at_module_scale_group<-ddply(.data = dat_group,
                                  .variables = c("genotype","Index"),
                                  summarise,
                                  MeanTotalLeave= mean(x = nb_total_leaves,
                                                       na.rm = T),
```

```r
                                SdTotalLeave= sd(x = nb_total_leaves,
                                                 na.rm = T),
                                MeanTotalFlower= mean(x = nb_total_flowers,
                                                      na.rm = T),
                                SdTotalFlower= sd(x = nb_total_flowers,
                                                  na.rm = T),
                                MeanStolon= mean(x = stolons,
                                                 na.rm = T),
                                SdStolon= sd(x = stolons,
                                             na.rm = T),
                         N=length(nb_total_leaves))

kable(x = data_at_module_scale_group,
      digits = 2,
      caption = " Data at module scale after grouping")
```

Table 5: Data at module scale after grouping

| genotype | Index | MeanTotalLeave | SdTotalLeave | MeanTotalFlower | SdTotalFlower | MeanStolon | SdStolon | N |
|---|---|---|---|---|---|---|---|---|
| Gariguette | 0 | 10.43 | 2.35 | 18.71 | 3.70 | 0.67 | 0.75 | 54 |
| Gariguette | 1 | 3.28 | 1.28 | 8.20 | 3.25 | 0.00 | 0.00 | 94 |
| Gariguette | 2 | 3.66 | 1.55 | 6.85 | 2.41 | 0.10 | 0.65 | 62 |
| Gariguette | 3 | 2.81 | 0.51 | 6.08 | 1.61 | 0.29 | 0.56 | 21 |
| Gariguette | 4 | 2.80 | 0.42 | 5.30 | 1.25 | 1.20 | 0.79 | 10 |
| Ciflorette | 0 | 7.63 | 2.57 | 10.95 | 2.76 | 1.09 | 0.96 | 54 |
| Ciflorette | 1 | 3.33 | 0.90 | 6.66 | 2.06 | 0.00 | 0.00 | 115 |
| Ciflorette | 2 | 3.60 | 1.01 | 5.95 | 1.64 | 0.00 | 0.00 | 78 |
| Ciflorette | 3 | 2.94 | 0.63 | 5.89 | 1.85 | 0.87 | 0.85 | 31 |
| Ciflorette | 4 | 3.75 | 1.65 | 6.71 | 1.33 | 1.80 | 0.77 | 20 |
| Clery | 0 | 8.33 | 2.97 | 13.71 | 3.34 | 1.65 | 1.25 | 54 |
| Clery | 1 | 3.09 | 1.04 | 6.34 | 2.13 | 0.01 | 0.10 | 98 |
| Clery | 2 | 3.46 | 0.78 | 4.24 | 1.46 | 0.10 | 0.35 | 63 |
| Clery | 3 | 2.94 | 0.65 | 4.35 | 1.30 | 0.38 | 0.70 | 34 |
| Clery | 4 | 2.86 | 0.77 | 3.89 | 1.17 | 0.79 | 0.70 | 14 |
| Capriss | 0 | 10.35 | 1.82 | 11.92 | 2.87 | 1.96 | 0.97 | 54 |
| Capriss | 1 | 3.43 | 1.04 | 4.28 | 1.28 | 0.00 | 0.00 | 190 |
| Capriss | 2 | 3.86 | 0.94 | 3.71 | 1.23 | 0.01 | 0.10 | 102 |
| Capriss | 3 | 2.91 | 0.74 | 3.33 | 0.82 | 0.20 | 0.41 | 35 |
| Darselect | 0 | 6.11 | 2.29 | 10.50 | 4.77 | 0.94 | 1.11 | 54 |
| Darselect | 1 | 3.34 | 1.08 | 7.69 | 3.03 | 0.01 | 0.11 | 87 |
| Darselect | 2 | 2.84 | 0.96 | 5.09 | 1.27 | 0.09 | 0.34 | 57 |
| Darselect | 3 | 2.56 | 0.68 | 5.00 | 0.79 | 0.23 | 0.48 | 39 |
| Darselect | 4 | 2.89 | 1.96 | 4.43 | 0.79 | 0.67 | 1.00 | 9 |
| Cir107 | 0 | 9.63 | 3.29 | 16.00 | 4.20 | 1.83 | 1.33 | 54 |
| Cir107 | 1 | 3.75 | 1.61 | 8.98 | 3.46 | 0.03 | 0.25 | 154 |
| Cir107 | 2 | 3.02 | 0.94 | 6.90 | 1.90 | 0.00 | 0.00 | 110 |
| Cir107 | 3 | 3.27 | 0.71 | 5.44 | 1.50 | 0.29 | 0.56 | 41 |
| Cir107 | 4 | 3.88 | 2.10 | 5.17 | 0.98 | 1.00 | 0.76 | 8 |

#### 3.2.4.2   No. leaves fonction of successive module order

##### 3.2.4.2.1   Cumulative distribution of no. leaves for each module orders

- **Table of distribution of one varname according to module orders**

```
tab4<-fc_dist_variable_by_order(data = dat_group,
                                genotype = "Gariguette",
                                varname = "nb_total_leaves",
                                prob = "cumulative")

kable(x = tab4,
      digits = 2,
      caption = "Cumulative distribution of total no. leaves by orders for Gariguette")
```

Table 6: Cumulative distribution of total no. leaves by orders for
Gariguette

|    | 0    | 1    | 2    | 3    | 4   |
|----|------|------|------|------|-----|
| 1  | 0.00 | 0.01 | 0.00 | 0.00 | 0.0 |
| 2  | 0.00 | 0.31 | 0.16 | 0.24 | 0.2 |
| 3  | 0.02 | 0.68 | 0.65 | 0.95 | 1.0 |
| 4  | 0.02 | 0.82 | 0.76 | 1.00 | NA  |
| 5  | 0.02 | 0.91 | 0.89 | NA   | NA  |
| 6  | 0.02 | 0.99 | 0.95 | NA   | NA  |
| 7  | 0.04 | 1.00 | 0.97 | NA   | NA  |
| 8  | 0.17 | 1.00 | 0.97 | NA   | NA  |
| 9  | 0.35 | 1.00 | 1.00 | NA   | NA  |
| 10 | 0.50 | 1.00 | NA   | NA   | NA  |
| 11 | 0.78 | 1.00 | NA   | NA   | NA  |
| 12 | 0.87 | 1.00 | NA   | NA   | NA  |
| 13 | 0.91 | 1.00 | NA   | NA   | NA  |
| 14 | 0.96 | 1.00 | NA   | NA   | NA  |
| 15 | 0.98 | 1.00 | NA   | NA   | NA  |
| 19 | 1.00 | 1.00 | NA   | NA   | NA  |

- **Visualization of distribution of varname for each module orders**

```
fc_dist_variable_by_order.plot(data = tab4)+
  xlab("No. Leaves")+
  ylab("Cumulative distribution function")
```

#### 3.2.4.2.2 Pointwise Mean of No.leaves of modules for successive orders for each varieties

```
fc_pointwise_mean_variable_by_order(data = data_at_module_scale_group,
                                    varname = "MeanTotalLeave")+
  ylab("Mean No. Flower")+
  ylim(2,10)
```

#### 3.2.4.2.3 Comparison of No. leaves for successive orders

Because pointwise of the mean no.leaves and mean no.flowers seems roughly constant for each varieties. In order to compare varieties we used trend linear regression, in particular we test the zero value of the slope parameter.

- **Identification from wich module variable was roughly constant for each varieties**

- *From Order 0*

```
Gariguette<- fc_linear_trend_reg(data = dat_group,
                                 genotype = "Gariguette",
                                 variable = "nb_total_leaves",
                                 Index = "Index")
```
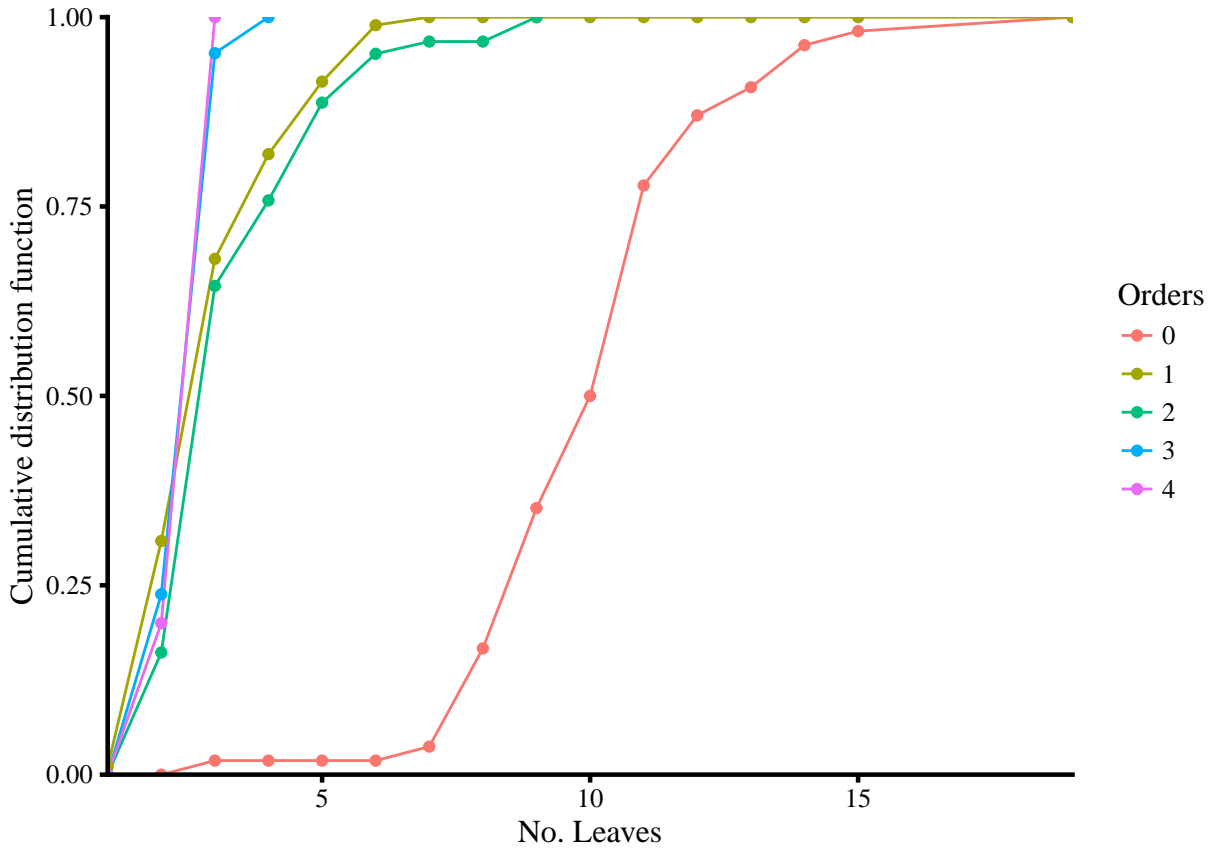
Figure 2: Plot distribution of leaves for each module orders and for Gariguette
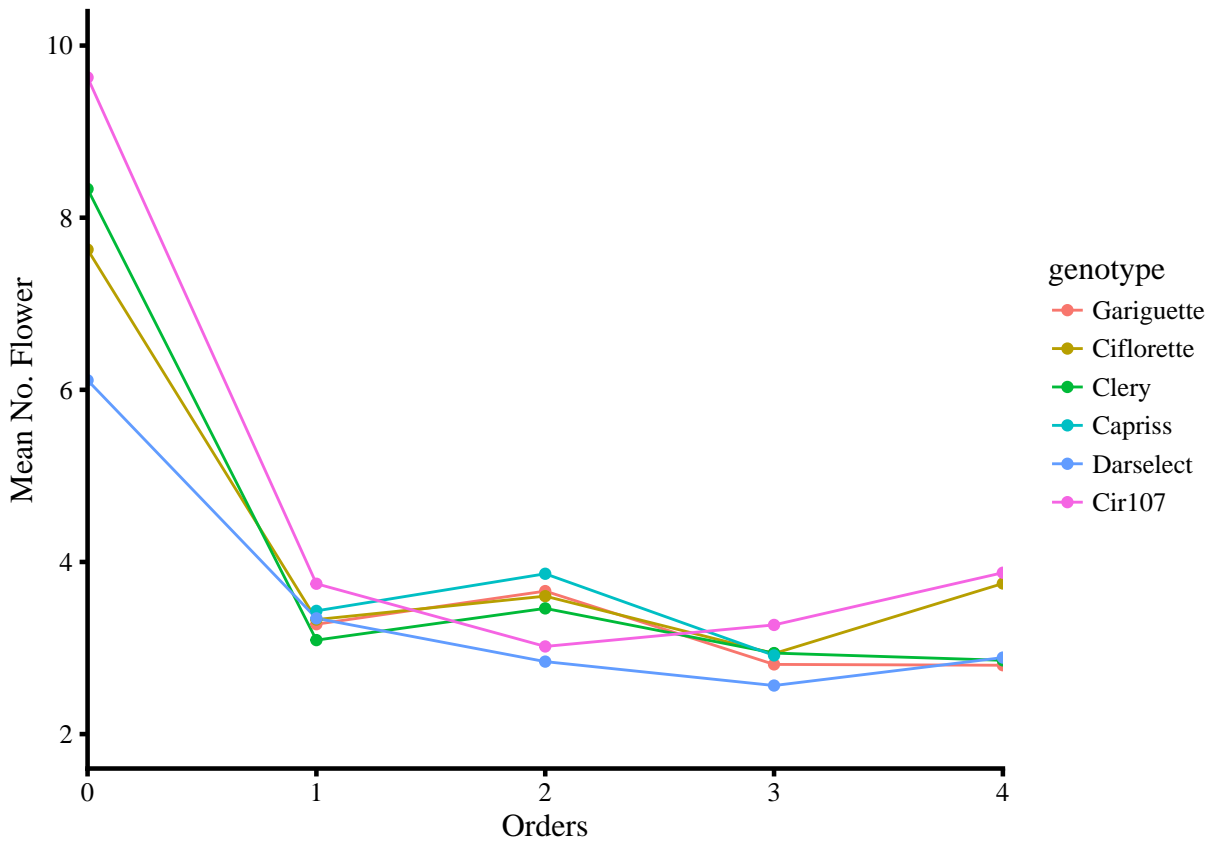
Figure 3: Pointwise Mean of No. leaves of modules for successive orders for each variety after grouping

```
Clery<- fc_linear_trend_reg(data = dat_group,
                            genotype = "Clery",
                            variable = "nb_total_leaves",
                            Index = "Index")

Capriss<- fc_linear_trend_reg(data = dat_group,
                              genotype = "Capriss",
                              variable = "nb_total_leaves",
                              Index = "Index")

Ciflorette<- fc_linear_trend_reg(data = dat_group,
                                 genotype = "Ciflorette",
                                 variable = "nb_total_leaves",
                                 Index = "Index")

Cir107<- fc_linear_trend_reg(data = dat_group,
                             genotype = "Cir107",
                             variable = "nb_total_leaves",
                             Index = "Index")

Darselect<- fc_linear_trend_reg(data = dat_group,
                                genotype = "Darselect",
                                variable = "nb_total_leaves",
                                Index = "Index")

tab5<- merge(x = Gariguette,
             y = Clery,
             all=T)

tab5<- merge(x = tab5,
             y = Capriss,
             all=T)

tab5<- merge(x = tab5,
             y = Ciflorette,
             all=T)

tab5<- merge(x = tab5,
             y = Cir107,
             all=T)

tab5<- merge(x = tab5,
             y = Darselect,
             all=T)

kable(x = tab5,
      digits = 2,
      caption = "Linear trend for no.leaves (estimate slope and 95% confidence interval -IC95%-) from order
```

Table 7: Linear trend for no.leaves (estimate slope and 95% confidence interval -IC95%-) from order 0 onwards

| Genotype | Slope | IC_lower | IC_upper |
|---|---|---|---|
| Capriss | -1.89 | -2.15 | -1.62 |
| Ciflorette | -0.91 | -1.11 | -0.71 |

| Genotype | Slope | IC_lower | IC_upper |
|---|---|---|---|
| Cir107 | -1.62 | -1.87 | -1.36 |
| Clery | -1.28 | -1.52 | -1.04 |
| Darselect | -0.96 | -1.14 | -0.78 |
| Gariguette | -2.00 | -2.32 | -1.68 |

- *From Order 1*

```r
dat_group_from_Order1<-dat_group[!dat_group[,'Index']=="0",]

Gariguette<- fc_linear_trend_reg(data = dat_group_from_Order1,
                                 genotype = "Gariguette",
                                 variable = "nb_total_leaves",
                                 Index = "Index")

Clery<- fc_linear_trend_reg(data = dat_group_from_Order1,
                            genotype = "Clery",
                            variable = "nb_total_leaves",
                            Index = "Index")

Capriss<- fc_linear_trend_reg(data = dat_group_from_Order1,
                              genotype = "Capriss",
                              variable = "nb_total_leaves",
                              Index = "Index")

Ciflorette<- fc_linear_trend_reg(data = dat_group_from_Order1,
                                 genotype = "Ciflorette",
                                 variable = "nb_total_leaves",
                                 Index = "Index")

Cir107<- fc_linear_trend_reg(data = dat_group_from_Order1,
                             genotype = "Cir107",
                             variable = "nb_total_leaves",
                             Index = "Index")

Darselect<- fc_linear_trend_reg(data = dat_group_from_Order1,
                                genotype = "Darselect",
                                variable = "nb_total_leaves",
                                Index = "Index")

tab6<- merge(x = Gariguette,
             y = Clery,
             all=T)

tab6<- merge(x = tab6,
             y = Capriss,
             all=T)

tab6<- merge(x = tab6,
             y = Ciflorette,
             all=T)

tab6<- merge(x = tab6,
             y = Cir107,
             all=T)
```

```r
tab6<- merge(x = tab6,
             y = Darselect,
             all=T)

kable(x = tab6,
      digits = 2,
      caption = "Linear trend for no.leaves (estimate slope and 95% confidence interval -IC95%-) for the f
```

Table 8: Linear trend for no.leaves (estimate slope and 95% confidence interval -IC95%-) for the first-order module onwards

| Genotype | Slope | IC_lower | IC_upper |
|----------|-------|----------|----------|
| Capriss | -0.04 | -0.20 | 0.12 |
| Ciflorette | 0.04 | -0.10 | 0.17 |
| Cir107 | -0.24 | -0.43 | -0.05 |
| Clery | -0.05 | -0.18 | 0.08 |
| Darselect | -0.31 | -0.47 | -0.15 |
| Gariguette | -0.12 | -0.34 | 0.10 |

**Result:** The no. leaves was roughly constant from first-order module

- **Comparison between variety for zeroth-order module and first-order modules**

- *From Order 0*

```r
dat_group_Order0<- dat_group[dat_group[,"Index"]=="0",]

tab7<-fc_comp_varieties_kruskal_posthoc(data = dat_group_Order0,
                                        varname = "nb_total_leaves",
                                        groupe = T)
```

```
##
##  Pairwise comparisons using Tukey and Kramer (Nemenyi) test
##                  with Tukey-Dist approximation for independent samples
##
## data:  data[, varname] and data[, "genotype"]
##
##            Gariguette Ciflorette Clery   Capriss Darselect
## Ciflorette 1.2e-05    -          -       -       -
## Clery      0.00929    0.62891    -       -       -
## Capriss    1.00000    9.9e-06    0.00831 -       -
## Darselect  6.3e-12    0.18977    0.00156 5.0e-12 -
## Cir107     0.98723    0.00026    0.06824 0.98413 6.1e-10
##
## P value adjustment method: none
```

```r
kable(x = tab7,
      digits = 2,
      caption = "Mean number with standard deviation and grouping of varieties using ANOVA on rank (Kruskal
```

Table 9: Mean number with standard deviation and grouping of varieties using ANOVA on rank (Kruskal Wallis and posthoc test) represented by letter for zeroth-order module

| | genotype | mean | std | groups |
|---|----------|------|-----|--------|
| 5 | Gariguette | 10.43 | 2.35 | a |

|   | genotype | mean | std | groups |
|---|----------|------|-----|--------|
| 6 | Capriss | 10.35 | 1.82 | a |
| 4 | Cir107 | 9.63 | 3.29 | a |
| 3 | Clery | 8.33 | 2.97 | b |
| 2 | Ciflorette | 7.63 | 2.57 | b |
| 1 | Darselect | 6.11 | 2.29 | c |

- *From Order 1*

```
tab8<-fc_comp_varieties_kruskal_posthoc(data = dat_group_from_Order1,
                                        varname = "nb_total_leaves",
                                        group = T)
```

```
##
##  Pairwise comparisons using Tukey and Kramer (Nemenyi) test
##                   with Tukey-Dist approximation for independent samples
##
## data:  data[, varname] and data[, "genotype"]
##
##            Gariguette Ciflorette Clery   Capriss Darselect
## Ciflorette 0.37781    -          -       -       -
## Clery      0.99986    0.20668    -       -       -
## Capriss    0.01311    0.76805    0.00312 -       -
## Darselect  0.38404    0.00086    0.51233 5.9e-07 -
## Cir107     0.82967    0.94849    0.63740 0.16064 0.00921
##
## P value adjustment method: none
```

```
kable(x = tab8,
      digits = 2,
      caption = "Mean number with standard deviation and grouping of varieties using ANOVA on rank (Kruskal
```

Table 10: Mean number with standard deviation and grouping of varieties using ANOVA on rank (Kruskal Wallis and posthoc test) represented by letter from the first-order modules onward

|   | genotype | mean | std | groups |
|---|----------|------|-----|--------|
| 6 | Capriss | 3.51 | 1.02 | a |
| 4 | Cir107 | 3.43 | 1.36 | bc |
| 5 | Ciflorette | 3.40 | 1.01 | ab |
| 3 | Gariguette | 3.33 | 1.31 | c |
| 2 | Clery | 3.16 | 0.91 | cd |
| 1 | Darselect | 3.02 | 1.07 | d |

- *pointwise Mean No .leaves of successive orders module (0 and >=1)*

  – convert dat in dat_group_from_order1

```
dat_group_from_Order1<-data[2:colend]

for (i in 1:nrow(data)){
  if( dat_group_from_Order1[i,"genotype"]=="Capriss"){
    if (data[i,'Index']=="0"){
      dat_group_from_Order1[i,"Index"]<- 0
      }else if (data[i,'Index']=="0-1"){
      dat_group_from_Order1[i,"Index"]<- 1
      }else if (data[i,'Index']=="0-1-2"){
```

```r
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="0-1-2-3"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="0-1-2-3-4"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="0-1-2-3-4-5"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="1"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="1-2"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="1-2-3"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="1-2-3-4"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="1-2-3-4-5"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="2"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="2-3"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="2-3-4"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="3"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="3-4"){
      dat_group_from_Order1[i,"Index"]<- 1
    }else if (data[i,'Index']=="4"){
      dat_group_from_Order1[i,"Index"]<- 1
    }
  }else
if (data[i,'Index']=="0"){
  dat_group_from_Order1[i,"Index"]<- 0
}else if (data[i,'Index']=="0-1"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="0-1-2"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="0-1-2-3"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="0-1-2-3-4"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="0-1-2-3-4-5"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="1"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="1-2"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="1-2-3"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="1-2-3-4"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="1-2-3-4-5"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="2"){
  dat_group_from_Order1[i,"Index"]<- 1
}else if (data[i,'Index']=="2-3"){
```

```
    dat_group_from_Order1[i,"Index"]<- 1
  }else if (data[i,'Index']=="2-3-4"){
    dat_group_from_Order1[i,"Index"]<- 1
  }else if (data[i,'Index']=="3"){
    dat_group_from_Order1[i,"Index"]<- 1
  }else if (data[i,'Index']=="3-4"){
    dat_group_from_Order1[i,"Index"]<- 1
  }else if (data[i,'Index']=="4"){
    dat_group_from_Order1[i,"Index"]<- 1
  }
}

#Remplacer les valeurs 0 dans la colone total flowers par NA
dat_group_from_Order1$nb_total_flowers[dat_group_from_Order1$nb_total_flowers==0]<-NA

dat_group_from_Order1$Index<-as.factor(dat_group_from_Order1$Index)
```

  * recalcule data_at_module_scale_group_from_Order1

```
data_at_module_scale_group_from_Order1<-ddply(.data = dat_group_from_Order1,
                                   .variables = c("genotype","Index"),
                                   summarise,
                                   MeanTotalLeave= mean(
                                     x = nb_total_leaves,
                                     na.rm = T),
                                   SdTotalLeave= sd(
                                     x = nb_total_leaves,
                                     na.rm = T),
                                   MeanTotalFlower= mean(
                                     x = nb_total_flowers,
                                     na.rm = T),
                                   SdTotalFlower= sd(
                                     x = nb_total_flowers,
                                     na.rm = T),
                                   MeanStolon= mean(
                                     x = stolons,
                                     na.rm = T),
                                   SdStolon= sd(
                                     x = stolons,
                                     na.rm = T),
                                   N=length(nb_total_leaves))

kable(x = data_at_module_scale_group_from_Order1,
      digits = 2,
      caption = " Data at module scale after grouping from order1")
```

Table 11: Data at module scale after grouping from order1

| genotype | Index | MeanTotalLeave | SdTotalLeave | MeanTotalFlower | SdTotalFlower | MeanStolon | SdStolon | N |
|---|---|---|---|---|---|---|---|---|
| Gariguette | 0 | 10.43 | 2.35 | 18.71 | 3.70 | 0.67 | 0.75 | 54 |
| Gariguette | 1 | 3.33 | 1.31 | 7.43 | 2.96 | 0.13 | 0.52 | 187 |
| Ciflorette | 0 | 7.63 | 2.57 | 10.95 | 2.76 | 1.09 | 0.96 | 54 |
| Ciflorette | 1 | 3.40 | 1.01 | 6.38 | 1.91 | 0.26 | 0.66 | 244 |
| Clery | 0 | 8.33 | 2.97 | 13.71 | 3.34 | 1.65 | 1.25 | 54 |
| Clery | 1 | 3.16 | 0.91 | 5.30 | 2.08 | 0.15 | 0.44 | 209 |

| genotype | Index | MeanTotalLeave | SdTotalLeave | MeanTotalFlower | SdTotalFlower | MeanStolon | SdStolon | N |
|---|---|---|---|---|---|---|---|---|
| Capriss | 0 | 10.35 | 1.82 | 11.92 | 2.87 | 1.96 | 0.97 | 54 |
| Capriss | 1 | 3.51 | 1.02 | 4.03 | 1.27 | 0.02 | 0.15 | 327 |
| Darselect | 0 | 6.11 | 2.29 | 10.50 | 4.77 | 0.94 | 1.11 | 54 |
| Darselect | 1 | 3.02 | 1.07 | 6.11 | 2.50 | 0.11 | 0.39 | 192 |
| Cir107 | 0 | 9.63 | 3.29 | 16.00 | 4.20 | 1.83 | 1.33 | 54 |
| Cir107 | 1 | 3.43 | 1.36 | 7.80 | 3.15 | 0.08 | 0.34 | 313 |

* Plot mean no. leaves for succesive module orders for 0 and from first-order module onwards

```
fc_pointwise_mean_variable_by_order(data = data_at_module_scale_group_from_Order1,
                                    varname = "MeanTotalLeave")+
  ylab("Mean no. leaves")+
  ylim(3,10)
```
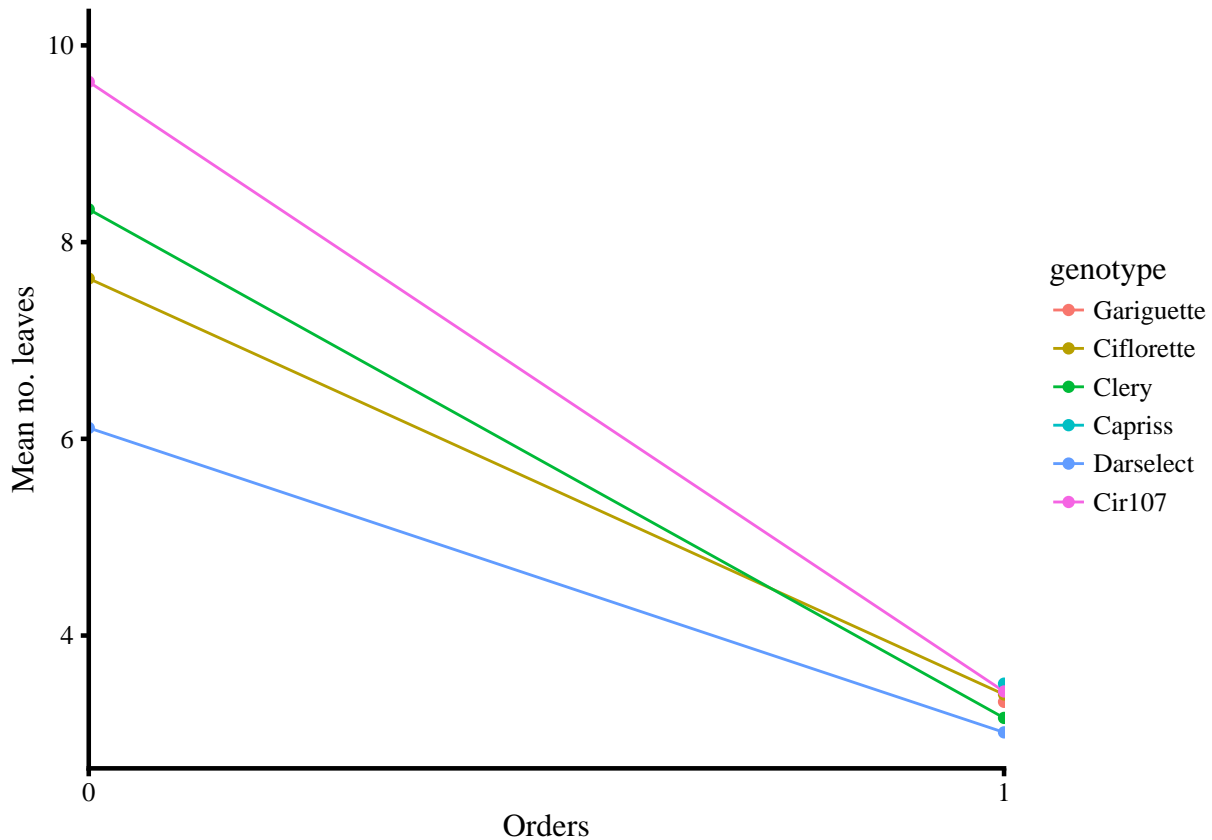


### 3.2.4.3 No. flowers fonction of successive module order

#### 3.2.4.3.1 Cumulative distribution of no. flowers for each module order

- Table of distribution of No.flowers according to module orders

```
tab9<-fc_dist_variable_by_order(data = dat_group,
                                genotype = "Gariguette",
                                varname = "nb_total_flowers",
                                prob = "cumulative")

kable(x = tab9,
```

```
      digits = 2,
      caption = "Cumulative distribution of total no. leaves by orders for Gariguette")
```

Table 12: Cumulative distribution of total no. leaves by orders for Gariguette

|    | 0    | 1    | 2    | 3    | 4   |
|----|------|------|------|------|-----|
| 2  | 0.00 | 0.01 | 0.03 | 0.00 | 0.0 |
| 3  | 0.00 | 0.01 | 0.03 | 0.00 | 0.1 |
| 4  | 0.00 | 0.05 | 0.15 | 0.08 | 0.2 |
| 5  | 0.00 | 0.11 | 0.35 | 0.46 | 0.6 |
| 6  | 0.00 | 0.29 | 0.44 | 0.69 | 0.8 |
| 7  | 0.00 | 0.45 | 0.62 | 0.85 | 1.0 |
| 8  | 0.00 | 0.64 | 0.79 | 0.92 | NA  |
| 9  | 0.00 | 0.76 | 0.88 | 0.92 | NA  |
| 10 | 0.02 | 0.86 | 0.94 | 1.00 | NA  |
| 11 | 0.05 | 0.93 | 0.97 | NA   | NA  |
| 12 | 0.05 | 0.96 | 0.97 | NA   | NA  |
| 13 | 0.07 | 0.96 | 0.97 | NA   | NA  |
| 14 | 0.17 | 0.97 | 1.00 | NA   | NA  |
| 15 | 0.22 | 0.97 | NA   | NA   | NA  |
| 17 | 0.34 | 0.97 | NA   | NA   | NA  |
| 18 | 0.49 | 0.97 | NA   | NA   | NA  |
| 19 | 0.59 | 0.97 | NA   | NA   | NA  |
| 20 | 0.63 | 0.97 | NA   | NA   | NA  |
| 21 | 0.73 | 0.97 | NA   | NA   | NA  |
| 22 | 0.83 | 0.97 | NA   | NA   | NA  |
| 23 | 0.90 | 1.00 | NA   | NA   | NA  |
| 24 | 0.98 | NA   | NA   | NA   | NA  |
| 25 | 1.00 | NA   | NA   | NA   | NA  |

- **Visualization of distribution of No. flowers for each module orders**

```
fc_dist_variable_by_order.plot(data = tab9)+
  xlab("No. Leaves")+
  ylab("Cumulative distribution function")
```

#### 3.2.4.3.2   Pointwise Mean of No.flowers of modules for successive orders for each varieties

```
fc_pointwise_mean_variable_by_order(data = data_at_module_scale_group,
                                    varname = "MeanTotalFlower")+
  ylab("Mean No. Flower")+
  ylim(0,20)
```

#### 3.2.4.3.3   Comparison of No. flowers for successive orders

- **Identification from wich module variable was roughly constant for each varieties**
  - *From Order 0*

```
Gariguette<- fc_linear_trend_reg(data = dat_group,
                              genotype = "Gariguette",
                              variable = "nb_total_flowers",
                              Index = "Index")

Clery<- fc_linear_trend_reg(data = dat_group,
```
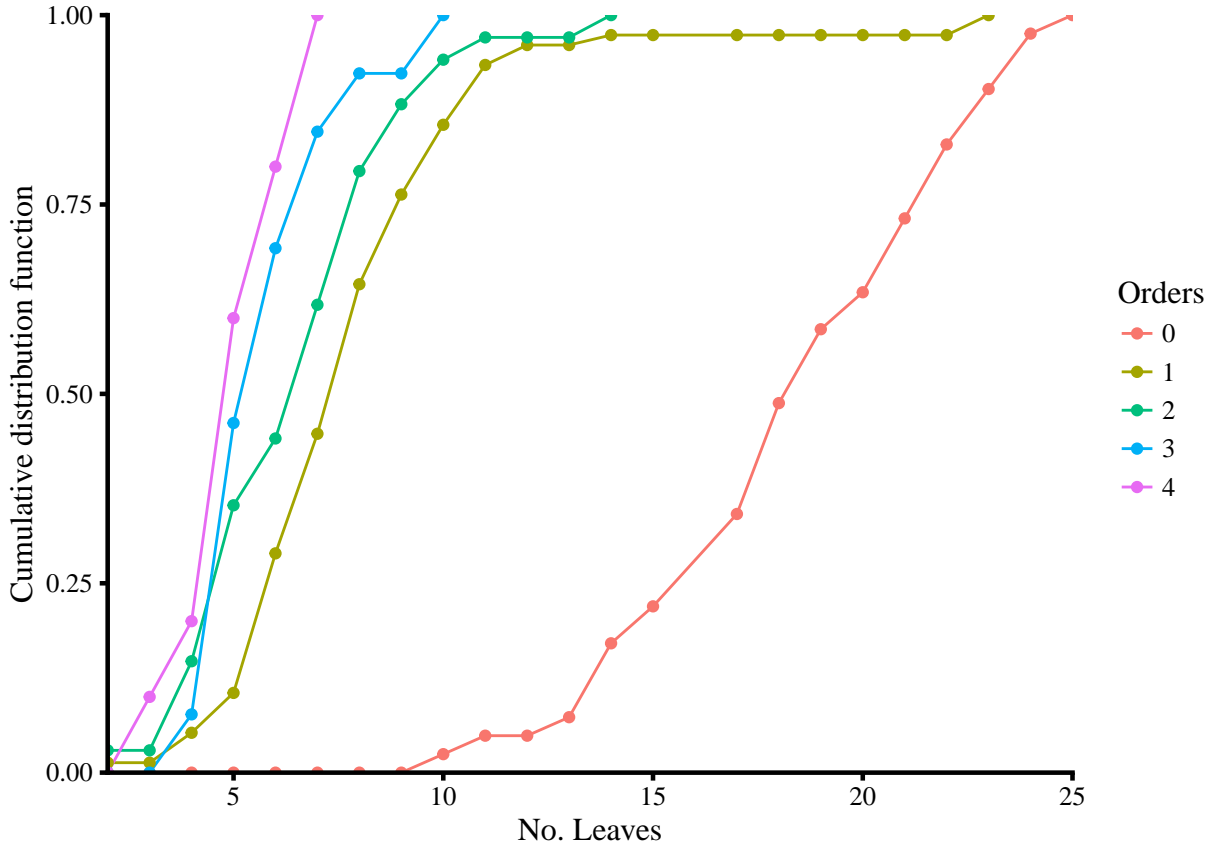
Figure 4: Plot distribution of leaves for each module orders and for Gariguette
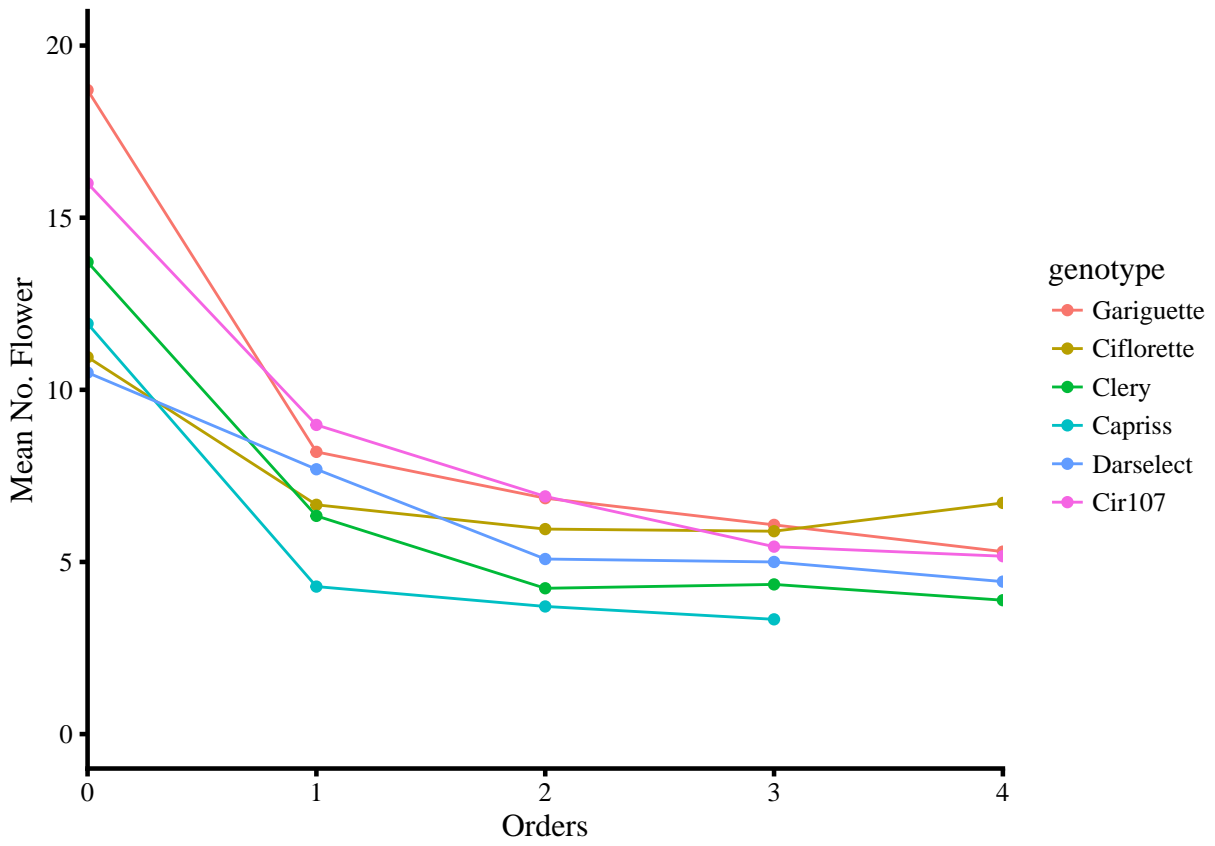
Figure 5: Pointwise Mean of No. leaves of modules for successive orders for each variety after grouping

```
                              genotype = "Clery",
                              variable = "nb_total_flowers",
                              Index = "Index")

Capriss<- fc_linear_trend_reg(data = dat_group,
                              genotype = "Capriss",
                              variable = "nb_total_flowers",
                              Index = "Index")

Ciflorette<- fc_linear_trend_reg(data = dat_group,
                              genotype = "Ciflorette",
                              variable = "nb_total_flowers",
                              Index = "Index")

Cir107<- fc_linear_trend_reg(data = dat_group,
                              genotype = "Cir107",
                              variable = "nb_total_flowers",
                              Index = "Index")

Darselect<- fc_linear_trend_reg(data = dat_group,
                              genotype = "Darselect",
                              variable = "nb_total_flowers",
                              Index = "Index")

tab10<- merge(x = Gariguette,
              y = Clery,
              all=T)

tab10<- merge(x = tab10,
              y = Capriss,
              all=T)

tab10<- merge(x = tab10,
              y = Ciflorette,
              all=T)

tab10<- merge(x = tab10,
              y = Cir107,
              all=T)

tab10<- merge(x = tab10,
              y = Darselect,
              all=T)

kable(x = tab10,
      digits = 2,
      caption = "Linear trend (estimate slope and 95% confidence interval -IC95%-) for the number of flowe
```

Table 13: Linear trend (estimate slope and 95% confidence interval -IC95%-) for the number of flowersfrom zeroth-order onward (orders >=0)

| Genotype | Slope | IC_lower | IC_upper |
|---|---|---|---|
| Capriss | -2.58 | -2.98 | -2.17 |
| Ciflorette | -1.08 | -1.37 | -0.79 |
| Cir107 | -2.86 | -3.33 | -2.40 |

| Genotype | Slope | IC_lower | IC_upper |
|---|---|---|---|
| Clery | -2.60 | -3.02 | -2.19 |
| Darselect | -1.85 | -2.28 | -1.42 |
| Gariguette | -3.50 | -4.10 | -2.90 |

- *From Order 1*

```r
Gariguette<- fc_linear_trend_reg(data = dat_group_from_Order1,
                                 genotype = "Gariguette",
                                 variable = "nb_total_flowers",
                                 Index = "Index")

Clery<- fc_linear_trend_reg(data = dat_group_from_Order1,
                            genotype = "Gariguette",
                            variable = "nb_total_flowers",
                            Index = "Index")

Capriss<- fc_linear_trend_reg(data = dat_group_from_Order1,
                              genotype = "Capriss",
                              variable = "nb_total_flowers",
                              Index = "Index")

Ciflorette<- fc_linear_trend_reg(data = dat_group_from_Order1,
                                 genotype = "Ciflorette",
                                 variable = "nb_total_flowers",
                                 Index = "Index")

Cir107<- fc_linear_trend_reg(data = dat_group_from_Order1,
                             genotype = "Cir107",
                             variable = "nb_total_flowers",
                             Index = "Index")

Darselect<- fc_linear_trend_reg(data = dat_group_from_Order1,
                                genotype = "Darselect",
                                variable = "nb_total_flowers",
                                Index = "Index")

tab11<- merge(x = Gariguette,
              y = Clery,
              all=T)

tab11<- merge(x = tab11,
              y = Capriss,
              all=T)

tab11<- merge(x = tab11,
              y = Ciflorette,
              all=T)

tab11<- merge(x = tab11,
              y = Cir107,
              all=T)

tab11<- merge(x = tab11,
              y = Darselect,
              all=T)
```

```r
kable(x = tab11,
      digits = 2,
      caption = "Linear trend (estimate slope and 95% confidence interval -IC95%-) for the number of flowe
```

Table 14: Linear trend (estimate slope and 95% confidence interval -IC95%-) for the number of flowers from first-order onward (orders >=1)

| Genotype | Slope | IC_lower | IC_upper |
|----------|-------|----------|----------|
| Capriss | -7.90 | -8.47 | -7.32 |
| Ciflorette | -4.57 | -5.29 | -3.86 |
| Cir107 | -8.20 | -9.44 | -6.97 |
| Darselect | -4.39 | -5.55 | -3.23 |
| Gariguette | -11.28 | -12.39 | -10.17 |

- *From Order 2*

```r
dat_group_from_Order2<-dat_group_from_Order1[!dat_group_from_Order1[,'Index']=="1",]

Gariguette<- fc_linear_trend_reg(data = dat_group_from_Order2,
                                 genotype = "Gariguette",
                                 variable = "nb_total_flowers",
                                 Index = "Index")

Clery<- fc_linear_trend_reg(data = dat_group_from_Order2,
                            genotype = "Gariguette",
                            variable = "nb_total_flowers",
                            Index = "Index")

Capriss<- fc_linear_trend_reg(data = dat_group_from_Order2,
                              genotype = "Capriss",
                              variable = "nb_total_flowers",
                              Index = "Index")

Ciflorette<- fc_linear_trend_reg(data = dat_group_from_Order2,
                                 genotype = "Ciflorette",
                                 variable = "nb_total_flowers",
                                 Index = "Index")

Cir107<- fc_linear_trend_reg(data = dat_group_from_Order2,
                             genotype = "Cir107",
                             variable = "nb_total_flowers",
                             Index = "Index")

Darselect<- fc_linear_trend_reg(data = dat_group_from_Order2,
                                genotype = "Darselect",
                                variable = "nb_total_flowers",
                                Index = "Index")

tab12<- merge(x = Gariguette,
              y = Clery,
              all=T)

tab12<- merge(x = tab12,
              y = Capriss,
```

```
            all=T)

tab12<- merge(x = tab12,
              y = Ciflorette,
              all=T)

tab12<- merge(x = tab12,
              y = Cir107,
              all=T)

tab12<- merge(x = tab12,
              y = Darselect,
              all=T)

kable(x = tab12,
      digits = 2,
      caption = "Linear trend (estimate slope and 95% confidence interval -IC95%-) for the number of flower
```

Table 15: Linear trend (estimate slope and 95% confidence interval -
IC95%-) for the number of flowers from second-order onward (orders
>=2)

| Genotype | Slope | IC_lower | IC_upper |
|----------|-------|----------|----------|
| Capriss | NA | NA | NA |
| Ciflorette | NA | NA | NA |
| Cir107 | NA | NA | NA |
| Darselect | NA | NA | NA |
| Gariguette | NA | NA | NA |

**Result:** The no. flowers was roughly constant from second-order module

- ** Comparison between variety for zeroth-order module and first-order modules and second-order module onwards**

- – For zeroth-order module*

```
tab13<-fc_comp_varieties_kruskal_posthoc(data = dat_group_Order0,
                                         varname = "nb_total_flowers",
                                         group = T)
```

```
##
##  Pairwise comparisons using Tukey and Kramer (Nemenyi) test
##              with Tukey-Dist approximation for independent samples
##
## data:  data[, varname] and data[, "genotype"]
##
##           Gariguette Ciflorette Clery   Capriss Darselect
## Ciflorette 7.1e-13    -          -       -       -
## Clery      0.00049    0.01310    -       -       -
## Capriss    4.4e-10    0.95953    0.14528 -       -
## Darselect  3.8e-12    1.00000    0.02249 0.98131 -
## Cir107     0.23032    1.2e-05    0.50281 0.00060 3.0e-05
##
## P value adjustment method: none
```

```
kable(x = tab13,
      digits = 2,
```

```
      caption = "Mean number with standard deviation and grouping of varieties using ANOVA on rank (Kruska
```

Table 16: Mean number with standard deviation and grouping of
varieties using ANOVA on rank (Kruskal Wallis and posthoc test)
represented by letter for zeroth-order module

|   | genotype | mean | std | groups |
|---|----------|------|-----|--------|
| 6 | Gariguette | 18.71 | 3.70 | a |
| 5 | Cir107 | 16.00 | 4.20 | b |
| 4 | Clery | 13.71 | 3.34 | c |
| 3 | Capriss | 11.92 | 2.87 | d |
| 1 | Ciflorette | 10.95 | 2.76 | d |
| 2 | Darselect | 10.50 | 4.77 | d |

- – For the first-order module*

```
dat_group_Order1<- dat_group[dat_group[,"Index"]==1,]

tab14<-fc_comp_varieties_kruskal_posthoc(data = dat_group_Order1,
                                         varname = "nb_total_flowers",
                                         group = T)
```

```
##
##  Pairwise comparisons using Tukey and Kramer (Nemenyi) test
##                 with Tukey-Dist approximation for independent samples
##
## data:  data[, varname] and data[, "genotype"]
##
##            Gariguette Ciflorette Clery   Capriss Darselect
## Ciflorette 0.0209     -          -       -       -
## Clery      0.0015     0.9020     -       -       -
## Capriss    5.5e-14    4.5e-13    1.2e-07 -       -
## Darselect  0.8175     0.6636     0.1942  1.1e-13 -
## Cir107     0.8682     5.3e-05    2.2e-06 < 2e-16 0.1849
##
## P value adjustment method: none
```

```
kable(x = tab14,
      digits = 2,
      caption = "Mean number with standard deviation and grouping of varieties using ANOVA on rank (Kruska
```

Table 17: Mean number with standard deviation and grouping of
varieties using ANOVA on rank (Kruskal Wallis and posthoc test)
represented by letter for first-order module

|   | genotype | mean | std | groups |
|---|----------|------|-----|--------|
| 6 | Cir107 | 8.98 | 3.46 | a |
| 5 | Gariguette | 8.20 | 3.25 | ab |
| 4 | Darselect | 7.69 | 3.03 | bc |
| 3 | Ciflorette | 6.66 | 2.06 | cd |
| 2 | Clery | 6.34 | 2.13 | d |
| 1 | Capriss | 4.28 | 1.28 | e |

* * For second-order module onwards*

```r
tab15<-fc_comp_varieties_kruskal_posthoc(data = dat_group_from_Order2,
                                         varname = "nb_total_flowers",
                                         group = T)
```

```
##
##  Pairwise comparisons using Tukey and Kramer (Nemenyi) test
##                   with Tukey-Dist approximation for independent samples
##
## data:  data[, varname] and data[, "genotype"]
##
##            Gariguette Ciflorette Clery   Capriss Darselect
## Ciflorette 7.1e-13    -          -       -       -
## Clery      0.00049    0.01310    -       -       -
## Capriss    4.4e-10    0.95953    0.14528 -       -
## Darselect  3.8e-12    1.00000    0.02249 0.98131 -
## Cir107     0.23032    1.2e-05    0.50281 0.00060 3.0e-05
##
## P value adjustment method: none
```

```r
kable(x = tab15,
      digits = 2,
      caption = "Mean number with standard deviation and grouping of varieties using ANOVA on rank (Kruskal
```

Table 18: Mean number with standard deviation and grouping of varieties using ANOVA on rank (Kruskal Wallis and posthoc test) represented by letter from the second-order modules onward

|   | genotype | mean | std | groups |
|---|----------|------|-----|--------|
| 6 | Gariguette | 18.71 | 3.70 | a |
| 5 | Cir107 | 16.00 | 4.20 | b |
| 4 | Clery | 13.71 | 3.34 | c |
| 3 | Capriss | 11.92 | 2.87 | d |
| 1 | Ciflorette | 10.95 | 2.76 | d |
| 2 | Darselect | 10.50 | 4.77 | d |

- *Pointwise Mean No. flowers of succesive orders module (0, 1 and >=2)*

    – convert dat in dat_group_from_order2

```r
dat_group_from_Order2<-data[2:colend]

for (i in 1:nrow(data)){
  if( dat_group_from_Order2[i,"genotype"]=="Capriss"){
    if (data[i,'Index']=="0"){
      dat_group_from_Order2[i,"Index"]<- 0
      }else if (data[i,'Index']=="0-1"){
      dat_group_from_Order2[i,"Index"]<- 1
      }else if (data[i,'Index']=="0-1-2"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="0-1-2-3"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="0-1-2-3-4"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="0-1-2-3-4-5"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="1"){
        dat_group_from_Order2[i,"Index"]<- 1
```

```r
      }else if (data[i,'Index']=="1-2"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="1-2-3"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="1-2-3-4"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="1-2-3-4-5"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="2"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="2-3"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="2-3-4"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="3"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="3-4"){
        dat_group_from_Order2[i,"Index"]<- 2
      }else if (data[i,'Index']=="4"){
        dat_group_from_Order2[i,"Index"]<- 2
      }
  }else
if (data[i,'Index']=="0"){
  dat_group_from_Order2[i,"Index"]<- 0
}else if (data[i,'Index']=="0-1"){
  dat_group_from_Order2[i,"Index"]<- 1
}else if (data[i,'Index']=="0-1-2"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="0-1-2-3"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="0-1-2-3-4"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="0-1-2-3-4-5"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="1"){
  dat_group_from_Order2[i,"Index"]<- 1
}else if (data[i,'Index']=="1-2"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="1-2-3"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="1-2-3-4"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="1-2-3-4-5"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="2"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="2-3"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="2-3-4"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="3"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="3-4"){
  dat_group_from_Order2[i,"Index"]<- 2
}else if (data[i,'Index']=="4"){
  dat_group_from_Order2[i,"Index"]<- 2
```

```
  }
}

#Remplacer les valeurs 0 dans la colone total flowers par NA
dat_group_from_Order2$nb_total_flowers[dat_group_from_Order2$nb_total_flowers==0]<-NA

dat_group_from_Order2$Index<-as.factor(dat_group_from_Order2$Index)
```

* recalcule data_at_module_scale_group_from_Order2

```
data_at_module_scale_group_from_Order2<-ddply(.data = dat_group_from_Order2,
                                    .variables = c("genotype","Index"),
                                    summarise,
                                    MeanTotalLeave= mean(
                                      x = nb_total_leaves,
                                      na.rm = T),
                                    SdTotalLeave= sd(
                                      x = nb_total_leaves,
                                      na.rm = T),
                                    MeanTotalFlower= mean(
                                      x = nb_total_flowers,
                                      na.rm = T),
                                    SdTotalFlower= sd(
                                      x = nb_total_flowers,
                                      na.rm = T),
                                    MeanStolon= mean(
                                      x = stolons,
                                      na.rm = T),
                                    SdStolon= sd(
                                      x = stolons,
                                      na.rm = T),
                                    N=length(nb_total_leaves))

kable(x = data_at_module_scale_group_from_Order2,
      digits = 2,
      caption = " Data at module scale after grouping from order1")
```

Table 19: Data at module scale after grouping from order1

| genotype | Index | MeanTotalLeave | SdTotalLeave | MeanTotalFlower | SdTotalFlower | MeanStolon | SdStolon | N |
|---|---|---|---|---|---|---|---|---|
| Gariguette | 0 | 10.43 | 2.35 | 18.71 | 3.70 | 0.67 | 0.75 | 54 |
| Gariguette | 1 | 3.28 | 1.28 | 8.20 | 3.25 | 0.00 | 0.00 | 94 |
| Gariguette | 2 | 3.38 | 1.35 | 6.40 | 2.15 | 0.26 | 0.72 | 93 |
| Ciflorette | 0 | 7.63 | 2.57 | 10.95 | 2.76 | 1.09 | 0.96 | 54 |
| Ciflorette | 1 | 3.33 | 0.90 | 6.66 | 2.06 | 0.00 | 0.00 | 115 |
| Ciflorette | 2 | 3.47 | 1.10 | 6.06 | 1.68 | 0.49 | 0.84 | 129 |
| Clery | 0 | 8.33 | 2.97 | 13.71 | 3.34 | 1.65 | 1.25 | 54 |
| Clery | 1 | 3.09 | 1.04 | 6.34 | 2.13 | 0.01 | 0.10 | 98 |
| Clery | 2 | 3.23 | 0.78 | 4.23 | 1.36 | 0.27 | 0.57 | 111 |
| Capriss | 0 | 10.35 | 1.82 | 11.92 | 2.87 | 1.96 | 0.97 | 54 |
| Capriss | 1 | 3.43 | 1.04 | 4.28 | 1.28 | 0.00 | 0.00 | 190 |
| Capriss | 2 | 3.62 | 0.99 | 3.57 | 1.10 | 0.06 | 0.24 | 137 |
| Darselect | 0 | 6.11 | 2.29 | 10.50 | 4.77 | 0.94 | 1.11 | 54 |
| Darselect | 1 | 3.34 | 1.08 | 7.69 | 3.03 | 0.01 | 0.11 | 87 |
| Darselect | 2 | 2.74 | 0.99 | 5.00 | 1.12 | 0.19 | 0.50 | 105 |

| genotype | Index | MeanTotalLeave | SdTotalLeave | MeanTotalFlower | SdTotalFlower | MeanStolon | SdStolon | N |
|---|---|---|---|---|---|---|---|---|
| Cir107 | 0 | 9.63 | 3.29 | 16.00 | 4.20 | 1.83 | 1.33 | 54 |
| Cir107 | 1 | 3.75 | 1.61 | 8.98 | 3.46 | 0.03 | 0.25 | 154 |
| Cir107 | 2 | 3.13 | 0.99 | 6.32 | 1.87 | 0.13 | 0.40 | 159 |

```
* Plot mean no. leaves for succesive module orders for 0, 1 and from second-order module onwards
fc_pointwise_mean_variable_by_order(data = data_at_module_scale_group_from_Order2,
                                    varname = "MeanTotalFlower")+
  ylab("Mean no. flowers")+
  ylim(3,20)
```
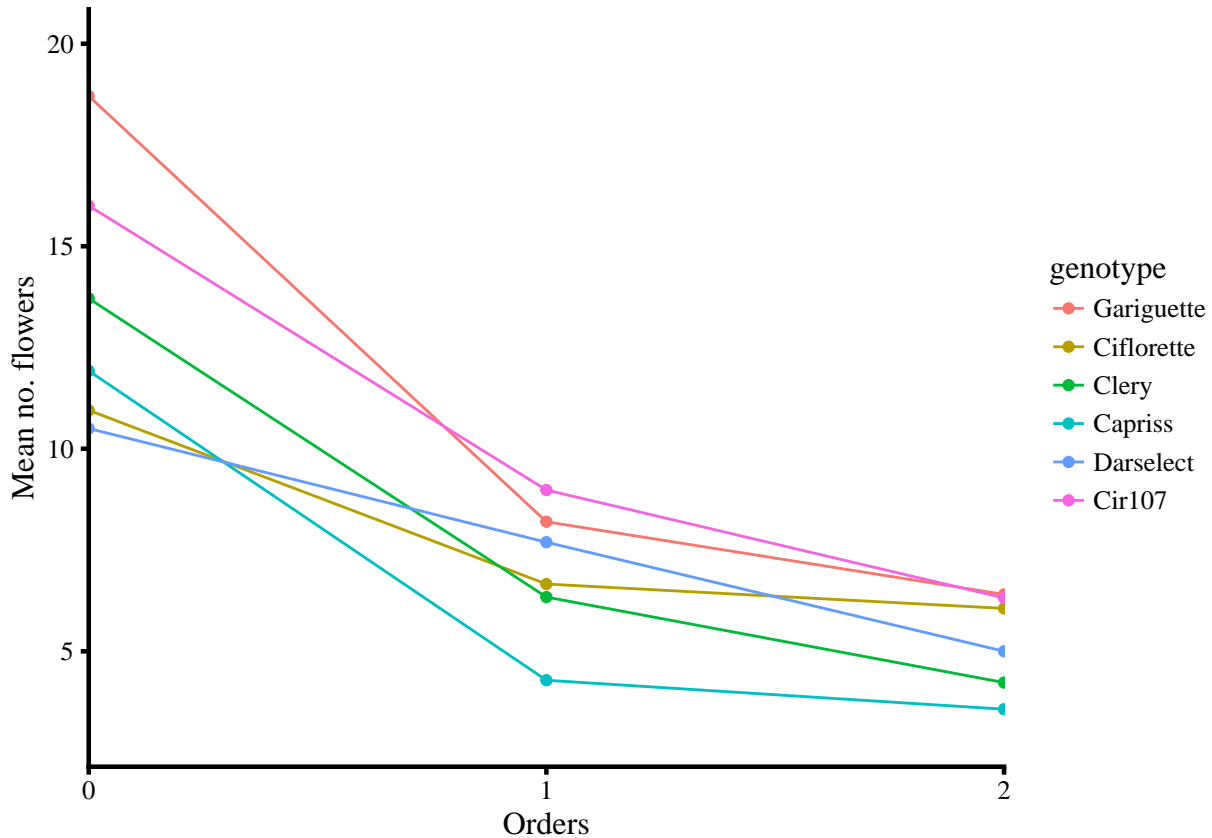


#### No. stolons fonction of successive module order

**3.2.4.3.4   Cumulative distribution of no. stolons for each module order**

- **Table of distribution of No. stolons according to module orders**

```
tab16<-fc_dist_variable_by_order(data = dat_group,genotype = "Gariguette",varname = "stolons",prob = T)

kable(x = tab16,
      digits = 2,
      caption = "Relative distribution of no. stolon by orders"
      )
```

Table 20: Relative distribution of no. stolon by orders

|  | 0 | 1 | 2 | 3 | 4 |
|---|---|---|---|---|---|
| 0 | 0.48 | 1 | 0.97 | 0.76 | 0.2 |
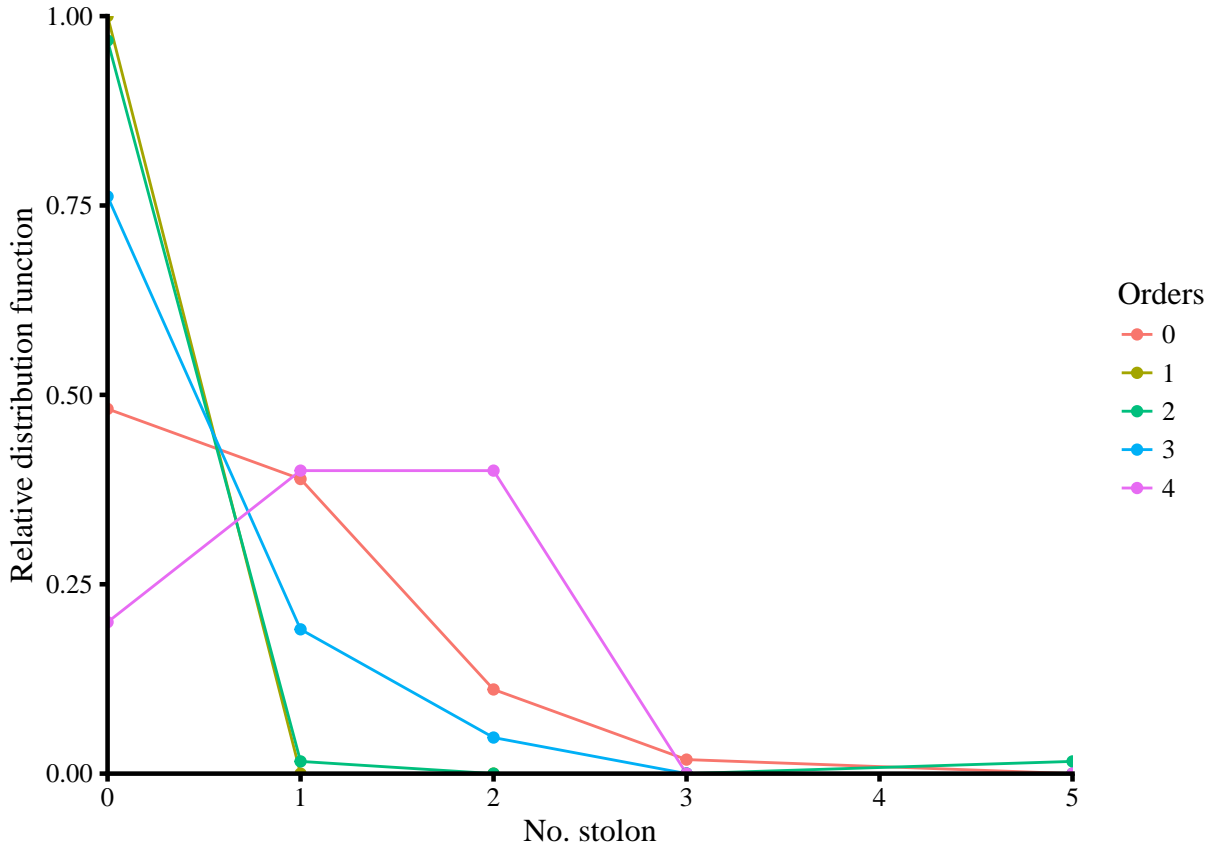
Figure 6: Relative frequency distribution of the number of stolons for successive orders for XX

|           | 0    | 1 | 2    | 3    | 4   |
|-----------|------|---|------|------|-----|
| 1         | 0.39 | 0 | 0.02 | 0.19 | 0.4 |
| 2         | 0.11 | 0 | 0.00 | 0.05 | 0.4 |
| 3         | 0.02 | 0 | 0.00 | 0.00 | 0.0 |
| 5         | 0.00 | 0 | 0.02 | 0.00 | 0.0 |
| Frequency | 1.00 | 1 | 1.00 | 1.00 | 1.0 |

- **Visualization of distribution of No stolons for each module orders**

```
fc_dist_variable_by_order.plot(data = tab16)+
  xlab("No. stolon")+
  ylab("Relative distribution function")
```

#### 3.2.4.3.5   Pointwise Mean of No. stolons of modules for successive orders for each varieties

```
fc_pointwise_mean_variable_by_order(data = data_at_module_scale_group,
                                    varname = "MeanStolon")+
  ylab("Mean No. Stolon")
```

**Results:** Not stationary so we are forced to compare varieties for each module orders

#### 3.2.4.3.6   Comparison of No. stolons for successive orders

- **For Order 0**
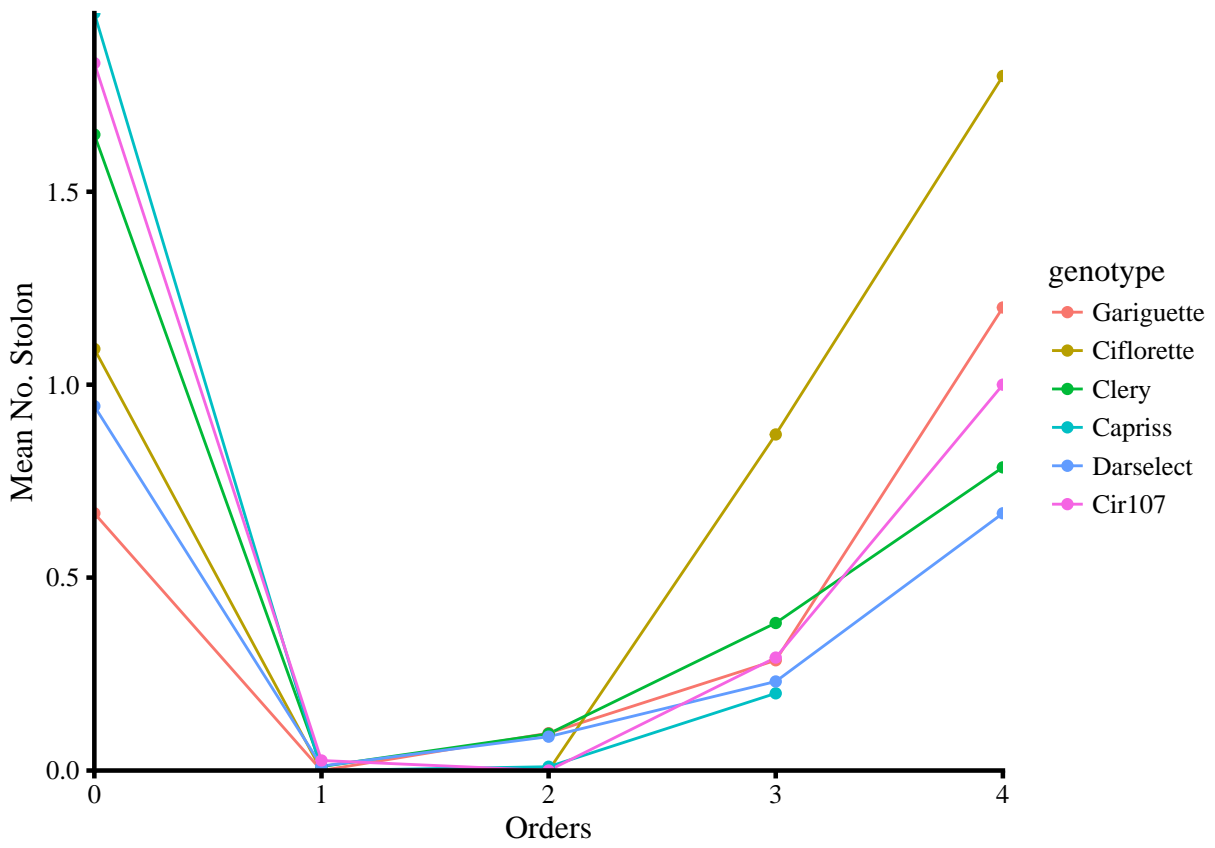
Figure 7: Pointwise Mean of No. leaves of modules for successive orders for each variety after grouping

```
tab17<- fc_comp_varieties_kruskal_posthoc(data = dat_group_Order0,
                                          varname = "stolons",
                                          groupe = T)
```

```
##
##  Pairwise comparisons using Tukey and Kramer (Nemenyi) test
##                   with Tukey-Dist approximation for independent samples
##
## data:  data[, varname] and data[, "genotype"]
##
##            Gariguette Ciflorette Clery   Capriss Darselect
## Ciflorette 0.34782    -          -       -       -
## Clery      0.00035    0.22244    -       -       -
## Capriss    1.4e-07    0.00246    0.65514 -       -
## Darselect  0.86235    0.95905    0.02543 6.4e-05 -
## Cir107     2.0e-05    0.05149    0.99064 0.94460 0.00314
##
## P value adjustment method: none
```

```
kable(x = tab17,
      digits = 2,
      caption = "Mean number of stolons with standard deviation and grouping of varieties using ANOVA on r
```

Table 21: Mean number of stolons with standard deviation and grouping of varieties using ANOVA on rank (Kruskal Wallis and posthoc test) represented by letter for zeroth-order module

|   | genotype | mean | std | groups |
|---|----------|------|-----|--------|
| 6 | Capriss | 1.96 | 0.97 | a |
| 5 | Cir107 | 1.83 | 1.33 | a |
| 4 | Clery | 1.65 | 1.25 | a |
| 3 | Ciflorette | 1.09 | 0.96 | b |
| 2 | Darselect | 0.94 | 1.11 | bc |
| 1 | Gariguette | 0.67 | 0.75 | c |

- **For Order 1**

```
tab18<-fc_comp_varieties_kruskal_posthoc(data = dat_group_Order1,
                                         varname = "stolons",
                                         groupe = T)
```

```
##
##  Pairwise comparisons using Tukey and Kramer (Nemenyi) test
##                   with Tukey-Dist approximation for independent samples
##
## data:  data[, varname] and data[, "genotype"]
##
##            Gariguette Ciflorette Clery Capriss Darselect
## Ciflorette 1          -          -     -       -
## Clery      1          1          -     -       -
## Capriss    1          1          1     -       -
## Darselect  1          1          1     1       -
## Cir107     1          1          1     1       1
##
## P value adjustment method: none
```

```
kable(x = tab18,
      digits = 2,
      caption = "Mean no.stolons with standard deviation and grouping of varieties using ANOVA on rank (Kr
```

Table 22: Mean no.stolons with standard deviation and grouping of varieties using ANOVA on rank (Kruskal Wallis and posthoc test) represented by letter for zeroth-order module

|    | genotype   | mean | std  | groups |
|----|------------|------|------|--------|
| 12 | Cir107     | 0.03 | 0.25 | a      |
| 11 | Darselect  | 0.01 | 0.11 | a      |
| 10 | Clery      | 0.01 | 0.10 | a      |
| 1  | Capriss    | 0.00 | 0.00 | a      |
| 2  | Capriss    | 0.00 | 0.00 | a      |
| 3  | Capriss    | 0.00 | 0.00 | a      |
| 4  | Ciflorette | 0.00 | 0.00 | a      |
| 5  | Ciflorette | 0.00 | 0.00 | a      |
| 6  | Ciflorette | 0.00 | 0.00 | a      |
| 7  | Gariguette | 0.00 | 0.00 | a      |
| 8  | Gariguette | 0.00 | 0.00 | a      |
| 9  | Gariguette | 0.00 | 0.00 | a      |

- **For Order 2**

```
dat_group_order2<-dat_group[dat_group[,"Index"]==2,]

tab19<-fc_comp_varieties_kruskal_posthoc(data = dat_group_order2,
                                         varname = "stolons",
                                         groupe = T)
```

```
##
##  Pairwise comparisons using Tukey and Kramer (Nemenyi) test
##                  with Tukey-Dist approximation for independent samples
##
## data:  data[, varname] and data[, "genotype"]
##
##            Gariguette Ciflorette Clery Capriss Darselect
## Ciflorette 1.00       -          -     -       -
## Clery      1.00       0.97       -     -       -
## Capriss    1.00       1.00       0.98  -       -
## Darselect  1.00       0.98       1.00  0.99    -
## Cir107     1.00       1.00       0.95  1.00    0.98
##
## P value adjustment method: none
```

```
kable(x = tab19,
      digits = 2,
      caption = "Mean No.stolons with standard deviation and grouping of varieties using ANOVA on rank (Kr
```

Table 23: Mean No.stolons with standard deviation and grouping of varieties using ANOVA on rank (Kruskal Wallis and posthoc test) represented by letter for second-order module

|   | genotype   | mean | std  | groups |
|---|------------|------|------|--------|
| 6 | Gariguette | 0.10 | 0.65 | ab     |
| 8 | Clery      | 0.10 | 0.35 | a      |

|   | genotype | mean | std | groups |
|---|----------|------|-----|--------|
| 7 | Darselect | 0.09 | 0.34 | a |
| 5 | Capriss | 0.01 | 0.10 | b |
| 1 | Ciflorette | 0.00 | 0.00 | b |
| 2 | Ciflorette | 0.00 | 0.00 | b |
| 3 | Cir107 | 0.00 | 0.00 | b |
| 4 | Cir107 | 0.00 | 0.00 | b |

- **For Order 3**

```
dat_group_order3<-dat_group[dat_group[,"Index"]==3,]

tab20<-fc_comp_varieties_kruskal_posthoc(data = dat_group_order3,
                                         varname = "stolons",
                                         groupe = T)
```

```
##
##  Pairwise comparisons using Tukey and Kramer (Nemenyi) test
##                   with Tukey-Dist approximation for independent samples
##
## data:  data[, varname] and data[, "genotype"]
##
##            Gariguette Ciflorette Clery Capriss Darselect
## Ciflorette 0.141      -          -     -       -
## Clery      1.000      0.132      -     -       -
## Capriss    1.000      0.021      0.985 -       -
## Darselect  1.000      0.021      0.991 1.000   -
## Cir107     1.000      0.048      1.000 0.999   1.000
##
## P value adjustment method: none
```

```
kable(x = tab20,
      digits = 2,
      caption = "Mean No. stolons with standard deviation and grouping of varieties using ANOVA on rank (K
```

Table 24: Mean No. stolons with standard deviation and grouping of varieties using ANOVA on rank (Kruskal Wallis and posthoc test) represented by letter for third-order module

|   | genotype | mean | std | groups |
|---|----------|------|-----|--------|
| 6 | Ciflorette | 0.87 | 0.85 | a |
| 5 | Clery | 0.38 | 0.70 | b |
| 4 | Cir107 | 0.29 | 0.56 | b |
| 3 | Gariguette | 0.29 | 0.56 | b |
| 2 | Darselect | 0.23 | 0.48 | b |
| 1 | Capriss | 0.20 | 0.41 | b |

- **For Order 4**

```
dat_group_order4<-dat_group[dat_group[,"Index"]==4,]

tab21<-fc_comp_varieties_kruskal_posthoc(data = dat_group_order4,
                                         varname = "stolons",
                                         groupe = T)
```

```
##
##  Pairwise comparisons using Tukey and Kramer (Nemenyi) test
```

```
##                         with Tukey-Dist approximation for independent samples
##
## data:  data[, varname] and data[, "genotype"]
##
##            Gariguette Ciflorette Clery Darselect
## Ciflorette 0.542      -          -     -
## Clery      0.759      0.016      -     -
## Darselect  0.572      0.013      0.992 -
## Cir107     0.987      0.269      0.980 0.893
##
## P value adjustment method: none
```

```r
kable(x = tab21,
      digits = 2,
      caption = "Mean No. stolons with standard deviation and grouping of varieties using ANOVA on rank (K:
```

Table 25: Mean No. stolons with standard deviation and grouping of varieties using ANOVA on rank (Kruskal Wallis and posthoc test) represented by letter for four-order module

|   | genotype | mean | std | groups |
|---|----------|------|-----|--------|
| 5 | Ciflorette | 1.80 | 0.77 | a |
| 4 | Gariguette | 1.20 | 0.79 | ab |
| 3 | Cir107 | 1.00 | 0.76 | b |
| 2 | Clery | 0.79 | 0.70 | b |
| 1 | Darselect | 0.67 | 1.00 | b |

### 3.2.5 Comparison of categorical variables

#### 3.2.5.1 Branch crown function of successive modules orders

Because the zeroth-order module is primary crown, to compare ramification for each module order we compare only from first-order module

##### 3.2.5.1.1 Relative frequency of proportion of Branch/Extention crown

- **Table of relative frequency of proportion of branch/Extention crown**

```r
dat_ramif<- dat_group[!dat_group[,"type_of_crown"]=="Primary_Crown",]

Capriss<-fc_dist_cat_variable_by_order(data = dat_ramif,
                                       genotype = "Capriss",
                                       varname = "type_of_crown",
                                       prob = T)

Ciflorette<-fc_dist_cat_variable_by_order(data = dat_ramif,
                                          genotype = "Ciflorette",
                                          varname = "type_of_crown",
                                          prob = T)

Cir107<-fc_dist_cat_variable_by_order(data = dat_ramif,
                                      genotype = "Cir107",
                                      varname = "type_of_crown",
                                      prob = T)

Clery<-fc_dist_cat_variable_by_order(data = dat_ramif,
```

```
                                 genotype = "Clery",
                                 varname = "type_of_crown",
                                 prob = T)

Darselect<-fc_dist_cat_variable_by_order(data = dat_ramif,
                                 genotype = "Darselect",
                                 varname = "type_of_crown",
                                 prob = T)

Gariguette<-fc_dist_cat_variable_by_order(data = dat_ramif,
                                 genotype = "Gariguette",
                                 varname = "type_of_crown",
                                 prob = T)

tab12<-merge(x = Capriss,
           y = Ciflorette,
           all=T)

tab12<-merge(x = tab12,
           y = Cir107,
           all=T)

tab12<-merge(x = tab12,
           y = Clery,
           all=T)

tab12<-merge(x = tab12,
           y = Darselect,
           all=T)

tab12<-merge(x = tab12,
           y = Gariguette,
           all=T)

tab12<- tab12[order(tab12$genotype),]

kable(x = tab12,
     digits = 2,
     caption = "Relative frequency distribution or branch crown and extention crown as function of module
```

Table 26: Relative frequency distribution or branch crown and
extention crown as function of module orders for each variety

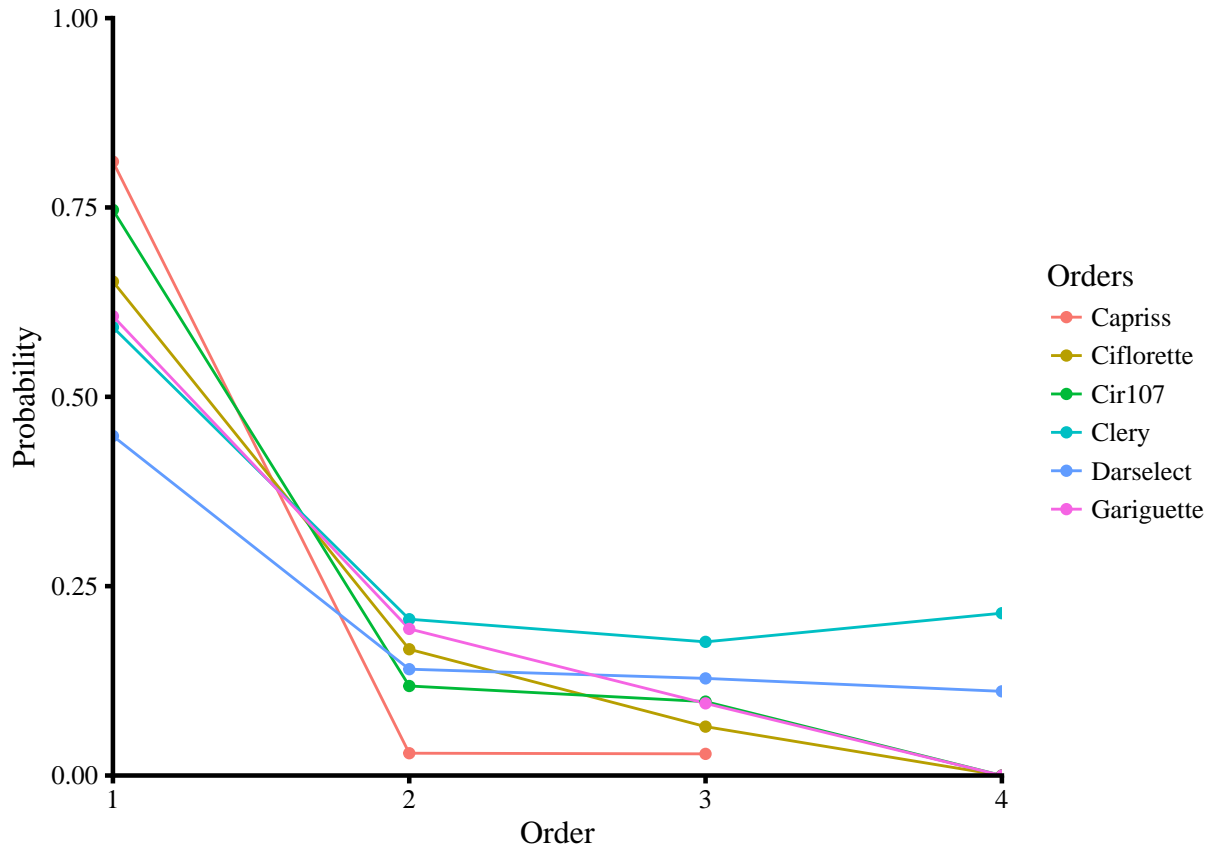|  | Primary_Crown | Extention_Crown | Branch_Crown | Frequency | genotype | Index |
|---|---|---|---|---|---|---|
| 1 | 0 | 0.19 | 0.81 | 1 | Capriss | 1 |
| 19 | 0 | 0.97 | 0.03 | 1 | Capriss | 2 |
| 20 | 0 | 0.97 | 0.03 | 1 | Capriss | 3 |
| 3 | 0 | 0.35 | 0.65 | 1 | Ciflorette | 1 |
| 11 | 0 | 0.83 | 0.17 | 1 | Ciflorette | 2 |
| 18 | 0 | 0.94 | 0.06 | 1 | Ciflorette | 3 |
| 21 | 0 | 1.00 | 0.00 | 1 | Ciflorette | 4 |
| 2 | 0 | 0.25 | 0.75 | 1 | Cir107 | 1 |
| 14 | 0 | 0.88 | 0.12 | 1 | Cir107 | 2 |
| 16 | 0 | 0.90 | 0.10 | 1 | Cir107 | 3 |
| 22 | 0 | 1.00 | 0.00 | 1 | Cir107 | 4 |
| 5 | 0 | 0.41 | 0.59 | 1 | Clery | 1 |

Figure 8: Relative frequencies of branch crown as a function of module orders for each varieties

|    | Primary_Crown | Extention_Crown | Branch_Crown | Frequency | genotype | Index |
|----|---------------|-----------------|--------------|-----------|-----------|-------|
| 7  | 0 | 0.79 | 0.21 | 1 | Clery | 4 |
| 8  | 0 | 0.79 | 0.21 | 1 | Clery | 2 |
| 10 | 0 | 0.82 | 0.18 | 1 | Clery | 3 |
| 6  | 0 | 0.55 | 0.45 | 1 | Darselect | 1 |
| 12 | 0 | 0.86 | 0.14 | 1 | Darselect | 2 |
| 13 | 0 | 0.87 | 0.13 | 1 | Darselect | 3 |
| 15 | 0 | 0.89 | 0.11 | 1 | Darselect | 4 |
| 4  | 0 | 0.39 | 0.61 | 1 | Gariguette | 1 |
| 9  | 0 | 0.81 | 0.19 | 1 | Gariguette | 2 |
| 17 | 0 | 0.90 | 0.10 | 1 | Gariguette | 3 |
| 23 | 0 | 1.00 | 0.00 | 1 | Gariguette | 4 |

- **Visualization of relative frequency of proportion of Branch/Extension crown**
    - *Plot of relative frequencies of branch crown*

```
fc_dist_cat_variable_by_order.plot(data = tab12,
                                   varname = "Branch_Crown")
```

* * Plot of relative frequency of extension crown*

```
fc_dist_cat_variable_by_order.plot(data = tab12,
                                   varname = "Extention_Crown")
```

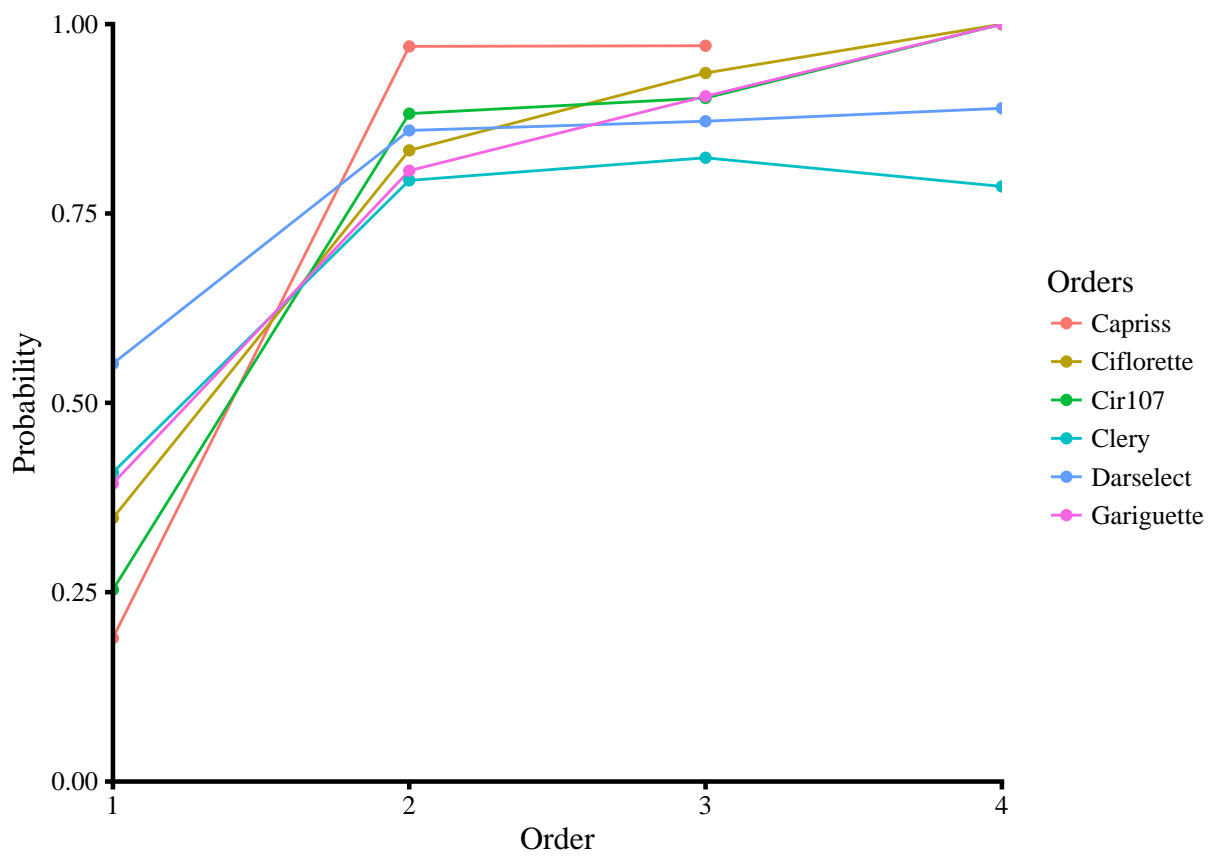#### 3.2.5.1.2 Comparison of Branch crown for successive order

Figure 9: Relative frequencies of extension crown as a function of module orders for each varieties

- **Identification from wich module variable was roughly constant for each varieties (chi2-test)**
  - *Comparison from zeroth-order module (from >= 1)*

```r
Capriss<- fc_chi_by_order(data = dat_group,
                          genotype = "Capriss",
                          varname = "type_of_crown",
                          var.comp = c("Branch_Crown",
                                       "Extention_Crown"),
                          idx.comp = c("1","2","3"),
                          parameter = ">=1",
                          table = F)


Ciflorette<- fc_chi_by_order(data = dat_group,
                             genotype = "Ciflorette",
                             varname = "type_of_crown",
                             var.comp = c("Branch_Crown",
                                          "Extention_Crown"),
                             idx.comp = c("1","2","3","4"),
                             parameter = ">=1",
                             table = F)


Cir107<- fc_chi_by_order(data = dat_group,
                         genotype = "Cir107",
                         varname = "type_of_crown",
                         var.comp = c("Branch_Crown",
                                      "Extention_Crown"),
                         idx.comp = c("1","2","3","4"),
                         parameter = ">=1",
                         table = F)


Clery<- fc_chi_by_order(data = dat_group,
                        genotype = "Clery",
                        varname = "type_of_crown",
                        var.comp = c("Branch_Crown",
                                     "Extention_Crown"),
                        idx.comp = c("1","2","3","4"),
                        parameter = ">=1",
                        table = F)


Darselect<- fc_chi_by_order(data = dat_group,
                            genotype = "Darselect",
                            varname = "type_of_crown",
                            var.comp = c("Branch_Crown",
                                         "Extention_Crown"),
                            idx.comp = c("1","2","3","4"),
                            parameter = ">=1",
                            table = F)


Gariguette<- fc_chi_by_order(data = dat_group,
                             genotype = "Gariguette",
                             varname = "type_of_crown",
                             var.comp = c("Branch_Crown",
                                          "Extention_Crown"),
                             idx.comp = c("1","2","3","4"),
                             parameter = ">=1",
                             table = F)
```

```
tab13<-merge(x = Capriss,
             y = Ciflorette,
             all=T)

tab13<-merge(x = tab13,
             y = Cir107,
             all=T)

tab13<-merge(x = tab13,
             y = Clery,
             all=T)

tab13<-merge(x = tab13,
             y = Darselect,
             all=T)

tab13<-merge(x = tab13,
             y = Gariguette,
             all=T)

tab13<- tab13[order(tab13$genotype),]

kable(x = tab13,
      digits = 2,
      caption = "Chi2 Comparaison of proportion of branch/extension crown for successive module order from
```

Table 27: Chi2 Comparaison of proportion of branch/extension crown for successive module order from first-order module onward

| genotype | parameter | p.value |
|---|---|---|
| Capriss | >=1 | 0 |
| Ciflorette | >=1 | 0 |
| Cir107 | >=1 | 0 |
| Clery | >=1 | 0 |
| Darselect | >=1 | 0 |
| Gariguette | >=1 | 0 |

* *Comparison from zeroth-order module (from >= 2)*

```
Capriss<- fc_chi_by_order(data = dat_group,
                          genotype = "Capriss",
                          varname = "type_of_crown",
                          var.comp = c("Branch_Crown",
                                       "Extention_Crown"),
                          idx.comp = c("2","3"),
                          parameter = ">=2",
                          table = F)

Ciflorette<- fc_chi_by_order(data = dat_group,
                             genotype = "Ciflorette",
                             varname = "type_of_crown",
                             var.comp = c("Branch_Crown",
                                          "Extention_Crown"),
                             idx.comp = c("2","3","4"),
```

```r
                                parameter = ">=2",
                                table = F)


Cir107<- fc_chi_by_order(data = dat_group,
                         genotype = "Cir107",
                         varname = "type_of_crown",
                         var.comp = c("Branch_Crown",
                                      "Extention_Crown"),
                         idx.comp = c("2","3","4"),
                         parameter = ">=2",
                         table = F)


Clery<- fc_chi_by_order(data = dat_group,
                        genotype = "Clery",
                        varname = "type_of_crown",
                        var.comp = c("Branch_Crown",
                                     "Extention_Crown"),
                        idx.comp = c("2","3","4"),
                        parameter = ">=2",
                        table = F)


Darselect<- fc_chi_by_order(data = dat_group,
                            genotype = "Darselect",
                            varname = "type_of_crown",
                            var.comp = c("Branch_Crown",
                                         "Extention_Crown"),
                            idx.comp = c("2","3","4"),
                            parameter = ">=2",
                            table = F)


Gariguette<- fc_chi_by_order(data = dat_group,
                             genotype = "Gariguette",
                             varname = "type_of_crown",
                             var.comp = c("Branch_Crown",
                                          "Extention_Crown"),
                             idx.comp = c("2","3","4"),
                             parameter = ">=2",
                             table = F)



tab14<-merge(x = Capriss,
             y = Ciflorette,
             all=T)

tab14<-merge(x = tab14,
             y = Cir107,
             all=T)

tab14<-merge(x = tab14,
             y = Clery,
             all=T)

tab14<-merge(x = tab14,
             y = Darselect,
             all=T)
```

```
tab14<-merge(x = tab14,
             y = Gariguette,
             all=T)

tab14<- tab14[order(tab14$genotype),]

kable(x = tab14,
      digits = 2,
      caption = "Chi2 Comparaison of proportion of branch/extension crown for successive module order from
```

Table 28: Chi2 Comparaison of proportion of branch/extension crown for successive module order from second-order module onwards

| genotype | parameter | p.value |
|---|---|---|
| Capriss | >=2 | 1.00 |
| Ciflorette | >=2 | 0.07 |
| Cir107 | >=2 | 0.57 |
| Clery | >=2 | 0.93 |
| Darselect | >=2 | 0.96 |
| Gariguette | >=2 | 0.20 |

- ** Comparison between varieties for zeroth-order modules and from first-order module onward**

- *Comparison between varieties for first-order module*

```
dat_group_Order1<- dat_group[dat_group[,"Index"]=="1",]

tab15<-fc_comp_varieties_chi2.fisher(data = dat_group_Order1,
                                     varname = "type_of_crown",
                                     comp = "genotype")

kable(x = tab15,
      digits = 2,
      caption = "Fisher comparison of proportion of branch crown extension crown for the first-order modul
```

Table 29: Fisher comparison of proportion of branch crown extension crown for the first-order module (Order1)

| comparison | p.value |
|---|---|
| Gariguette:Ciflorette | 0.60 |
| Gariguette:Clery | 0.88 |
| Gariguette:Capriss | 0.00 |
| Gariguette:Darselect | 0.06 |
| Gariguette:Cir107 | 0.04 |
| Ciflorette:Clery | 0.46 |
| Ciflorette:Capriss | 0.01 |
| Ciflorette:Darselect | 0.01 |
| Ciflorette:Cir107 | 0.14 |
| Clery:Capriss | 0.00 |
| Clery:Darselect | 0.08 |
| Clery:Cir107 | 0.03 |
| Capriss:Darselect | 0.00 |
| Capriss:Cir107 | 0.24 |
| Darselect:Cir107 | 0.00 |

- *Comparison between varieties from second-order module onwards*

```
tab15<-fc_comp_varieties_chi2.fisher(data = dat_group_from_Order2,
                                     varname = "type_of_crown",
                                     comp = "genotype")


kable(x = tab15,
      digits = 2,
      caption = "Fisher comparison of proportion of branch crown extension crown from second-order module
```

Table 30: Fisher comparison of proportion of branch crown extension crown from second-order module onwards (Order>=2)

| comparison | p.value |
|---|---|
| Gariguette:Ciflorette | 0.90 |
| Gariguette:Clery | 1.00 |
| Gariguette:Capriss | 0.07 |
| Gariguette:Darselect | 0.08 |
| Gariguette:Cir107 | 0.52 |
| Ciflorette:Clery | 0.89 |
| Ciflorette:Capriss | 0.04 |
| Ciflorette:Darselect | 0.10 |
| Ciflorette:Cir107 | 0.33 |
| Clery:Capriss | 0.07 |
| Clery:Darselect | 0.07 |
| Clery:Cir107 | 0.52 |
| Capriss:Darselect | 0.00 |
| Capriss:Cir107 | 0.22 |
| Darselect:Cir107 | 0.01 |