

# Architecture\_analysis

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## 1 Requierevements

### 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")
install.packages("tinytex")
install.packages("dplyr")
#install.packages("RCurl")
```

### 1.2 Packages loading

```
library(plyr)
library(ggplot2)
library(gtable)
library(grid)
library(cowplot)
library(reshape2)
library(scales)
library(knitr)
library(tinytex)
```

```
library(dplyr)
#library(RCurl)
library(rmarkdown)
```

## 1.3 Functions importing

```
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 January, 3: mid February, 4: early March, 5: early April, 6: end May/early June) VARIABLE 15 : INT # plant. plant index

```
DataSet <- read.csv(
  "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 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),
                      labels = c("Gariguetete", "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", "E

                  )

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_Flor
```

```
#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)

```

### 3 Exploratory analysis

#### 3.1 At module scale

**\*\* \* Extraction of data at module scale \*\***

```

data_at_module_scale<-ddply(.data = dat,
  .variables = c("genotype","Index"),
  summarise,
  MeanTotalLeave= round(x = mean(x = nb_total_leaves,
                                na.rm = T),
                        digits = 0),
  SdTotalLeave= sd(x = nb_total_leaves,
                  na.rm = T),
  MeanTotalFlower= round(mean(x = nb_total_flowers,
                              na.rm = T),
                          digits = 0),
  SdTotalFlower= sd(x = nb_total_flowers,
                    na.rm = T),
  MeanStolon= round(mean(x = stolons,
                         na.rm = T),
                     digits = 0),
  SdStolon= sd(x = stolons,
               na.rm = T),
  N=length(nb_total_leaves))

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

```

Table 1: Data at module scale

genotype	Index	MeanTotalLeave	SdTotalLeave	MeanTotalFlower	SdTotalFlower	MeanStolon	SdStolon	N
Gariguet	0	10	2.3520513	14	8.690441	1	0.7523548	54
Gariguet	1	3	1.2818355	7	4.365022	0	0.0000000	94
Gariguet	2	4	1.5464772	4	3.869534	0	0.6455314	62
Gariguet	3	3	0.5117663	4	3.269629	0	0.5606119	21
Gariguet	4	3	0.4409586	5	1.166667	1	0.7817360	9
Gariguet	5	3	NA	7	NA	2	NA	1
Ciflorette	0	8	2.5719554	8	5.392751	1	0.9569708	54
Ciflorette	1	3	0.8956203	6	3.076745	0	0.0000000	115
Ciflorette	2	4	1.0108469	3	3.215120	0	0.0000000	78
Ciflorette	3	3	0.6290460	5	2.495157	1	0.8462441	31
Ciflorette	4	4	1.5434873	5	3.041381	2	0.7812132	17
Ciflorette	5	5	2.3094011	3	5.196152	1	0.5773503	3
Clery	0	8	2.9652070	10	6.909543	2	1.2462382	54
Clery	1	3	1.0363172	4	3.430427	0	0.1010153	98
Clery	2	3	0.7792759	2	2.378862	0	0.3461440	63
Clery	3	3	0.6485965	3	2.321718	0	0.6969503	34
Clery	4	3	0.7703289	2	2.139375	1	0.6992932	14
Capriss	0	10	1.8239229	9	5.912624	2	0.9705661	54
Capriss	1	3	1.0404784	3	2.321914	0	0.0000000	190
Capriss	2	4	0.9443864	1	1.983821	0	0.0990148	102
Capriss	3	3	0.7063460	2	1.709556	0	0.4016097	31
Capriss	4	2	1.0000000	1	1.154700	0	0.5000000	4
Darselect	0	6	2.2875105	7	6.271880	1	1.1060156	54
Darselect	1	3	1.0764669	5	4.455098	0	0.1072113	87
Darselect	2	3	0.9597149	4	2.263362	0	0.3422980	57
Darselect	3	3	0.6803587	3	2.593462	0	0.4845800	39
Darselect	4	3	2.0701967	3	2.121320	1	1.0606602	8
Darselect	5	2	NA	5	NA	1	NA	1
Cir107	0	10	3.2868882	10	8.522261	2	1.3282134	54
Cir107	1	4	1.6110796	6	5.063588	0	0.2543235	154
Cir107	2	3	0.9382965	3	3.698939	0	0.0000000	110
Cir107	3	3	0.7079686	4	2.880760	0	0.5587442	41
Cir107	4	4	2.1001701	4	2.531939	1	0.7559289	8

### 3.1.1 Number of Module for successive orders

```

tab1<- fc_dist_module_by_order(data = dat)
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
Gariguet	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

### 3.1.2 Occurrence of the higher order along time

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

Table 3: Module order frequency distribution for successive date

	Mid-December	Early-January	Mid-February	Early-March	Early-April	Early-June	Frequency
0	9	9	9	9	9	9	54
1	0	7	24	17	26	20	94
2	0	0	0	11	28	23	62
3	0	0	0	1	3	17	21
4	0	0	0	0	0	9	9
5	0	0	0	0	0	1	1
Frequency	9	16	33	38	66	79	241