Architecture\_analysis

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# Requierements

## 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")

## 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)

## Functions importing

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

# Import and transformation of dataset

## 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(  
 "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)]

## 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 ...

## 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)

## 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("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","Early-June")  
 )  
  
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\_Floral\_bud","Terminal\_Inflorescence"))

#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)

# Exploratory analysis

## 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")

Data at module scale

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| genotype | Index | MeanTotalLeave | SdTotalLeave | MeanTotalFlower | SdTotalFlower | MeanStolon | SdStolon | N |
| Gariguette | 0 | 10 | 2.3520513 | 14 | 8.690441 | 1 | 0.7523548 | 54 |
| Gariguette | 1 | 3 | 1.2818355 | 7 | 4.365022 | 0 | 0.0000000 | 94 |
| Gariguette | 2 | 4 | 1.5464772 | 4 | 3.869534 | 0 | 0.6455314 | 62 |
| Gariguette | 3 | 3 | 0.5117663 | 4 | 3.269629 | 0 | 0.5606119 | 21 |
| Gariguette | 4 | 3 | 0.4409586 | 5 | 1.166667 | 1 | 0.7817360 | 9 |
| Gariguette | 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 |

### 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 "  
 )

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 |

### Occurence 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)

Module order frequency distribution for successive date

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Mid-December | Early-Junuary | 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 |