ALSIA Data Analysis Timepoints

Elise

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Set the right working directory.

```
rm(list = ls())

setwd("C:/Users/elise/Documents/Mémoire/Main/Data/Templates/ALSIA")
platform <- "ALSIA"
```

Data importation

Reimport the data sets extracted from the Data Preparation and Data Analysis R Markdown.

```
list.files()
```

```
## [1] "endpoint.txt"     "plant_info.txt"   "S_timeseries.txt" "T_timeseries.txt"
## [5] "timeseries.txt"
```

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

# plant_info
plant_info <- lapply(plant_info, factor)

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

# timeseries
# No data for ALSIA

# S_timeseries
matching_cols <- intersect(names(S_timeseries), names(plant_info))
S_timeseries[, matching_cols] <- lapply(S_timeseries[, matching_cols], factor)
S_timeseries$Timestamp <- as.POSIXct(S_timeseries$Timestamp, format = "%Y-%m-%d %H:%M:%
S")
S_timeseries$Date <- date(S_timeseries$Date)

# T_timeseries
# No data

platform <- "ALSIA"

# endpoint
df <- endpoint[,colSums(is.na(endpoint))<nrow(endpoint)]
genotype_index <- which(colnames(df) == "Genotype")
variables <- c("FW_shoot_g", "Plant_height_cm")

# timeseries
# no data

# S_timeseries
df_S_timeseries <- S_timeseries[,colSums(is.na(S_timeseries))<nrow(S_timeseries)]
genotype_index <- which(colnames(df_S_timeseries) == "Genotype")
variables_S <- colnames(df_S_timeseries[, c(5:(genotype_index - 1))]) # We remove the t
hree first columns that are "Unit.ID","Time" and "Date"

# T_timeseries
# no data

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

```
## [1] "ALSIA : The variables for endpoint are FW_shoot_g, Plant_height_cm"
```

```
print(paste(platform, ": The variables for S_timeseries are", paste(variables_S, collap
se = ", "), sep = " "))
```

```
## [1] "ALSIA : The variables for S_timeseries are S_Height_cm, S_Area_cmsquared, S_Con
vex_hull_area_cmsquared, S_Solidity, S_Leaf_area_cmsquared"
```

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

Get the cleaned endpoint data

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



# We add a Plant_type variable that is H or L, with T being L
S_timeseries$Plant_type <- substr(S_timeseries$Genotype, nchar(as.character(S_timeserie
s$Genotype)), nchar(as.character(S_timeseries$Genotype)))

S_timeseries$Plant_type <- ifelse(S_timeseries$Plant_type %in% c("T", "L"), "Line",
                                  ifelse(S_timeseries$Plant_type == "H", "Hybrid", S_ti
meseries$Plant_type))
```

Time point objects

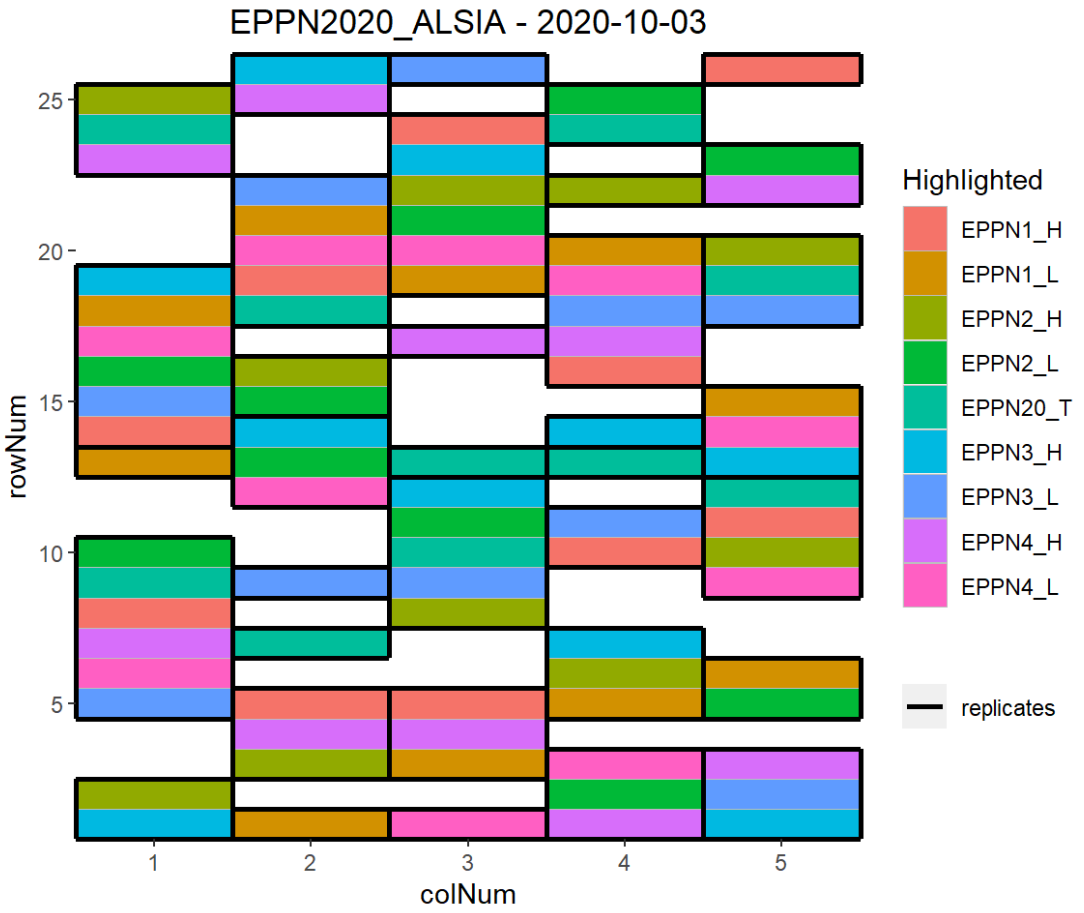
Generation of the timePoints objects using the function “createTimePoints”.

```
timePoint_endpoint <- createTimePoints(dat = endpoint,
                                       experimentName = "EPPN2020_ALSIA",
                                       genotype = "Genotype",
                                       timePoint = "Date",
                                       plotId = "Unit.ID",
                                       rowNum = "Row",
                                       colNum = "Column",
                                       repId = "Replication")

timePoint_endpoint_clean <- createTimePoints(dat = endpoint_clean,
                                       experimentName = "EPPN2020_ALSIA",
                                       genotype = "Genotype",
                                       timePoint = "Date",
                                       plotId = "Unit.ID",
                                       rowNum = "Row",
                                       colNum = "Column",
                                       repId = "Replication")

timePoint_S <- createTimePoints(dat = S_timeseries,
                                experimentName = "EPPN2020_ALSIA",
                                genotype = "Genotype",
                                timePoint = "Date",
                                plotId = "Unit.ID",
                                rowNum = "Row",
                                colNum = "Column",
                                repId = "Replication",
                                addCheck = TRUE,
                                checkGenotypes = "EPPN20_T")
```

Gentoypic layout

Check the layout of the platforms' genotypes.

```
genotypes_list <- as.character(unique(endpoint$Genotype))

plot(timePoint_endpoint,
     plotType = "layout",
     highlight =  genotypes_list,
     showGeno = FALSE)
```



1. endpoint

Comparisons between raw and cleaned data

View timePoint object.

```
summary(timePoint_endpoint)
```

```
## timePoint_endpoint contains data for experiment EPPN2020_ALSIA.
##
## It contains 1 time points.
## First time point: 2020-10-03
## Last time point: 2020-10-03
##
## No check genotypes are defined.
```

```
getTimePoints(timePoint_endpoint)
```

```
##   timeNumber  timePoint
## 1          1 2020-10-03
```

Count the number of observations per trait.

```
traits <- variables

for (trait_name in traits) {
  print(paste("How many data observations for", trait_name))
  num_observations <- countValid(timePoint_endpoint, trait_name)
  print(num_observations)
}
```

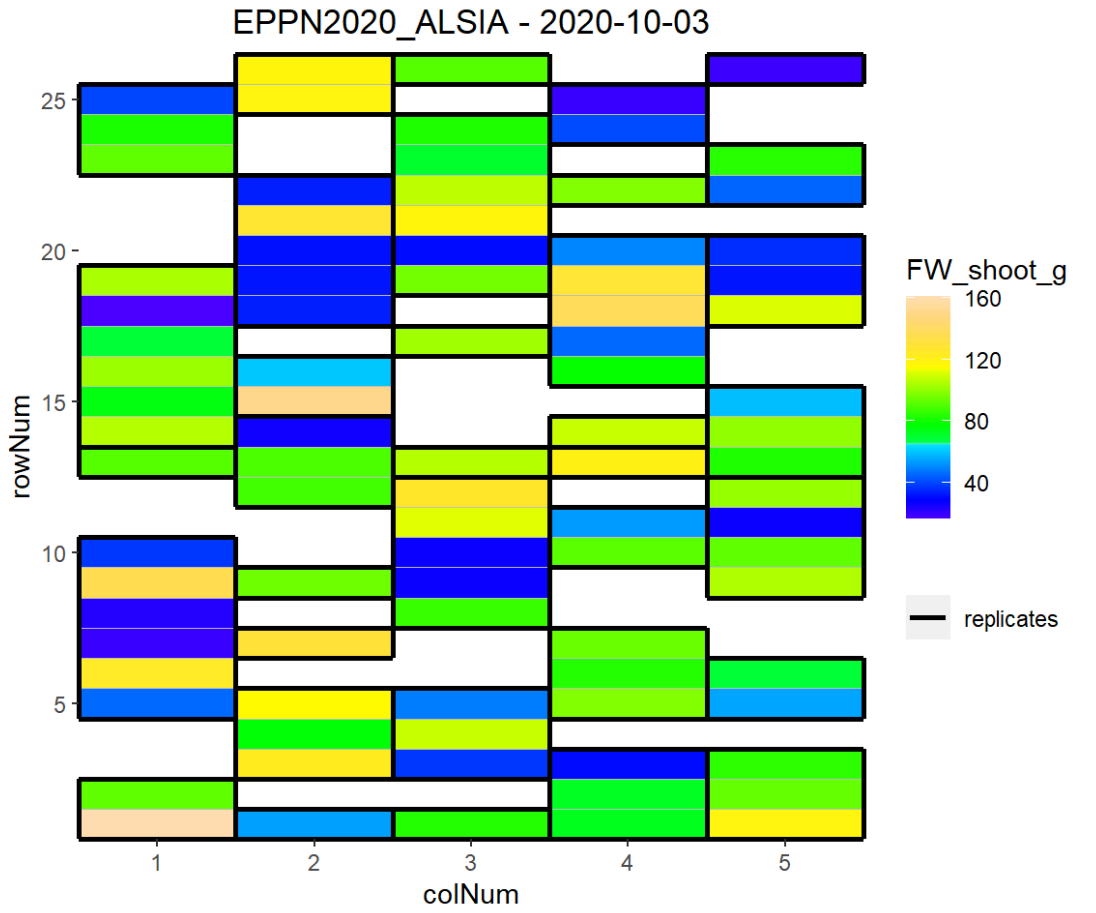
```
## [1] "How many data observations for FW_shoot_g"
## 2020-10-03
##         90
## [1] "How many data observations for Plant_height_cm"
## 2020-10-03
##         90
```

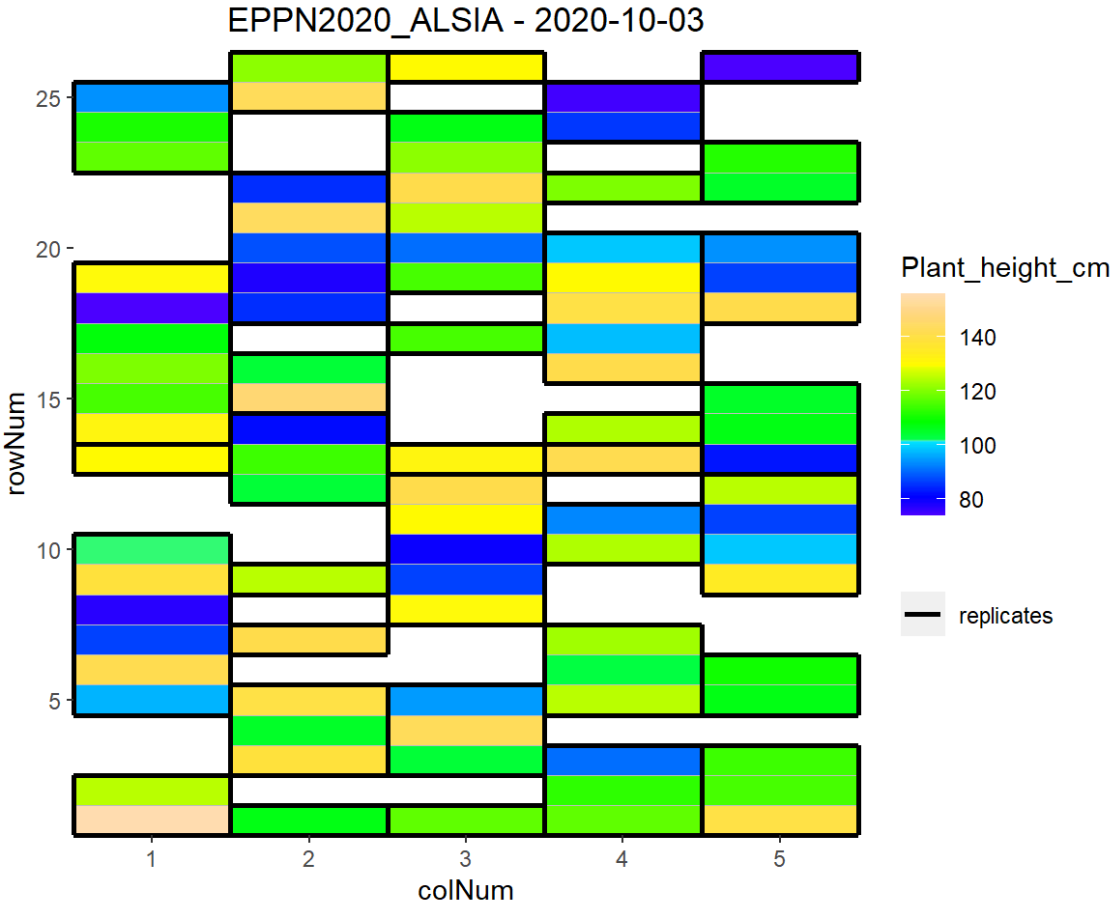
```
for (trait_name in traits) {
  print(paste("How many cleaned data observations for", trait_name))
  num_observations <- countValid(timePoint_endpoint_clean, trait_name)
  print(num_observations)
}
```

```
## [1] "How many cleaned data observations for FW_shoot_g"
## 2020-10-03
##         89
## [1] "How many cleaned data observations for Plant_height_cm"
## 2020-10-03
##         84
```

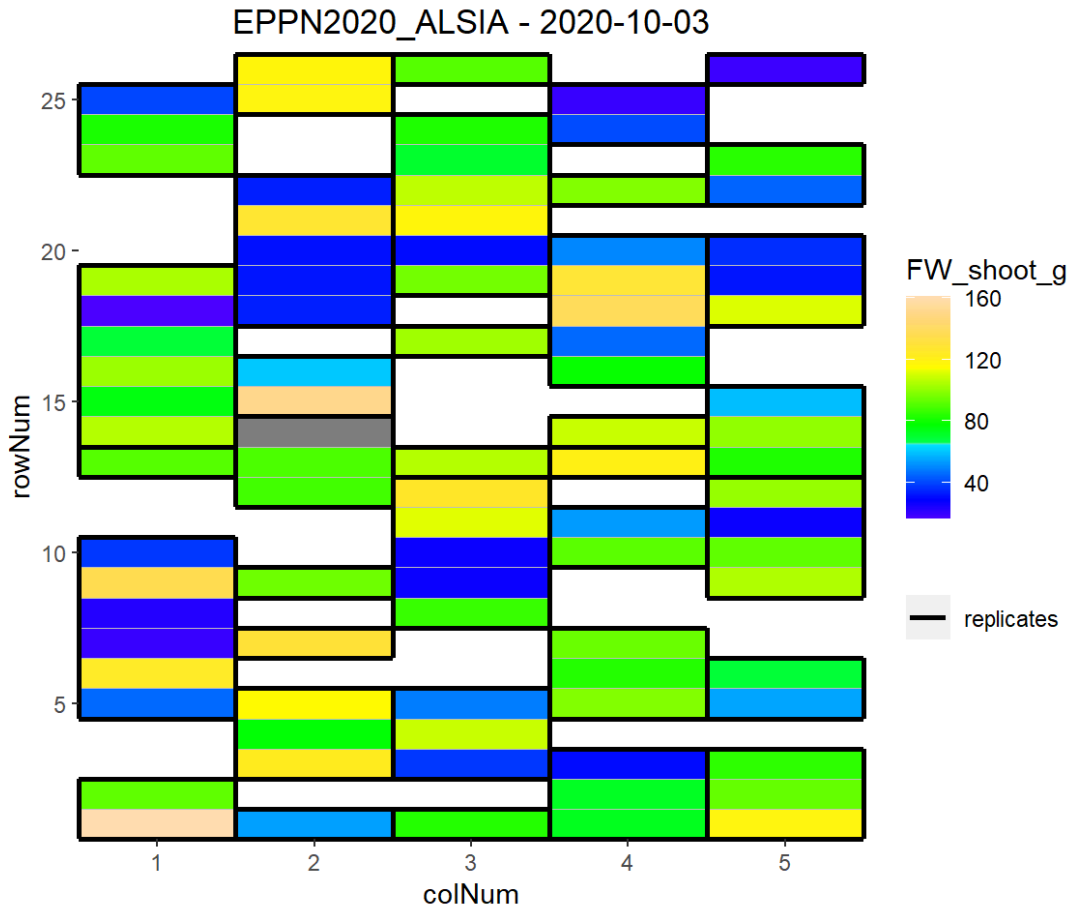
Check the heatmap of the data at harvest

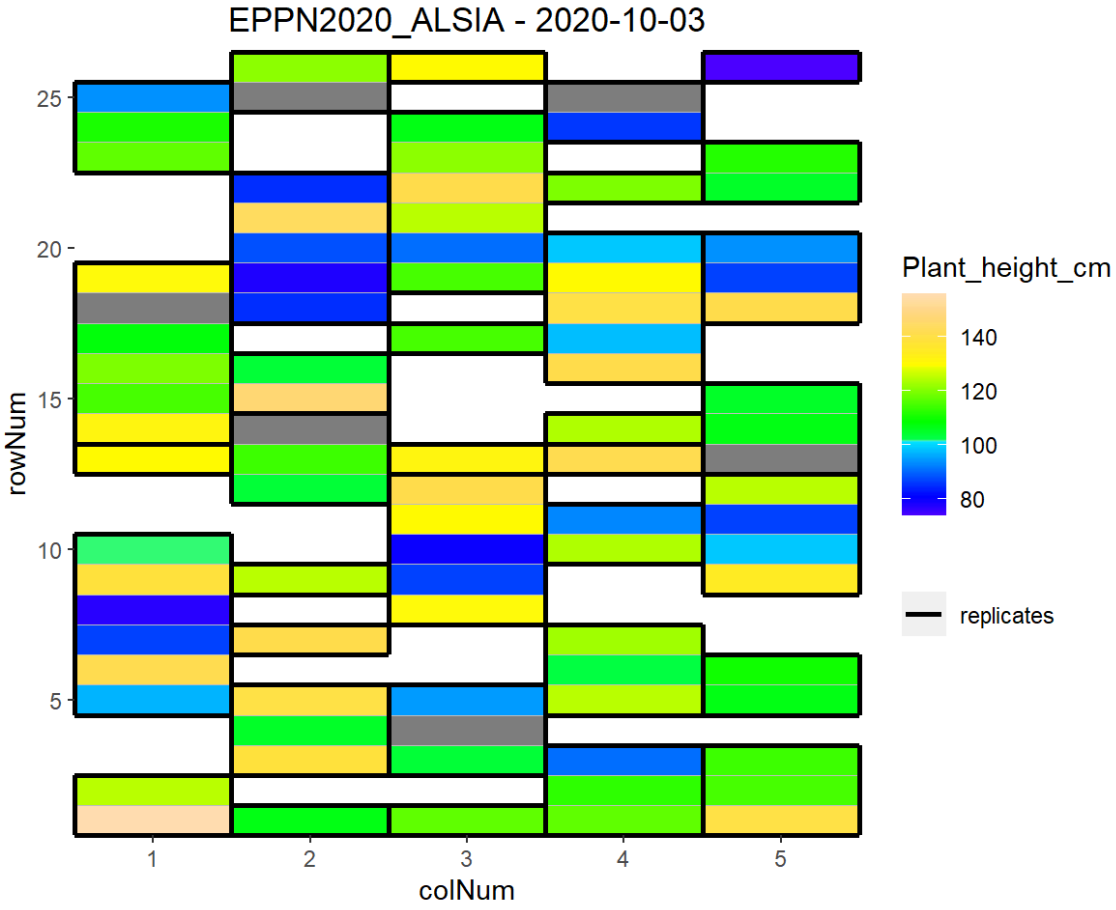
```
for (trait_name in traits) {
  plot(timePoint_endpoint,
     plotType = "layout",
     timePoints = 1,
     traits = trait_name)
}
```


EPPN2020_ALSIA - 2020-10-03
rowNum
colNum
FW_shoot_g
160
120
80
40
replicates


EPPN2020_ALSIA - 2020-10-03
rowNum
colNum
Plant_height_cm
140
120
100
80
replicates

```
for (trait_name in traits) {
  plot(timePoint_endpoint_clean,
     plotType = "layout",
     timePoints = 1,
     traits = trait_name)
}
```





2. S_timeseries

Raw data

View timePoint object

```
summary(timePoint_S)
```

```
## timePoint_S contains data for experiment EPPN2020_ALSIA.
##
## It contains 11 time points.
## First time point: 2020-09-10
## Last time point: 2020-10-05
##
## The following genotypes are defined as check genotypes: EPPN20_T.
```

```
getTimePoints(timePoint_S)
```

```
##    timeNumber  timePoint
## 1           1 2020-09-10
## 2           2 2020-09-14
## 3           3 2020-09-16
## 4           4 2020-09-18
## 5           5 2020-09-21
## 6           6 2020-09-23
## 7           7 2020-09-25
## 8           8 2020-09-28
## 9           9 2020-09-30
## 10         10 2020-10-02
## 11         11 2020-10-05
```

```
num_timepoints <- getTimePoints(timePoint_S)
```

Count the number of observations per trait and time point

We focus on the Height [cm] and Leaf area, because these are the two most common among the platforms.

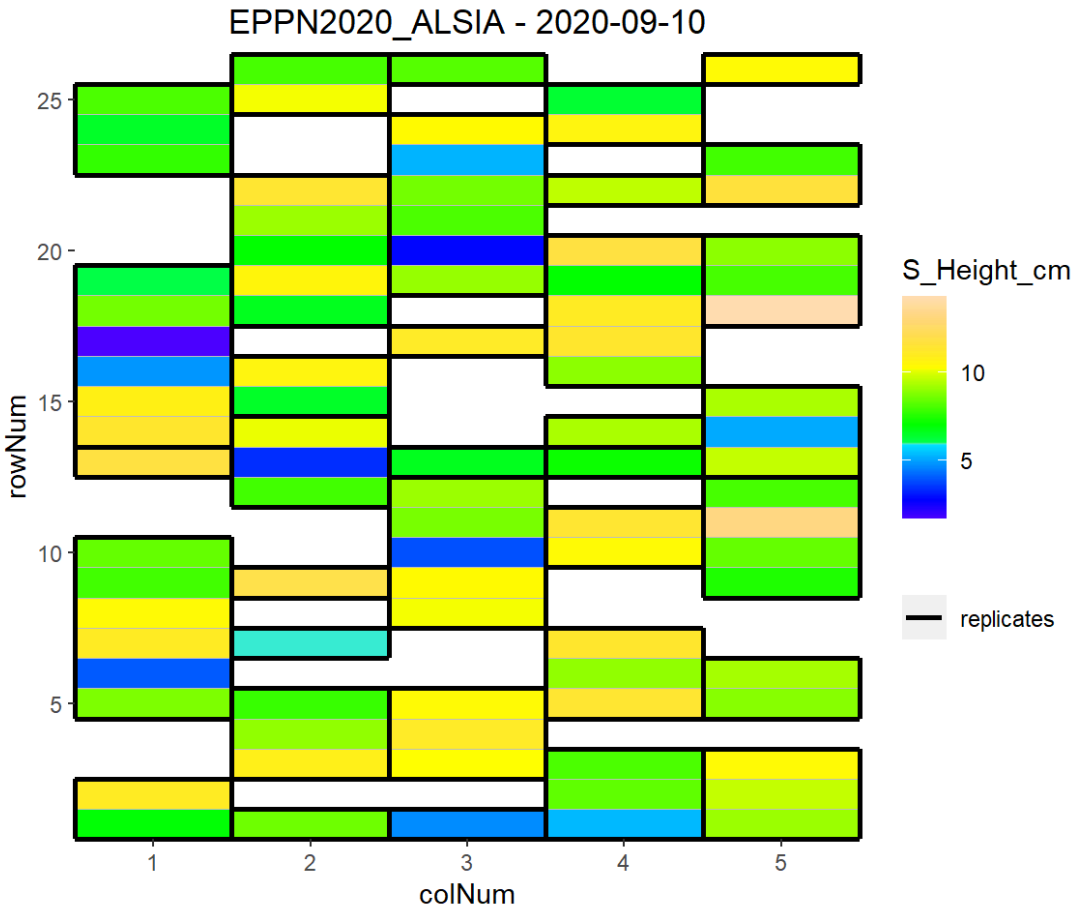
Height is computed for 6 platforms out of 9 and area for 4 out of 9.

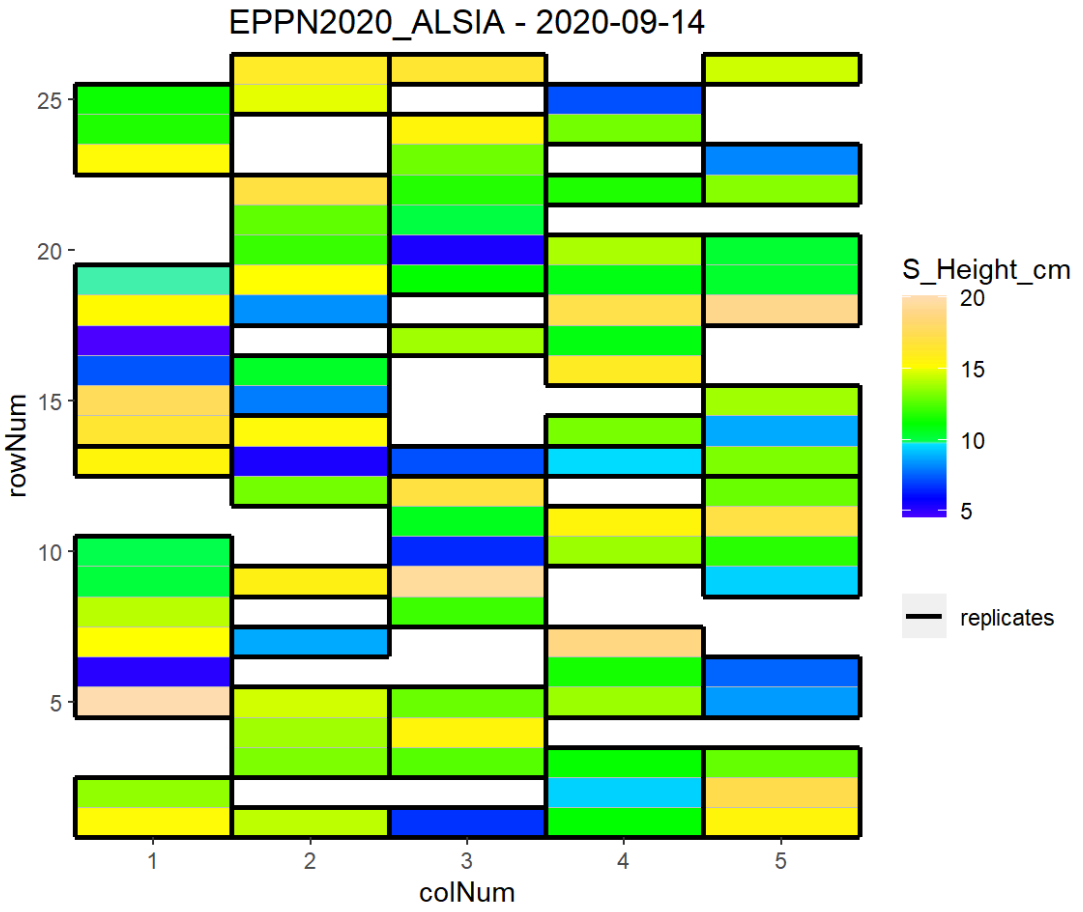
```
var_voulues <- c(variables_S[1], variables_S[5])
traits <- var_voulues

for (trait_name in traits) {
  print(paste("How many observations for", trait_name))
  valid_count <- countValid(timePoint_S, trait_name)
  print(valid_count)
}
```

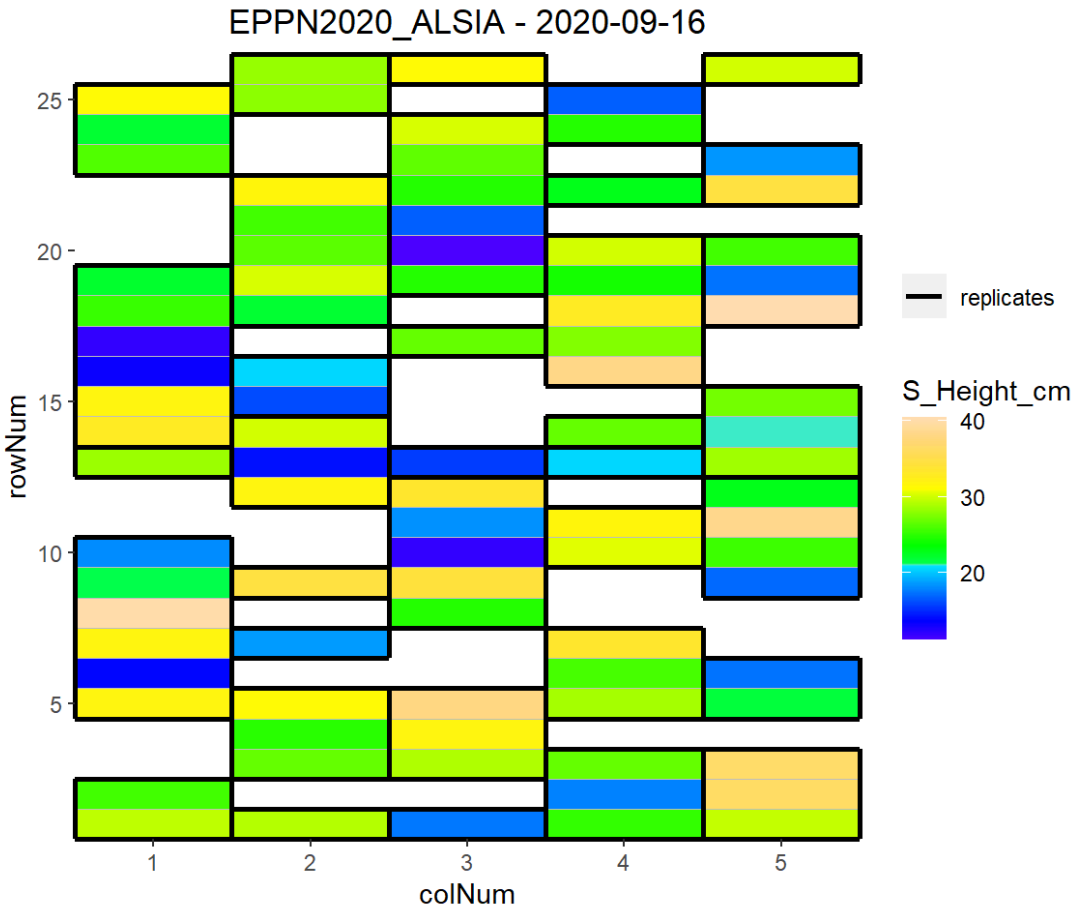
```
## [1] "How many observations for S_Height_cm"
## 2020-09-10 2020-09-14 2020-09-16 2020-09-18 2020-09-21 2020-09-23 2020-09-25
##         90         90         90         90         90         90         90
## 2020-09-28 2020-09-30 2020-10-02 2020-10-05
##         90         90         90         90
## [1] "How many observations for S_Leaf_area_cmsquared"
## 2020-09-10 2020-09-14 2020-09-16 2020-09-18 2020-09-21 2020-09-23 2020-09-25
##         90         90         90         90         90         90         90
## 2020-09-28 2020-09-30 2020-10-02 2020-10-05
##         90         90         90         90
```

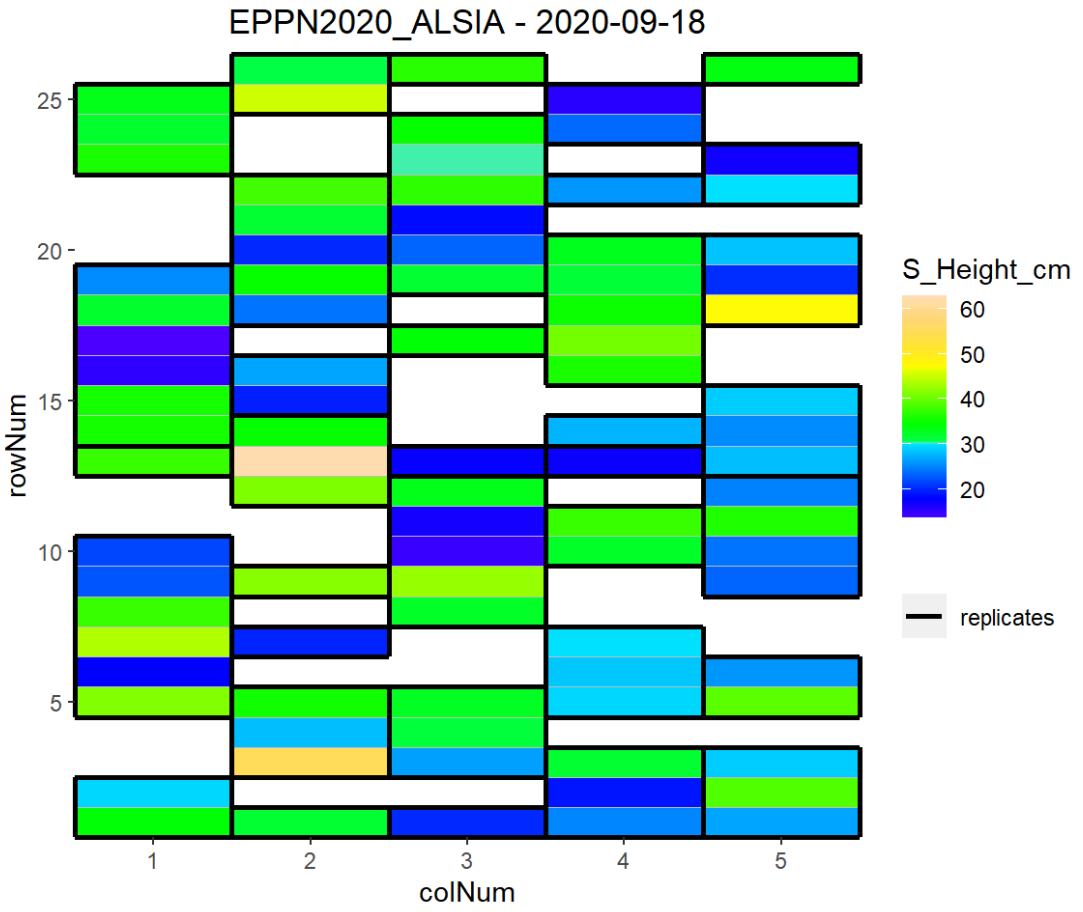
Check the heatmap of the raw data per time point

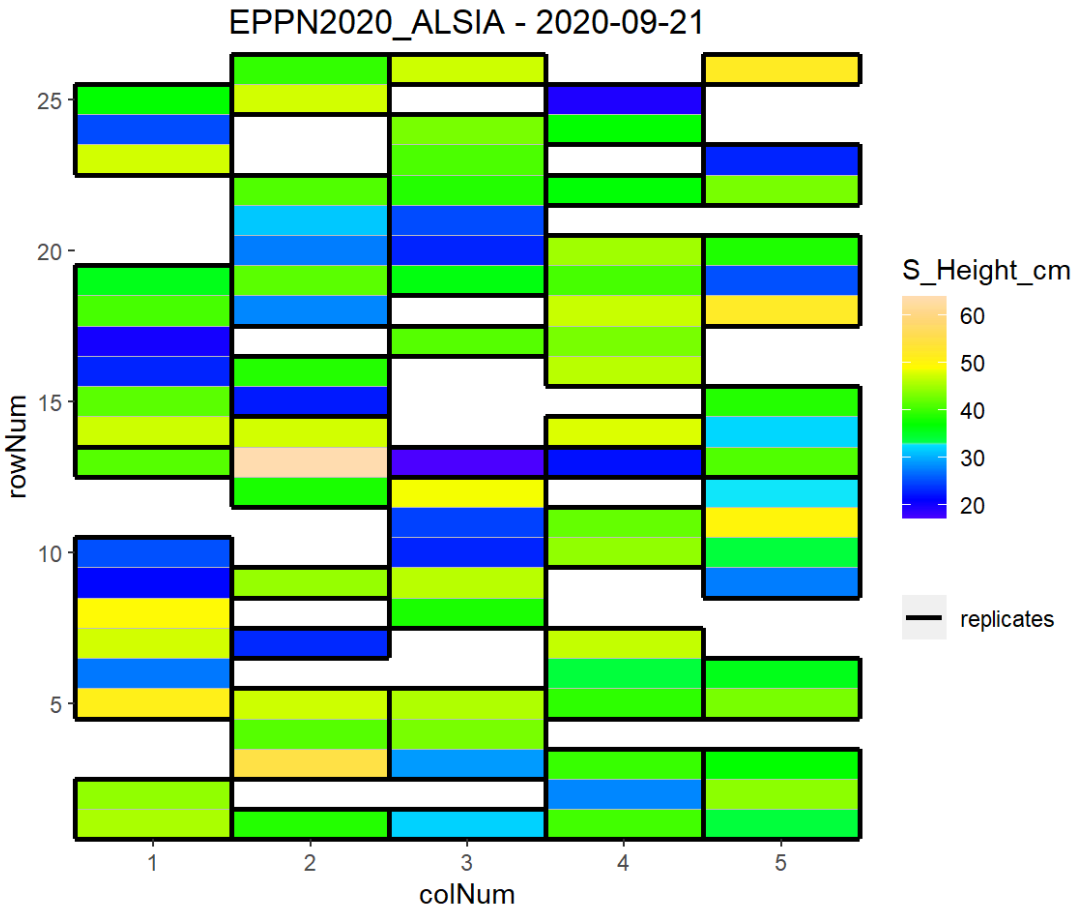
```
for (trait_name in traits) {
  for (tp in 1:length(num_timepoints$timeNumber)) {
    plot(timePoint_S,
         plotType = "layout",
         timePoints = tp,
         traits = trait_name)
  }
}
```

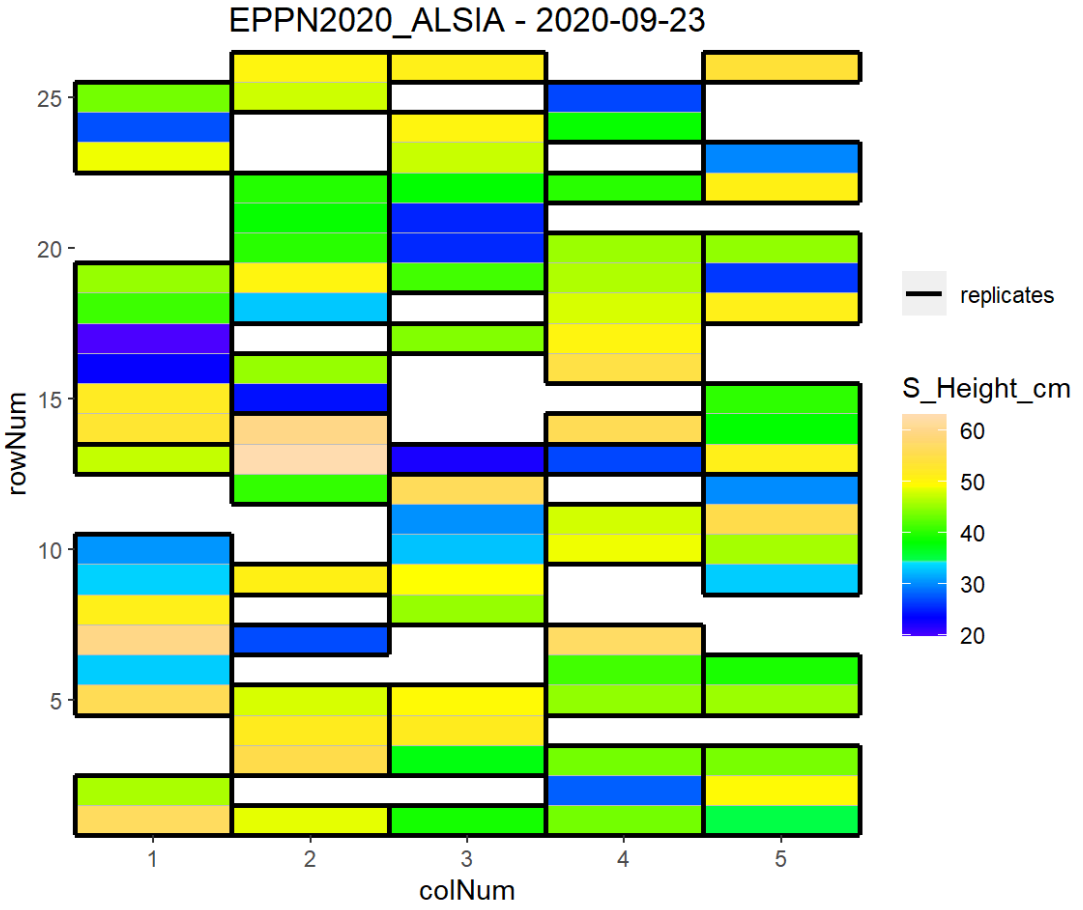

EPPN2020_ALSIA - 2020-09-10
rowNum
colNum
S_Height_cm
10
5
replicates

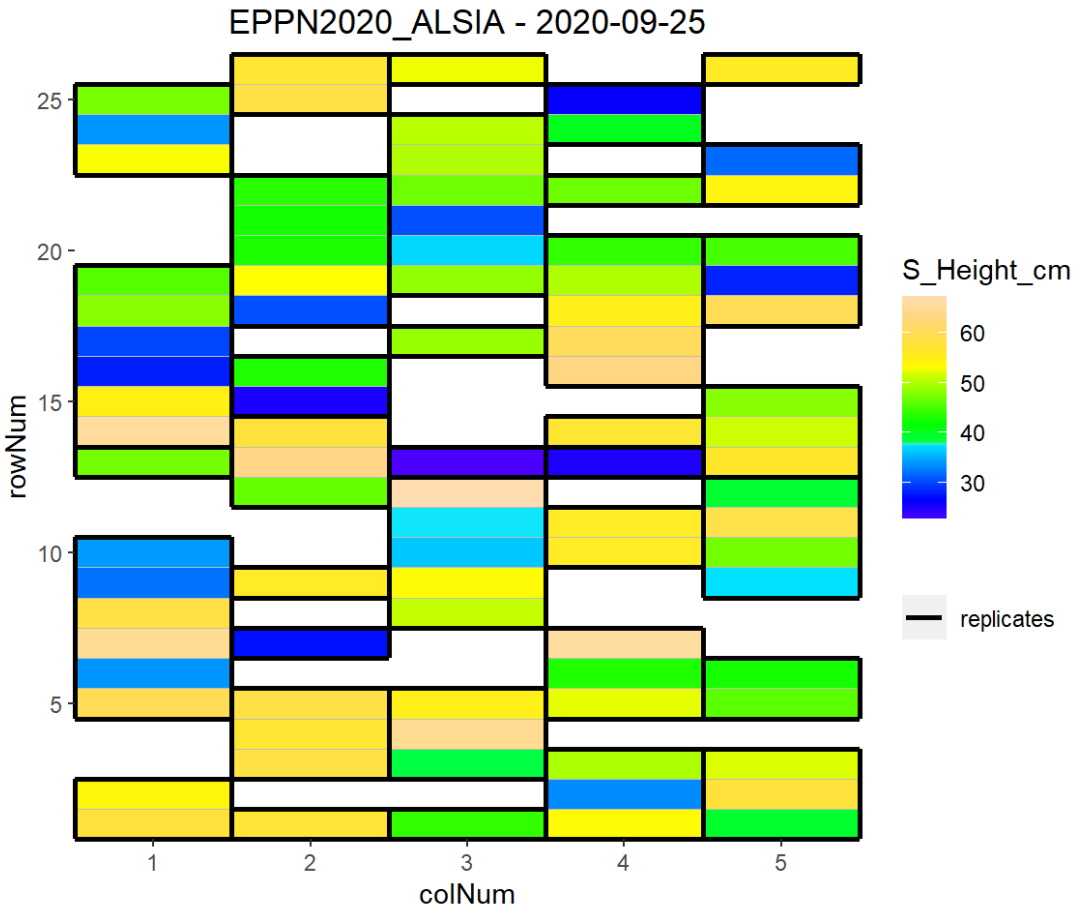

EPPN2020_ALSIA - 2020-09-14
rowNum
colNum
S_Height_cm
20
15
10
5
replicates

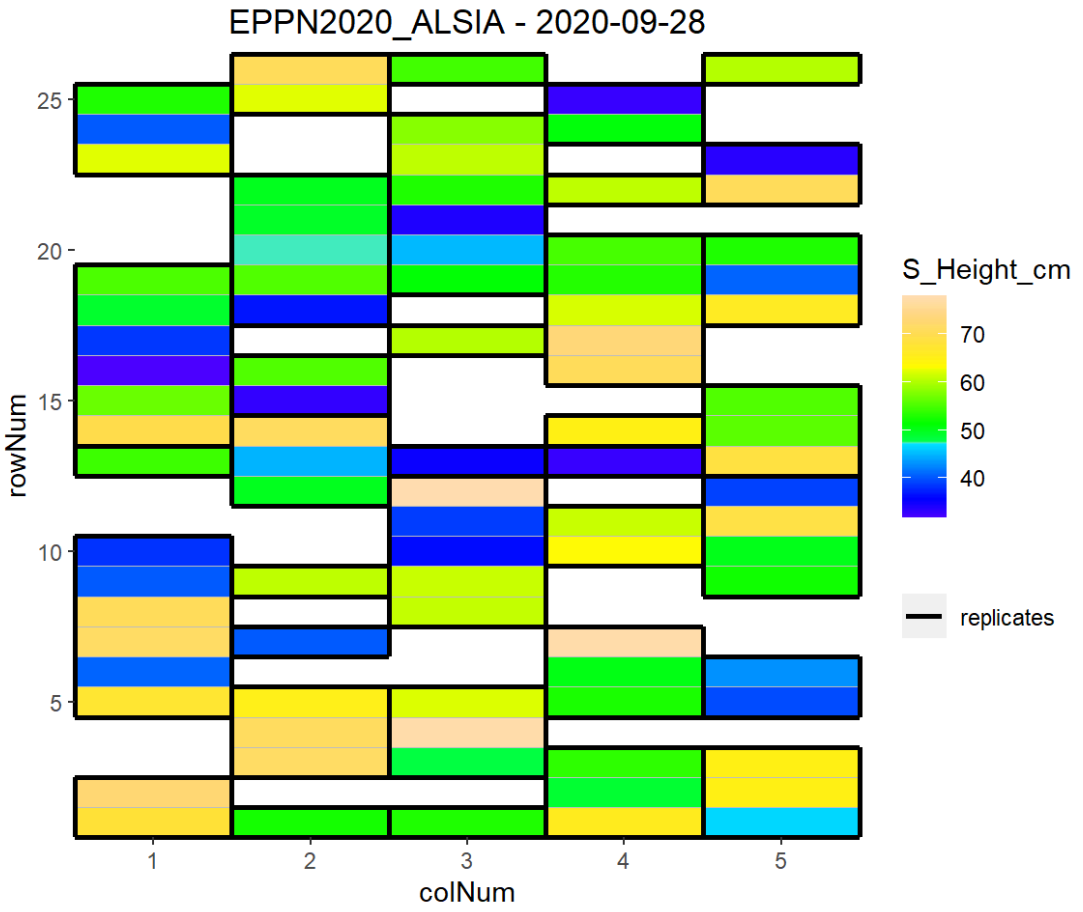

EPPN2020_ALSIA - 2020-09-16
rowNum
colNum
25
20
15
10
5
1
2
3
4
5
replicates
S_Height_cm
40
30
20

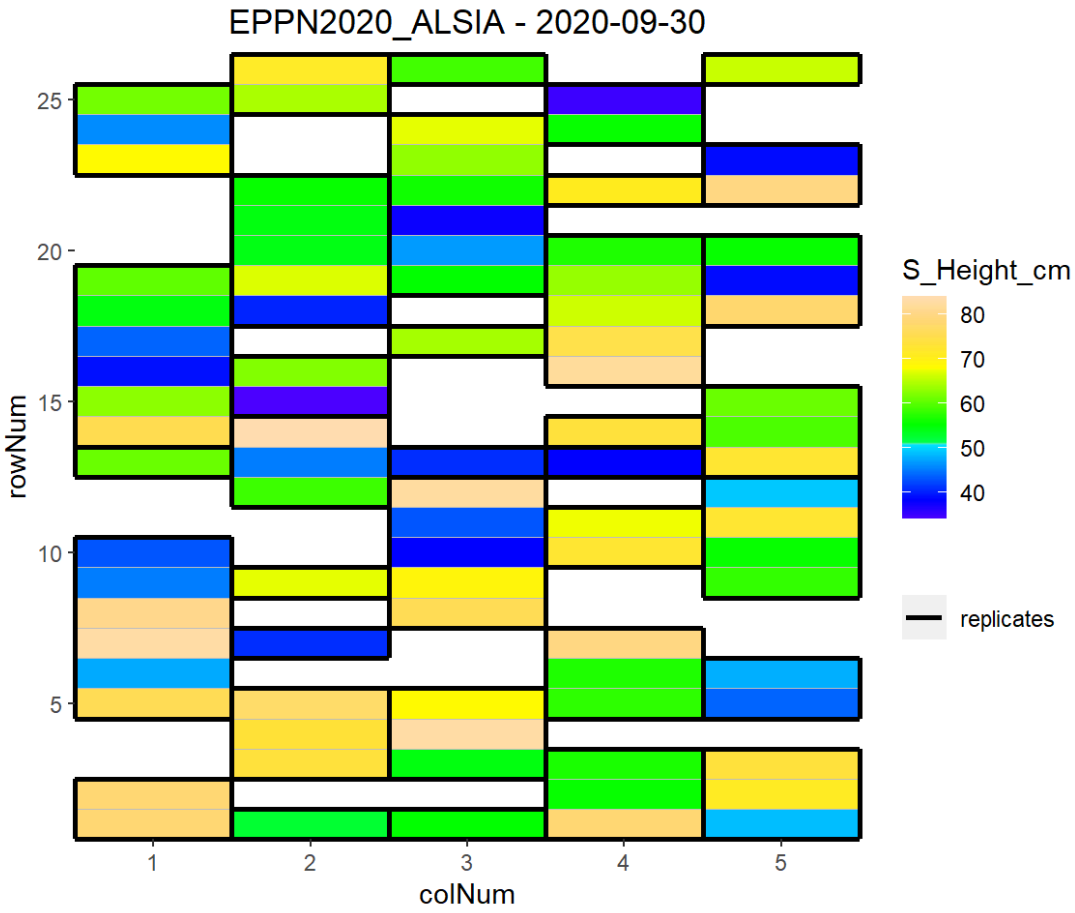

EPPN2020_ALSIA - 2020-09-18
rowNum
colNum
25
20
15
10
5
1
2
3
4
5
S_Height_cm
60
50
40
30
20
replicates

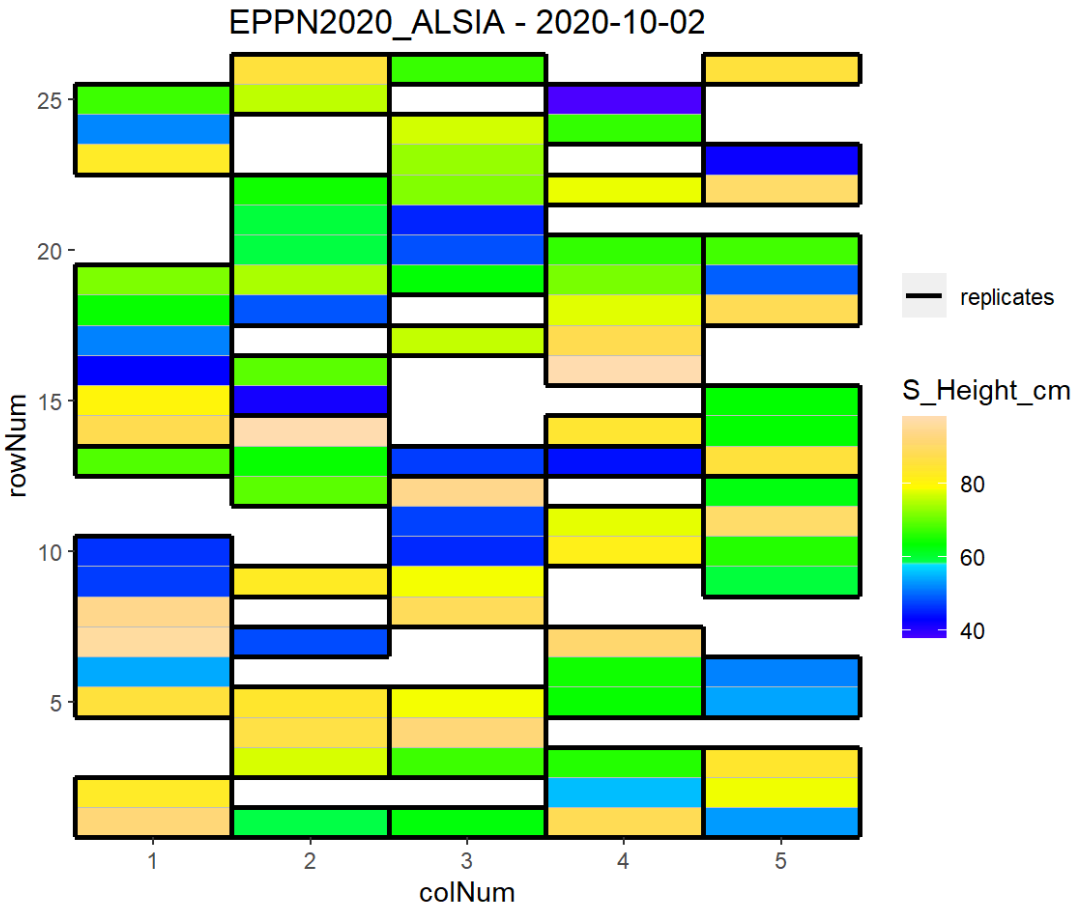

EPPN2020_ALSIA - 2020-09-21
rowNum
colNum
S_Height_cm
60
50
40
30
20
replicates

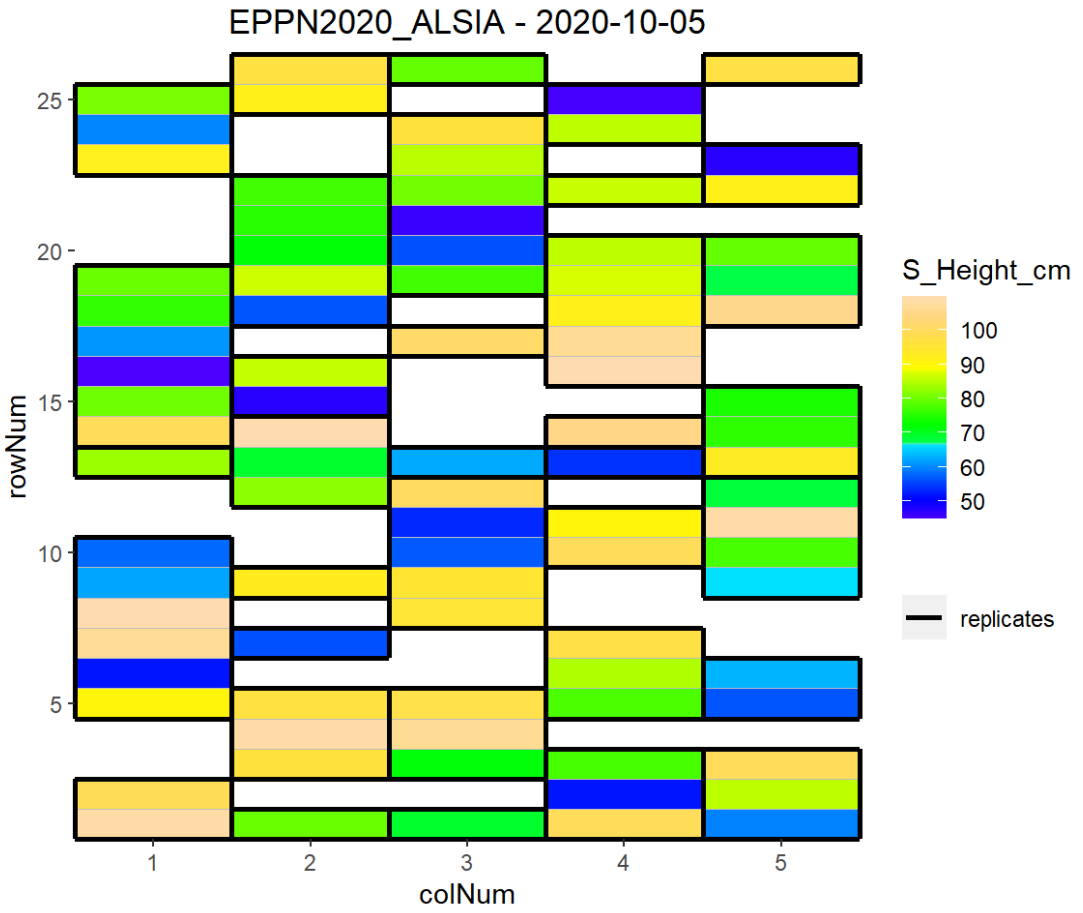

EPPN2020_ALSIA - 2020-09-23
rowNum
colNum
replicates
S_Height_cm
60
50
40
30
20

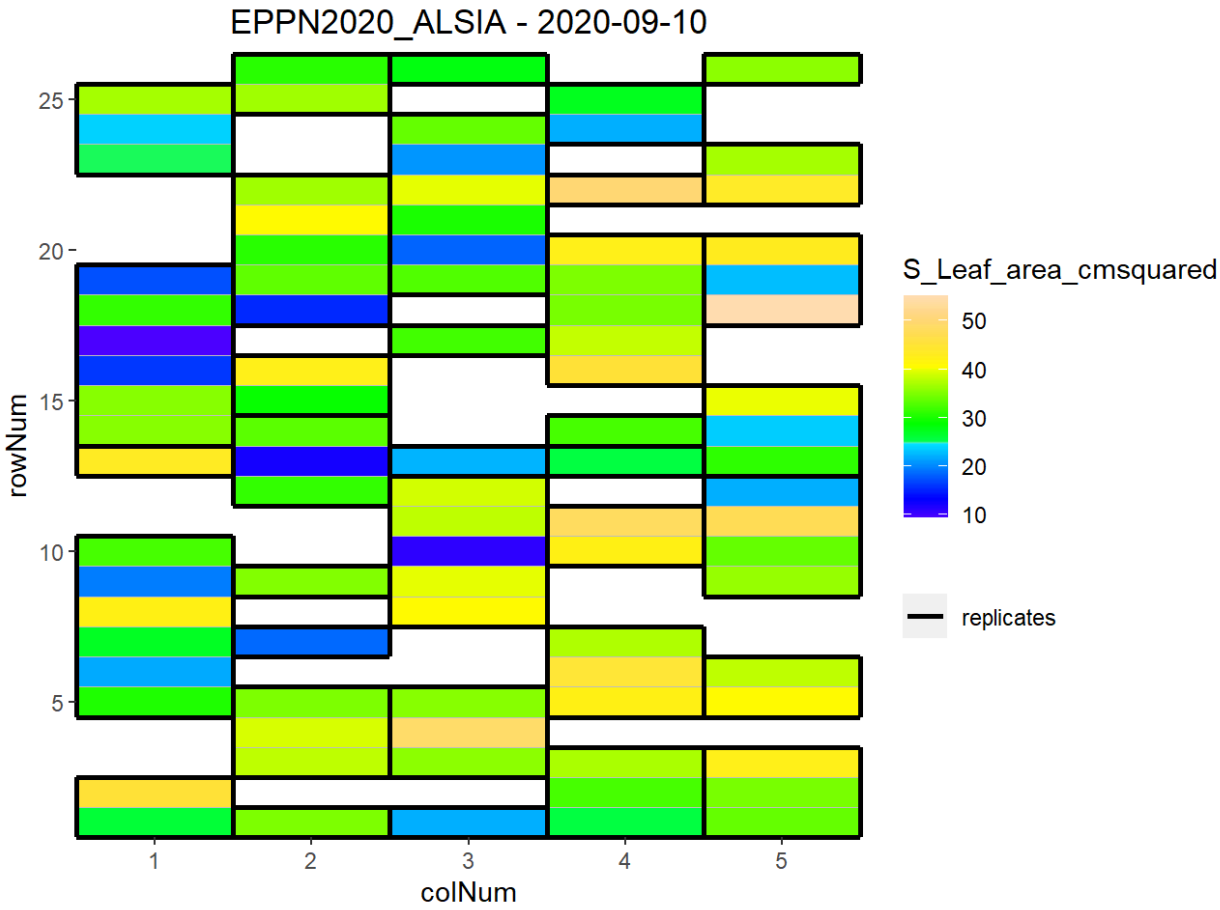

EPPN2020_ALSIA - 2020-09-25
rowNum
colNum
S_Height_cm
60
50
40
30
replicates

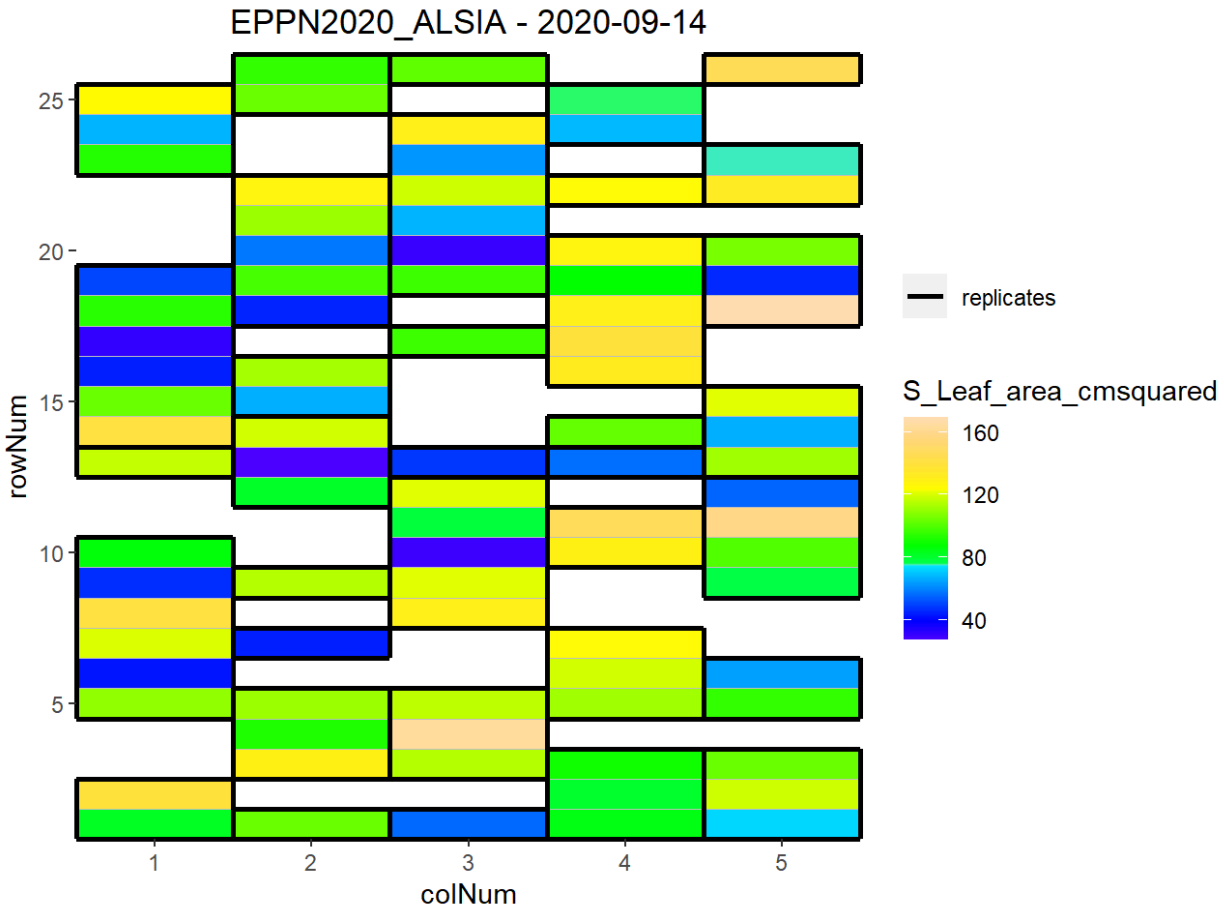

EPPN2020_ALSIA - 2020-09-28
rowNum
colNum
S_Height_cm
70
60
50
40
replicates

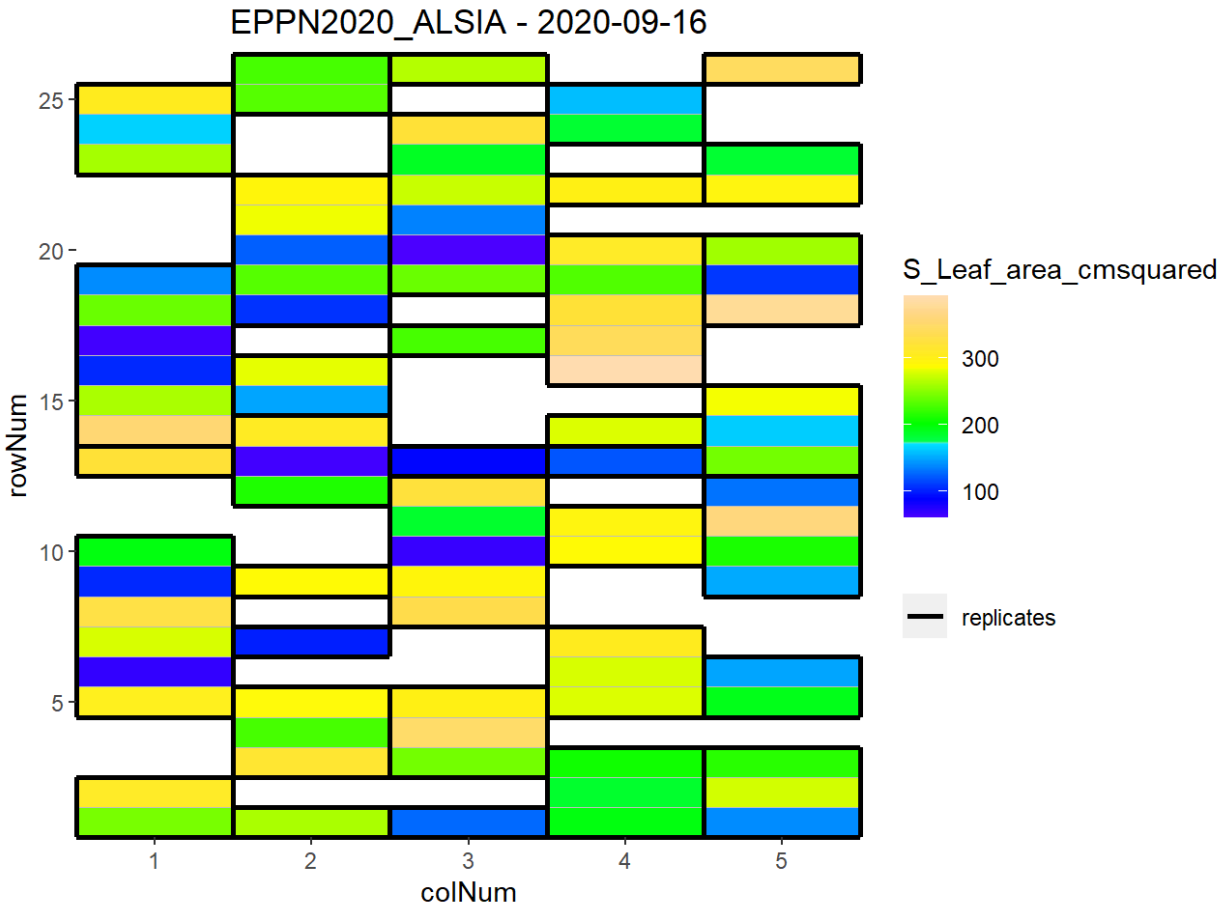

EPPN2020_ALSIA - 2020-09-30
rowNum
colNum
S_Height_cm
80
70
60
50
40
replicates

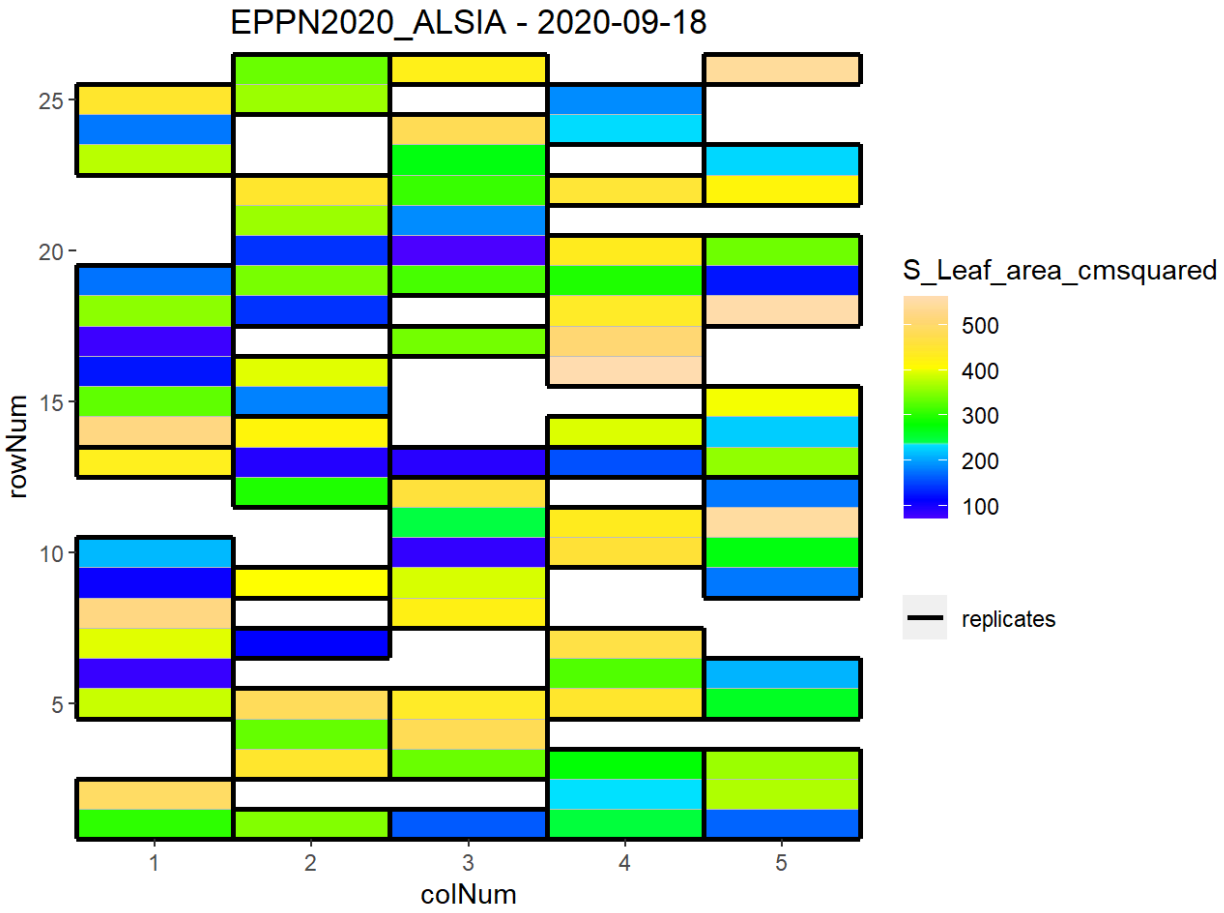

EPPN2020_ALSIA - 2020-10-02
rowNum
colNum
replicates
S_Height_cm
80
60
40

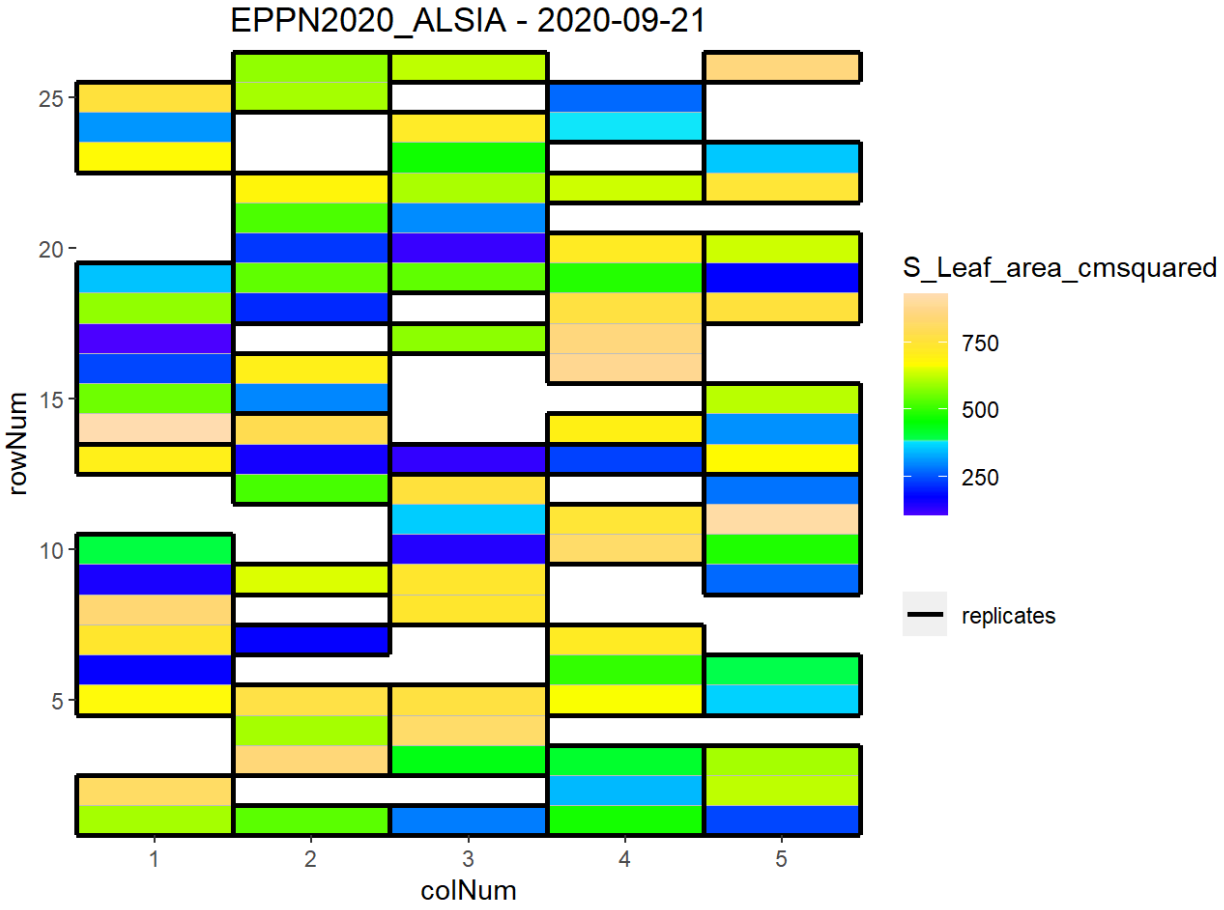

EPPN2020_ALSIA - 2020-10-05
rowNum
colNum
S_Height_cm
100
90
80
70
60
50
replicates

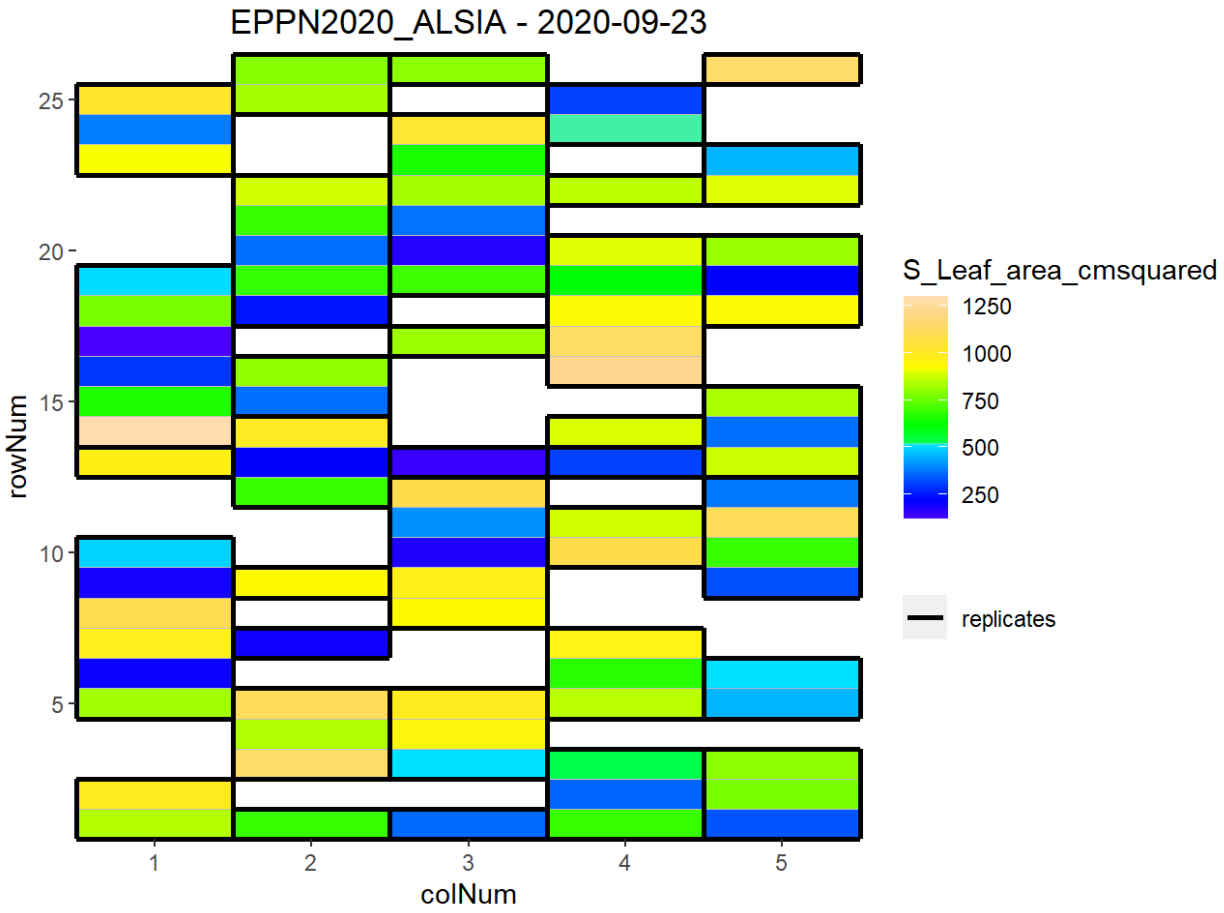

EPPN2020_ALSIA - 2020-09-10
rowNum
colNum
S_Leaf_area_cmsquared
50
40
30
20
10
replicates

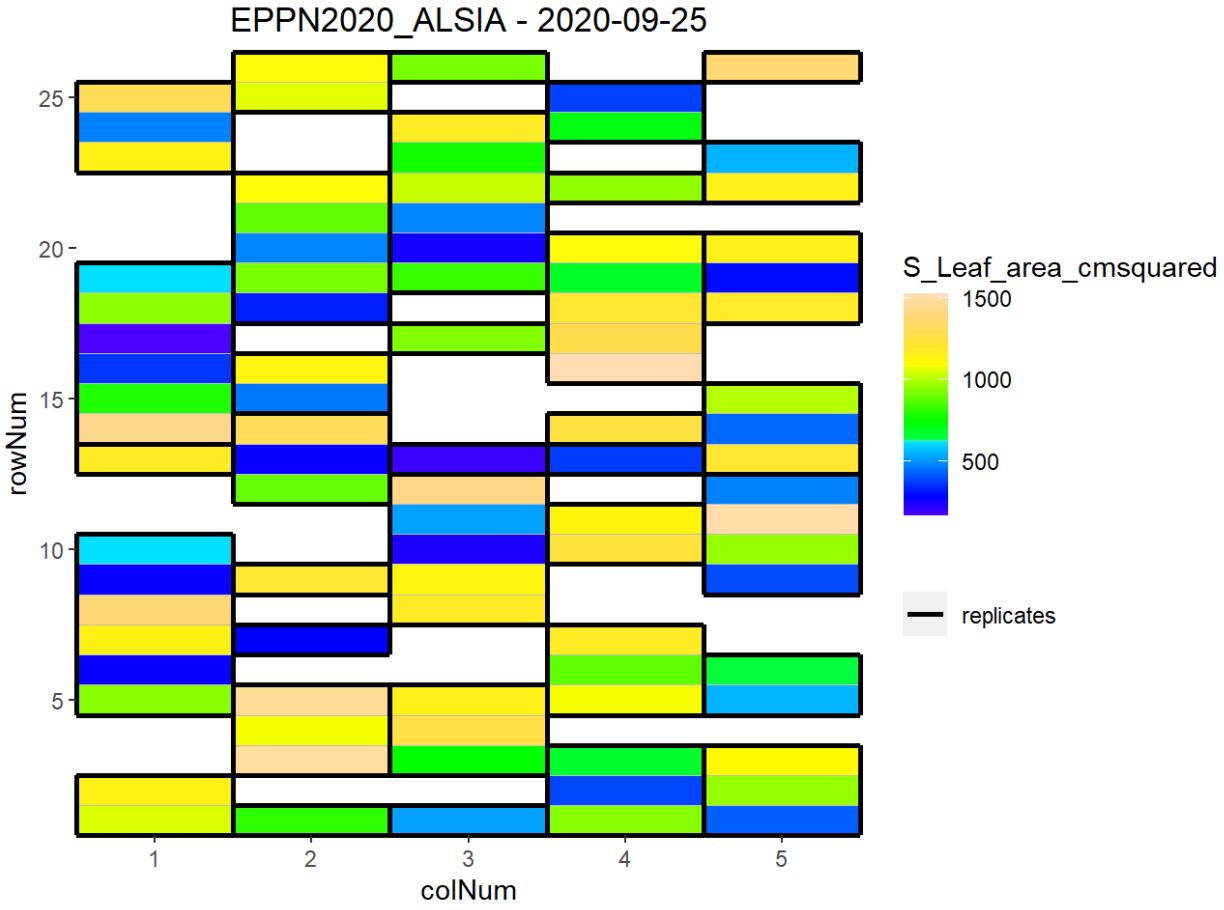

EPPN2020_ALSIA - 2020-09-14
rowNum
colNum
25
20
15
10
5
1
2
3
4
5
replicates
S_Leaf_area_cmsquared
160
120
80
40

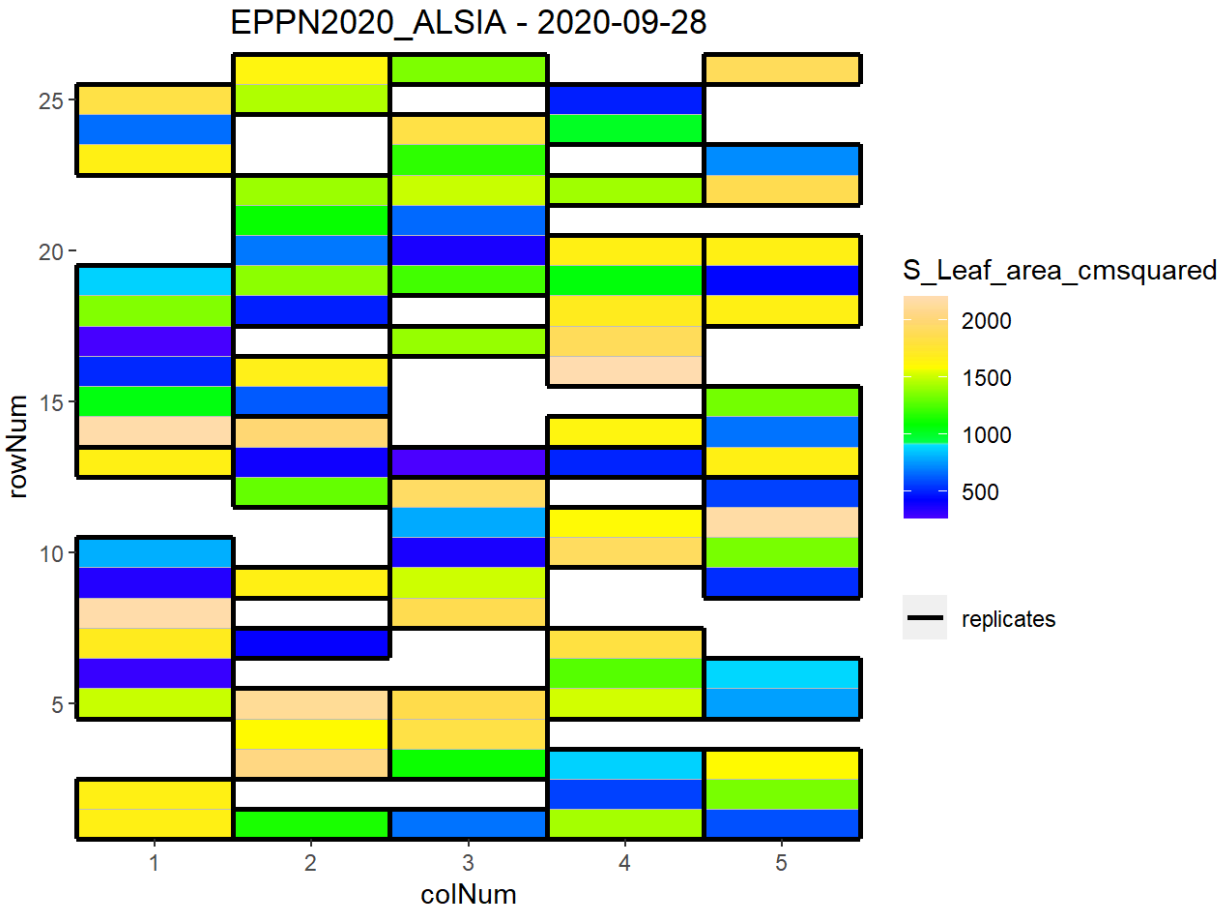

EPPN2020_ALSIA - 2020-09-16
rowNum
colNum
25
20
15
10
5
1
2
3
4
5
S_Leaf_area_cmsquared
300
200
100
replicates

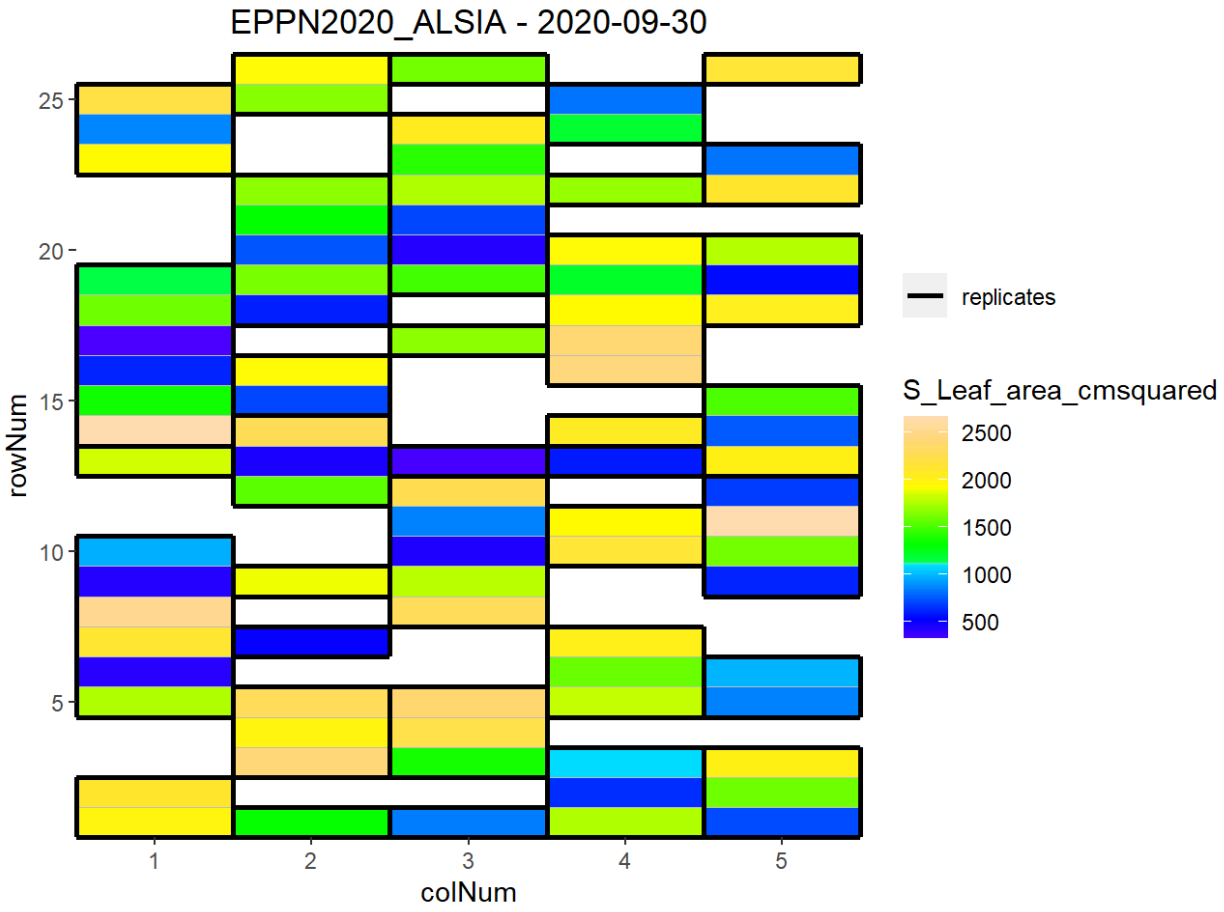

EPPN2020_ALSIA - 2020-09-18
rowNum
colNum
S_Leaf_area_cmsquared
500
400
300
200
100
replicates

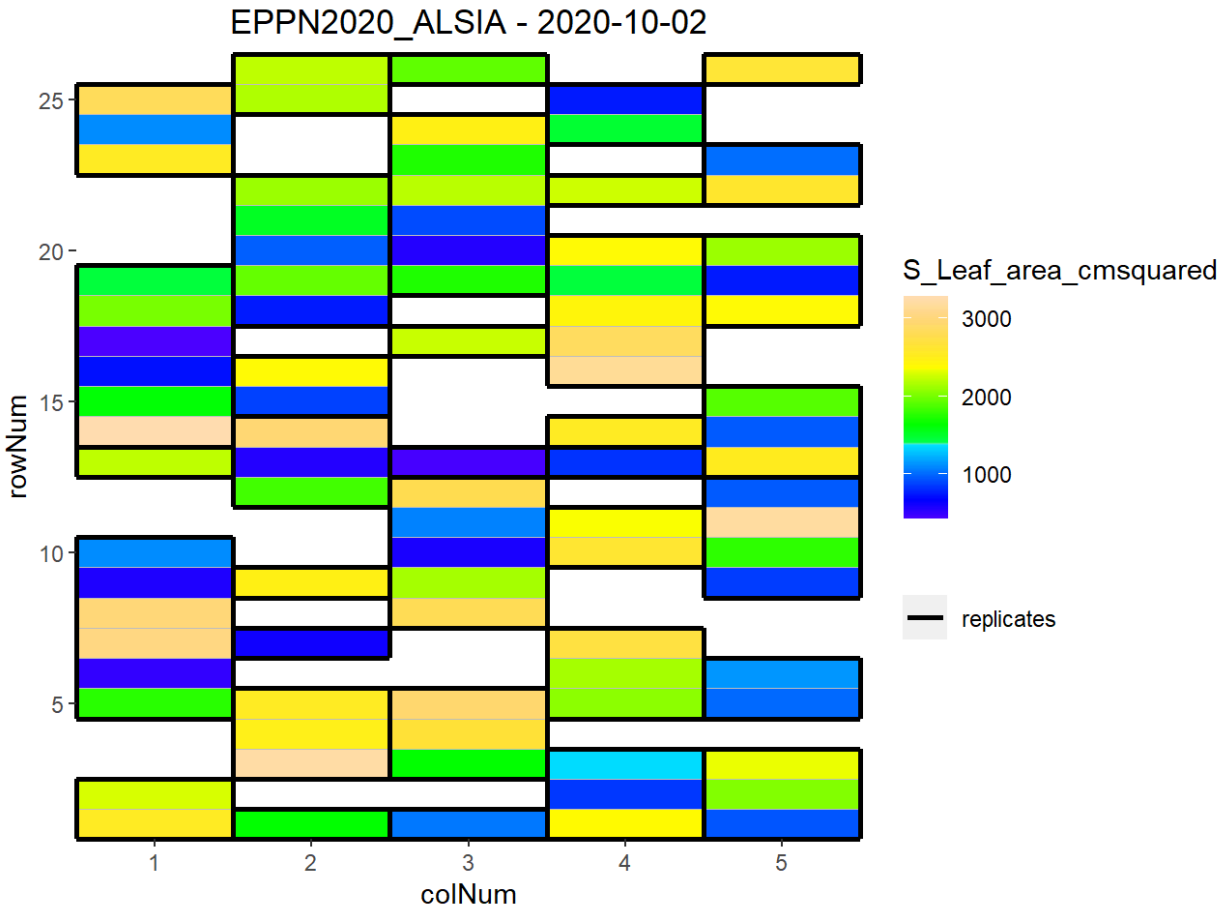

EPPN2020_ALSIA - 2020-09-21
rowNum
colNum
S_Leaf_area_cmsquared
750
500
250
replicates

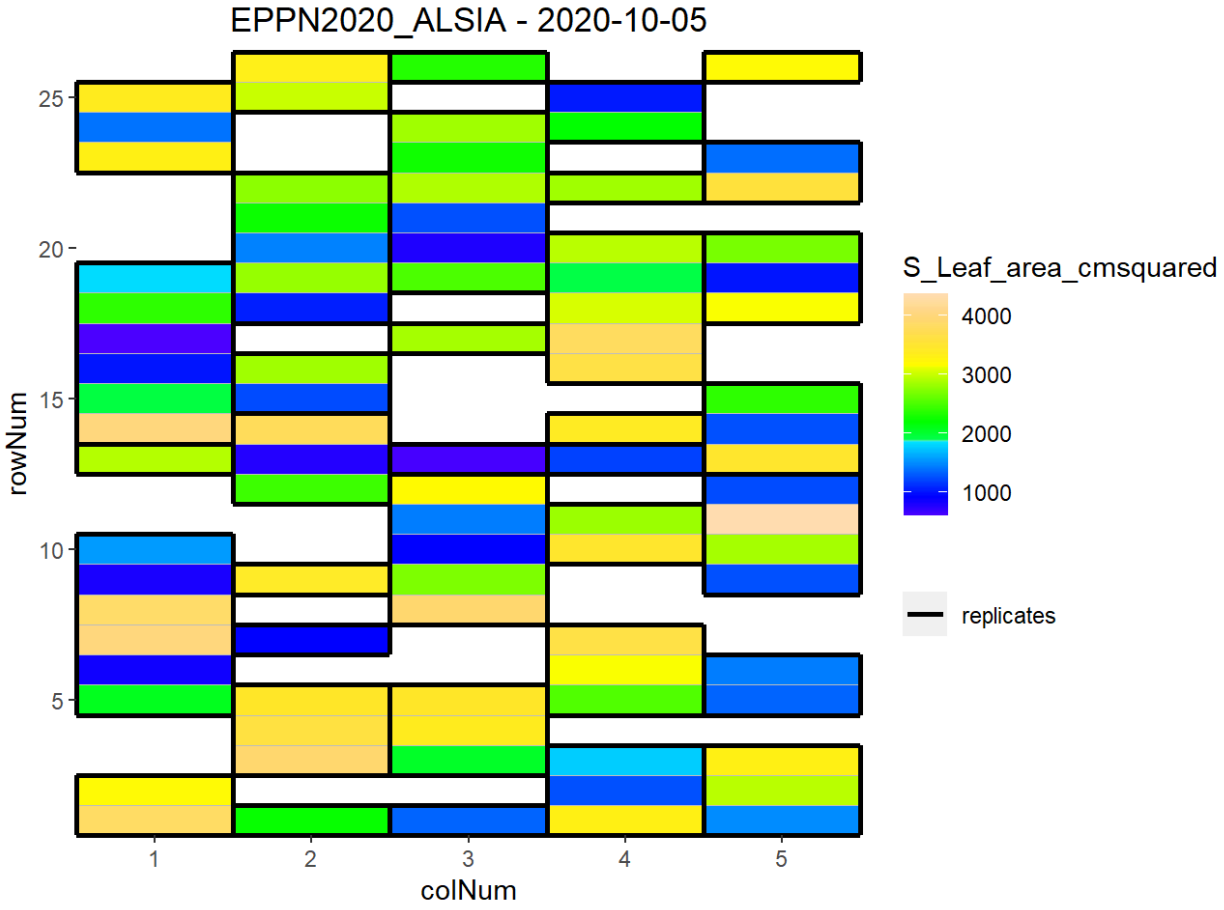

EPPN2020_ALSIA - 2020-09-23
rowNum
colNum
S_Leaf_area_cmsquared
1250
1000
750
500
250
replicates


EPPN2020_ALSIA - 2020-09-25
rowNum
colNum
S_Leaf_area_cmsquared
1500
1000
500
replicates


EPPN2020_ALSIA - 2020-09-28
rowNum
colNum
S_Leaf_area_cmsquared
2000
1500
1000
500
replicates

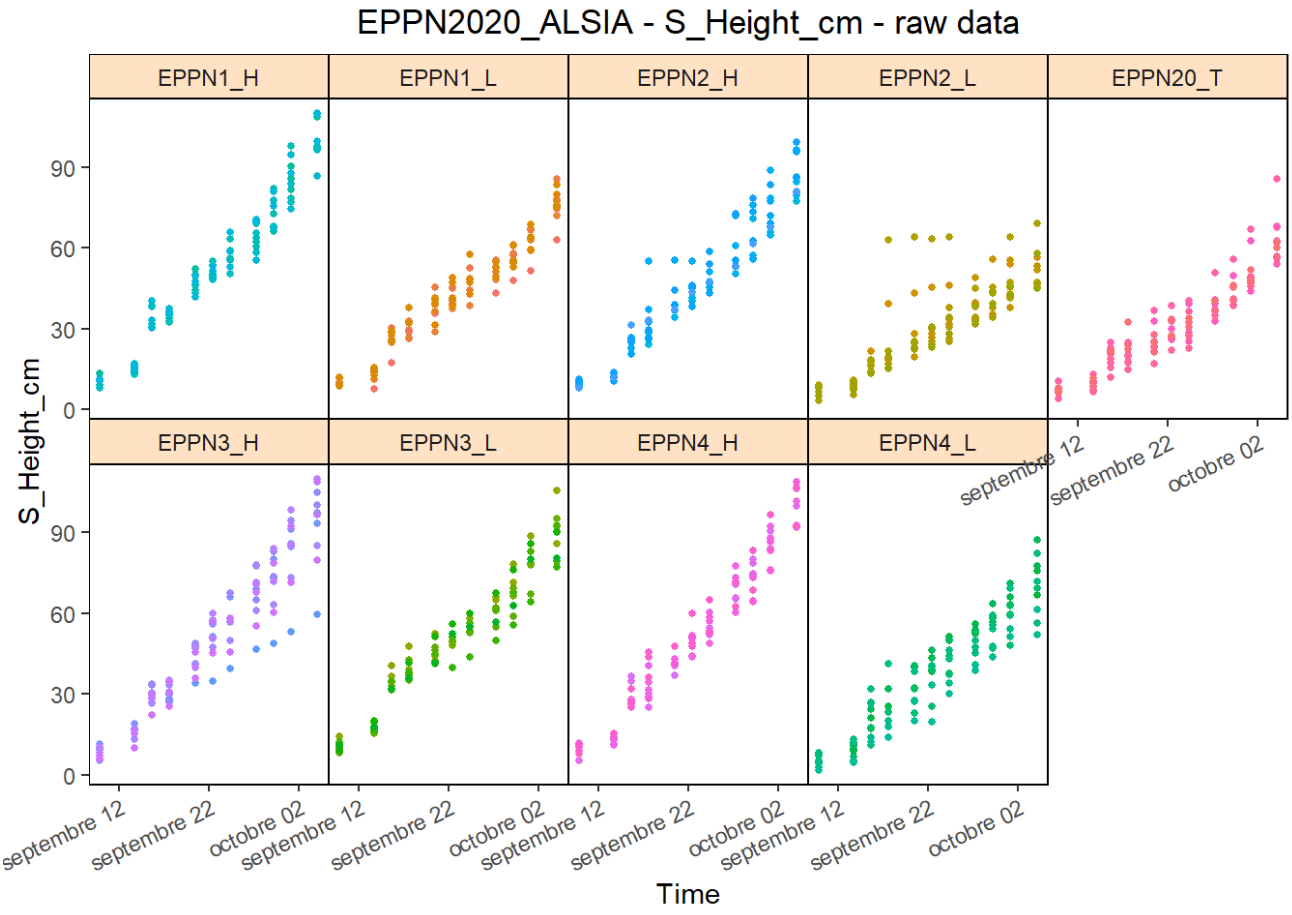

EPPN2020_ALSIA - 2020-09-30
rowNum
colNum
replicates
S_Leaf_area_cmsquared
2500
2000
1500
1000
500

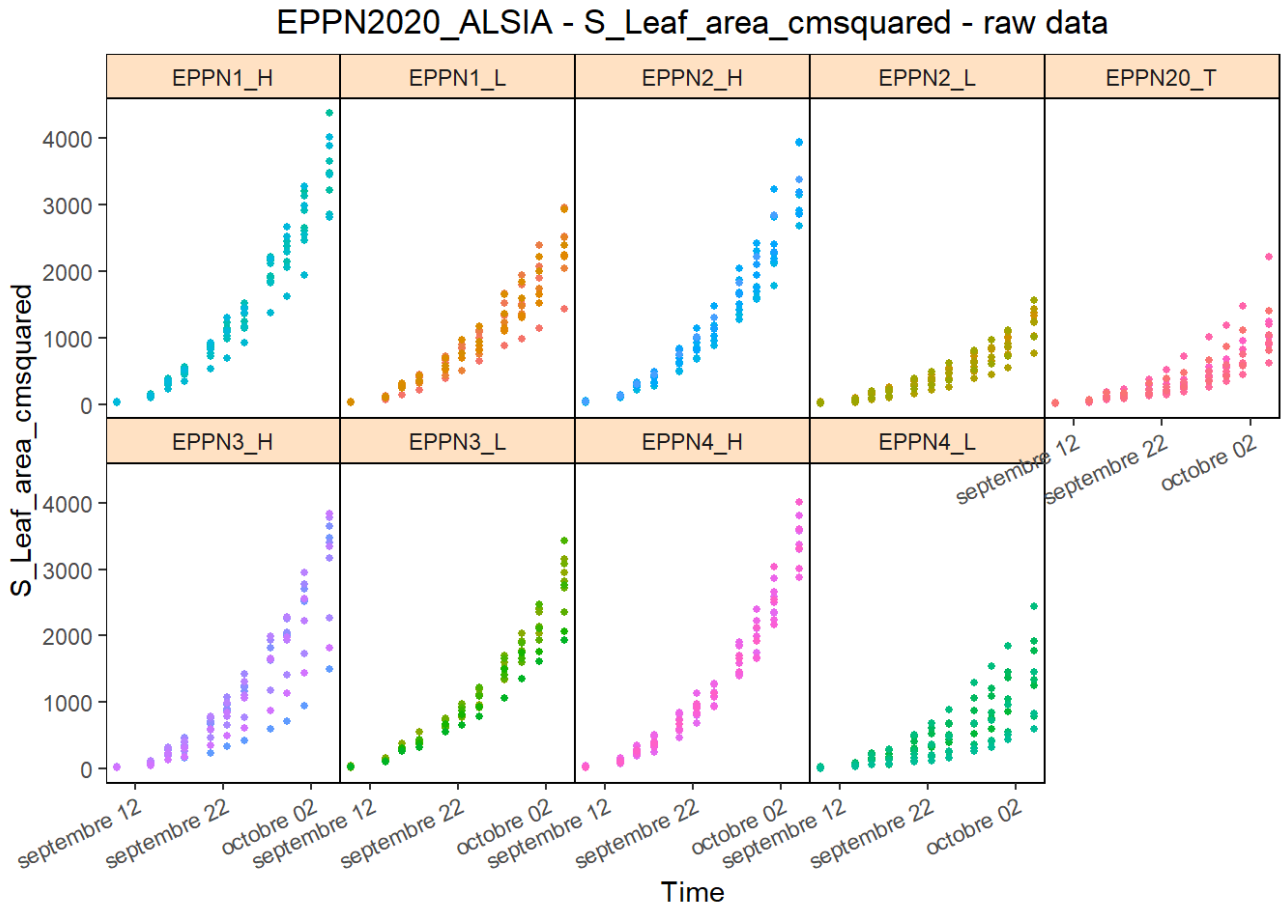




Check time course of raw data per time point

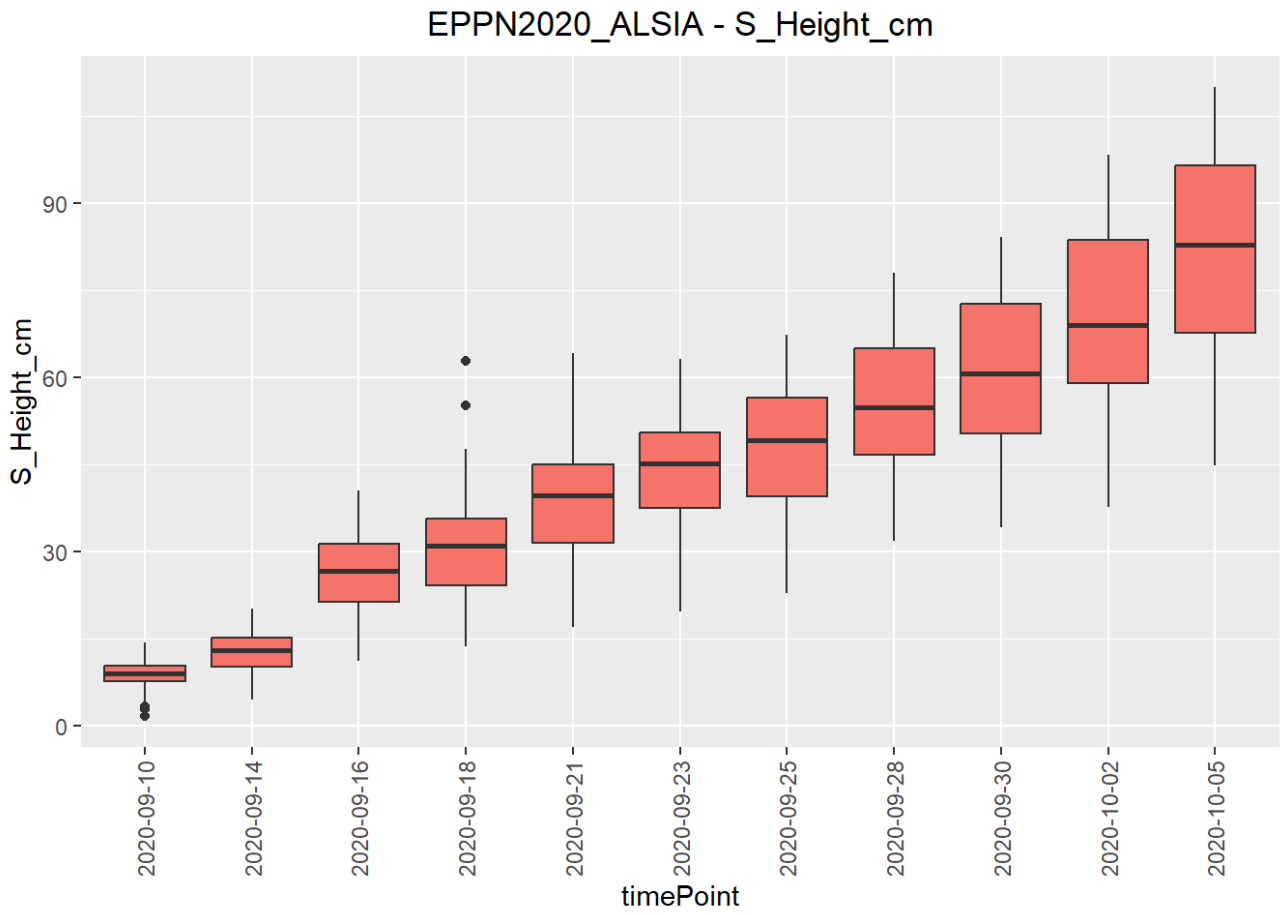
```
for (trait_name in traits) {
  plot(timePoint_S,
     traits = trait_name,
     plotType = "raw")
}
```

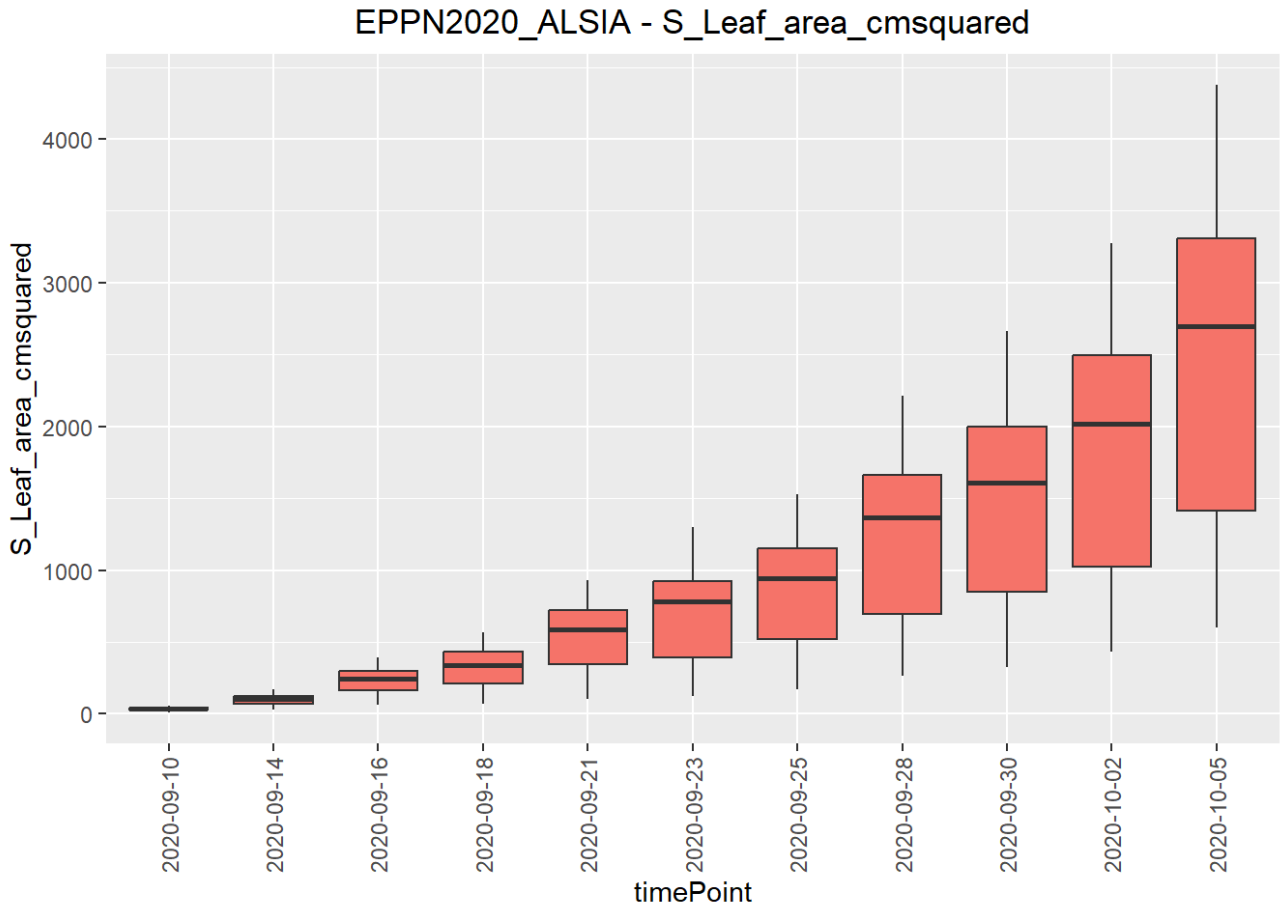




Check the boxplots of raw data per time point

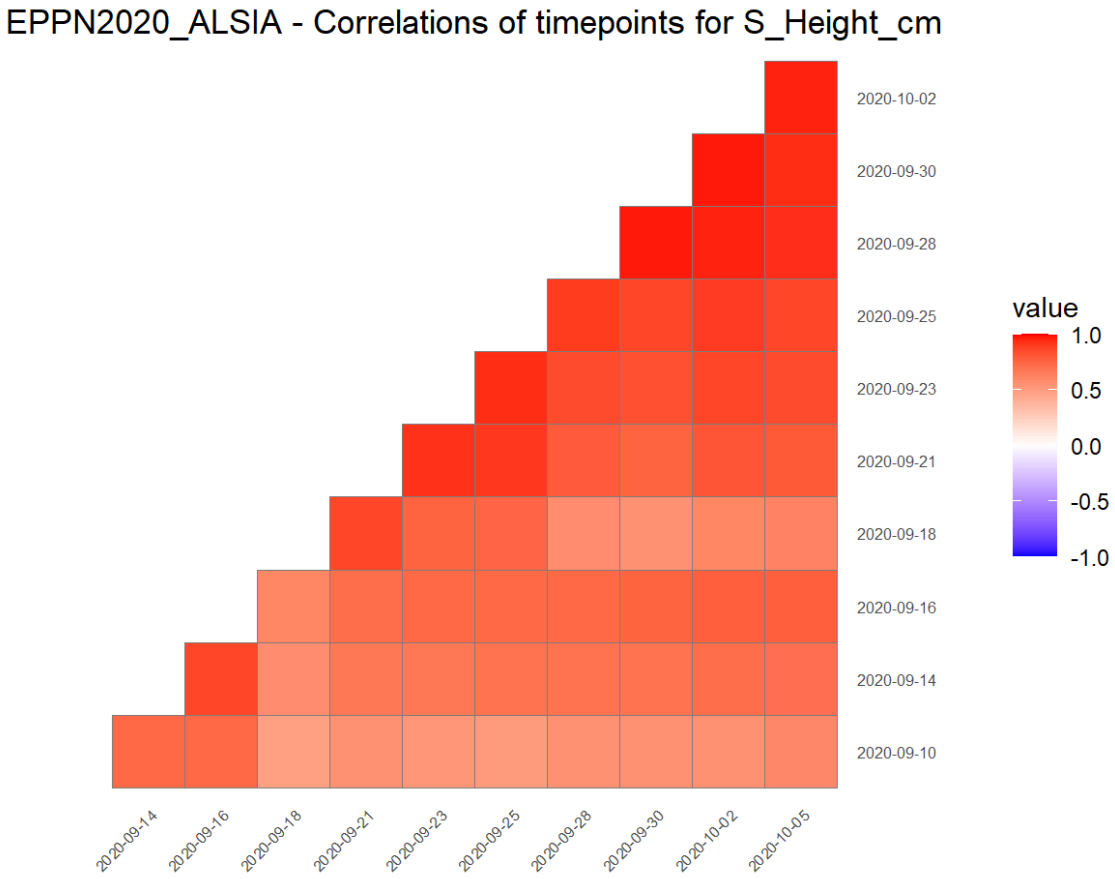
```
for (trait_name in traits) {
  plot(timePoint_S,
     plotType = "box",
     traits = trait_name)
}
```

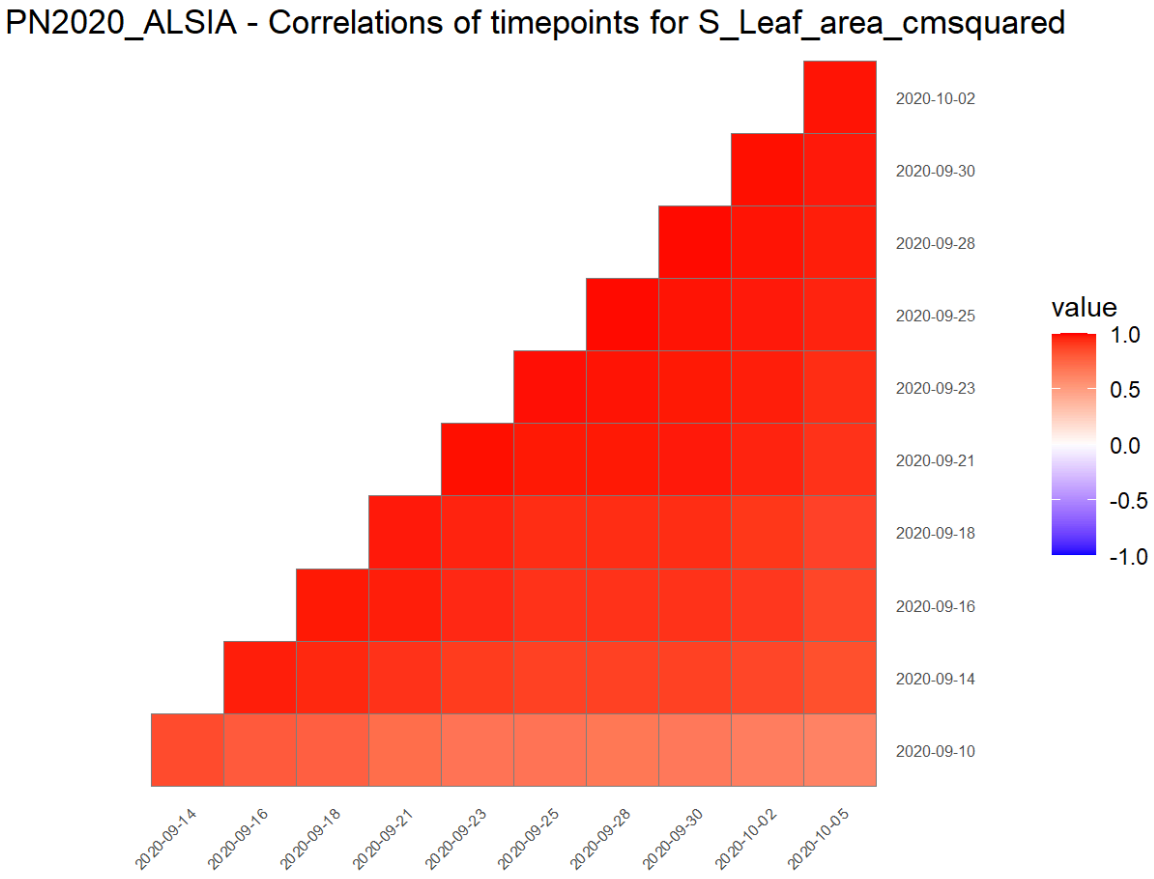




Check the correlation plots of raw data per time point

```
for (trait_name in traits) {
  plot(timePoint_S,
     plotType = "cor",
     traits = trait_name)
}
```



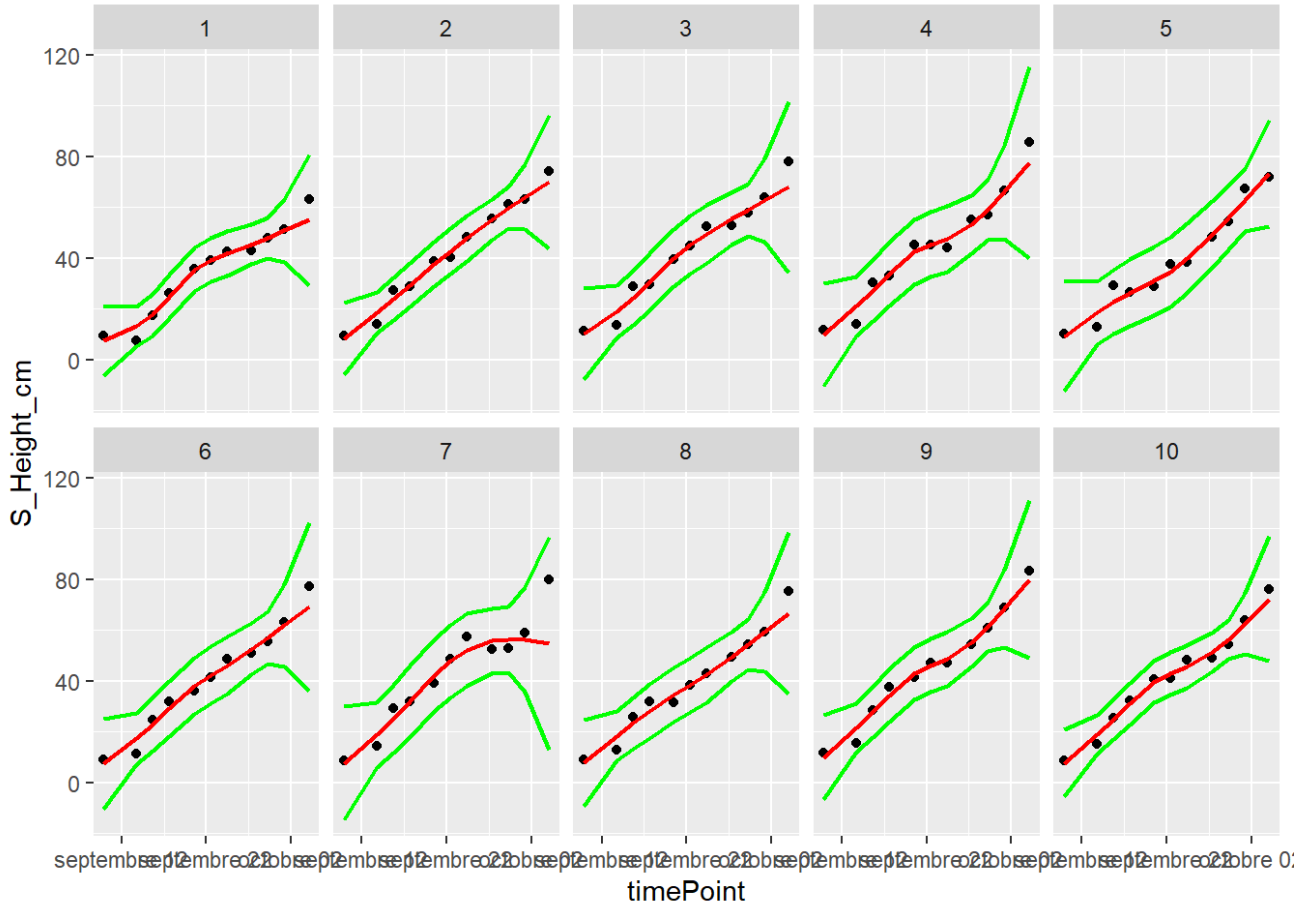


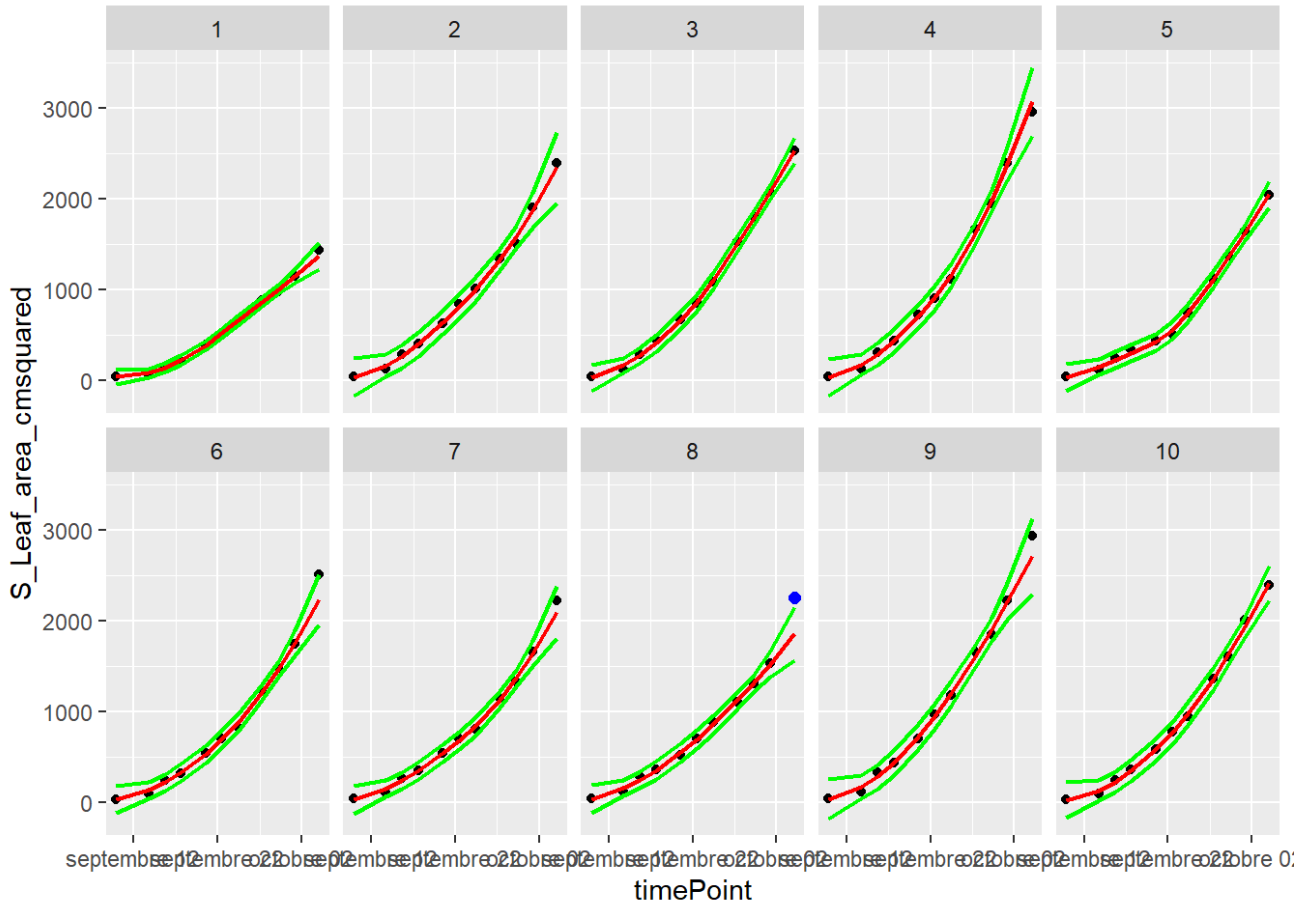
1. Detection of outliers for single observations

Using the SingleOut detect and single functions. We select a subset of plants to adjust the settings for the confIntSize and nnLocfit.

```
plantSel<- c(1,2,3,4,5,6,7,8,9,10)

ci <- 5 # confidence interval
nn <- 0.8 # nearest neighbor
ce <- FALSE
```

```
for (trait_name in traits) {
  variable_name <- paste0("Single_test_", trait_name)

  single_test <- detectSingleOut(
    TP = timePoint_S,
    trait = trait_name,
    plotIds = plantSel,
    confIntSize = ci,
    nnLocfit = nn,
    checkEdges = TRUE # check for outlier values in start and end of experiment
  )

  assign(variable_name, single_test)

  plot(single_test, outOnly = FALSE)
}
```





We can then run on all plants of the data set.

```
for (trait_name in traits) {
  single_test_object_name <- paste0("Single_test_", trait_name)
  Single_test <- get(single_test_object_name)
    if (any(Single_test$outlier == 1)) {
    outliers_count <- with(Single_test[Single_test$outlier == 1,], table(timePoint))
    print(trait_name)
    print(outliers_count)

    Single_outliers <- removeSingleOut(timePoint_S, Single_test)
    assign(paste0("Single_outliers_", trait_name), Single_outliers)

    readr::write_tsv(Single_test, sprintf("%s/single_outliers_%s.tsv", datadir, trait_n
ame))
  } else {
    cat("No outlier for", trait_name, "\n")
  }
}
```

```
## No outlier for S_Height_cm
## [1] "S_Leaf_area_cmsquared"
## timePoint
## 2020-10-05
##          1
```

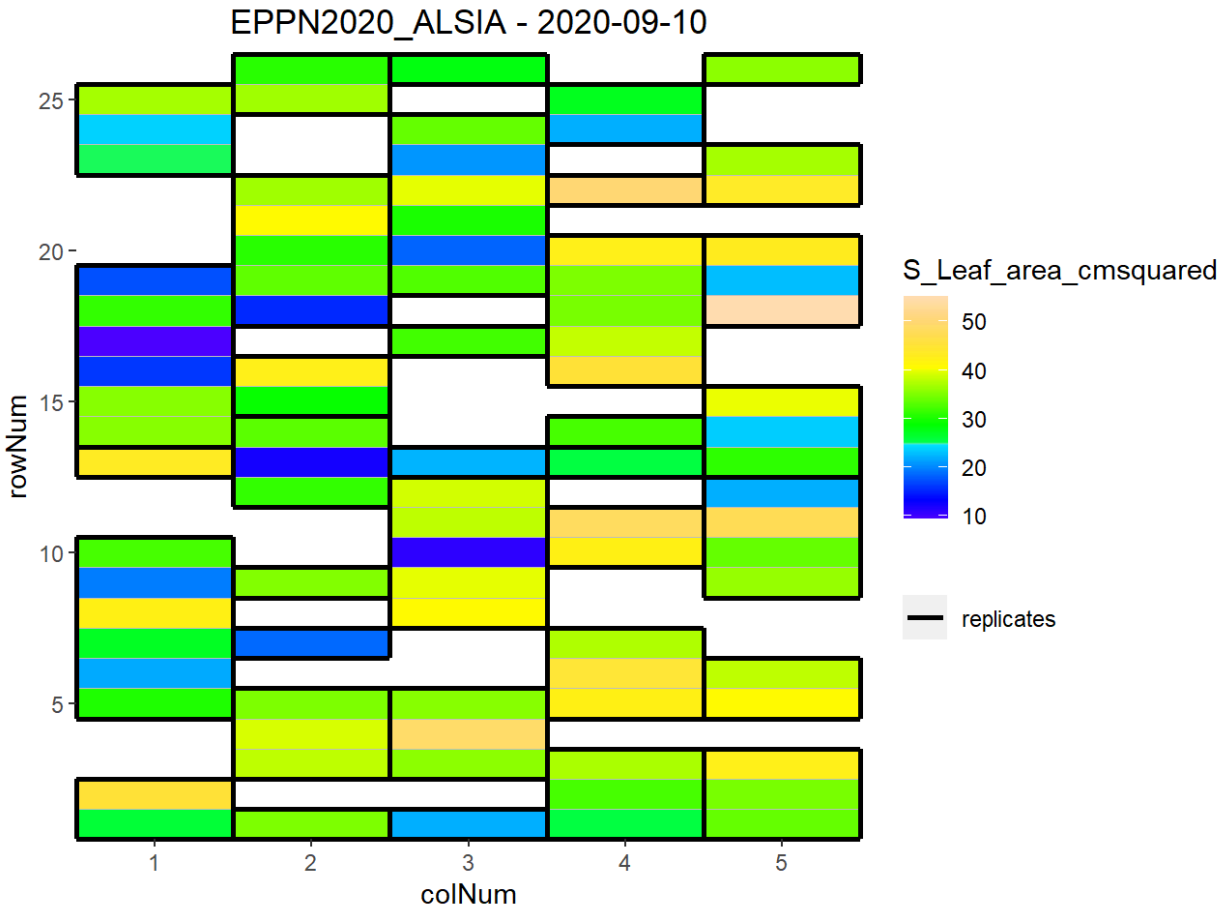
Data visualisation after single observations outliers removal

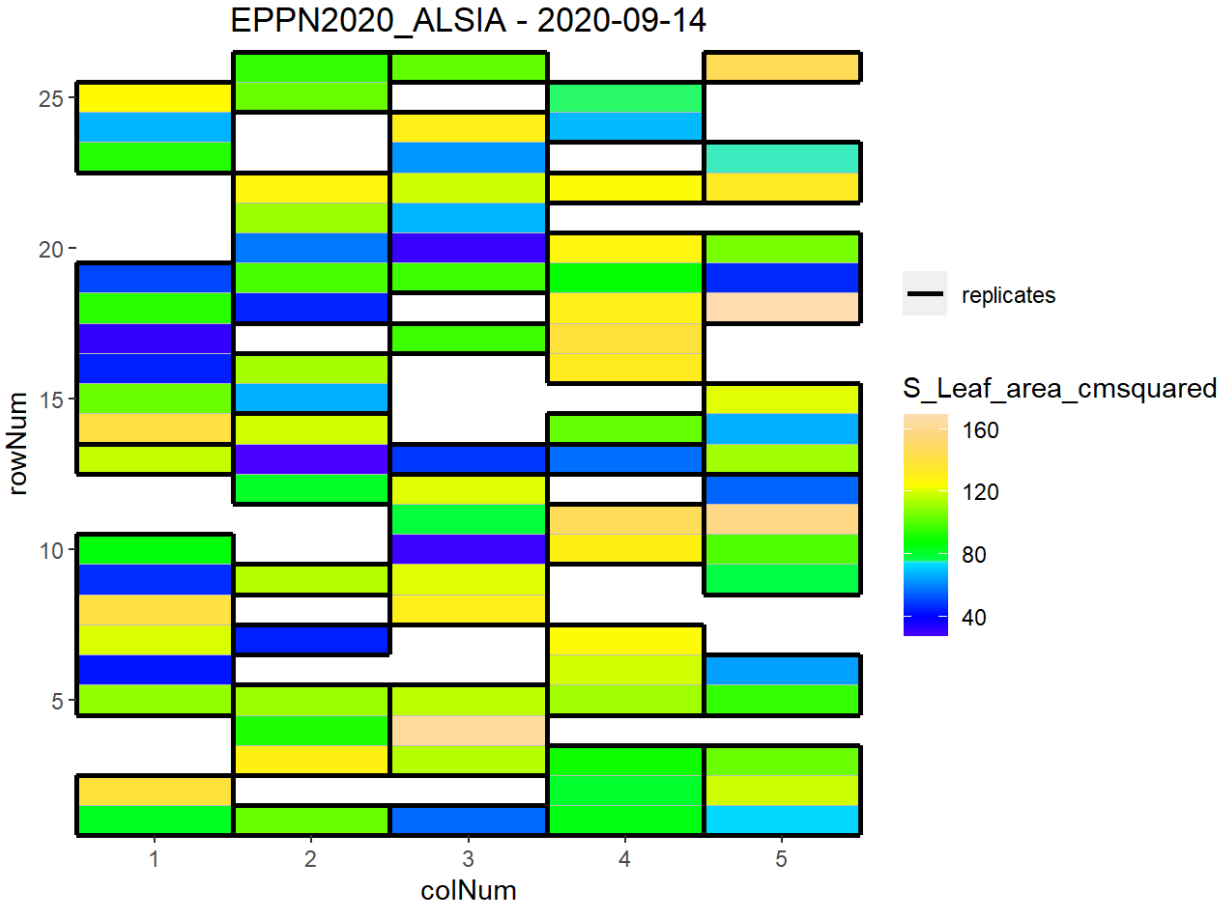
Heatmap of data

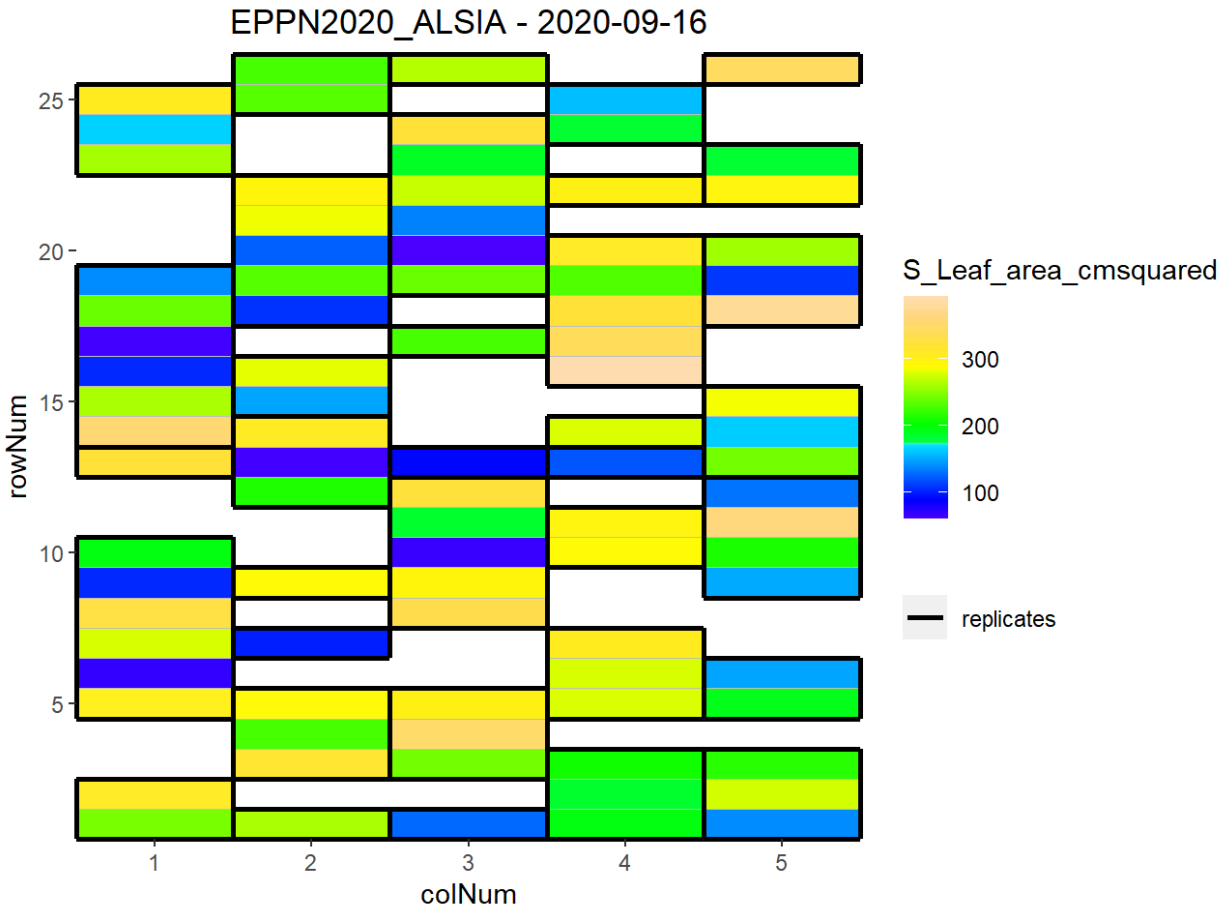
Check the heatmap of the data with outliers detection at all the time points.

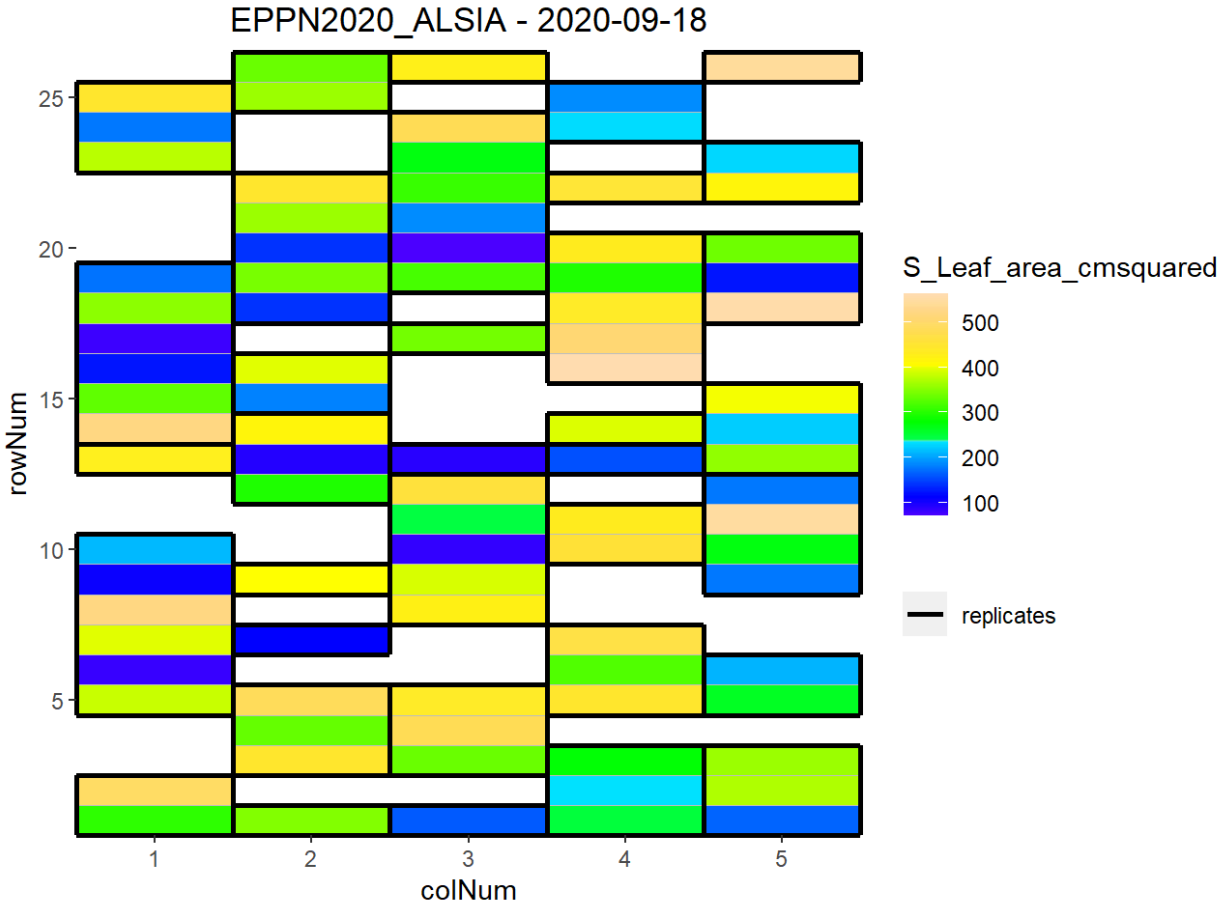
```
for (trait_name in traits) {
  single_outliers_name <- paste0("Single_outliers_", trait_name)

  if (exists(single_outliers_name)) {
    Single_outliers <- get(single_outliers_name)

    for (tp in 1:length(num_timepoints$timeNumber)) {
      plot(Single_outliers,
           plotType = "layout",
           timePoints = tp,
           traits = trait_name)
    }
  } else {
    cat("No object Single_outliers found for trait", trait_name, "\n")
  }
}
```

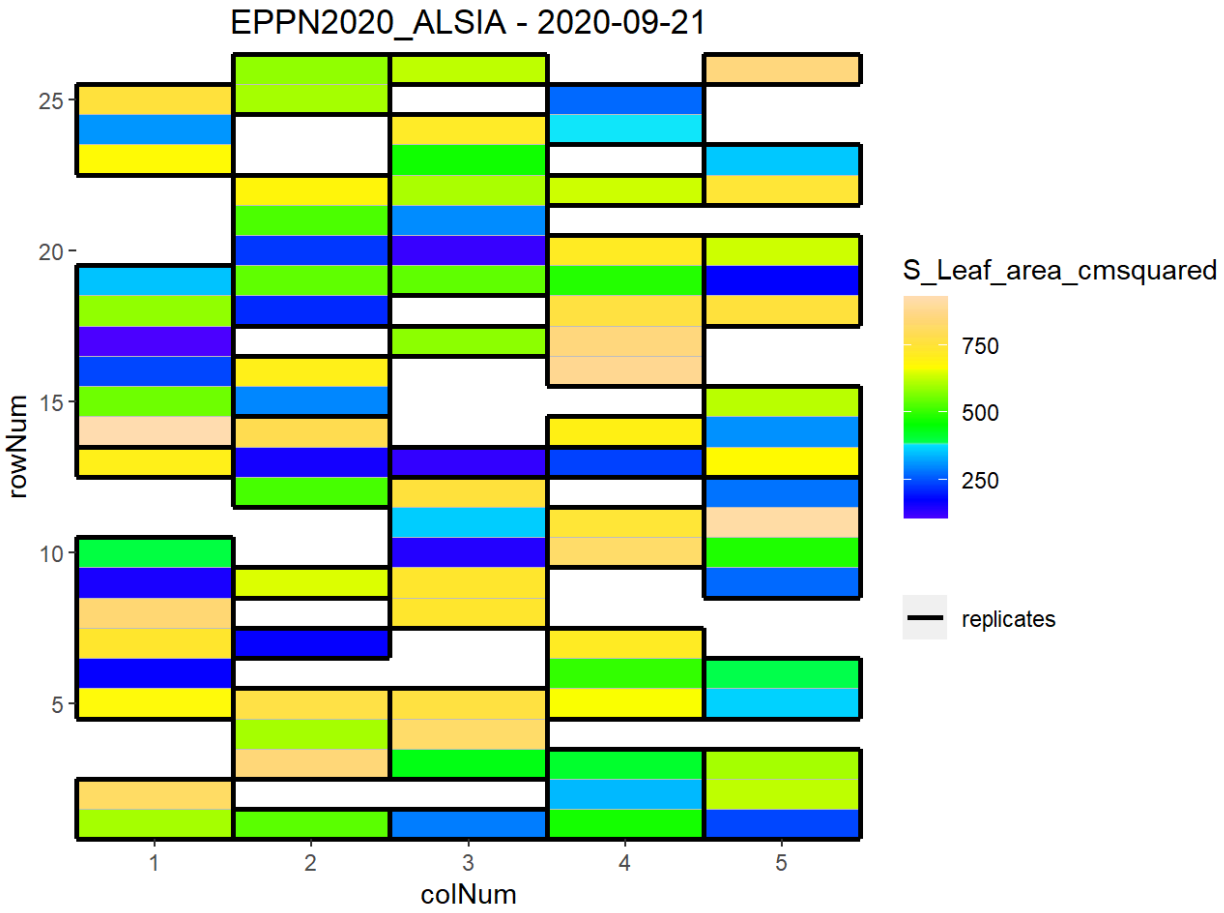
```
## No object Single_outliers found for trait S_Height_cm
```

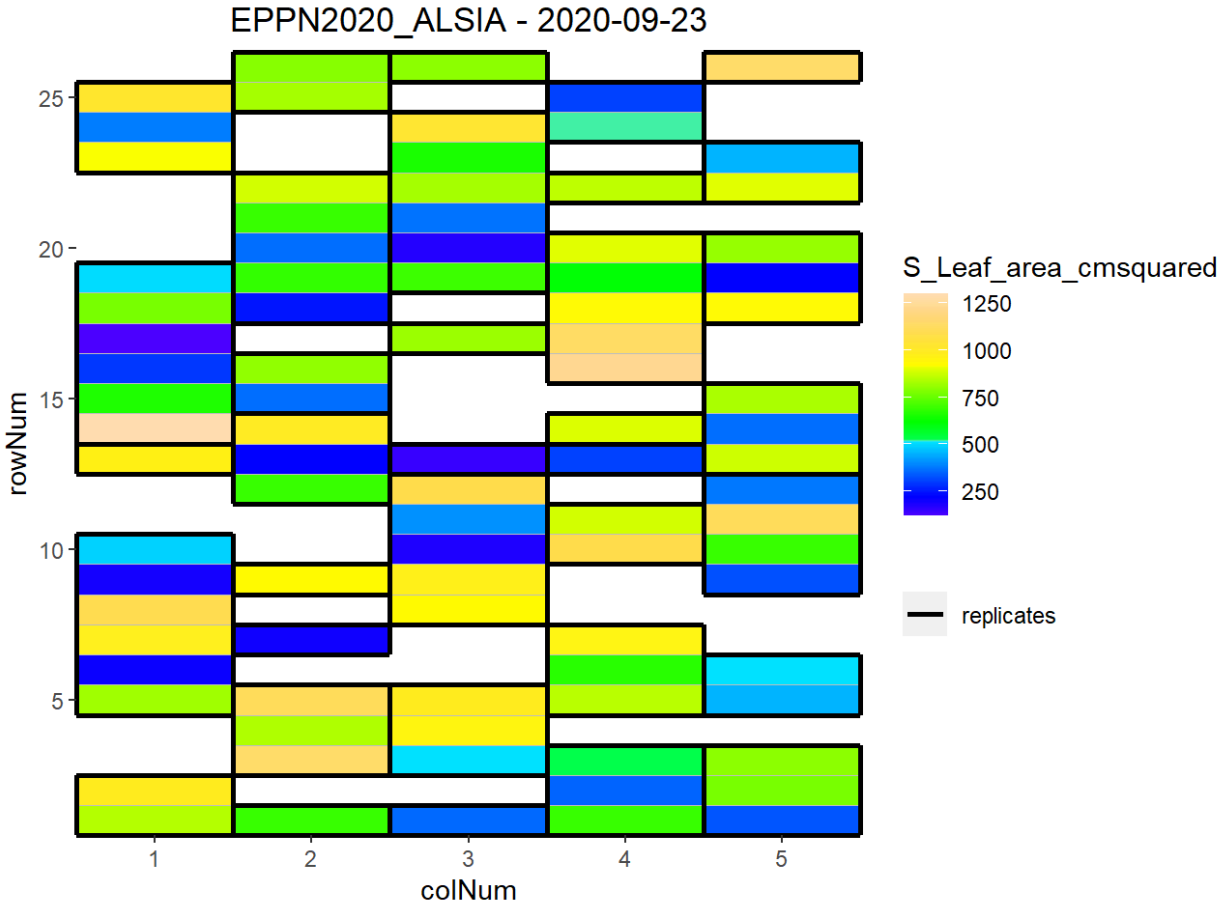

EPPN2020_ALSIA - 2020-09-10
rowNum
colNum
S_Leaf_area_cmsquared
50
40
30
20
10
replicates

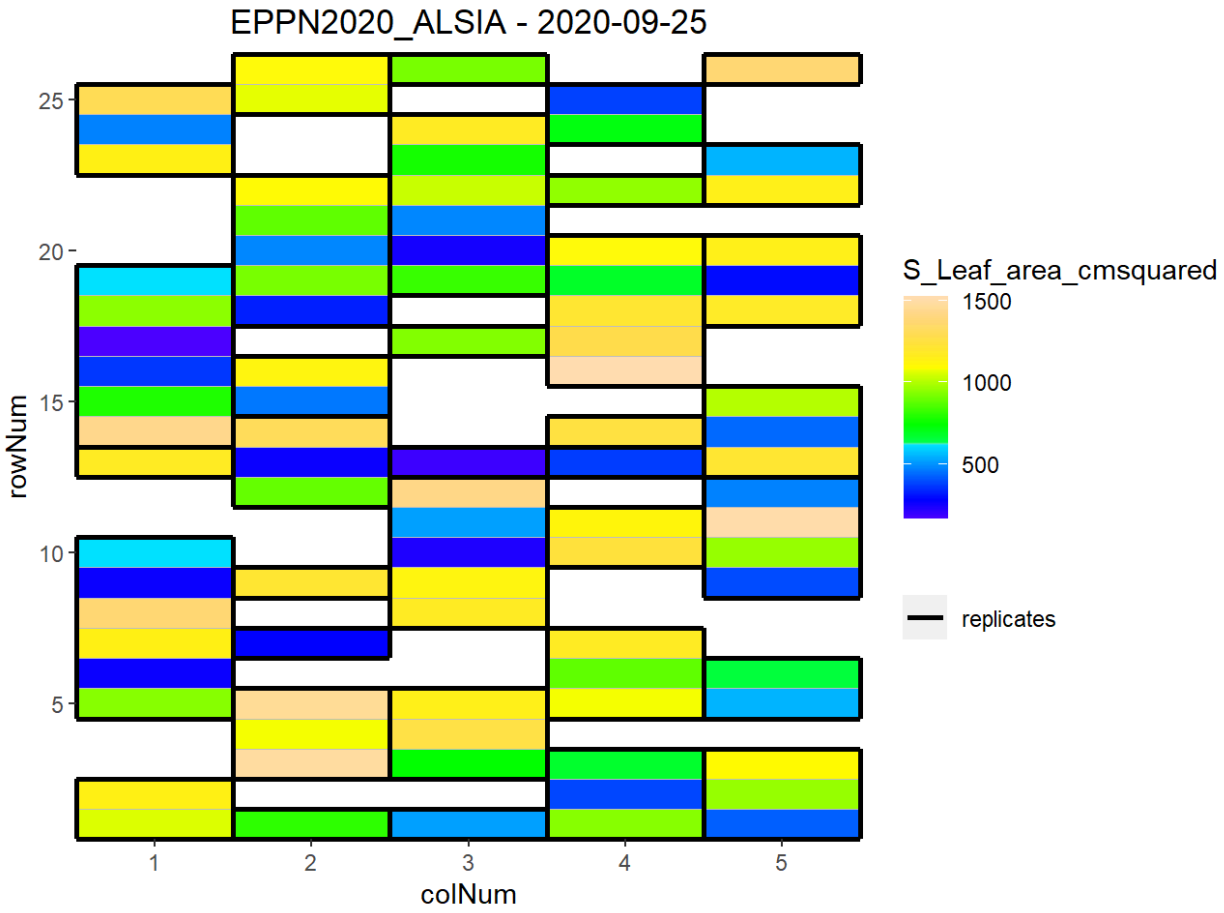

EPPN2020_ALSIA - 2020-09-14
rowNum
colNum
replicates
S_Leaf_area_cmsquared
160
120
80
40

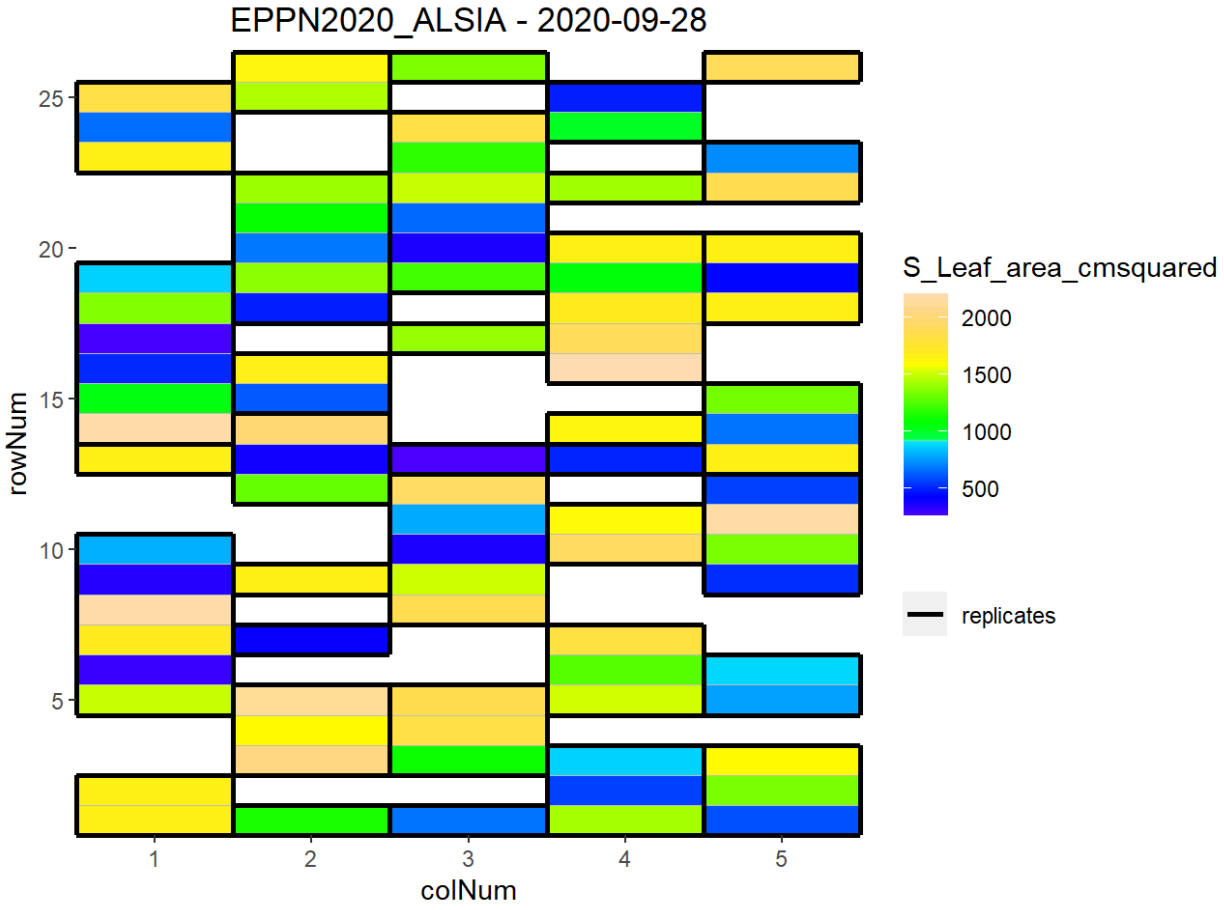

EPPN2020_ALSIA - 2020-09-16
rowNum
colNum
S_Leaf_area_cmsquared
300
200
100
replicates

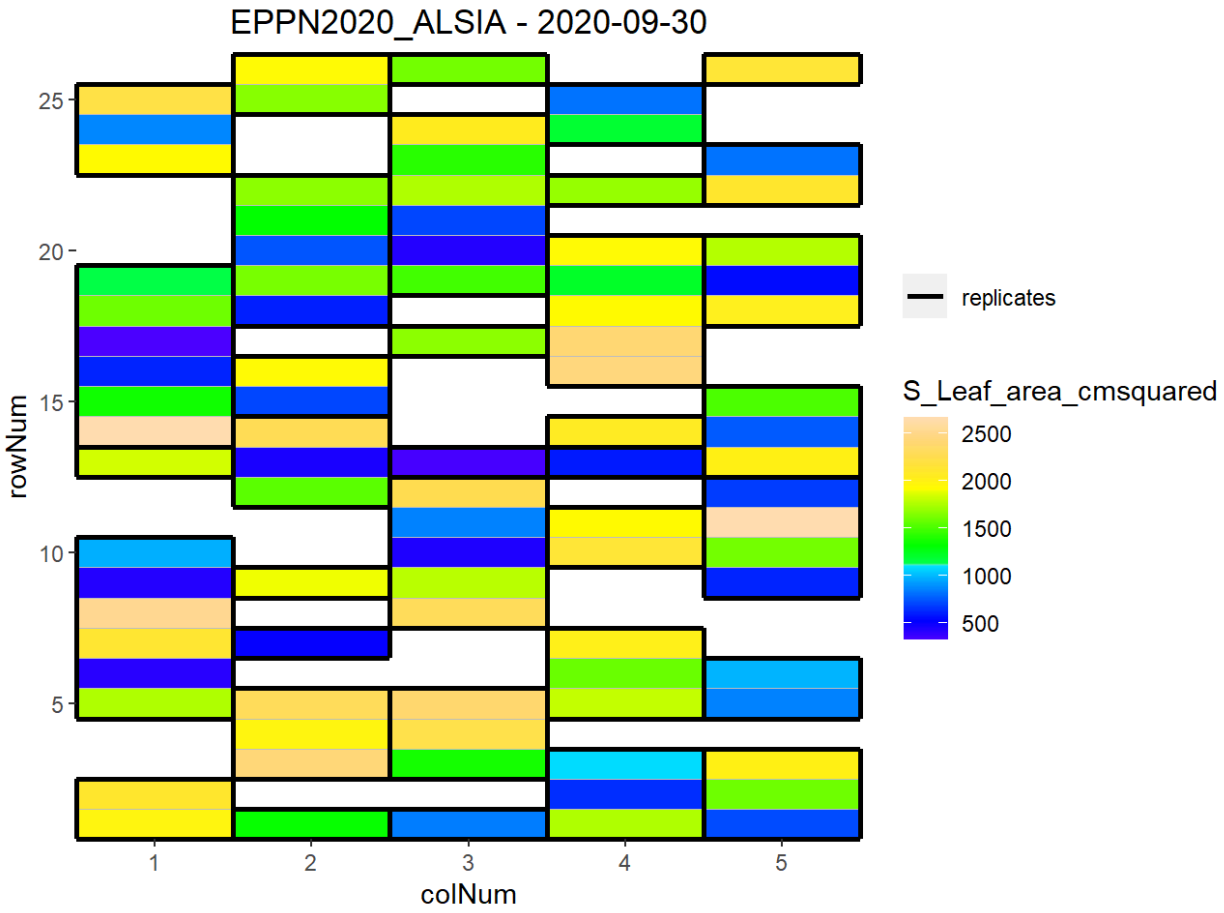

EPPN2020_ALSIA - 2020-09-18
rowNum
colNum
S_Leaf_area_cmsquared
500
400
300
200
100
replicates

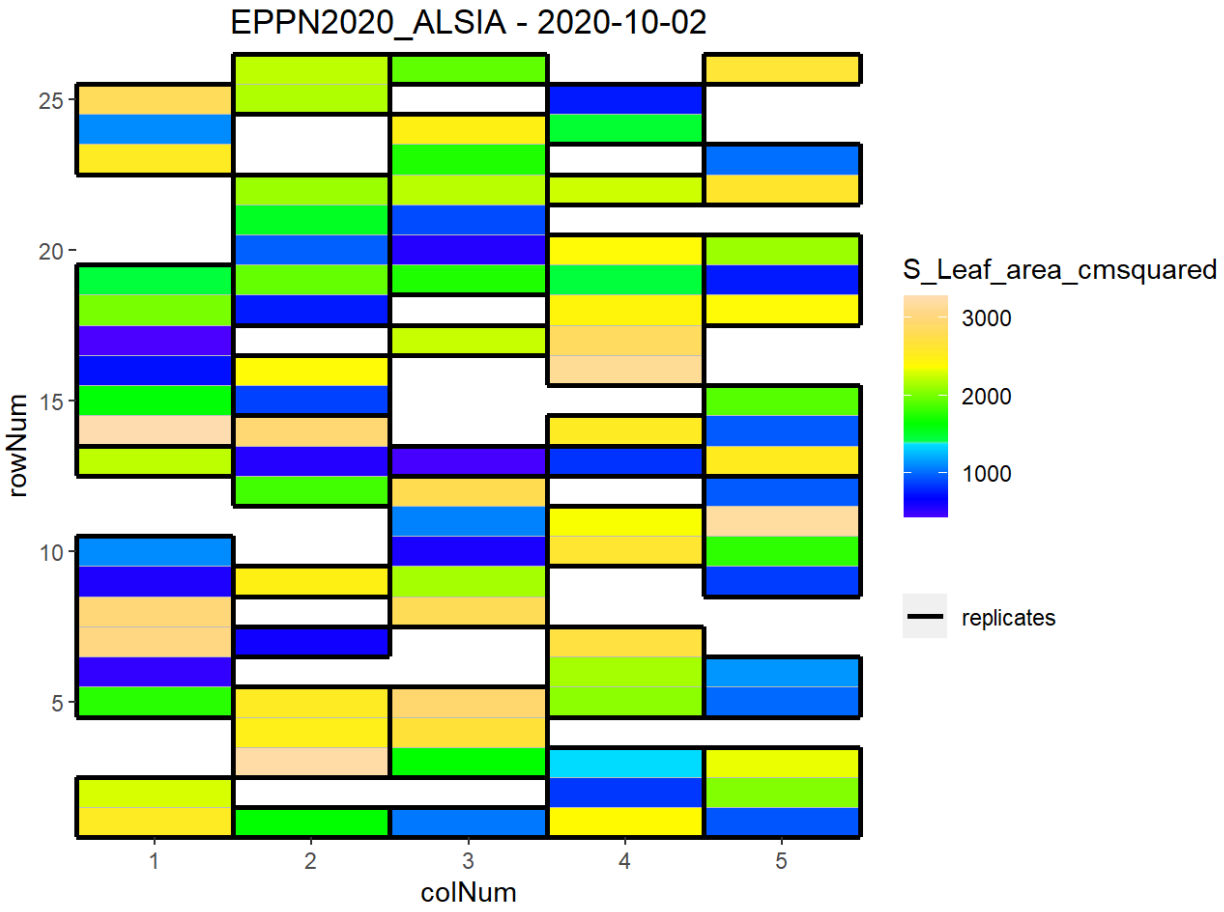

EPPN2020_ALSIA - 2020-09-21
rowNum
colNum
S_Leaf_area_cmsquared
750
500
250
replicates

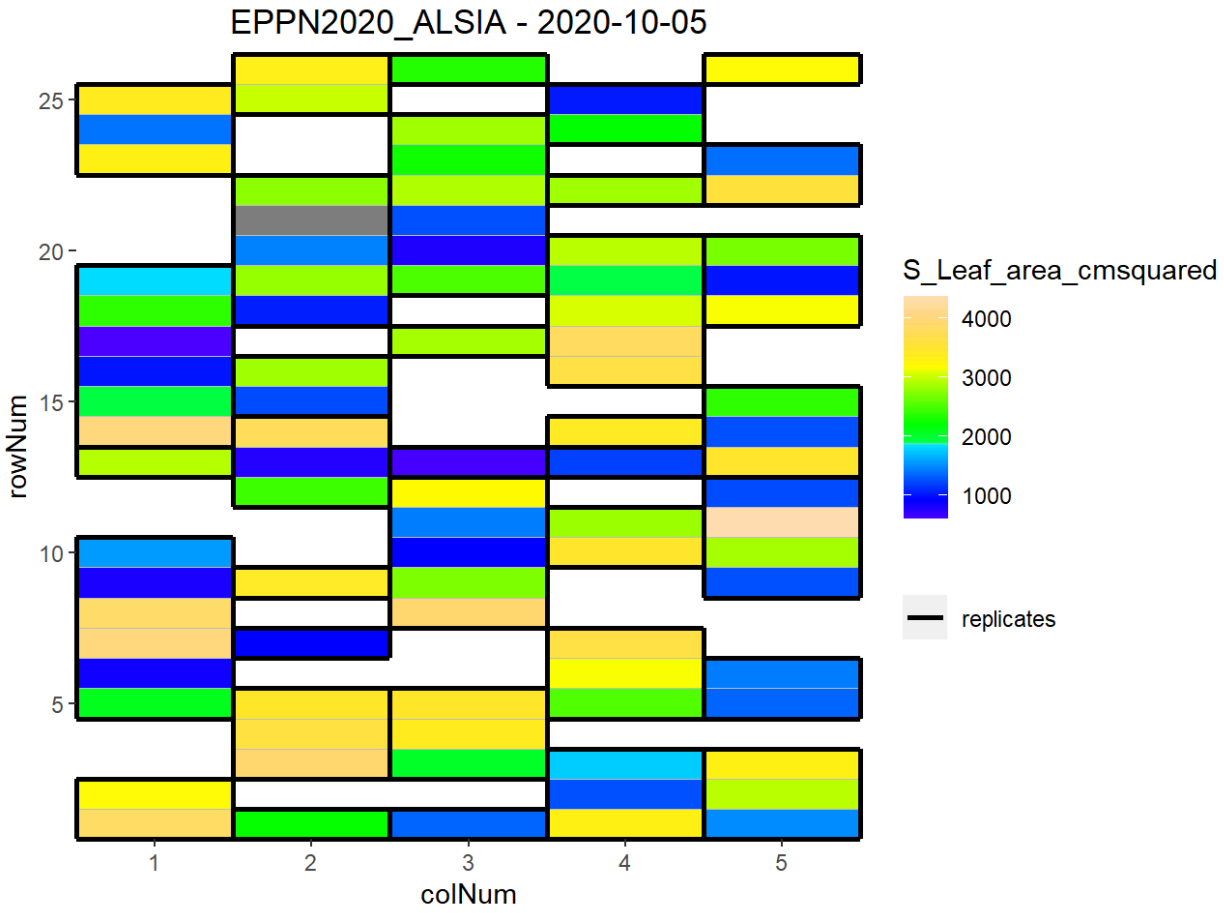

EPPN2020_ALSIA - 2020-09-23
rowNum
colNum
S_Leaf_area_cmsquared
1250
1000
750
500
250
replicates


EPPN2020_ALSIA - 2020-09-25
rowNum
colNum
S_Leaf_area_cmsquared
1500
1000
500
replicates


EPPN2020_ALSIA - 2020-09-28
rowNum
colNum
S_Leaf_area_cmsquared
2000
1500
1000
500
replicates


EPPN2020_ALSIA - 2020-09-30
rowNum
colNum
25
20
15
10
5
1
2
3
4
5
replicates
S_Leaf_area_cmsquared
2500
2000
1500
1000
500

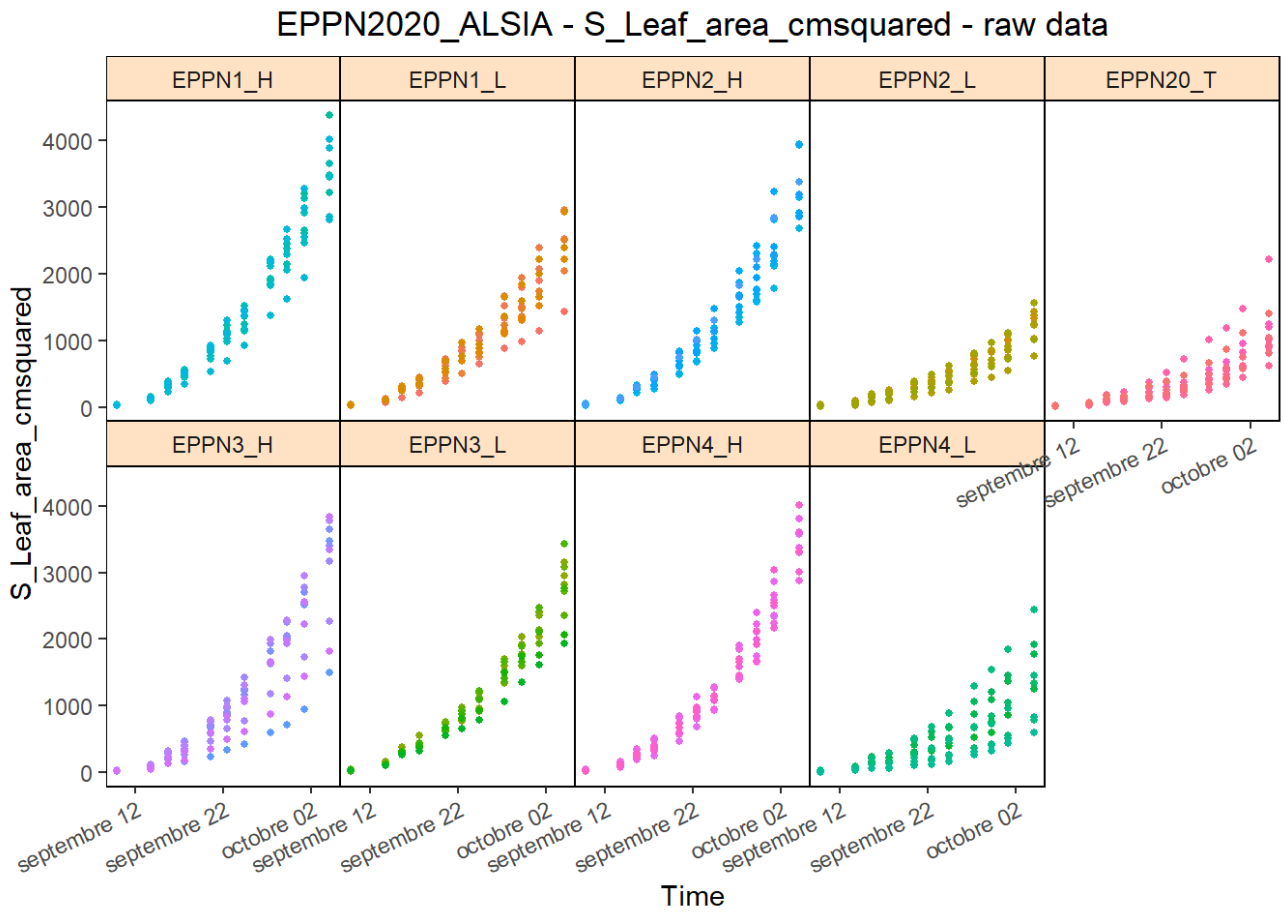

EPPN2020_ALSIA - 2020-10-02
rowNum
colNum
25
20
15
10
5
1
2
3
4
5
S_Leaf_area_cmsquared
3000
2000
1000
replicates

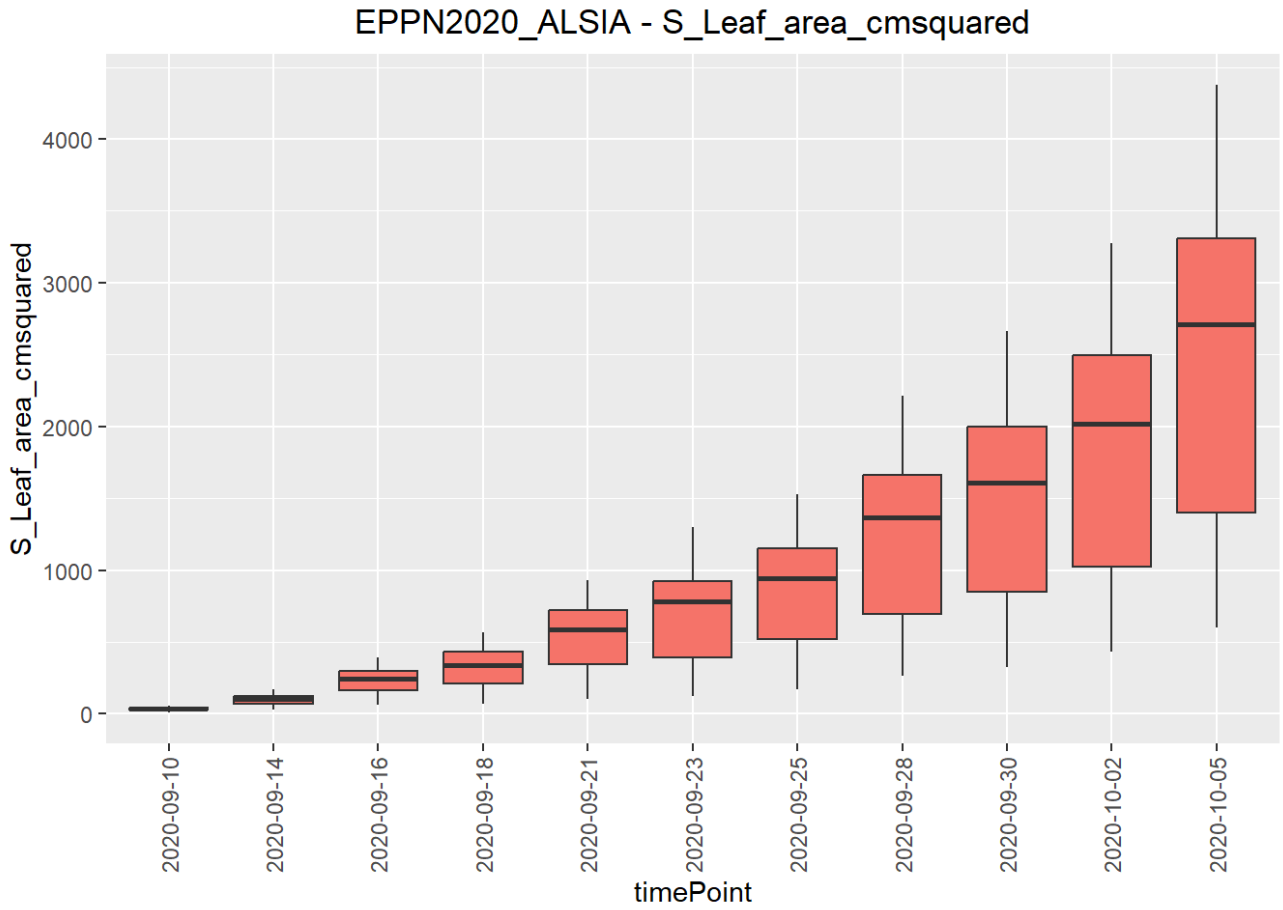


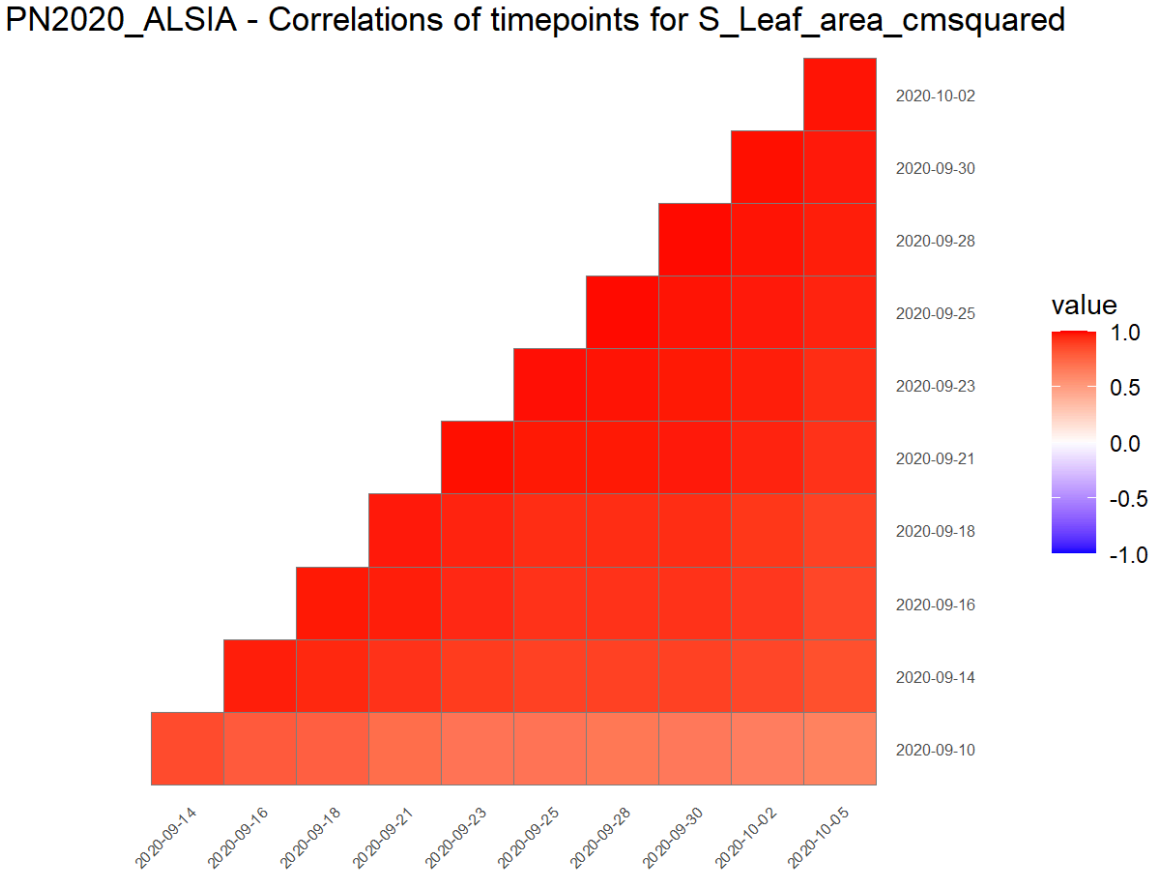
Time course, boxplots and correlation plots of data

```
for (trait_name in traits) {
  single_outliers_name <- paste0("Single_outliers_", trait_name)

  if (exists(single_outliers_name)) {
    Single_outliers <- get(single_outliers_name)

    plot(Single_outliers,
         traits = trait_name,
         plotType = "raw")

    plot(Single_outliers,
         plotType = "box",
         traits = trait_name)

    plot(Single_outliers,
         plotType = "cor",
         traits = trait_name)

  } else {
    cat("No Single_outliers object found for trait", trait_name, "\n")
  }
}
```

```
## No Single_outliers object found for trait S_Height_cm
```


EPPN2020_ALSIA - S_Leaf_area_cmsquared - raw data
EPPN1_H
EPPN1_L
EPPN2_H
EPPN2_L
EPPN20_T
EPPN3_H
EPPN3_L
EPPN4_H
EPPN4_L
S_Leaf_area_cmsquared
0
1000
2000
3000
4000
septembre 12
septembre 22
octobre 02
Time


EPPN2020_ALSIA - S_Leaf_area_cmsquared
S_Leaf_area_cmsquared
0
1000
2000
3000
4000
2020-09-10
2020-09-14
2020-09-16
2020-09-18
2020-09-21
2020-09-23
2020-09-25
2020-09-28
2020-09-30
2020-10-02
2020-10-05
timePoint



2. Correction for spatial trends

Fit a model for all time points with no extra fixed effects.

```
for (trait_name in traits) {
  single_outliers_name <- paste0("Single_outliers_", trait_name)

  if (exists(single_outliers_name)) {
    Single_outliers <- get(single_outliers_name)

    assign(paste0("modTP_", trait_name),
           fitModels(TP = Single_outliers,
                     trait = trait_name,
                     geno.decomp = "Plant_type"))
  } else {
    assign(paste0("modTP_", trait_name),
           fitModels(TP = timePoint_S,
                     trait = trait_name,
                     geno.decomp = "Plant_type"))
  }
}
```

```
## 2020-09-10
```

```
## 2020-09-14
```

```
## 2020-09-16
```

```
## 2020-09-18
```

```
## 2020-09-21
```

```
## 2020-09-23
```

```
## 2020-09-25
```

```
## 2020-09-28
```

```
## 2020-09-30
```

```
## 2020-10-02
```

```
## 2020-10-05
```

```
## 2020-09-10
```

```
## 2020-09-14
```

```
## 2020-09-16
```

```
## 2020-09-18
```

```
## 2020-09-21
```

```
## 2020-09-23
```

```
## 2020-09-25
```

```
## 2020-09-28
```

```
## 2020-09-30
```

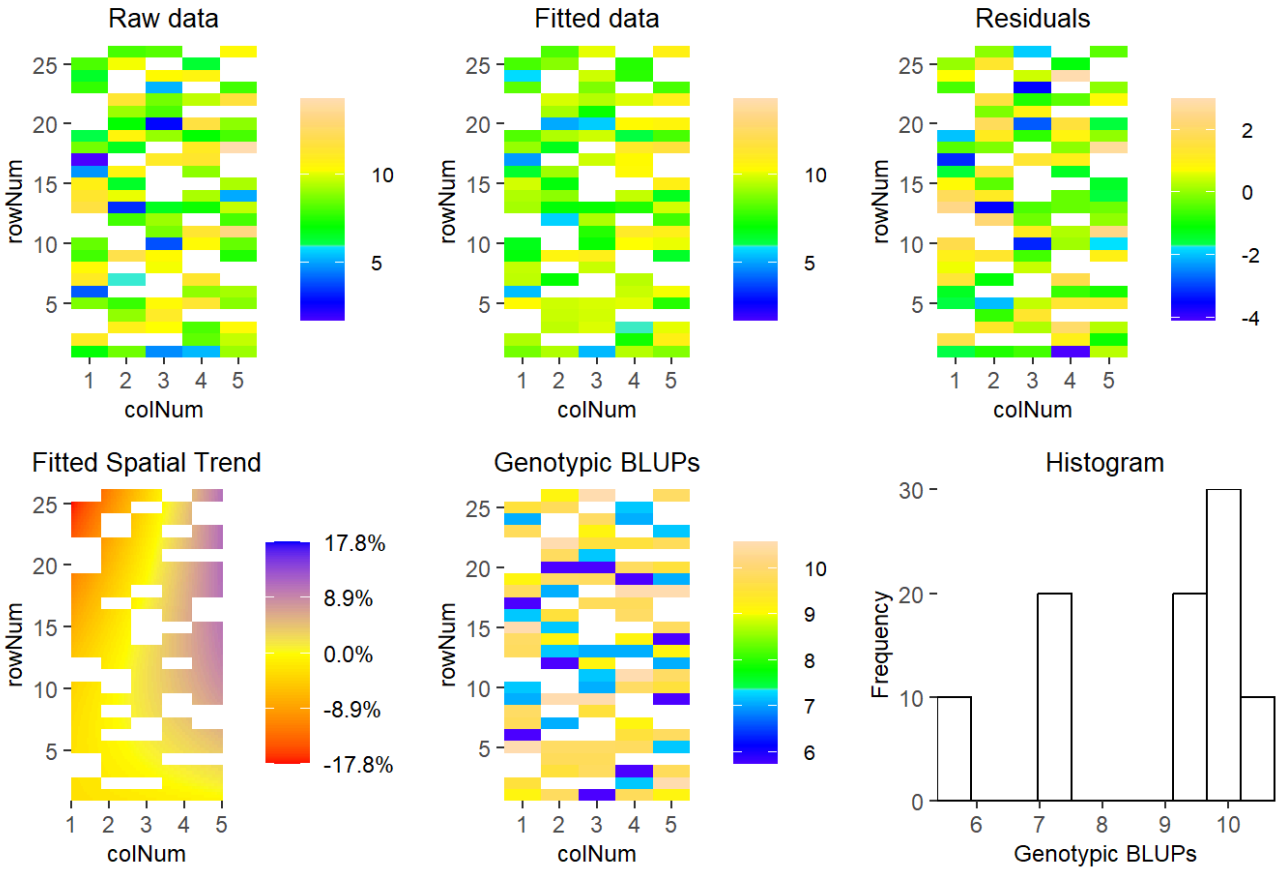
```
## 2020-10-02
```

```
## 2020-10-05
```

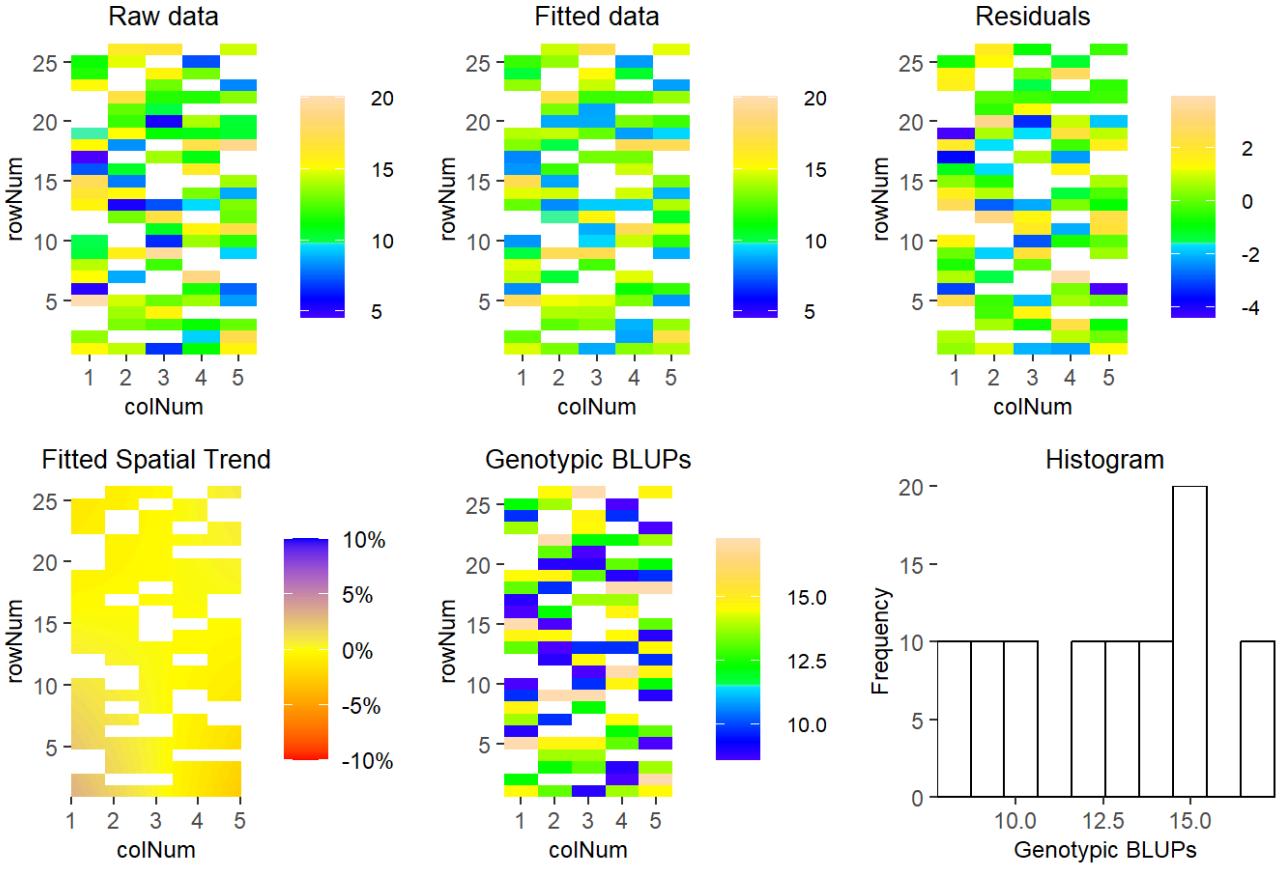
Model visualisation

```
for (trait_name in traits) {
  mod_name <- paste0("modTP_", trait_name)

  if (exists(mod_name)) {
    mod <- get(mod_name)

    for (tp in 1:length(num_timepoints$timeNumber)) {
      plot(mod,
           timePoints = tp,
           plotType = "spatial",
           spaTrend = "percentage")
    }

    gif_file <- sprintf("%s/%s_mod.gif", datadir, trait_name)

    plot(mod,
         plotType = "timeLapse",
         spaTrend = "percentage",
         outFile = gif_file)
  } else {
    cat("No model found for", trait_name, "\n")
  }
}
```

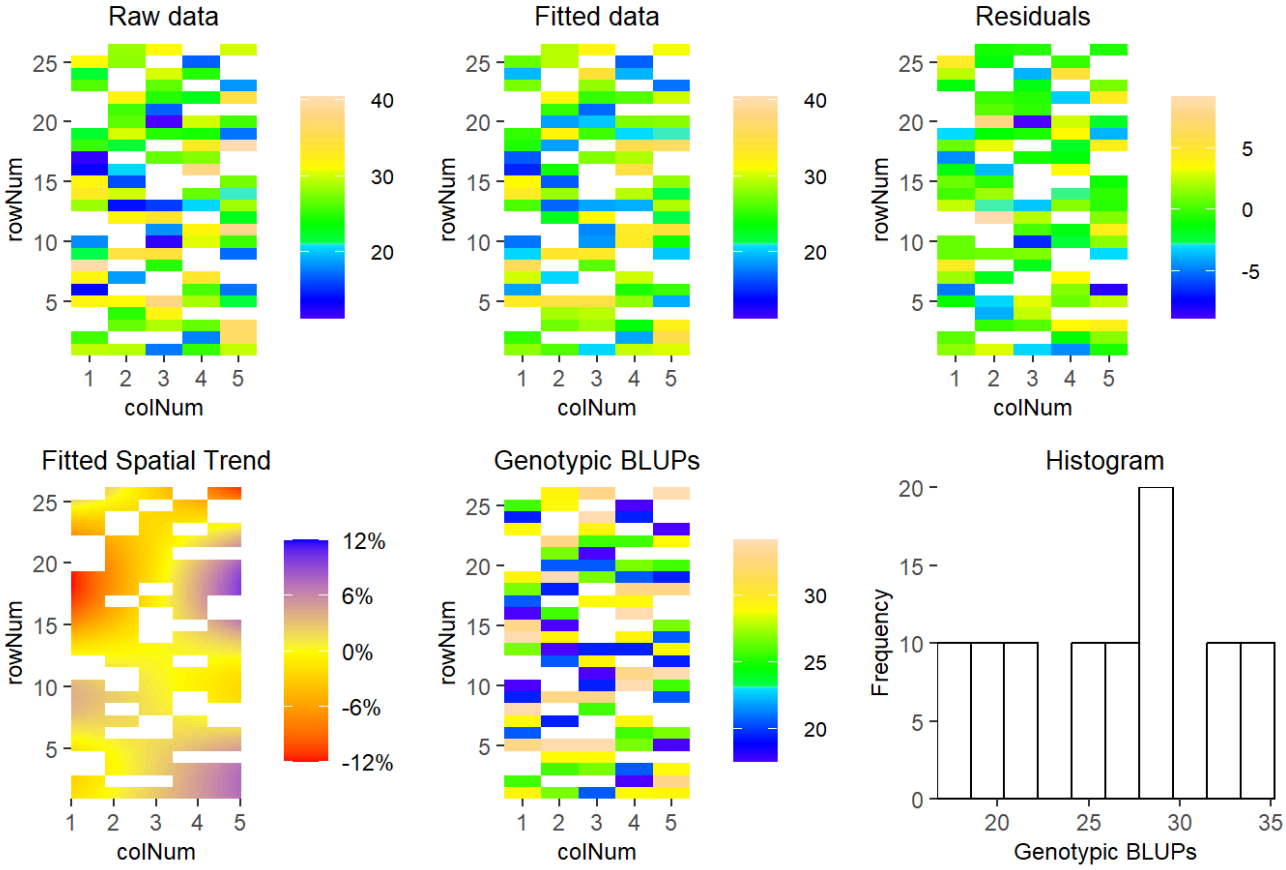
EPPN2020_ALSIA - S_Height_cm - 2020-09-10



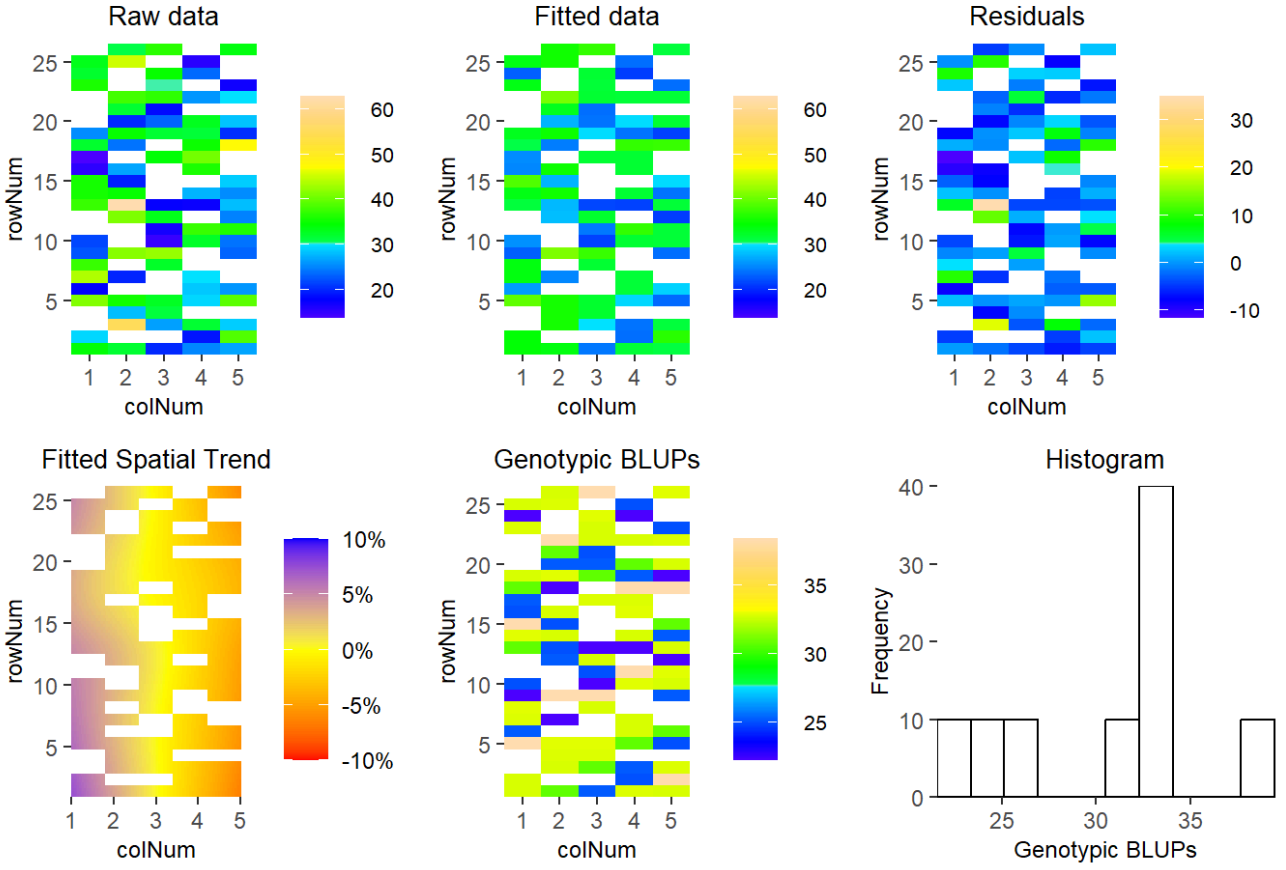
EPPN2020_ALSIA - S_Height_cm - 2020-09-14



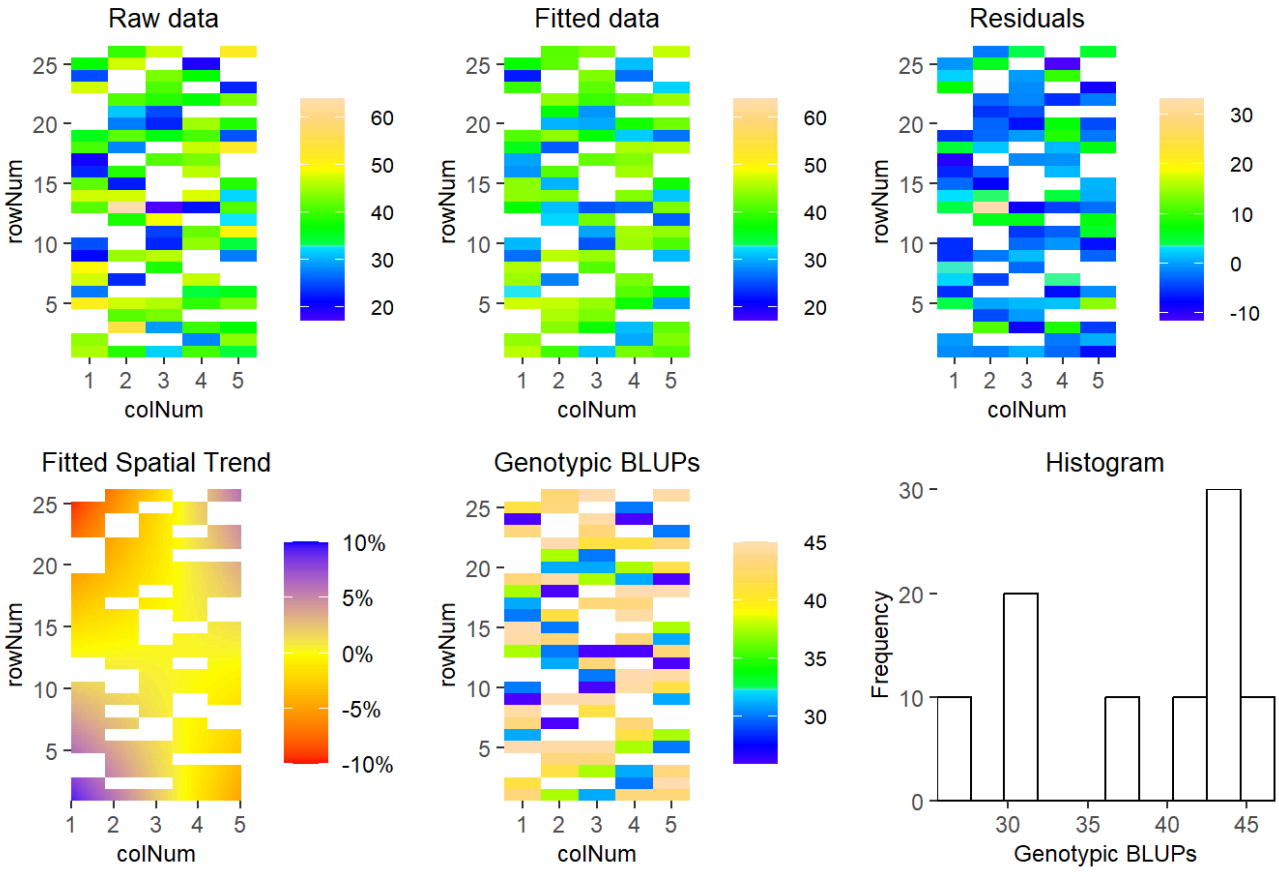
EPPN2020_ALSIA - S_Height_cm - 2020-09-16



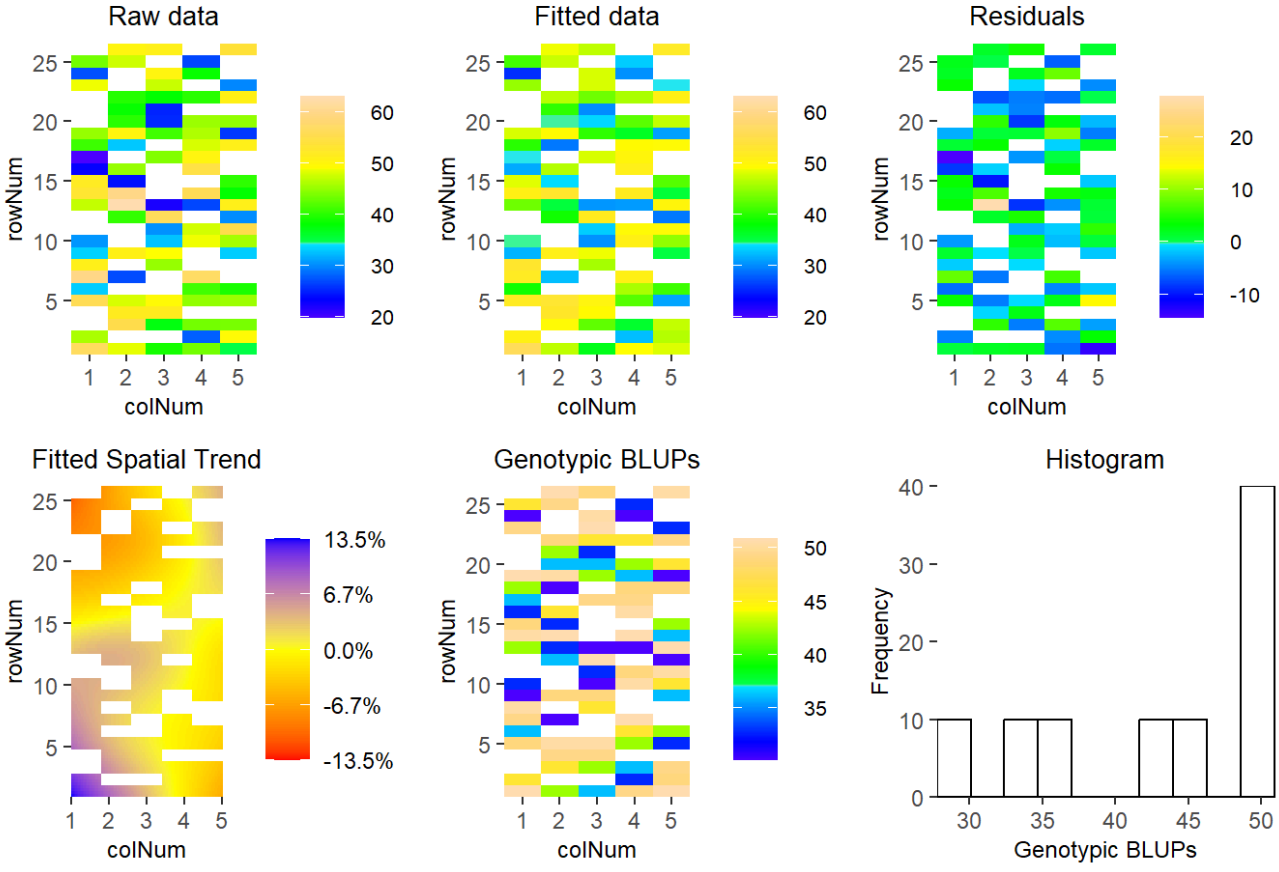
EPPN2020_ALSIA - S_Height_cm - 2020-09-18



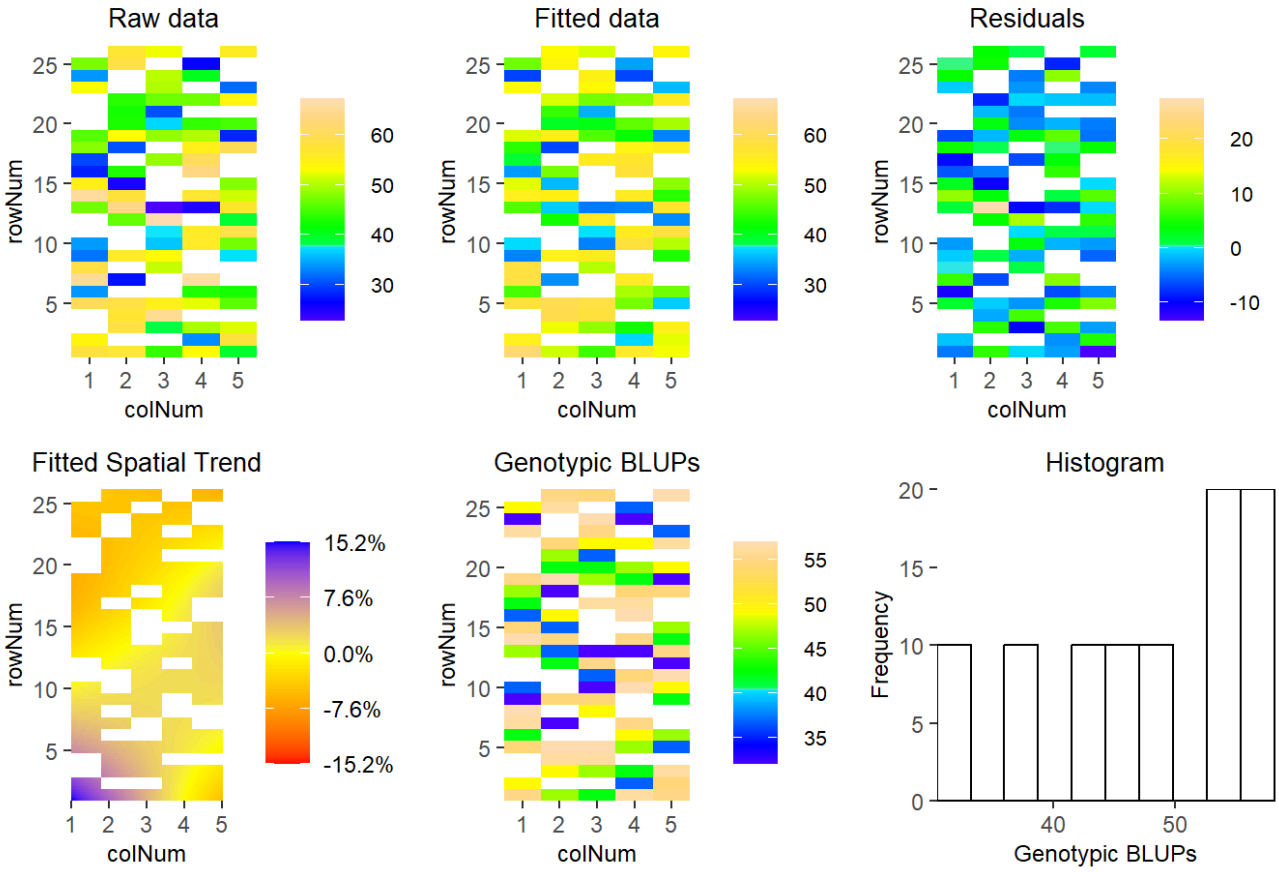
EPPN2020_ALSIA - S_Height_cm - 2020-09-21



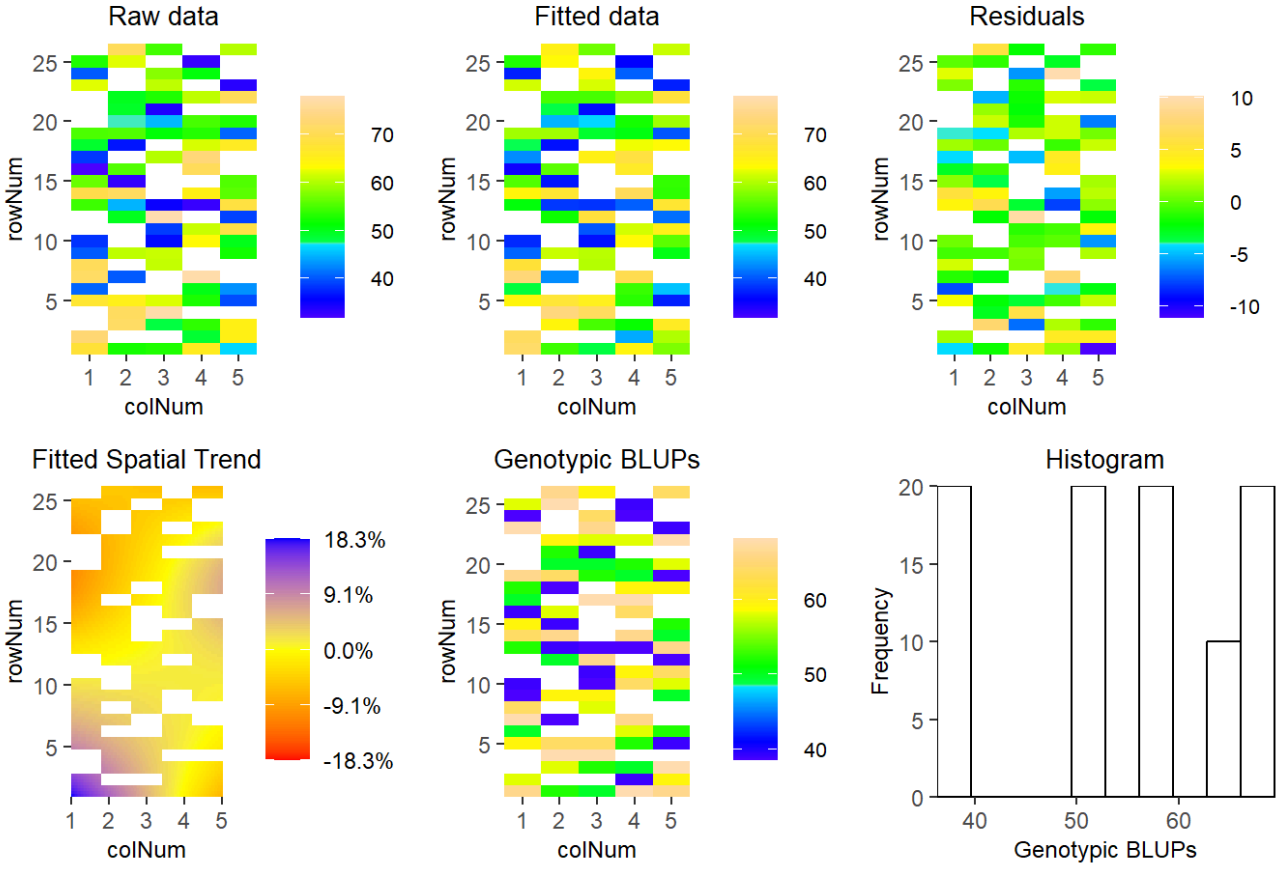
EPPN2020_ALSIA - S_Height_cm - 2020-09-23

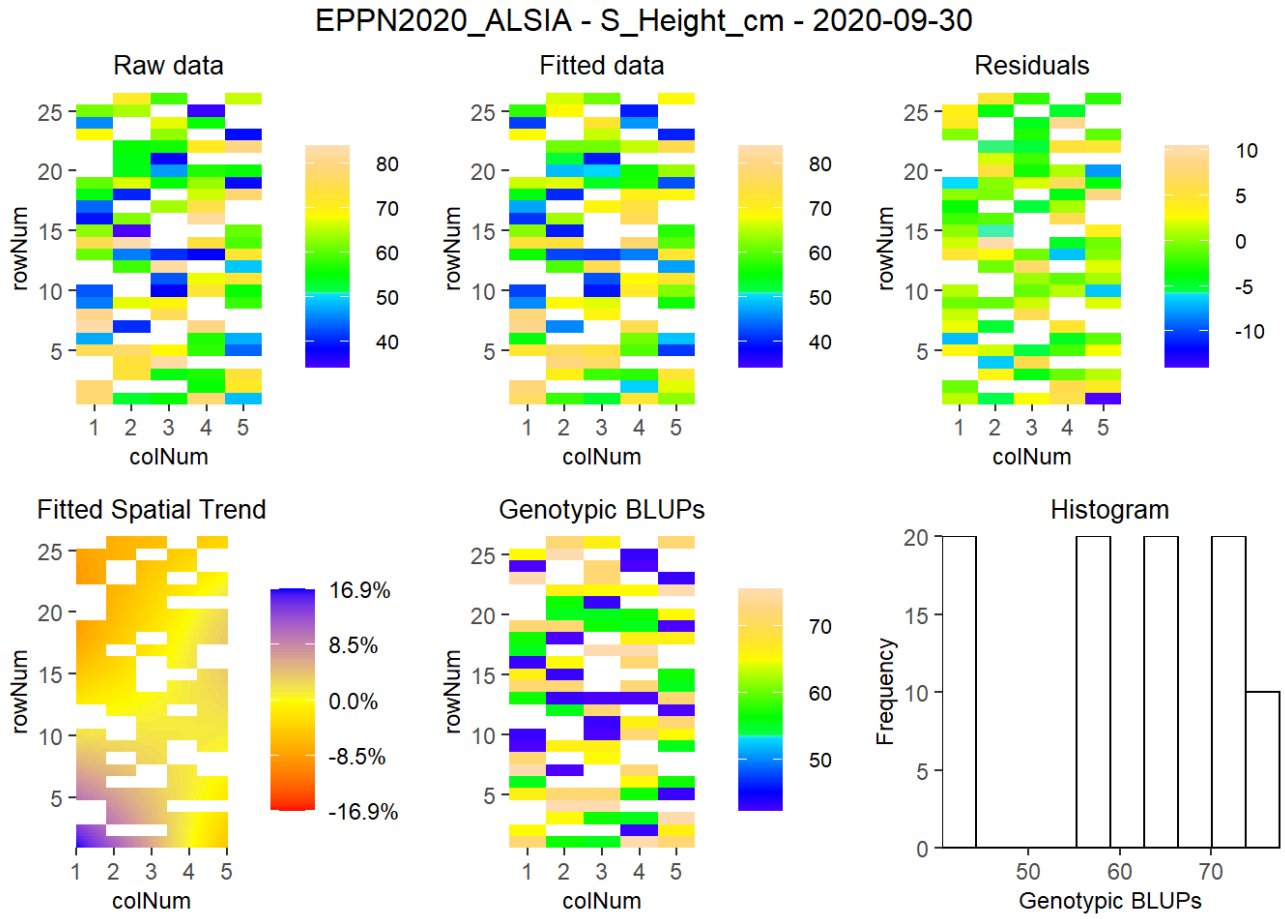


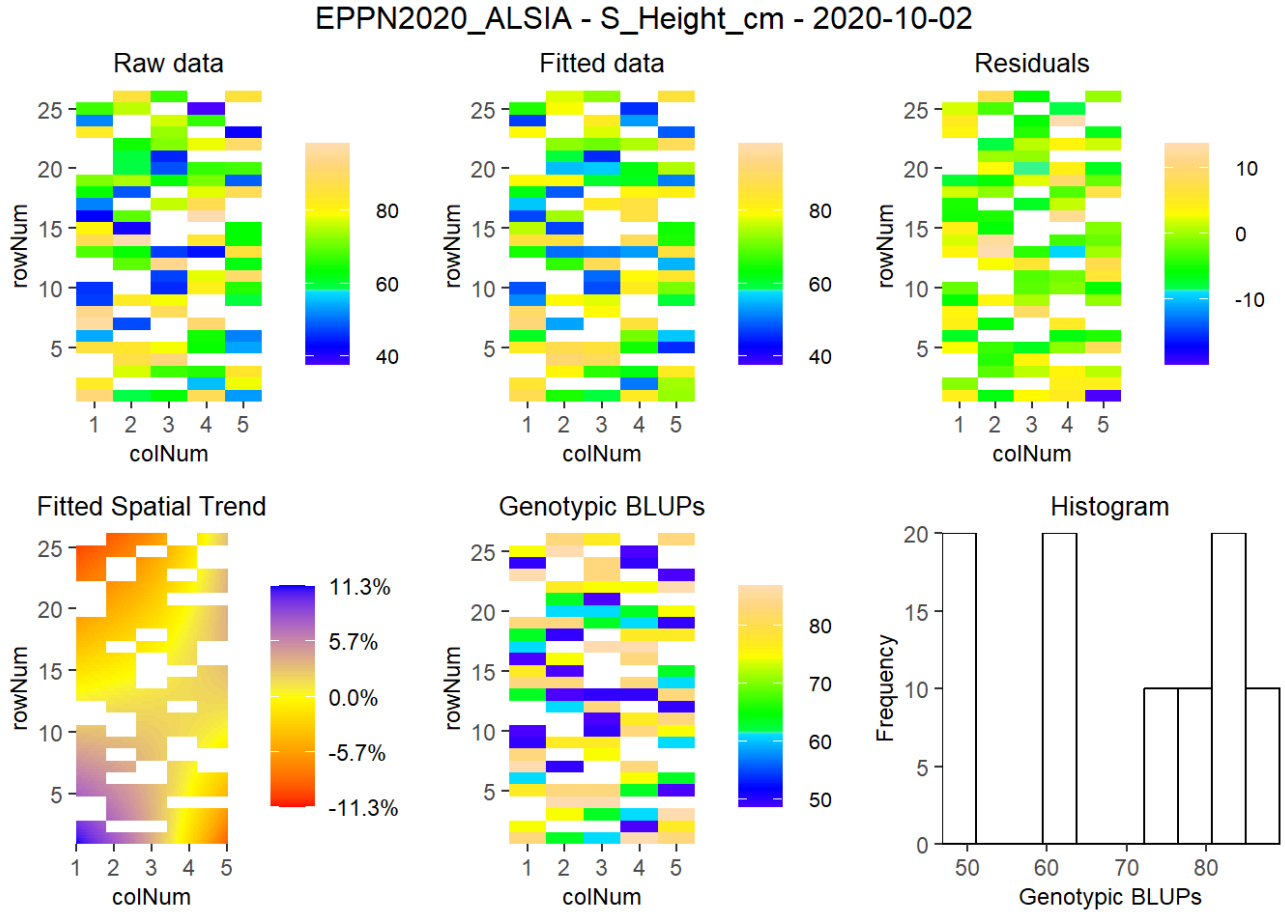
EPPN2020_ALSIA - S_Height_cm - 2020-09-25



EPPN2020_ALSIA - S_Height_cm - 2020-09-28

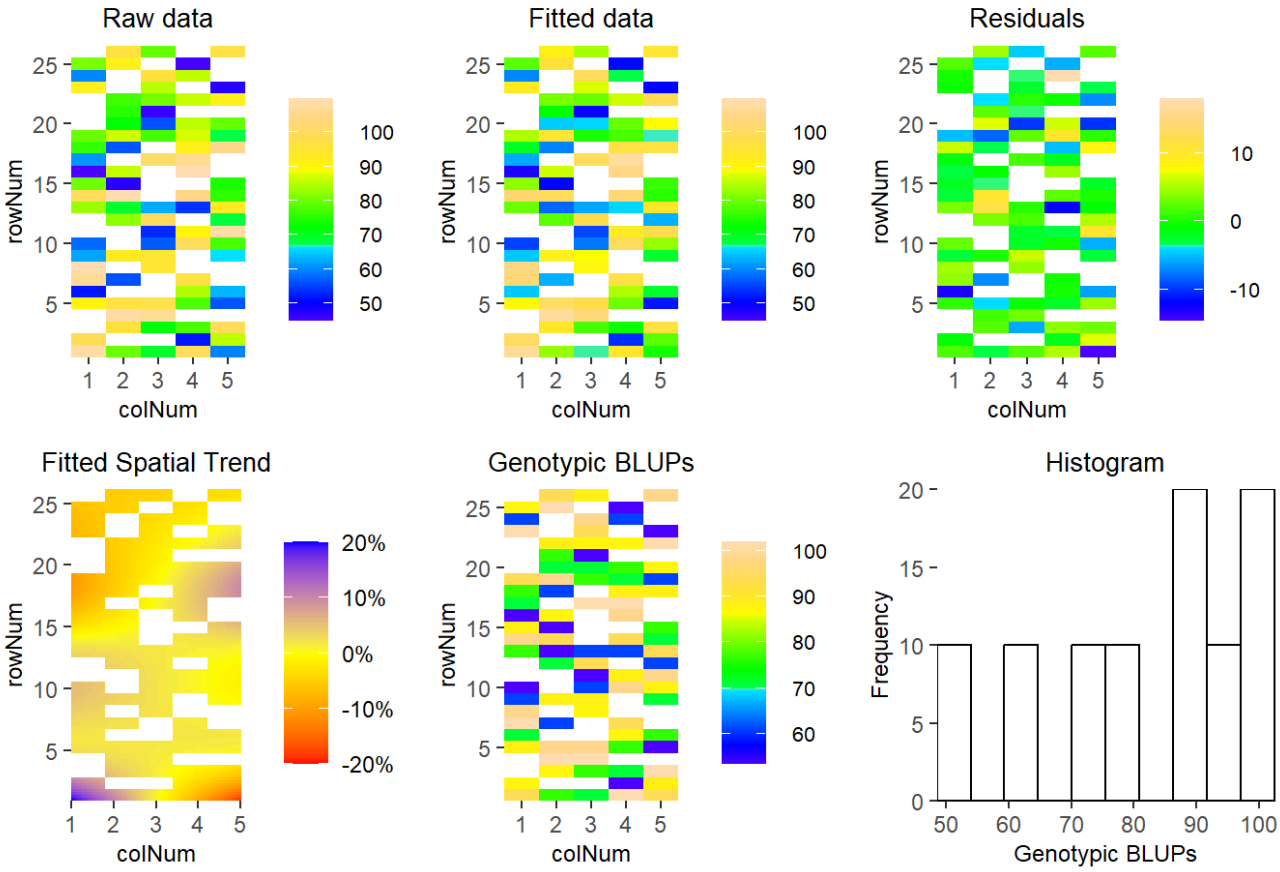




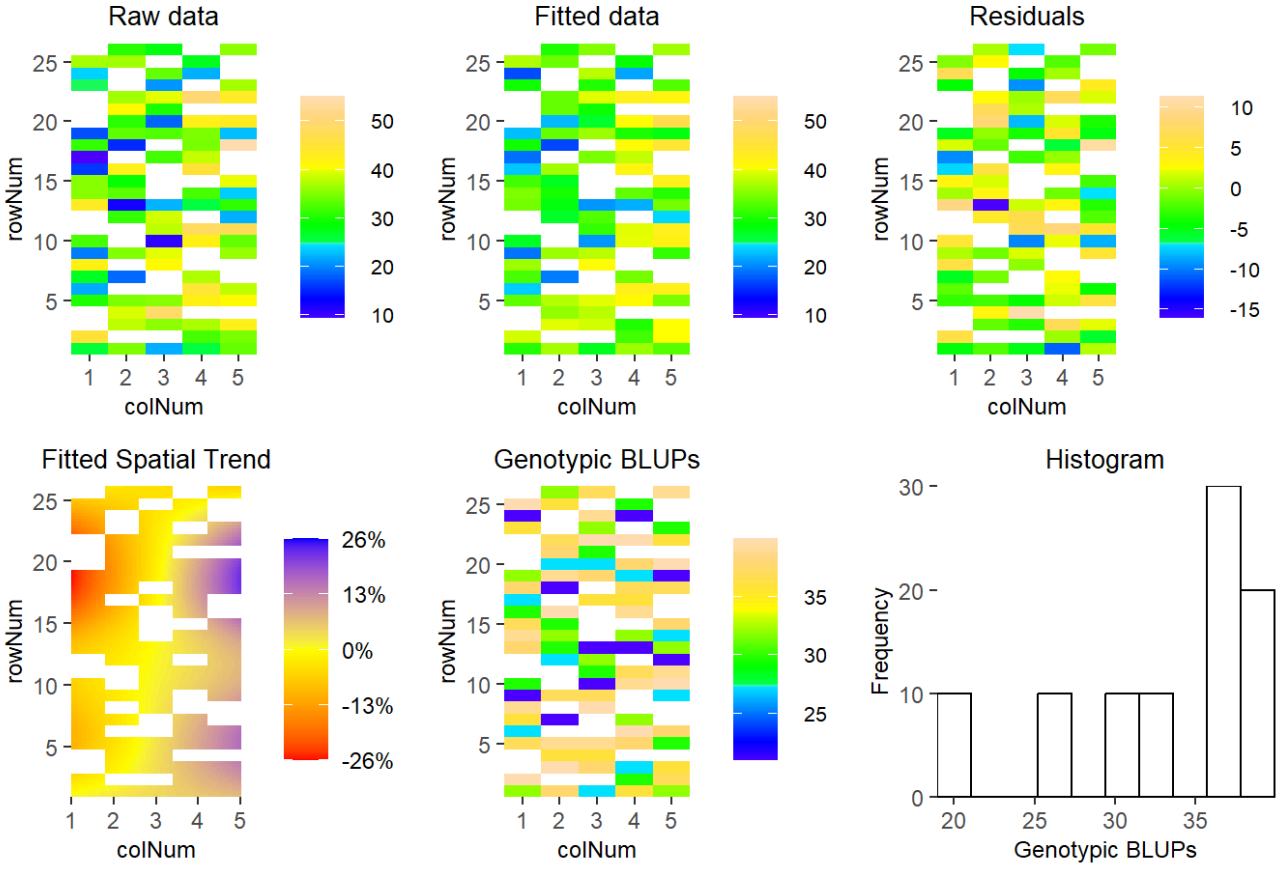



```
## Output at: C:/Users/elise/Documents/Mémoire/Main/Data/Extracted/ALSIA/S_Height_cm_mo
d.gif
```

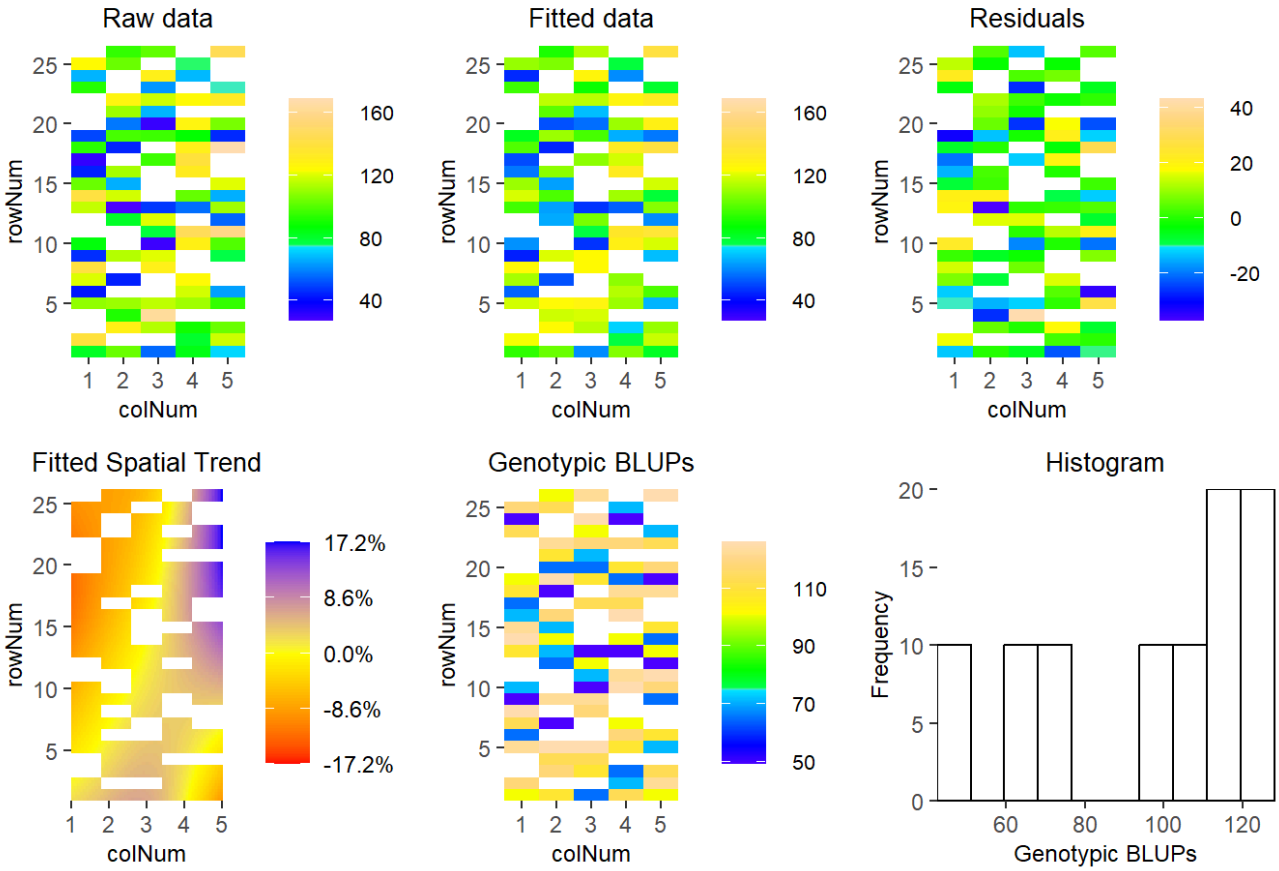
EPPN2020_ALSIA - S_Height_cm - 2020-10-05



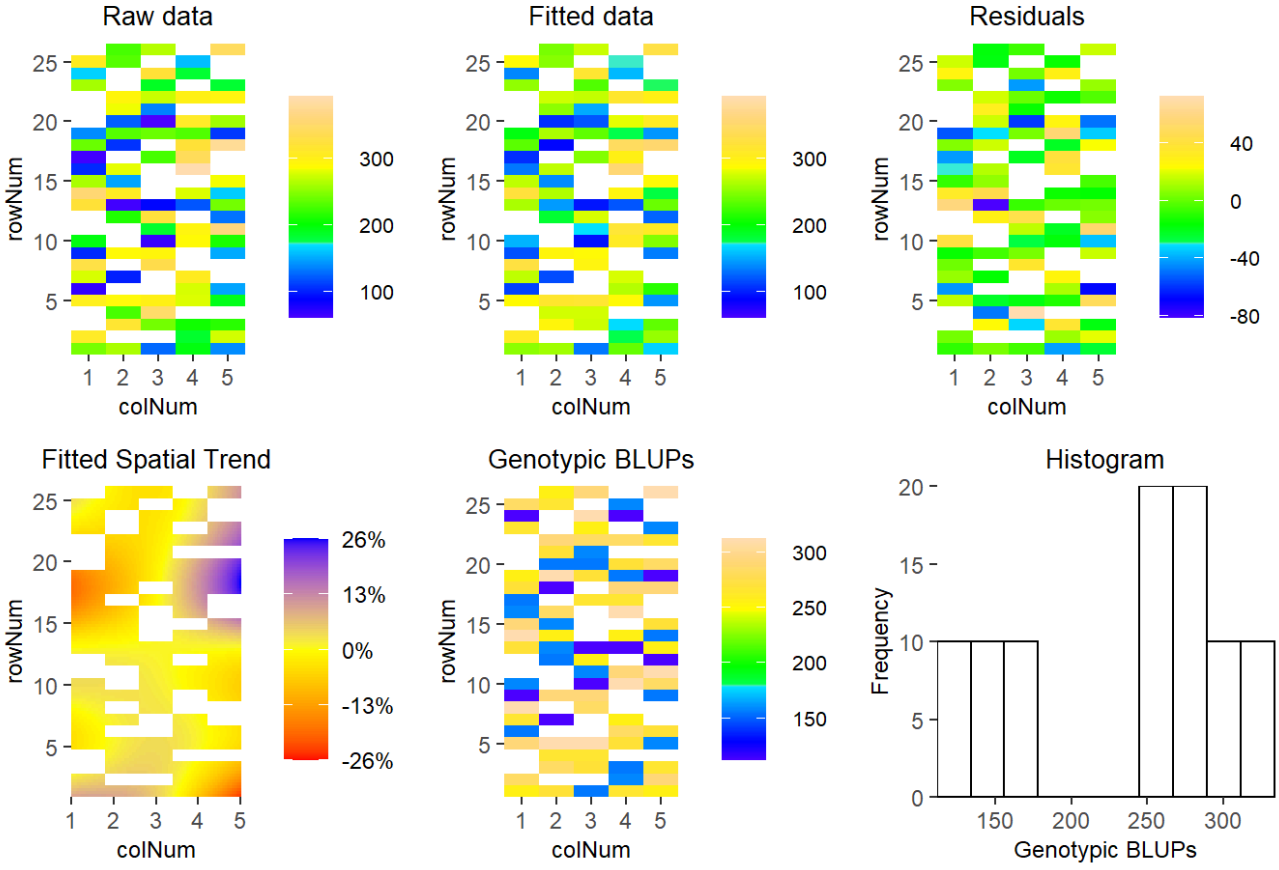
EPPN2020_ALSIA - S_Leaf_area_cmsquared - 2020-09-10



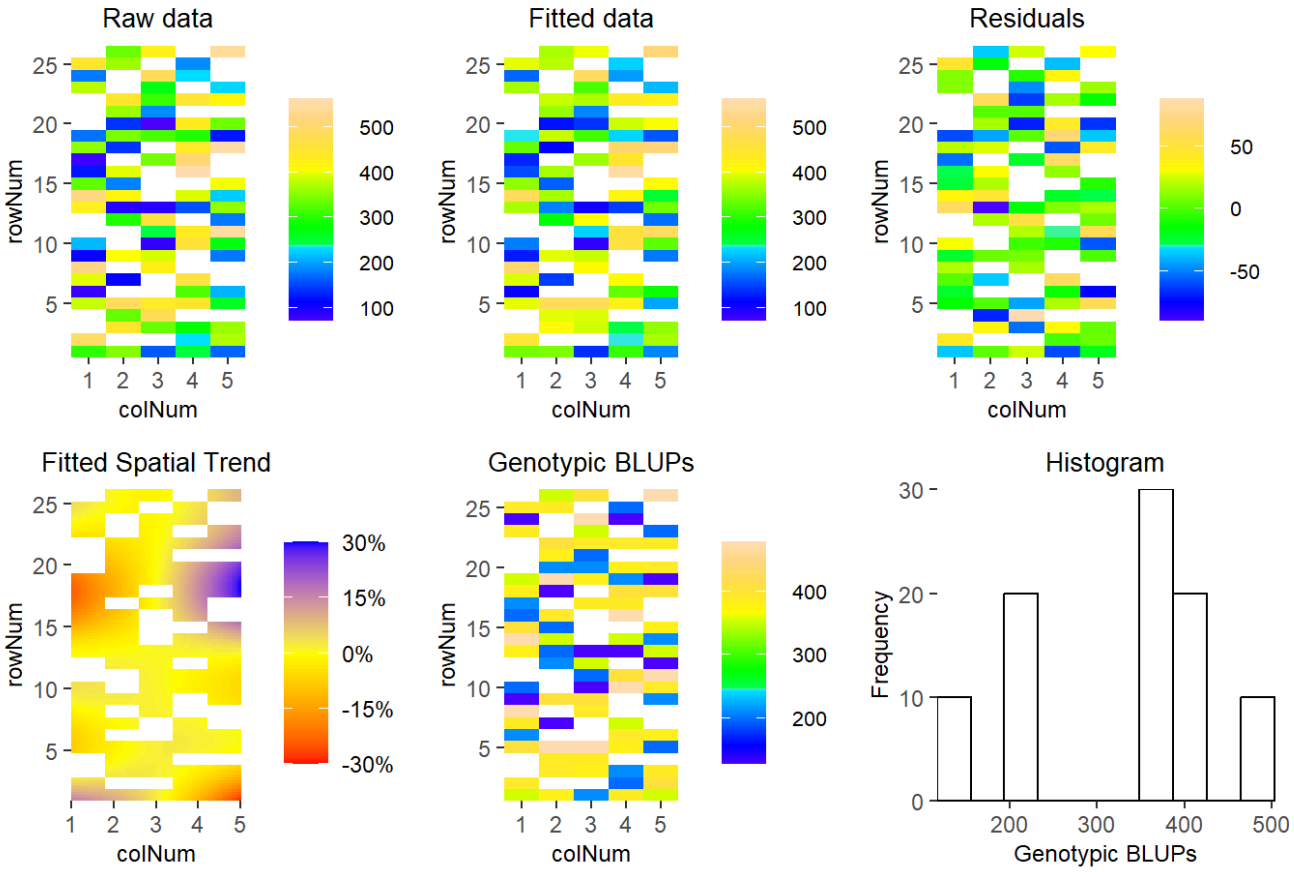
EPPN2020_ALSIA - S_Leaf_area_cmsquared - 2020-09-14



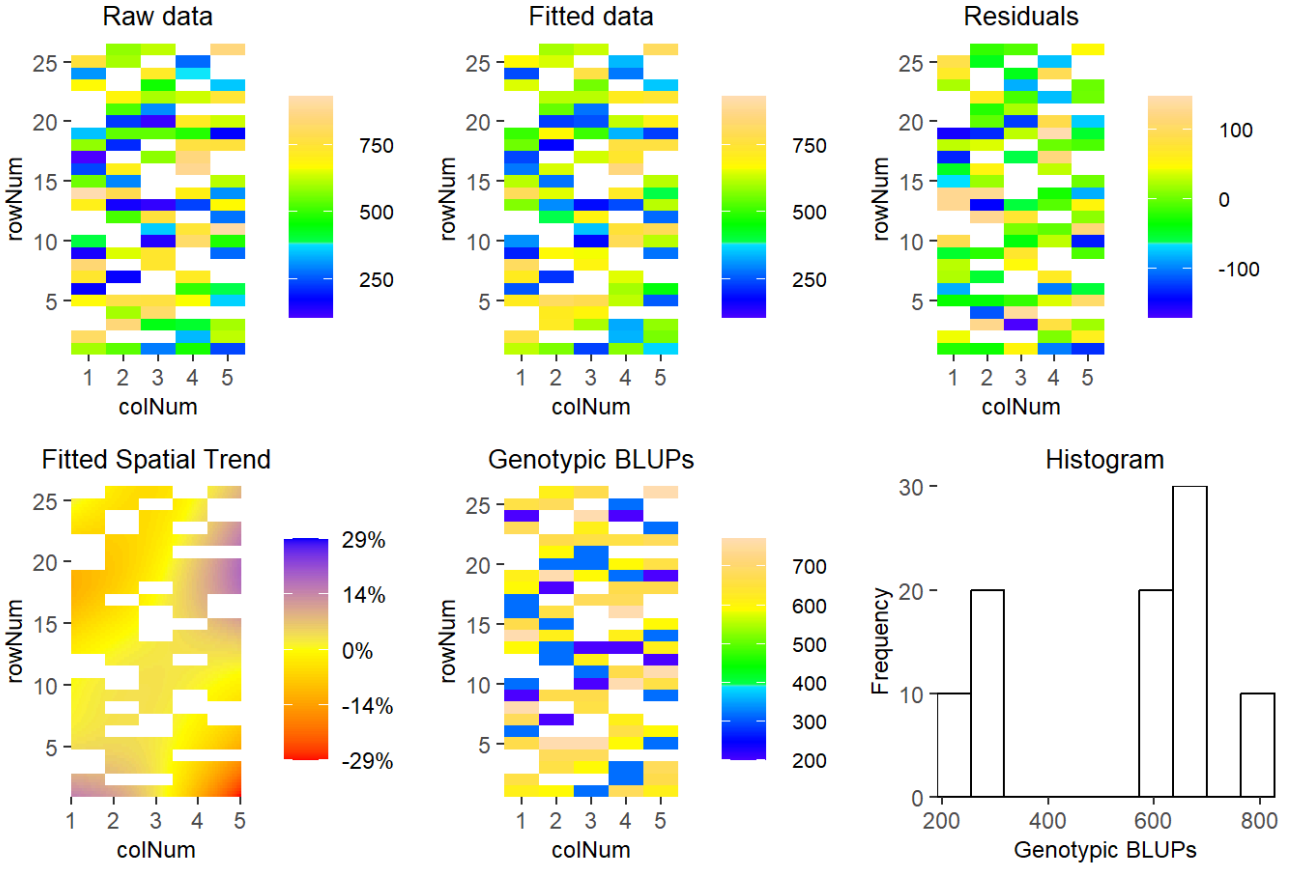
EPPN2020_ALSIA - S_Leaf_area_cmsquared - 2020-09-16

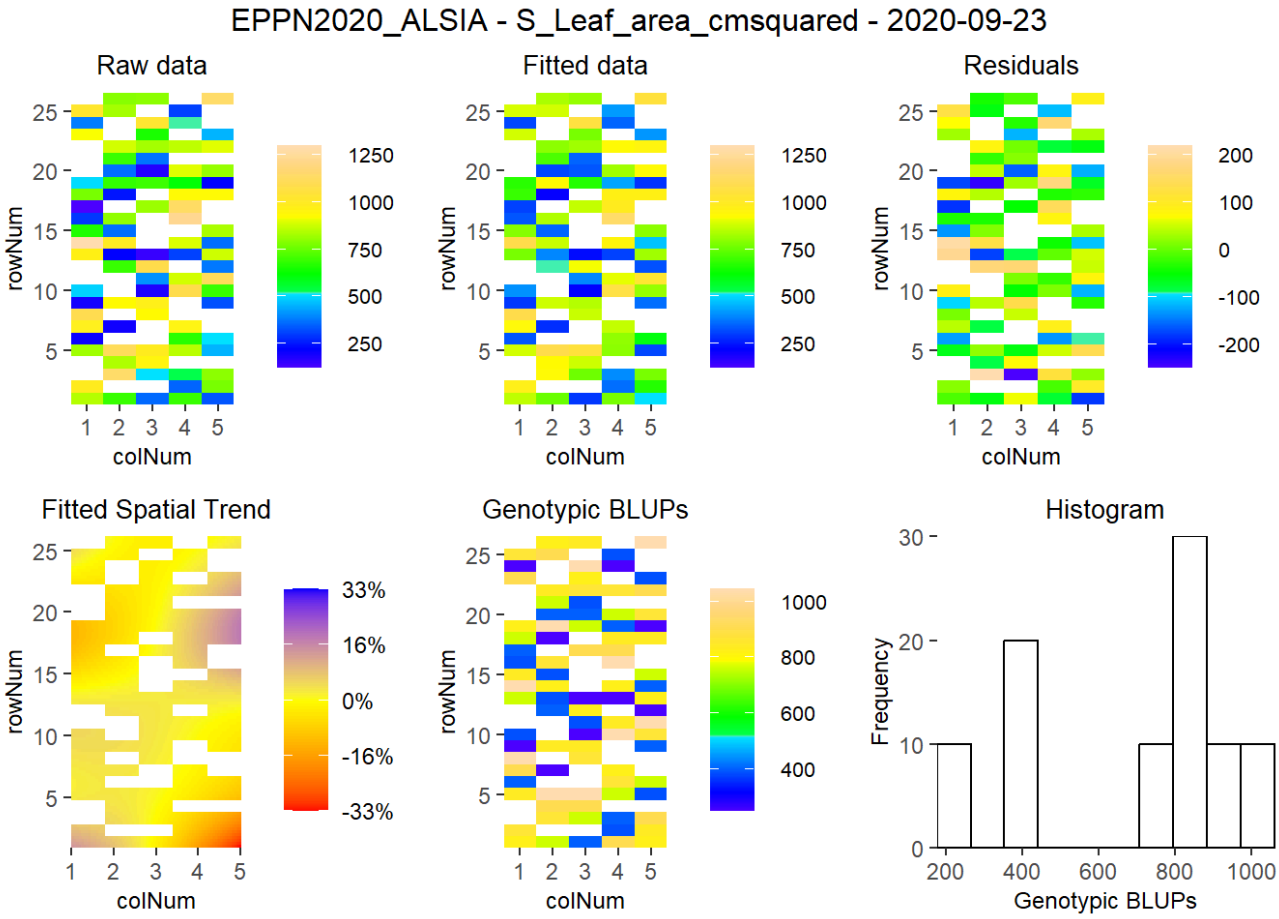


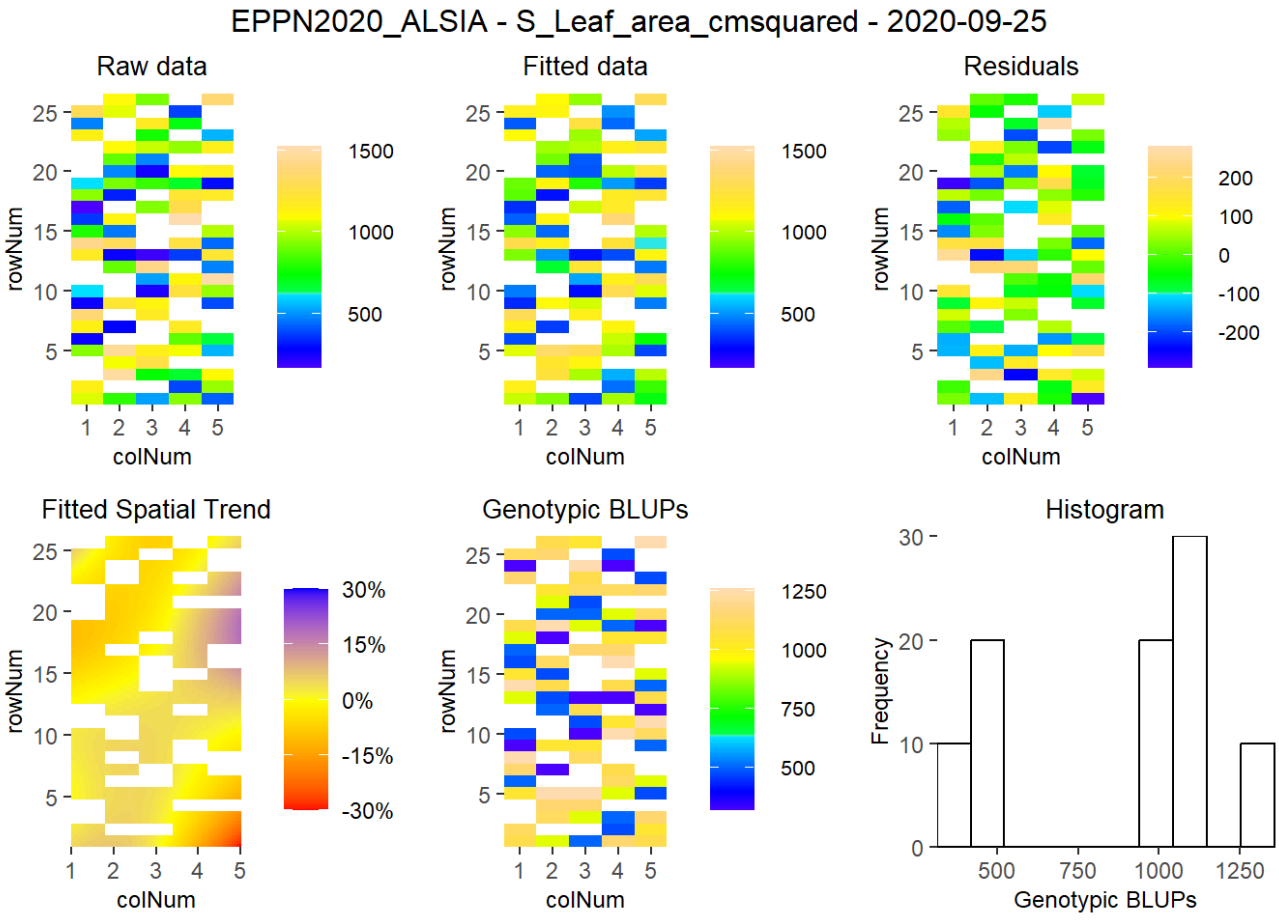
EPPN2020_ALSIA - S_Leaf_area_cmsquared - 2020-09-18



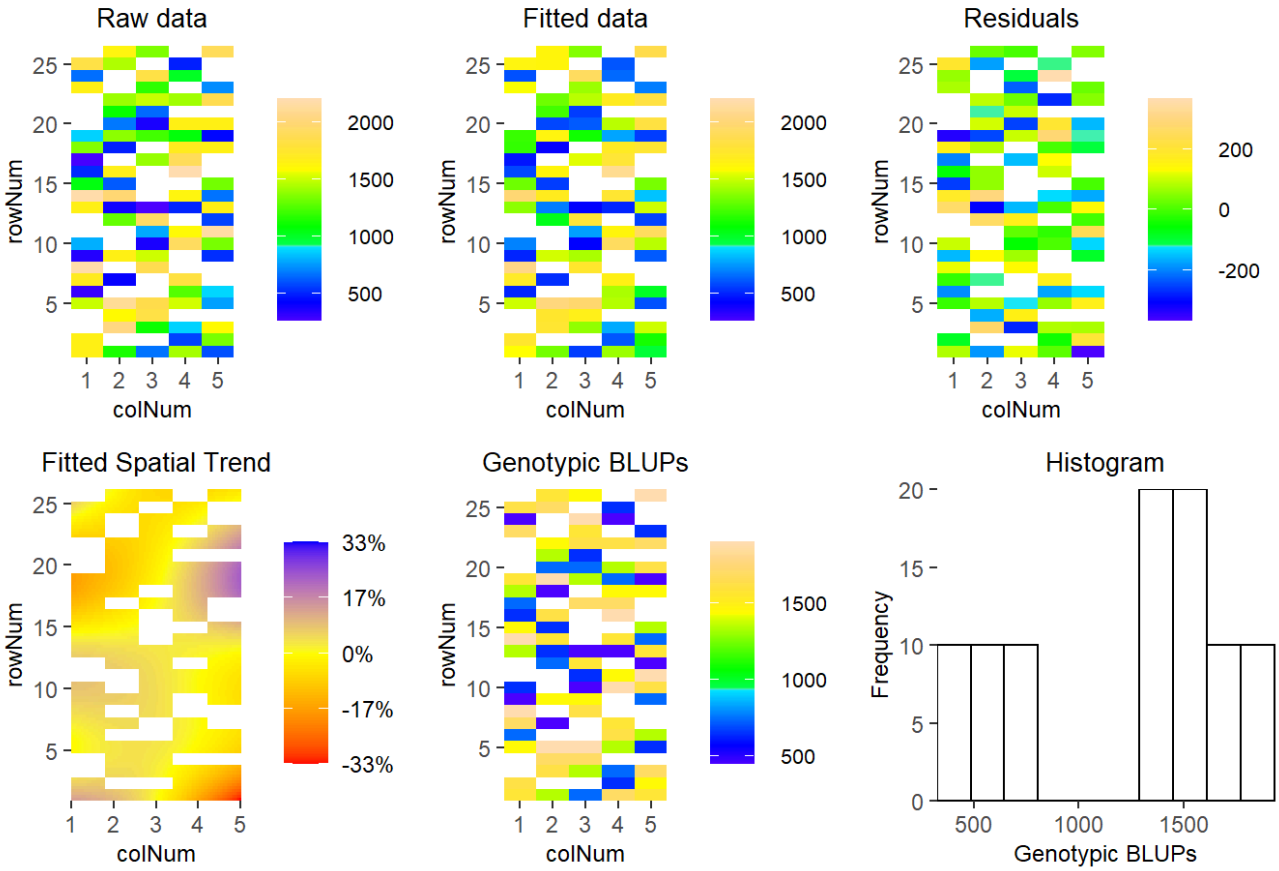
EPPN2020_ALSIA - S_Leaf_area_cmsquared - 2020-09-21



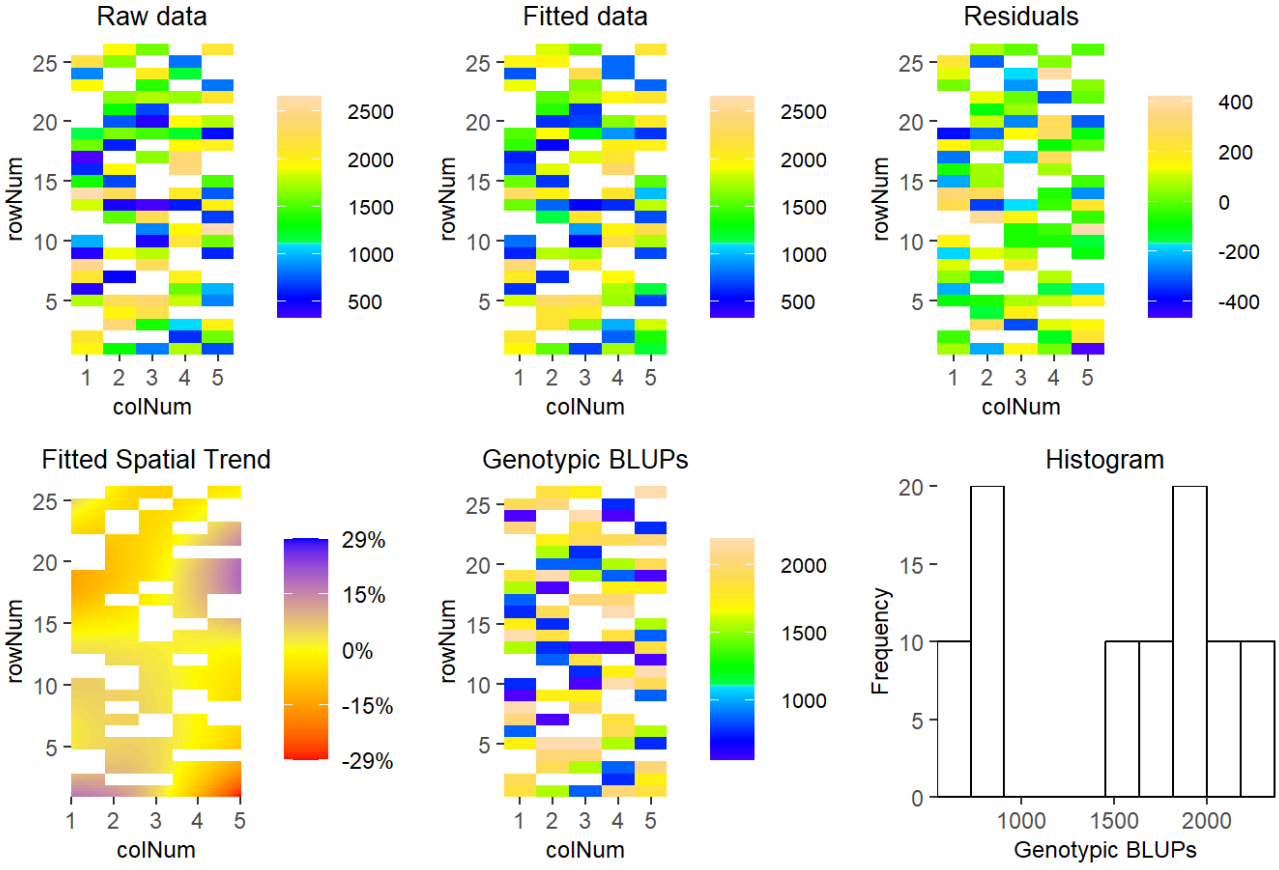

EPPN2020_ALSIA - S_Leaf_area_cmsquared - 2020-09-23
Raw data
Fitted data
Residuals
Fitted Spatial Trend
Genotypic BLUPs
Histogram
rowNum
colNum
Frequency
Genotypic BLUPs

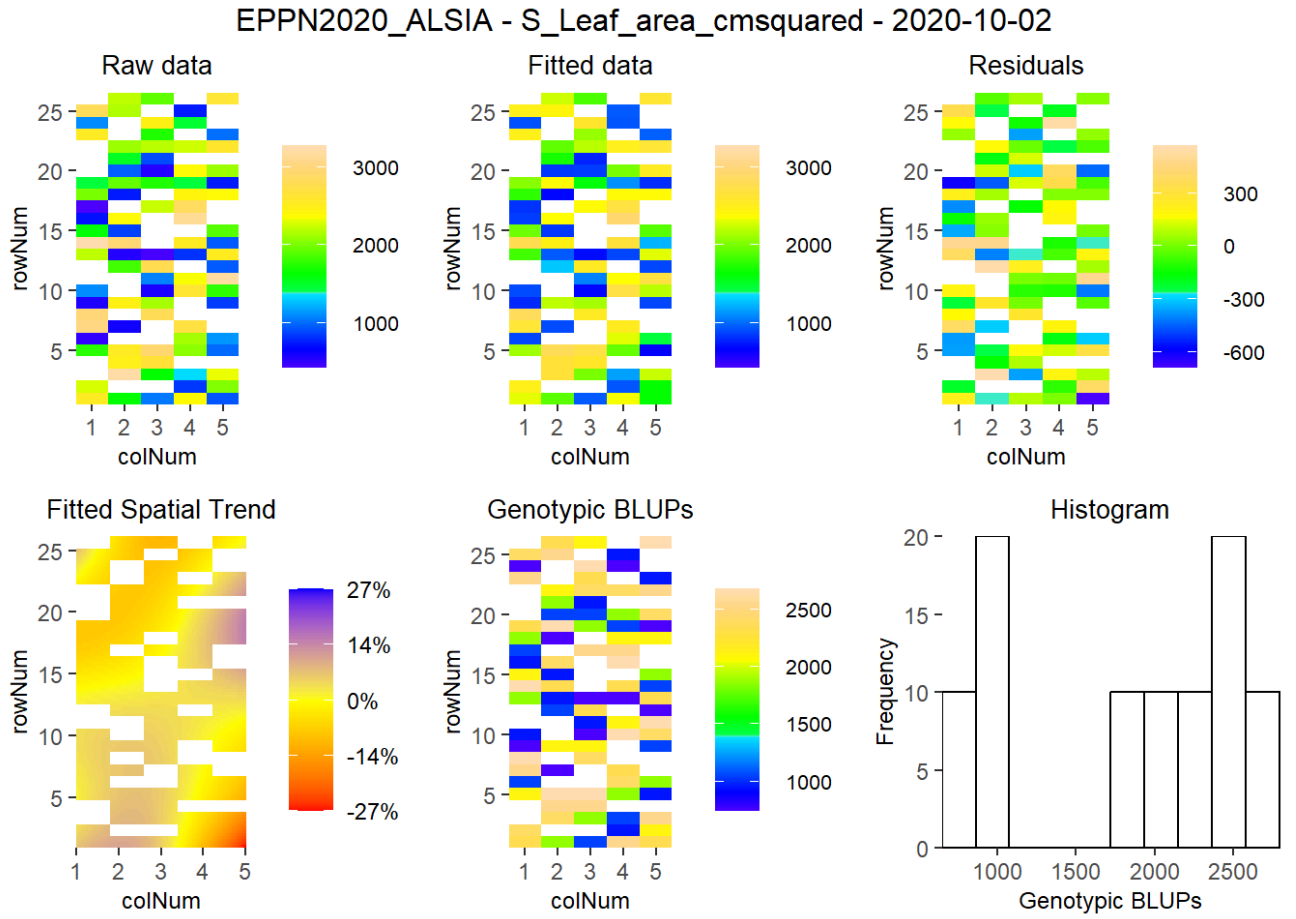

EPPN2020_ALSIA - S_Leaf_area_cmsquared - 2020-09-25
Raw data
Fitted data
Residuals
Fitted Spatial Trend
Genotypic BLUPs
Histogram
rowNum
colNum
Frequency
Genotypic BLUPs

EPPN2020_ALSIA - S_Leaf_area_cmsquared - 2020-09-28

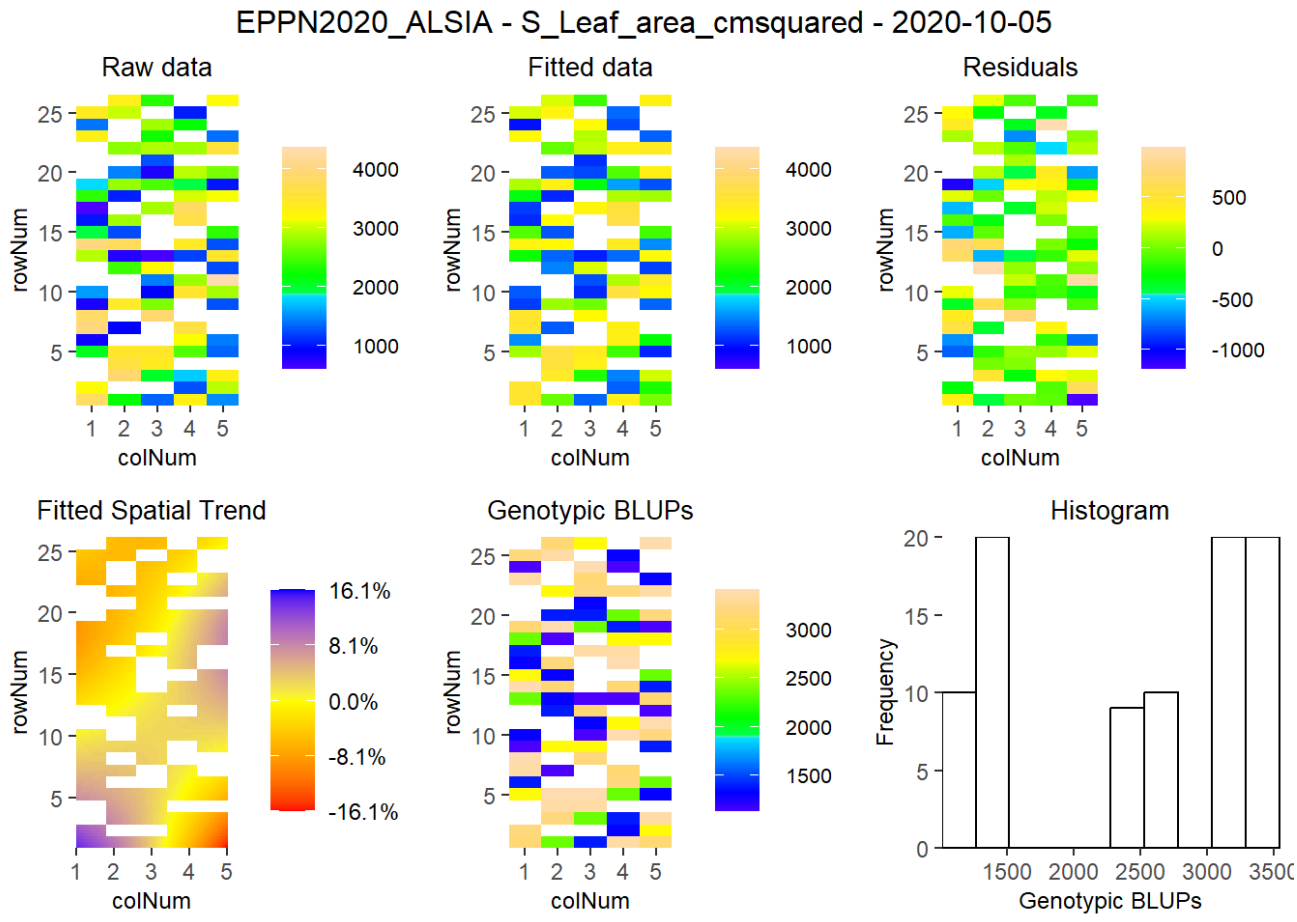


EPPN2020_ALSIA - S_Leaf_area_cmsquared - 2020-09-30

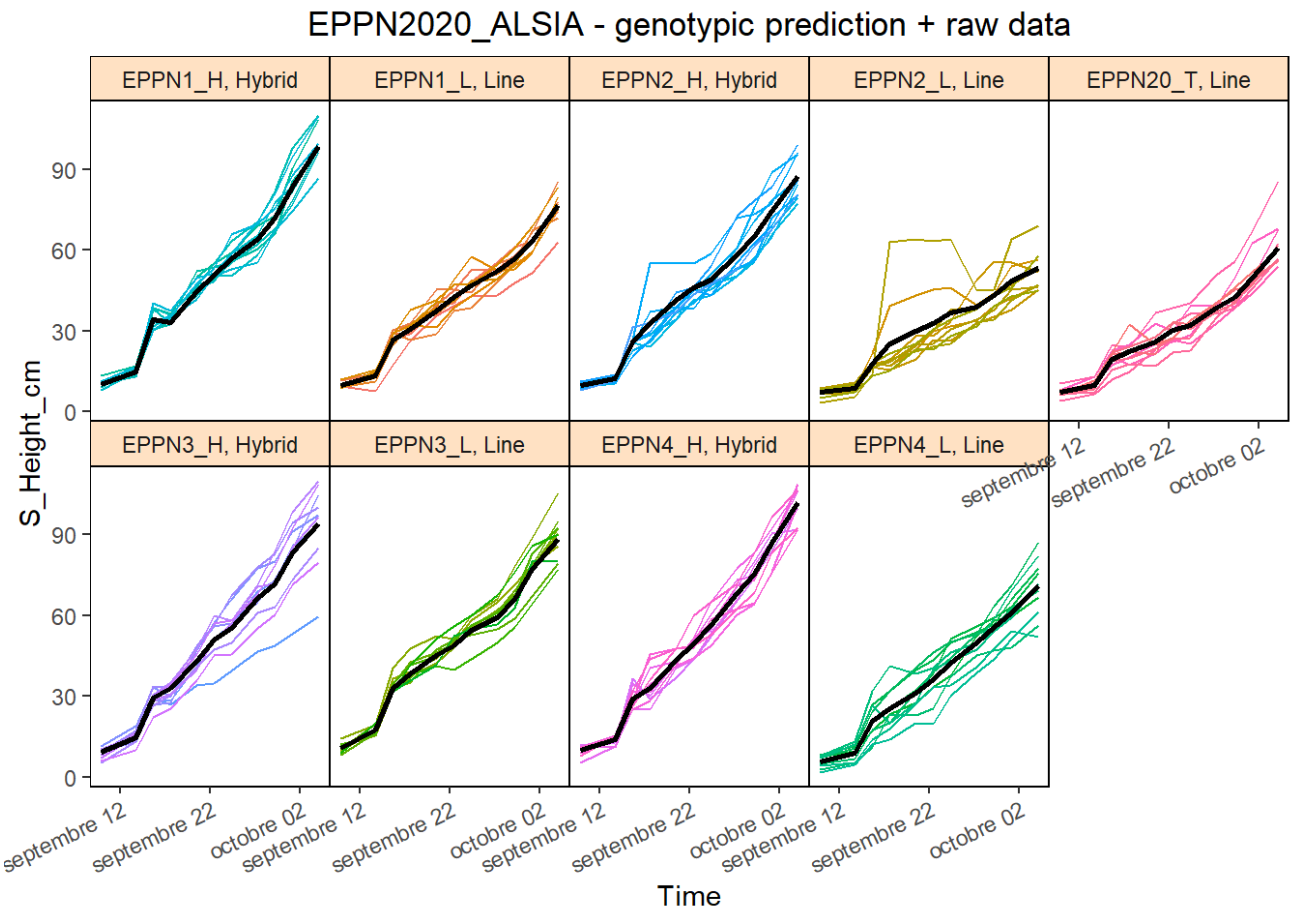


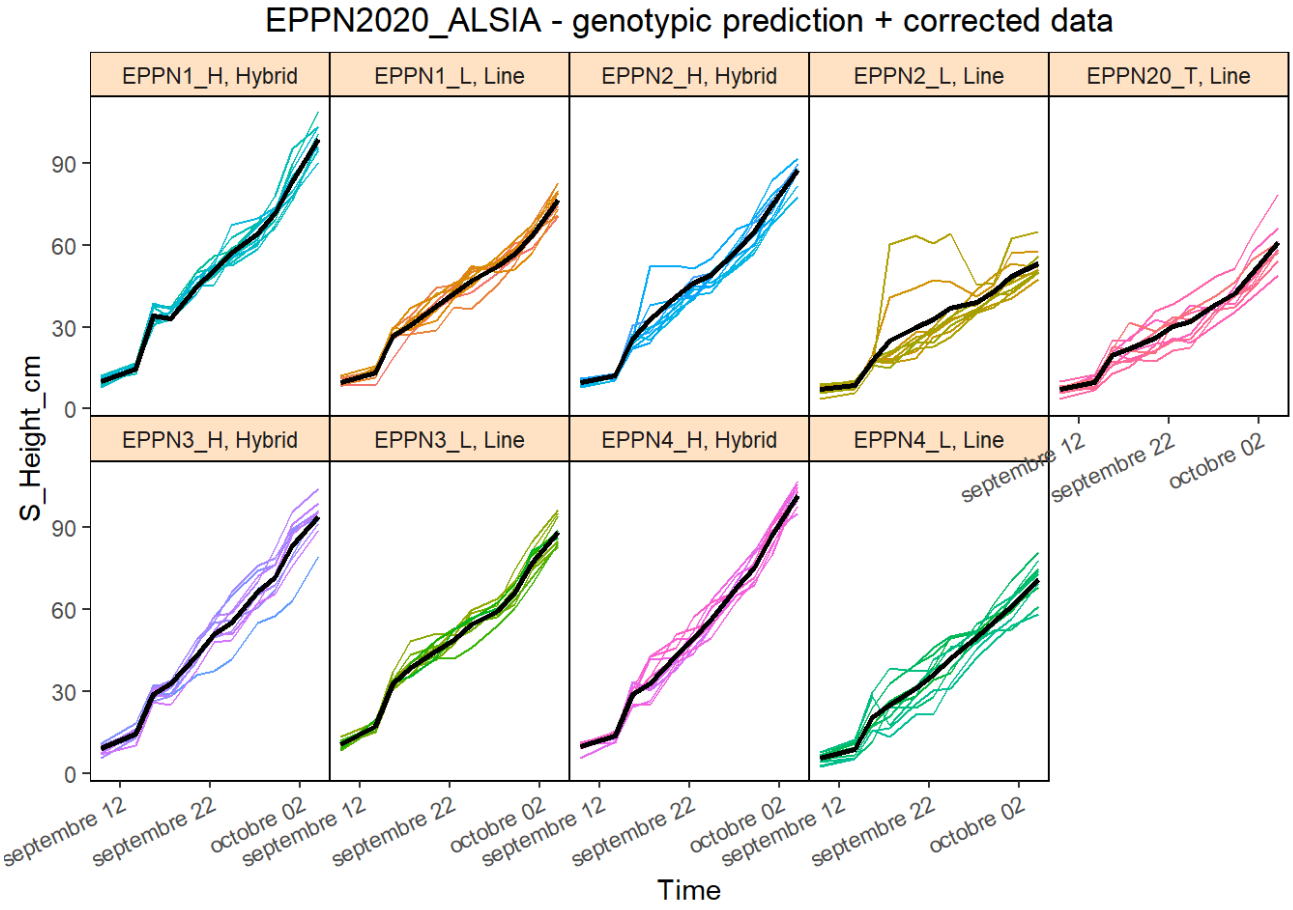


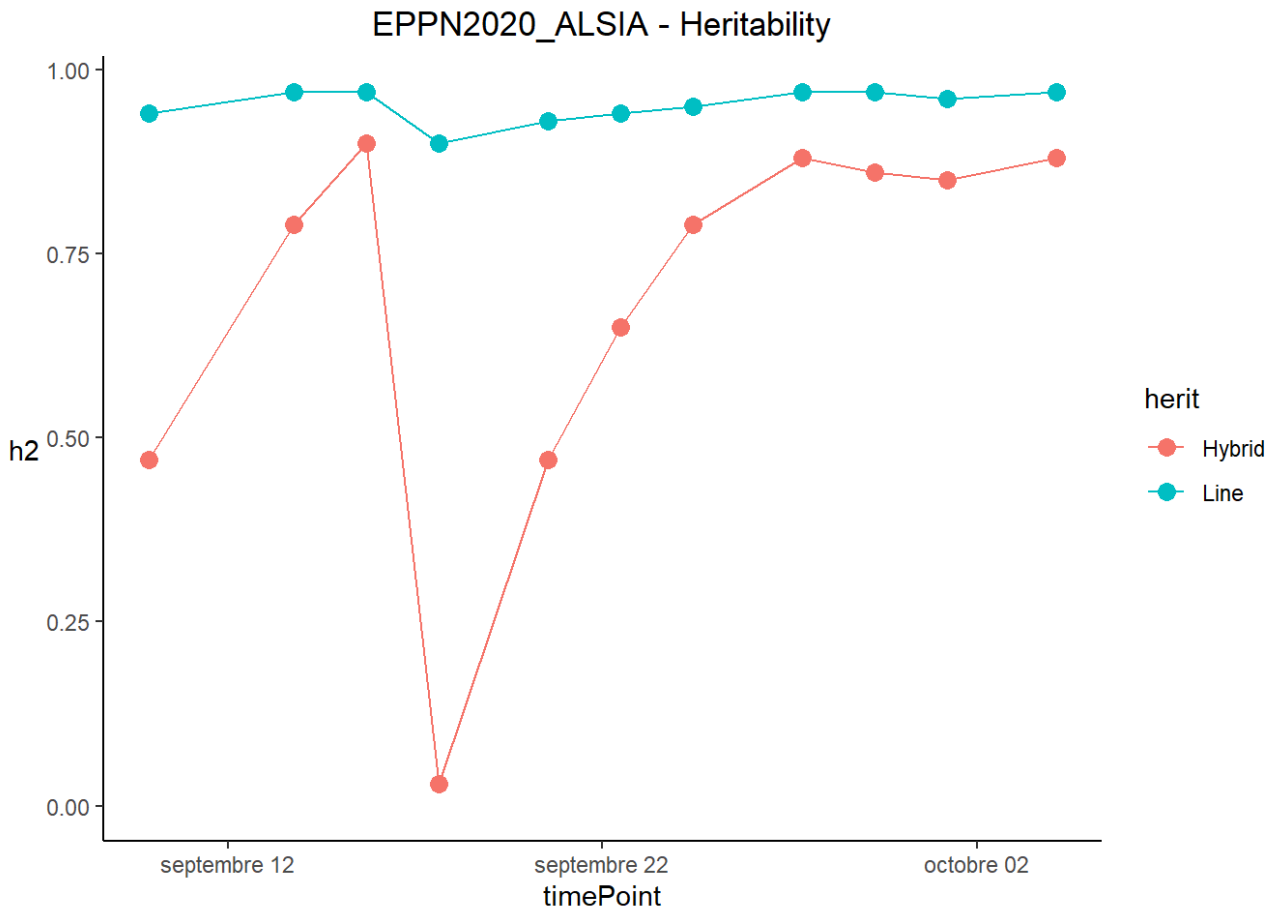

```
## Output at: C:/Users/elise/Documents/Mémoire/Main/Data/Extracted/ALSIA/S_Leaf_area_cm
squared_mod.gif
```

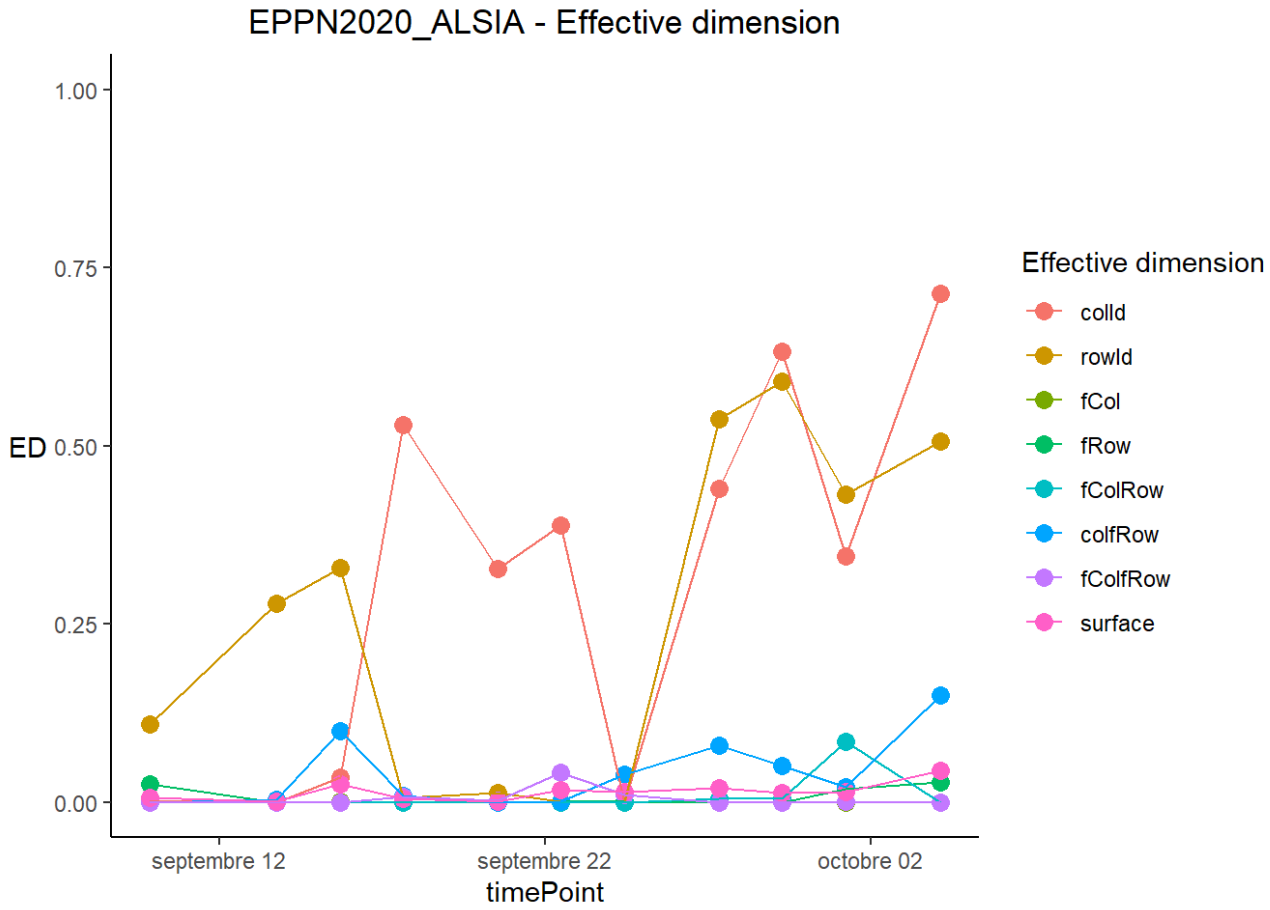


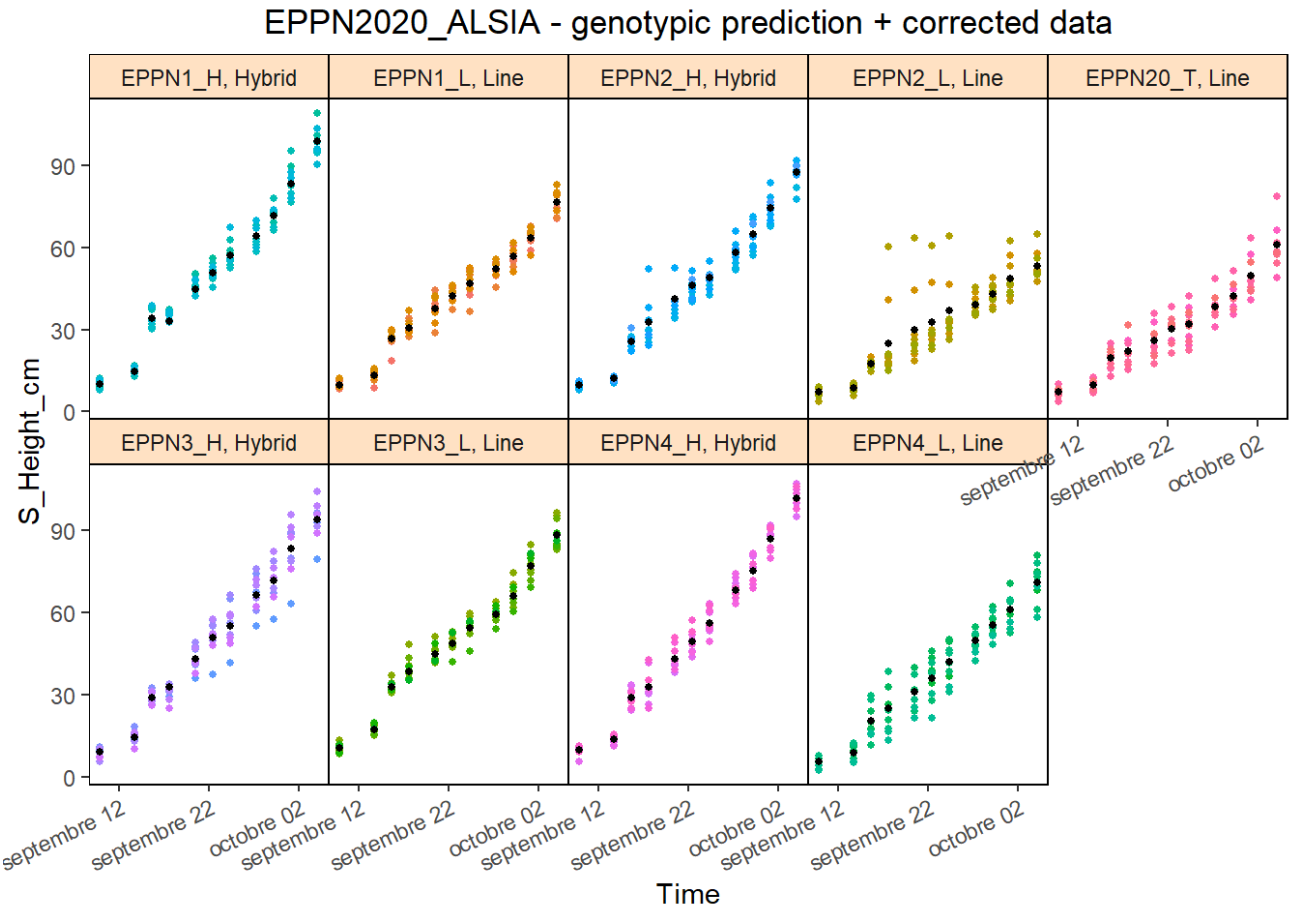
```
for (trait_name in traits) {
  mod_name <- paste0("modTP_", trait_name)
    if (exists(mod_name)) {
    mod <- get(mod_name)

    plot(mod,
         plotType = "rawPred",
         plotLine = TRUE)

    plot(mod,
         plotType = "corrPred",
         plotLine = TRUE)

    plot(mod,
         plotType = "herit",
         yLim = c(0, 0.5))

    plot(mod,
         plotType = "effDim",
         EDType = "ratio",
         yLim = c(0, 1))

    plot(mod,
         plotType = "corrPred")
  } else {
    cat("No model found for the trait", trait_name, "\n")
  }
}
```

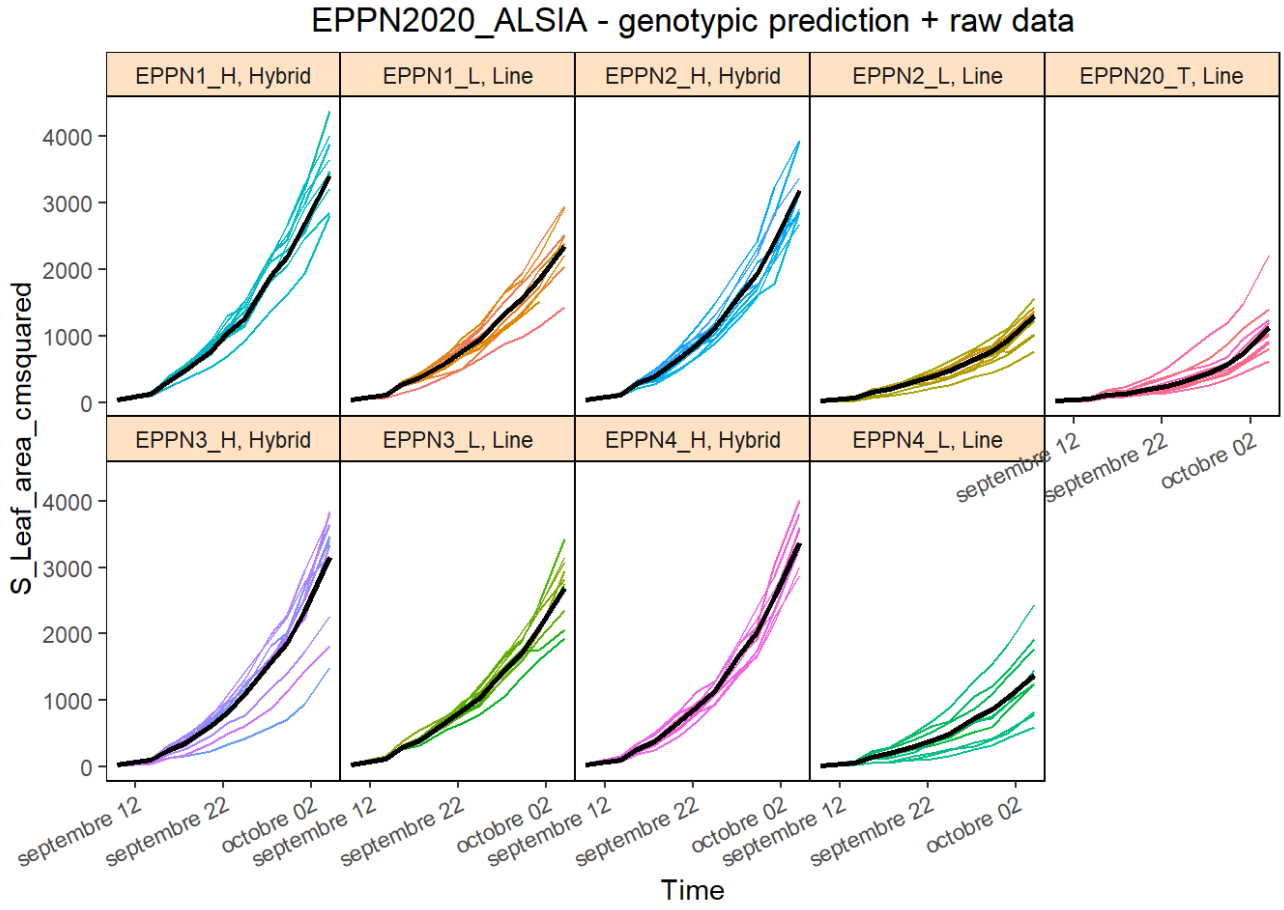

EPPN2020_ALSIA - genotypic prediction + raw data
EPPN1_H, Hybrid
EPPN1_L, Line
EPPN2_H, Hybrid
EPPN2_L, Line
EPPN20_T, Line
EPPN3_H, Hybrid
EPPN3_L, Line
EPPN4_H, Hybrid
EPPN4_L, Line
S_Height_cm
0
30
60
90
septembre 12
septembre 22
octobre 02
Time

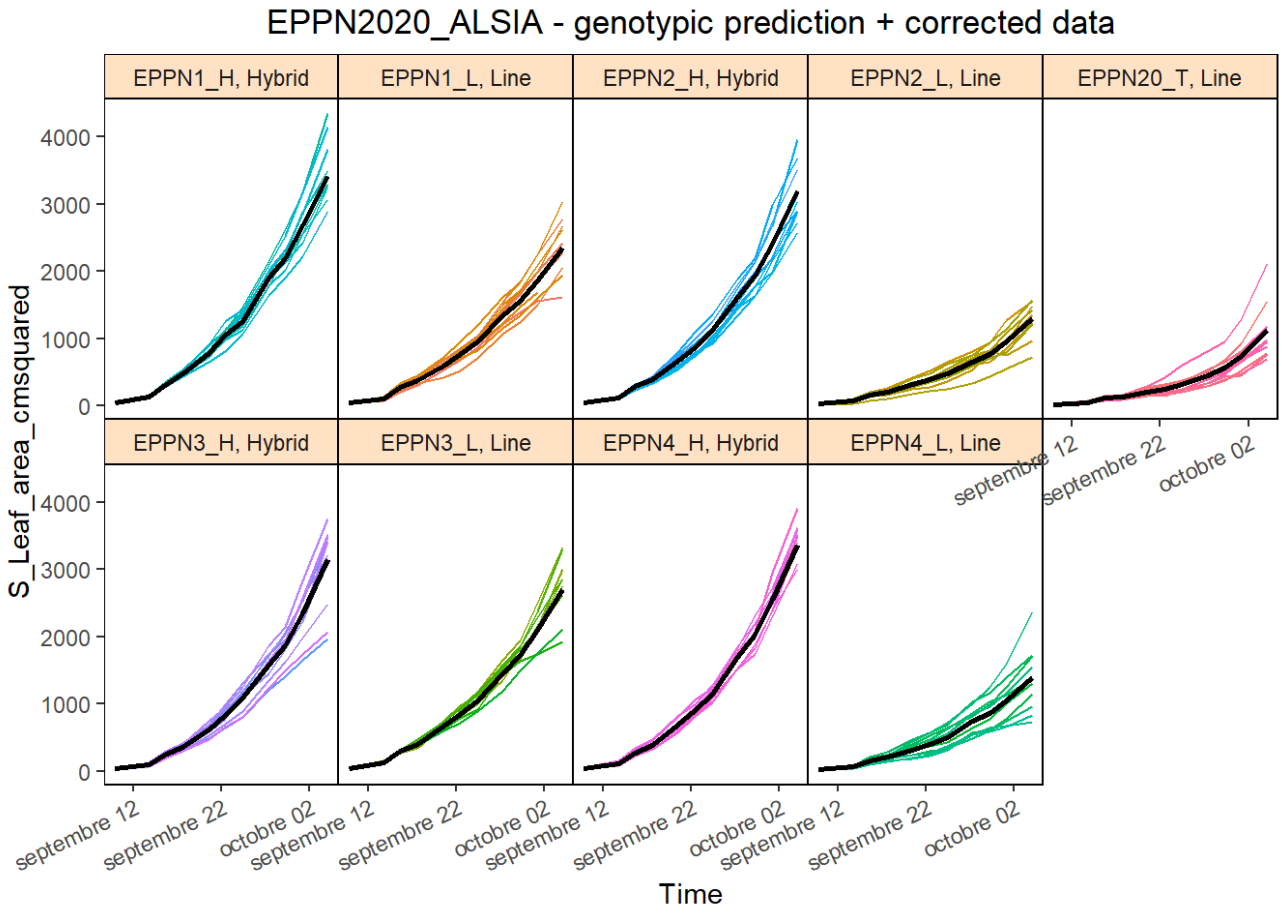

EPPN2020_ALSIA - genotypic prediction + corrected data
EPPN1_H, Hybrid
EPPN1_L, Line
EPPN2_H, Hybrid
EPPN2_L, Line
EPPN20_T, Line
EPPN3_H, Hybrid
EPPN3_L, Line
EPPN4_H, Hybrid
EPPN4_L, Line
S_Height_cm
0
30
60
90
septembre 12
septembre 22
octobre 02
Time

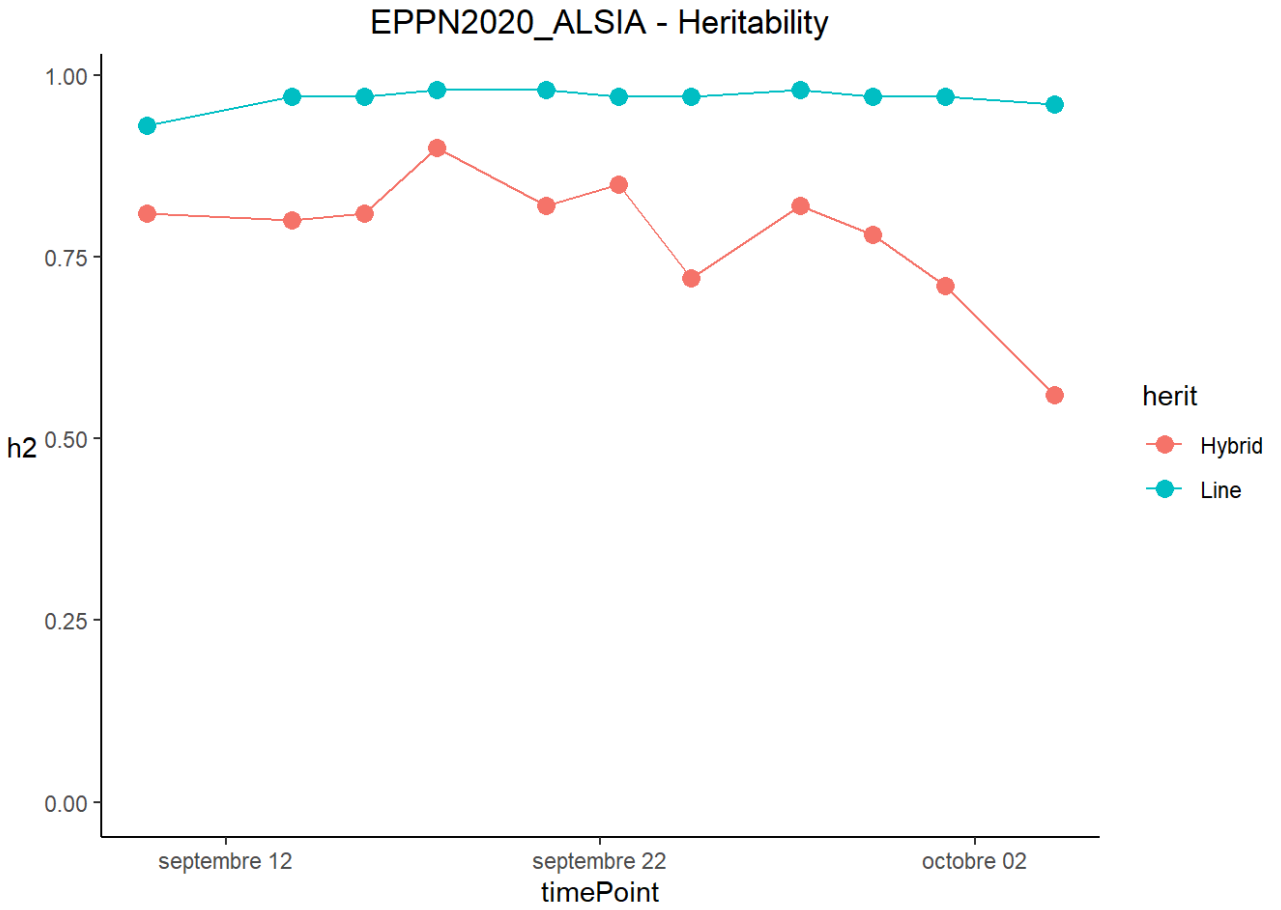

EPPN2020_ALSIA - Heritability
1.00
0.75
0.50
0.25
0.00
h2
septembre 12
septembre 22
octobre 02
timePoint
herit
Hybrid
Line

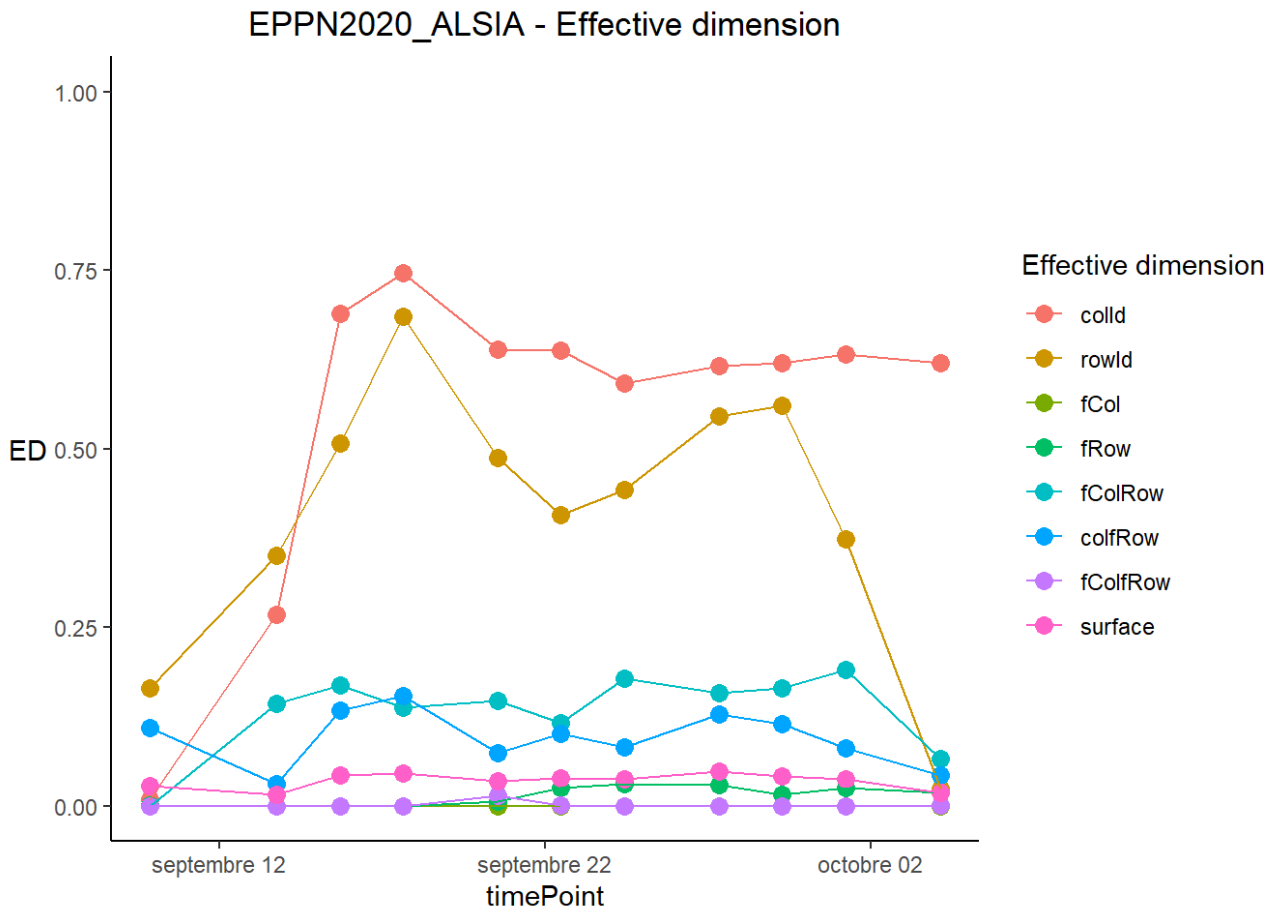

EPPN2020_ALSIA - Effective dimension
1.00
0.75
0.50
0.25
0.00
ED
septembre 12
septembre 22
octobre 02
timePoint
Effective dimension
colId
rowId
fCol
fRow
fColRow
colfRow
fColfRow
surface

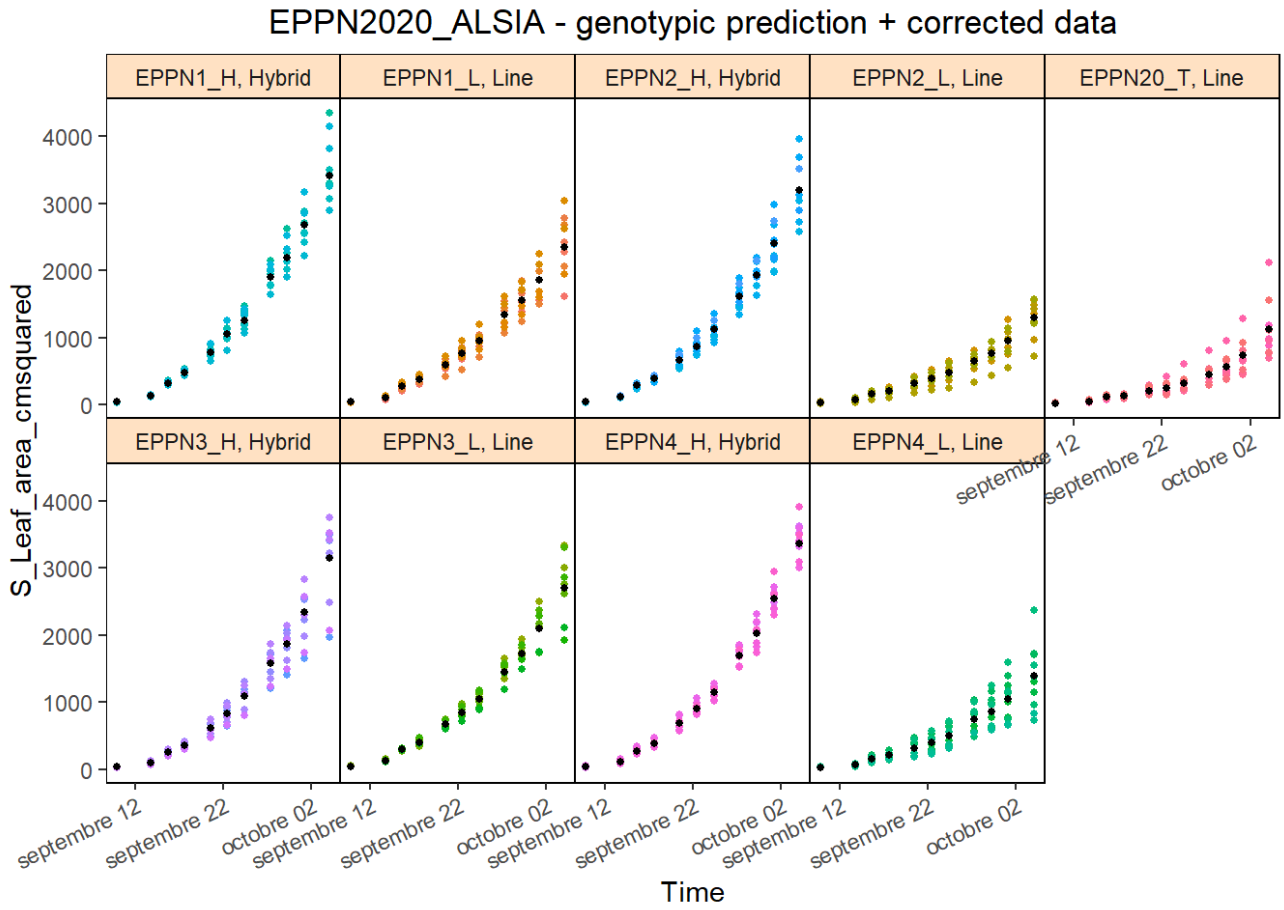

EPPN2020_ALSIA - genotypic prediction + corrected data
EPPN1_H, Hybrid
EPPN1_L, Line
EPPN2_H, Hybrid
EPPN2_L, Line
EPPN20_T, Line
EPPN3_H, Hybrid
EPPN3_L, Line
EPPN4_H, Hybrid
EPPN4_L, Line
S_Height_cm
0
30
60
90
septembre 12
septembre 22
octobre 02
Time


EPPN2020_ALSIA - genotypic prediction + raw data
EPPN1_H, Hybrid
EPPN1_L, Line
EPPN2_H, Hybrid
EPPN2_L, Line
EPPN20_T, Line
EPPN3_H, Hybrid
EPPN3_L, Line
EPPN4_H, Hybrid
EPPN4_L, Line
S_Leaf_area_cmsquared
0
1000
2000
3000
4000
septembre 12
septembre 22
octobre 02
Time


EPPN2020_ALSIA - genotypic prediction + corrected data
EPPN1_H, Hybrid
EPPN1_L, Line
EPPN2_H, Hybrid
EPPN2_L, Line
EPPN20_T, Line
EPPN3_H, Hybrid
EPPN3_L, Line
EPPN4_H, Hybrid
EPPN4_L, Line
S_Leaf_area_cmsquared
0
1000
2000
3000
4000
septembre 12
septembre 22
octobre 02
Time


EPPN2020_ALSIA - Heritability
h2
0.00
0.25
0.50
0.75
1.00
septembre 12
septembre 22
octobre 02
timePoint
herit
Hybrid
Line





3. Outlier detection for series of observations

By using the splines.

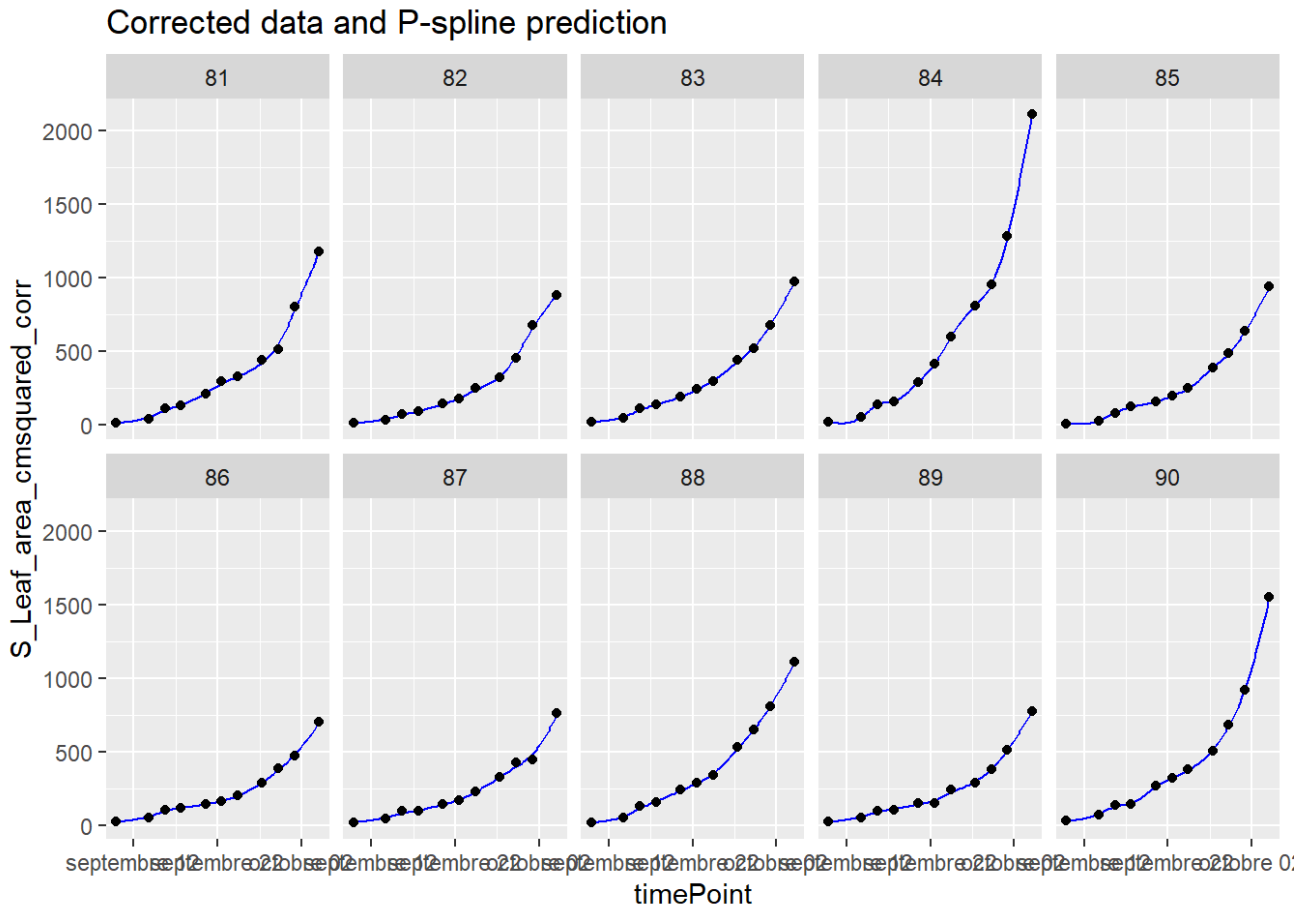
fitModels

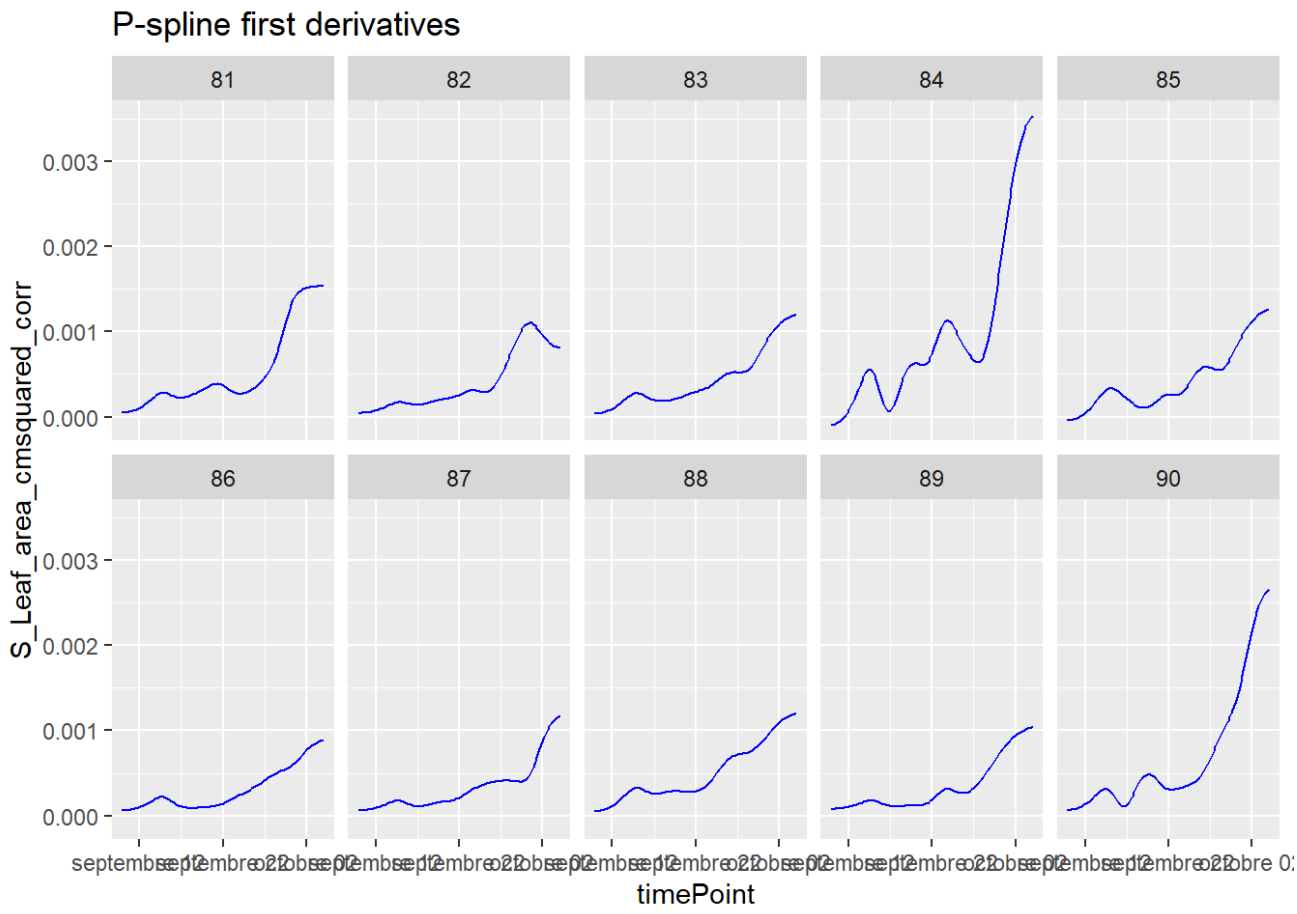
```
for (trait_name in traits) {
  Spatial_Corrected_name <- paste0("Spatial_Corrected_", trait_name)
  modTP_name <- paste0("modTP_", trait_name)
}
```

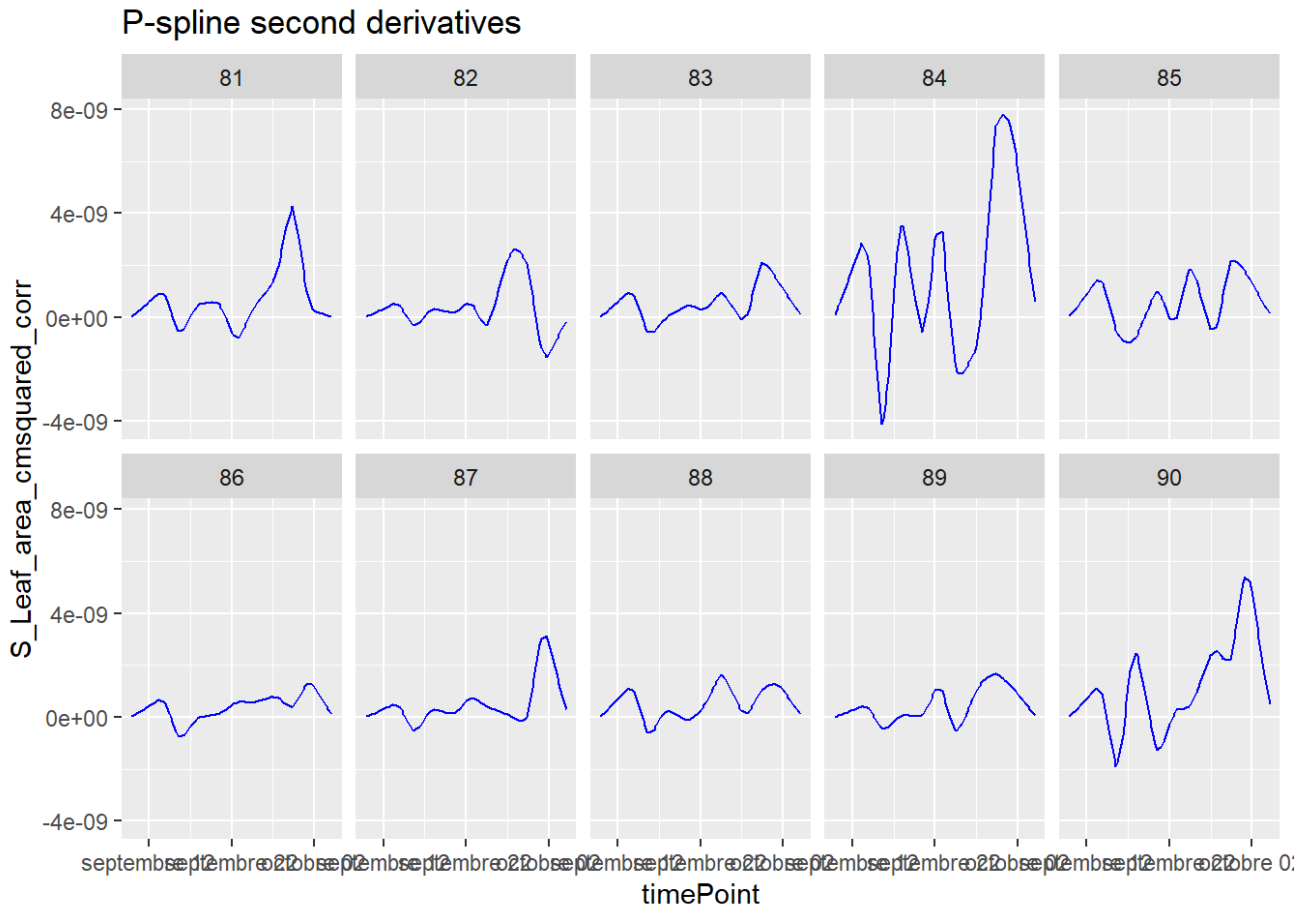
```
knots <- c(30)
mintimepoints <- c(9) # Minimal number of observations

for (trait_name in traits) {
  # Nom de la variable pour les données corrigées
  Spatial_Corrected_name <- paste0("Spatial_Corrected_", trait_name)
  modTP_name <- paste0("modTP_", trait_name)

  # Vérifier si le modèle existe
  if (exists(modTP_name)) {
    modTP <- get(modTP_name)
    Spatial_Corrected <- getCorrected(modTP)
    assign(Spatial_Corrected_name, Spatial_Corrected)

    # Ajuster les splines pour les données corrigées
    fit.spline <- fitSpline(inDat = Spatial_Corrected,
                            trait = paste0(trait_name, "_corr"),
                            knots = knots,
                            minNoTP = mintimepoints)

    # Extraire les tables de valeurs prédites et coefficients de splines
    predDat_name <- paste0("predDat_", trait_name)
    coefDat_name <- paste0("coefDat_", trait_name)

    assign(predDat_name, fit.spline$predDat)
    assign(coefDat_name, fit.spline$coefDat)
  } else {
    cat("No model found for", trait_name, "\n")
  }
}
```

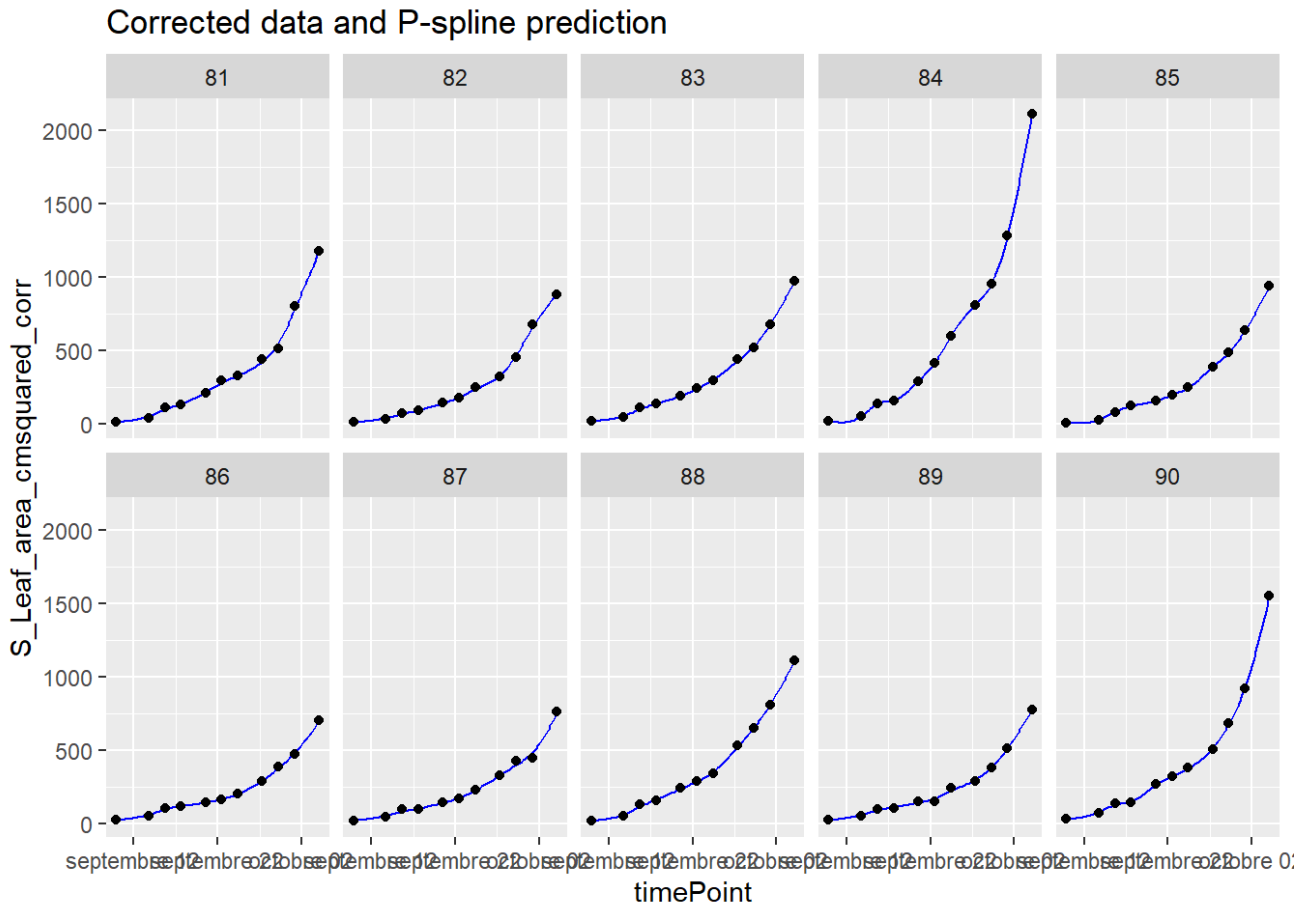
Plot the splines for a plant selection

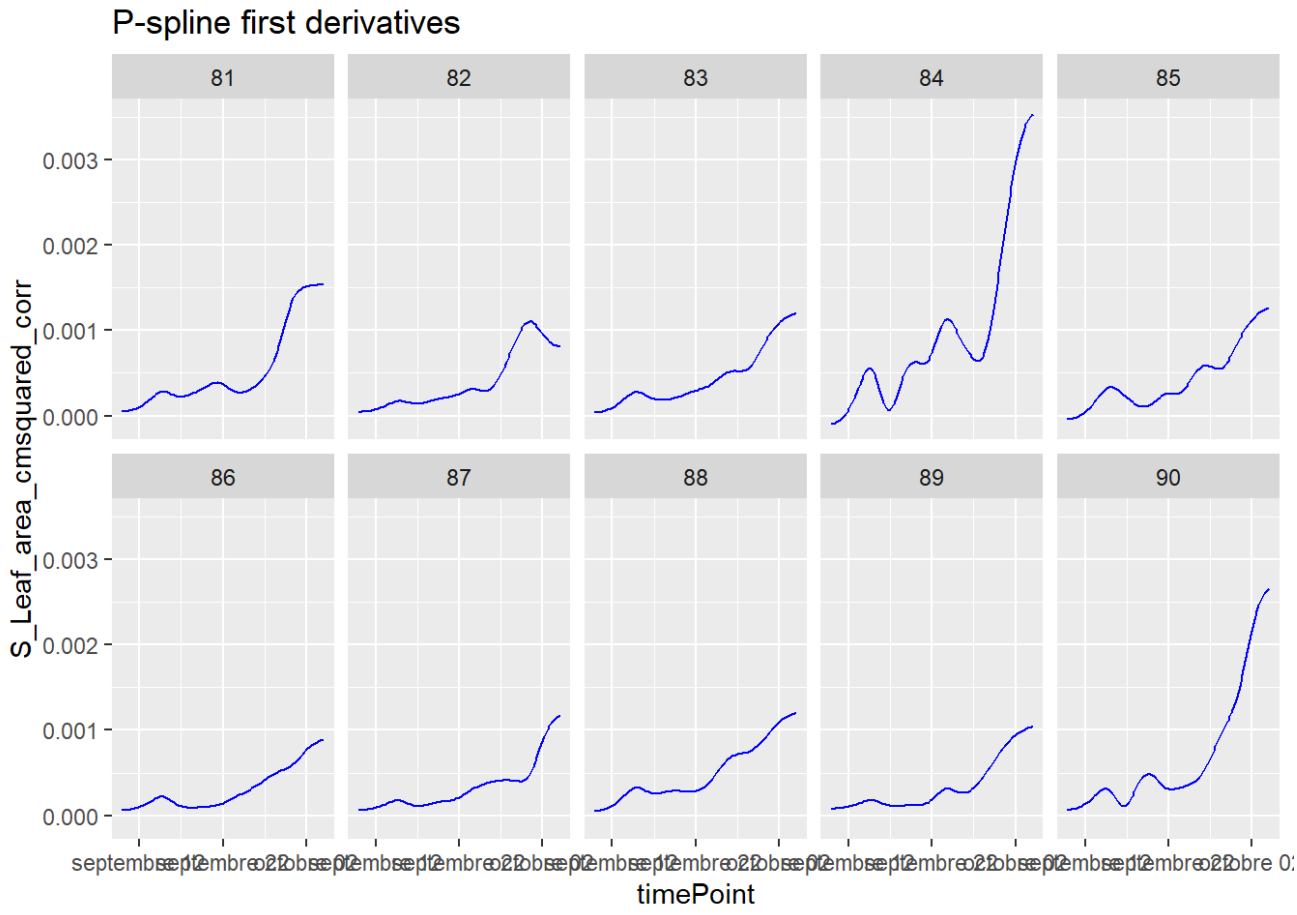
```
for (trait_name in traits) {
  plantSel <- S_timeseries[grepl('EPPN20_T', S_timeseries$Genotype), "Unit.ID", drop =
TRUE]
  plantSel <- as.character(plantSel)

  plot(fit.spline,
       plotIds = plantSel,
       plotType = "predictions",
       main = paste("Predictions for", trait_name))

  plot(fit.spline,
       plotIds = plantSel,
       plotType = "derivatives",
       main = paste("Derivatives for", trait_name))

  plot(fit.spline,
       plotIds = plantSel,
       plotType = "derivatives2",
       main = paste("Second Derivatives for", trait_name))
}
```

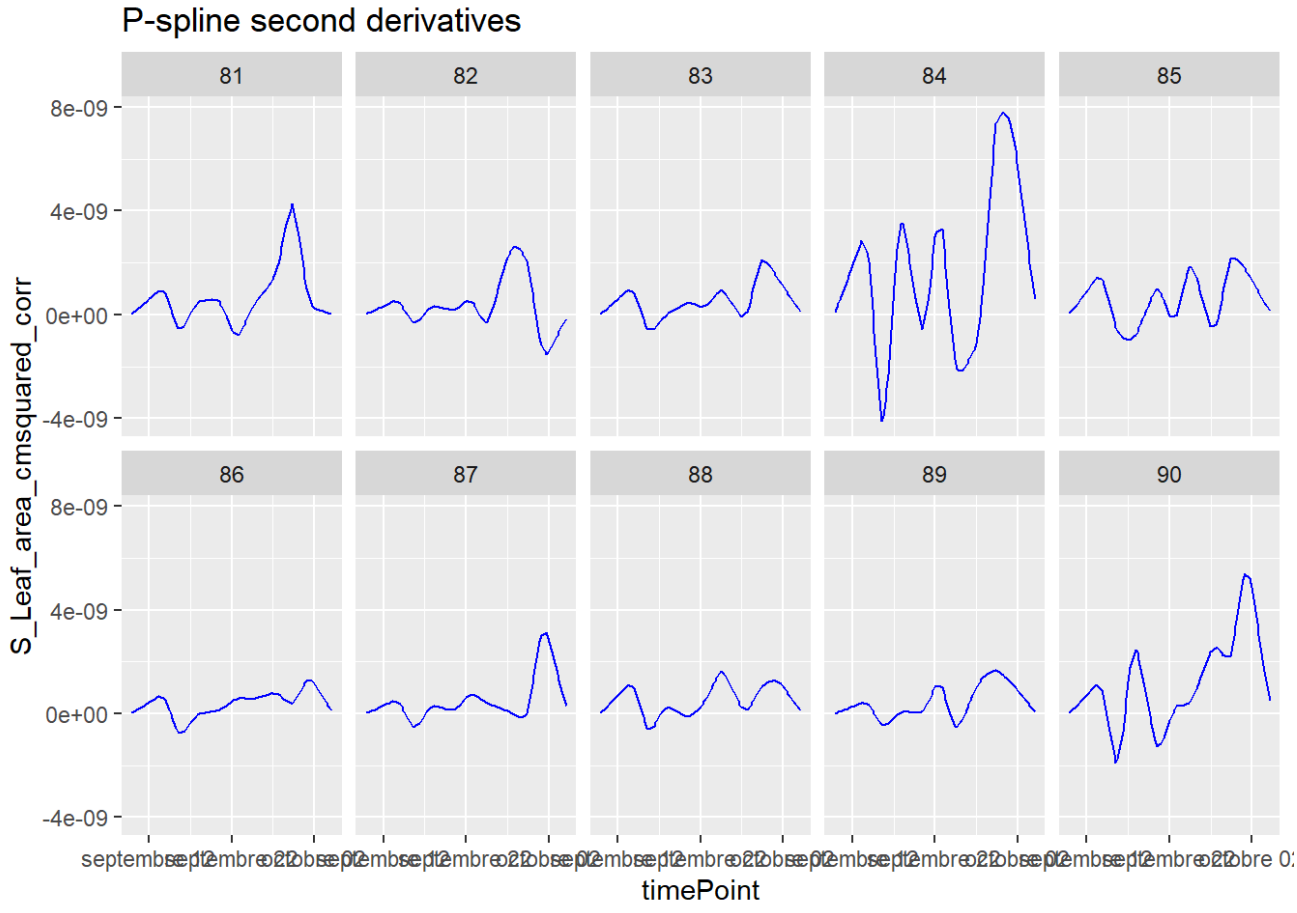

Corrected data and P-spline prediction
81
82
83
84
85
86
87
88
89
90
S_Leaf_area_cmsquared_corr
timePoint


P-spline first derivatives
81
82
83
84
85
86
87
88
89
90
S_Leaf_area_cmsquared_corr
timePoint


P-spline second derivatives
81
82
83
84
85
86
87
88
89
90
8e-09
4e-09
0e+00
-4e-09
S_Leaf_area_cmsquared_corr
timePoint


Corrected data and P-spline prediction
81
82
83
84
85
86
87
88
89
90
2000
1500
1000
500
0
S_Leaf_area_cmsquared_corr
timePoint

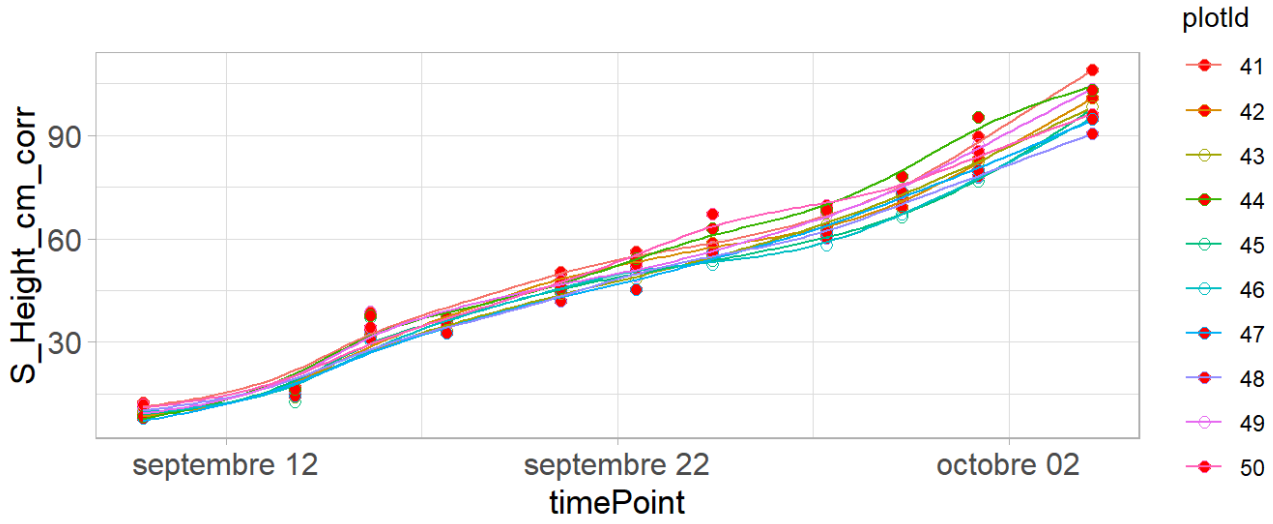


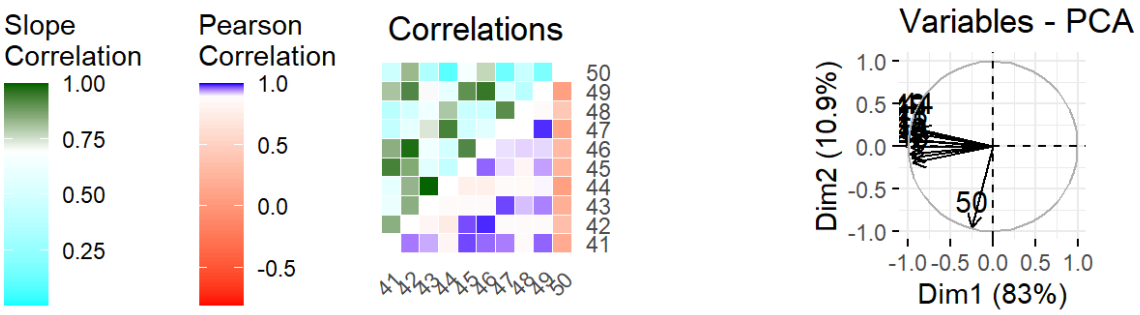


detectSerieOut

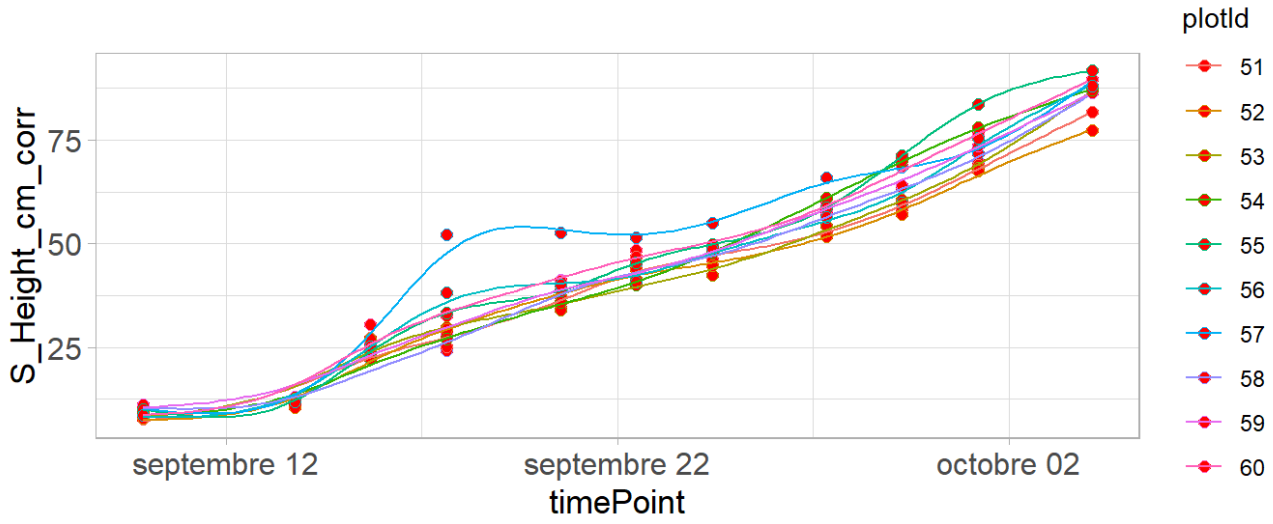
```
thrCor <- c(0.9) # correlation threshold
thrPca <- c(30) # pca angle threshold
thrSlope <- c(0.7) # slope threshold

for (trait_name in traits) {
  Spatial_Corrected_name <- paste0("Spatial_Corrected_", trait_name)
  predDat_name <- paste0("predDat_", trait_name)
  coefDat_name <- paste0("coefDat_", trait_name)

  if (exists(Spatial_Corrected_name) && exists(predDat_name) && exists(coefDat_name)) {
    Spatial_Corrected <- get(Spatial_Corrected_name)
    predDat <- get(predDat_name)
    coefDat <- get(coefDat_name)

    Series_test <- detectSerieOut(corrDat = Spatial_Corrected,
                                  predDat = predDat,
                                  coefDat = coefDat,
                                  trait = paste0(trait_name, "_corr"),
                                  thrCor = thrCor,
                                  thrPca = thrPca,
                                  thrSlope = thrSlope,
                                  geno.decomp = "geno.decomp")

    plot(Series_test, genotypes = levels(factor(Series_test$genotype)))

    assign(paste0("Series_test_", trait_name), Series_test)

    assign(paste0("Spatial_Corrected_Out_", trait_name), Spatial_Corrected)
  } else {
    cat("No corrected data or prediction data found for", trait_name, "\n")
  }
}
```

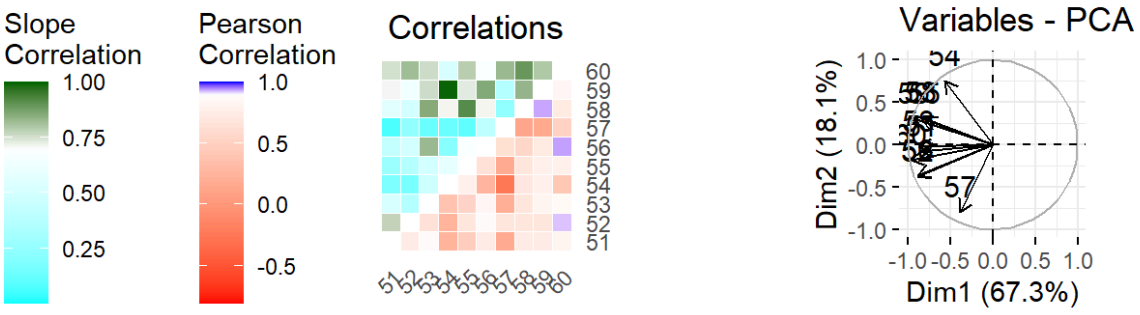
Geno EPPN1_H.Hybrid



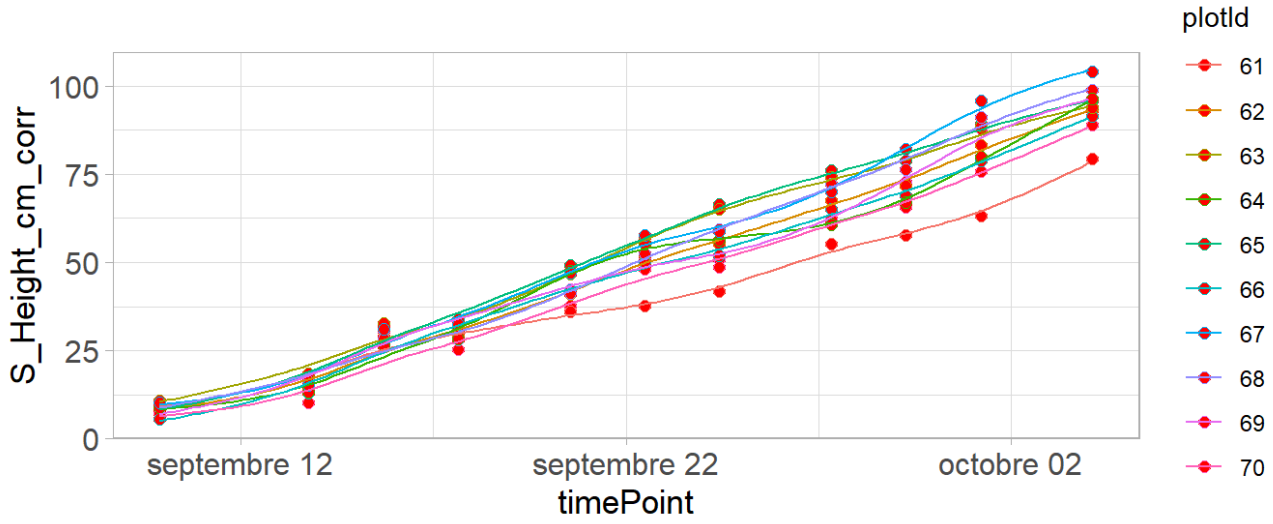


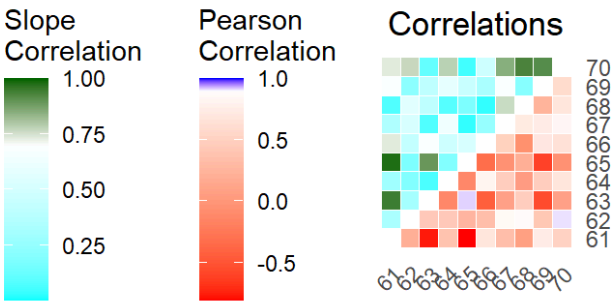
Geno EPPN2_H.Hybrid

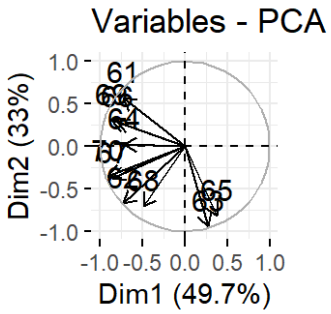




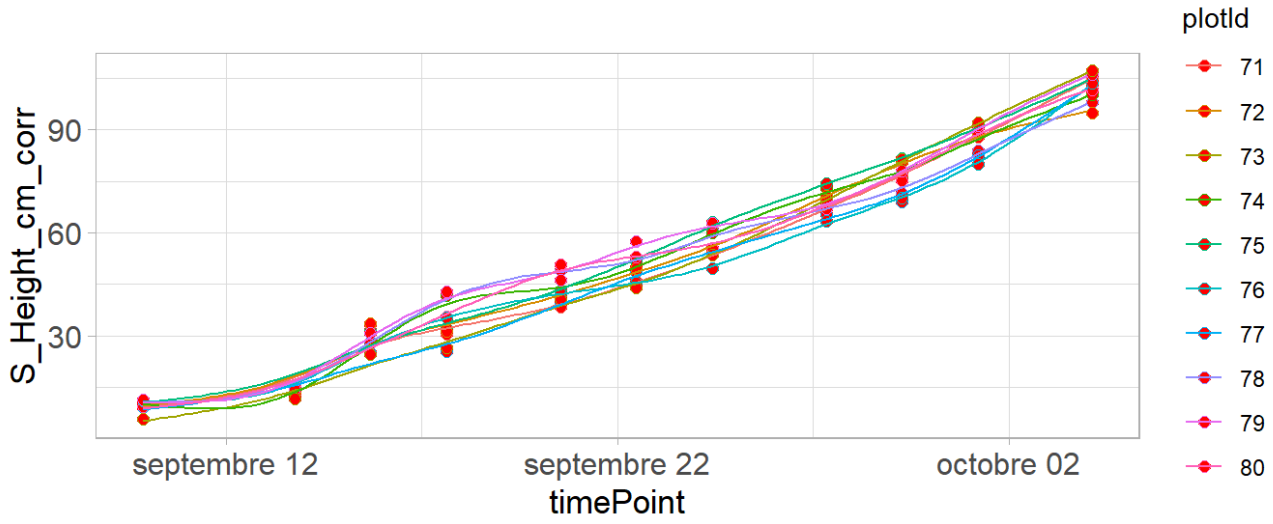
Geno EPPN3_H.Hybrid

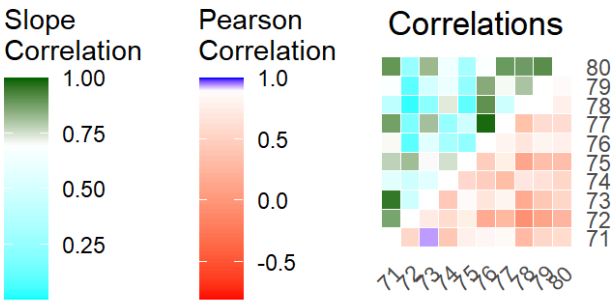


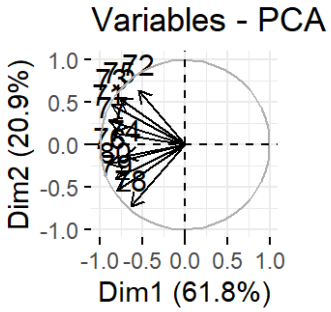




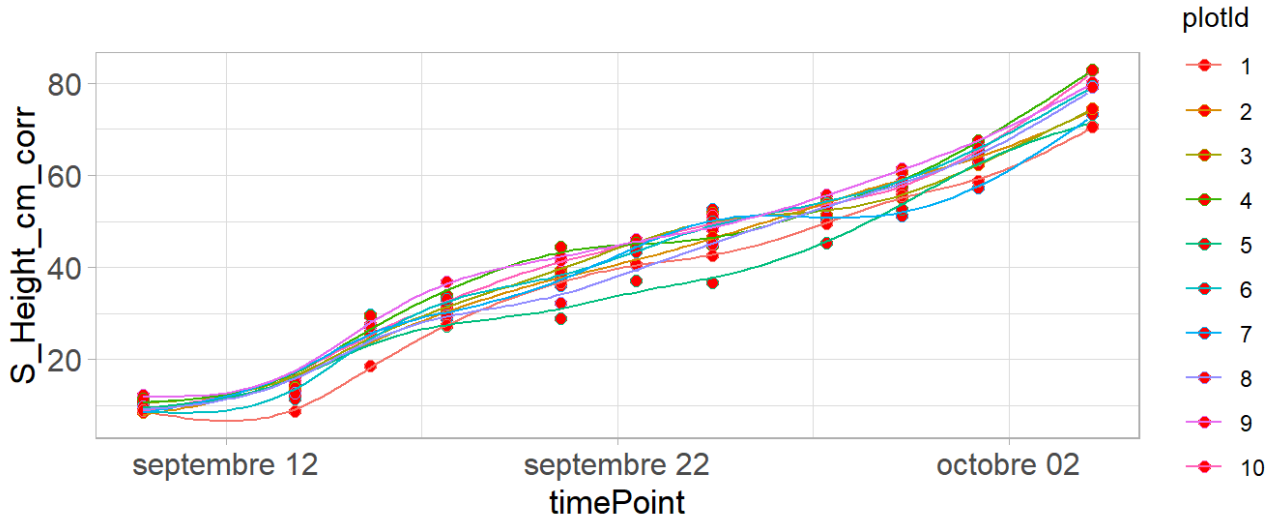
Geno EPPN4_H.Hybrid

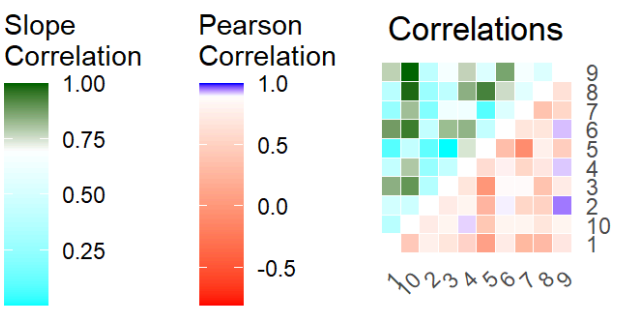


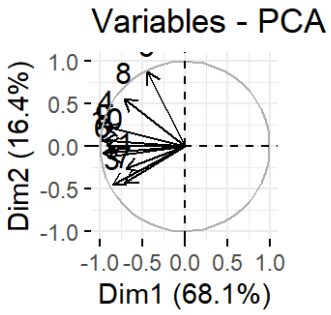




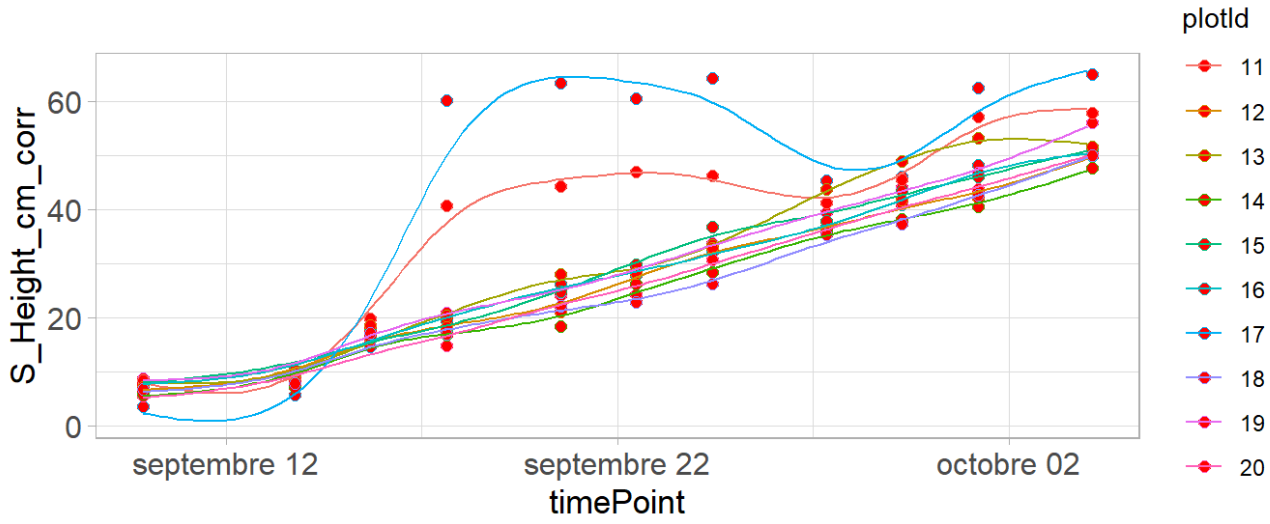
Geno EPPN1_L.Line

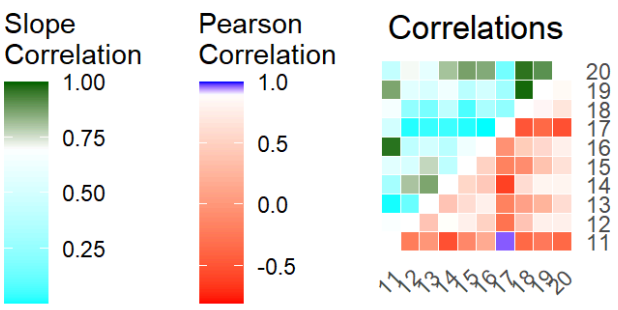


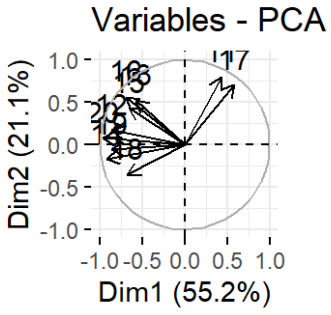




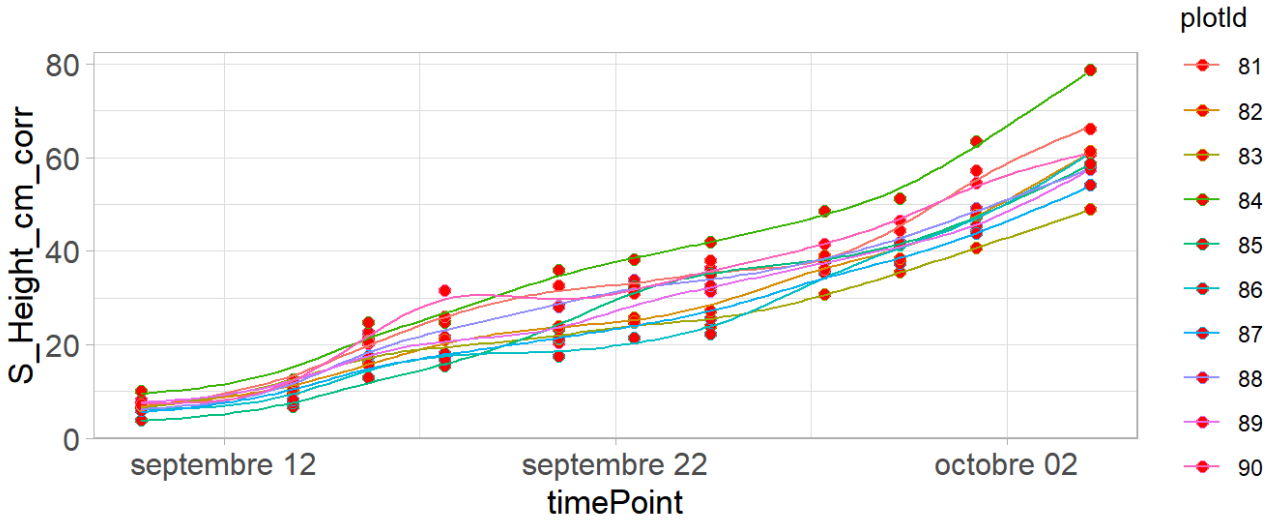
Geno EPPN2_L.Line

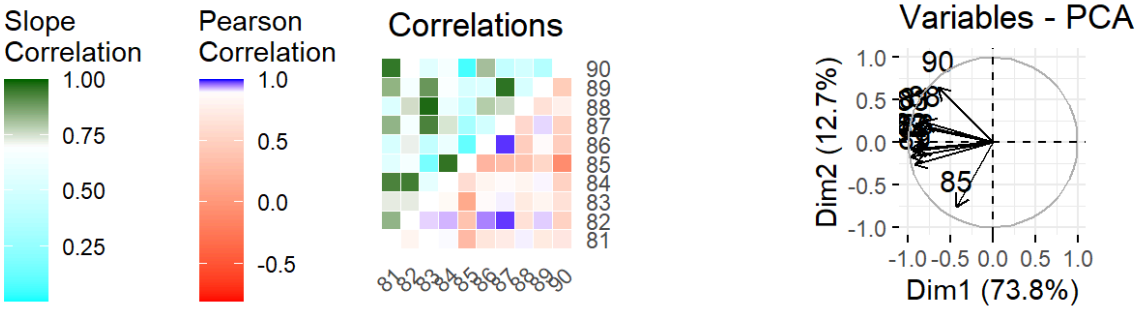




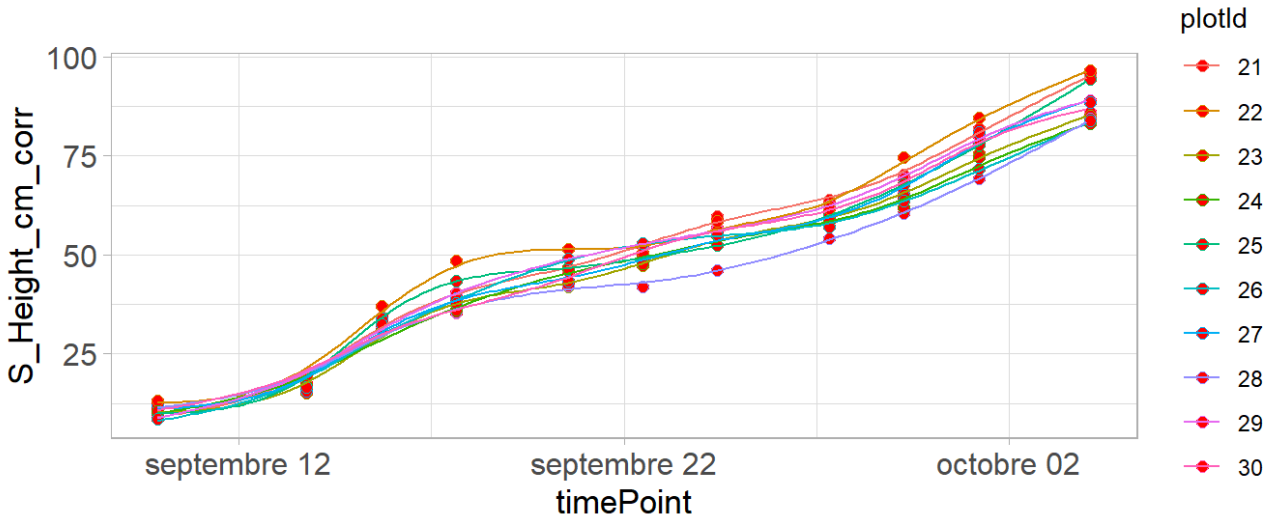


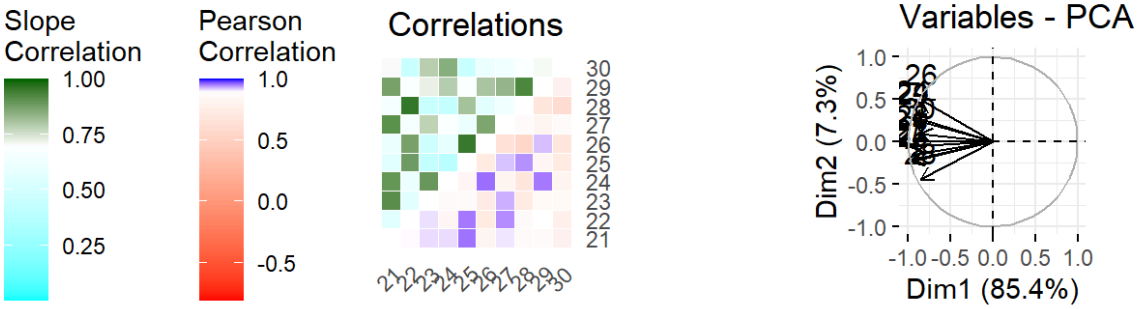
Geno EPPN20_T.Line



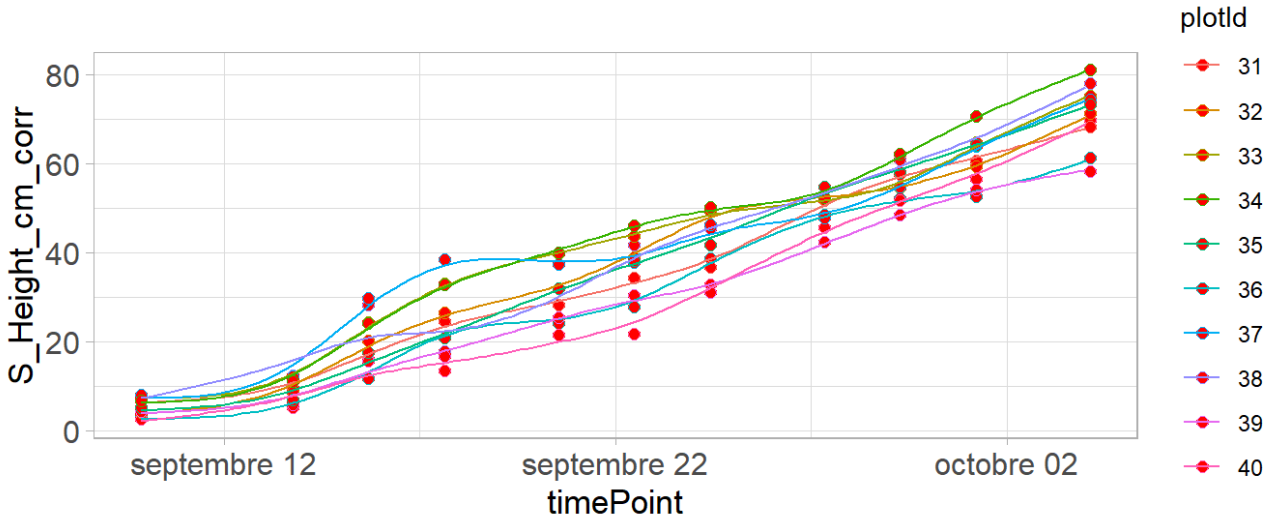


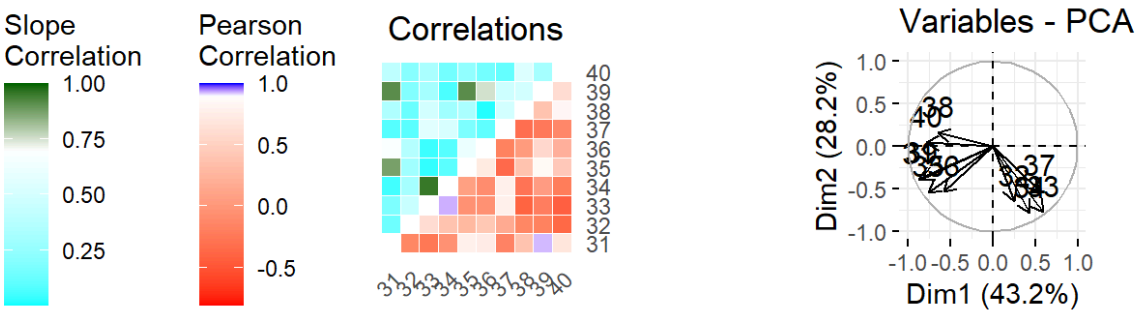
Geno EPPN3_L.Line



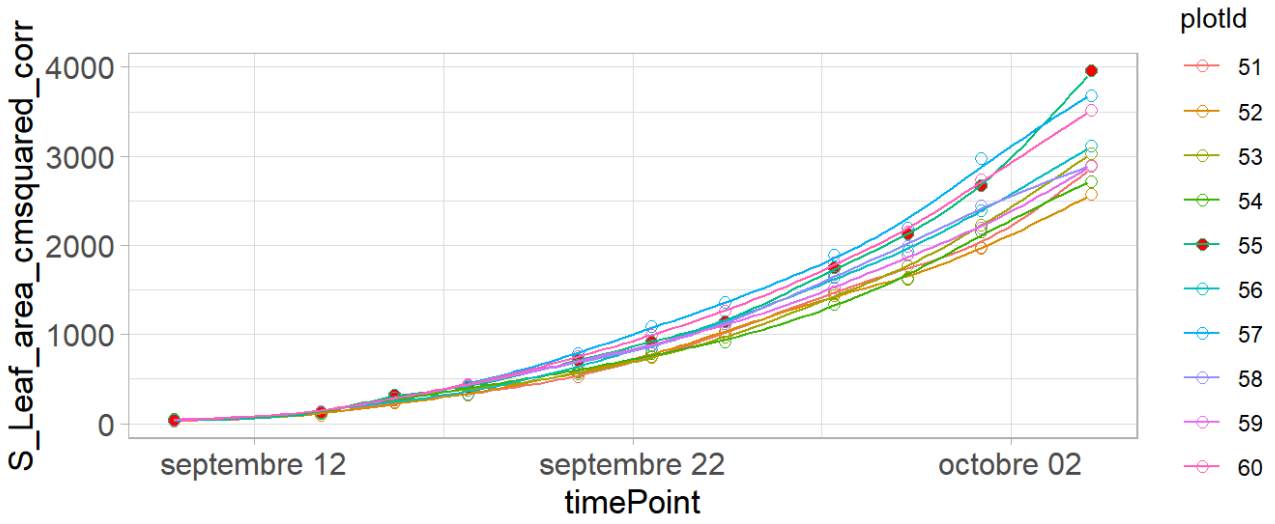


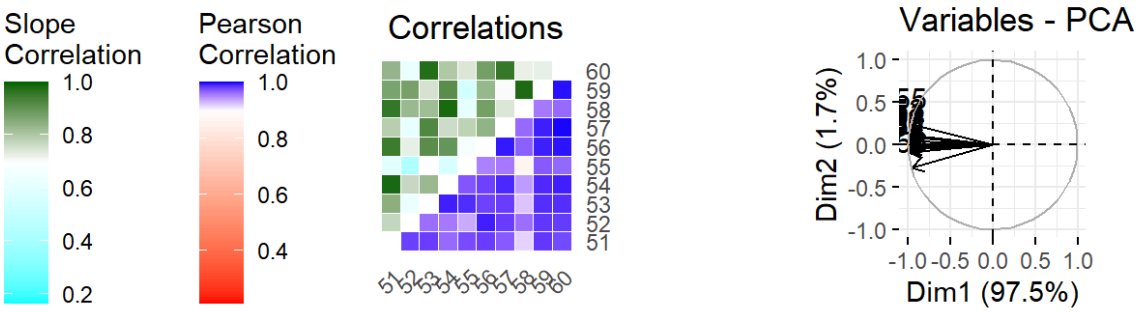
Geno EPPN4_L.Line



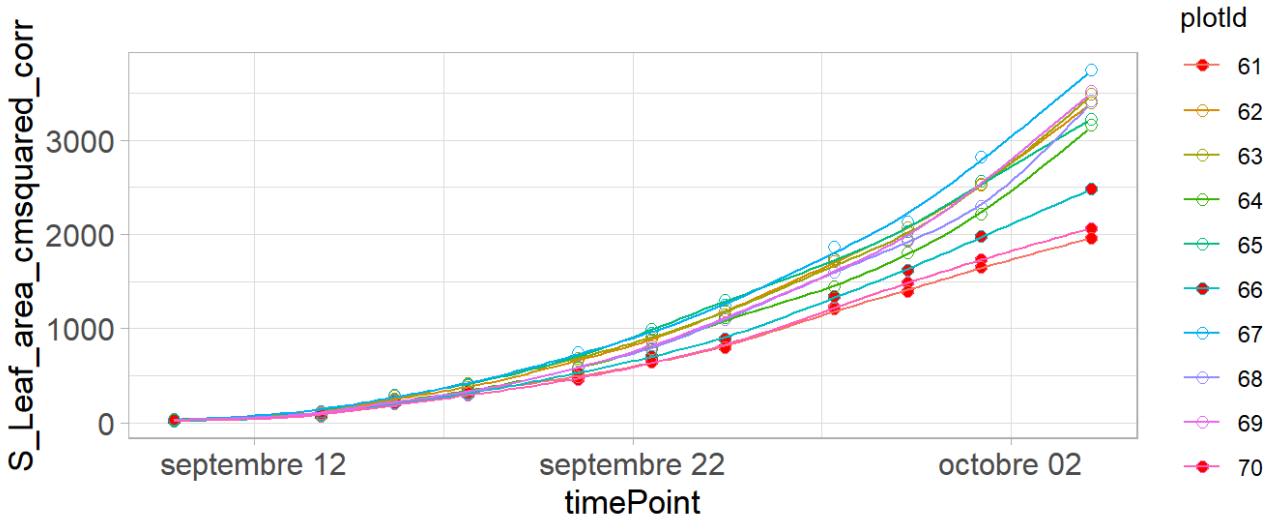


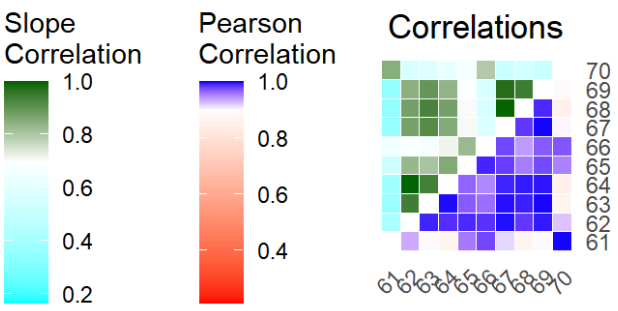
Geno EPPN2_H.Hybrid

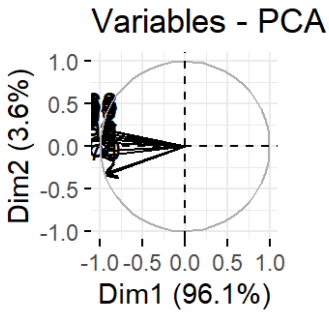




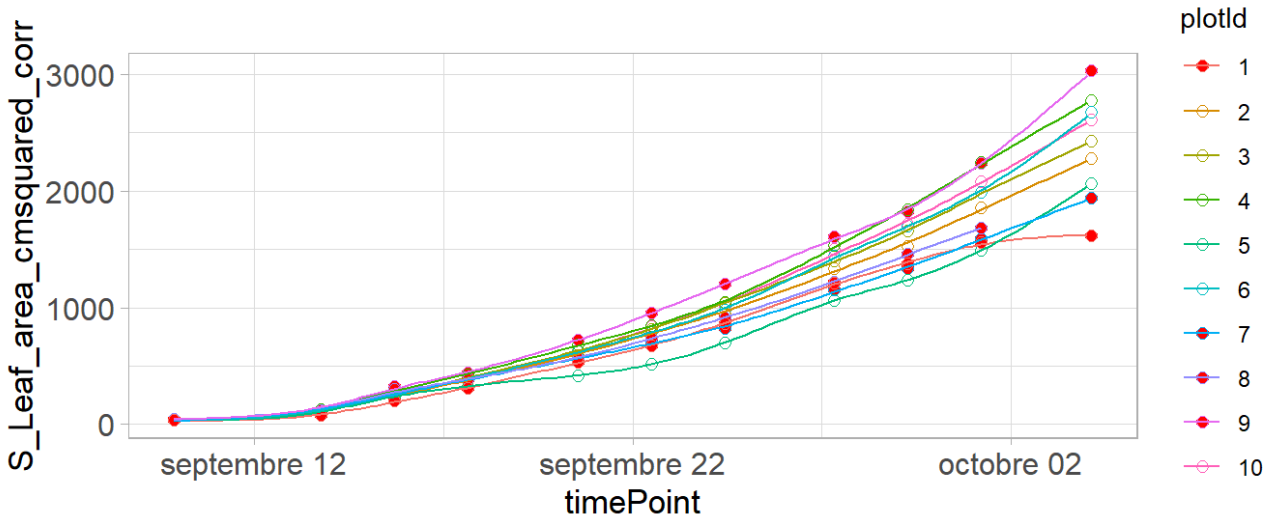
Geno EPPN3_H.Hybrid

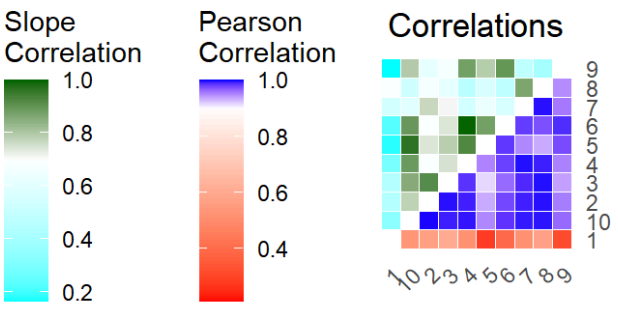


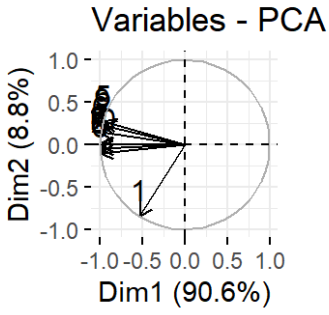




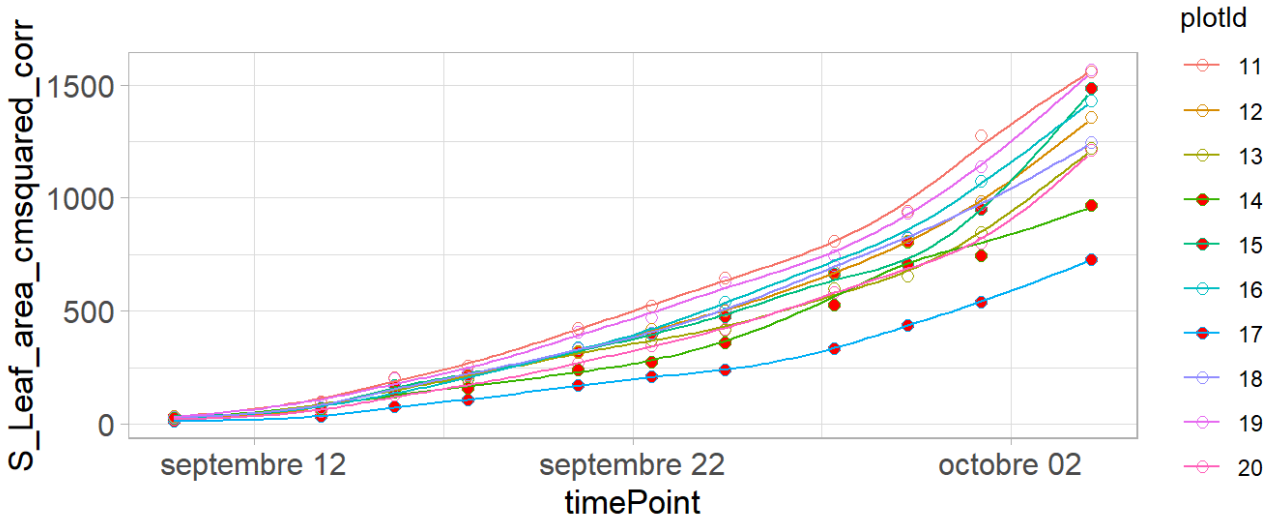
Geno EPPN1_L.Line

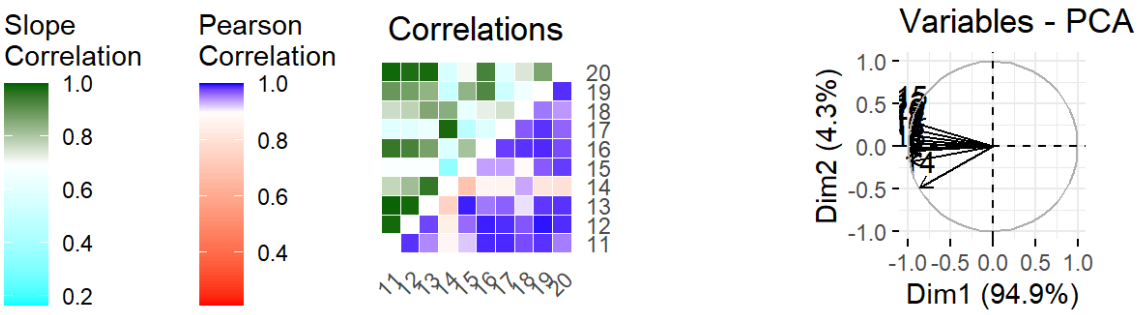




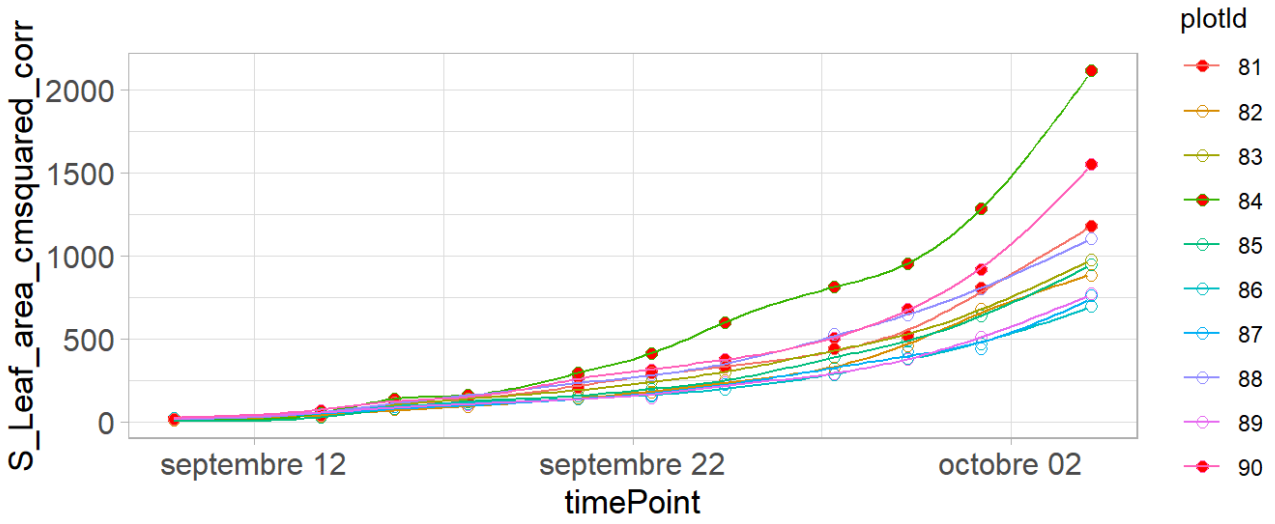


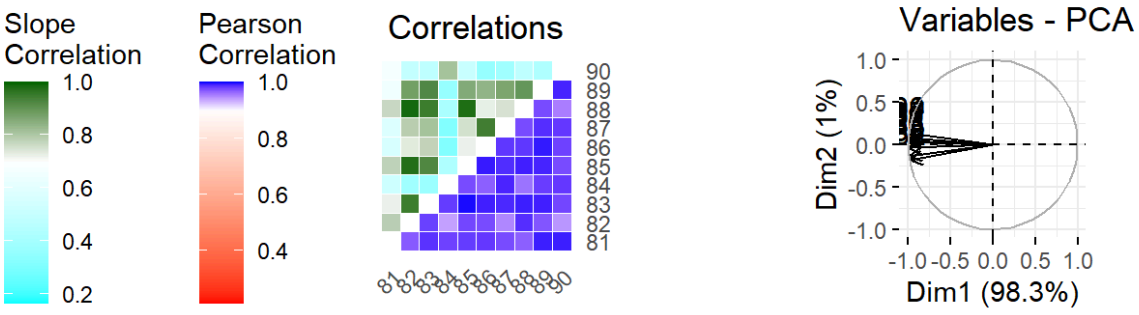
Geno EPPN2_L.Line



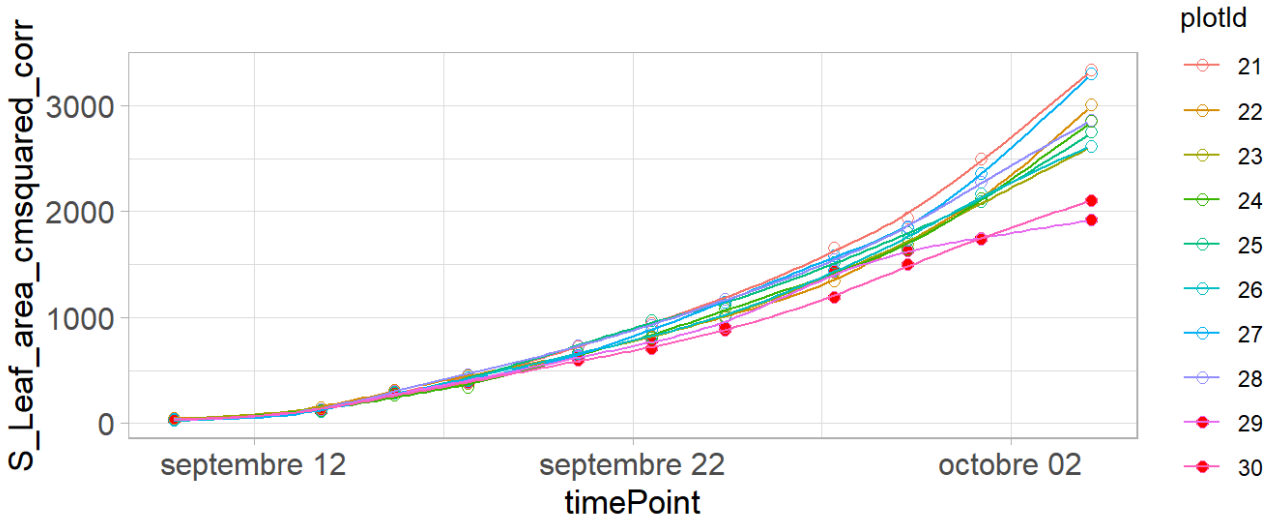


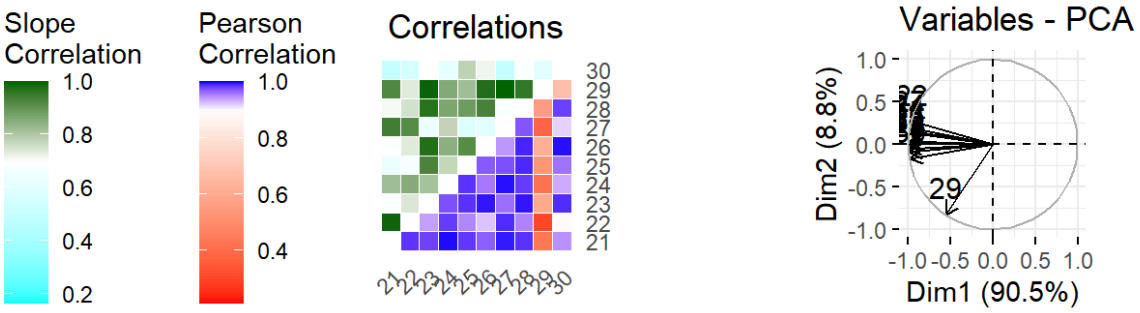
Geno EPPN20_T.Line



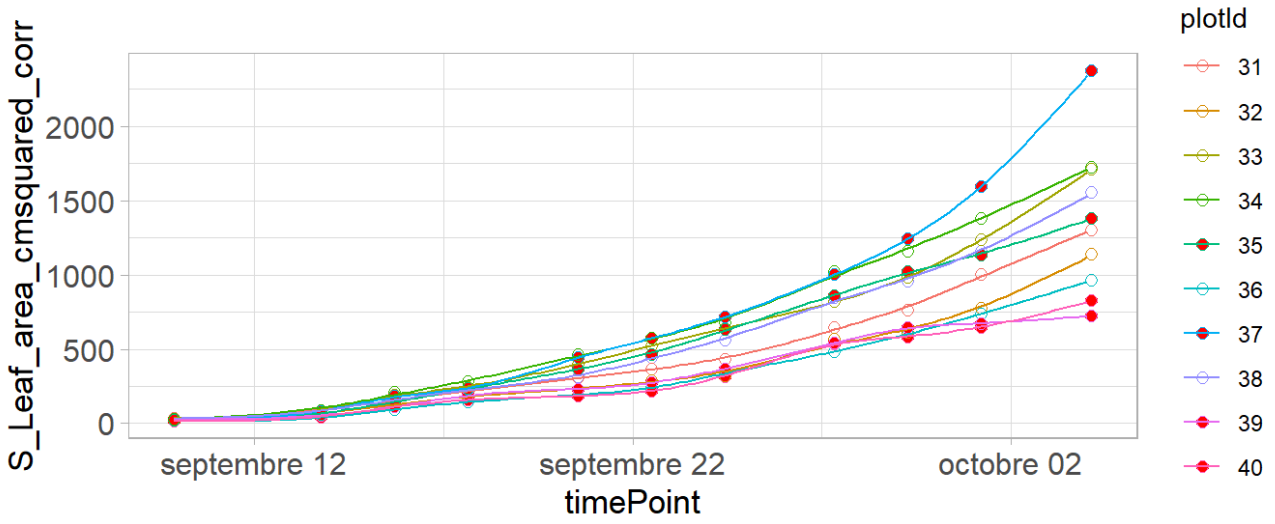


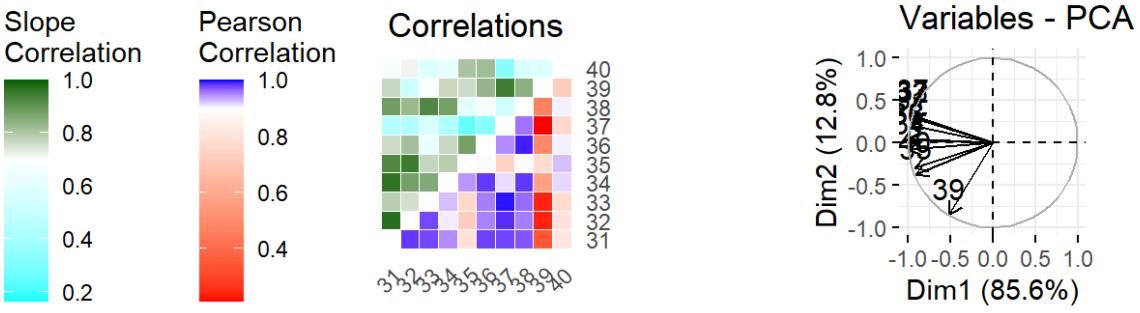
Geno EPPN3_L.Line





Geno EPPN4_L.Line





removeSerieOut

```
for (trait_name in traits) {
  # Nom de la variable pour les données corrigées
  Spatial_Corrected_name <- paste0("Spatial_Corrected_", trait_name)
  Series_test_name <- paste0("Series_test_", trait_name)

  # Extraire les données corrigées et les résultats des séries
  if (exists(Spatial_Corrected_name) && exists(Series_test_name)) {
    Spatial_Corrected <- get(Spatial_Corrected_name)
    Series_test <- get(Series_test_name)

    # Supprimer les outliers de la série
    Spatial_Corrected_Out <- removeSerieOut(dat = Spatial_Corrected, serieOut = Series_
test)

    # Assigner le résultat à une nouvelle variable
    assign(paste0("Spatial_Corrected_Out_", trait_name), Spatial_Corrected_Out)
  } else {
    cat("No corrected data or series test data found for", trait_name, "\n")
  }
}
```

```
for (trait_name in traits) {
  Spatial_Corrected_Out_name <- paste0("Spatial_Corrected_Out_", trait_name)

  if (exists(Spatial_Corrected_Out_name)) {
    Spatial_Corrected_Out <- get(Spatial_Corrected_Out_name)
    output_file <- sprintf("%s/timeSeriesOutliers_%s.tsv", datadir, trait_name)
    readr::write_tsv(Spatial_Corrected_Out, output_file)

    cat("Data written to:", output_file, "\n")
  } else {
    cat("No corrected data found for", trait_name, "\n")
  }
}
```

```
## Data written to: C:/Users/elise/Documents/Mémoire/Main/Data/Extracted/ALSIA/timeSeri
esOutliers_S_Height_cm.tsv
## Data written to: C:/Users/elise/Documents/Mémoire/Main/Data/Extracted/ALSIA/timeSeri
esOutliers_S_Leaf_area_cmsquared.tsv
```

4. With the cleaned data, re-do the spatial correction

This is used to compare the values before and after.

Need to write a for loop for all the variables.

For S_Height_cm

```
trait_name <- "S_Height_cm"

timePoint_S_2 <- createTimePoints(dat = Spatial_Corrected_Out_S_Height_cm,
                                  experimentName = "EPPN2020_clean",
                                  genotype = "genotype",
                                  timePoint = "timePoint",
                                  plotId = "plotId",
                                  rowNum = "rowId",
                                  colNum = "colId")

## Correct for spatial
modTP_2 <- fitModels(TP = timePoint_S_2,
                           trait = trait_name,
                           geno.decomp = c("geno.decomp"))
```

```
## 2020-09-10
```

```
## 2020-09-14
```

```
## 2020-09-16
```

```
## 2020-09-18
```

```
## 2020-09-21
```

```
## 2020-09-23
```

```
## 2020-09-25
```

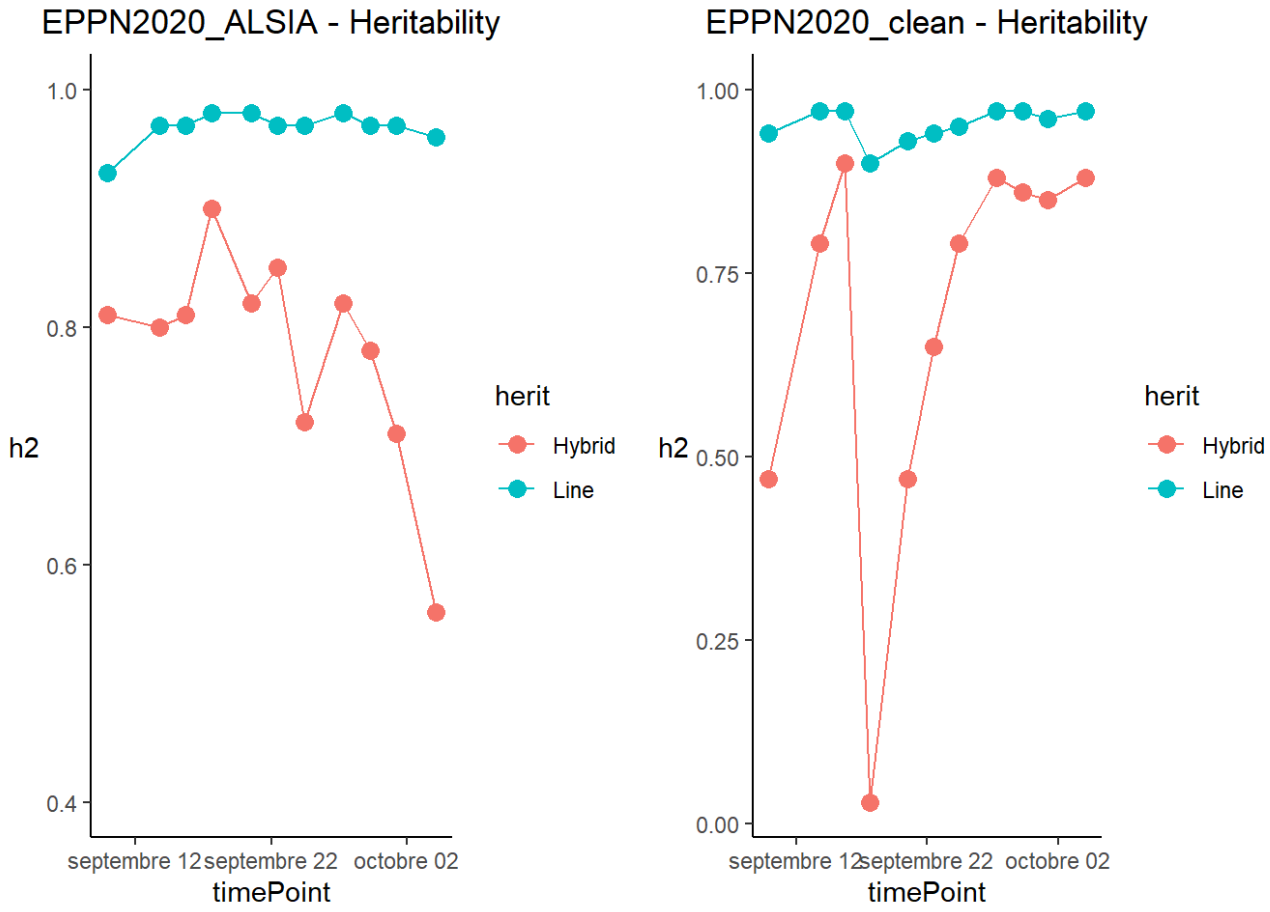
```
## 2020-09-28
```

```
## 2020-09-30
```

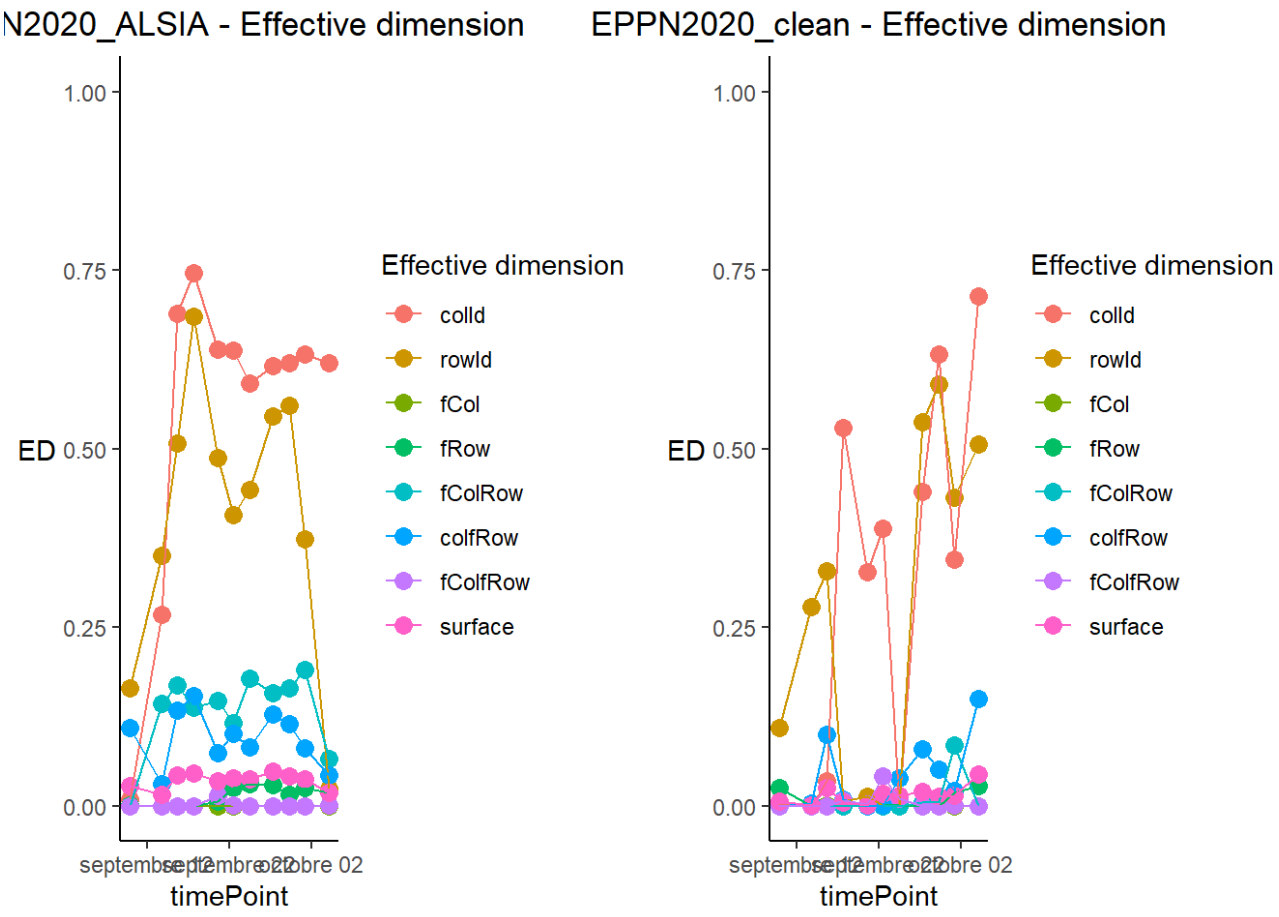
```
## 2020-10-02
```

```
## 2020-10-05
```

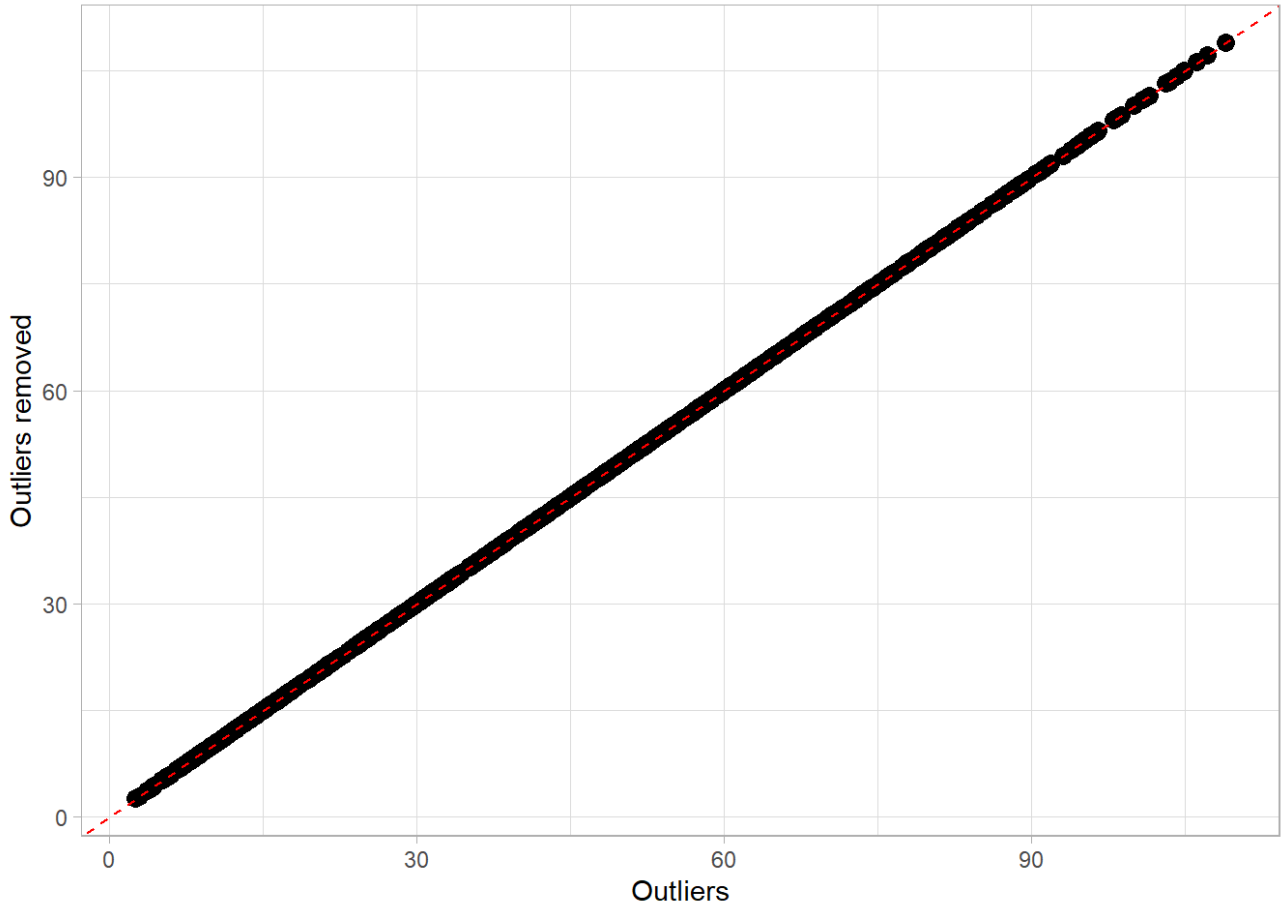
```
## Extract corrected values
Spatial_Corrected_2 <- getCorrected(modTP_2)

#Check the values before and after:

h21<-plot(modTP, output = FALSE,
          plotType = "herit",
          yLim = c(0.4,1))

h22<-plot(modTP_2, output = FALSE,
          plotType = "herit",
          yLim = c(0.4,1))

grid.arrange(h21, h22,  nrow = 1)
```




```
#
ed2<-plot(modTP_2,output = FALSE,
          plotType = "effDim",
          EDType = "ratio",
          yLim = c(0,1))

ed1<-plot(modTP,output = FALSE,
          plotType = "effDim",
          EDType = "ratio",
          yLim = c(0,1))

grid.arrange(ed1, ed2,  nrow = 1)
```




```
spatial_Corr <-
  inner_join(Spatial_Corrected_S_Height_cm[,c("timeNumber","plotId",paste0(trait_name,
"_corr"))],
             Spatial_Corrected_2[,c("timeNumber","plotId",paste0(trait_name, "_cor
r"))],
             by = c("timeNumber","plotId") )


col1 <- paste0(trait_name, "_corr.x")
col2 <- paste0(trait_name, "_corr.y")
ggplot(spatial_Corr, aes(x = .data[[col1]], y = .data[[col2]])) +
  geom_point(size=3) +
  geom_abline(slope=1, intercept = 0,col="red",lty=2) +
  ylab("Outliers removed") + xlab("Outliers") + theme_light()
```



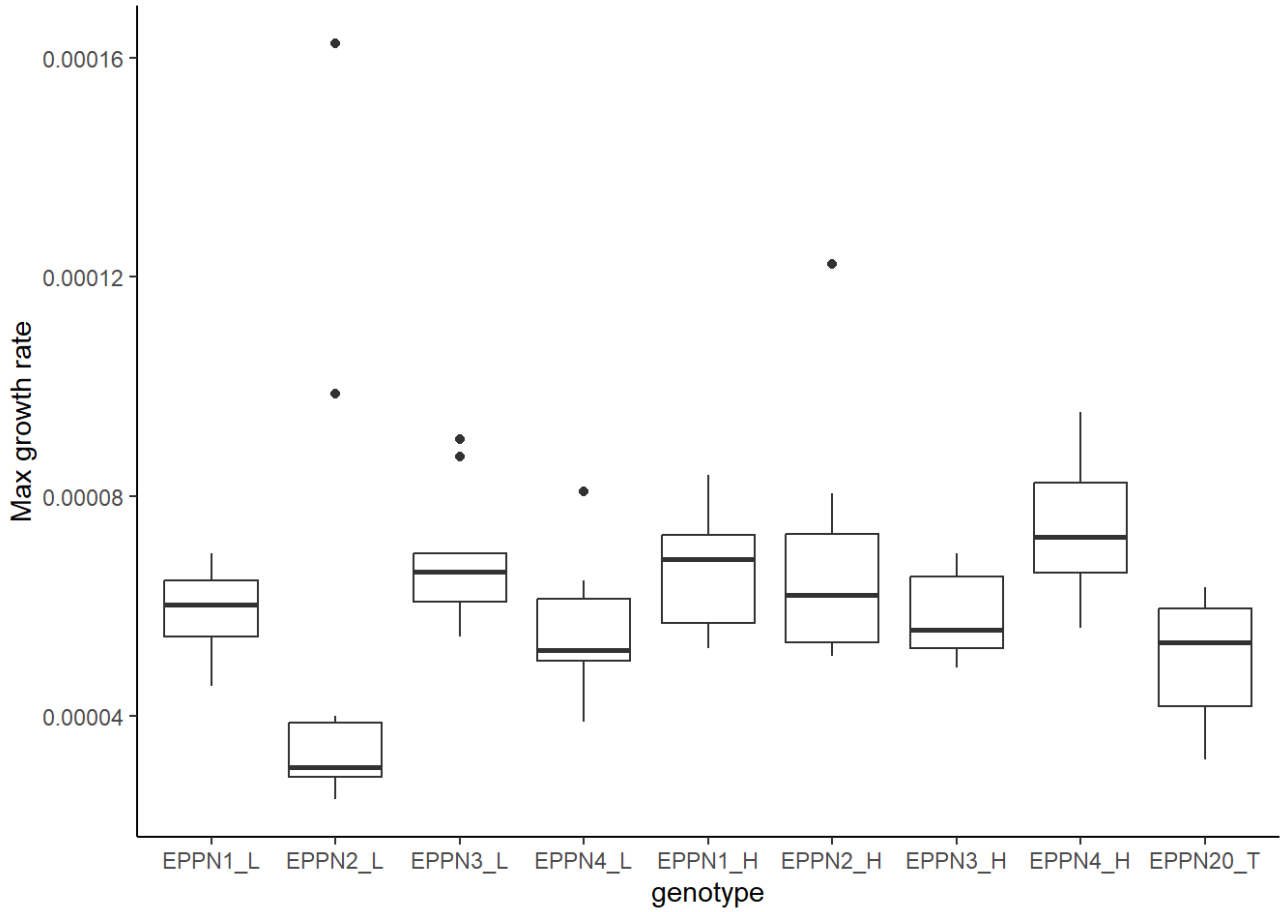

```
# fit Spline again
fit.spline_2 <- fitSpline(inDat = Spatial_Corrected_2,
                                trait = paste0(trait_name, "_corr"),
                                knots = 30,
                                minNoTP = 9)
```

Estimation of parameter from time series

```
param1bis <- estimateSplineParameters(x = fit.spline_2,
                            estimate = "derivatives",
                            what = "max")
head(param1bis)
```

```
##   genotype geno.decomp plotId max_derivatives max_timeNumber
## 1  EPPN1_H      Hybrid     41    8.125181e-05        2150400
## 2  EPPN1_H      Hybrid     42    7.329501e-05        2150400
## 3  EPPN1_H      Hybrid     43    6.195831e-05        2150400
## 4  EPPN1_H      Hybrid     44    7.197570e-05        1785600
## 5  EPPN1_H      Hybrid     45    8.390040e-05        2150400
## 6  EPPN1_H      Hybrid     46    6.862990e-05        2150400
##         max_timePoint
## 1 2020-10-04 21:20:00
## 2 2020-10-04 21:20:00
## 3 2020-10-04 21:20:00
## 4 2020-09-30 16:00:00
## 5 2020-10-04 21:20:00
## 6 2020-10-04 21:20:00
```

```
param1bis[,'genotype'] <- factor( param1bis[, 'genotype'],
                                  levels = genotypes_list)

# Visualize the variability
ggplot(param1bis,
       aes(x = genotype, y = max_derivatives)) +
  geom_boxplot(na.rm = TRUE) +
  ylab("Max growth rate") +
  theme_classic()
```



For S_Leaf_area_cmsquared

```
trait_name <- "S_Leaf_area_cmsquared"

timePoint_S_2 <- createTimePoints(dat = Spatial_Corrected_Out_S_Leaf_area_cmsquared,
                                  experimentName = "EPPN2020_clean",
                                  genotype = "genotype",
                                  timePoint = "timePoint",
                                  plotId = "plotId",
                                  rowNum = "rowId",
                                  colNum = "colId")

## Correct for spatial
modTP_2 <- fitModels(TP = timePoint_S_2,
                           trait = trait_name,
                           geno.decomp = c("geno.decomp"))
```

```
## 2020-09-10
```

```
## 2020-09-14
```

```
## 2020-09-16
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## 2020-09-18
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## 2020-09-21
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## 2020-09-23
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## 2020-09-25
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## 2020-09-28
```
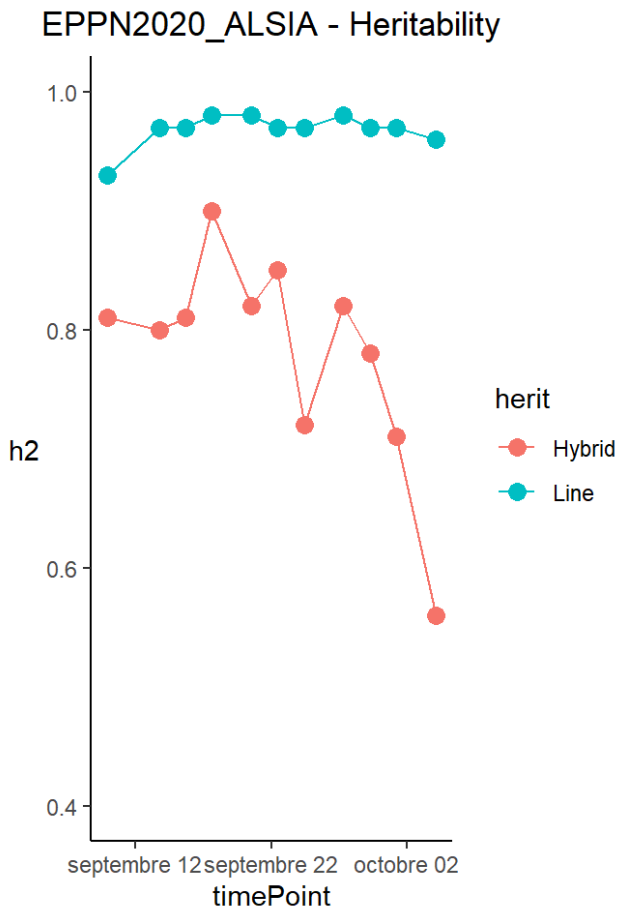
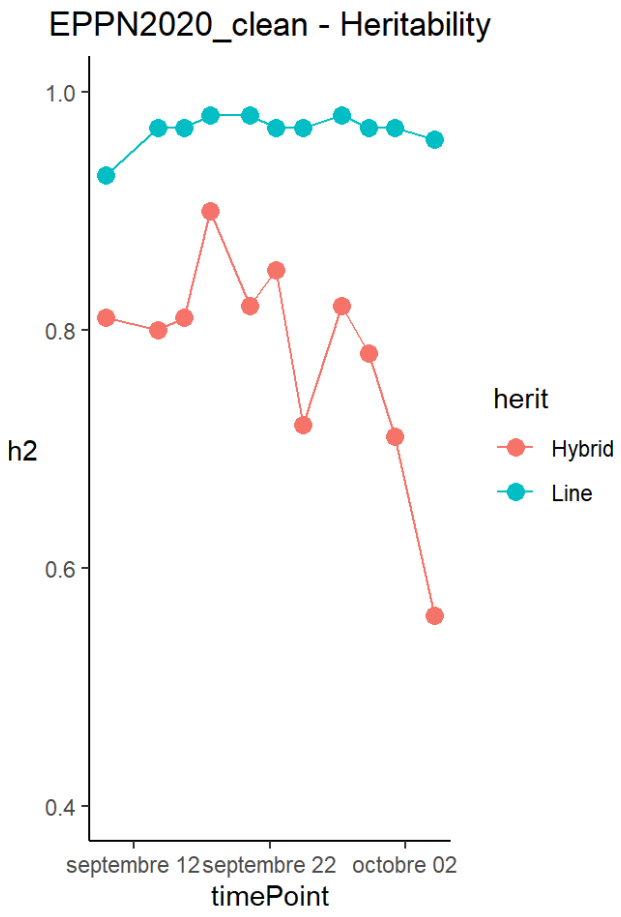

```
## 2020-09-30
```

```
## 2020-10-02
```

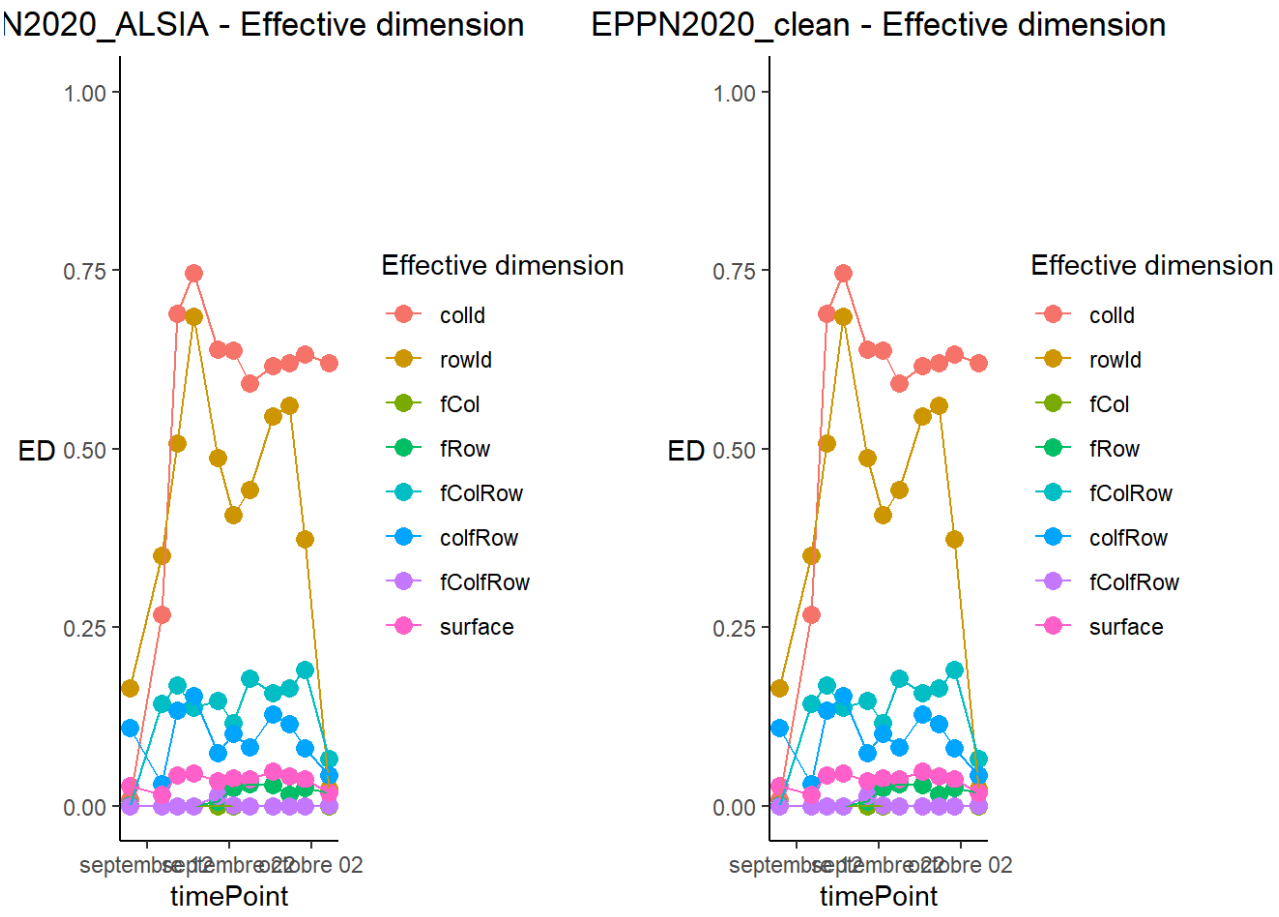
```
## 2020-10-05
```

```
## Extract corrected values
Spatial_Corrected_2 <- getCorrected(modTP_2)

#Check the values before and after:

h21<-plot(modTP, output = FALSE,
          plotType = "herit",
          yLim = c(0.4,1))

h22<-plot(modTP_2, output = FALSE,
          plotType = "herit",
          yLim = c(0.4,1))

grid.arrange(h21, h22,  nrow = 1)
```



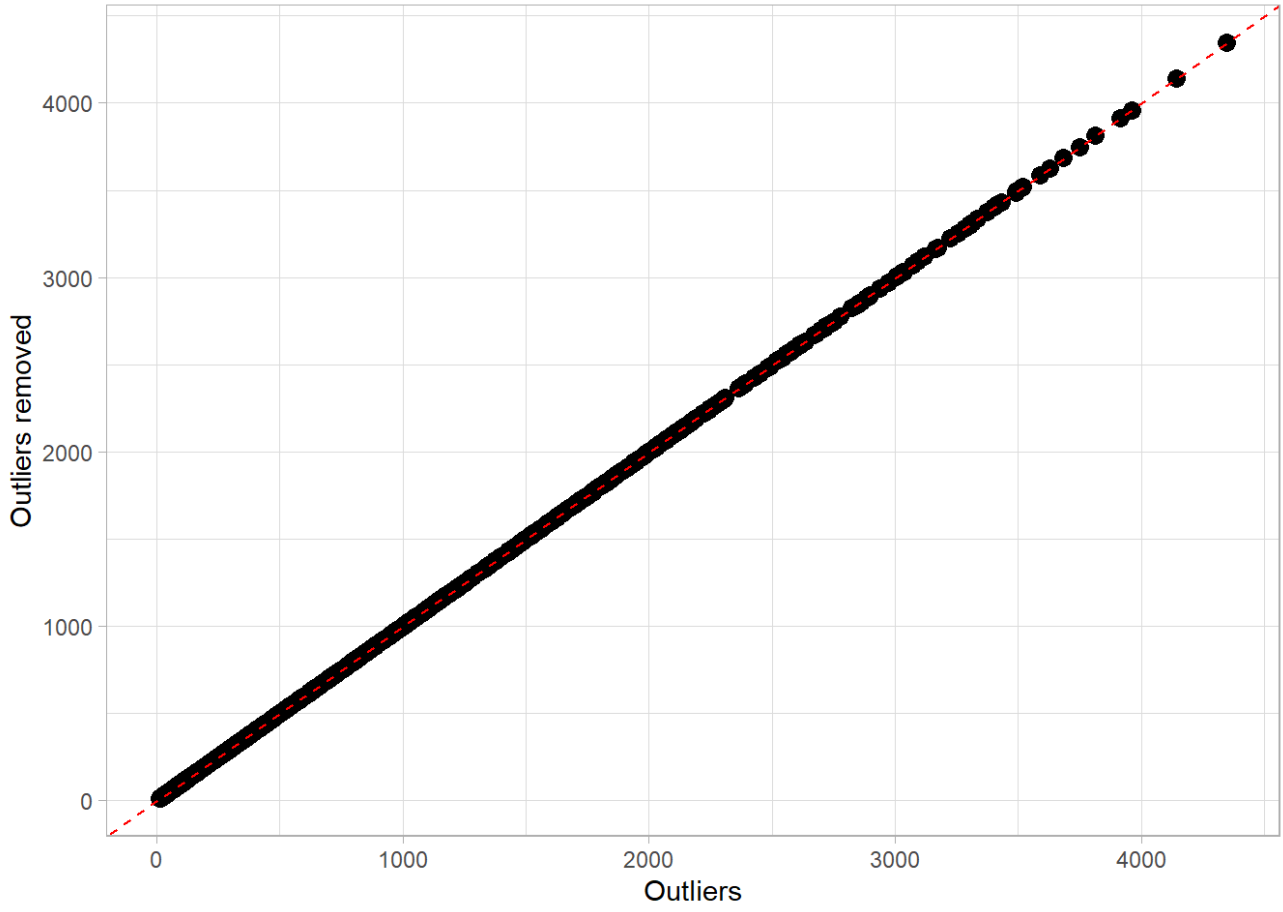



```
#
ed2<-plot(modTP_2,output = FALSE,
          plotType = "effDim",
          EDType = "ratio",
          yLim = c(0,1))

ed1<-plot(modTP,output = FALSE,
          plotType = "effDim",
          EDType = "ratio",
          yLim = c(0,1))

grid.arrange(ed1, ed2,  nrow = 1)
```




```
spatial_Corr <-
  inner_join(Spatial_Corrected_S_Leaf_area_cmsquared[,c("timeNumber","plotId",paste0(tr
ait_name, "_corr"))],
             Spatial_Corrected_2[,c("timeNumber","plotId",paste0(trait_name, "_cor
r"))],
             by = c("timeNumber","plotId") )


col1 <- paste0(trait_name, "_corr.x")
col2 <- paste0(trait_name, "_corr.y")
ggplot(spatial_Corr, aes(x = .data[[col1]], y = .data[[col2]])) +
  geom_point(size=3) +
  geom_abline(slope=1, intercept = 0,col="red",lty=2) +
  ylab("Outliers removed") + xlab("Outliers") + theme_light()
```

```
## Warning: Removed 1 rows containing missing values (`geom_point()`).
```




```
# fit Spline again
fit.spline_2 <- fitSpline(inDat = Spatial_Corrected_2,
                                trait = paste0(trait_name, "_corr"),
                                knots = 30,
                                minNoTP = 9)
```

Estimation of parameter from time series

```
param1bis <- estimateSplineParameters(x = fit.spline_2,
                           estimate = "derivatives",
                           what = "max")
head(param1bis)
```

```
##   genotype geno.decomp plotId max_derivatives max_timeNumber
## 1  EPPN1_H      Hybrid     41     0.004880555        2150400
## 2  EPPN1_H      Hybrid     42     0.002473484        1920000
## 3  EPPN1_H      Hybrid     43     0.002802800        2150400
## 4  EPPN1_H      Hybrid     44     0.002701529        1843200
## 5  EPPN1_H      Hybrid     45     0.003210063        1766400
## 6  EPPN1_H      Hybrid     46     0.002370769        1843200
##         max_timePoint
## 1 2020-10-04 21:20:00
## 2 2020-10-02 05:20:00
## 3 2020-10-04 21:20:00
## 4 2020-10-01 08:00:00
## 5 2020-09-30 10:40:00
## 6 2020-10-01 08:00:00
```

```
param1bis[,'genotype'] <- factor( param1bis[, 'genotype'],
                                  levels = genotypes_list)

# Visualize the variability
ggplot(param1bis,
       aes(x = genotype, y = max_derivatives)) +
  geom_boxplot(na.rm = TRUE) +
  ylab("Max growth rate of area") +
  theme_classic()
```