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A. Exploration of the timeseries dataframe

B. Exploration of the S_timeseries dataframe

C. Exploration of the T_timeseries dataframe

SPPU Data Analysis

Elise

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Set the right working directory.

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

Data importation

Import the data sets extracted from the Data Preparation 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")
S_timeseries <- read.table("S_timeseries.txt", header = TRUE, sep = "\t")
T_timeseries <- read.table("T_timeseries.txt", header = TRUE, sep = "\t")
```

Convert the columns to factor and date formats.

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

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

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

```
platform <- "SPPU"

# 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 three first columns that are "Unit.ID", "Time" and "Date"

# T_timeseries
df_T_timeseries <- T_timeseries[, colSums(is.na(T_timeseries)) < nrow(T_timeseries)]
genotype_index <- which(colnames(df_T_timeseries) == "Genotype")
variables_T <- colnames(df_T_timeseries[, c(5:(genotype_index - 1))]) # We remove the three first columns that are "Unit.ID", "Time" and "Date"

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

```
## [1] "SPPU : The variables for S_timeseries are S_Height_cm, S_Height_pixel, S_Area_cm_squared, S_Area_pixel, S_Perimeter_cm, S_Perimeter_pixel, S_Compactness, S_Width_cm, S_Width_pixel"
```

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

```
## [1] "SPPU : The variables for T_timeseries are T_Area_cm_squared, T_Area_pixel, T_Perimeter_cm, T_Perimeter_pixel, T_Compactness, T_Roundness, T_Roundness2, T_Isotropy, T_Eccentricity, T_Rms, T_Sol"
```

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

```
S_timeseries$Plant_type <- substr(S_timeseries$Genotype, nchar(as.character(S_timeseries$Genotype)), nchar(as.character(S_timeseries$Genotype)))
T_timeseries$Plant_type <- substr(T_timeseries$Genotype, nchar(as.character(T_timeseries$Genotype)), nchar(as.character(T_timeseries$Genotype)))
```

1. Endpoint dataframe

A. Exploration of data

Exploration tables using the rstatix, janitor and skimr packages

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

```
## [1] "No data for SPPU"
```

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

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

Data visualization

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

Boxplots

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

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

Correlation plots

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

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

B. Normality hypothesis and outlier detection

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

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

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

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

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

Then run the function on all variables of the dataset.

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

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

Boxplots after outlier detection

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

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

Violin and sine plots after outlier detection

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

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

Exploration statistics for the variables after outlier detection

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

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

2. Exploration of the timeseries data

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

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

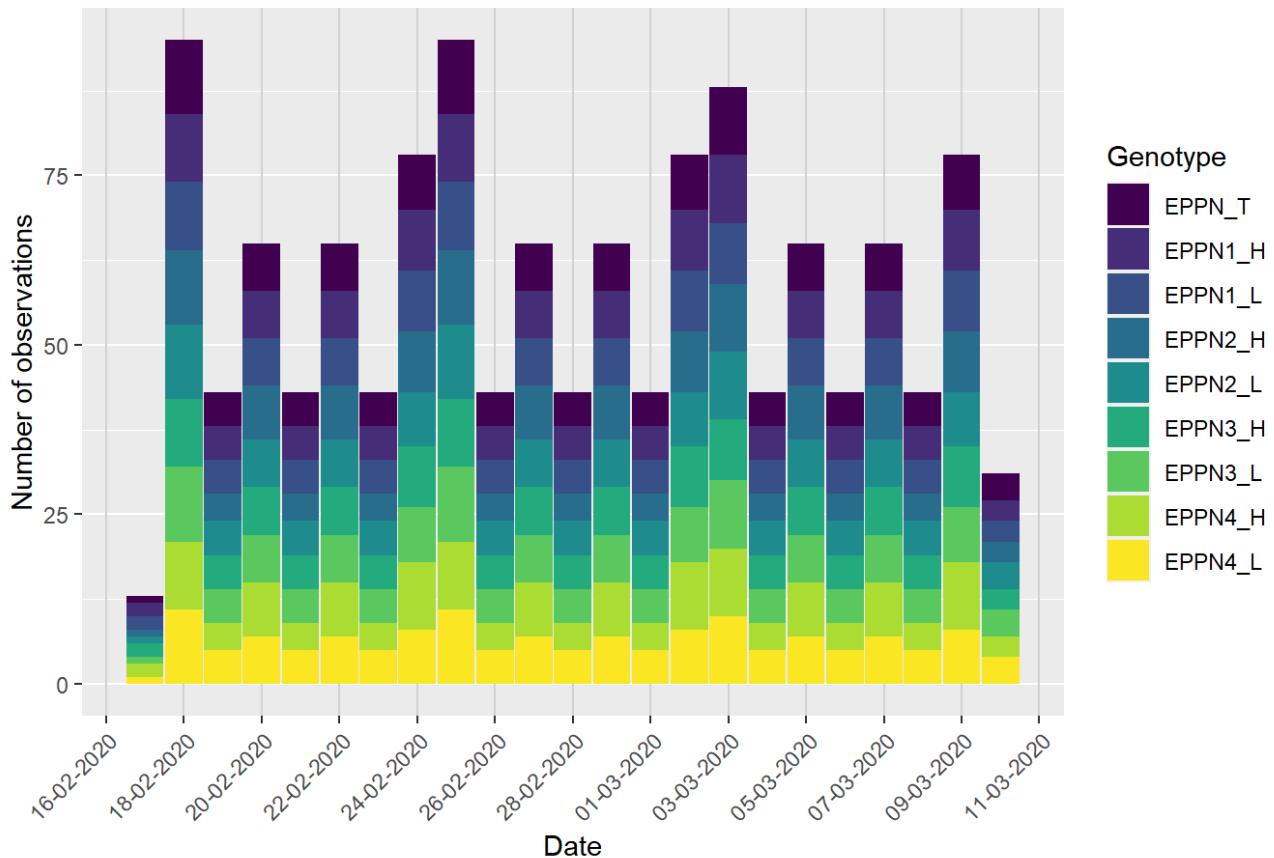
```
h2 <- ggplot(S_timeseries, aes(x = Date)) +
  geom_bar(aes(fill = Genotype), position = "stack", width = 0.96) +
  scale_fill_viridis_d(option = "D") +
  labs(x = "Date", y = "Number of observations", title = "Observations per day for S_timeseries") +
  scale_y_continuous(breaks = seq(from = 0, to = 325, by = 25)) +
  scale_x_date(date_breaks = "2 days", date_labels = "%d-%m-%Y") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        panel.grid.major.x = element_line(color = "lightgray", size = 0.5),
        panel.grid.minor.x = element_blank())
```

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

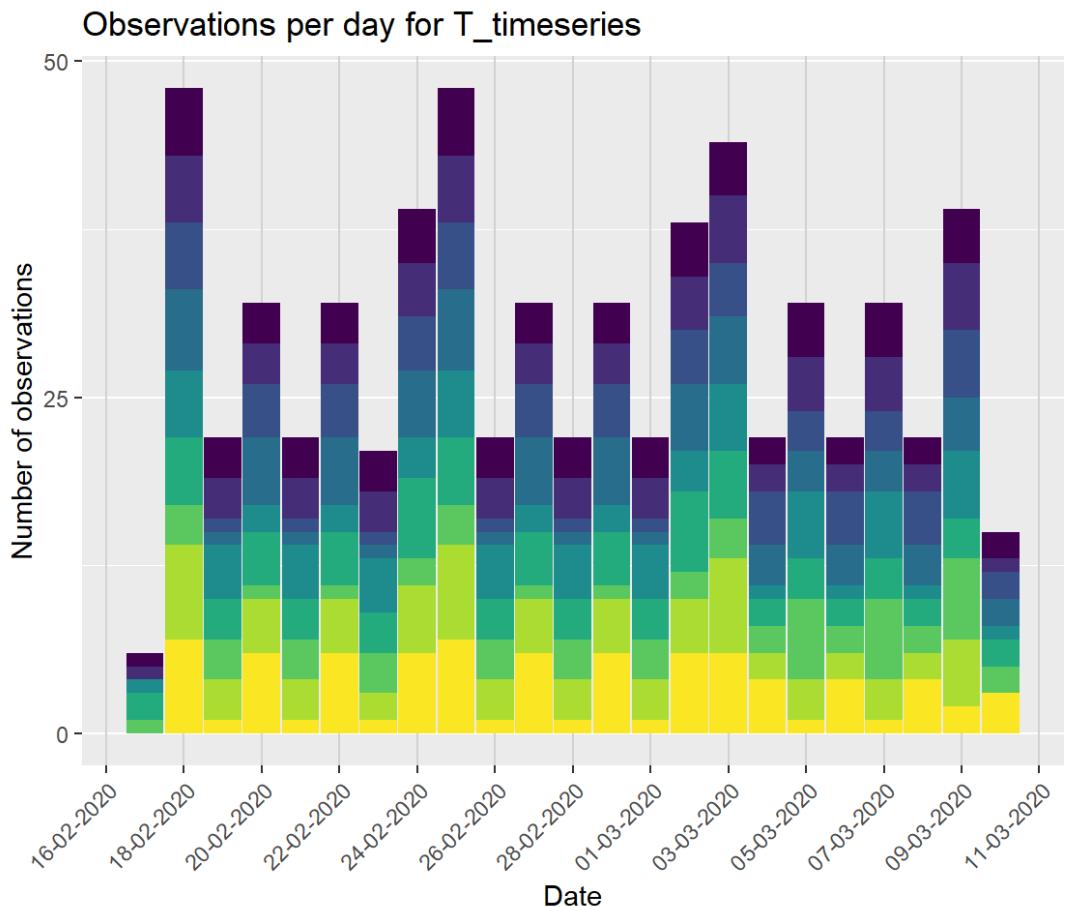
```
h3 <- ggplot(T_timeseries, aes(x = Date)) +
  geom_bar(aes(fill = Genotype), position = "stack", width = 0.96) +
  scale_fill_viridis_d(option = "D") +
  labs(x = "Date", y = "Number of observations", title = "Observations per day for T_timeseries") +
  scale_y_continuous(breaks = seq(0, to = 325, by = 25)) +
  scale_x_date(date_breaks = "2 days", date_labels = "%d-%m-%Y") +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
        panel.grid.major.x = element_line(color = "lightgray", size = 0.5),
        panel.grid.minor.x = element_blank())
```

h2

Observations per day for S_timeseries



h3



A. Exploration of the timeseries dataframe

Scatter plots by Genotype

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

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

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

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

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

Scatter plots for all genotypes by water treatment

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

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

B. Exploration of the S_timeseries dataframe

Scatter plots by Genotype

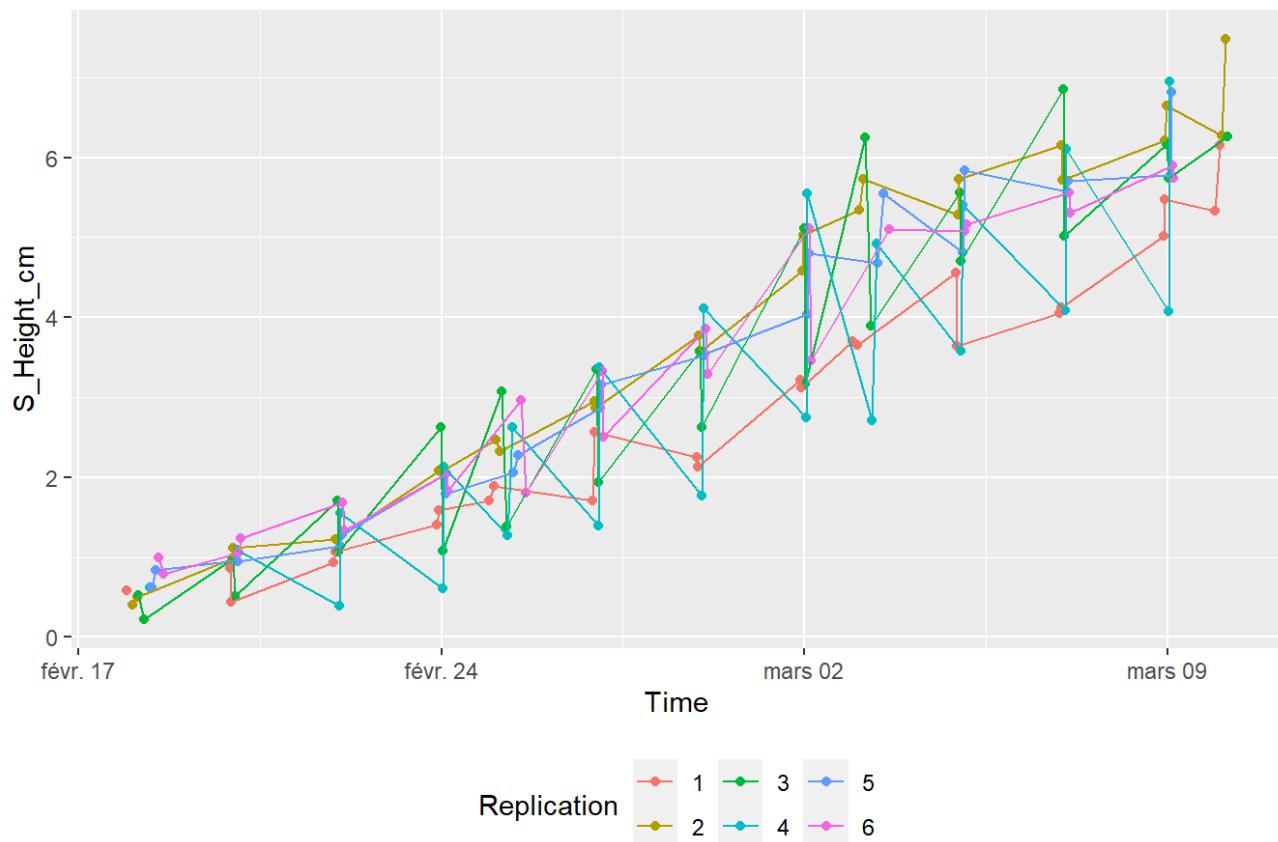
```
plot_scatter_by_genotype(S_timeseries, variables_S, "EPPN_T")
```

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

```
## Warning: Removed 3 rows containing missing values (`geom_point()`).
```

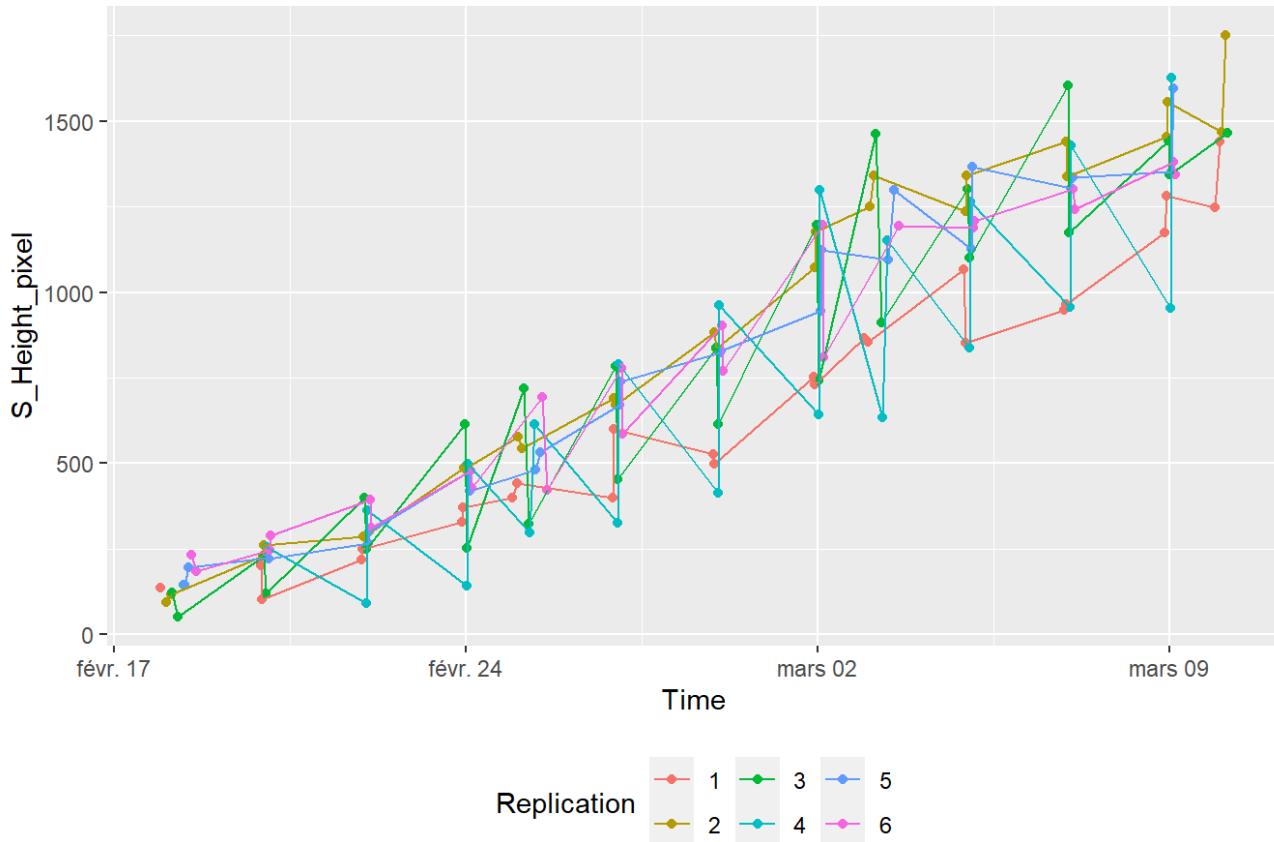
```
## Warning: Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of S_Height_cm for Genotype EPPN_T



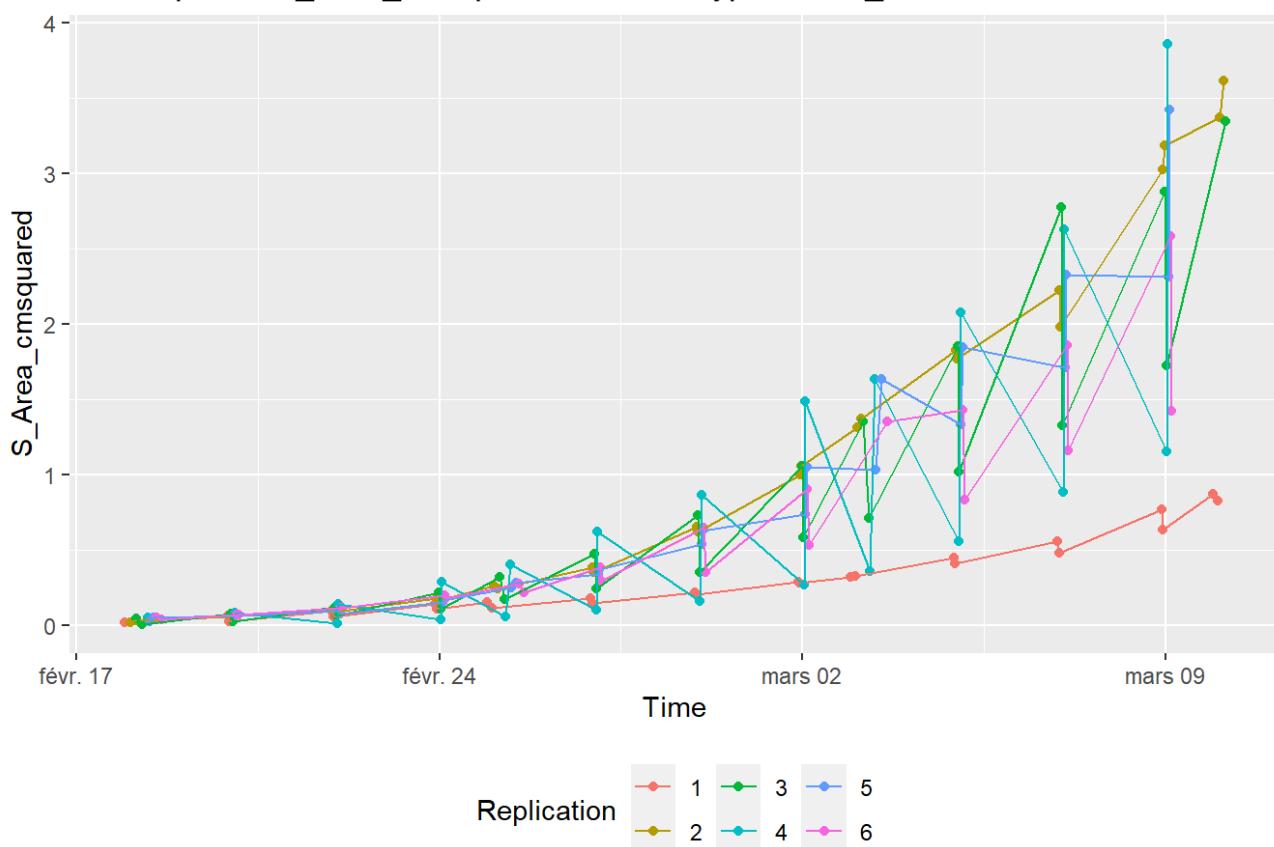
```
## Warning: Removed 3 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of S_Height_pixel for Genotype EPPN_T

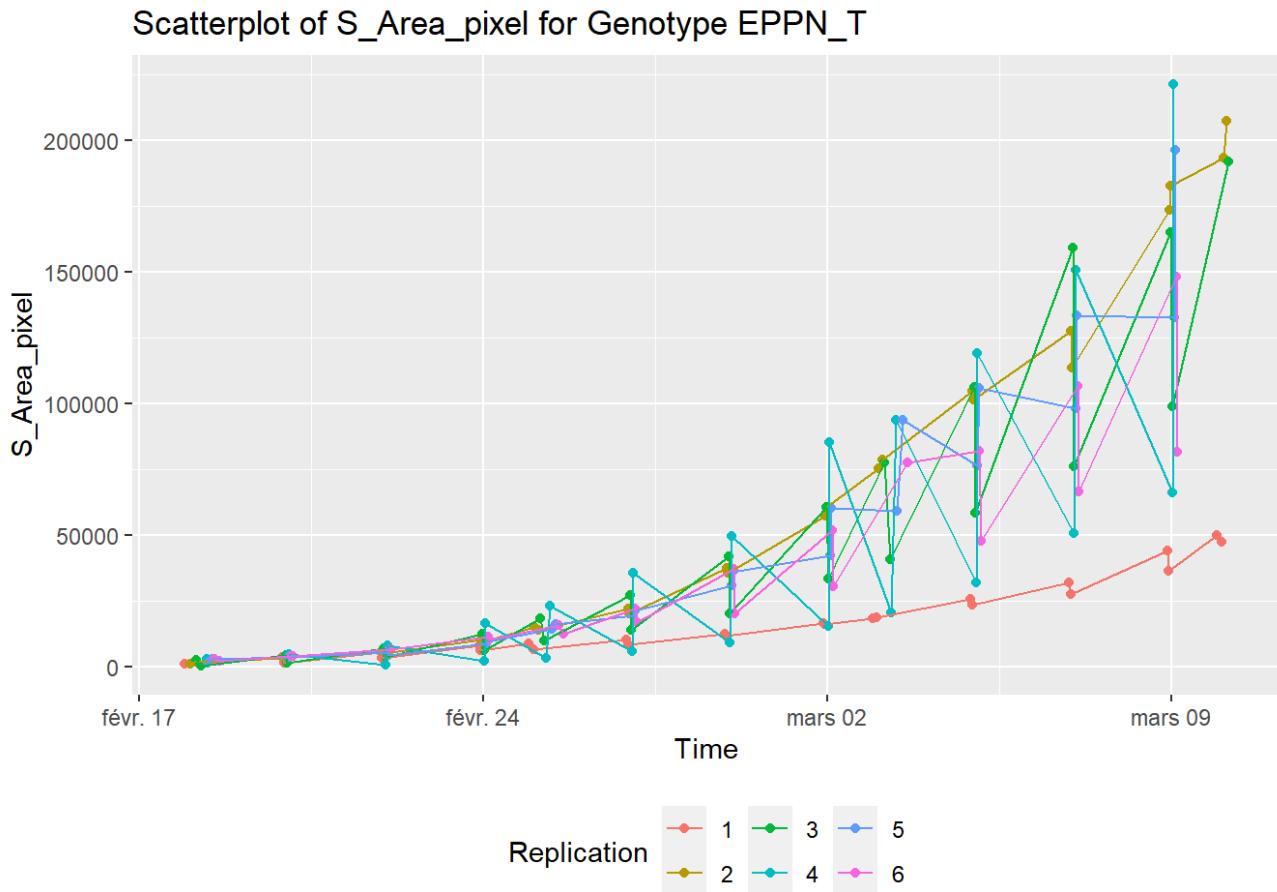


```
## Warning: Removed 3 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of S_Area_cmsquared for Genotype EPPN_T

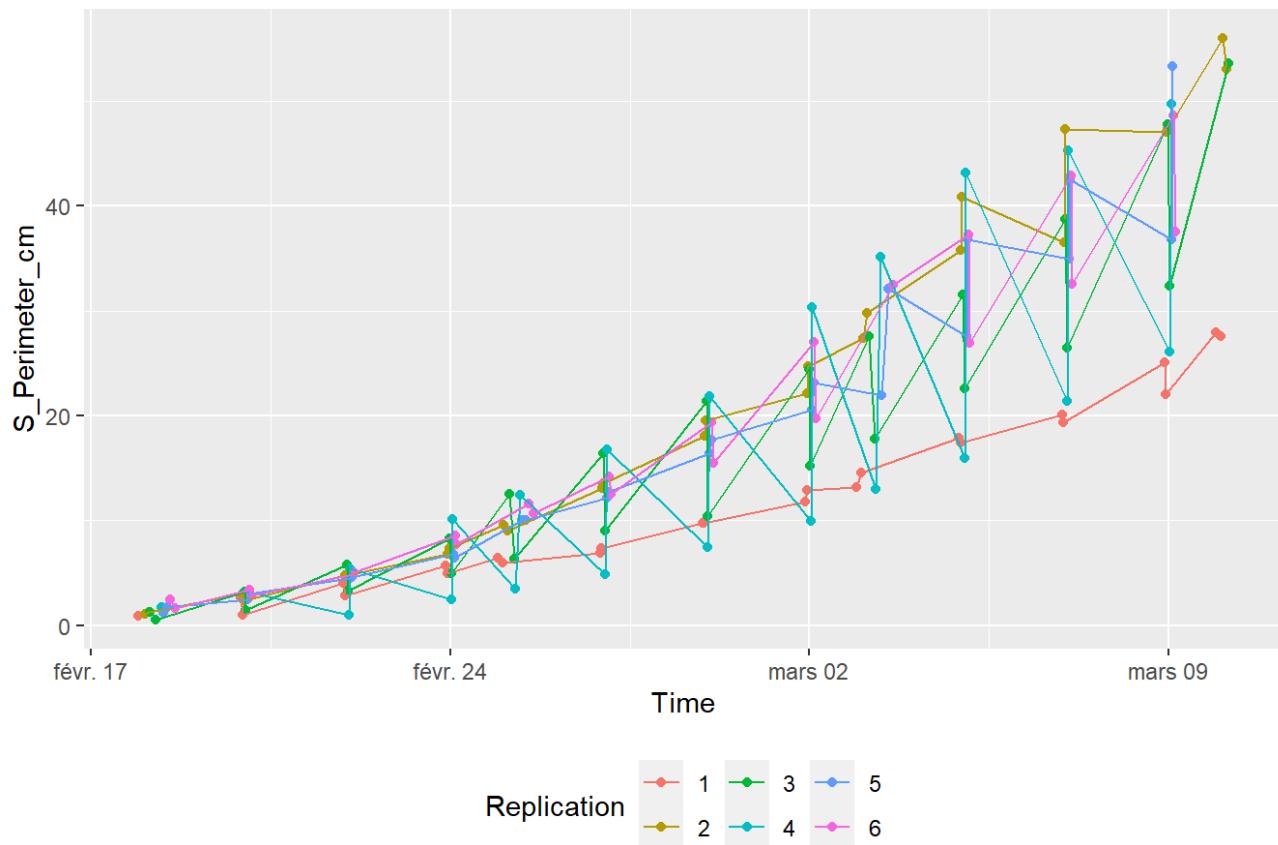


```
## Warning: Removed 3 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```



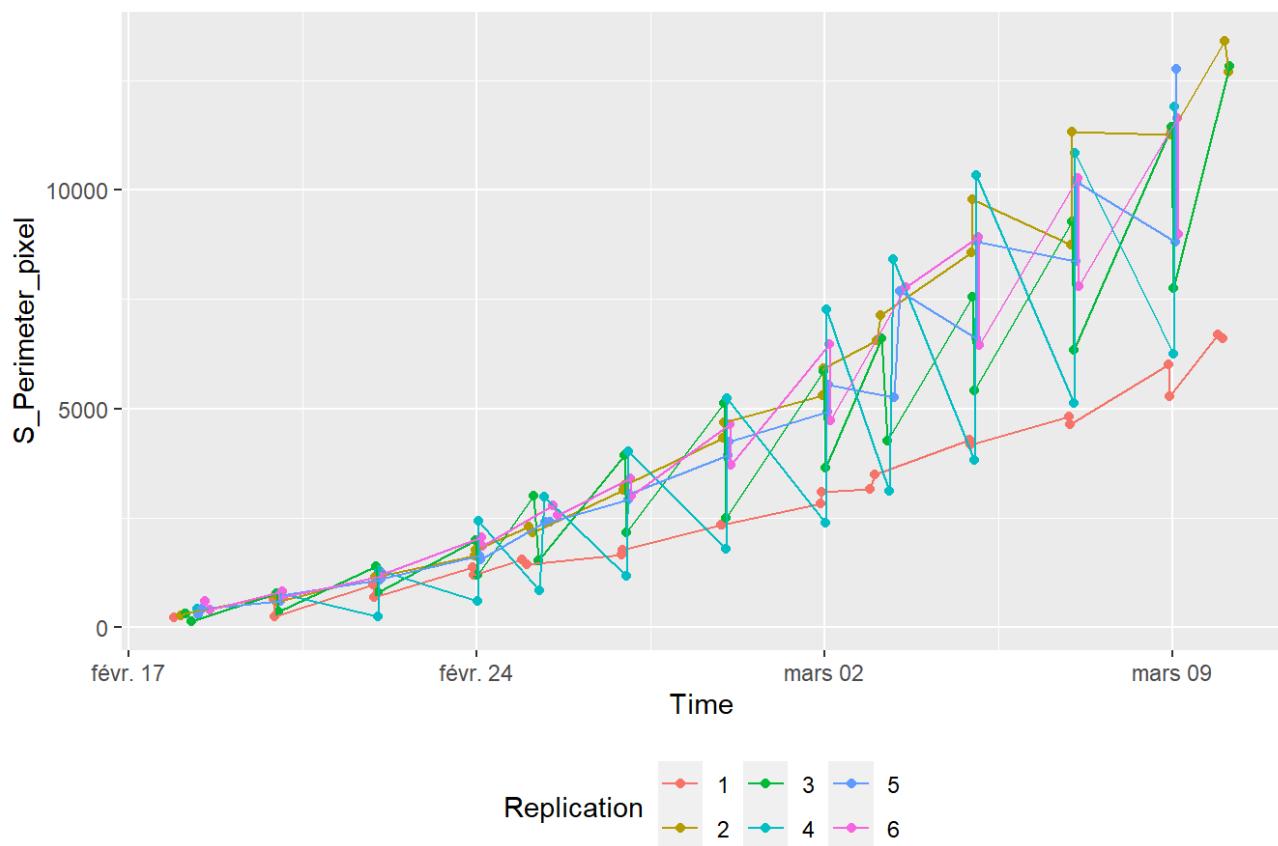
```
## Warning: Removed 3 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of S_Perimeter_cm for Genotype EPPN_T



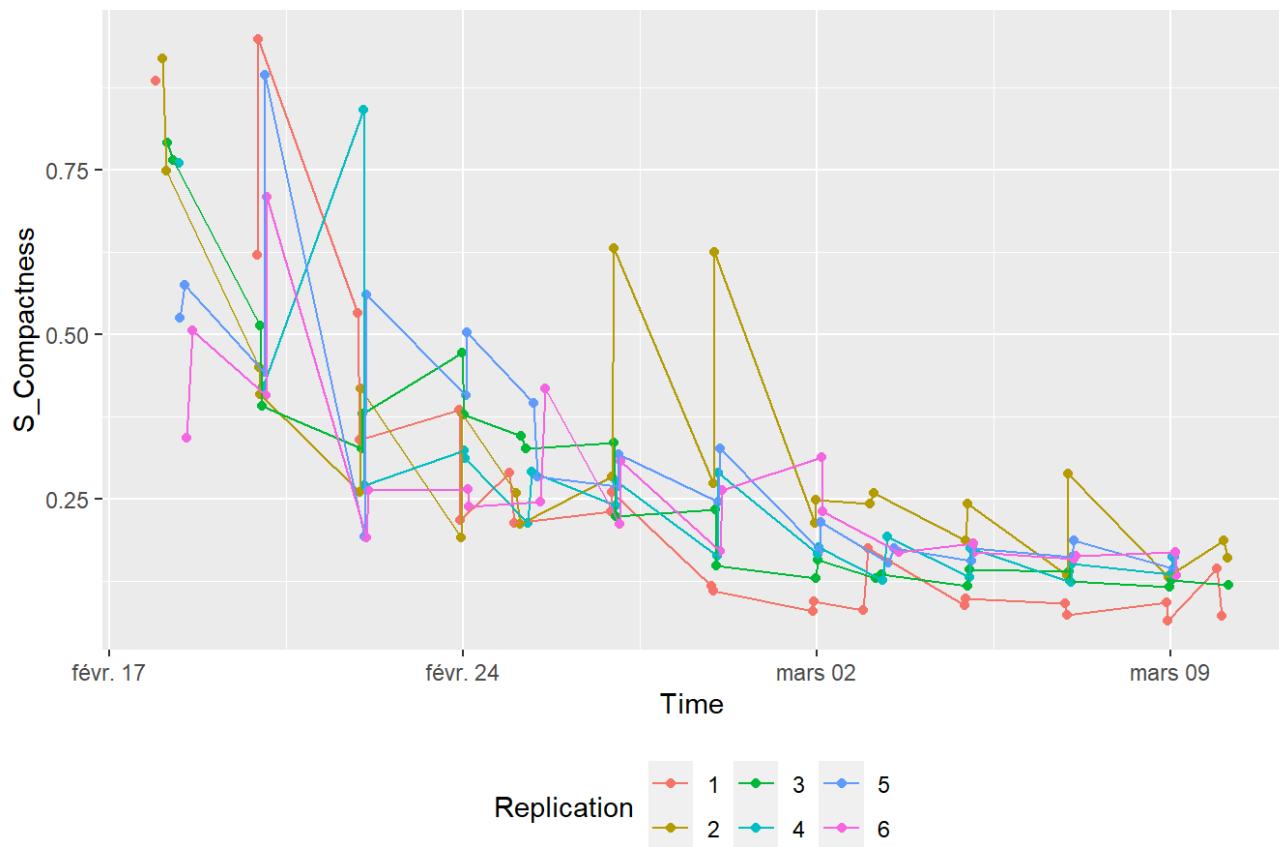
```
## Warning: Removed 3 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of S_Perimeter_pixel for Genotype EPPN_T



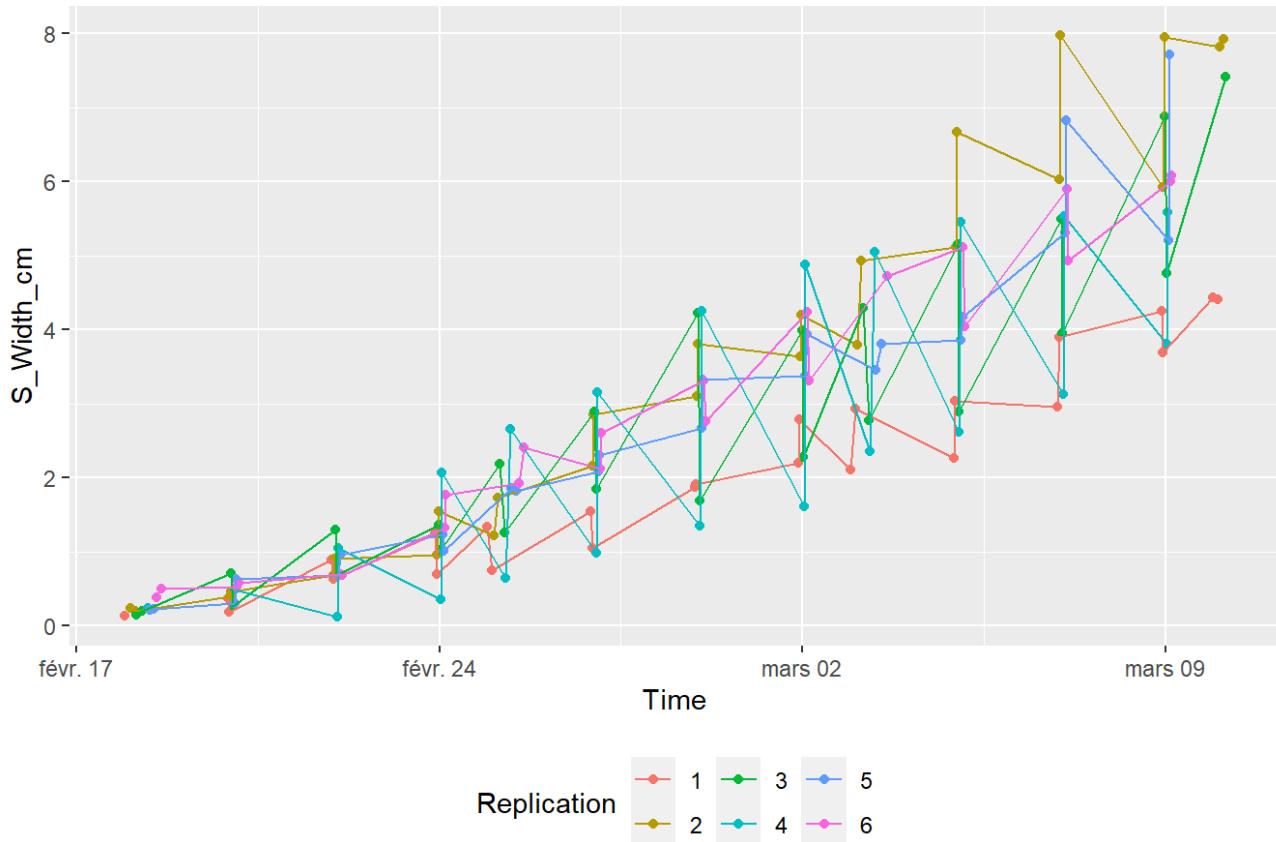
```
## Warning: Removed 3 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of S_Compactness for Genotype EPPN_T



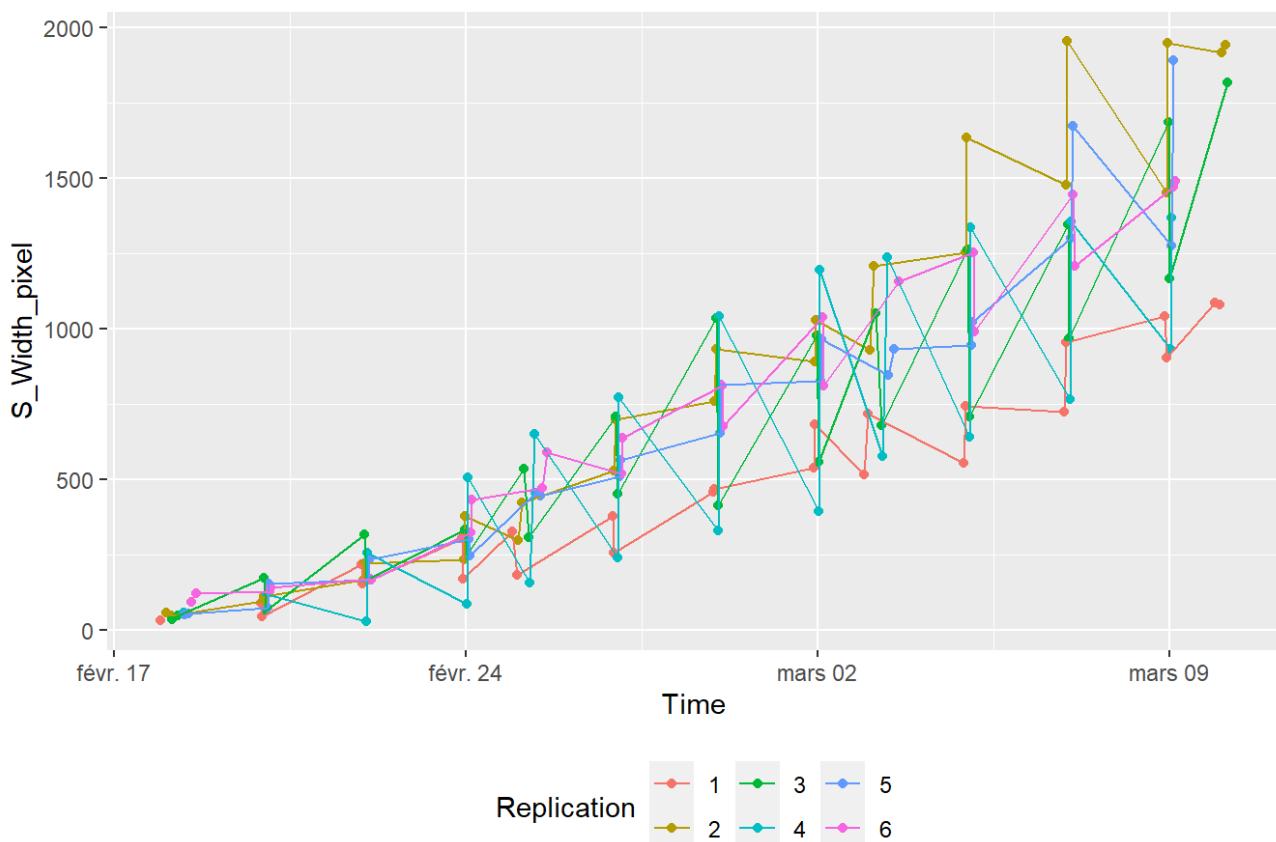
```
## Warning: Removed 3 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of S_Width_cm for Genotype EPPN_T



```
## Warning: Removed 3 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of S_Width_pixel for Genotype EPPN_T



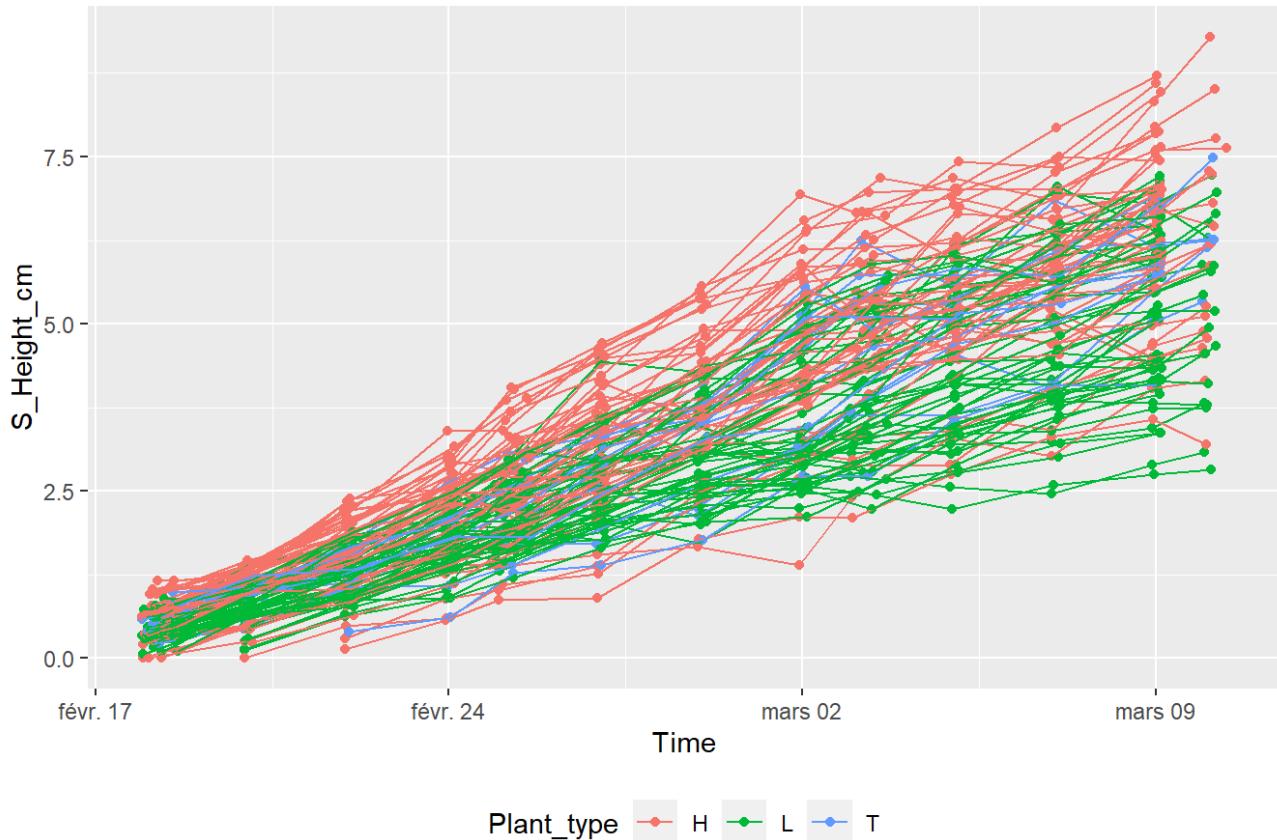
Scatterplots for all genotypes by Plant type (Hybride, Line, EPPN20_T) with smooth line.

```
plot_scatter_with_smooth(S_timeseries, variables_S)
```

```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 30 rows containing missing values (`geom_line()`).
```

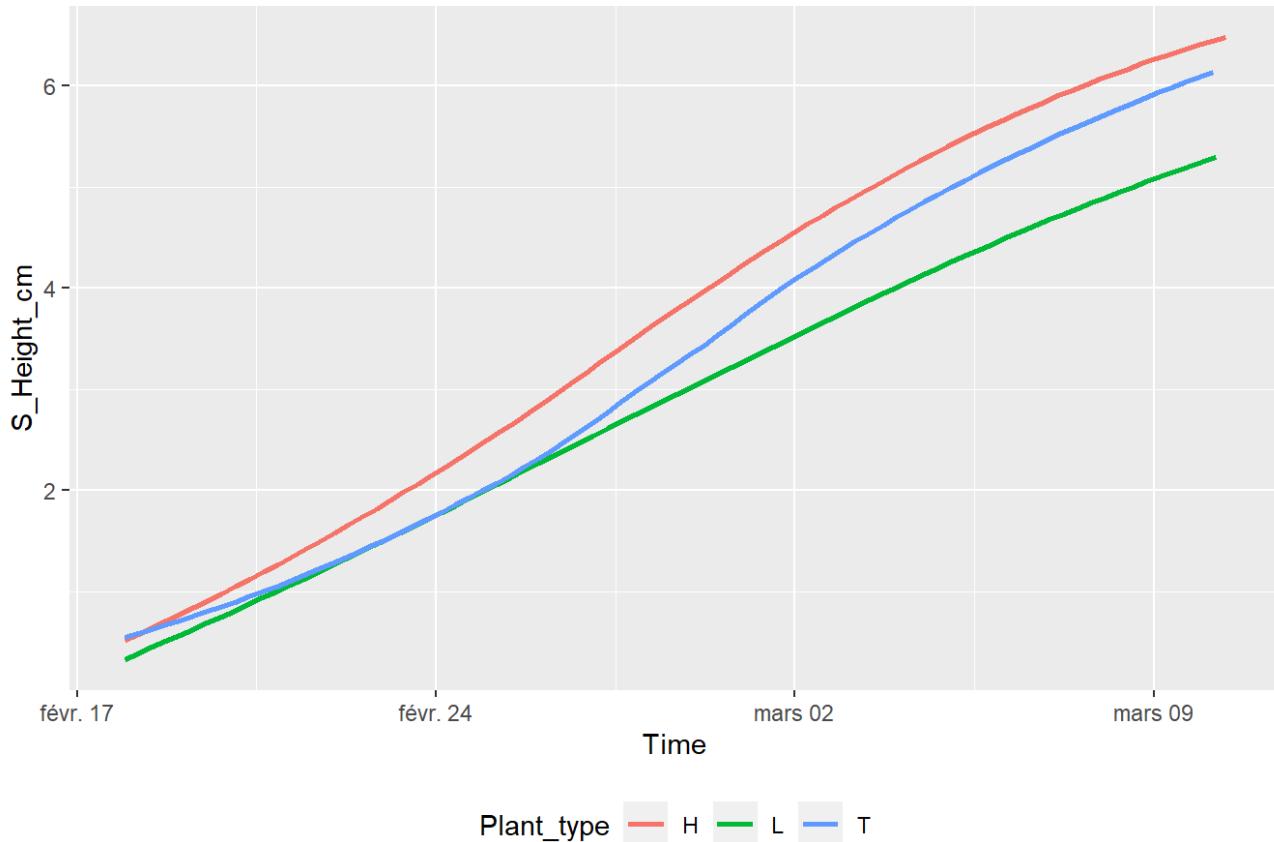
Scatterplot of S_Height_cm by Plant type



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

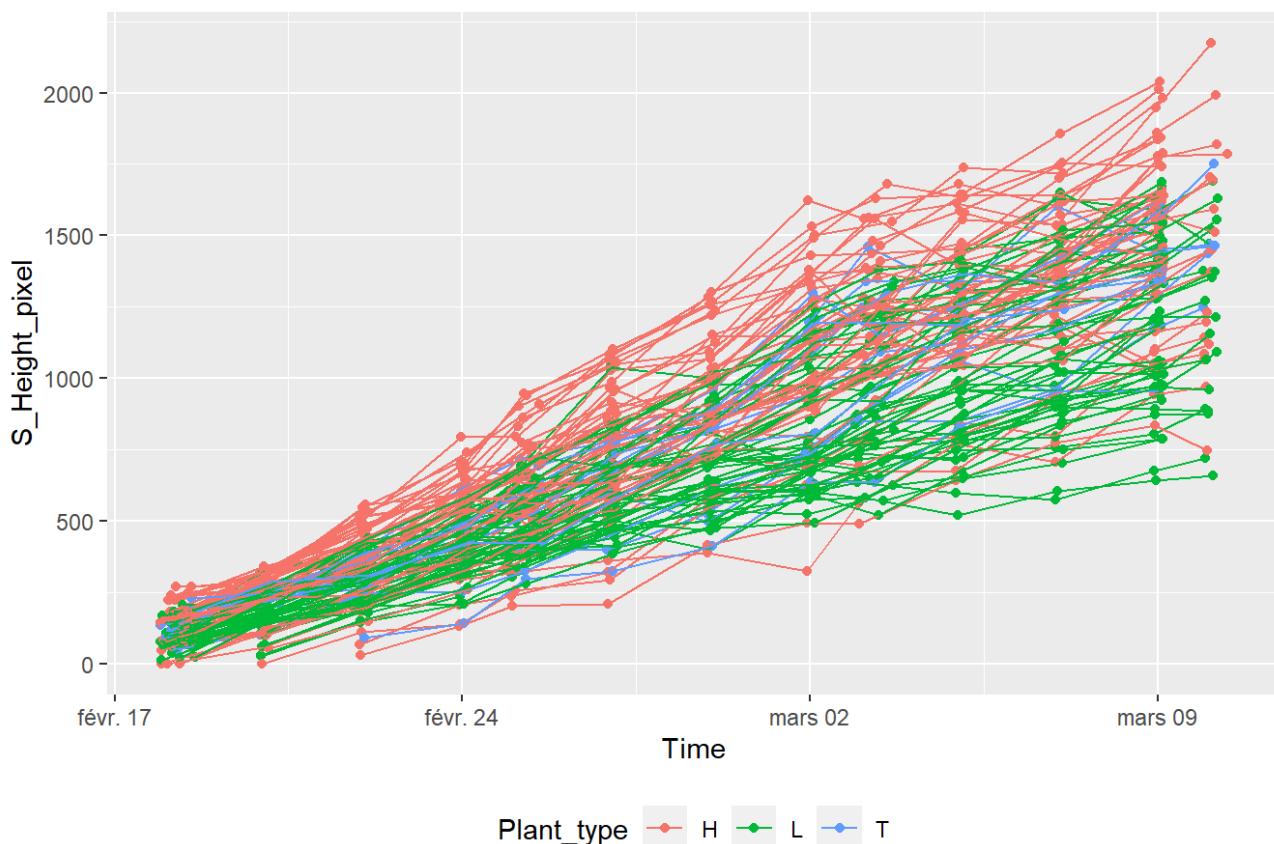
```
## Warning: Removed 30 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of S_Height_cm by Plant type



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
## Removed 30 rows containing missing values (`geom_line()`).
```

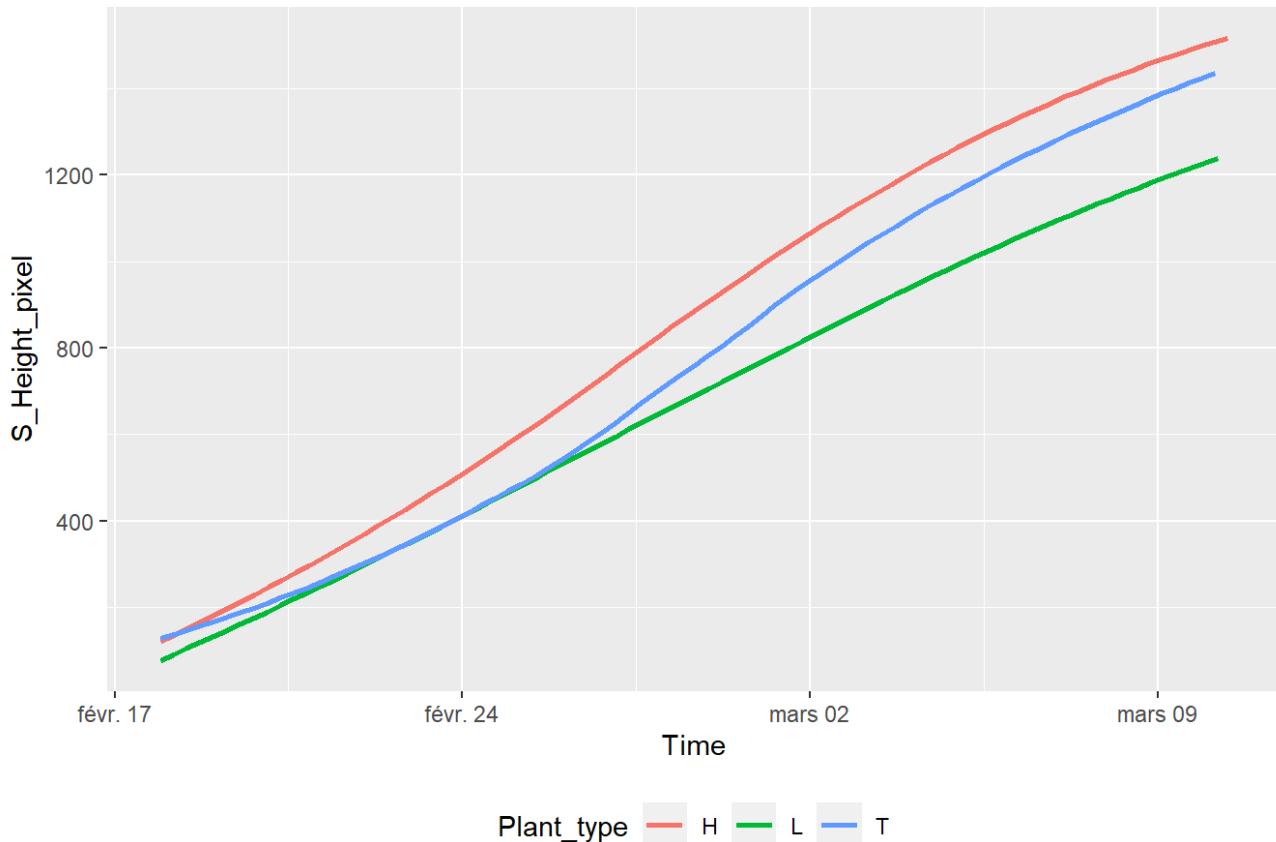
Scatterplot of S_Height_pixel by Plant type



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

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

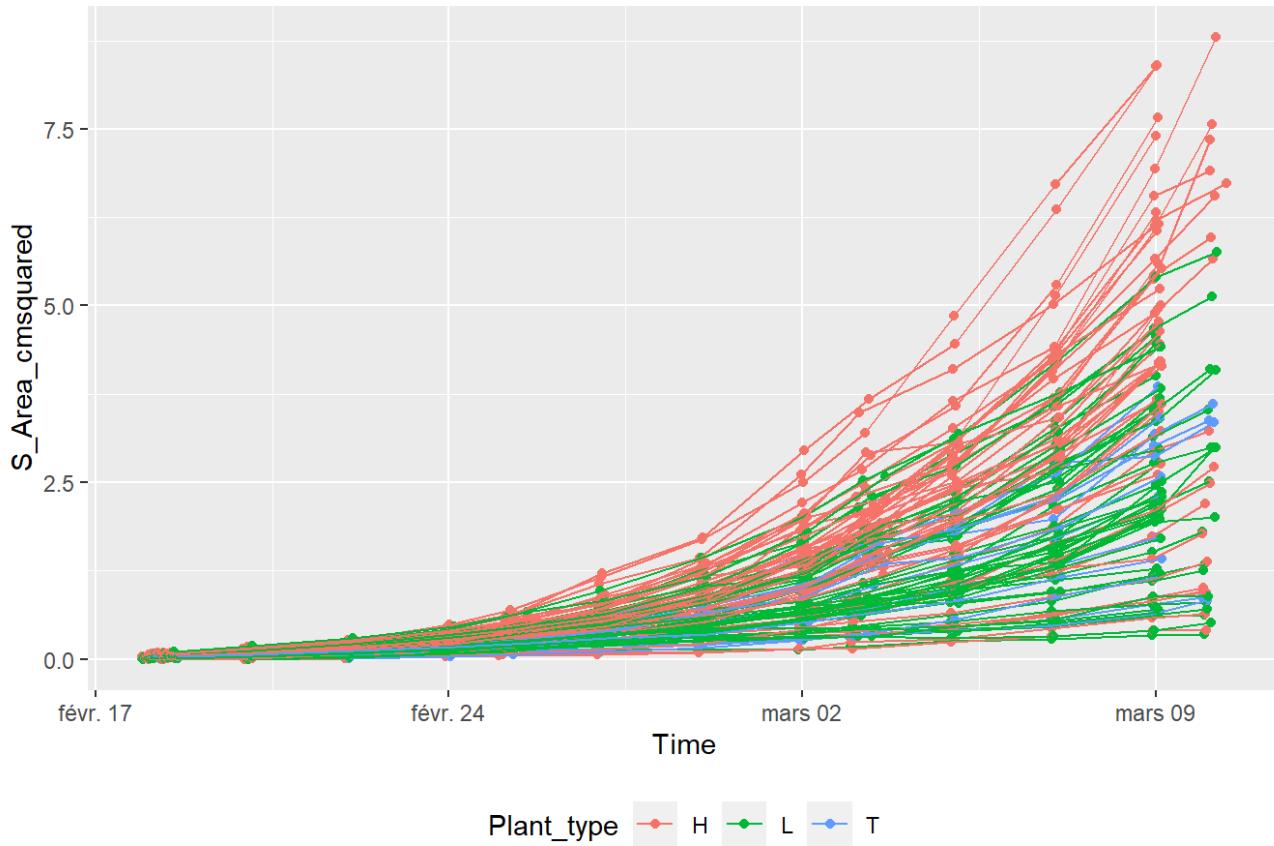
Smooth line of S_Height_pixel by Plant type



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
```

```
## Removed 30 rows containing missing values (`geom_line()`).
```

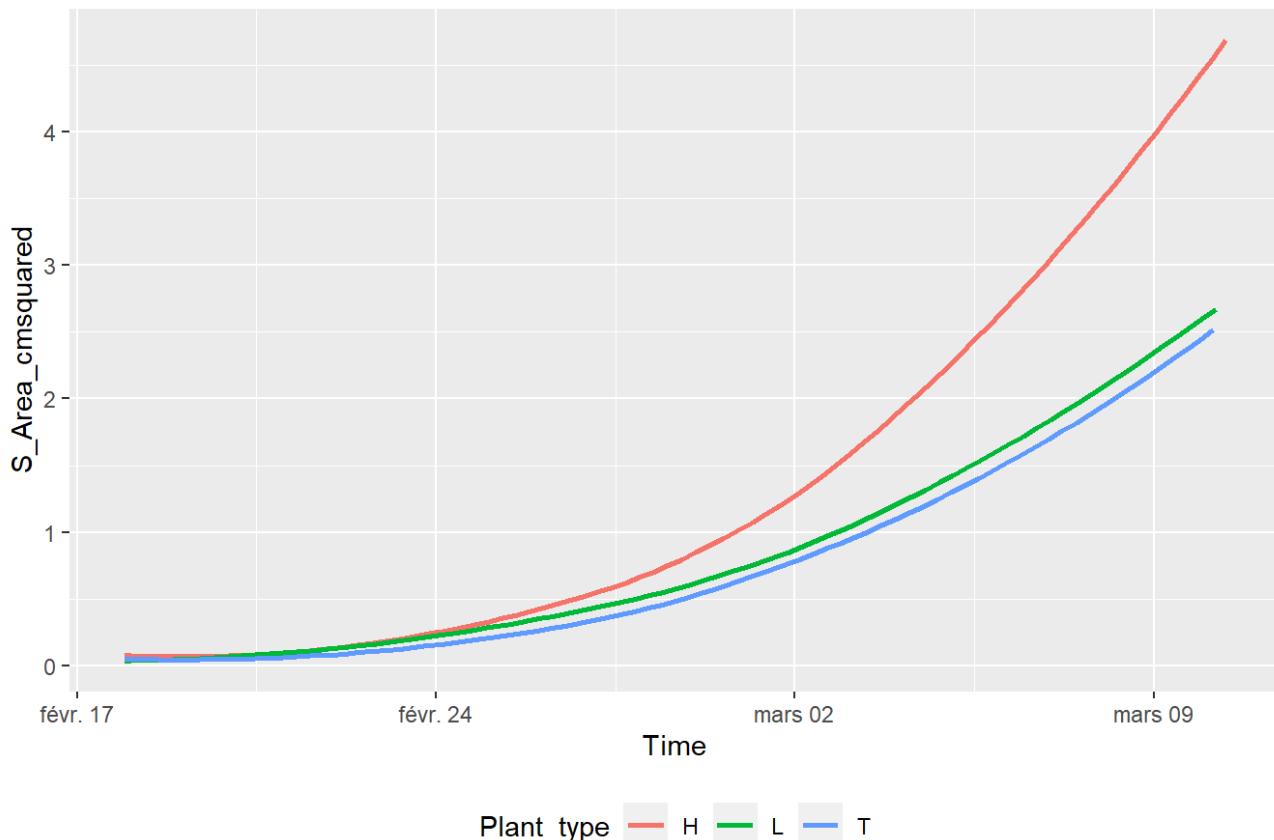
Scatterplot of S_Area_cmsquared by Plant type



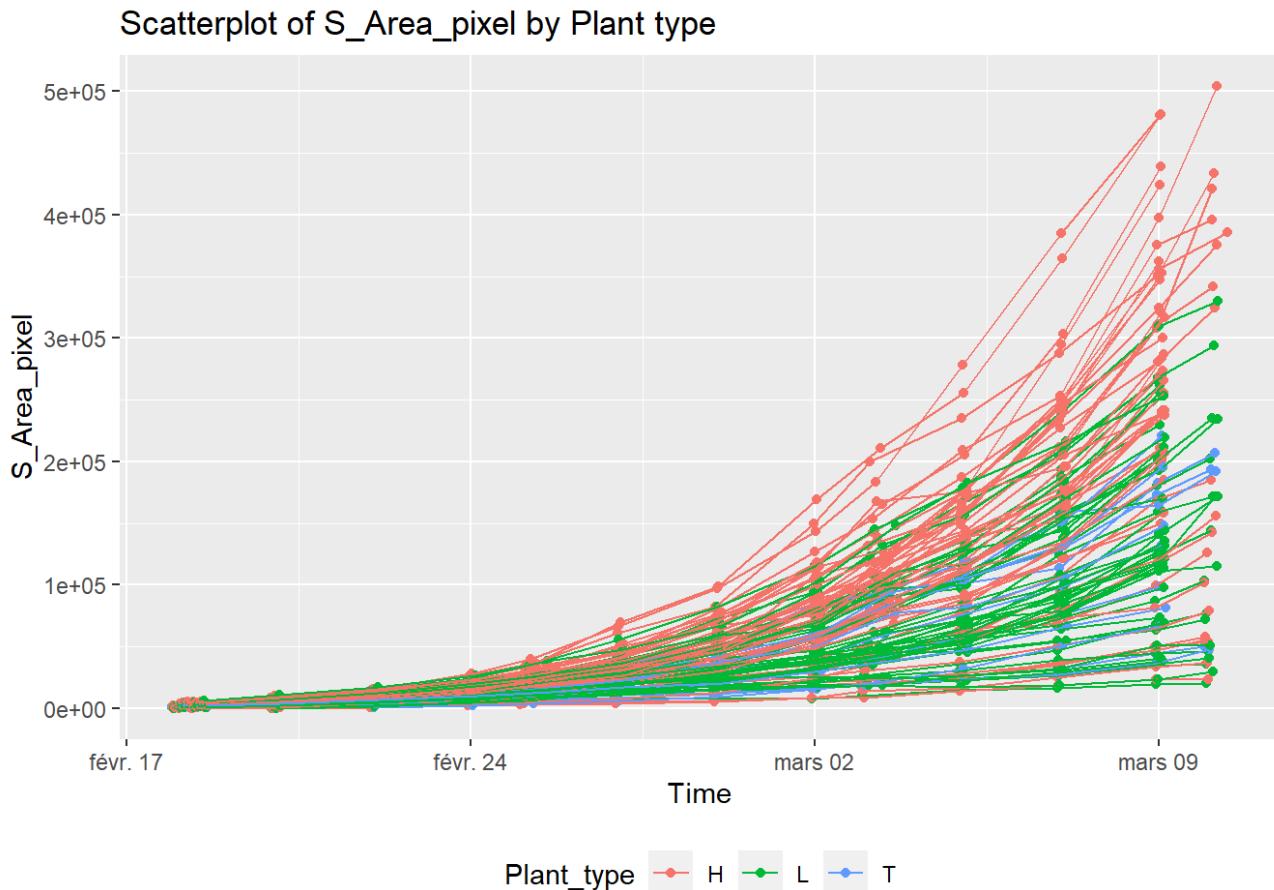
```
## `geom_smooth()` using formula = 'y ~ x'
```

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

Smooth line of S_Area_cmsquared by Plant type



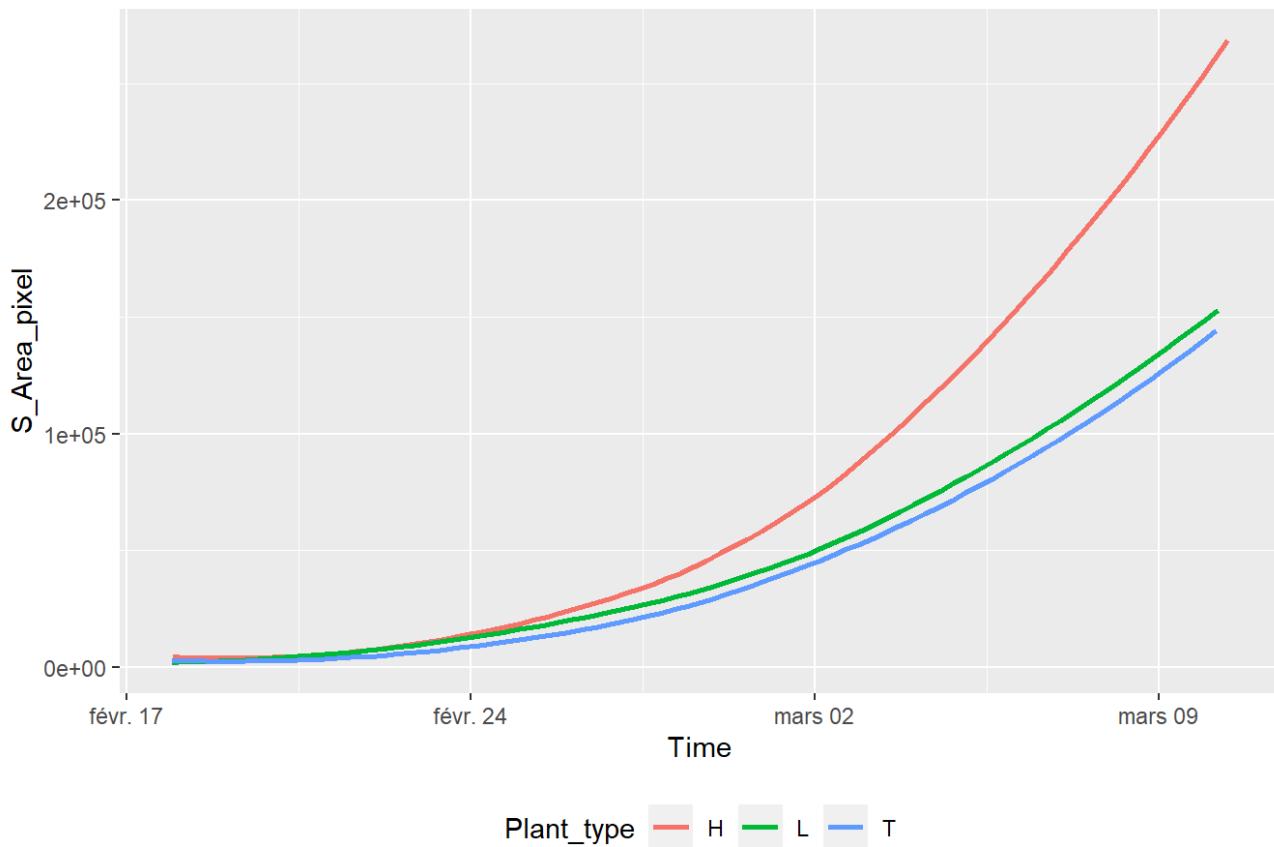
```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
## Removed 30 rows containing missing values (`geom_line()`).
```



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

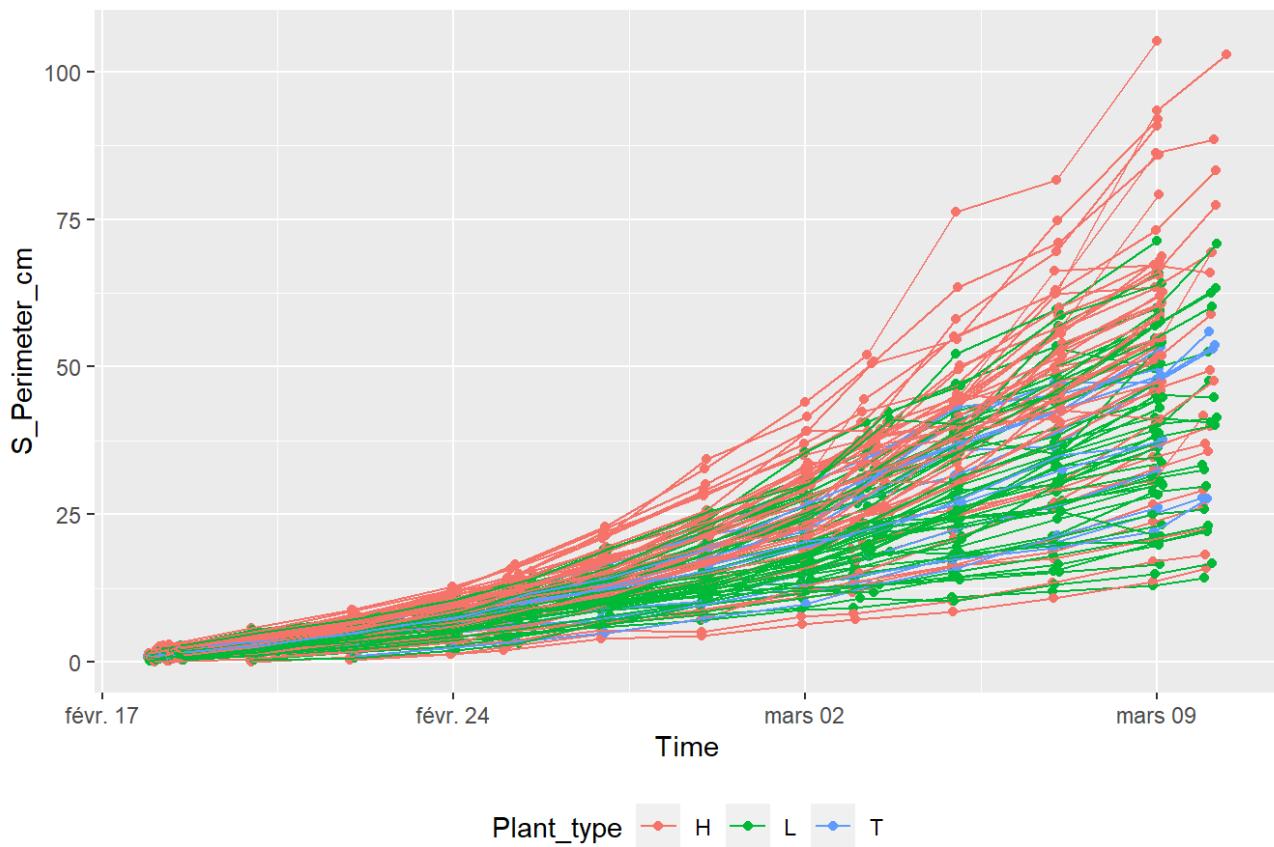
```
## Warning: Removed 30 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of S_Area_pixel by Plant type



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
## Removed 30 rows containing missing values (`geom_line()`).
```

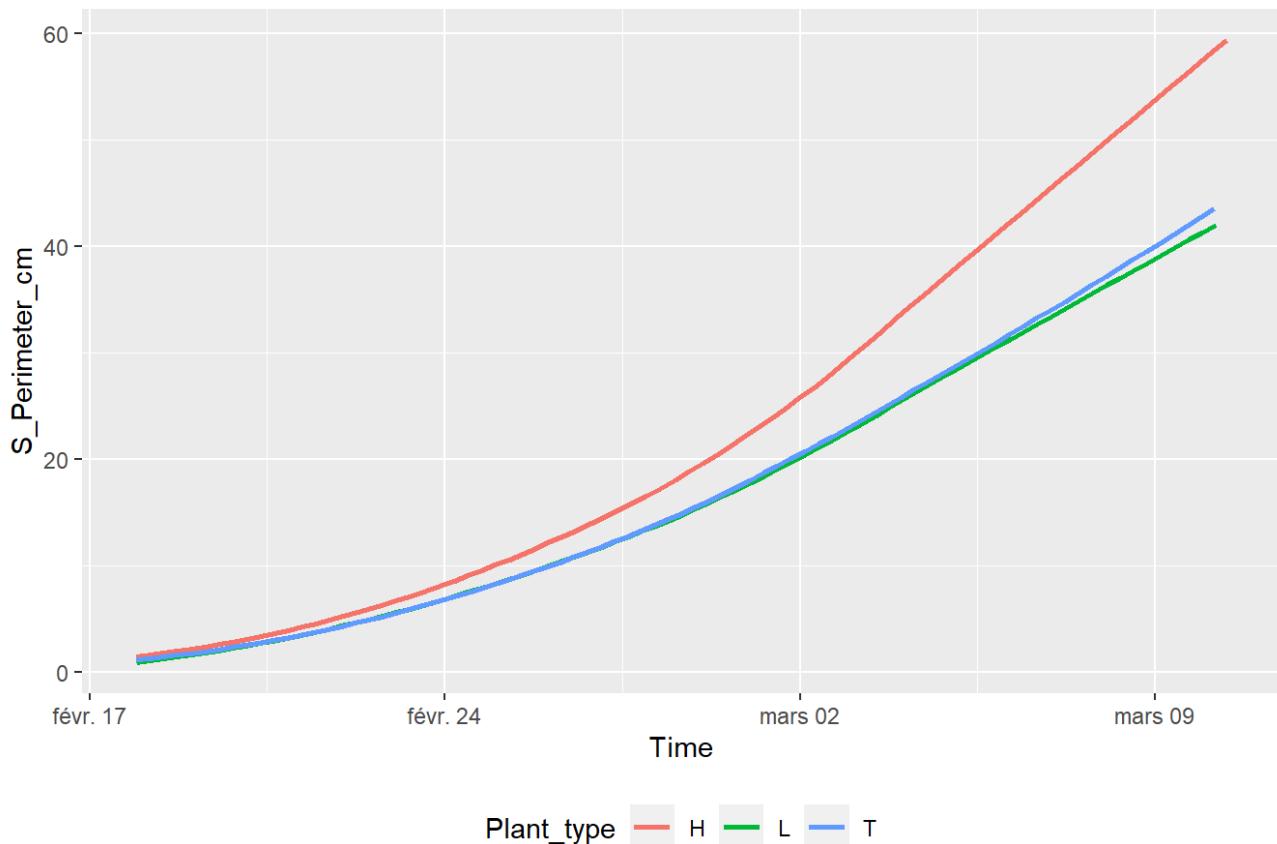
Scatterplot of S_Perimeter_cm by Plant type



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

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

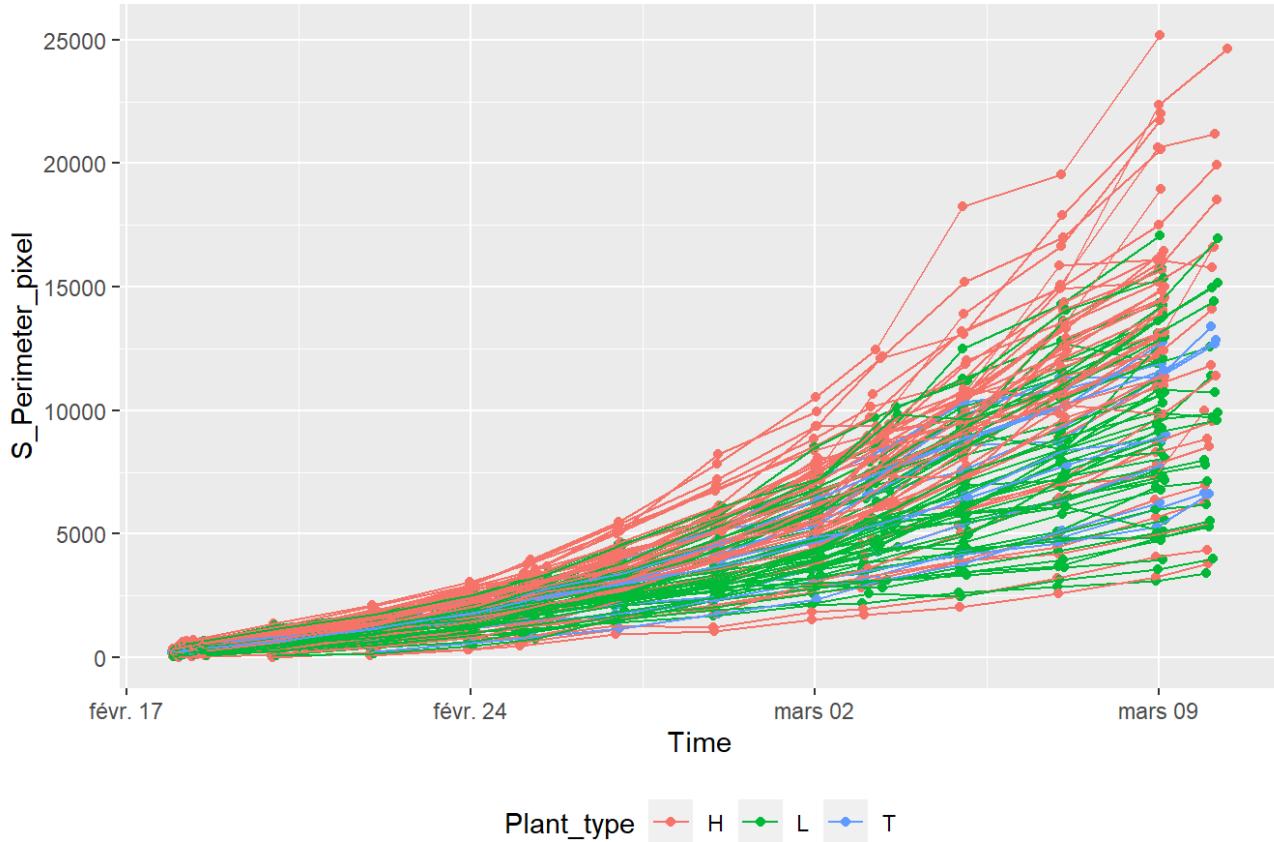
Smooth line of S_Perimeter_cm by Plant type



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
```

```
## Removed 30 rows containing missing values (`geom_line()`).
```

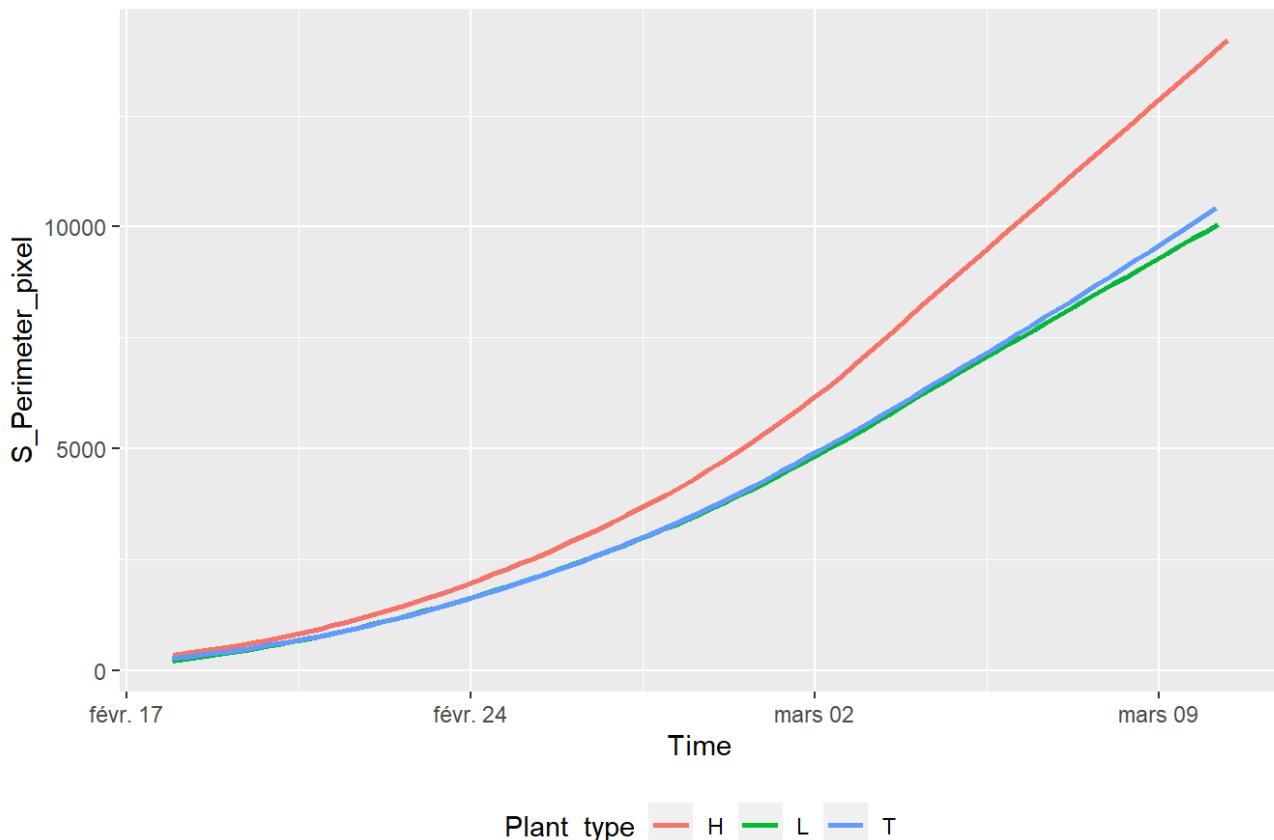
Scatterplot of S_Perimeter_pixel by Plant type



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

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

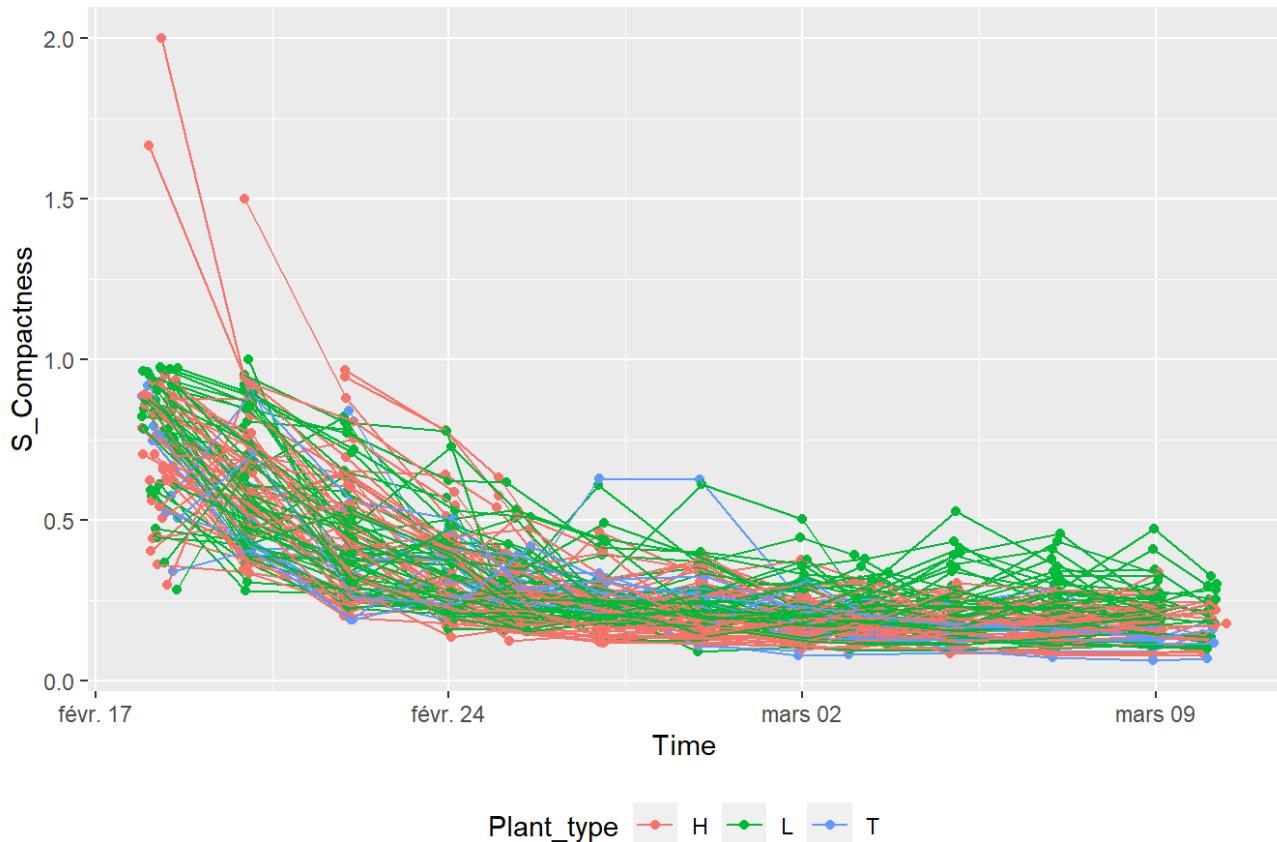
Smooth line of S_Perimeter_pixel by Plant type



```
## Warning: Removed 31 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 31 rows containing missing values (`geom_line()`).
```

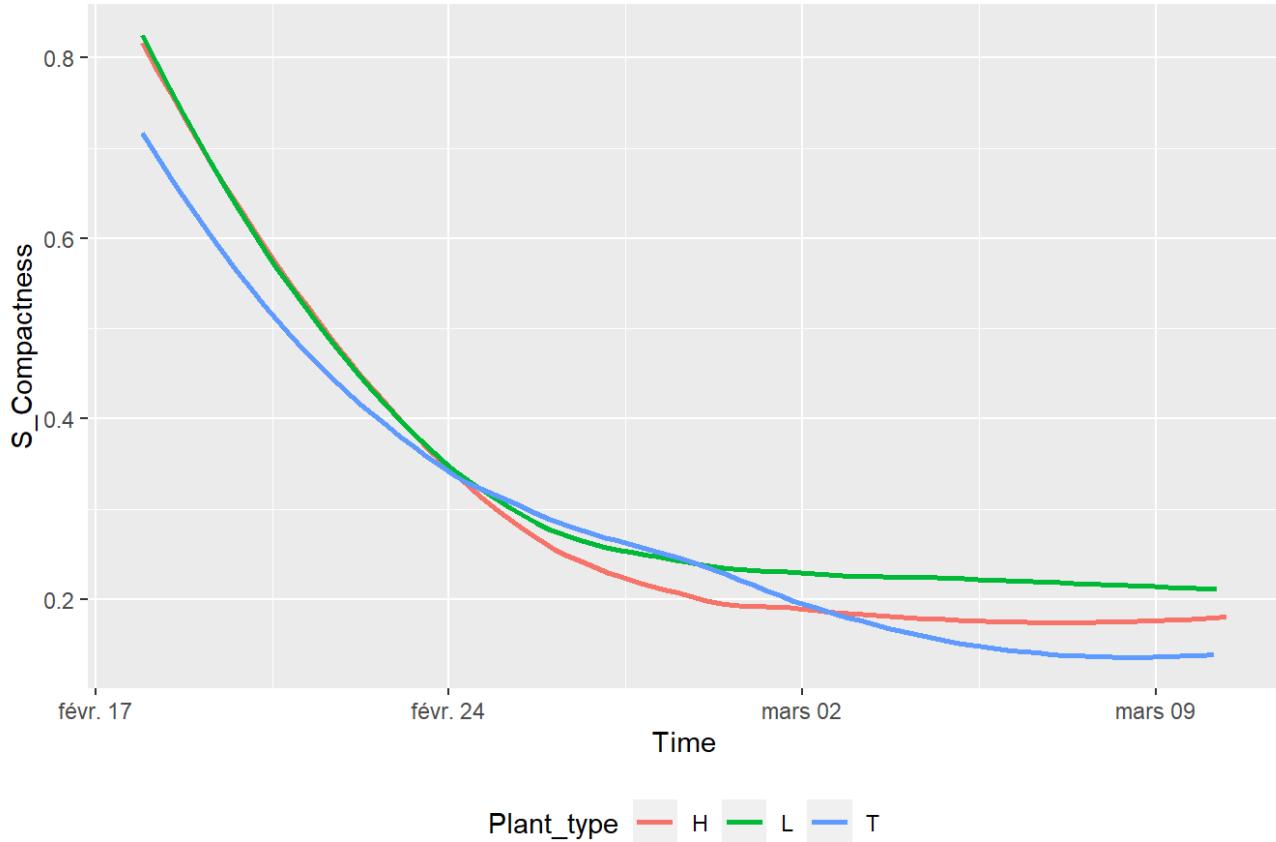
Scatterplot of S_Compactness by Plant type



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

```
## Warning: Removed 31 rows containing non-finite values (`stat_smooth()`).
```

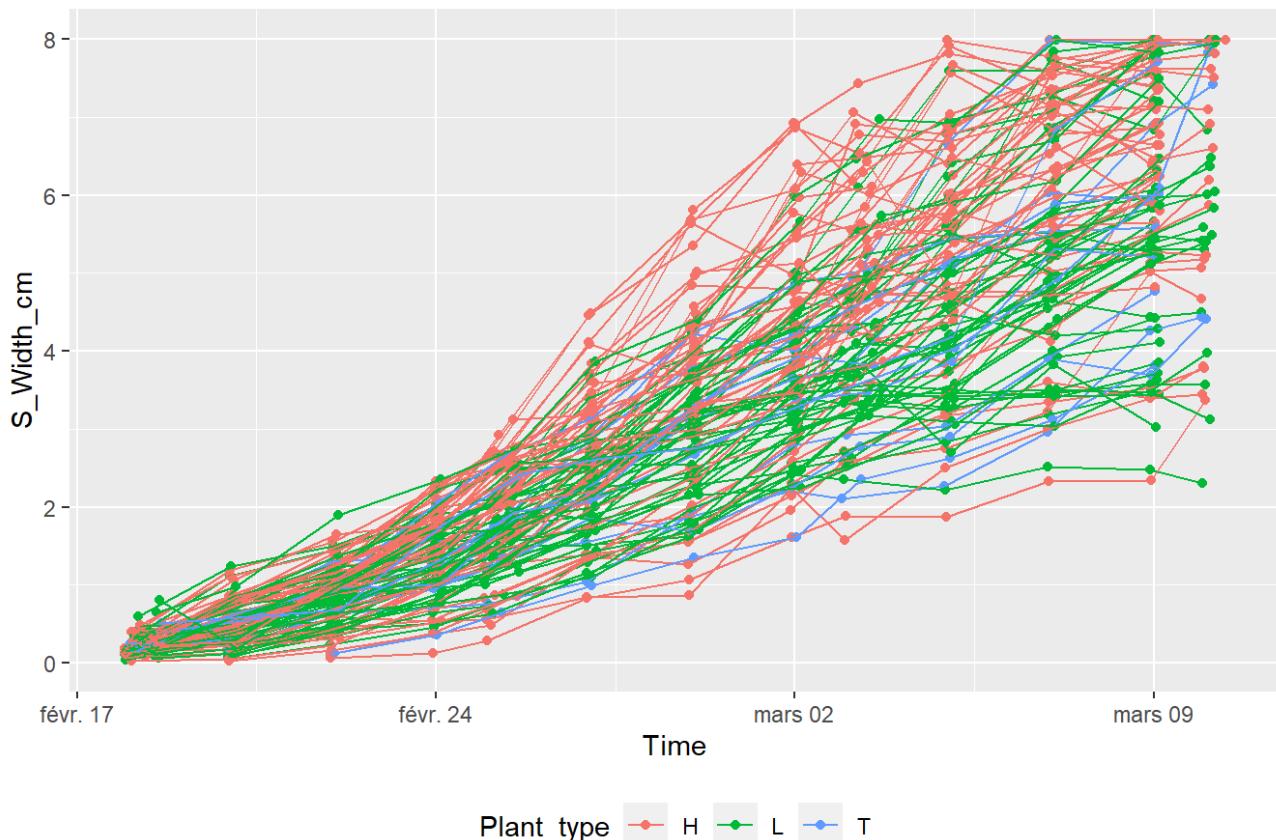
Smooth line of S_Compactness by Plant type



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 30 rows containing missing values (`geom_line()`).
```

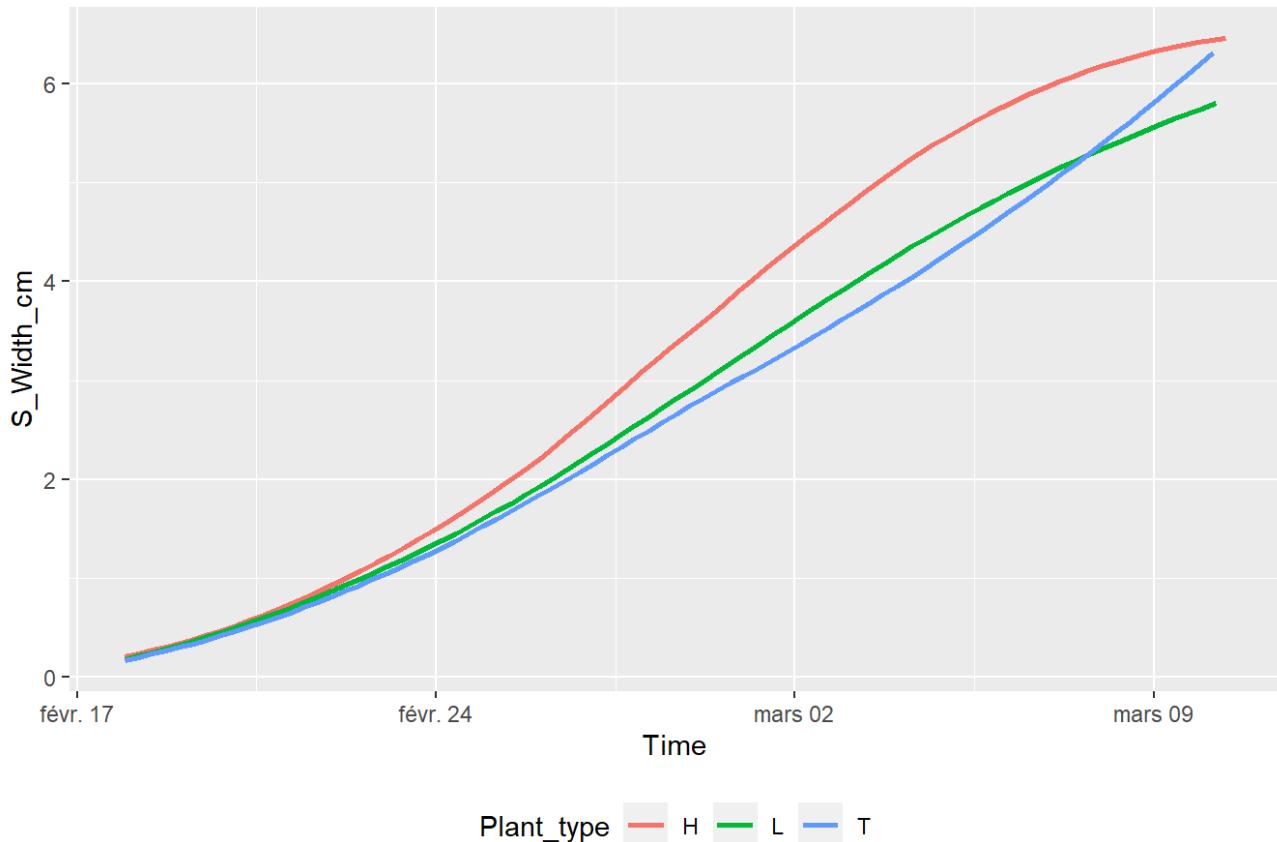
Scatterplot of S_Width_cm by Plant type



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

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

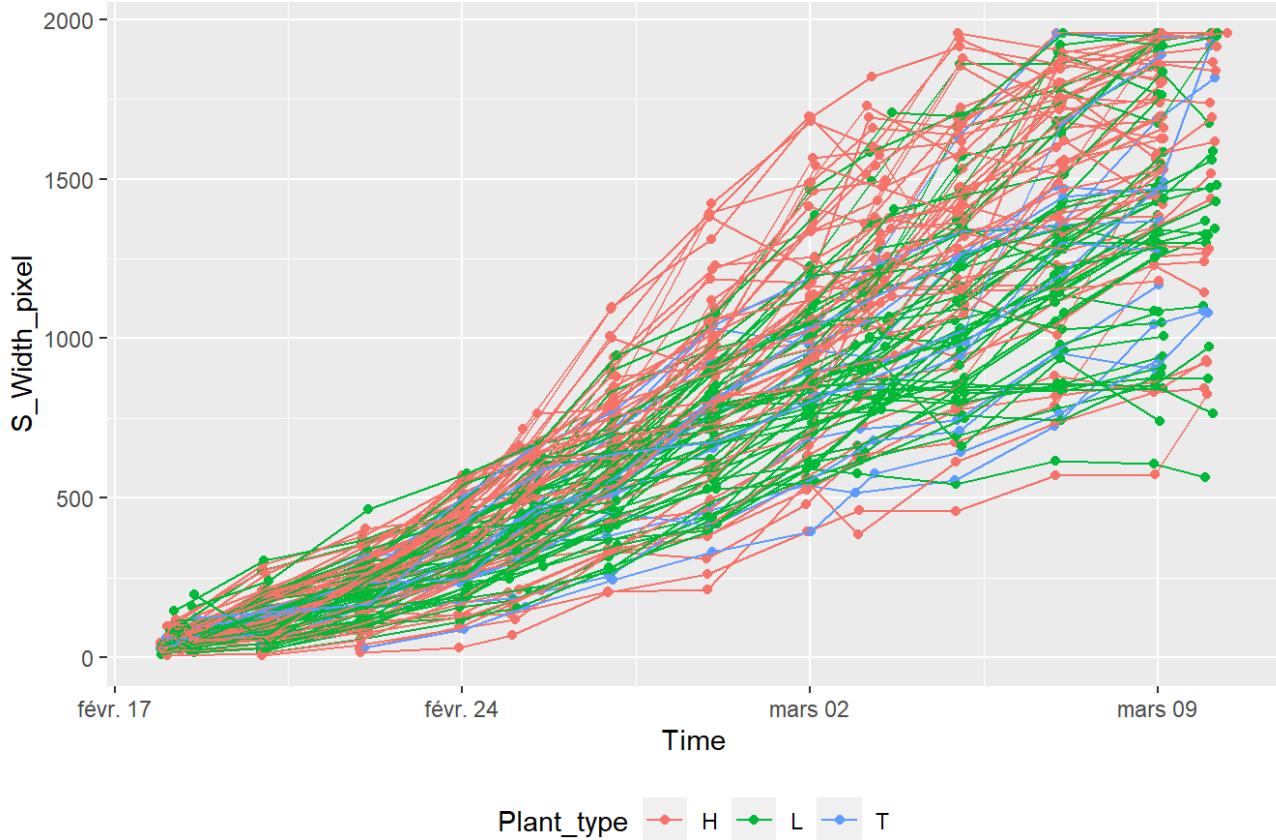
Smooth line of S_Width_cm by Plant type



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
```

```
## Removed 30 rows containing missing values (`geom_line()`).
```

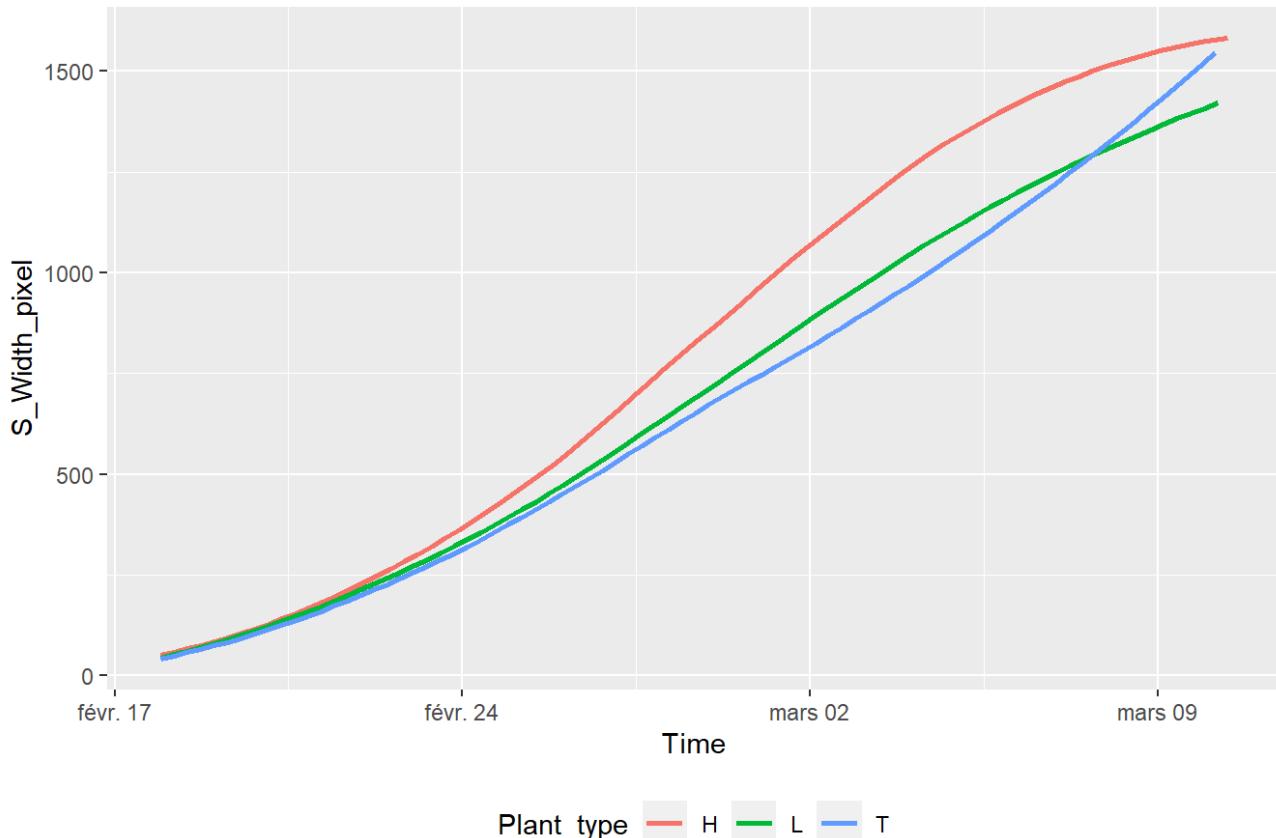
Scatterplot of S_Width_pixel by Plant type



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

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

Smooth line of S_Width_pixel by Plant type



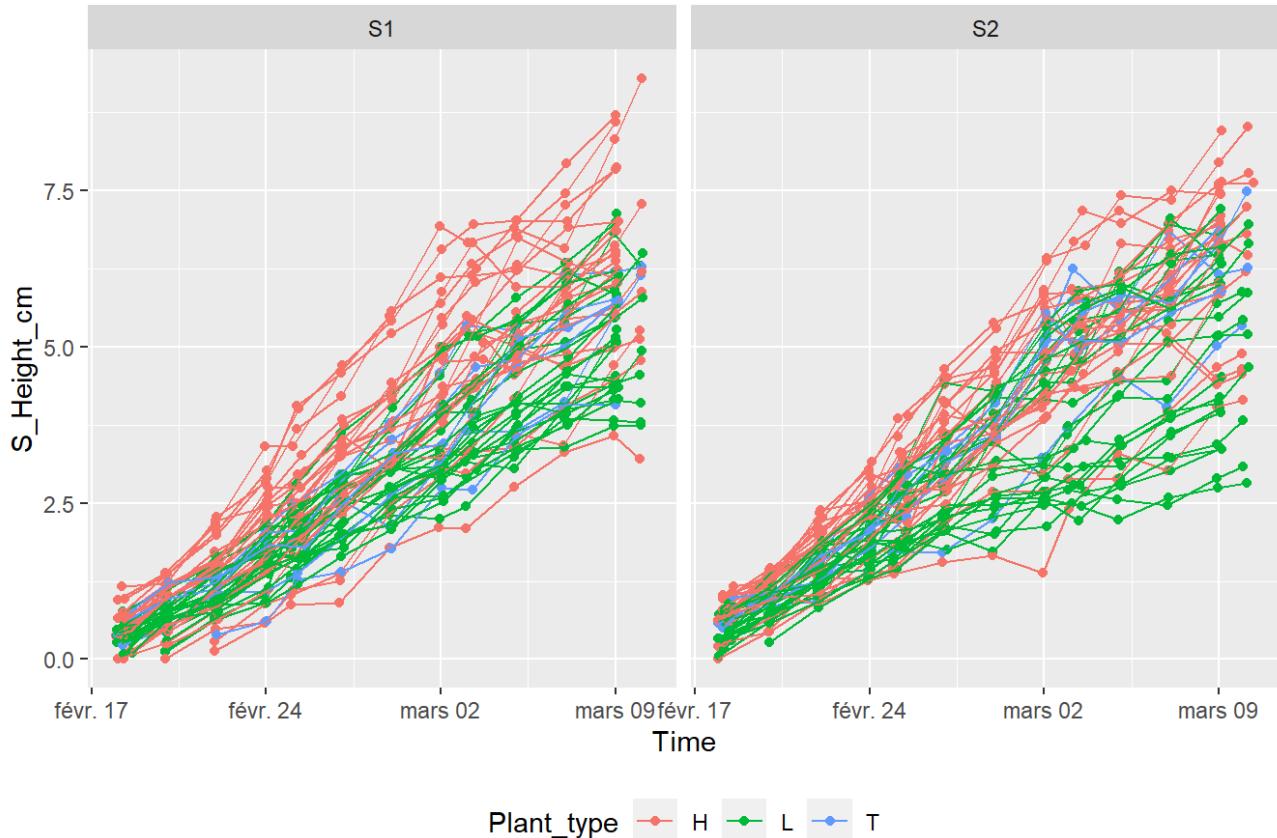
Scatter plots for all genotypes by water treatment

```
plot_scatter_with_smooth_water(S_timeseries, variables_S)
```

```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 30 rows containing missing values (`geom_line()`).
```

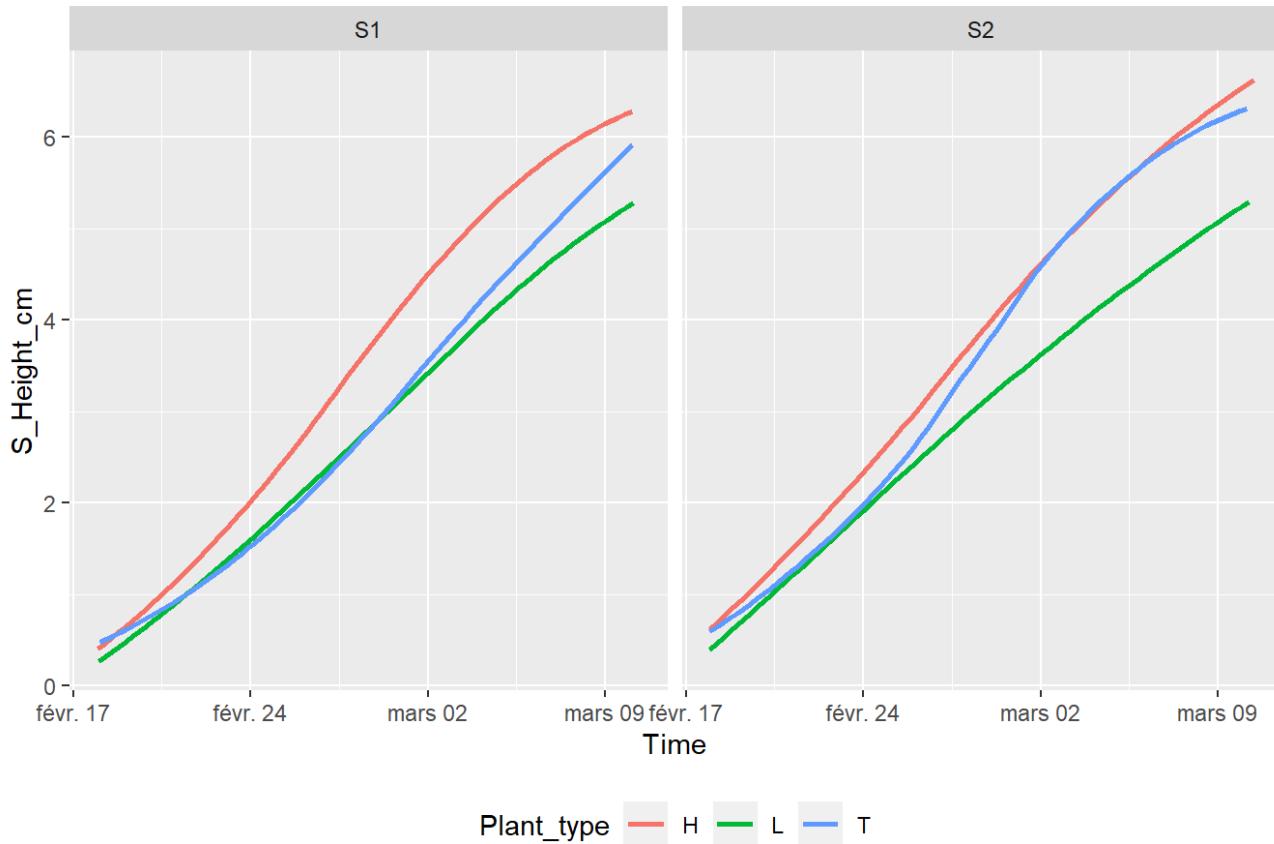
Scatterplot of S_Height_cm by Plant type and Soil



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

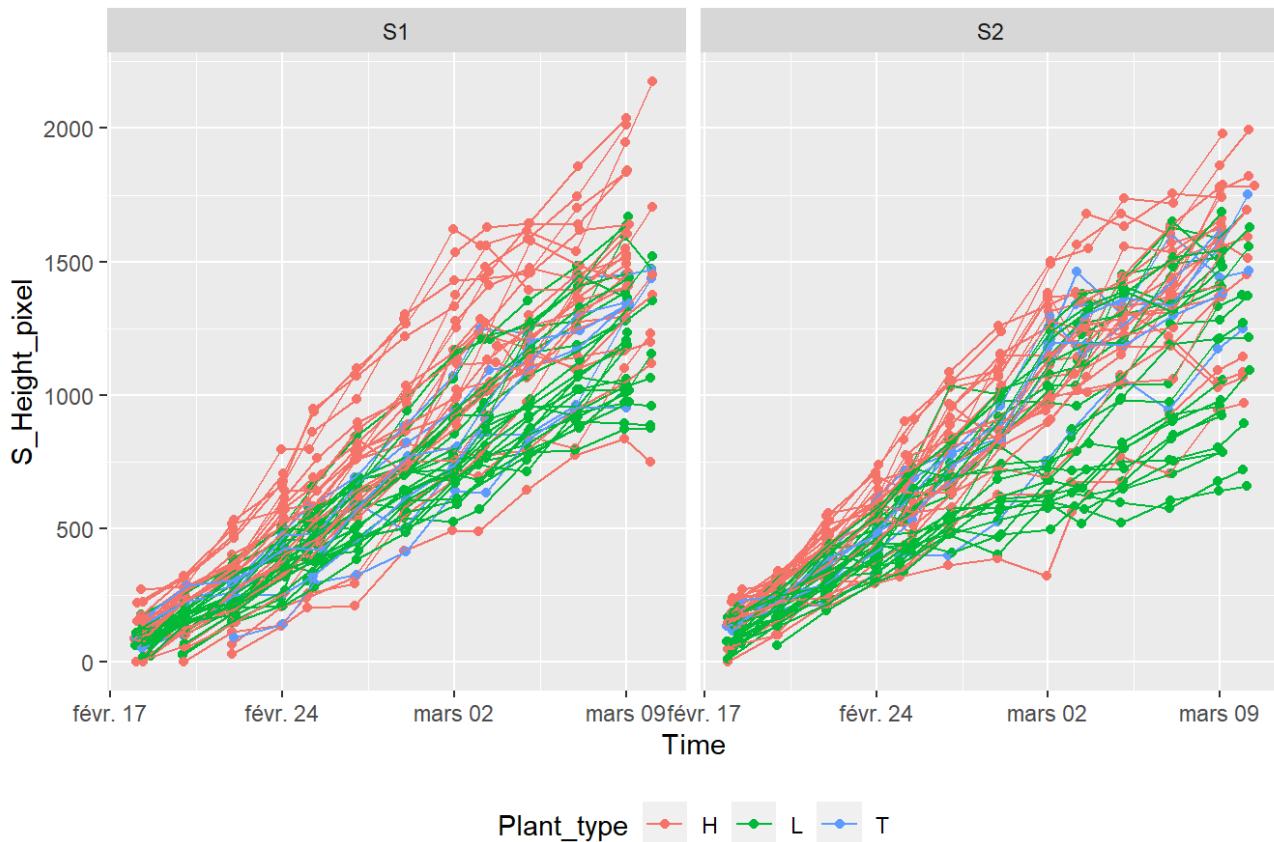
```
## Warning: Removed 30 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of S_Height_cm by Plant type and Soil



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
## Removed 30 rows containing missing values (`geom_line()`).
```

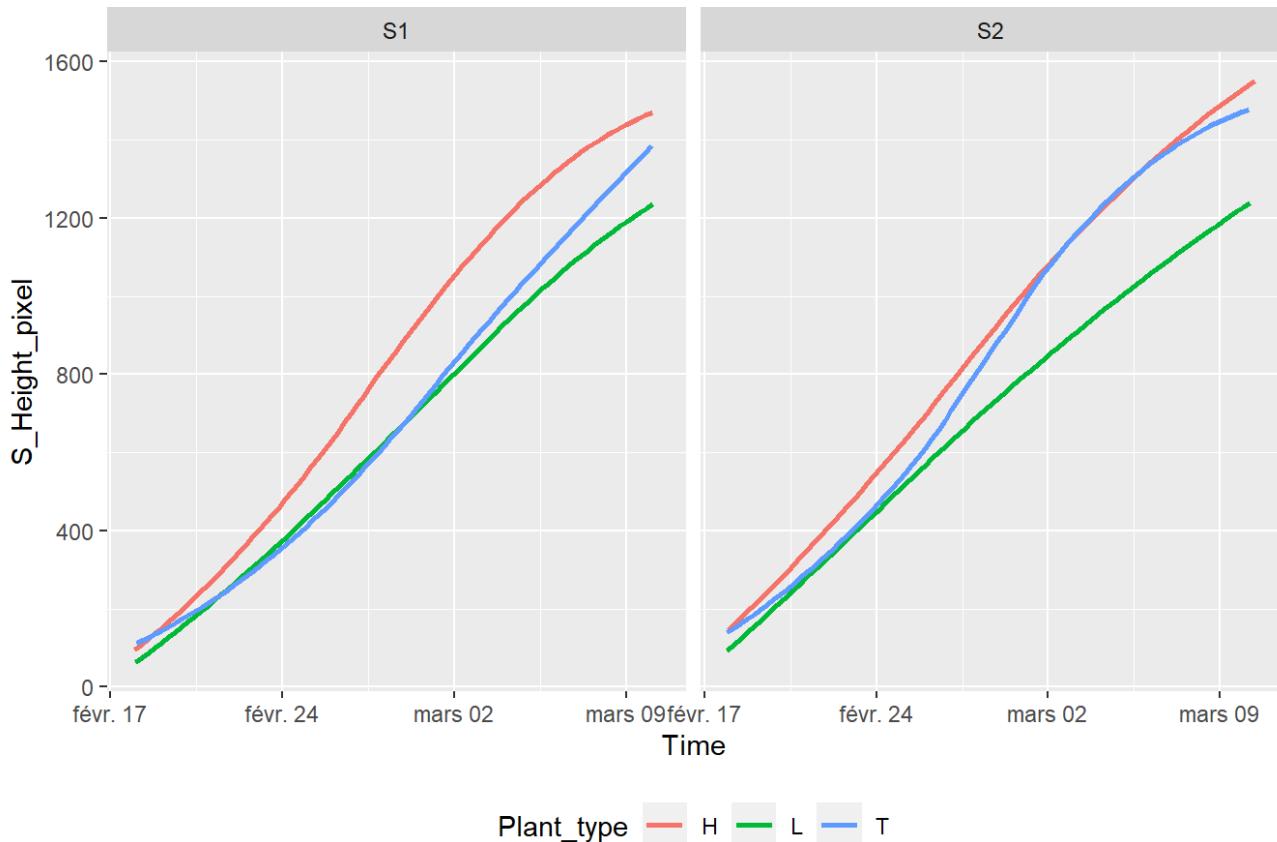
Scatterplot of S_Height_pixel by Plant type and Soil



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

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

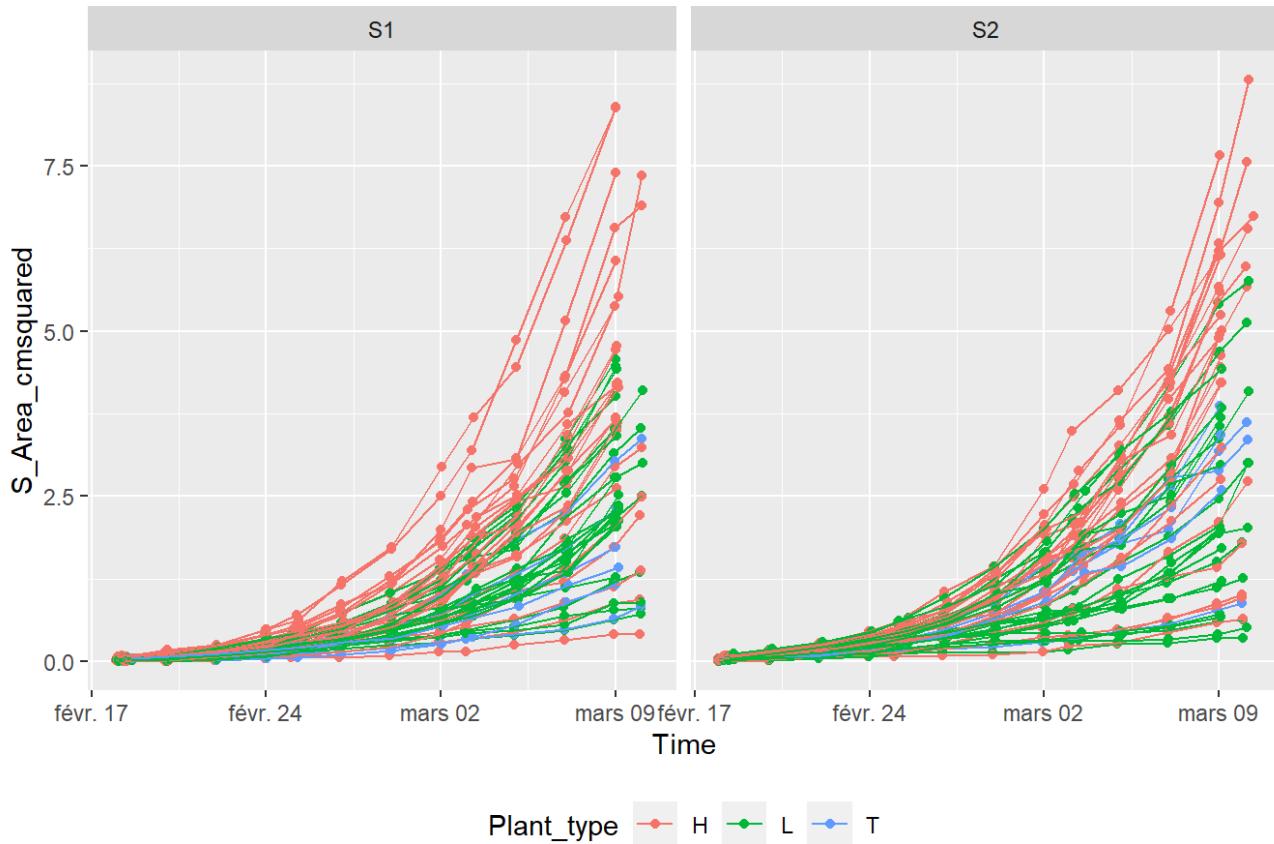
Smooth line of S_Height_pixel by Plant type and Soil



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
```

```
## Removed 30 rows containing missing values (`geom_line()`).
```

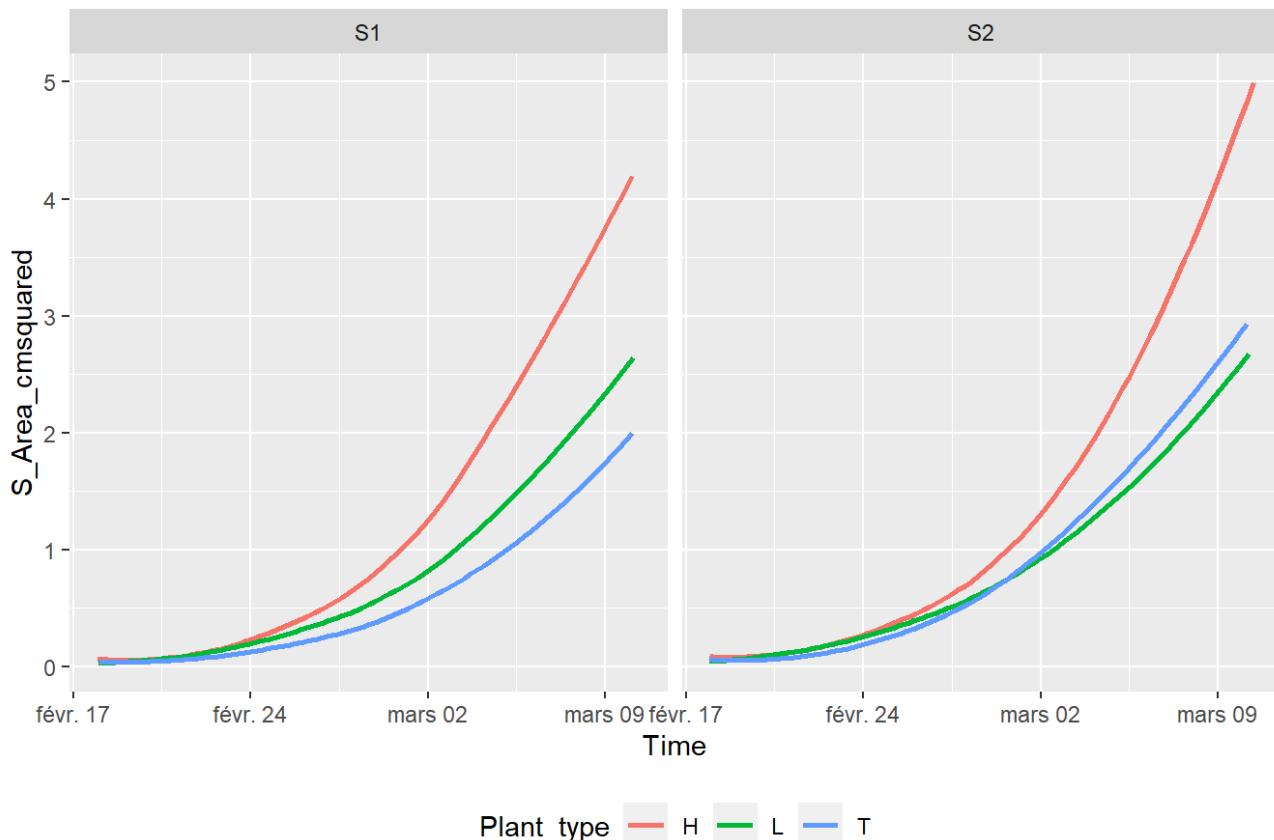
Scatterplot of S_Area_cmsquared by Plant type and Soil



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

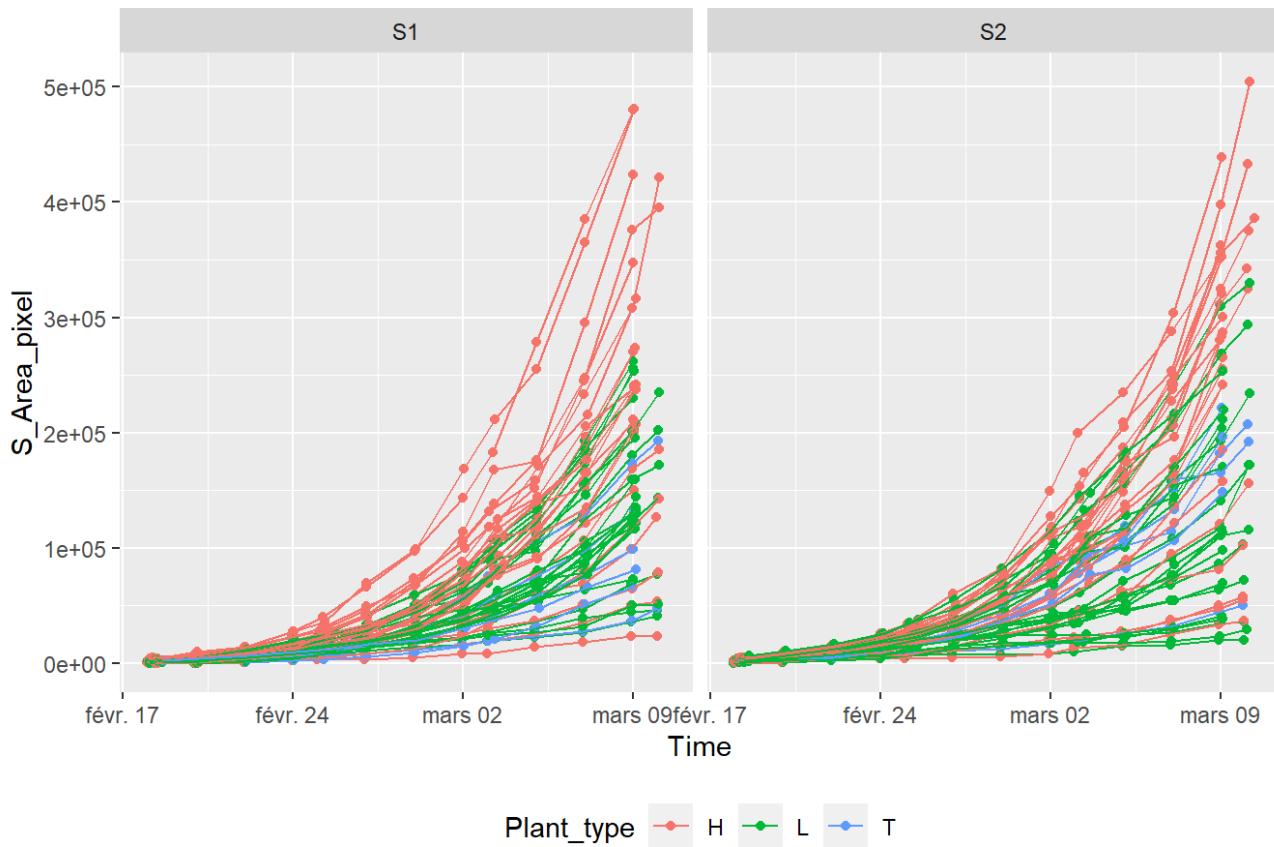
```
## Warning: Removed 30 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of S_Area_cmsquared by Plant type and Soil



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
## Removed 30 rows containing missing values (`geom_line()`).
```

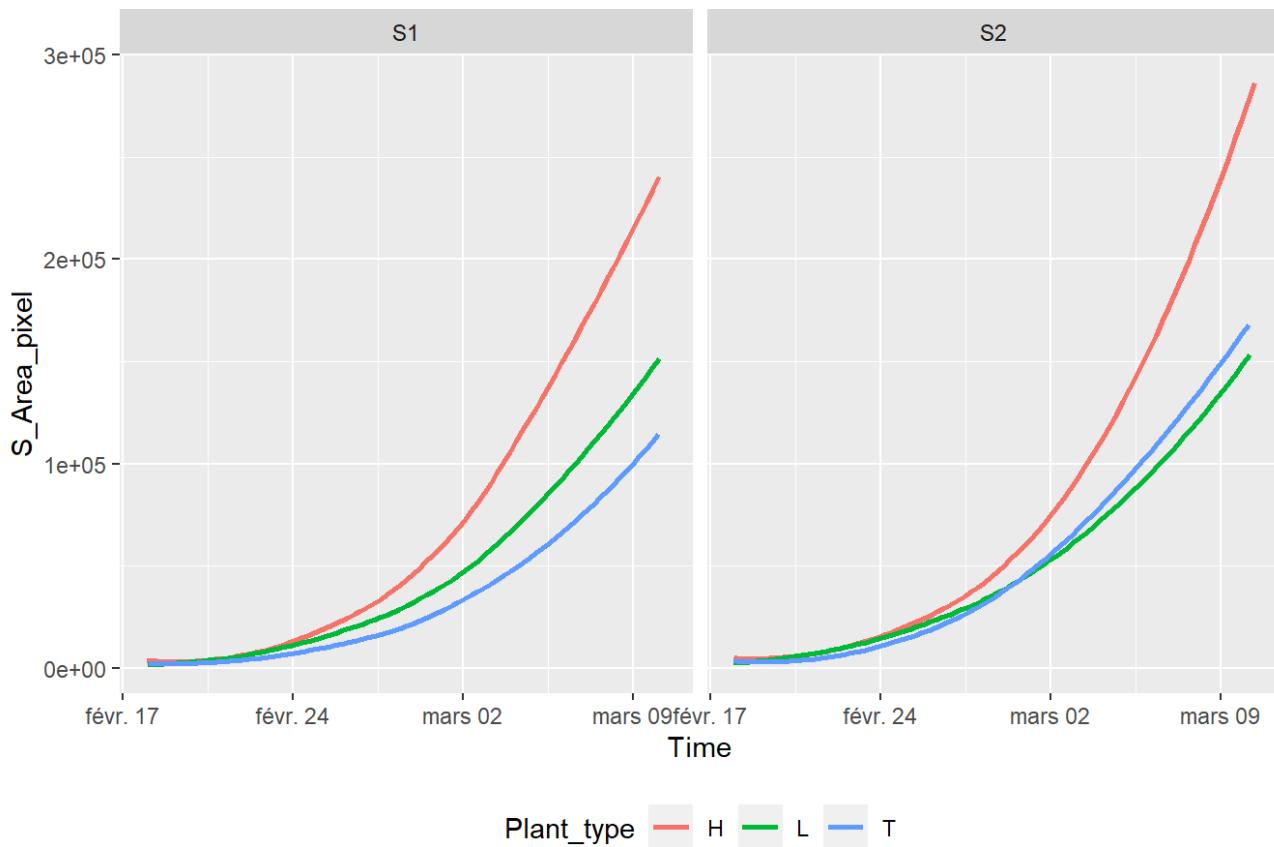
Scatterplot of S_Area_pixel by Plant type and Soil



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

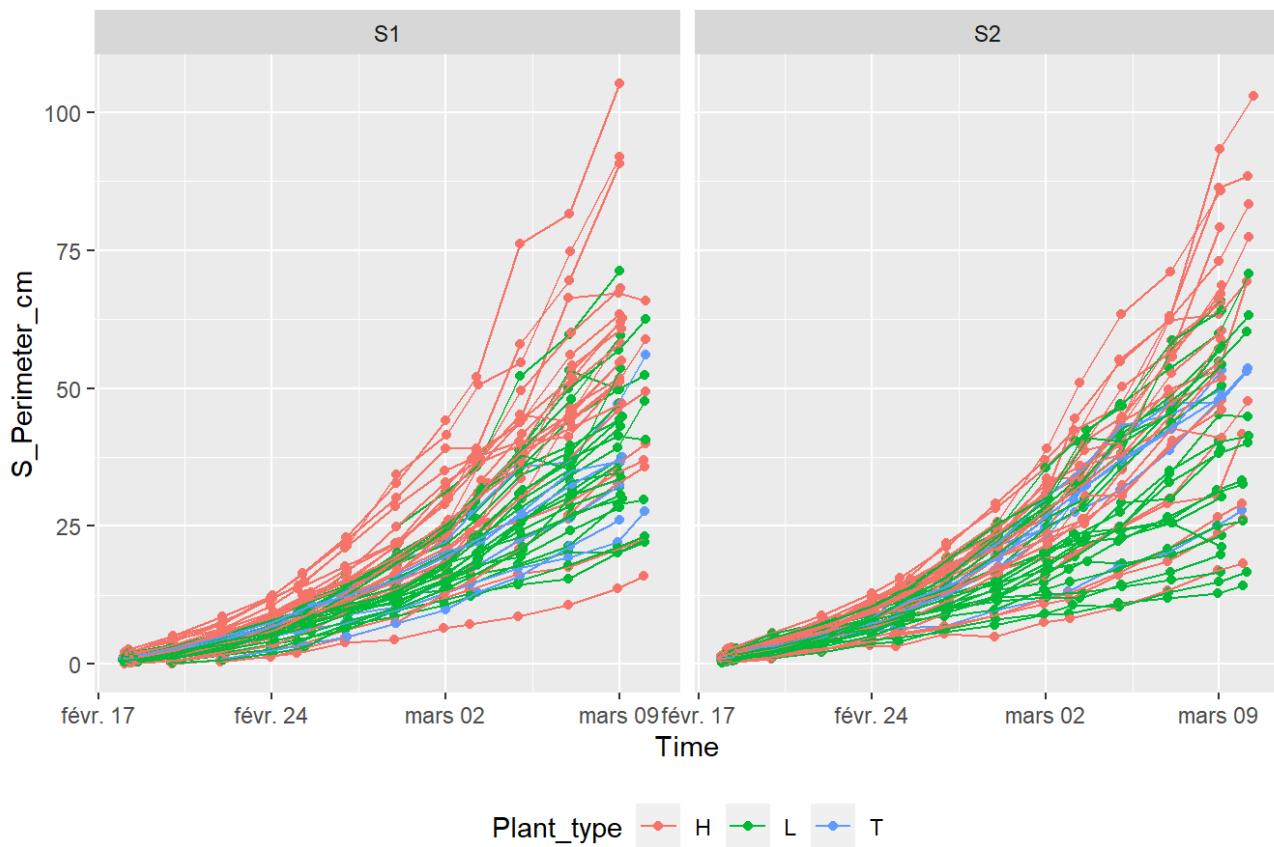
```
## Warning: Removed 30 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of S_Area_pixel by Plant type and Soil



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
## Removed 30 rows containing missing values (`geom_line()`).
```

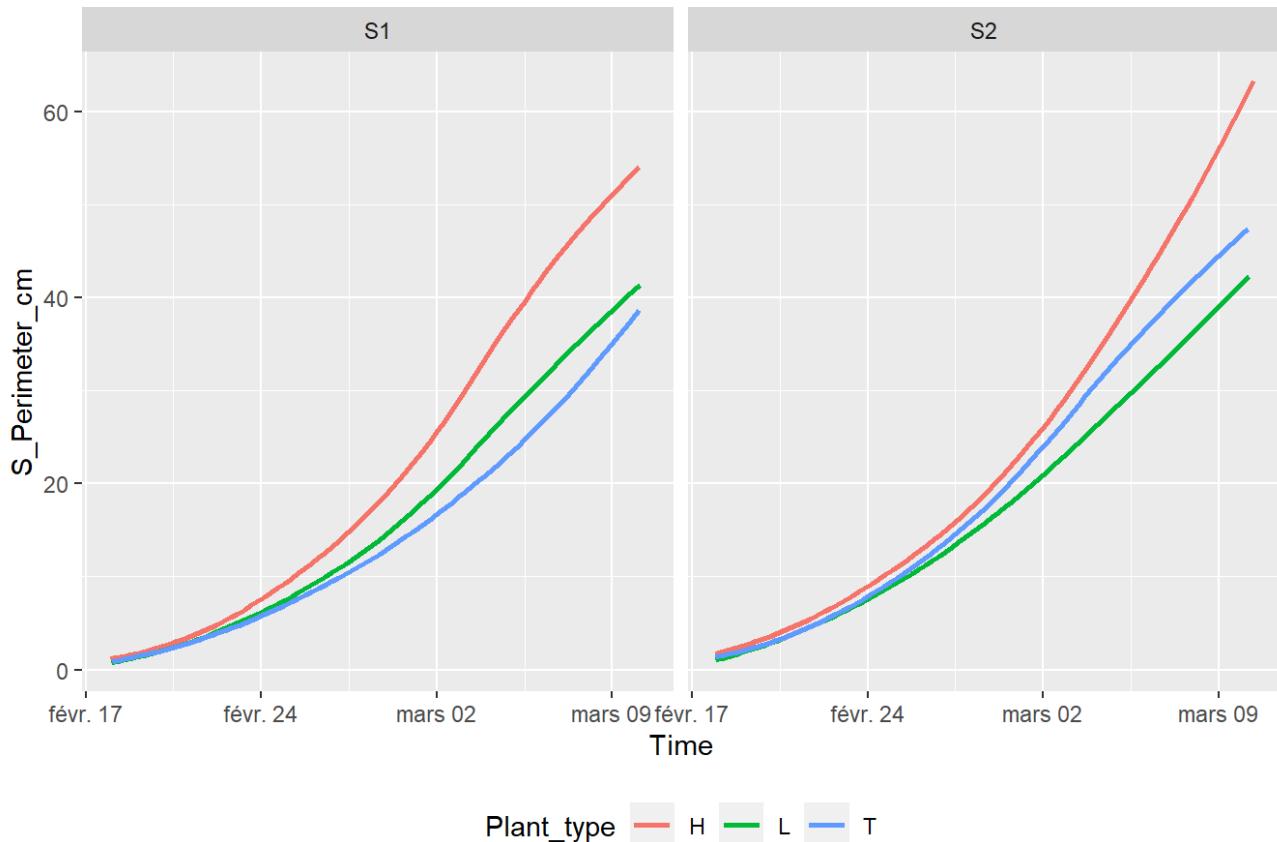
Scatterplot of S_Perimeter_cm by Plant type and Soil



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

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

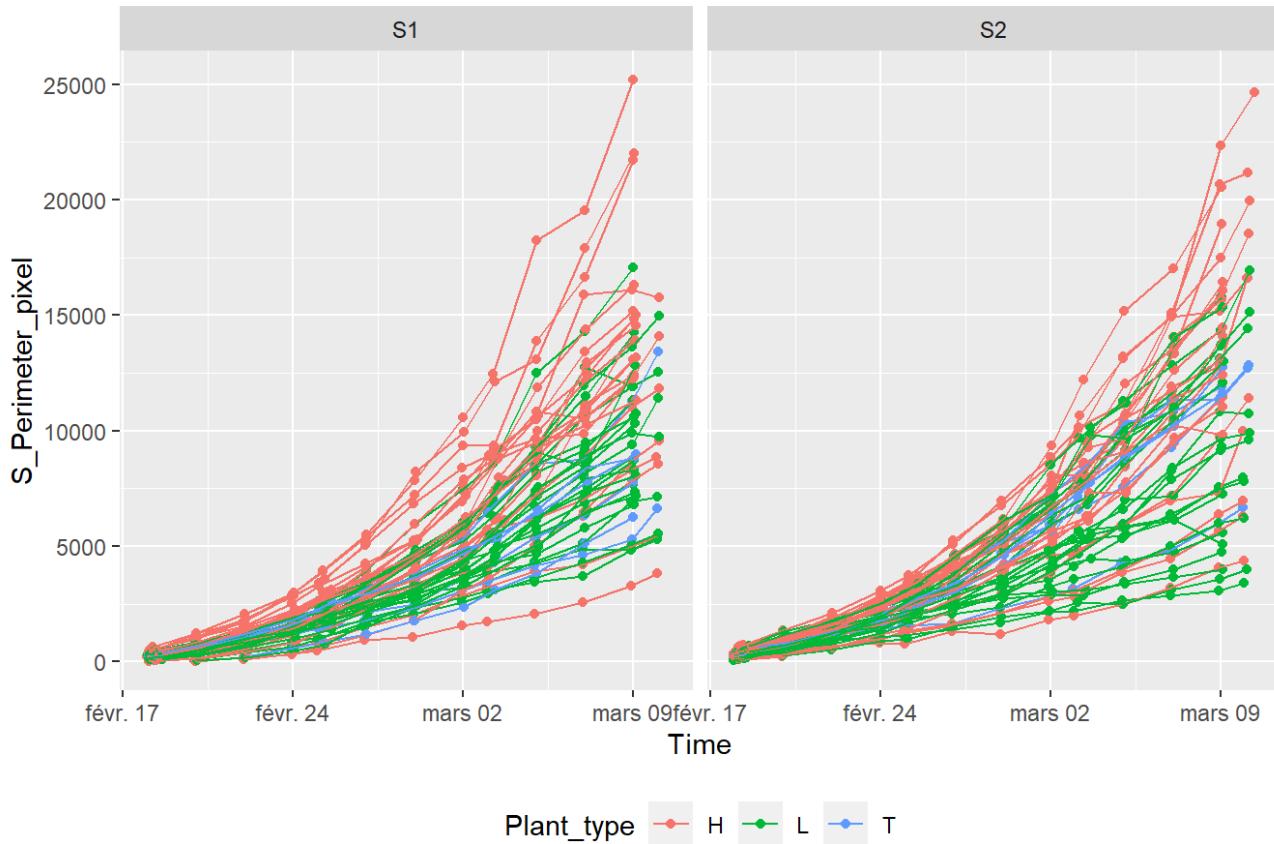
Smooth line of S_Perimeter_cm by Plant type and Soil



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
```

```
## Removed 30 rows containing missing values (`geom_line()`).
```

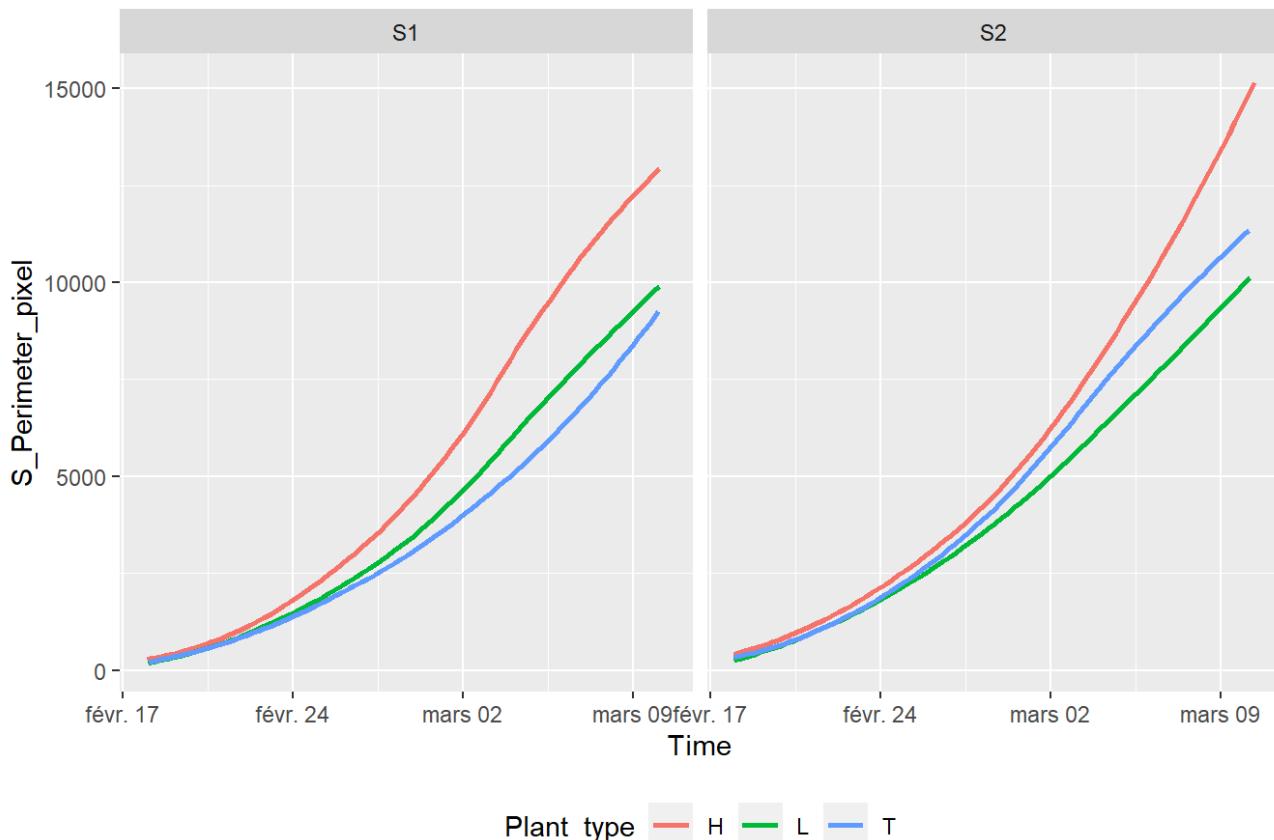
Scatterplot of S_Perimeter_pixel by Plant type and Soil



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

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

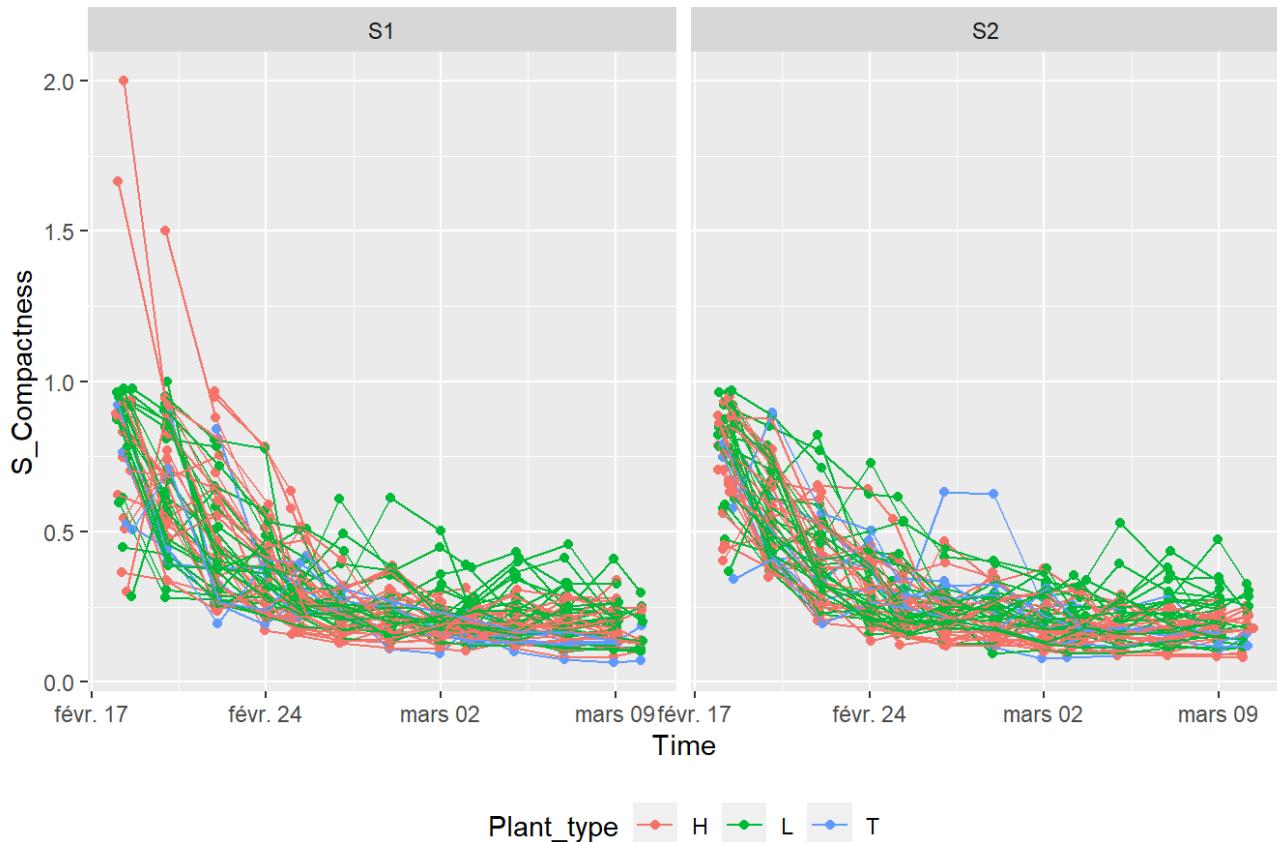
Smooth line of S_Perimeter_pixel by Plant type and Soil



```
## Warning: Removed 31 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 31 rows containing missing values (`geom_line()`).
```

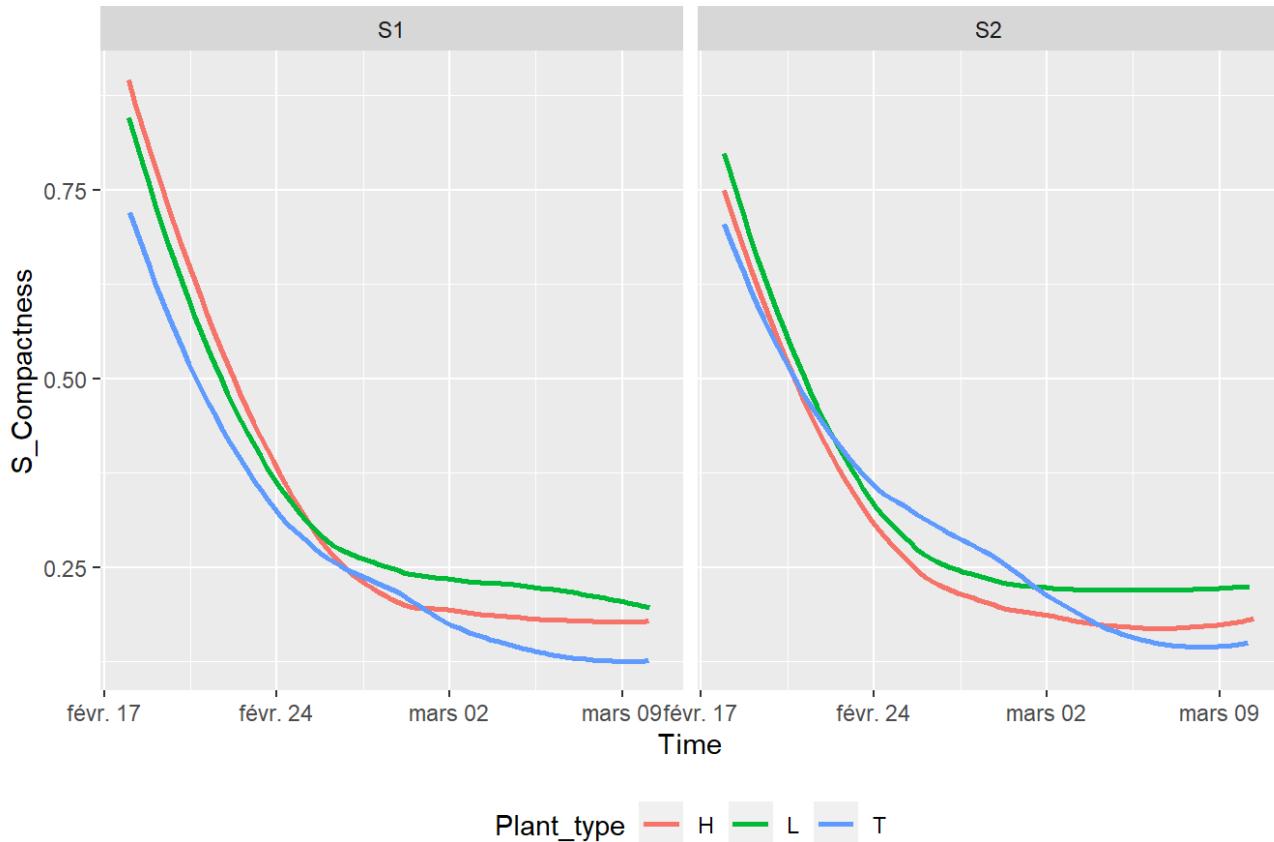
Scatterplot of S_Compactness by Plant type and Soil



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

```
## Warning: Removed 31 rows containing non-finite values (`stat_smooth()`).
```

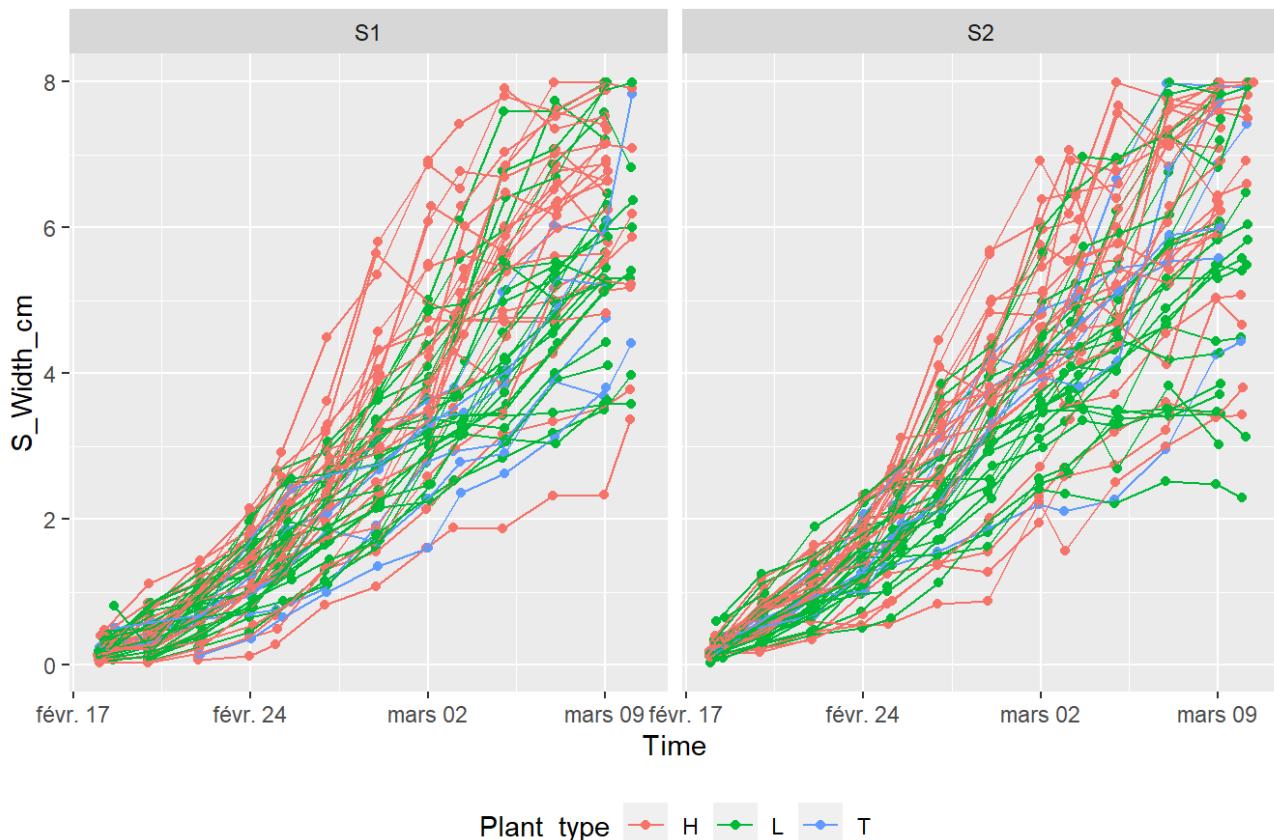
Smooth line of S_Compactness by Plant type and Soil



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 30 rows containing missing values (`geom_line()`).
```

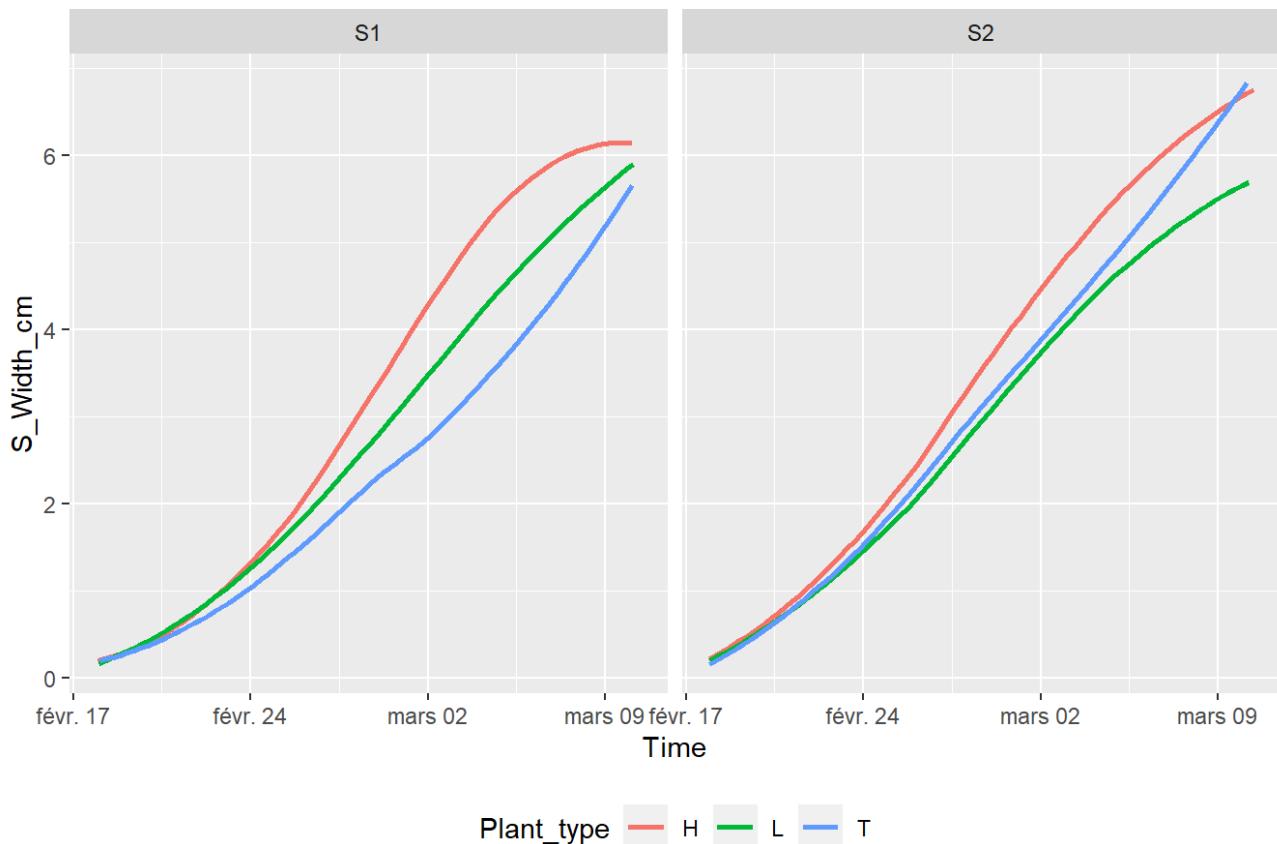
Scatterplot of S_Width_cm by Plant type and Soil



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

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

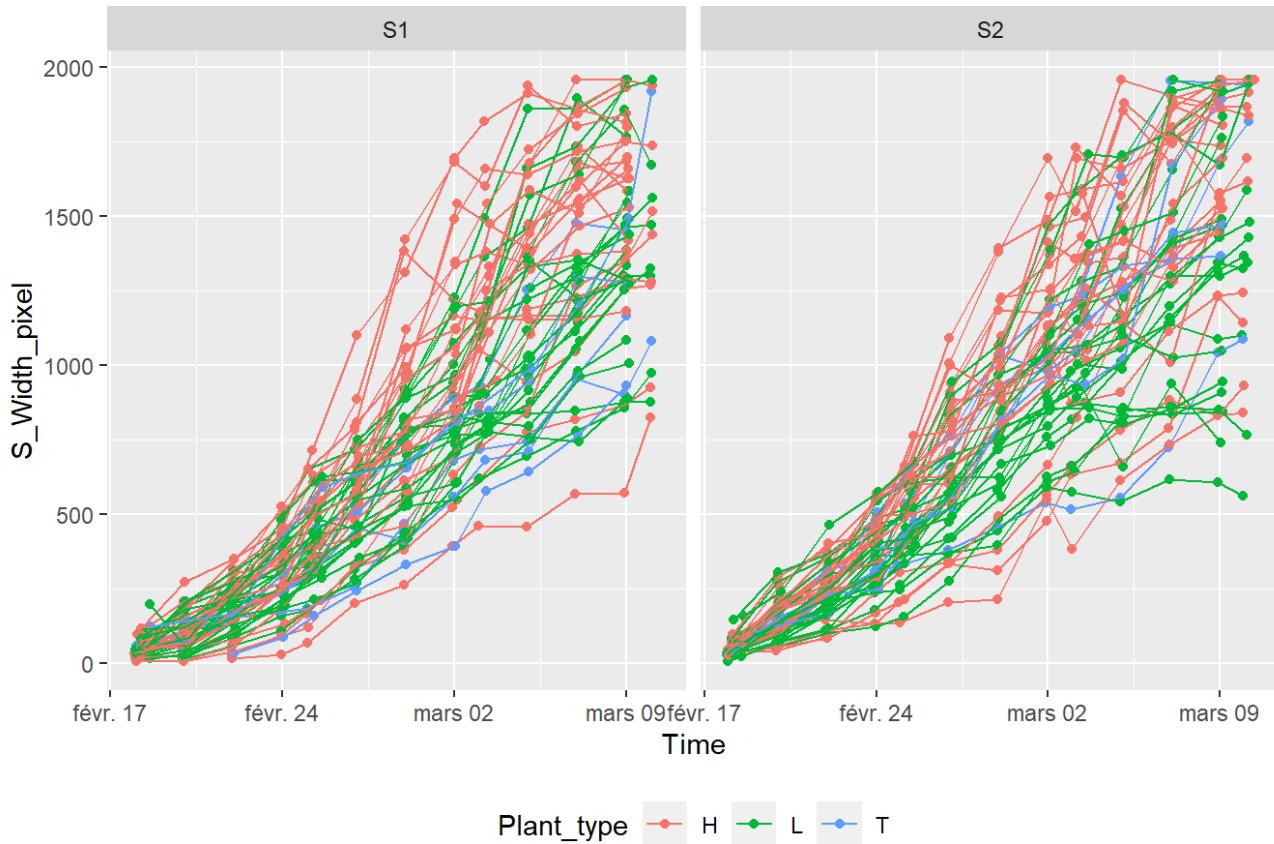
Smooth line of S_Width_cm by Plant type and Soil



```
## Warning: Removed 30 rows containing missing values (`geom_point()`).
```

```
## Removed 30 rows containing missing values (`geom_line()`).
```

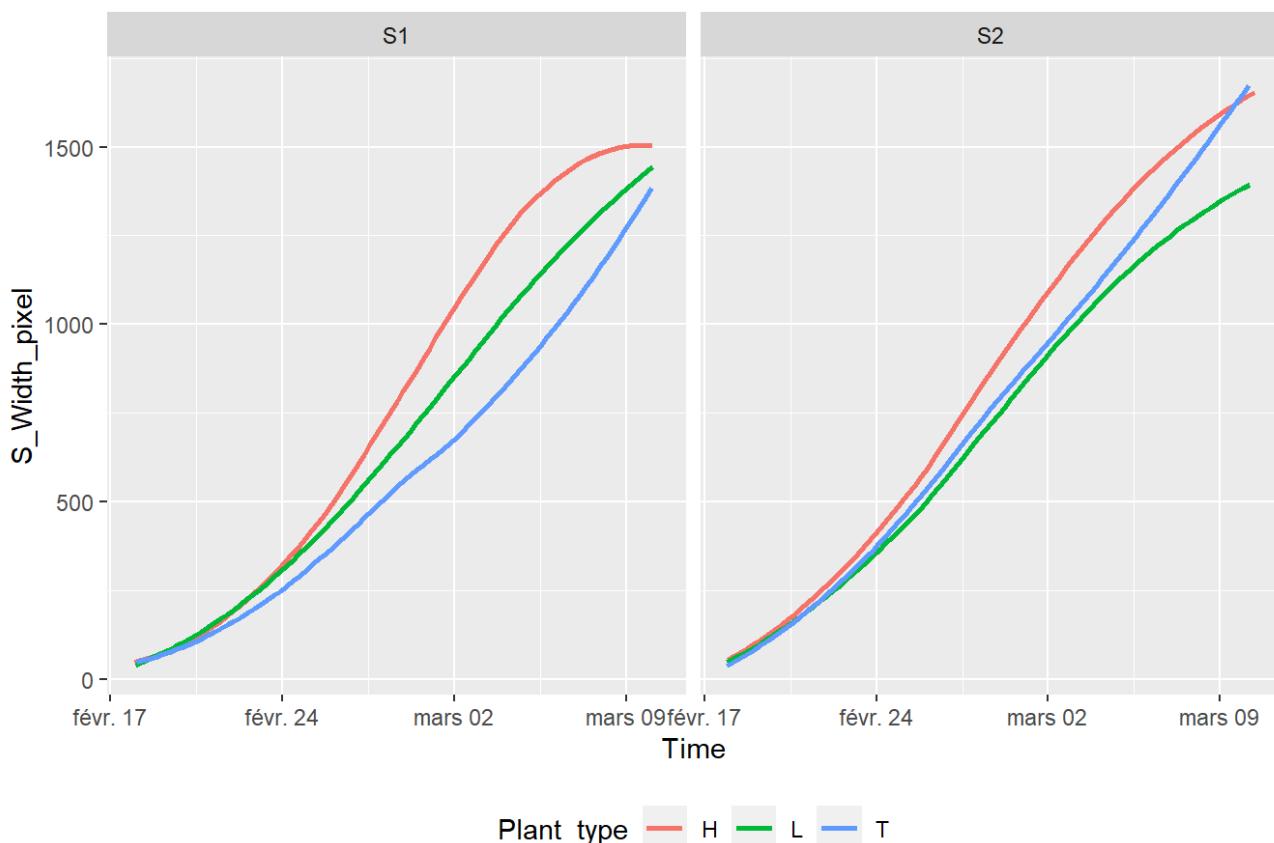
Scatterplot of S_Width_pixel by Plant type and Soil



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

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

Smooth line of S_Width_pixel by Plant type and Soil



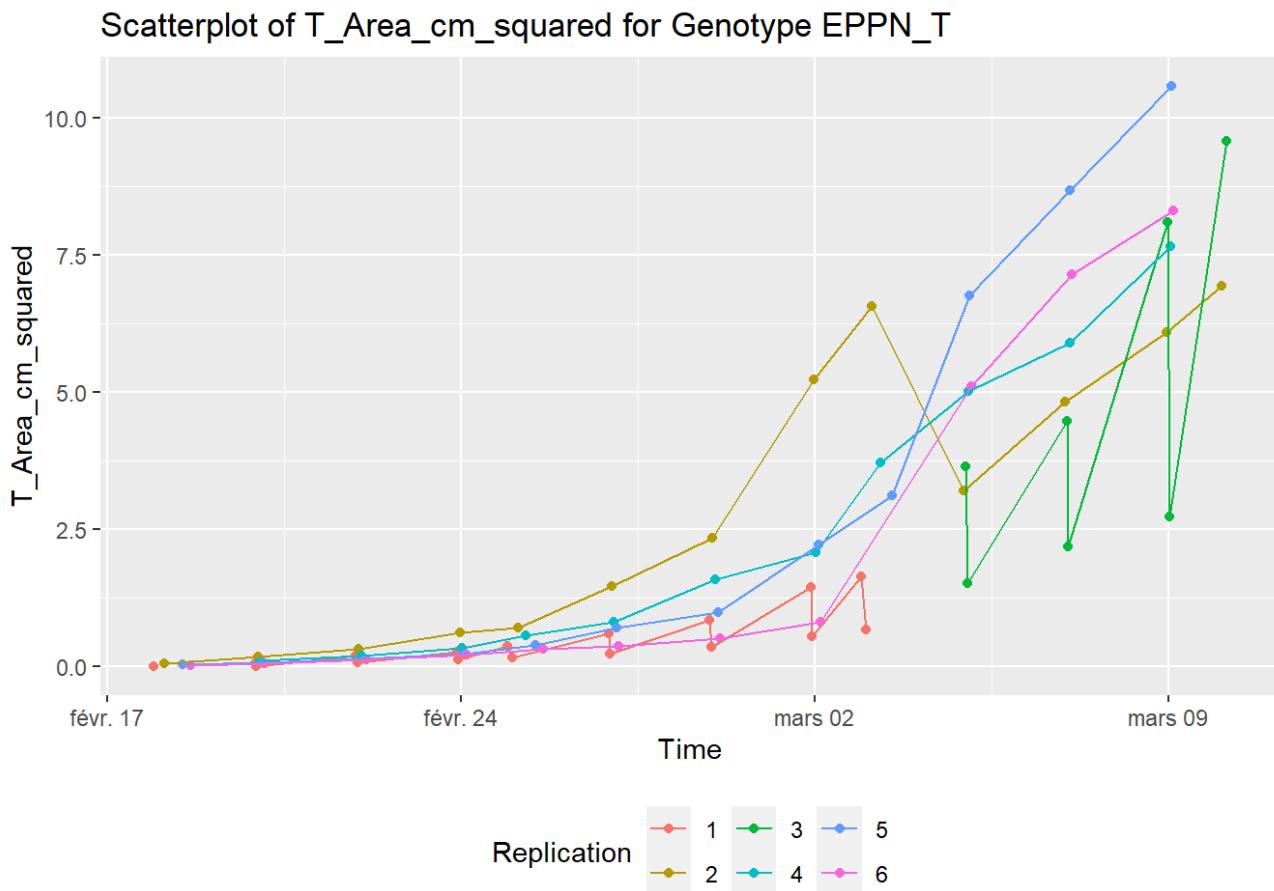
C. Exploration of the T_timeseries dataframe

Scatter plots by Genotype

```
plot_scatter_by_genotype(T_timeseries, variables_T, "EPPN_T")
```

```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
```

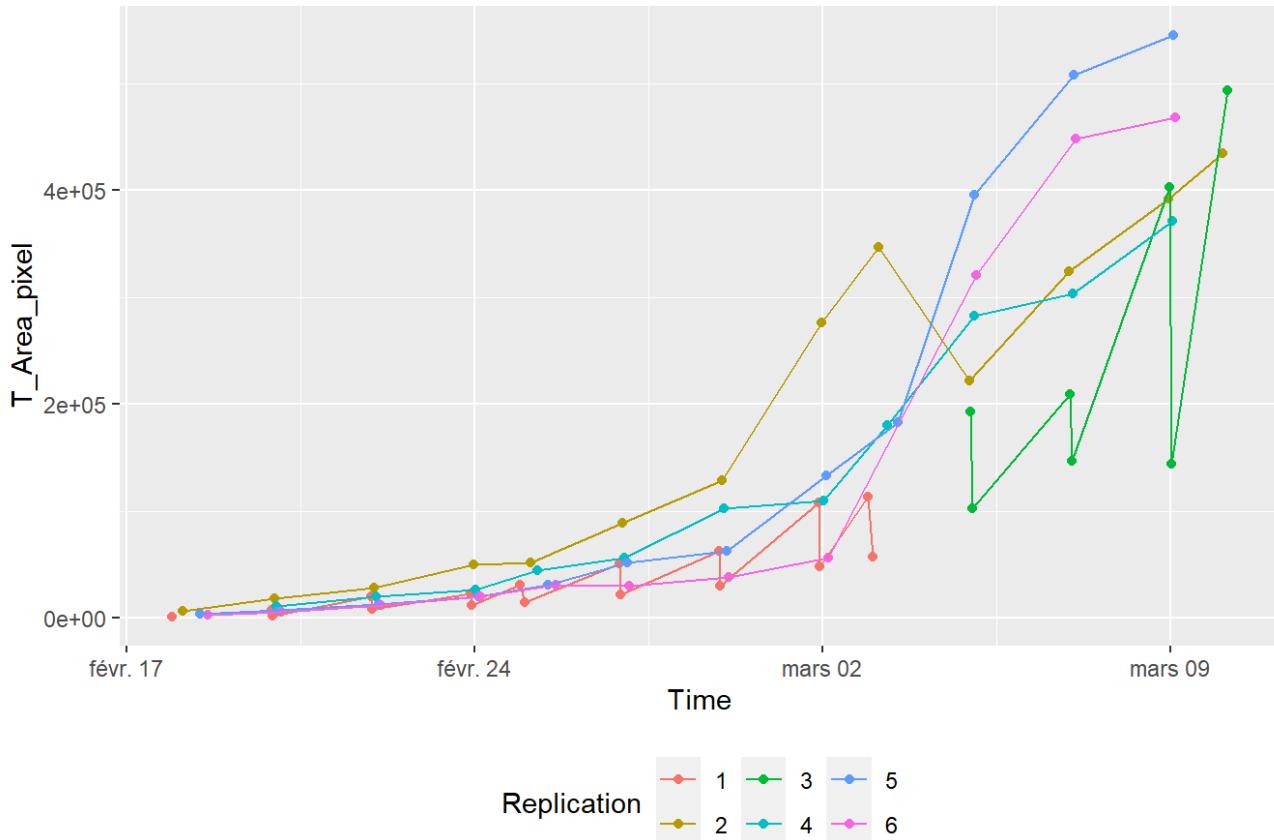
```
## Warning: Removed 1 row containing missing values (`geom_line()`).
```



```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
```

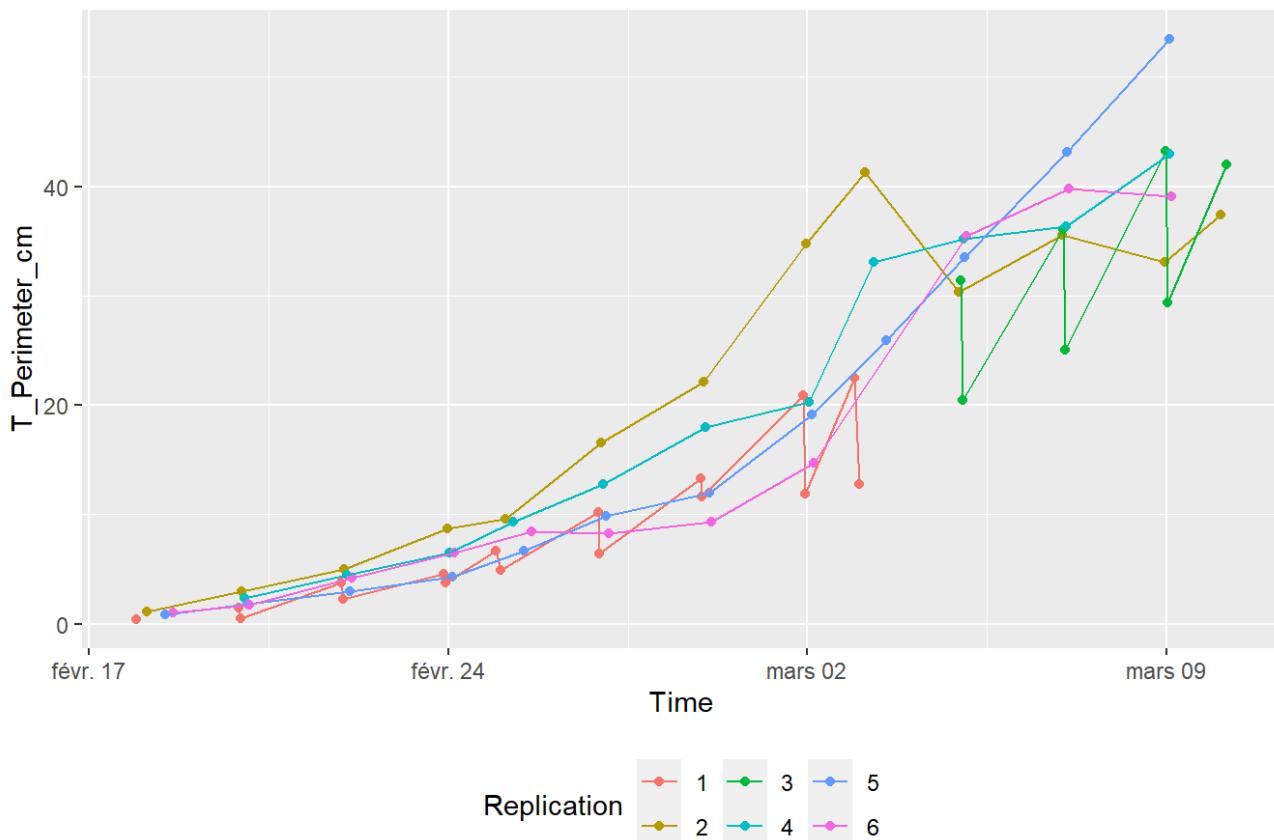
```
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of T_Area_pixel for Genotype EPPN_T

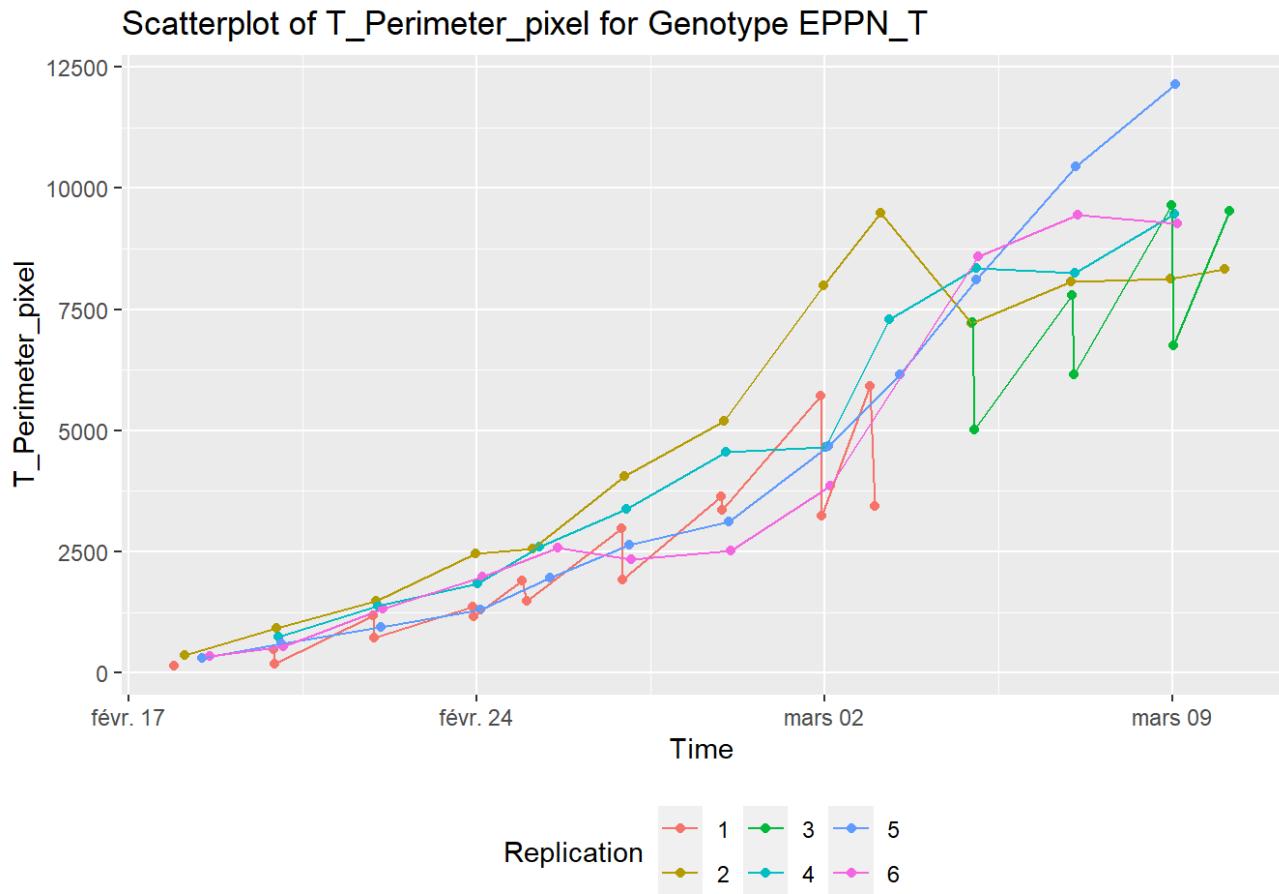


```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of T_Perimeter_cm for Genotype EPPN_T

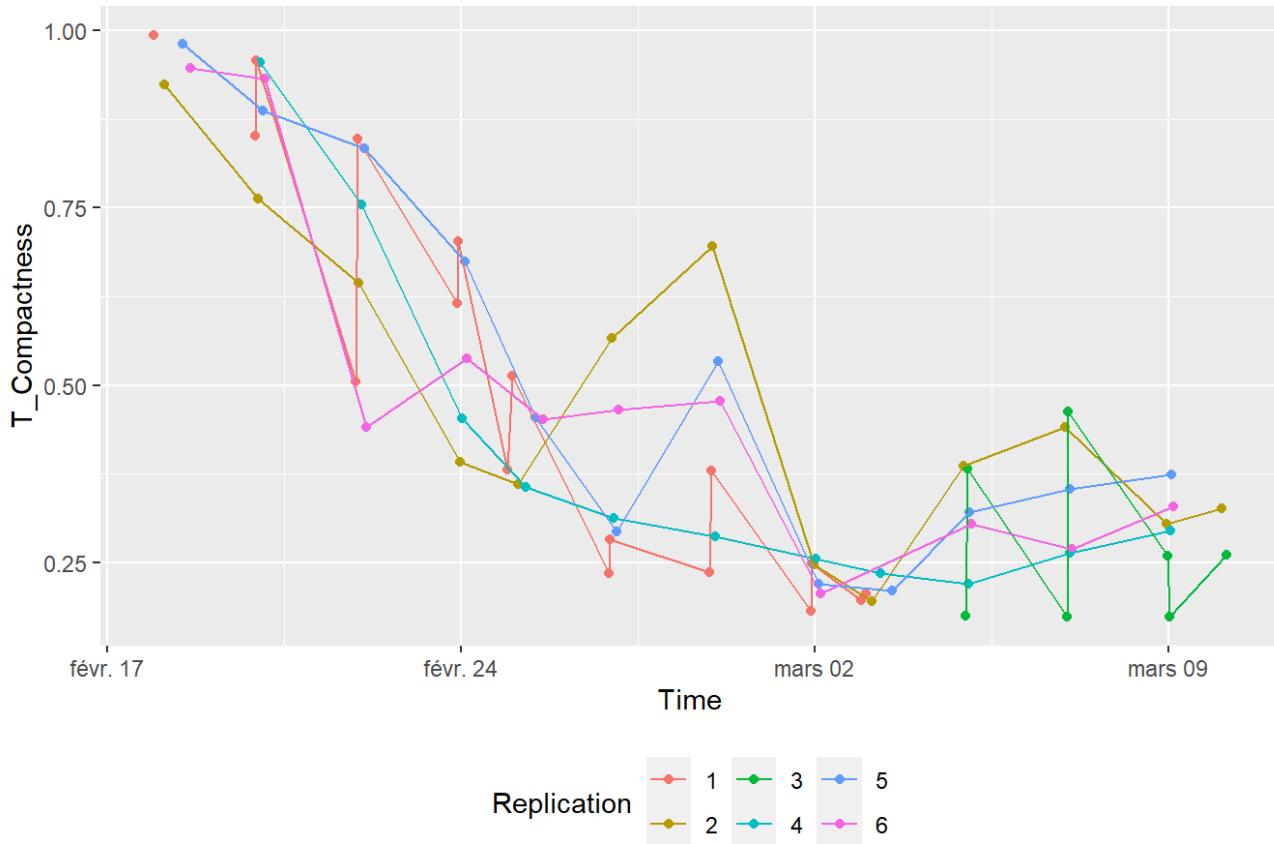


```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```



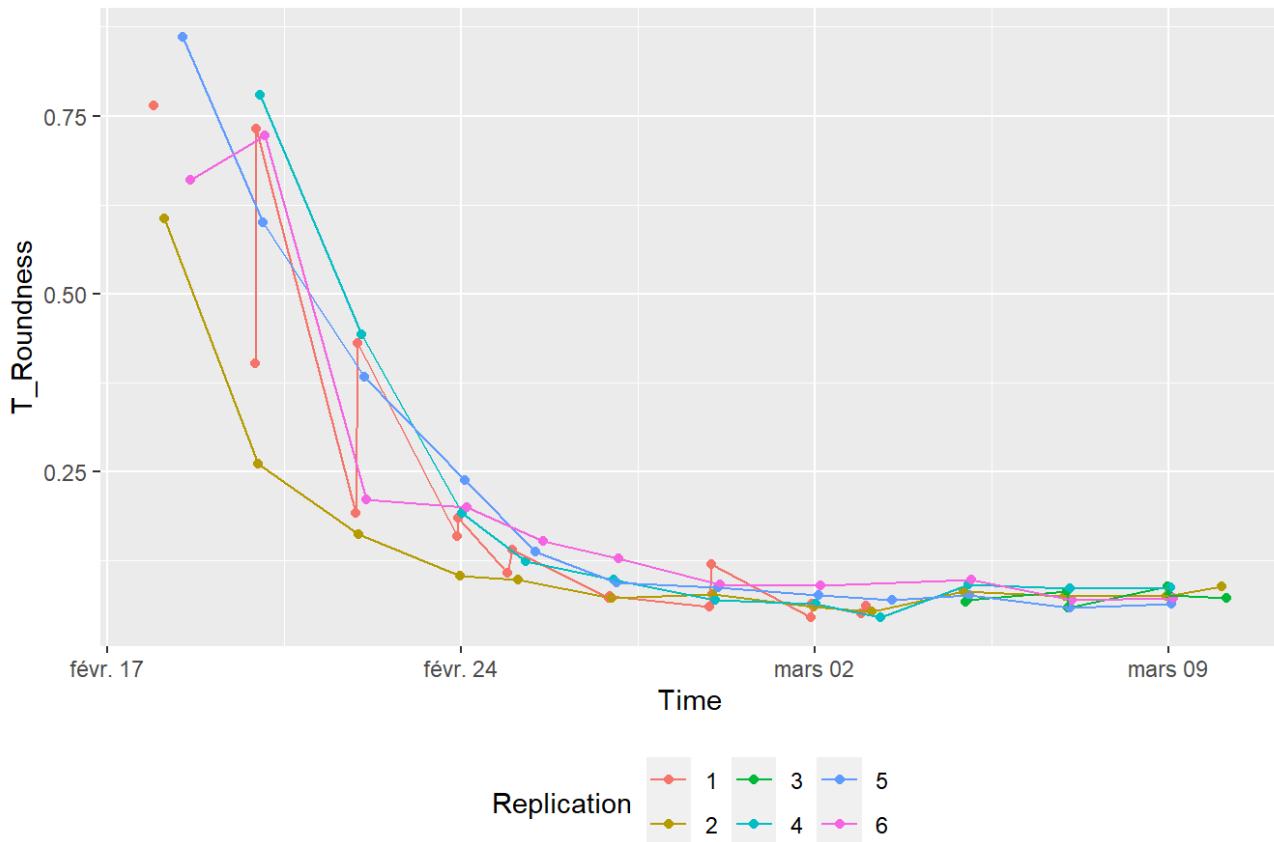
```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of T_Compactness for Genotype EPPN_T



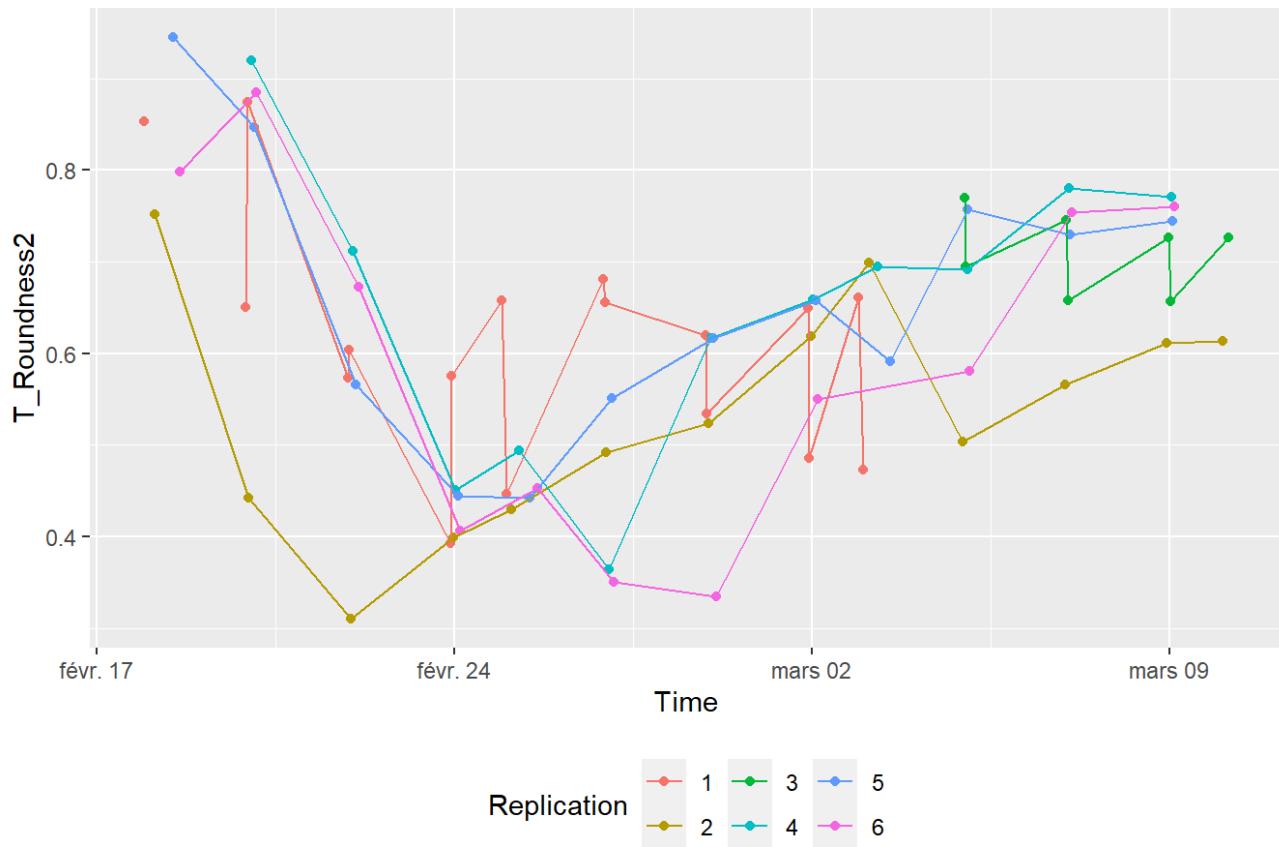
```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of T_Roundness for Genotype EPPN_T



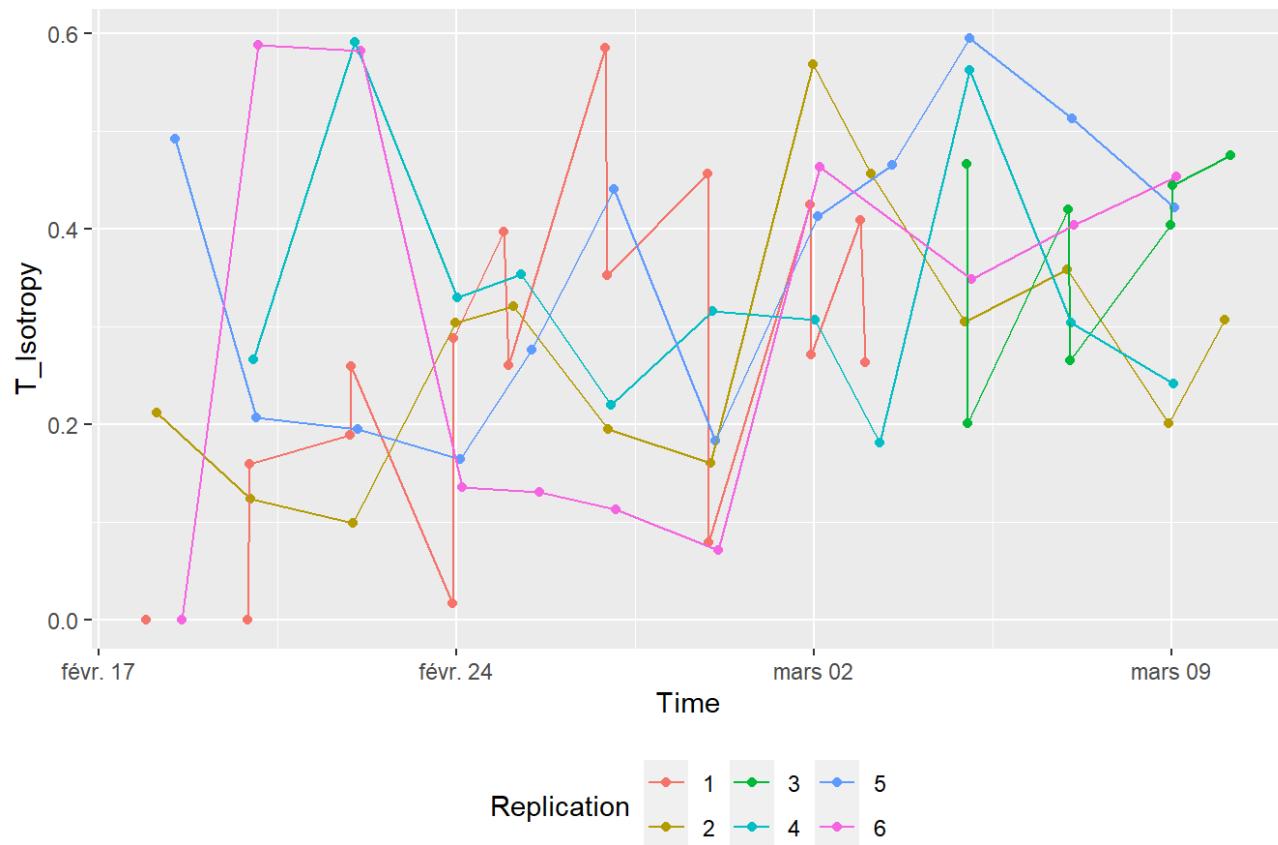
```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of T_Roundness2 for Genotype EPPN_T



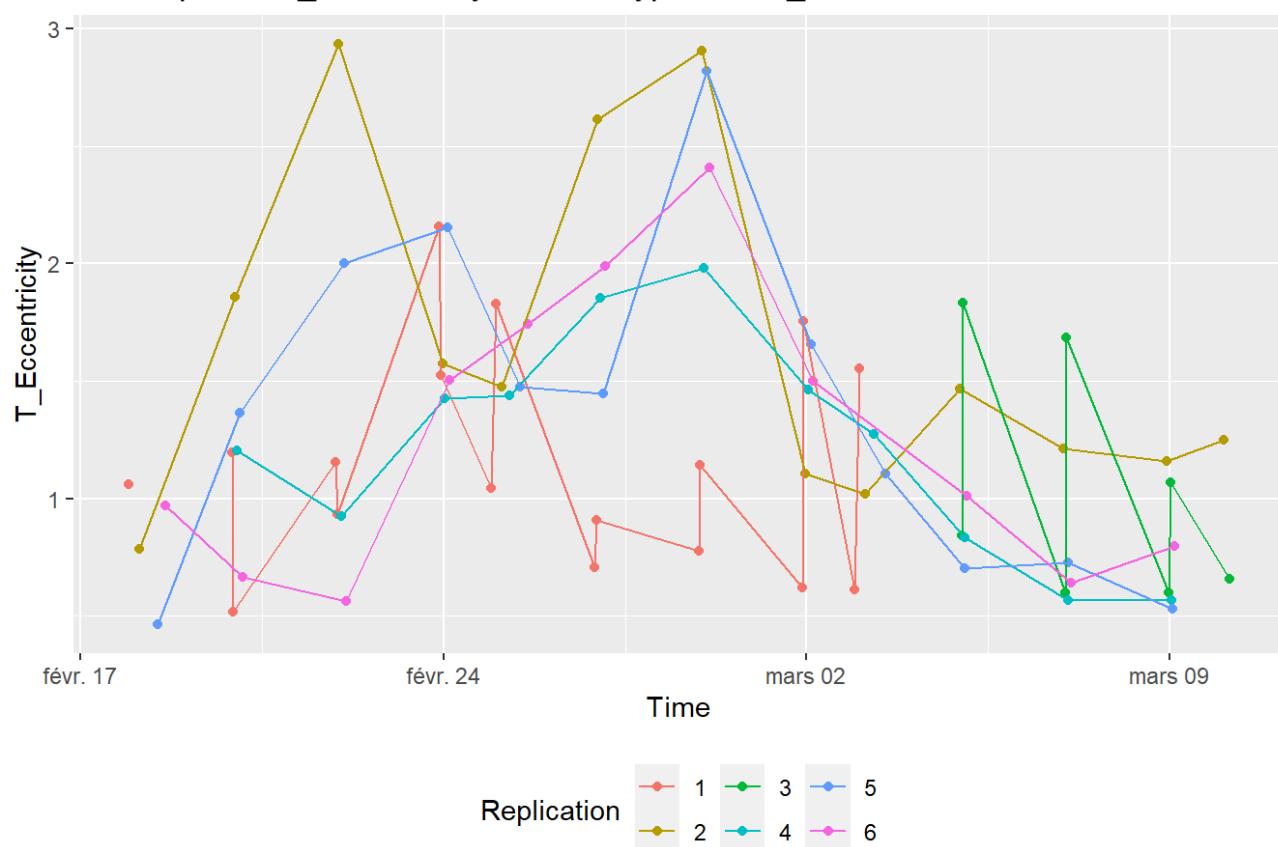
```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of T_Isotropy for Genotype EPPN_T

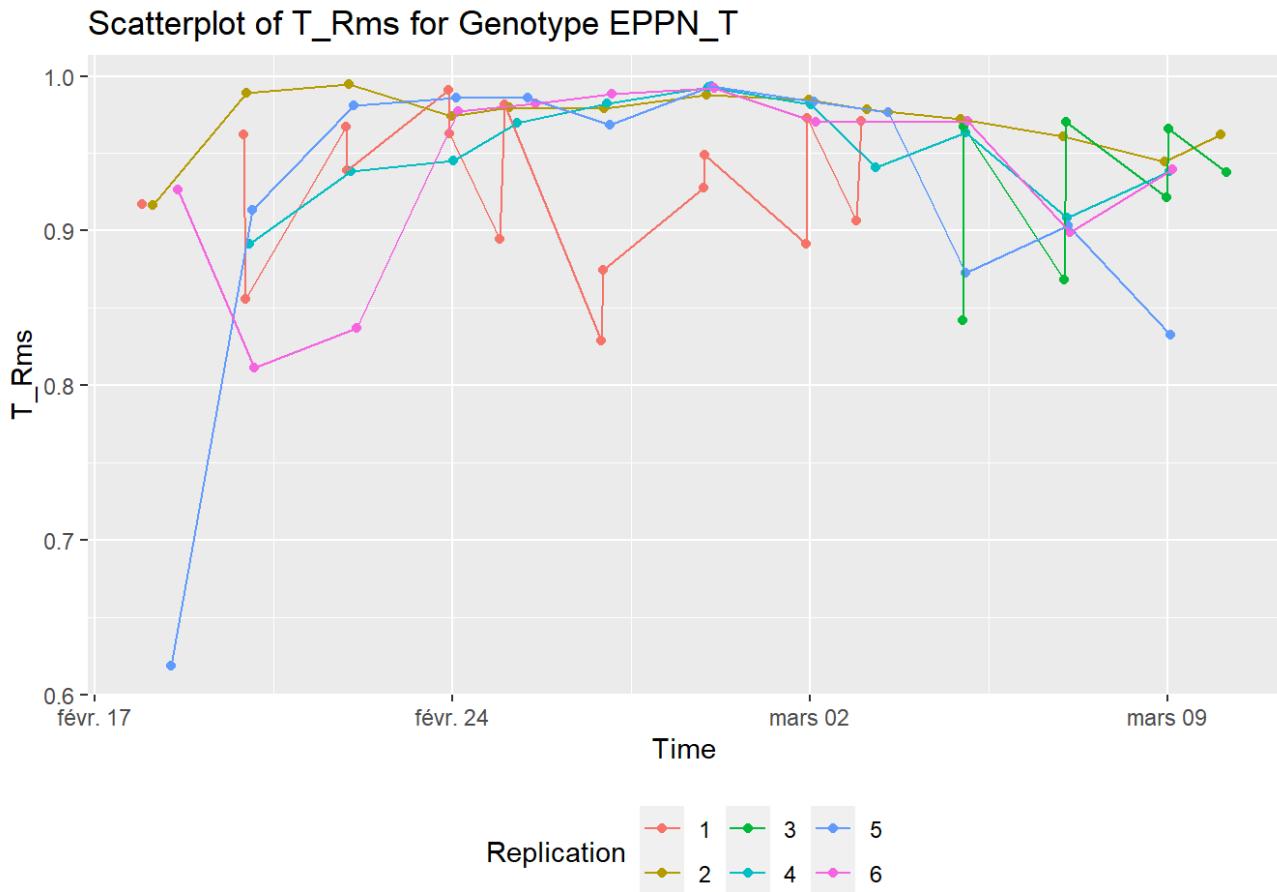


```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of T_Eccentricity for Genotype EPPN_T

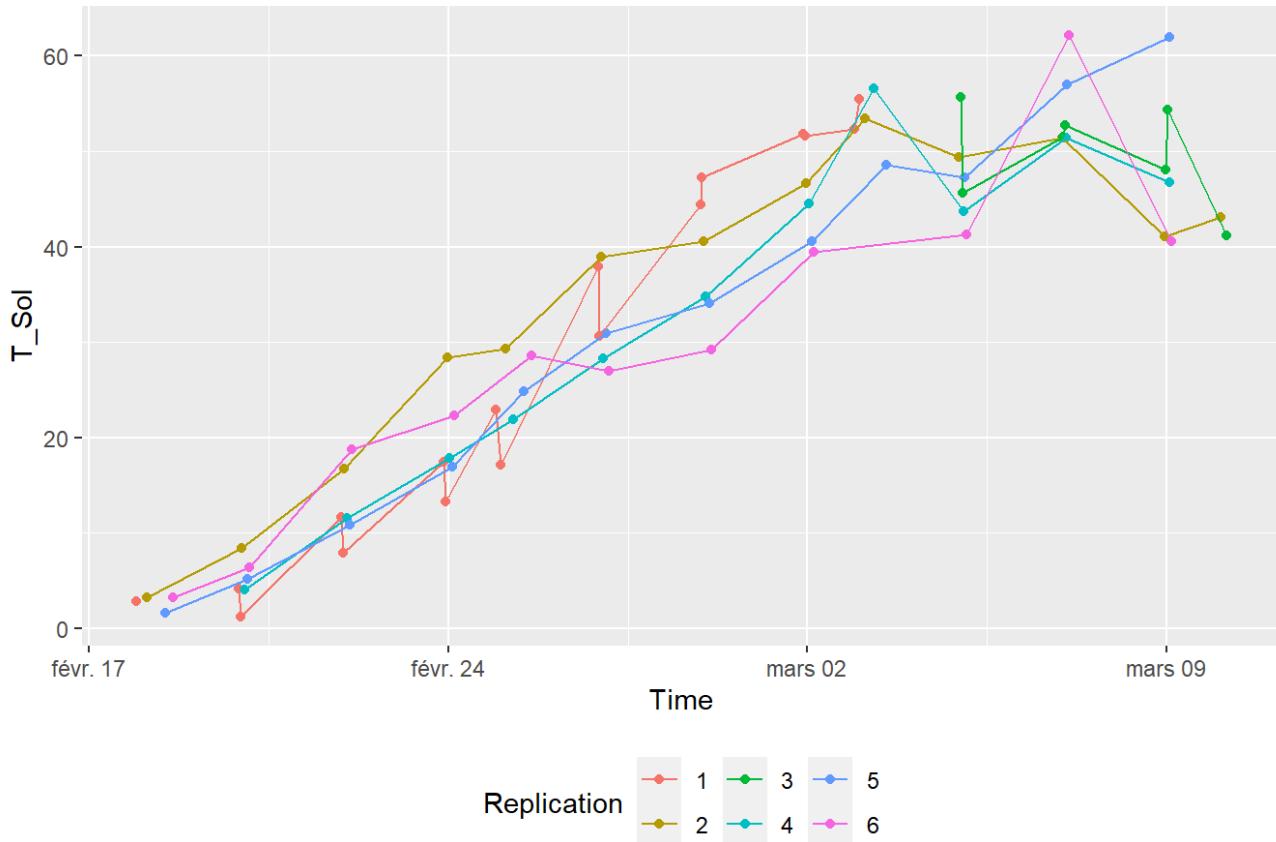


```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```



```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
## Removed 1 row containing missing values (`geom_line()`).
```

Scatterplot of T_Sol for Genotype EPPN_T



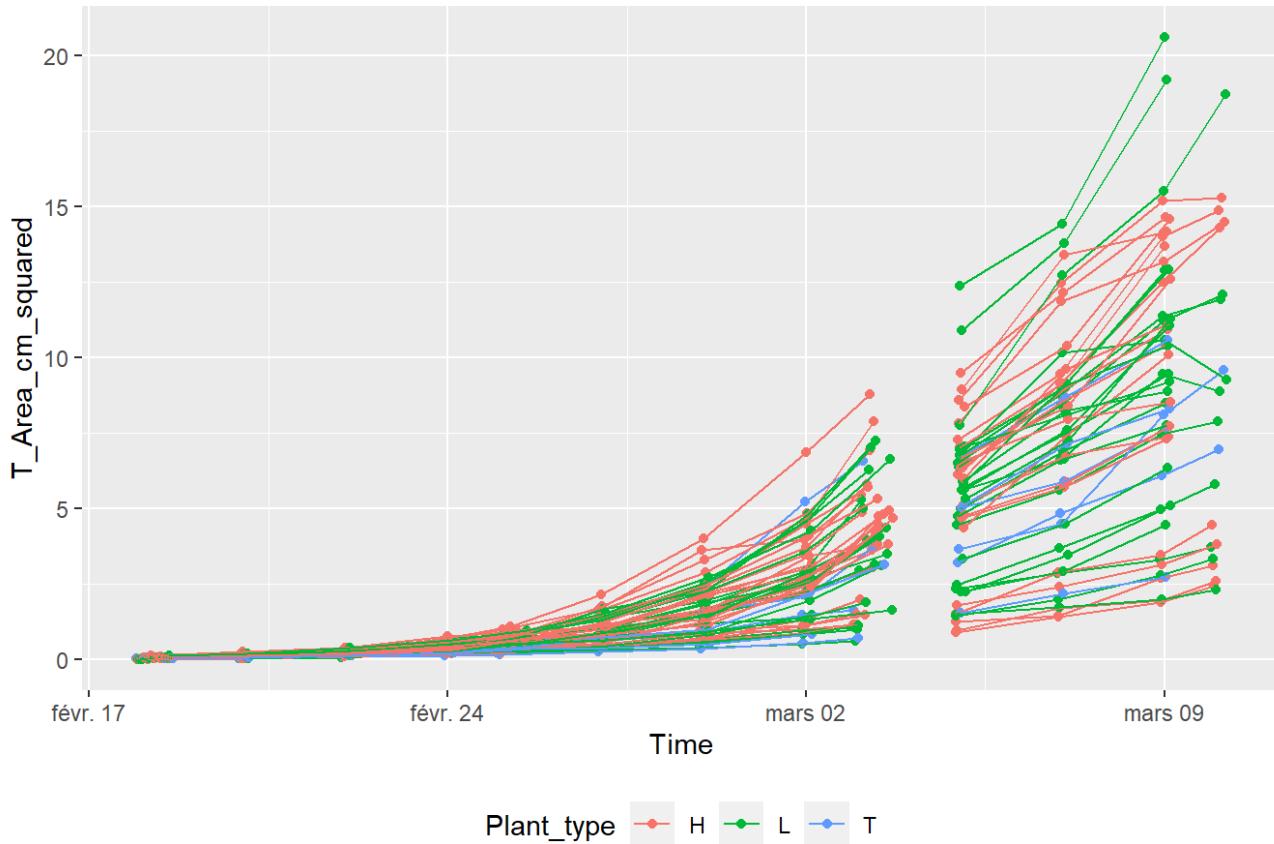
Scatterplots for all genotypes by Plant type (Hybride, Line, EPPN20_T) with smooth line.

```
plot_scatter_with_smooth(T_timeseries, variables_T)
```

```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 22 rows containing missing values (`geom_line()`).
```

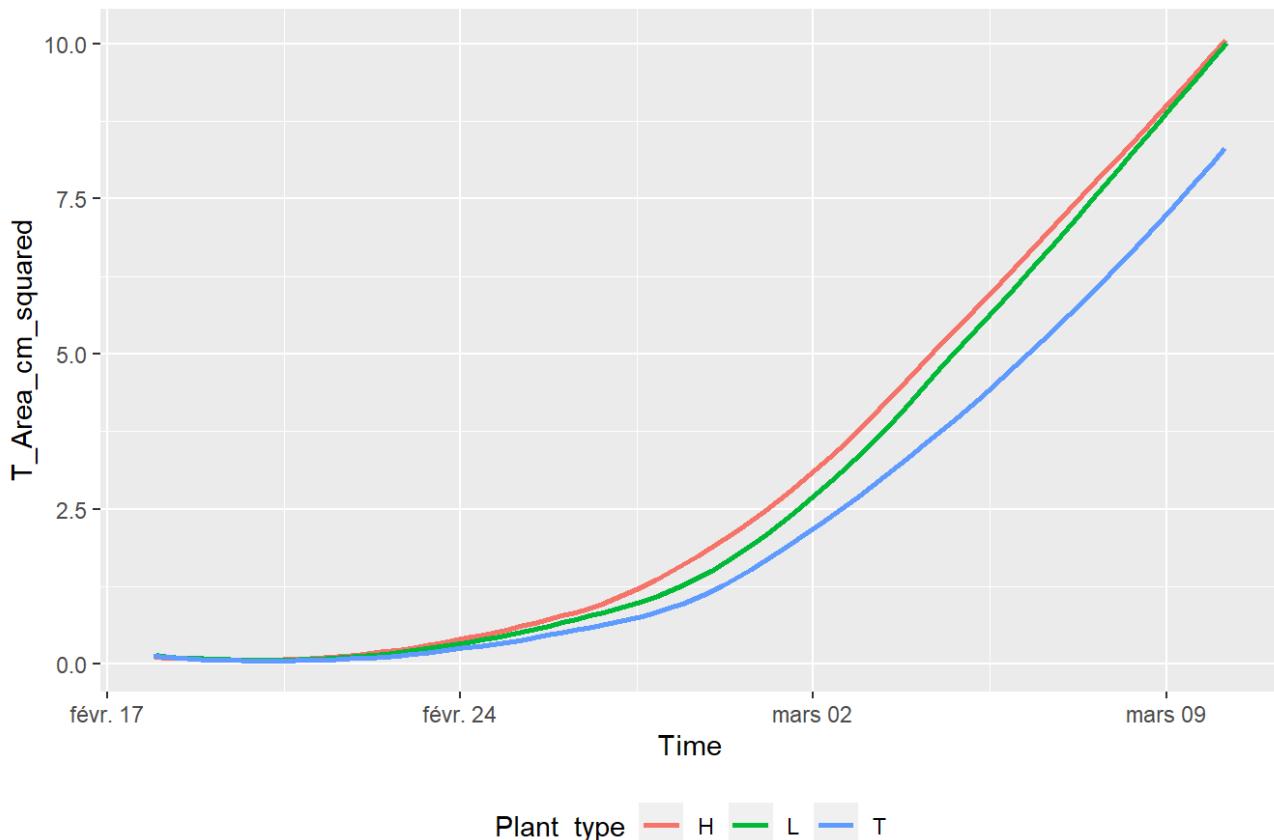
Scatterplot of T_Area_cm_squared by Plant type



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

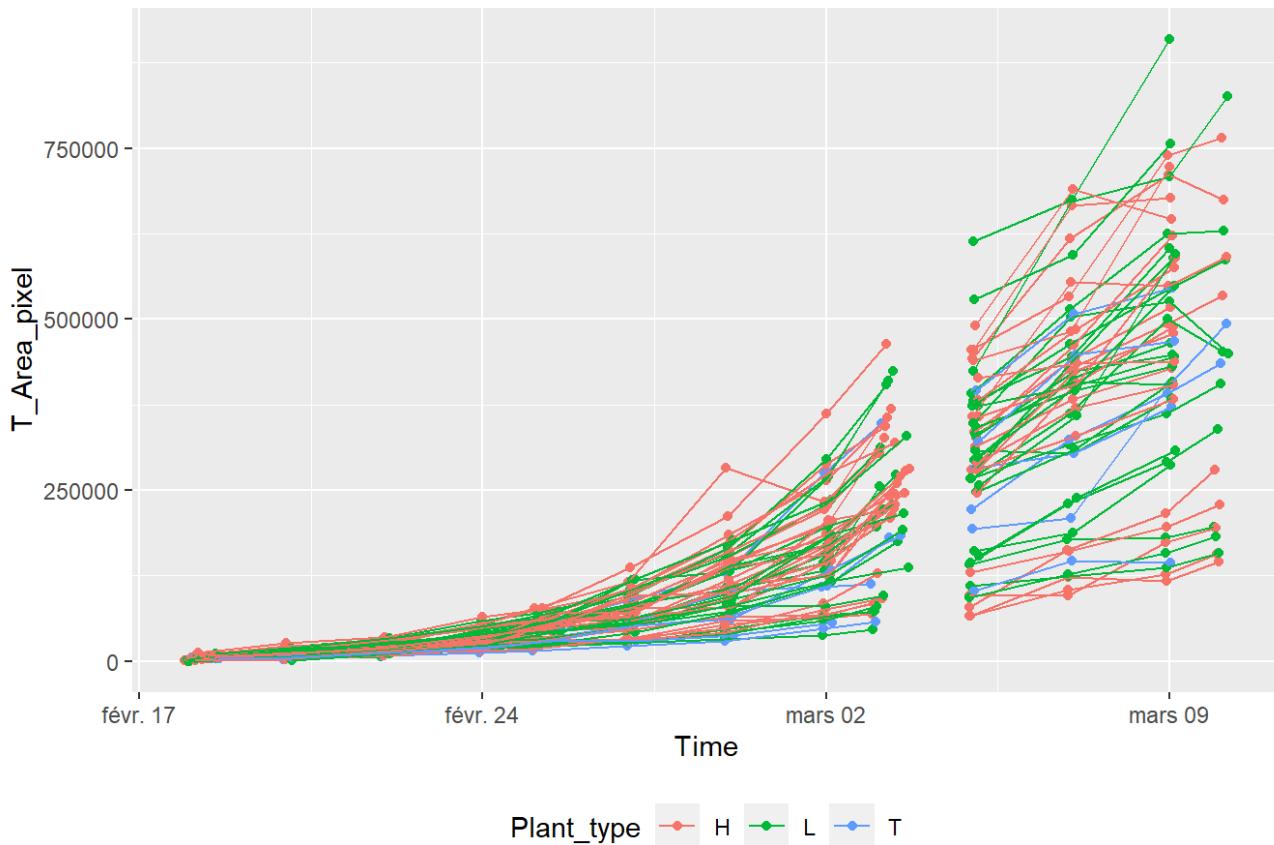
```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Area_cm_squared by Plant type



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
## Removed 22 rows containing missing values (`geom_line()`).
```

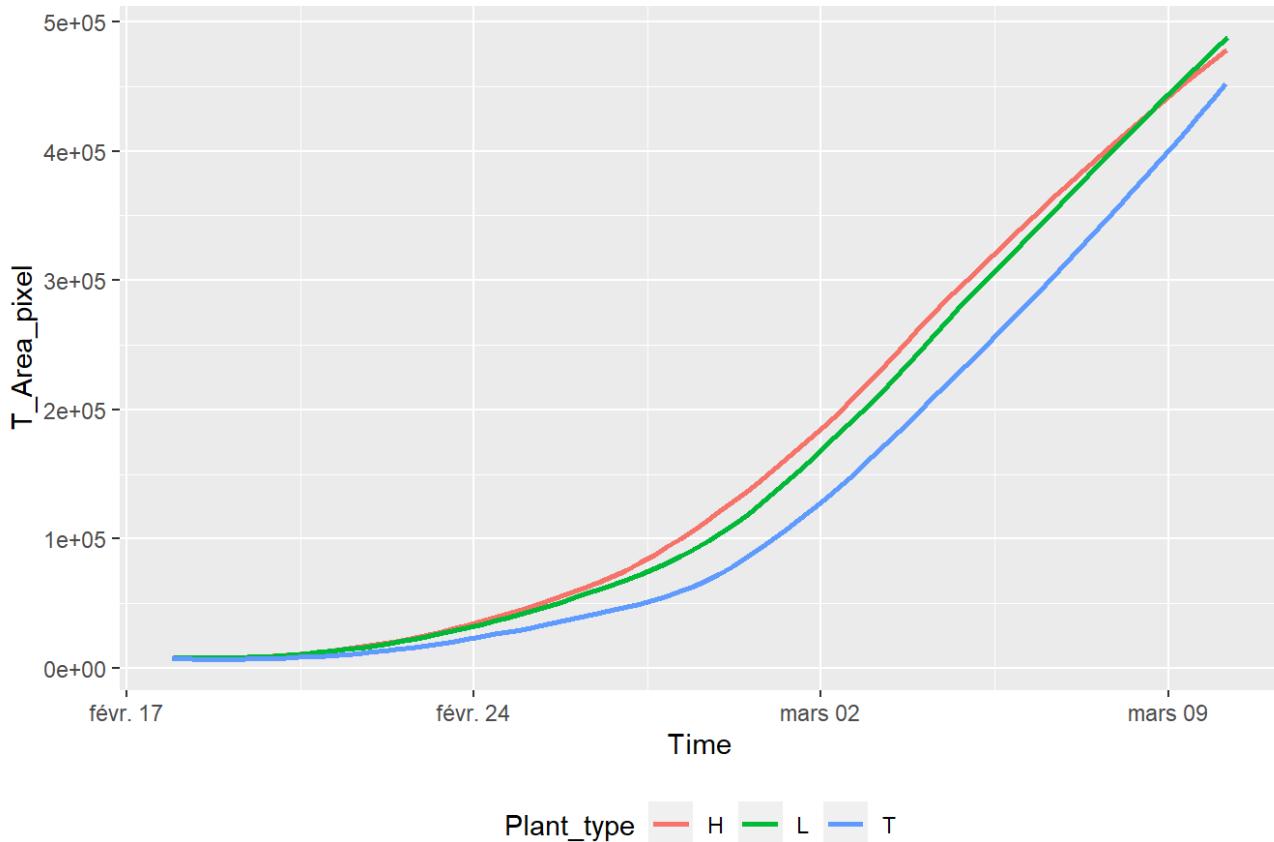
Scatterplot of T_Area_pixel by Plant type



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

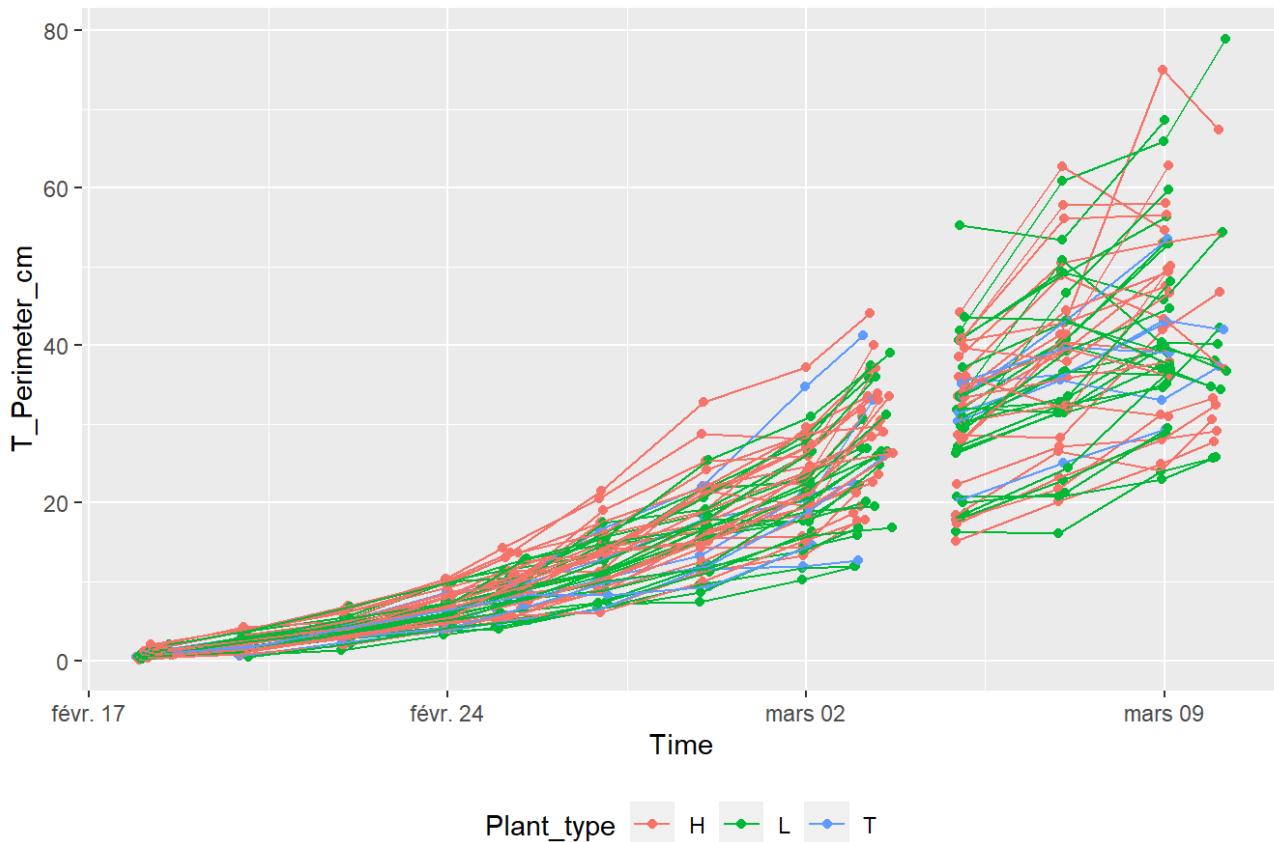
```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Area_pixel by Plant type



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
## Removed 22 rows containing missing values (`geom_line()`).
```

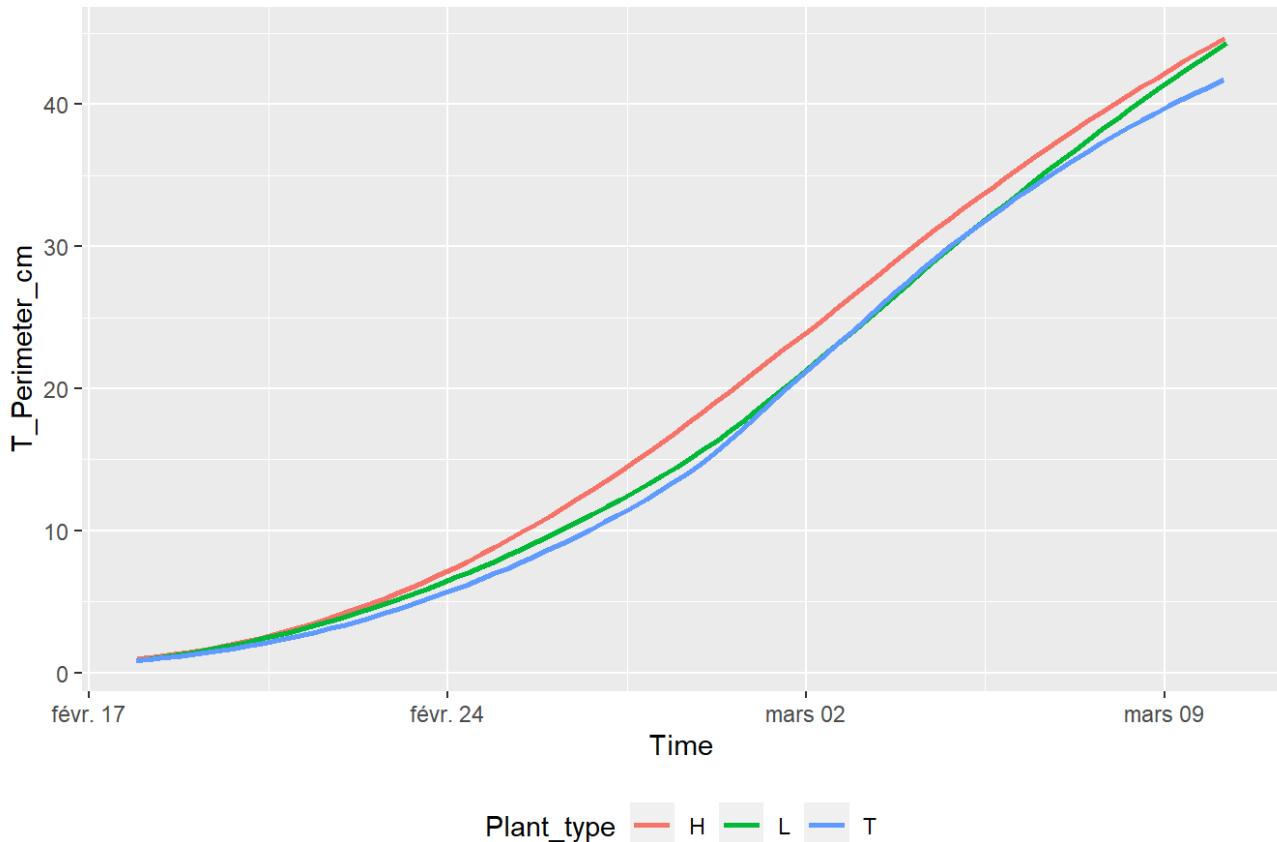
Scatterplot of T_Perimeter_cm by Plant type



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

```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

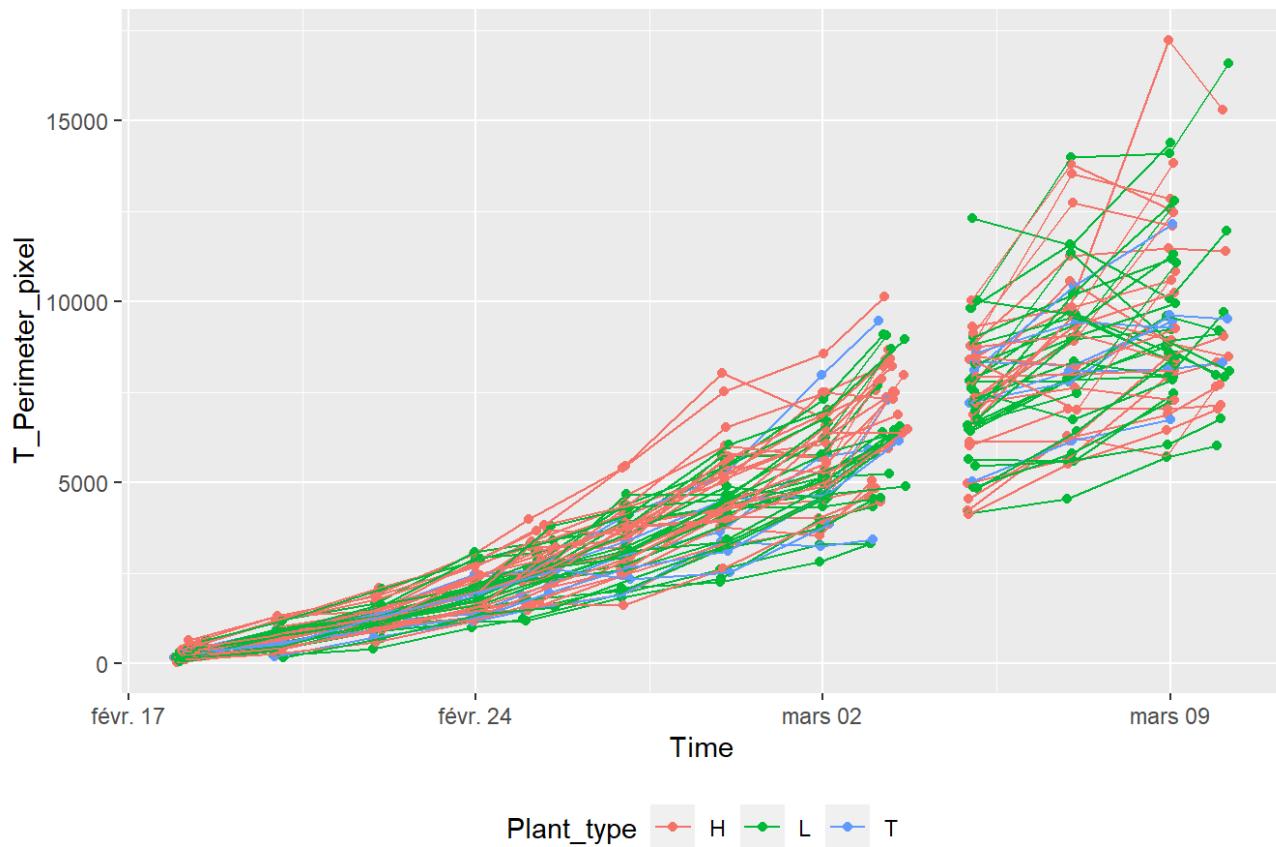
Smooth line of T_Perimeter_cm by Plant type



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
```

```
## Removed 22 rows containing missing values (`geom_line()`).
```

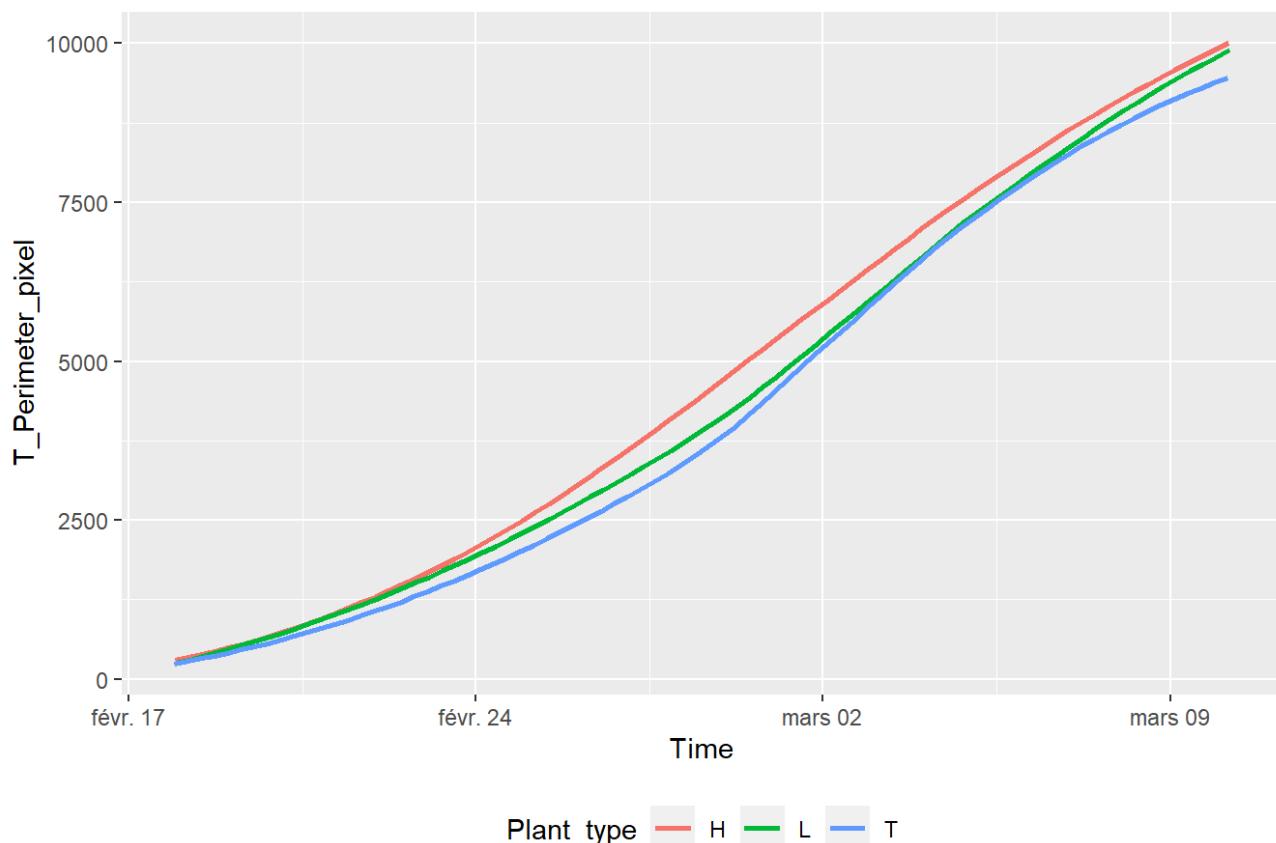
Scatterplot of T_Perimeter_pixel by Plant type



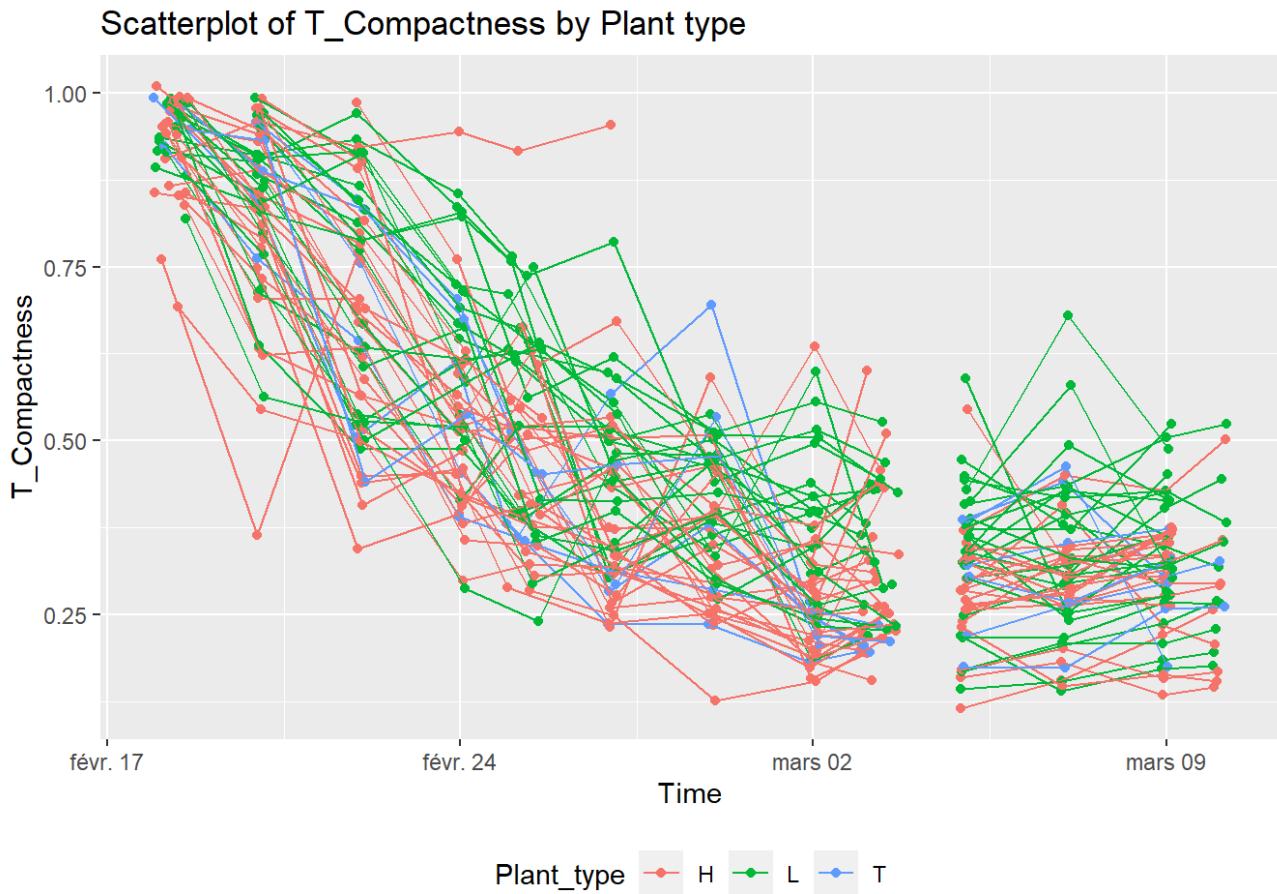
```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Perimeter_pixel by Plant type



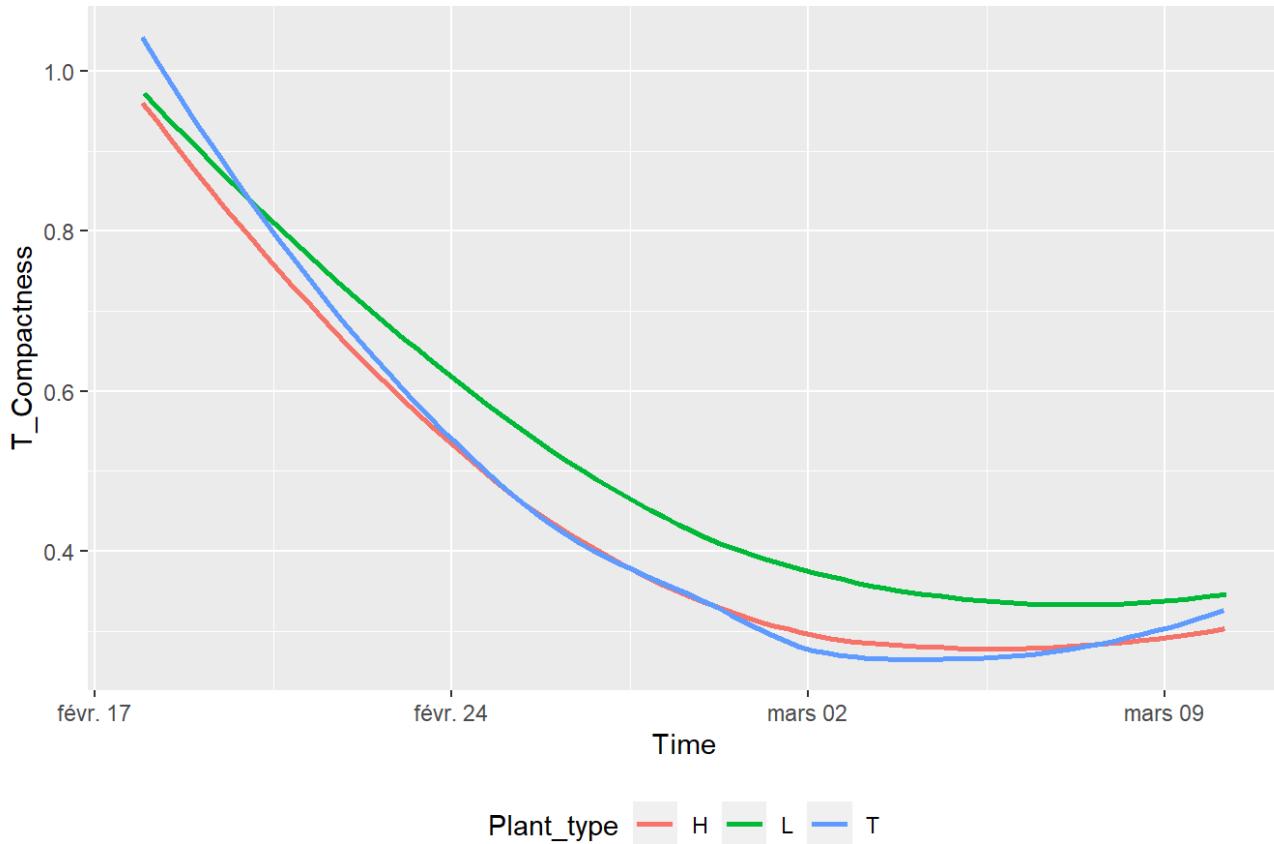
```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
## Removed 22 rows containing missing values (`geom_line()`).
```



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

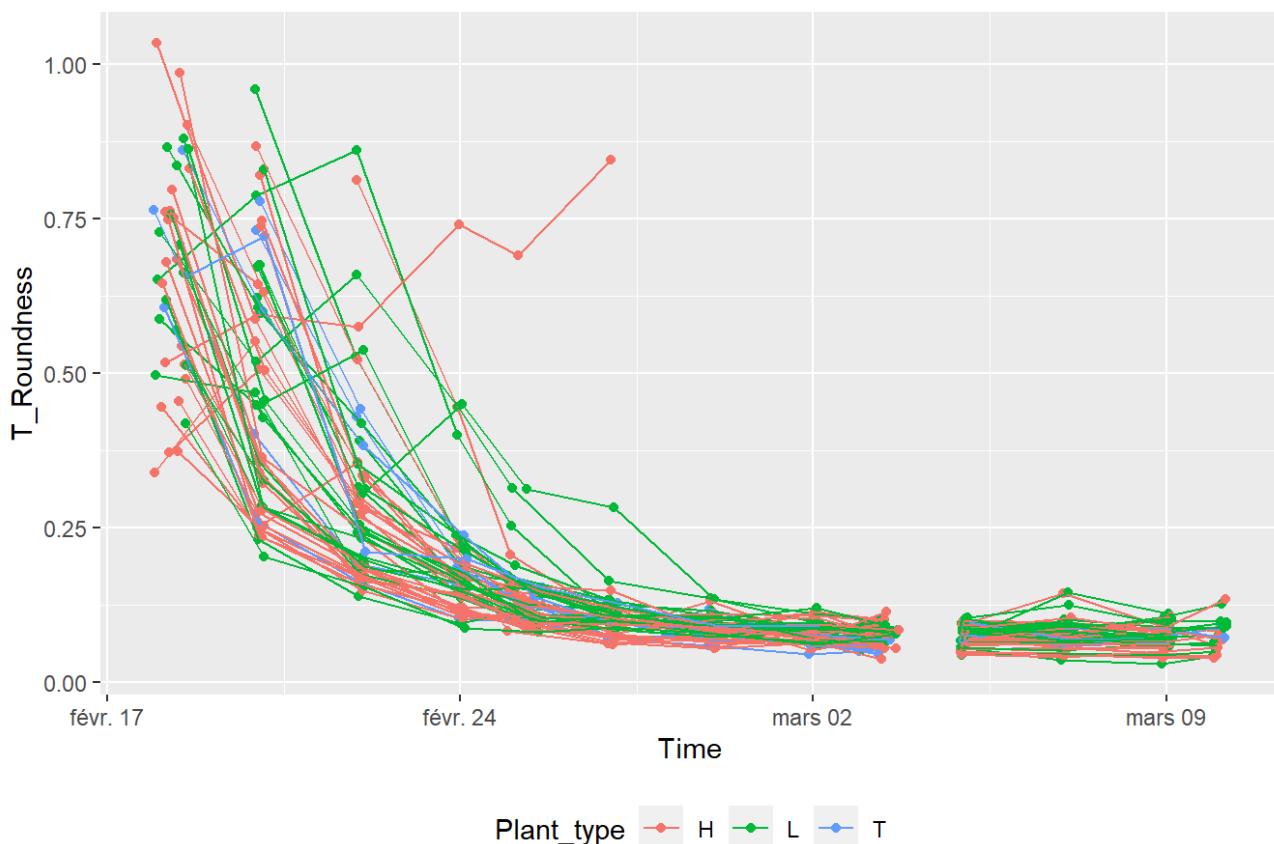
```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Compactness by Plant type



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
## Removed 22 rows containing missing values (`geom_line()`).
```

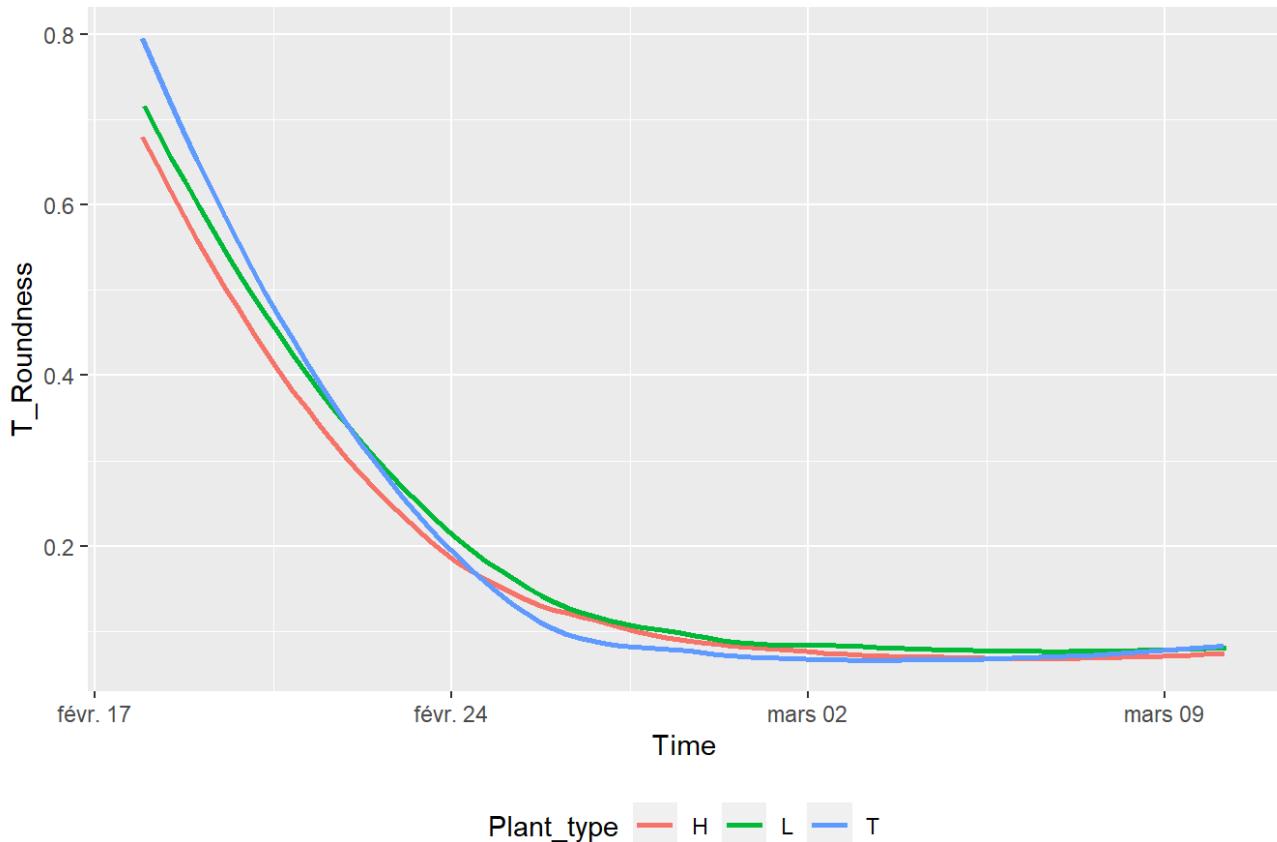
Scatterplot of T_Roundness by Plant type



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

```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

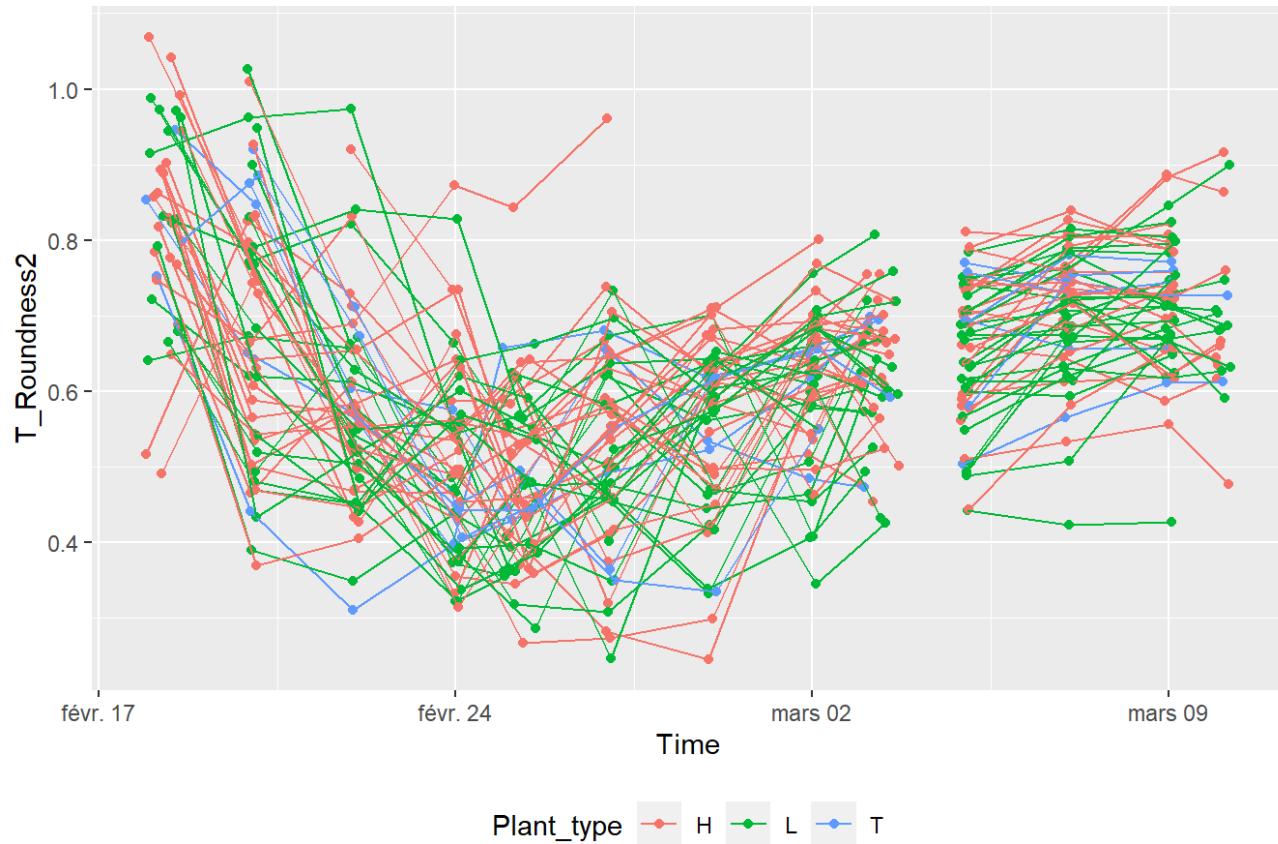
Smooth line of T_Roundness by Plant type



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
```

```
## Removed 22 rows containing missing values (`geom_line()`).
```

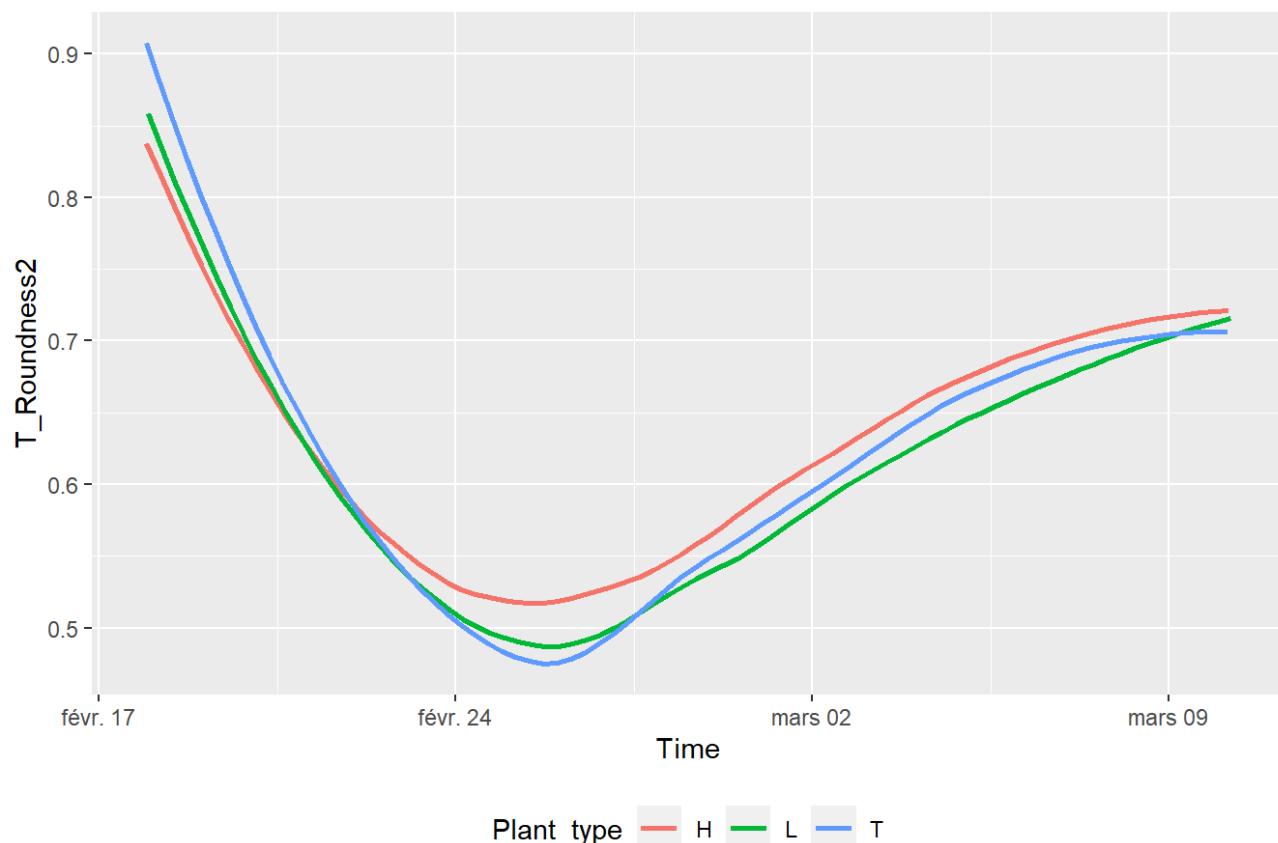
Scatterplot of T_Roundness2 by Plant type



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

```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

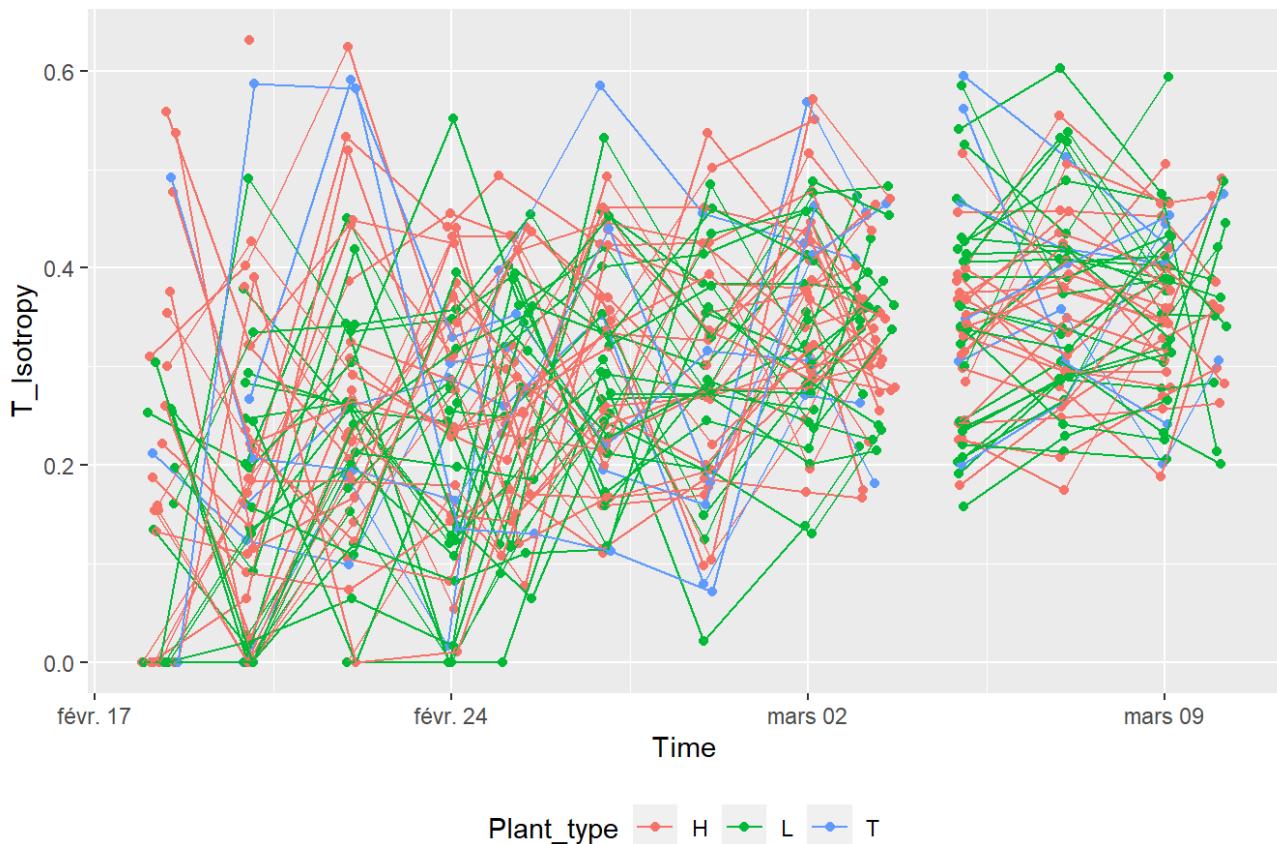
Smooth line of T_Roundness2 by Plant type



```
## Warning: Removed 27 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 26 rows containing missing values (`geom_line()`).
```

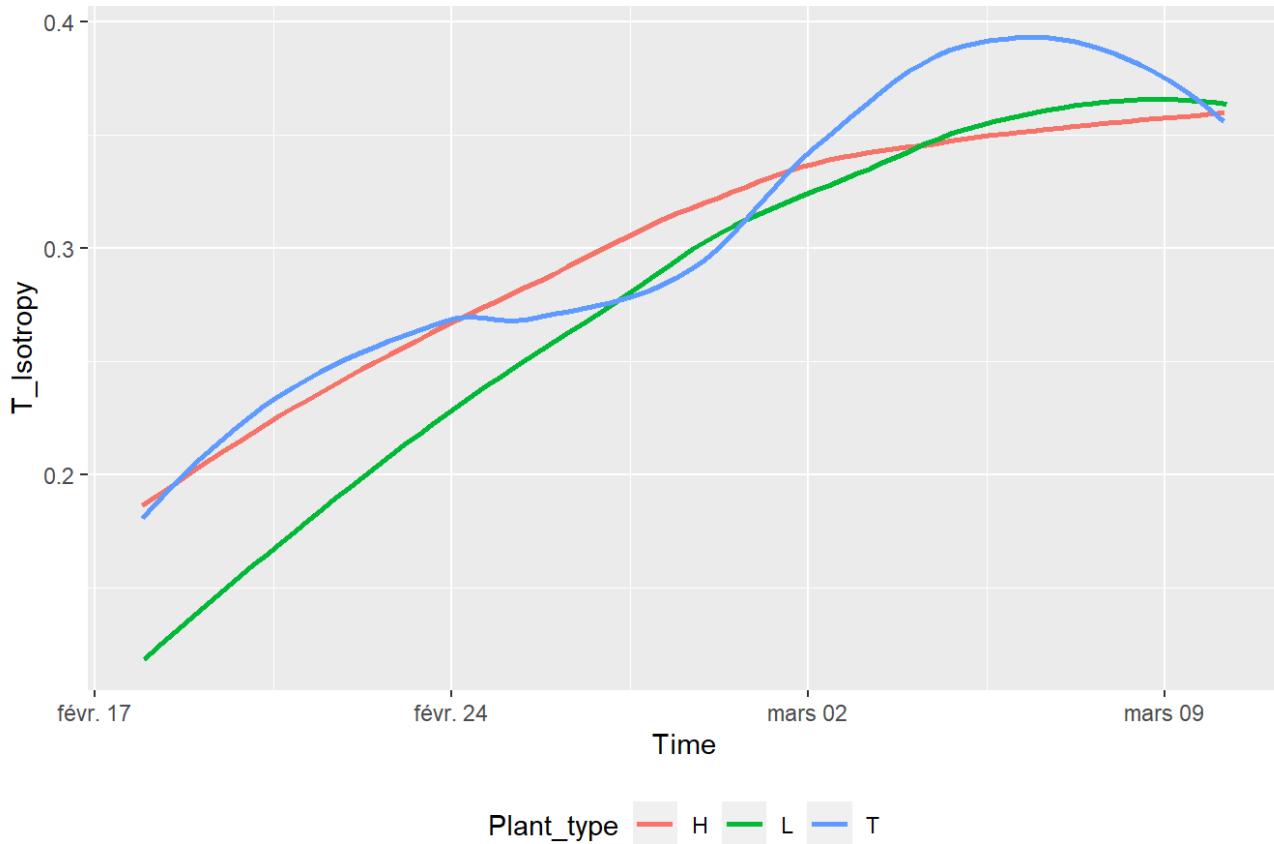
Scatterplot of T_Isotropy by Plant type



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

```
## Warning: Removed 27 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Isotropy by Plant type

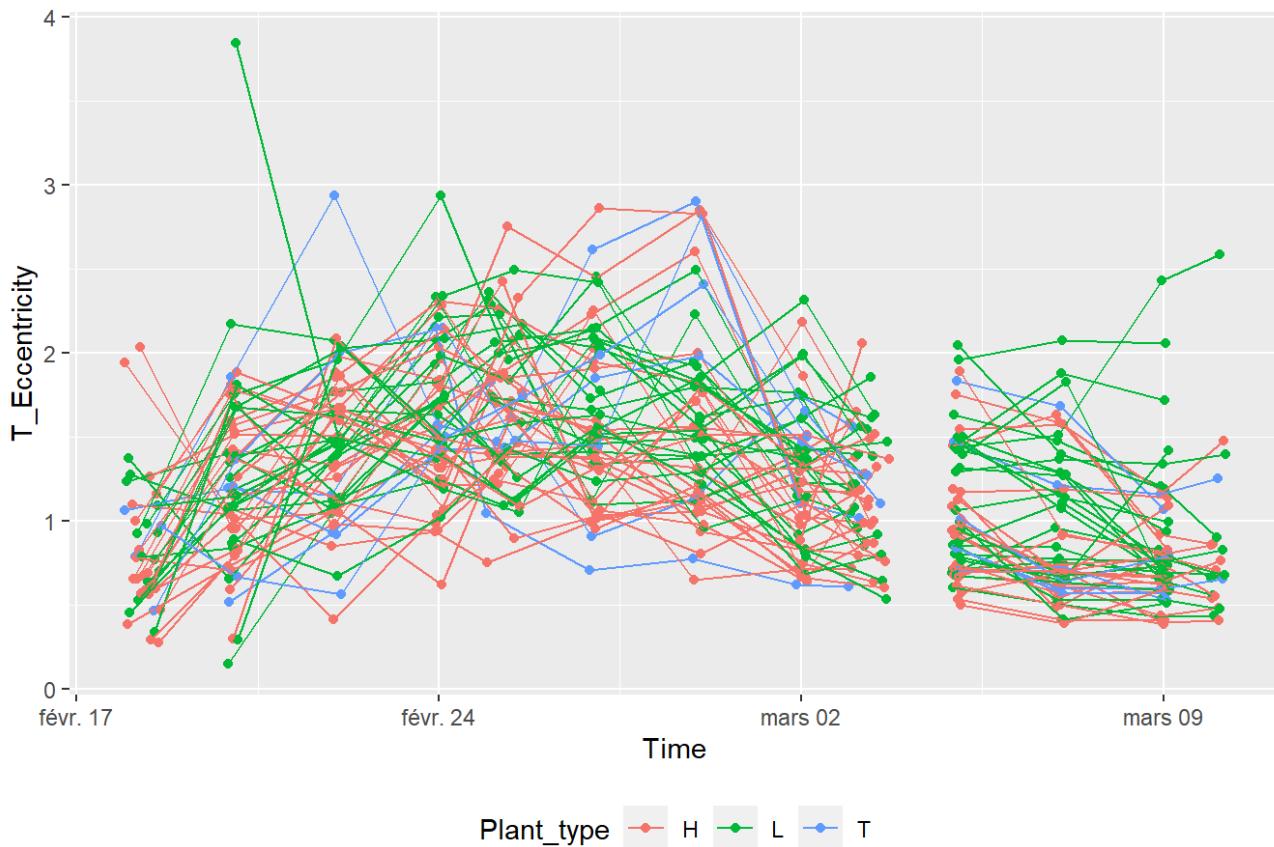


```
Plant_type — H — L — T
```

```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 22 rows containing missing values (`geom_line()`).
```

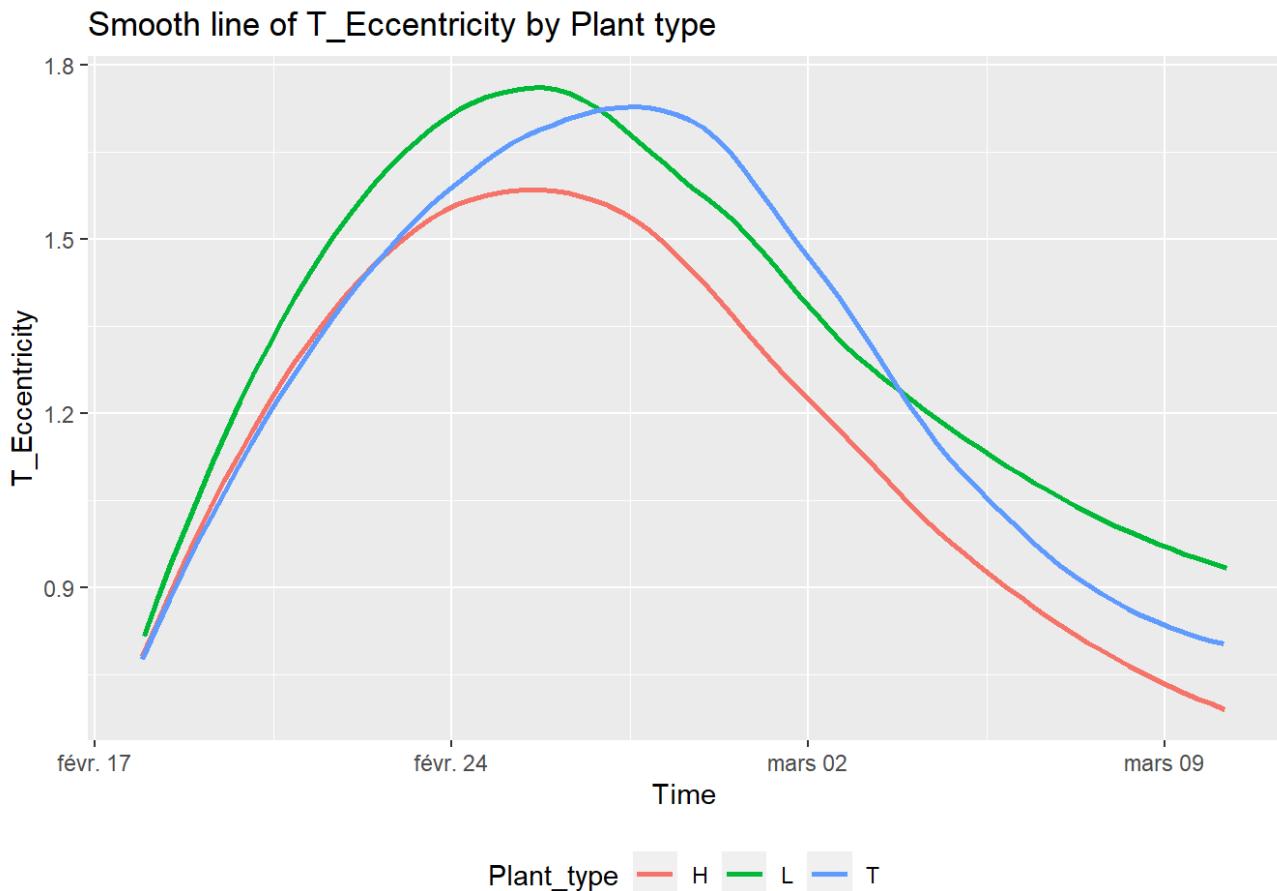
Scatterplot of T_Eccentricity by Plant type



```
Plant_type — H — L — T
```

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

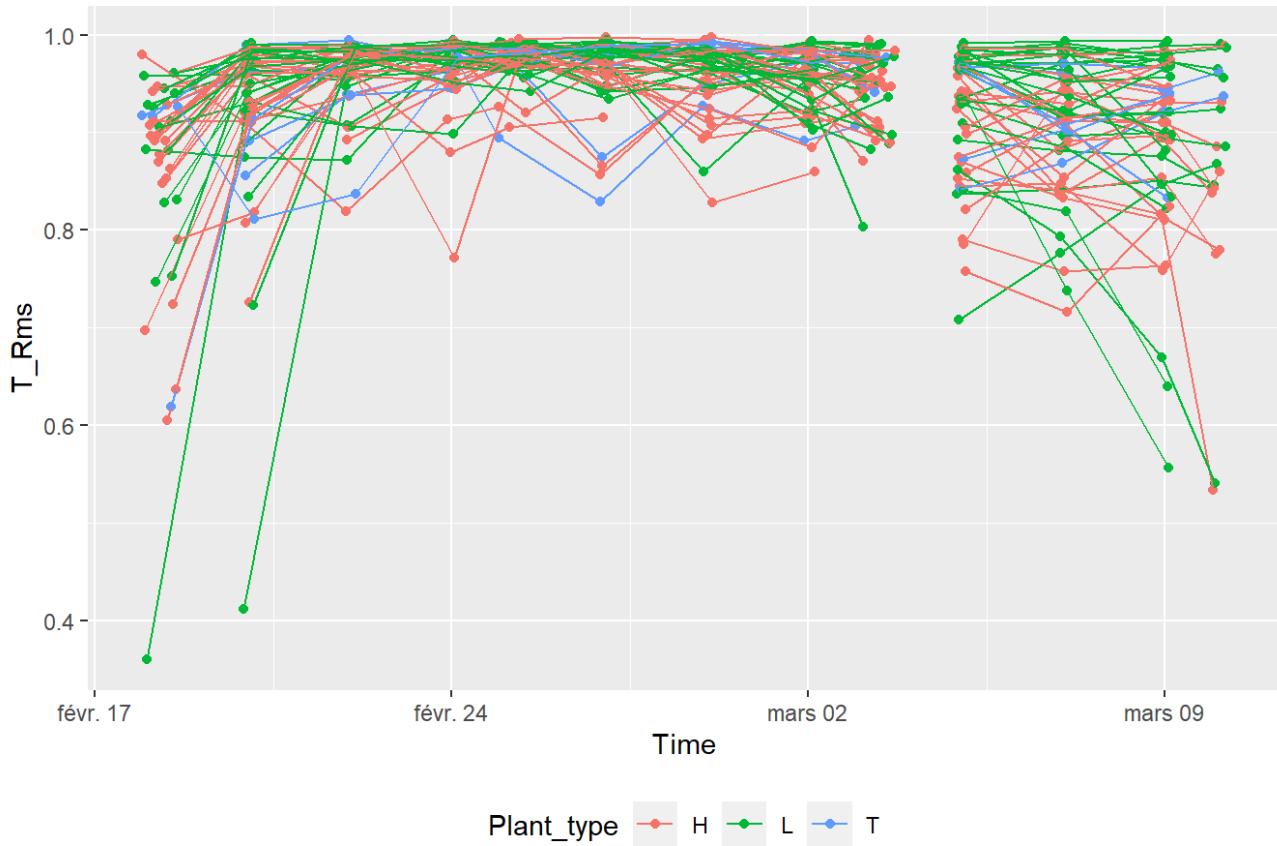
```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
```

```
## Removed 22 rows containing missing values (`geom_line()`).
```

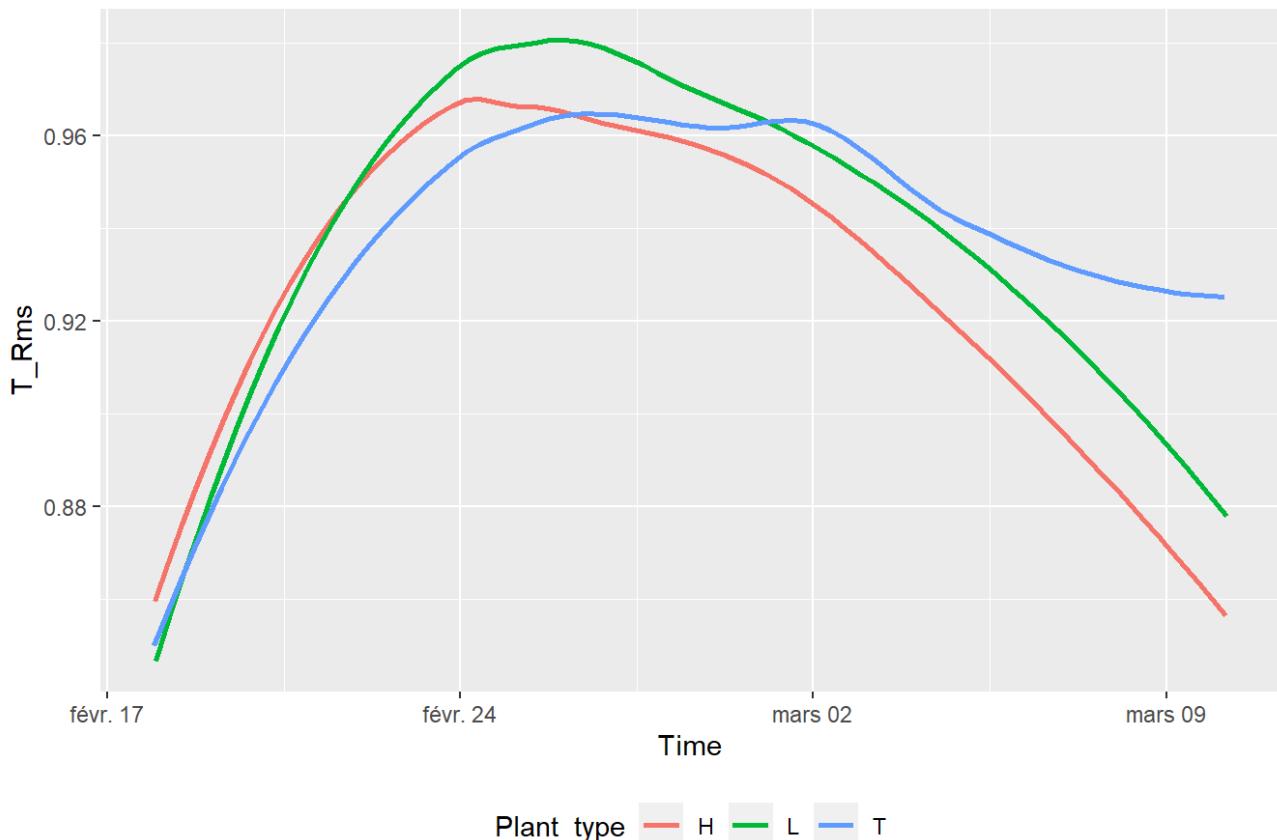
Scatterplot of T_Rms by Plant type



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

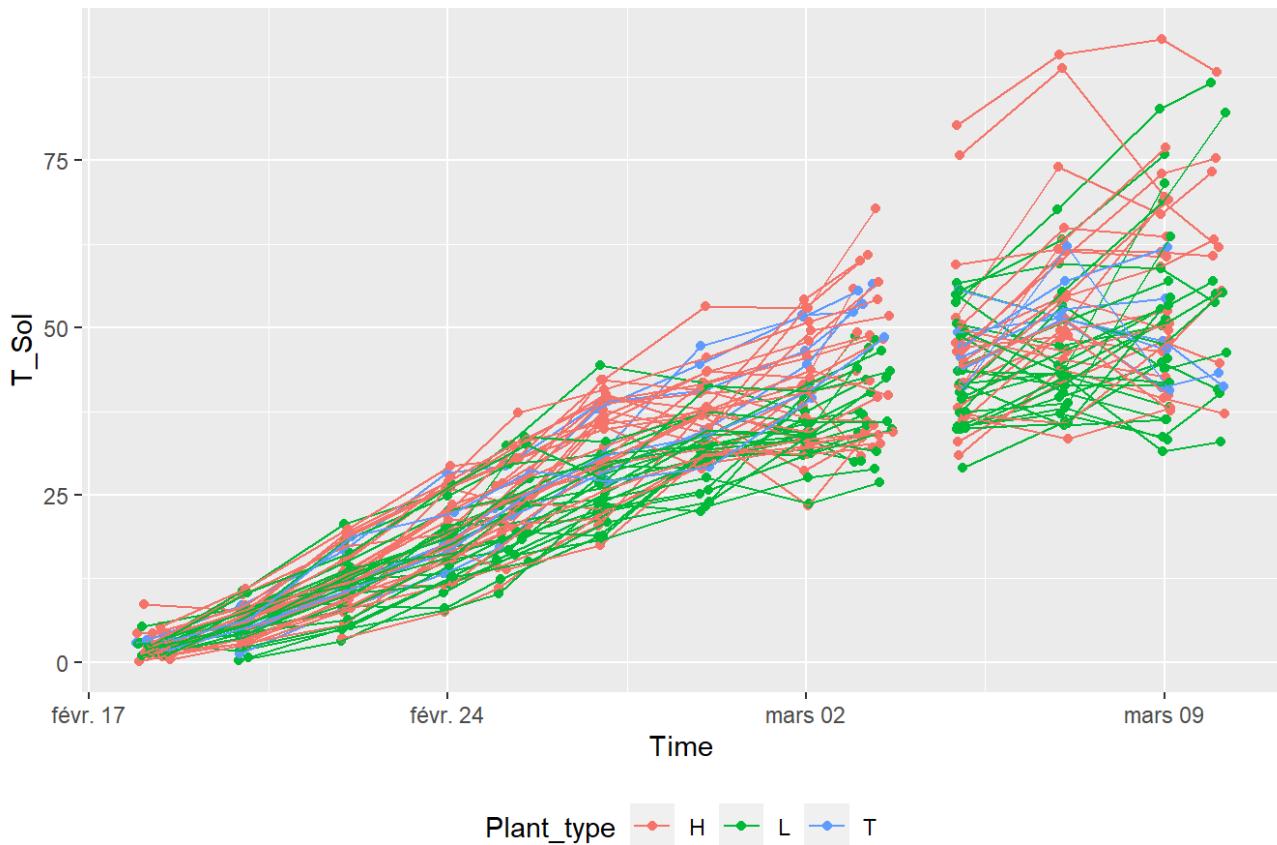
```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Rms by Plant type



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
## Removed 22 rows containing missing values (`geom_line()`).
```

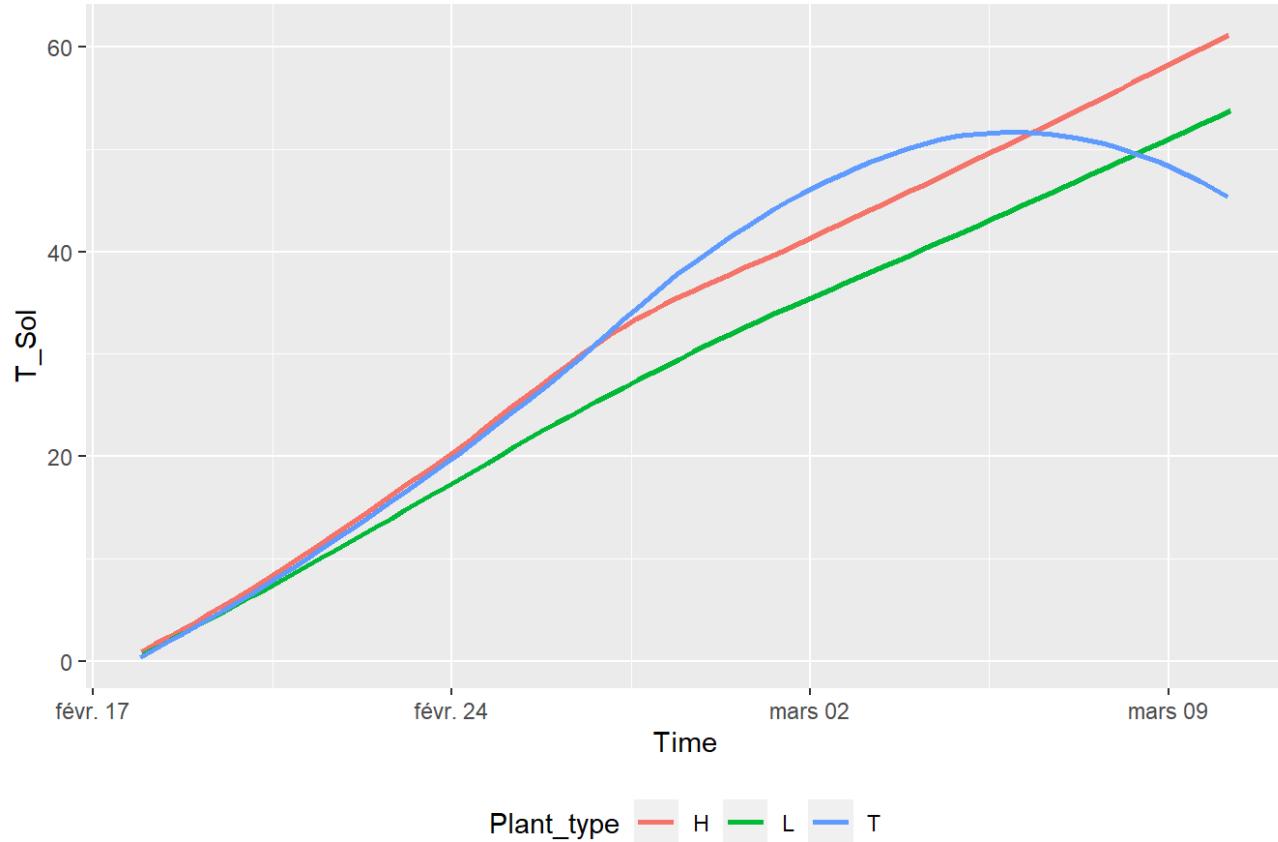
Scatterplot of T_Sol by Plant type



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

```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Sol by Plant type



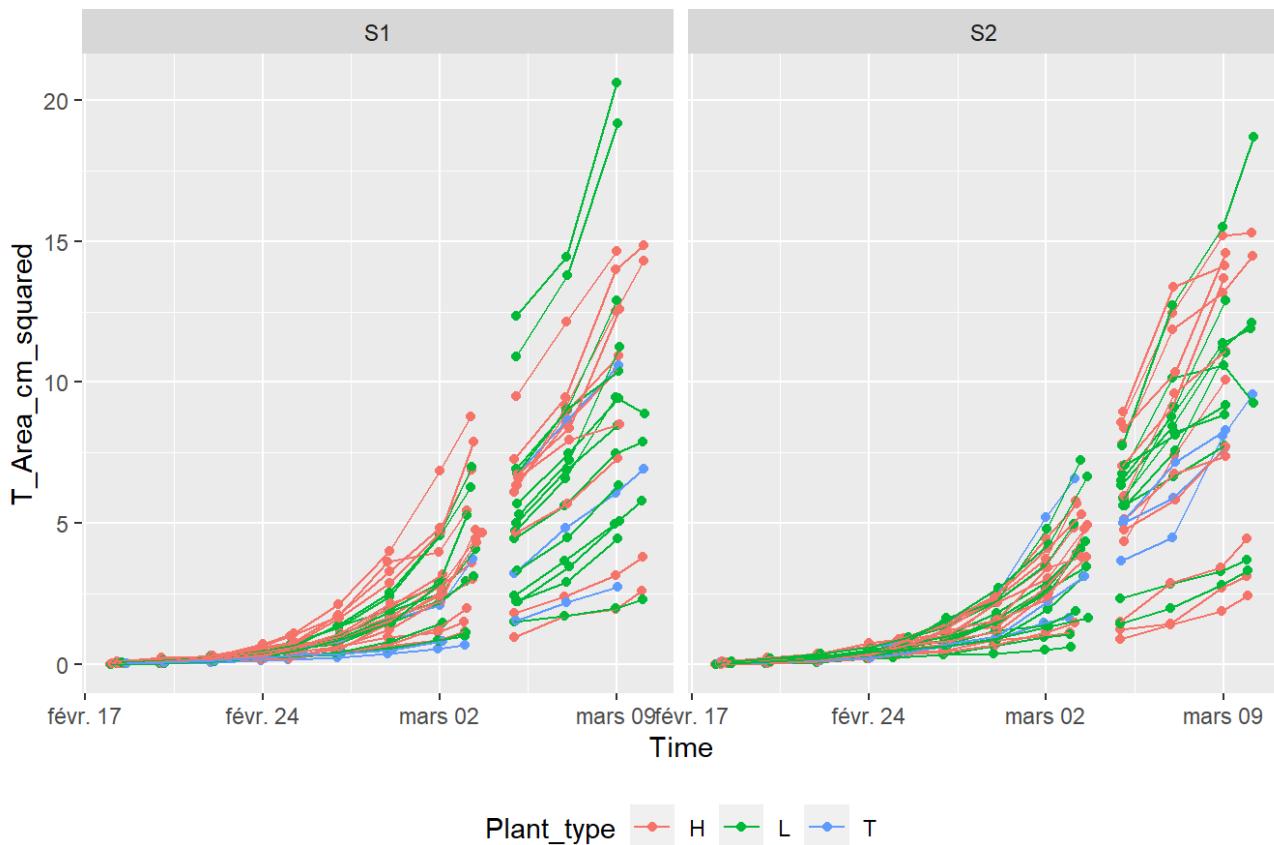
Scatter plots for all genotypes by water treatment

```
plot_scatter_with_smooth_water(T_timeseries, variables_T)
```

```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 22 rows containing missing values (`geom_line()`).
```

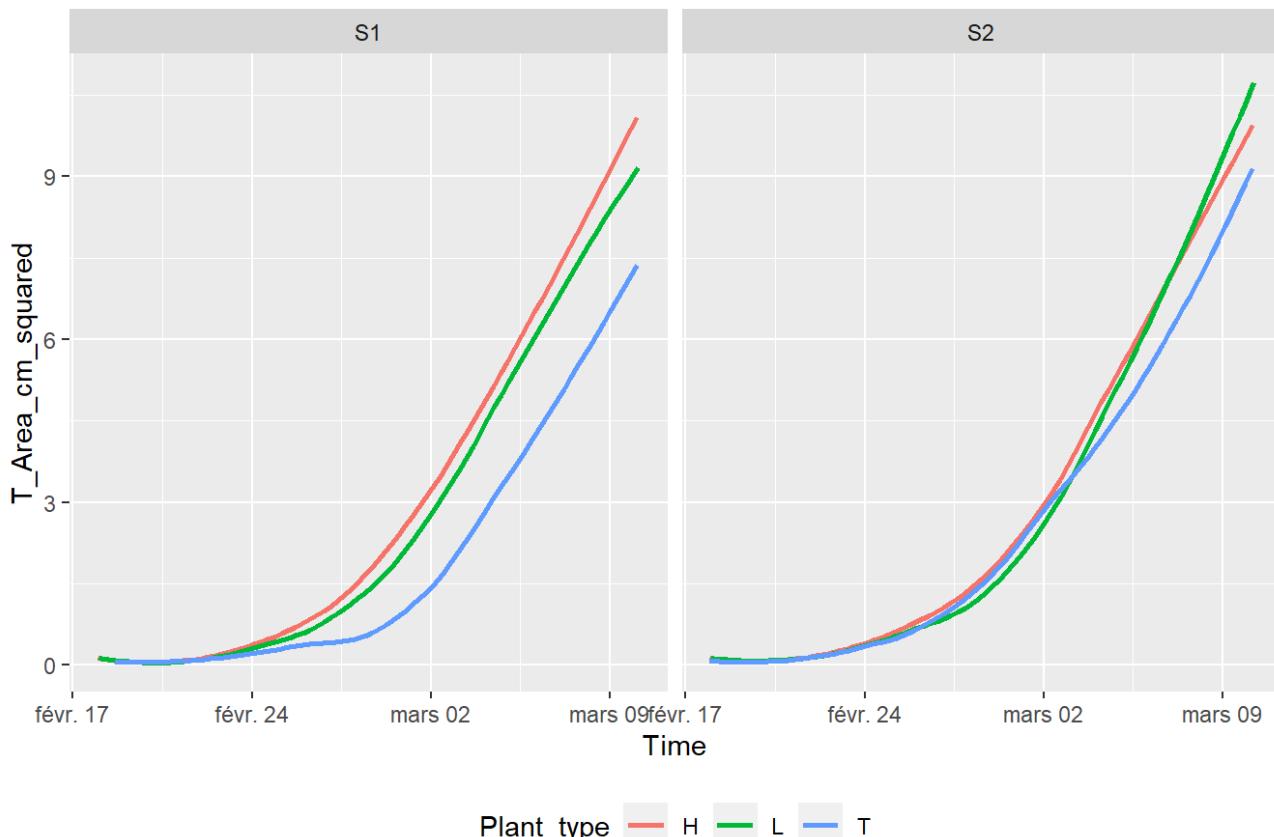
Scatterplot of T_Area_cm_squared by Plant type and Soil



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

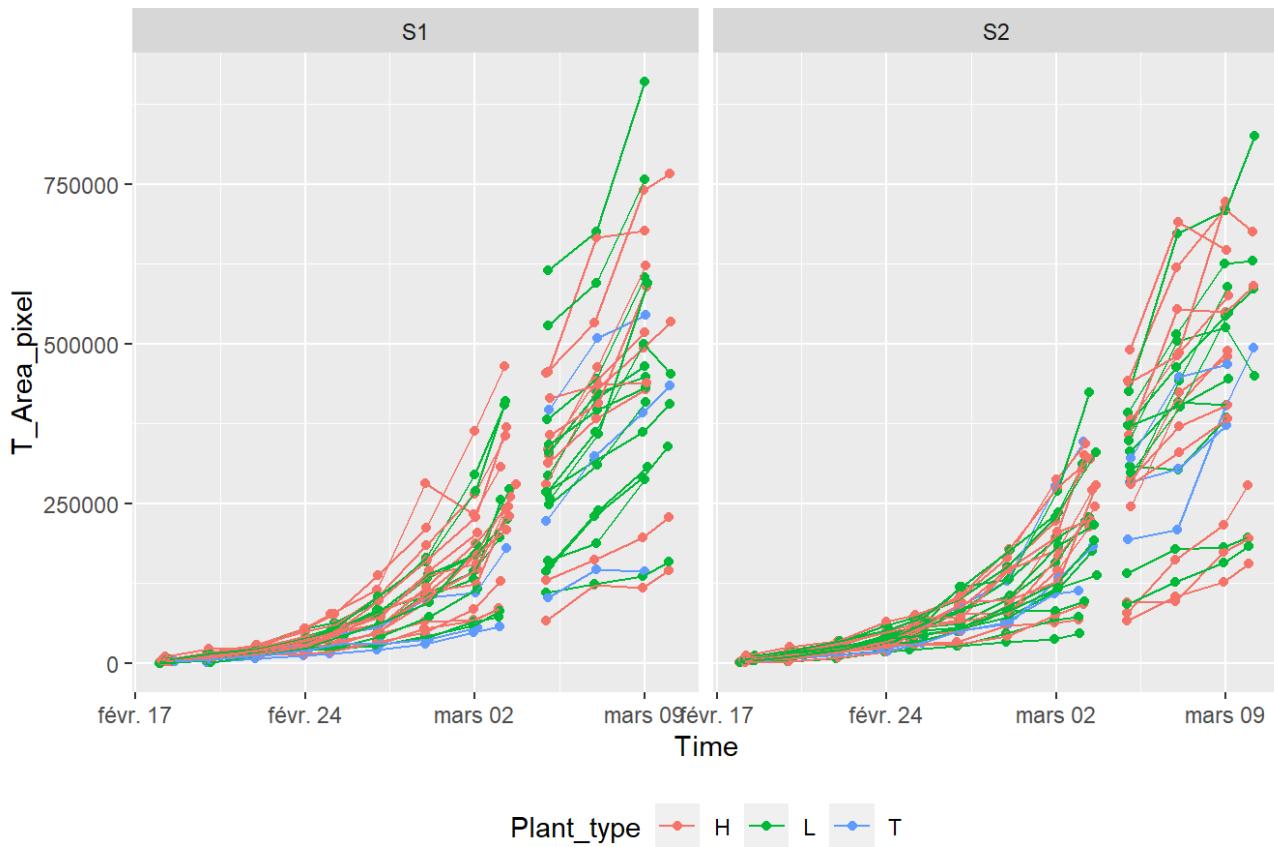
```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Area_cm_squared by Plant type and Soil



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
## Removed 22 rows containing missing values (`geom_line()`).
```

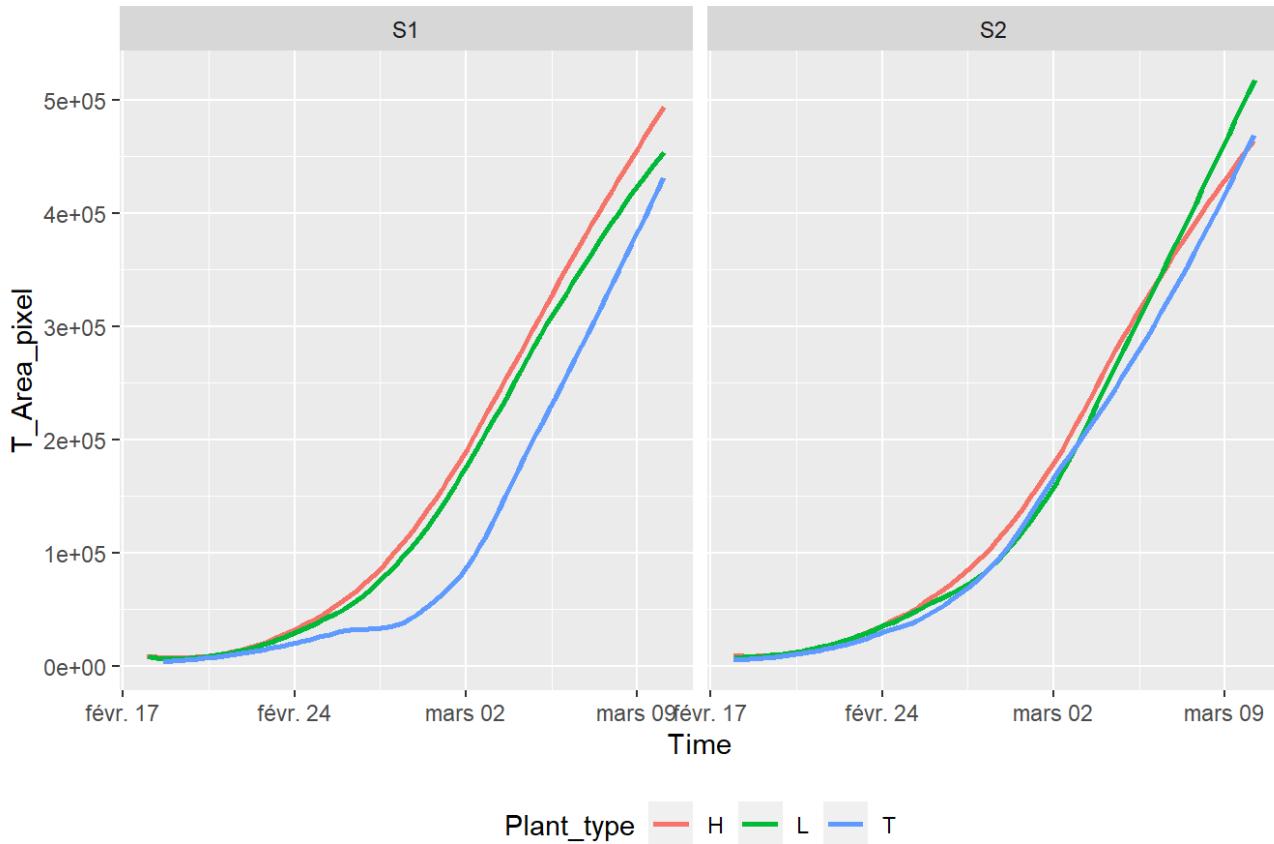
Scatterplot of T_Area_pixel by Plant type and Soil



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

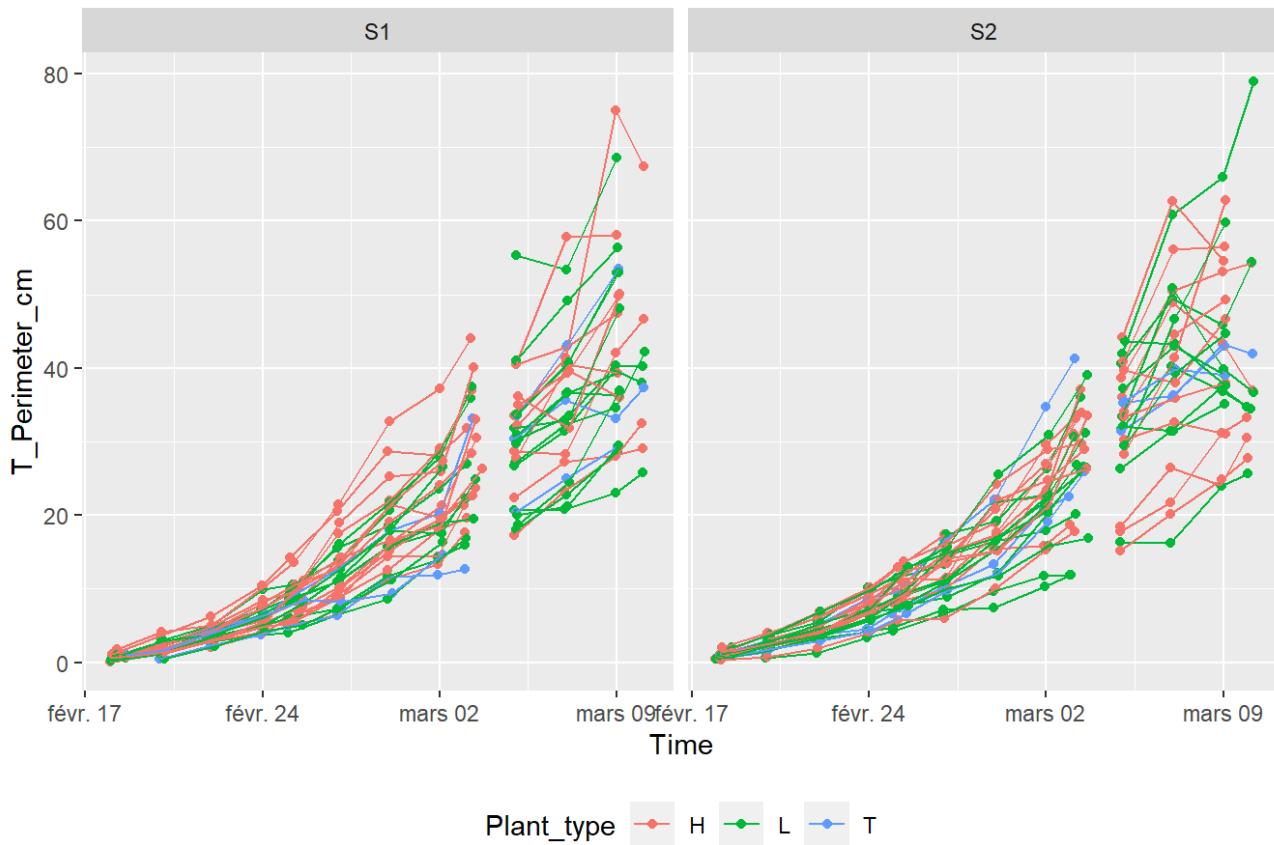
```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Area_pixel by Plant type and Soil



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
## Removed 22 rows containing missing values (`geom_line()`).
```

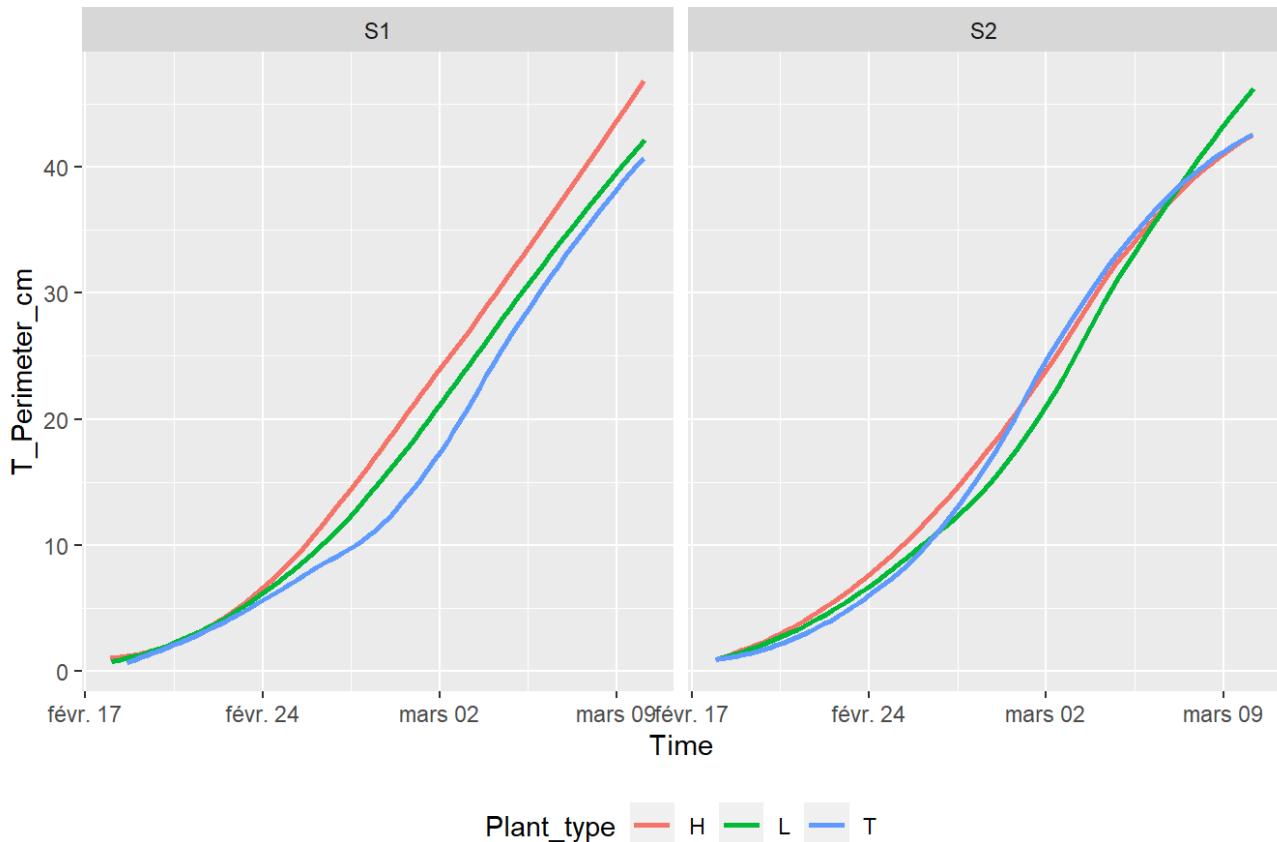
Scatterplot of T_Perimeter_cm by Plant type and Soil



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

```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

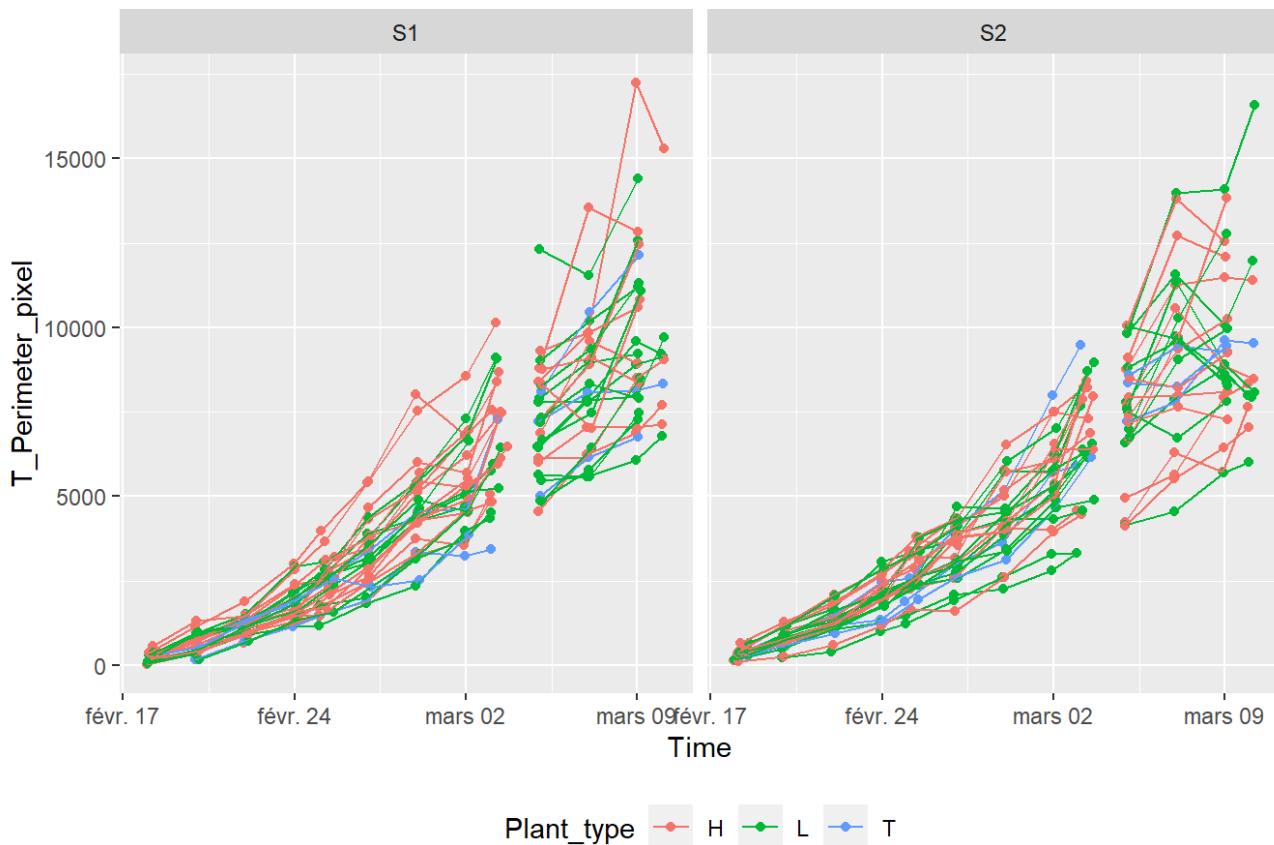
Smooth line of T_Perimeter_cm by Plant type and Soil



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
```

```
## Removed 22 rows containing missing values (`geom_line()`).
```

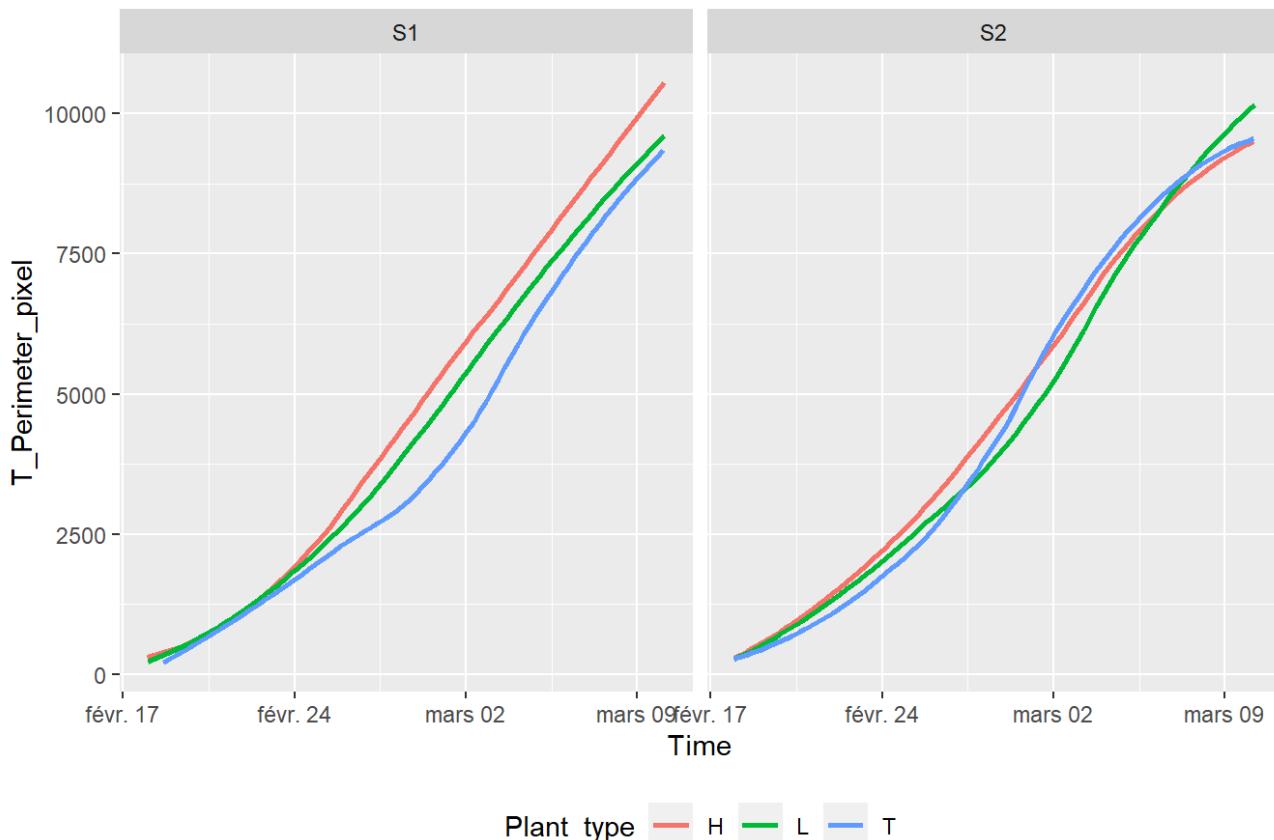
Scatterplot of T_Perimeter_pixel by Plant type and Soil



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

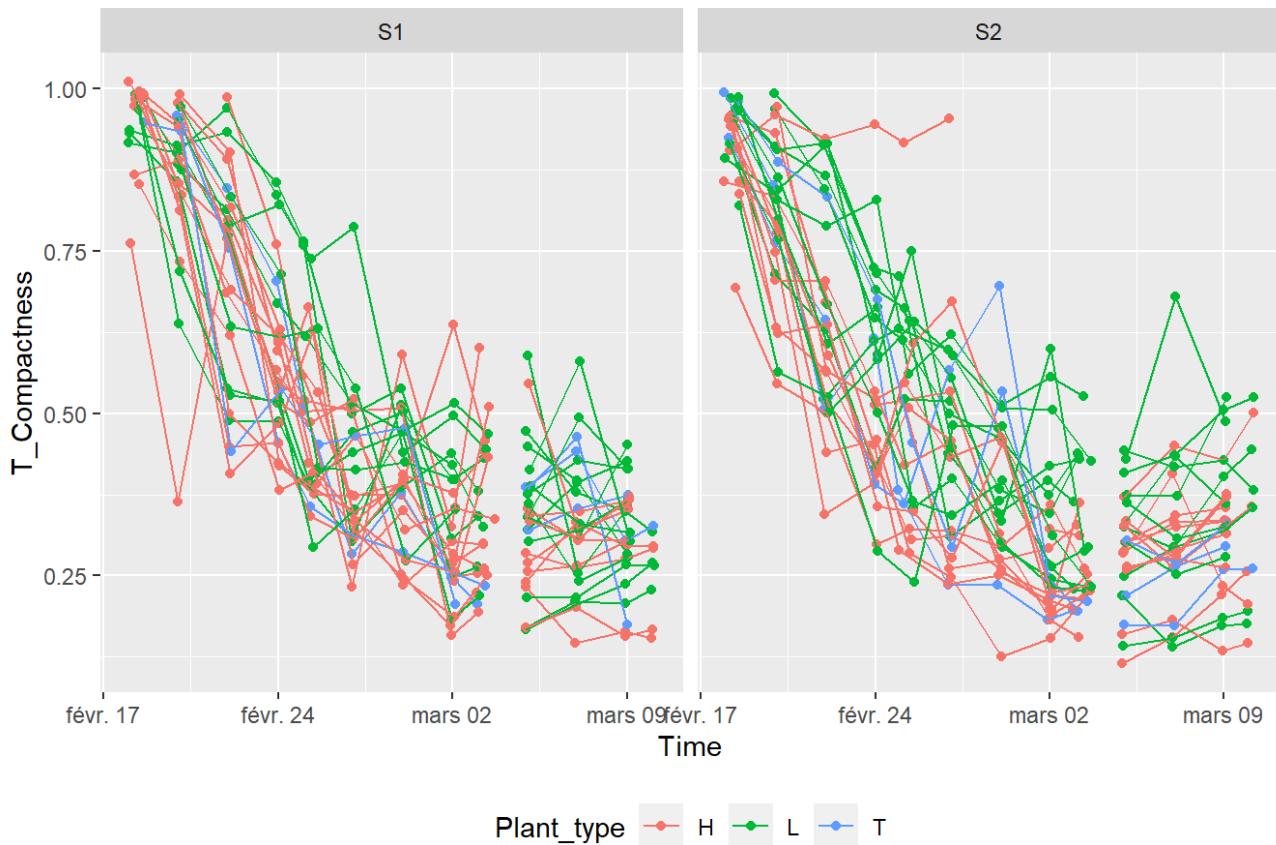
```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Perimeter_pixel by Plant type and Soil



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
## Removed 22 rows containing missing values (`geom_line()`).
```

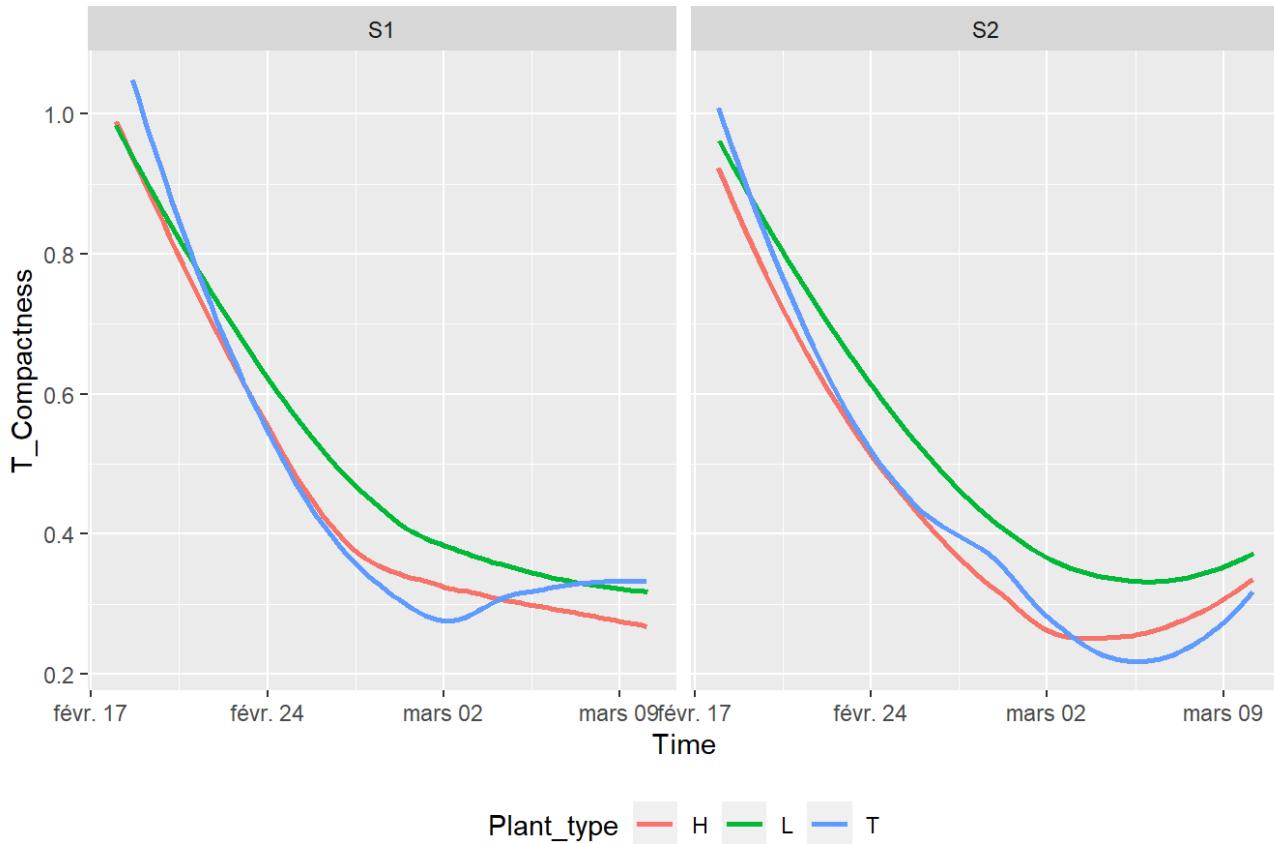
Scatterplot of T_Compactness by Plant type and Soil



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

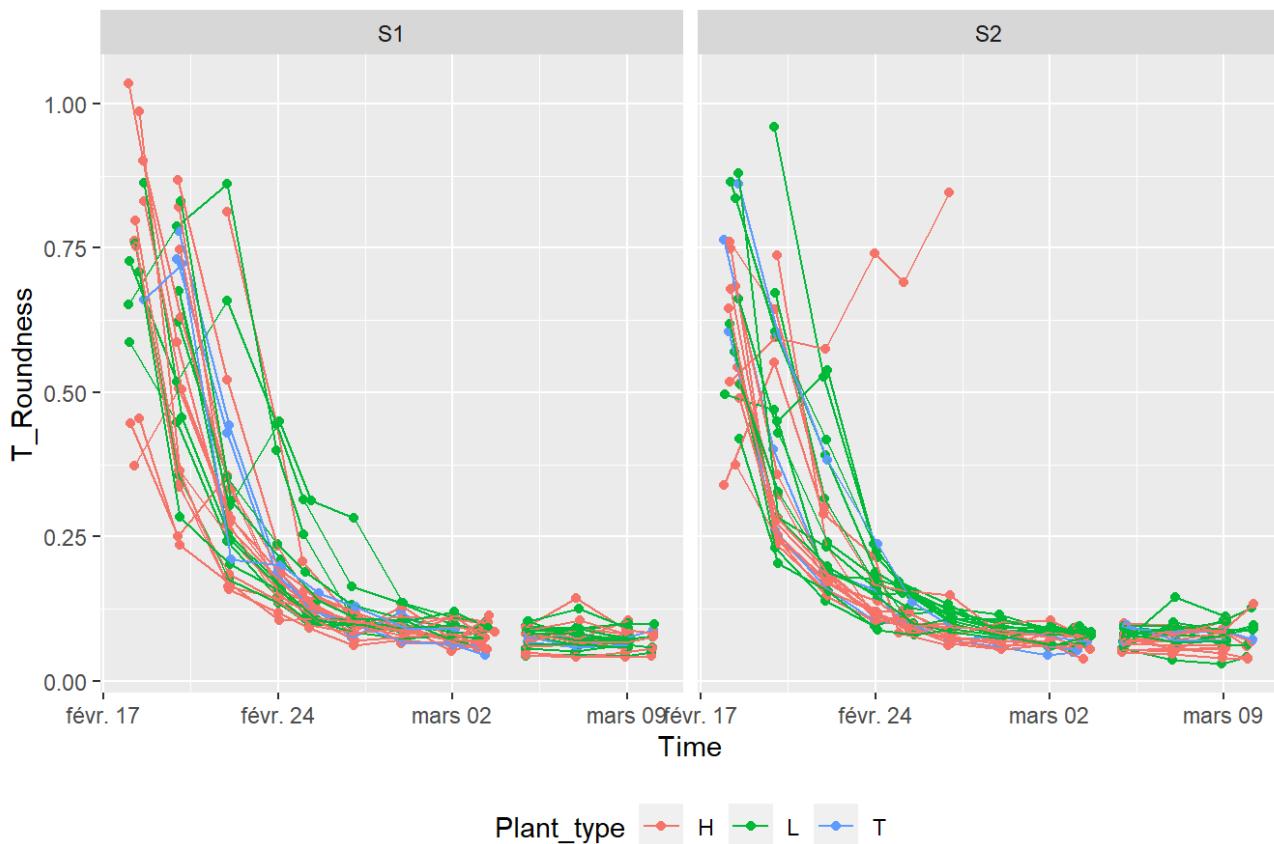
```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Compactness by Plant type and Soil



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
## Removed 22 rows containing missing values (`geom_line()`).
```

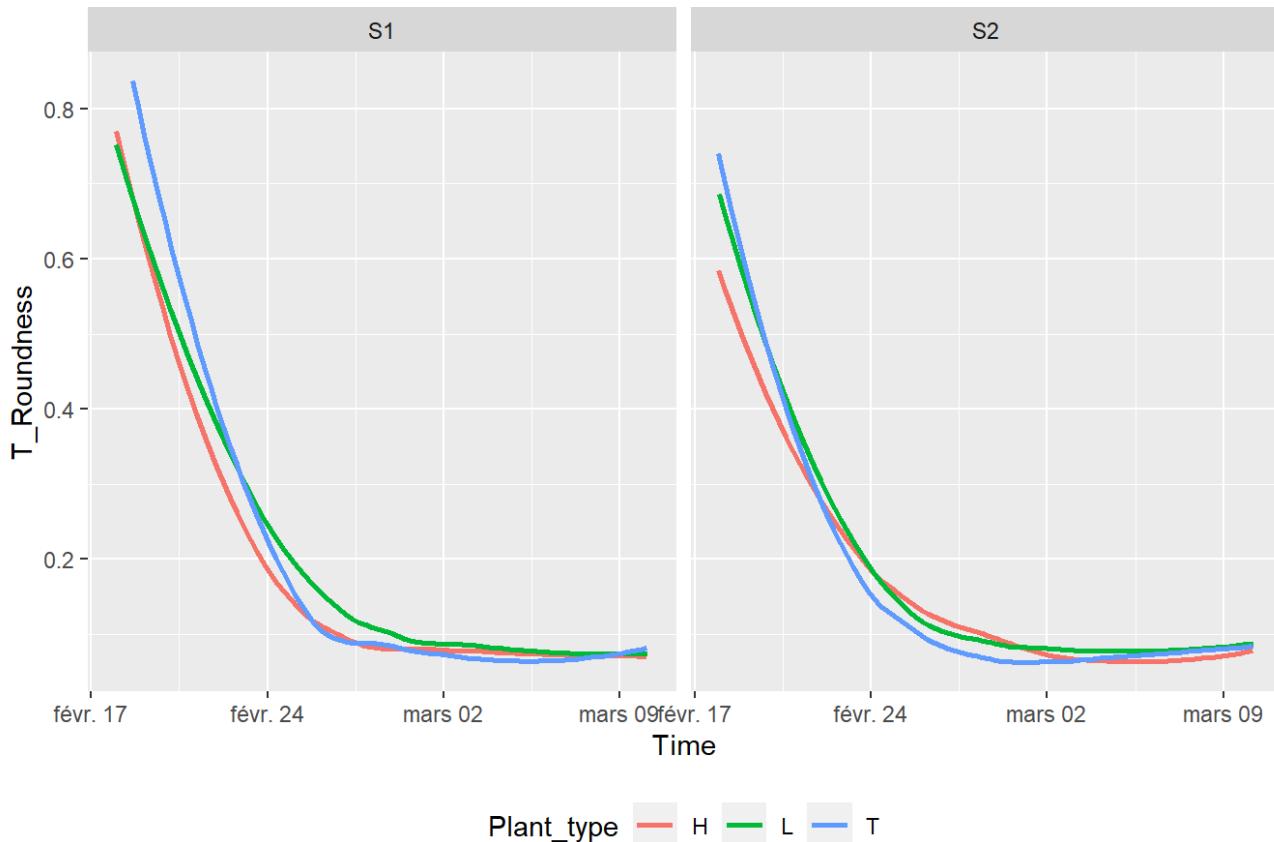
Scatterplot of T_Roundness by Plant type and Soil



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

```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

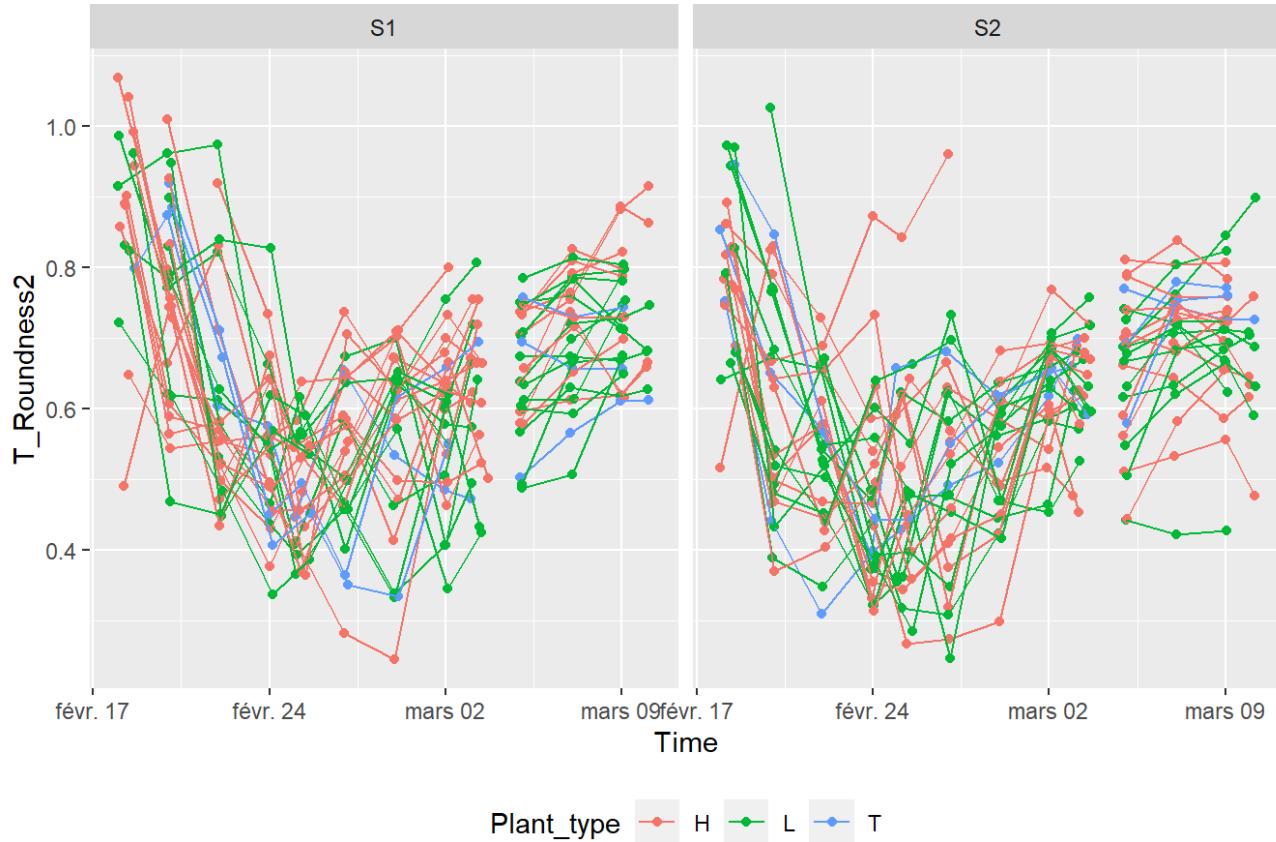
Smooth line of T_Roundness by Plant type and Soil



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
```

```
## Removed 22 rows containing missing values (`geom_line()`).
```

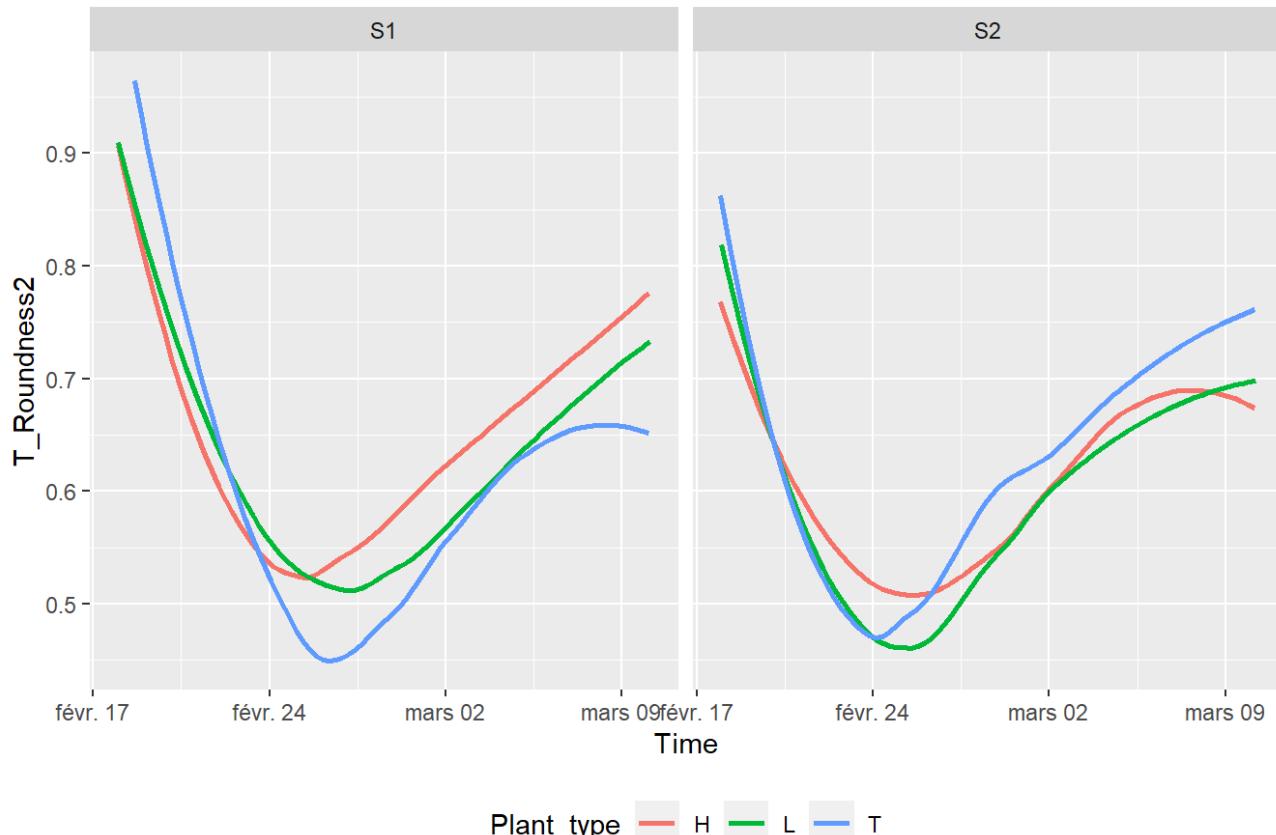
Scatterplot of T_Roundness2 by Plant type and Soil



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

```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

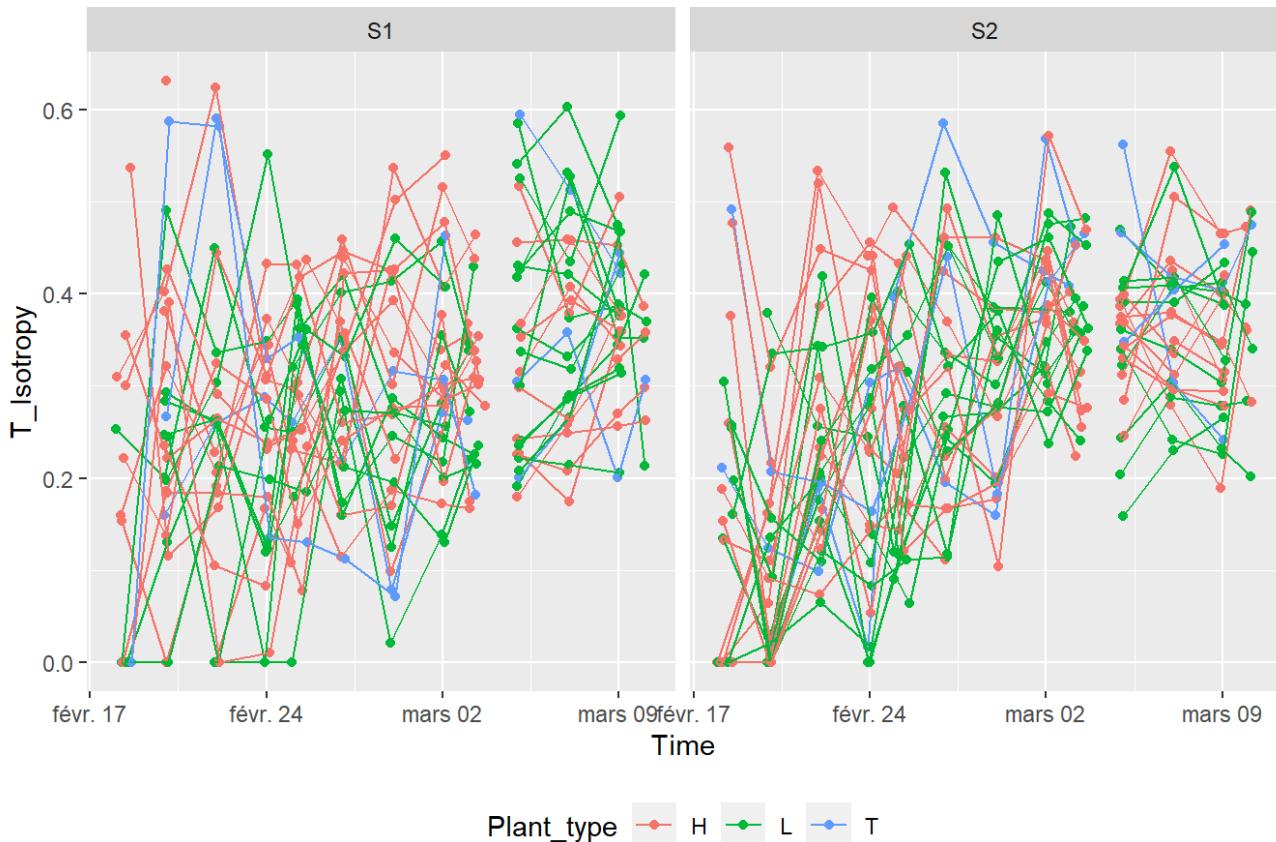
Smooth line of T_Roundness2 by Plant type and Soil



```
## Warning: Removed 27 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 26 rows containing missing values (`geom_line()`).
```

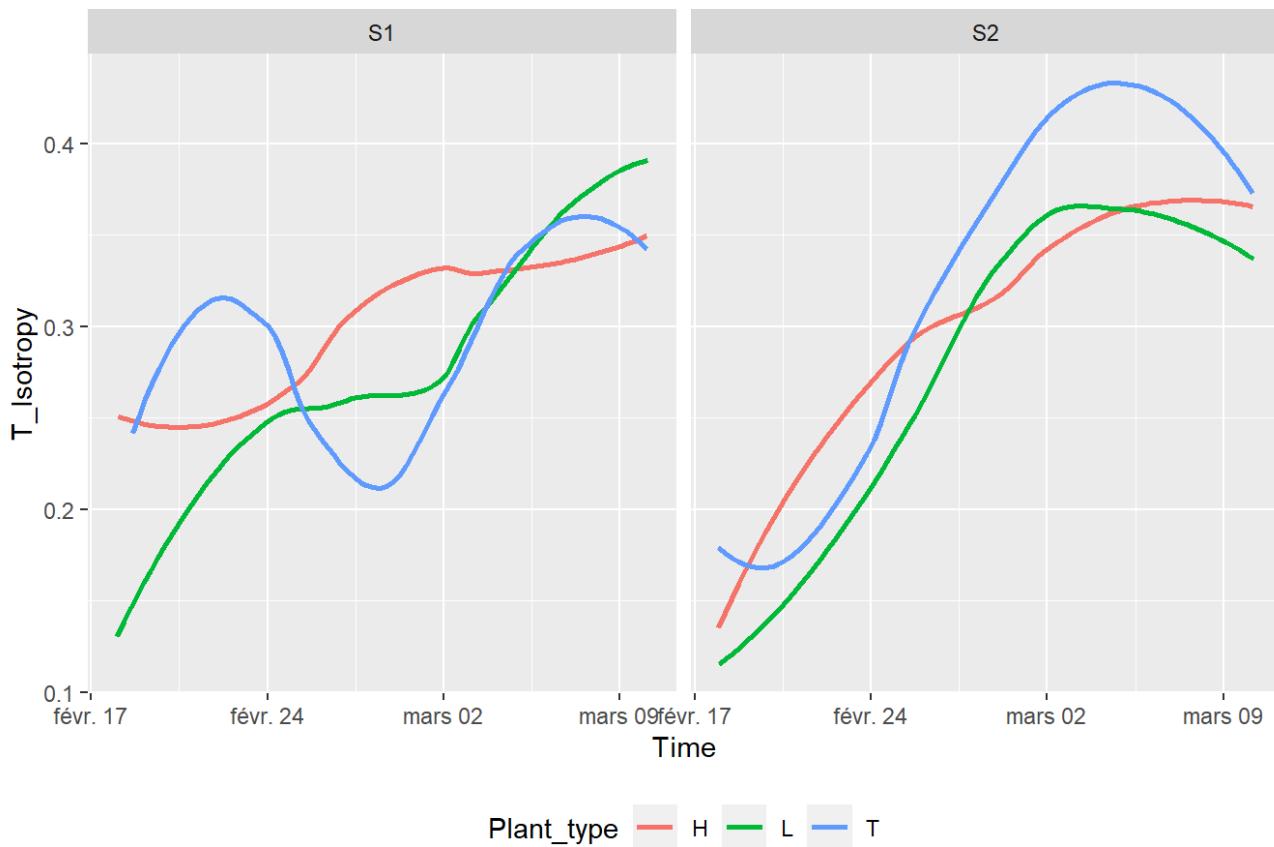
Scatterplot of T_Isotropy by Plant type and Soil



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

```
## Warning: Removed 27 rows containing non-finite values (`stat_smooth()`).
```

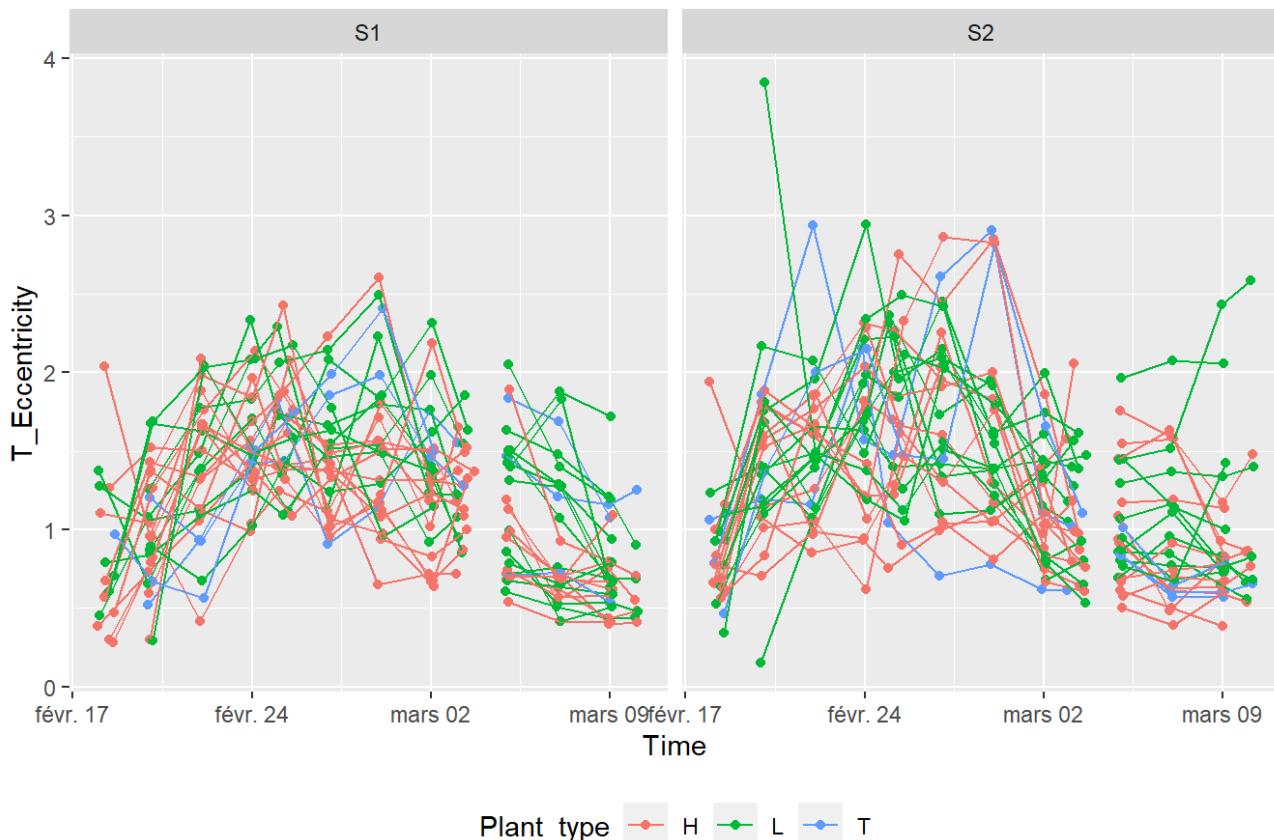
Smooth line of T_Isotropy by Plant type and Soil



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 22 rows containing missing values (`geom_line()`).
```

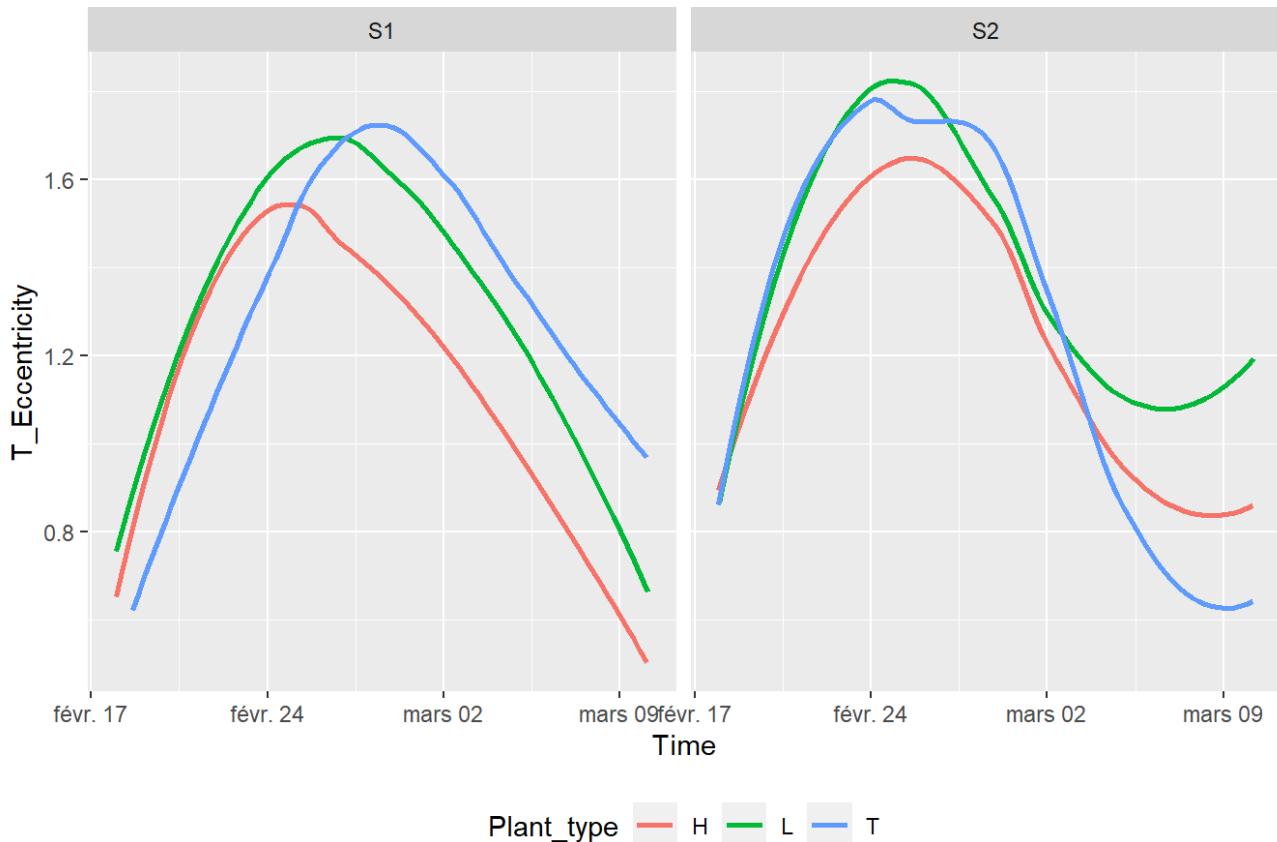
Scatterplot of T_Eccentricity by Plant type and Soil



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

```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

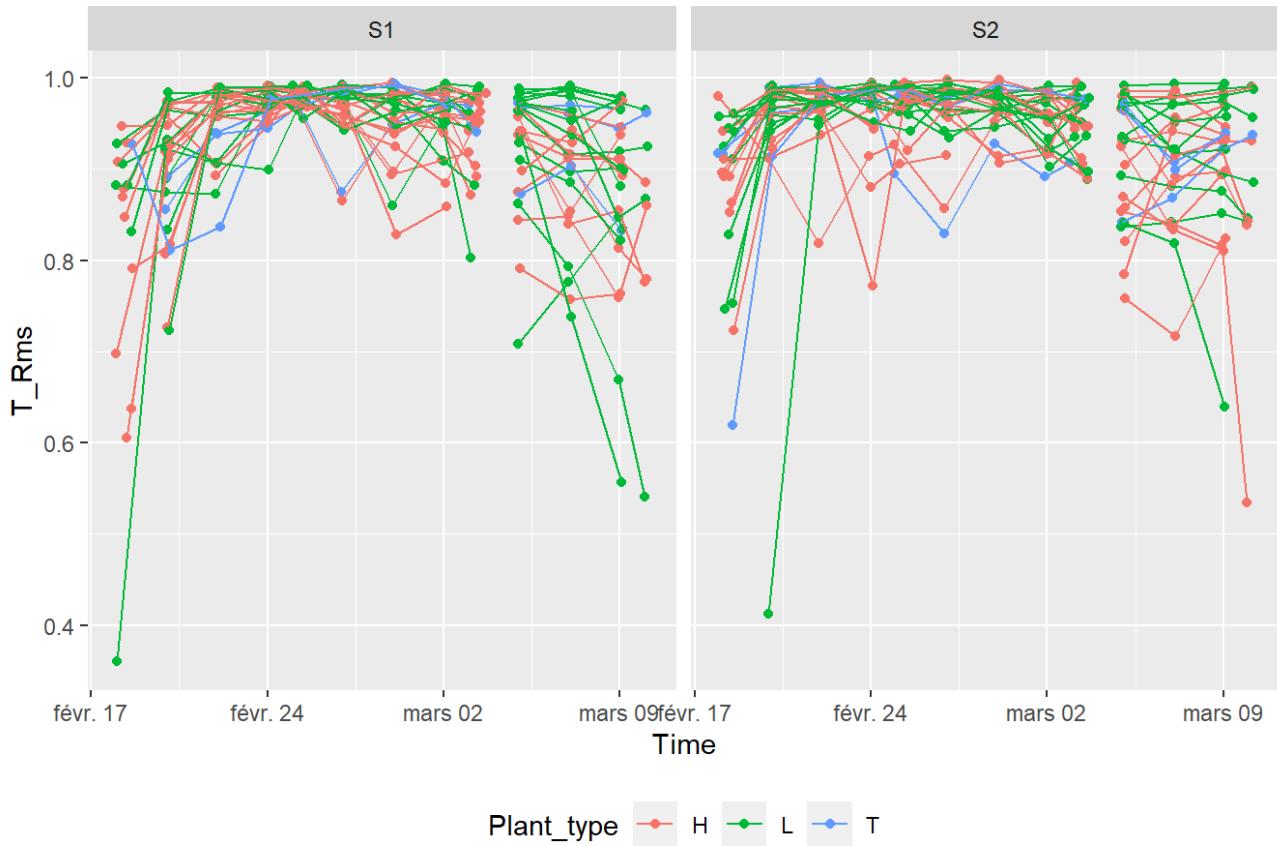
Smooth line of T_Eccentricity by Plant type and Soil



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
```

```
## Removed 22 rows containing missing values (`geom_line()`).
```

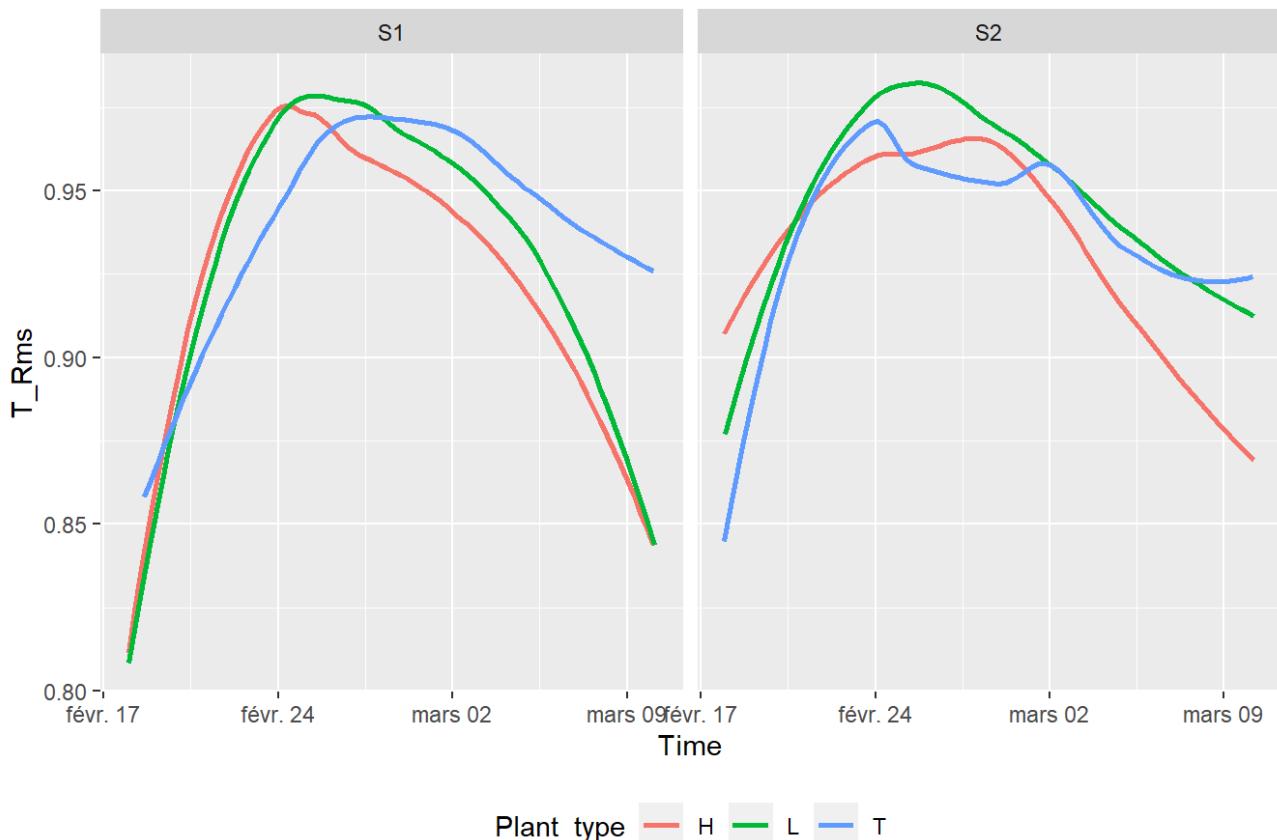
Scatterplot of T_Rms by Plant type and Soil



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

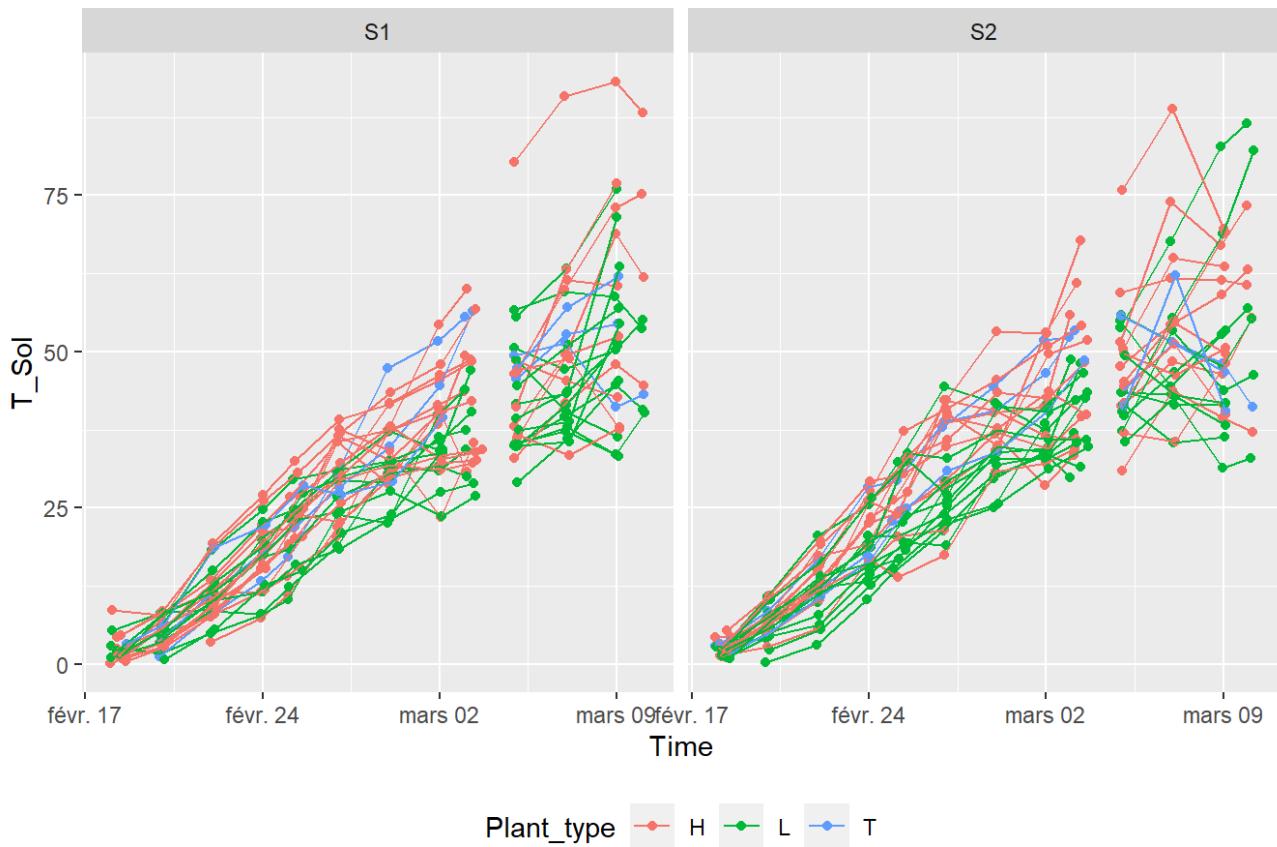
```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Rms by Plant type and Soil



```
## Warning: Removed 22 rows containing missing values (`geom_point()`).
## Removed 22 rows containing missing values (`geom_line()`).
```

Scatterplot of T_Sol by Plant type and Soil



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

```
## Warning: Removed 22 rows containing non-finite values (`stat_smooth()`).
```

Smooth line of T_Sol by Plant type and Soil

