M3P Data Preparation

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Set the right working directory.

```
setwd("C:/Users/elise/Documents/Mémoire/Main/Data/Drive/M3P")
```

Packages importation

1. Data importation

The first step in this data preparation process involves importing all the pertinent datasets listed in the Google Sheets “Variables template” document. Fist we find the files, then import them.

```
## [1] "env_multisensor.txt"    "img_extracted.txt"      "img_raw.txt"
## [4] "ISA_EPPN2020_M3P.xlsx"  "M3P.Rmd"                "M3P_Initial Code Draft"
## [7] "multisensor.txt"
```

We can extract the coordinates of each plant with the ISA_EPPN.xlsx dataset, using a made-up function “coordinates_isaTAB”.

```
# Get the coordinates
isaTAB <- read_excel("ISA_EPPN2020_M3P.xlsx", sheet = "s_exp")
```

```
## New names:
## • `Unit` -> `Unit...9`
## • `Term Source REF` -> `Term Source REF...10`
## • `Term Accession Number` -> `Term Accession Number...11`
## • `Unit` -> `Unit...13`
## • `Term Source REF` -> `Term Source REF...14`
## • `Term Accession Number` -> `Term Accession Number...15`
## • `Unit` -> `Unit...21`
## • `Term Source REF` -> `Term Source REF...22`
## • `Term Accession Number` -> `Term Accession Number...23`
## • `Unit` -> `Unit...25`
## • `Term Source REF` -> `Term Source REF...26`
## • `Term Accession Number` -> `Term Accession Number...27`
```

```
coordinates <- coordinates_isaTAB(isaTAB)
```

A. Datasets structures

We can take a quick look at all the datasets.

- coordinates
- data_pheno
- data_imaging
- data_environment

```
head(coordinates)
```

```
##                                             Sample.Name nrow ncol rep
## 1  0001/ZM4531/EPPN7_L/WD1/EPPN_Rep_1/01_01/ARCH2020-02-03    1    1   1
## 2 0002/ZM4534/EPPN10_L/WD1/EPPN_Rep_1/01_02/ARCH2020-02-03    1    2   1
## 3  0003/ZM4532/EPPN8_L/WD1/EPPN_Rep_1/01_03/ARCH2020-02-03    1    3   1
## 4  0004/ZM4527/EPPN3_L/WD1/EPPN_Rep_1/01_04/ARCH2020-02-03    1    4   1
## 5  0005/ZM4525/EPPN1_L/WD1/EPPN_Rep_1/01_05/ARCH2020-02-03    1    5   1
## 6  0006/ZM4526/EPPN2_L/WD1/EPPN_Rep_1/01_06/ARCH2020-02-03    1    6   1
```

```
head(data_pheno)
```

```
##                                                Unit.ID           Timestamp
## 1  0001/ZM4531/EPPN7_L/WD1/EPPN_Rep_1/01_01/ARCH2020-02-03 2020-02-11 13:33:08
## 2 0002/ZM4534/EPPN10_L/WD1/EPPN_Rep_1/01_02/ARCH2020-02-03 2020-02-11 13:33:31
## 3  0003/ZM4532/EPPN8_L/WD1/EPPN_Rep_1/01_03/ARCH2020-02-03 2020-02-11 13:33:44
## 4  0004/ZM4527/EPPN3_L/WD1/EPPN_Rep_1/01_04/ARCH2020-02-03 2020-02-11 13:34:01
## 5  0005/ZM4525/EPPN1_L/WD1/EPPN_Rep_1/01_05/ARCH2020-02-03 2020-02-11 13:34:24
## 6  0006/ZM4526/EPPN2_L/WD1/EPPN_Rep_1/01_06/ARCH2020-02-03 2020-02-11 13:35:48
##   Device.ID           variable.ID Value
## 1     User1 m3p:variable/pv000007     2
## 2     User1 m3p:variable/pv000007     2
## 3     User1 m3p:variable/pv000007     2
## 4     User1 m3p:variable/pv000007     1
## 5     User1 m3p:variable/pv000007     2
## 6     User1 m3p:variable/pv000007     2
```

```
head(data_imaging)
```

```
##                                                Unit.ID           Timestamp
## 1 0001/ZM4531/EPPN7_L/WD1/EPPN_Rep_1/01_01/ARCH2020-02-03 2020-02-14 17:29:17
## 2 0001/ZM4531/EPPN7_L/WD1/EPPN_Rep_1/01_01/ARCH2020-02-03 2020-02-15 16:42:29
## 3 0001/ZM4531/EPPN7_L/WD1/EPPN_Rep_1/01_01/ARCH2020-02-03 2020-02-16 16:28:43
## 4 0001/ZM4531/EPPN7_L/WD1/EPPN_Rep_1/01_01/ARCH2020-02-03 2020-02-17 18:26:42
## 5 0001/ZM4531/EPPN7_L/WD1/EPPN_Rep_1/01_01/ARCH2020-02-03 2020-02-18 17:53:42
## 6 0001/ZM4531/EPPN7_L/WD1/EPPN_Rep_1/01_01/ARCH2020-02-03 2020-02-19 11:47:34
##                Device.ID Estimated_PlantLeafArea Estimated_PlantBiomass
## 1 m3p:arch/2019/sa190020               15.048832           0.0000000000
## 2 m3p:arch/2019/sa190020                4.417823           0.0009568383
## 3 m3p:arch/2019/sa190020               81.417398           0.0000000000
## 4 m3p:arch/2019/sa190020                5.762199           0.0014552102
## 5 m3p:arch/2019/sa190020                6.291897           0.0015154682
## 6 m3p:arch/2019/sa190020                6.805034           0.0016275418
##   Estimated_PlantHeight
## 1              334.5375
## 2               64.6800
## 3             1796.2725
## 4               70.3725
## 5               75.4875
## 6               82.5000
```

```
head(data_environment)
```

```
##             Timestamp                  Unit.ID              Device.ID
## 1 2020-01-18 00:15:00 EPPN2020_JRA1.4_OBJ3_M3P m3p:arch/2011/sa110001
## 2 2020-01-18 00:30:00 EPPN2020_JRA1.4_OBJ3_M3P m3p:arch/2011/sa110001
## 3 2020-01-18 00:45:00 EPPN2020_JRA1.4_OBJ3_M3P m3p:arch/2011/sa110001
## 4 2020-01-18 01:00:00 EPPN2020_JRA1.4_OBJ3_M3P m3p:arch/2011/sa110001
## 5 2020-01-18 01:15:00 EPPN2020_JRA1.4_OBJ3_M3P m3p:arch/2011/sa110001
## 6 2020-01-18 01:30:00 EPPN2020_JRA1.4_OBJ3_M3P m3p:arch/2011/sa110001
##             Variable.ID Value
## 1 m3p:variable/ev000020  68.2
## 2 m3p:variable/ev000020  67.9
## 3 m3p:variable/ev000020  67.4
## 4 m3p:variable/ev000020  66.8
## 5 m3p:variable/ev000020  66.6
## 6 m3p:variable/ev000020  66.5
```

B. Data manipulation

This next step standardizes diverse datasets by renaming variables for consistency, converting data into appropriate units, adding necessary columns, and merging the datasets.

```
################################################################################
# COORDINATES
################################################################################
# Unit.ID
coordinates$Unit.ID <- seq_len(nrow(coordinates))
# Reference for Sample.Name et Unit.ID
reference <- coordinates[, c("Sample.Name", "Unit.ID")]
## We can then copy dataset2$Unit.ID <- reference$Unit.ID[match(dataset2$Sample.Name, r
eference$Sample.Name)]

# Genotype, soil
reference$Genotype <- isaTAB$`Source Name`
reference$Soil <- isaTAB$`Factor Value[WaterTreatment]`

################################################################################
# DATA_PHENO
################################################################################

# Time, Date and Timestamp
data_pheno$Timestamp <- as.POSIXct(data_pheno$Timestamp, format = "%Y-%m-%d %H:%M:%S")
data_pheno$Date <- as.Date(data_pheno$Timestamp, format = "%Y-%m-%d")
data_pheno$Time <- sapply(strsplit(as.character(data_pheno$Timestamp), split = " "),
'[', 2)

# Name of the platform
data_pheno$Platform <- "M3P"

# Unit.ID
data_pheno$Unit.ID2 <- reference$Unit.ID[match(data_pheno$Unit.ID, reference$Sample.Nam
e)]
data_pheno$Unit.ID <- data_pheno$Unit.ID2

# Variables
Leaf_number <- data_pheno[data_pheno$variable.ID == "m3p:variable/pv000005", ]
Ligulated_leaf_number <- data_pheno[data_pheno$variable.ID == "m3p:variable/pv000006",
]
Plant_emergence <- data_pheno[data_pheno$variable.ID == "m3p:variable/pv000007", ]
DW_plant_g <- data_pheno[data_pheno$variable.ID == "m3p:variable/pv000008", ]
DW_plant_g$Date <- as.Date("2020-04-19")
Plant_transpiration <- data_pheno[data_pheno$variable.ID == "m3p:variable/pv000009", ]
Daily_wu <- data_pheno[data_pheno$variable.ID == "m3p:variable/pv000010", ]
Total_wu <- data_pheno[data_pheno$variable.ID == "m3p:variable/pv000011", ]
Wue <- data_pheno[data_pheno$variable.ID == "m3p:variable/pv000012", ]
Soil_water_potential <- data_pheno[data_pheno$variable.ID == "m3p:variable/pv000013", ]

################################################################################
# DATA_IMAGING
################################################################################
# Time, Date and Timestamp
data_imaging$Timestamp <- as.POSIXct(data_imaging$Timestamp, format = "%Y-%m-%d %H:%M:%
S")
data_imaging$Date <- as.Date(data_imaging$Timestamp, format = "%Y-%m-%d")
data_imaging$Time <- sapply(strsplit(as.character(data_imaging$Timestamp), split = "
"), '[', 2)
```

```
# Name of the platform
data_imaging$Platform <- "M3P"

# Unit.ID
data_imaging$Unit.ID <- reference$Unit.ID[match(data_imaging$Unit.ID, reference$Sample.
Name)]

# Rename the columns for the template
data_imaging <- rename(data_imaging,
                       S_Height_cm = Estimated_PlantHeight,
                       S_Leaf_area_cm_squared = Estimated_PlantLeafArea,
                       Plant_biomass_g = Estimated_PlantBiomass
                       )
```

2. Data template

A. Data template: plant_info

This dataset contains information about the plant: Unit.ID, genotype, replication, row and column location in the greenhouse, and soil treatment.

B. Data template: endpoint

This datasets contains information of the end of the experiment (variables at harvest). It is then linked by the Unit.ID to the plant_info data template.

C. Data template: timeseries

This section in divided in three data templates:

- timeseries
- S_timeseries (variables computed from sideview imaging or image processing)
- T_timeseries (variables computed from topview imaging or image processing)

The time interval between data timestamps varies in each platform. They are then linked by the Unit.ID to the plant_info data template.

```
# Remove the unknown genotypes
endpoint <- endpoint %>%
  filter(!Genotype %in% c("DZPG91", "DZPG72", "DZPG", "DZPG23", "DZPG100", "DZPG93", "D
ZPG999", "DZPG96"))

timeseries <- timeseries %>%
  filter(!Genotype %in% c("DZPG91", "DZPG72", "DZPG", "DZPG23", "DZPG100", "DZPG93", "D
ZPG999", "DZPG96"))

timeseries_Leaf_number <- timeseries_Leaf_number %>%
  filter(!Genotype %in% c("DZPG91", "DZPG72", "DZPG", "DZPG23", "DZPG100", "DZPG93", "D
ZPG999", "DZPG96"))

timeseries_Ligulated_leaf_number <- timeseries_Ligulated_leaf_number %>%
  filter(!Genotype %in% c("DZPG91", "DZPG72", "DZPG", "DZPG23", "DZPG100", "DZPG93", "D
ZPG999", "DZPG96"))

timeseries_Plant_emergence <- timeseries_Plant_emergence %>%
  filter(!Genotype %in% c("DZPG91", "DZPG72", "DZPG", "DZPG23", "DZPG100", "DZPG93", "D
ZPG999", "DZPG96"))

timeseries_Plant_transpiration <- timeseries_Plant_transpiration %>%
  filter(!Genotype %in% c("DZPG91", "DZPG72", "DZPG", "DZPG23", "DZPG100", "DZPG93", "D
ZPG999", "DZPG96"))

timeseries_Soil_water_potential <- timeseries_Soil_water_potential %>%
  filter(!Genotype %in% c("DZPG91", "DZPG72", "DZPG", "DZPG23", "DZPG100", "DZPG93", "D
ZPG999", "DZPG96"))

timeseries_Water <- timeseries_Water %>%
  filter(!Genotype %in% c("DZPG91", "DZPG72", "DZPG", "DZPG23", "DZPG100", "DZPG93", "D
ZPG999", "DZPG96"))

S_timeseries <- S_timeseries %>%
  filter(!Genotype %in% c("DZPG91", "DZPG72", "DZPG", "DZPG23", "DZPG100", "DZPG93", "D
ZPG999", "DZPG96"))
```

D. M3P data templates

- plant_info
- endpoint
- timeseries
- timeseries_Leaf_number, timeseries_Ligulated_leaf_number, timeseries_Plant_emergence, timeseries_Plant_transpiration, timeseries_Soil_water_potential, timeseries_Water
- S_timeseries
- T_timeseries

```
##   Unit.ID Genotype Soil Replication Row Column Platform
## 1       1  EPPN7_L  WD1           1   1      1      M3P
## 2       2 EPPN10_L  WD1           1   1      2      M3P
## 3       3  EPPN8_L  WD1           1   1      3      M3P
## 4       4  EPPN3_L  WD1           1   1      4      M3P
## 5       5  EPPN1_L  WD1           1   1      5      M3P
## 6       6  EPPN2_L  WD1           1   1      6      M3P
```

```
##   Unit.ID Time       Date Timestamp DW_shoot_g FW_shoot_g DW_root_g FW_root_g
## 1       1   NA 2020-04-19        NA         NA         NA        NA         NA
## 2       2   NA 2020-04-19        NA         NA         NA        NA         NA
## 3       3   NA 2020-04-19        NA         NA         NA        NA         NA
## 4       4   NA 2020-04-19        NA         NA         NA        NA         NA
## 5       5   NA 2020-04-19        NA         NA         NA        NA         NA
## 6       6   NA 2020-04-19        NA         NA         NA        NA         NA
##   Leaf_number Plant_height_cm DW_plant_g Root_length_cm Root_number Root_angle
## 1          NA              NA        113             NA          NA         NA
## 2          NA              NA        231             NA          NA         NA
## 3          NA              NA        156             NA          NA         NA
## 4          NA              NA        150             NA          NA         NA
## 5          NA              NA        138             NA          NA         NA
## 6          NA              NA         96             NA          NA         NA
##   Total_wu DW_seed_g FW_seed_g Leaf_area_cmsquared Genotype Soil Replication
## 1       NA        NA        NA                  NA  EPPN7_L  WD1           1
## 2       NA        NA        NA                  NA EPPN10_L  WD1           1
## 3       NA        NA        NA                  NA  EPPN8_L  WD1           1
## 4       NA        NA        NA                  NA  EPPN3_L  WD1           1
## 5       NA        NA        NA                  NA  EPPN1_L  WD1           1
## 6       NA        NA        NA                  NA  EPPN2_L  WD1           1
##   Row Column Platform
## 1   1      1      M3P
## 2   1      2      M3P
## 3   1      3      M3P
## 4   1      4      M3P
## 5   1      5      M3P
## 6   1      6      M3P
```

```
##   Unit.ID     Time       Date           Timestamp Manual_Plant_height_cm
## 1       1 17:29:17 2020-02-14 2020-02-14 17:29:17                     NA
## 2       1 16:42:29 2020-02-15 2020-02-15 16:42:29                     NA
## 3       1 16:28:43 2020-02-16 2020-02-16 16:28:43                     NA
## 4       1 18:26:42 2020-02-17 2020-02-17 18:26:42                     NA
## 5       1 17:53:42 2020-02-18 2020-02-18 17:53:42                     NA
## 6       1 11:47:34 2020-02-19 2020-02-19 11:47:34                     NA
##   Leaf_number Wue Plant_biomass_g Ligulated_leaf_number Plant_emergence
## 1          NA  NA    0.0000000000                    NA              NA
## 2          NA  NA    0.0009568383                    NA              NA
## 3          NA  NA    0.0000000000                    NA              NA
## 4          NA  NA    0.0014552102                    NA              NA
## 5          NA  NA    0.0015154682                    NA              NA
## 6          NA  NA    0.0016275418                    NA              NA
##   Plant_transpiration Daily_wu Soil_water_potential Genotype Soil Replication
## 1                  NA       NA                   NA  EPPN7_L  WD1           1
## 2                  NA       NA                   NA  EPPN7_L  WD1           1
## 3                  NA       NA                   NA  EPPN7_L  WD1           1
## 4                  NA       NA                   NA  EPPN7_L  WD1           1
## 5                  NA       NA                   NA  EPPN7_L  WD1           1
## 6                  NA       NA                   NA  EPPN7_L  WD1           1
##   Row Column Platform
## 1   1      1      M3P
## 2   1      1      M3P
## 3   1      1      M3P
## 4   1      1      M3P
## 5   1      1      M3P
## 6   1      1      M3P
```

```
##   Unit.ID     Time       Date           Timestamp Ligulated_leaf_number
## 1       1 14:02:01 2020-02-18 2020-02-18 14:02:01                     1
## 2       2 14:02:16 2020-02-18 2020-02-18 14:02:16                     1
## 3       3 14:03:10 2020-02-18 2020-02-18 14:03:10                     1
## 4       4 14:03:19 2020-02-18 2020-02-18 14:03:19                     1
## 5       5 14:03:31 2020-02-18 2020-02-18 14:03:31                     1
## 6       6 14:03:40 2020-02-18 2020-02-18 14:03:40                     1
##   Genotype Soil Replication Row Column Platform
## 1  EPPN7_L  WD1           1   1      1      M3P
## 2 EPPN10_L  WD1           1   1      2      M3P
## 3  EPPN8_L  WD1           1   1      3      M3P
## 4  EPPN3_L  WD1           1   1      4      M3P
## 5  EPPN1_L  WD1           1   1      5      M3P
## 6  EPPN2_L  WD1           1   1      6      M3P
```

```
##   Unit.ID     Time       Date           Timestamp Leaf_number Genotype Soil
## 1       1 13:42:21 2020-02-14 2020-02-14 13:42:21           2  EPPN7_L  WD1
## 2       2 15:46:42 2020-02-14 2020-02-14 15:46:42           2 EPPN10_L  WD1
## 3       3 15:46:55 2020-02-14 2020-02-14 15:46:55           3  EPPN8_L  WD1
## 4       4 15:47:02 2020-02-14 2020-02-14 15:47:02           2  EPPN3_L  WD1
## 5       5 15:47:15 2020-02-14 2020-02-14 15:47:15           3  EPPN1_L  WD1
## 6       6 15:47:26 2020-02-14 2020-02-14 15:47:26           2  EPPN2_L  WD1
##   Replication Row Column Platform
## 1           1   1      1      M3P
## 2           1   1      2      M3P
## 3           1   1      3      M3P
## 4           1   1      4      M3P
## 5           1   1      5      M3P
## 6           1   1      6      M3P
```

```
##   Unit.ID     Time       Date           Timestamp Plant_emergence Genotype Soil
## 1       1 13:33:08 2020-02-11 2020-02-11 13:33:08               2  EPPN7_L  WD1
## 2       2 13:33:31 2020-02-11 2020-02-11 13:33:31               2 EPPN10_L  WD1
## 3       3 13:33:44 2020-02-11 2020-02-11 13:33:44               2  EPPN8_L  WD1
## 4       4 13:34:01 2020-02-11 2020-02-11 13:34:01               1  EPPN3_L  WD1
## 5       5 13:34:24 2020-02-11 2020-02-11 13:34:24               2  EPPN1_L  WD1
## 6       6 13:35:48 2020-02-11 2020-02-11 13:35:48               2  EPPN2_L  WD1
##   Replication Row Column Platform
## 1           1   1      1      M3P
## 2           1   1      2      M3P
## 3           1   1      3      M3P
## 4           1   1      4      M3P
## 5           1   1      5      M3P
## 6           1   1      6      M3P
```

```
##   Unit.ID     Time       Date           Timestamp Plant_transpiration Genotype
## 1       1 15:23:07 2020-01-24 2020-01-24 15:23:07            6.866636  EPPN7_L
## 2       1 07:49:17 2020-01-31 2020-01-31 07:49:17           20.001392  EPPN7_L
## 3       1 10:41:40 2020-02-02 2020-02-02 10:41:40           18.512016  EPPN7_L
## 4       1 12:05:41 2020-02-08 2020-02-08 12:05:41          142.663045  EPPN7_L
## 5       1 17:13:36 2020-02-09 2020-02-09 17:13:36          110.346602  EPPN7_L
## 6       1 15:53:35 2020-02-10 2020-02-10 15:53:35          110.069825  EPPN7_L
##   Soil Replication Row Column Platform
## 1  WD1           1   1      1      M3P
## 2  WD1           1   1      1      M3P
## 3  WD1           1   1      1      M3P
## 4  WD1           1   1      1      M3P
## 5  WD1           1   1      1      M3P
## 6  WD1           1   1      1      M3P
```

```
##   Unit.ID     Time       Date           Timestamp Soil_water_potential Genotype
## 1       1 13:29:01 2020-02-03 2020-02-03 13:29:01          -0.03812094  EPPN7_L
## 2       2 13:28:55 2020-02-03 2020-02-03 13:28:55          -0.03884573 EPPN10_L
## 3       3 13:29:18 2020-02-03 2020-02-03 13:29:18          -0.03746740  EPPN8_L
## 4       4 13:29:10 2020-02-03 2020-02-03 13:29:10          -0.03346333  EPPN3_L
## 5       5 13:29:33 2020-02-03 2020-02-03 13:29:33          -0.03862930  EPPN1_L
## 6       6 13:29:26 2020-02-03 2020-02-03 13:29:26          -0.03564079  EPPN2_L
##   Soil Replication Row Column Platform
## 1  WD1           1   1      1      M3P
## 2  WD1           1   1      2      M3P
## 3  WD1           1   1      3      M3P
## 4  WD1           1   1      4      M3P
## 5  WD1           1   1      5      M3P
## 6  WD1           1   1      6      M3P
```

```
##   Unit.ID Time       Date Timestamp       Wue Daily_wu Total_wu Genotype Soil
## 1       1   NA 2020-01-23        NA  74.88403       26     1509  EPPN7_L  WD1
## 2       2   NA 2020-01-23        NA 115.09716       34     2007 EPPN10_L  WD1
## 3       3   NA 2020-01-23        NA  87.44395       28     1784  EPPN8_L  WD1
## 4       4   NA 2020-01-23        NA  87.10801       31     1722  EPPN3_L  WD1
## 5       5   NA 2020-01-23        NA  69.62664       34     1982  EPPN1_L  WD1
## 6       1   NA 2020-01-30        NA  74.88403       90     1509  EPPN7_L  WD1
##   Replication Row Column Platform
## 1           1   1      1      M3P
## 2           1   1      2      M3P
## 3           1   1      3      M3P
## 4           1   1      4      M3P
## 5           1   1      5      M3P
## 6           1   1      1      M3P
```

```
##   Unit.ID           Timestamp       Date     Time S_Height_cm S_Height_pixel
## 1       1 2020-02-14 17:29:17 2020-02-14 17:29:17    334.5375             NA
## 2       1 2020-02-15 16:42:29 2020-02-15 16:42:29     64.6800             NA
## 3       1 2020-02-16 16:28:43 2020-02-16 16:28:43   1796.2725             NA
## 4       1 2020-02-17 18:26:42 2020-02-17 18:26:42     70.3725             NA
## 5       1 2020-02-18 17:53:42 2020-02-18 17:53:42     75.4875             NA
## 6       1 2020-02-19 11:47:34 2020-02-19 11:47:34     82.5000             NA
##   S_Area_cmsquared S_Area_pixel S_Perimeter_cm S_Perimeter_pixel
## 1               NA           NA             NA                NA
## 2               NA           NA             NA                NA
## 3               NA           NA             NA                NA
## 4               NA           NA             NA                NA
## 5               NA           NA             NA                NA
## 6               NA           NA             NA                NA
##   S_Convex_hull_area_cmsquared S_Solidity S_Compactness S_Width_cm
## 1                           NA         NA            NA         NA
## 2                           NA         NA            NA         NA
## 3                           NA         NA            NA         NA
## 4                           NA         NA            NA         NA
## 5                           NA         NA            NA         NA
## 6                           NA         NA            NA         NA
##   S_Width_pixel S_Leaf_area_cmsquared Genotype Soil Replication Row Column
## 1            NA             15.048832  EPPN7_L  WD1           1   1      1
## 2            NA              4.417823  EPPN7_L  WD1           1   1      1
## 3            NA             81.417398  EPPN7_L  WD1           1   1      1
## 4            NA              5.762199  EPPN7_L  WD1           1   1      1
## 5            NA              6.291897  EPPN7_L  WD1           1   1      1
## 6            NA              6.805034  EPPN7_L  WD1           1   1      1
##   Platform
## 1      M3P
## 2      M3P
## 3      M3P
## 4      M3P
## 5      M3P
## 6      M3P
```

```
##   Unit.ID Time Date Timestamp T_Area_cm_squared T_Area_pixel T_Perimeter_cm
## 1    <NA>   NA   NA        NA                NA           NA             NA
##   T_Perimeter_pixel T_Convex_hull_area_cmsquared T_Solidity T_Compactness
## 1                NA                           NA         NA            NA
##   T_Roundness T_Roundness2 T_Isotropy T_Eccentricity T_Rms T_Sol Genotype Soil
## 1          NA           NA         NA             NA    NA    NA     <NA> <NA>
##   Replication  Row Column Platform
## 1        <NA> <NA>   <NA>     <NA>
```

3. Export the data templates in .txt

Stock the new data sets in a new folder.

```
setwd("C:/Users/elise/Documents/Mémoire/Main/Data/Templates/M3P")

write.table(plant_info, file = "plant_info.txt", sep = "\t", row.names = FALSE, quote =
FALSE)
write.table(endpoint, file = "endpoint.txt", sep = "\t", row.names = FALSE, quote = FAL
SE)
write.table(timeseries, file = "timeseries.txt", sep = "\t", row.names = FALSE, quote =
FALSE)

write.table(timeseries_Leaf_number, file = "timeseries_Leaf_number.txt", sep = "\t", ro
w.names = FALSE, quote = FALSE)
write.table(timeseries_Ligulated_leaf_number, file = "timeseries_Ligulated_leaf_number.
txt", sep = "\t", row.names = FALSE, quote = FALSE)
write.table(timeseries_Plant_emergence, file = "timeseries_Plant_emergence.txt", sep =
"\t", row.names = FALSE, quote = FALSE)
write.table(timeseries_Plant_transpiration, file = "timeseries_Plant_transpiration.tx
t", sep = "\t", row.names = FALSE, quote = FALSE)
write.table(timeseries_Soil_water_potential, file = "timeseries_Soil_water_potential.tx
t", sep = "\t", row.names = FALSE, quote = FALSE)
write.table(timeseries_Water, file = "timeseries_Water.txt", sep = "\t", row.names = FA
LSE, quote = FALSE)

write.table(S_timeseries, file = "S_timeseries.txt", sep = "\t", row.names = FALSE, quo
te = FALSE)
write.table(T_timeseries, file = "T_timeseries.txt", sep = "\t", row.names = FALSE, quo
te = FALSE)
```