- Input Files required:
    1. Loadcells
    2. Loadcells metadata
    3. Sensor climate data
    4. Sensor unit map
    5. Plant eye
- Merge all the data files into R data by executing the script **createExpData.R**
- Create folder: **results**, and within that 2 sub-folders;
  rawFeaturesTimeSeries and **smthFeaturesTimeSeries**
- Run the pipeline script **EZTr_main.R** by considering the following **experiment-specific changes:**

  ⇨ L 35. load("./data/**HTP_data_Exp41_PM**.RData")

  ⇨ L 36. allData <- **HTP_data_Exp41_PM**

  ⇨ L 38. LastDate="2020-01-28"

  ⇨ L 39. irrg.dts <- c("2019-12-28", "2019-12-30", "2020-01-02", "2020-01-04", "2020-01-06",
      "2020-01-08", "2020-01-10", "2020-01-11", "2020-01-13", "2020-01-14",
      "2020-01-16", "2020-01-17", "2020-01-18", "2020-01-20", "2020-01-22",
      "2020-01-23", "2020-01-25", "2020-01-27")

  ⇨ L 43. Date1="2019-12-27 23:46:00"

  ⇨ L 44. Date2="2020-01-28 23:45:00"

  ⇨ L 45. opPATH <- "./results/Exp41-PM-NOirrg/"

  ⇨ L 46. opPATH.smth="D:/EZTr-master/results/Exp41-PM-NOirrg/smthFeaturesTimeSeries/"

  ⇨ L 47. opPATH.raw="D:/EZTr-master/results/Exp41-PM-NOirrg/rawFeaturesTimeSeries/"

  ⇨ In **functions**,

  extractRawLCmatrix: L 10. m.lc.df$ts <- **dmy_hm(m.lc.df$timestamp)**

  calculateTr: L 38. LAI.mat[i,] <- **((((sec.lai.tmp/100))/0.36)***(1/0.26)/10000)

  ⇨ L 62. meta.d.sp <- meta.d[meta.d$Species==species.nm[**1**],]

  ⇨ L 92. meta.d.LCmat <- meta.d.sp[meta.d.sp$unit %in% colnames(LC.MAT.f)[-1], **c(1,2,6,7,8)]**

  (# "unit", "old_unit", "Genotype, "G..Alias", "Replicates" #)

  Based on **unq.clm.var,** *assign* **x**

  # [1] "Temperature (Â°C)" [2] "Relative humidity (%)" [3] "Windspeed average (m/s)" [4]
  *"Windspeed max (m/s)" [5] "Solar radiation (W/(s*mÂ²))" [6] "Precipitation (mm)"*
  [7] "Wind direction (Â°)"

  ⇨ L 175. **temperature**.DF <- extractWthrVar(**x = 1**, y = clm.df.mapped)

  ⇨ L 176. temperature.DF$ts <- temperature.DF$ts **+ 5.5*60*60**

  ⇨ L 178. **relHUM**.DF <- extractWthrVar(**x = 2**, y = clm.df.mapped)

  ⇨ L 179. relHUM.DF$ts <- relHUM.DF$ts **+ 5.5*60*60**

  ⇨ L 181. **windS**.DF <- extractWthrVar(**x = 3**, y = clm.df.mapped)

  ⇨ L 182. windS.DF$ts <- windS.DF$ts **+ 5.5*60*60**

  ⇨ L 184. **solarRad**.DF <- extractWthrVar(**x = 5**, y = clm.df.mapped)

  ⇨ L 185. solarRad.DF$ts <- solarRad.DF$ts **+ 5.5*60*60**

  ⇨ L 443. pe.df.ETr <- pe.df.ETr[, **c(1, 5, 7, 12, 17, 18)]**

  (# columns: "Sector", "Genotype", "Replicates", "LeafArea3D", "TS", "date" #)