Phenoarch platform - Cleaning procedure - Curve level - gss package

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Objective of cleaning procedure using smoothing splines anova

Smoothing spline analysis of variance on each genotype-scenario of an experiment. Detection of outlier repetition if significant TT*Rep (thermal time by repetition) interaction using a Kullblack-Leibler projection (KL). I consider a genotype-scenario as outlier:

- biovolume: if KL $>$ 0.05
- plantHeight: if KL $>$ 0.05
- leafArea: if KL $>$ 0.05

The input dataset must contain the following columns:

- experimentAlias
- genotypeAlias
- scenario
- repetition
- thermalTime (for thermal time)
- parameter of interest (biovolume, plantHeight etc...)

The five first column names are standard names extracted from the web service.

Import of data

```
library(ggplot2)
library(lubridate)
library(tidyr)
library(dplyr)
library(gss)
library(openSilexStatR)

myreport<-substr(now(),1,10)
```

```
data(plant3)
cat("-------------- plant3 dataset ---------------\n")
```

```
## -------------- plant3 dataset ---------------
```

```
printExperiment(datain=plant3)
```

```
## Experiment: manip3
```

```
## Genotypes: 10
##  [1] "A3_H"     "A310_H"   "11430_H"  "A554_H"   "A374_H"   "A347_H"
##  [7] "B100_H"   "A375_H"   "AS5707_H" "A347"
## Scenario: 2
## [1] "WW" "WD"
## Repetition-scenario: 6
## [1] "1-WW" "2-WW" "3-WW" "1-WD" "2-WD" "3-WD"
## Pots (number of plants): 60
## Line: 25
## Position: 42
```

```
  # Import data, here is a dataset in the phisStatR package, You have to import your own dataset
  # using a read.table() statement or a request to the web service
  # You can add some datamanagement statements...
  #-------------------------------------------------------------------------
  # Please, add the 'Ref' and 'Genosce' columns if don't exist.
  # 'Ref' is the concatenation of experimentAlias-Line-Position-scenario
  # 'Genosce' is the concatenation of experimentAlias-genotypeAlias-scenario
  #-------------------------------------------------------------------------

  mydata<-unite(plant3,Genosce,experimentAlias,genotypeAlias,scenario,
                sep="-",remove=FALSE)
  mydata<-arrange(mydata,Genosce)
```

```
  # For one parameter, for example biovolume
  resbio<-fitGSS(datain=mydata,trait="biovolume",loopId="Genosce")
```

Curves by genotype-scenario

Biovolume

```
  outlierbio<-printGSS(object=resbio,threshold = 0.05)
  klbio<-printGSS(object=resbio,threshold = NULL)

  cat("Detection of outlier curve with KL projection:\n")
```

```
## Detection of outlier curve with KL projection:
```

```
  print(outlierbio)
```

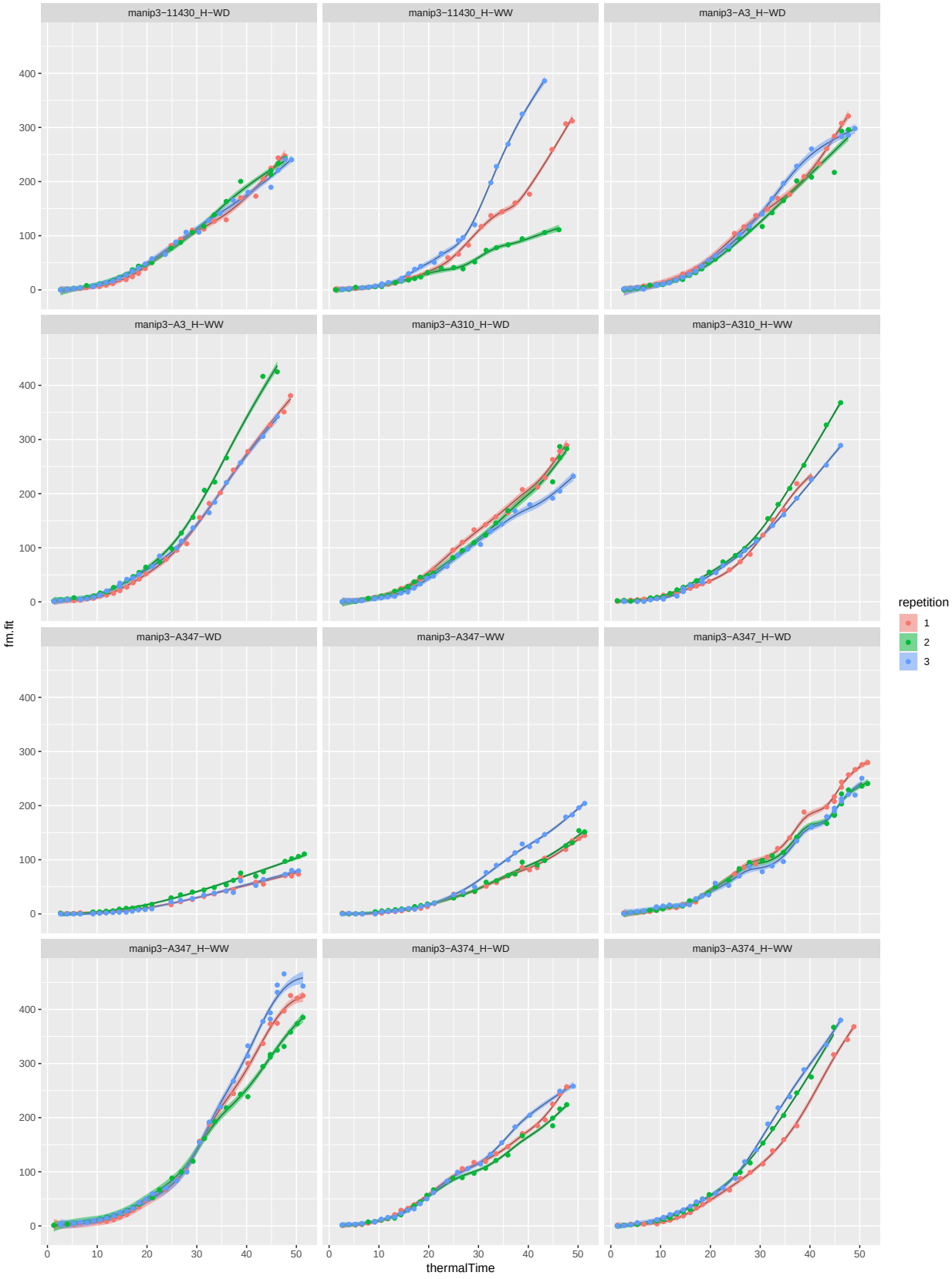
```
##              Genosce      ratio        kl     check
## 1  manip3-11430_H-WW 0.15015910 1175.7782 0.9999887
## 2 manip3-AS5707_H-WD 0.07205993  633.0729 0.9999874
```

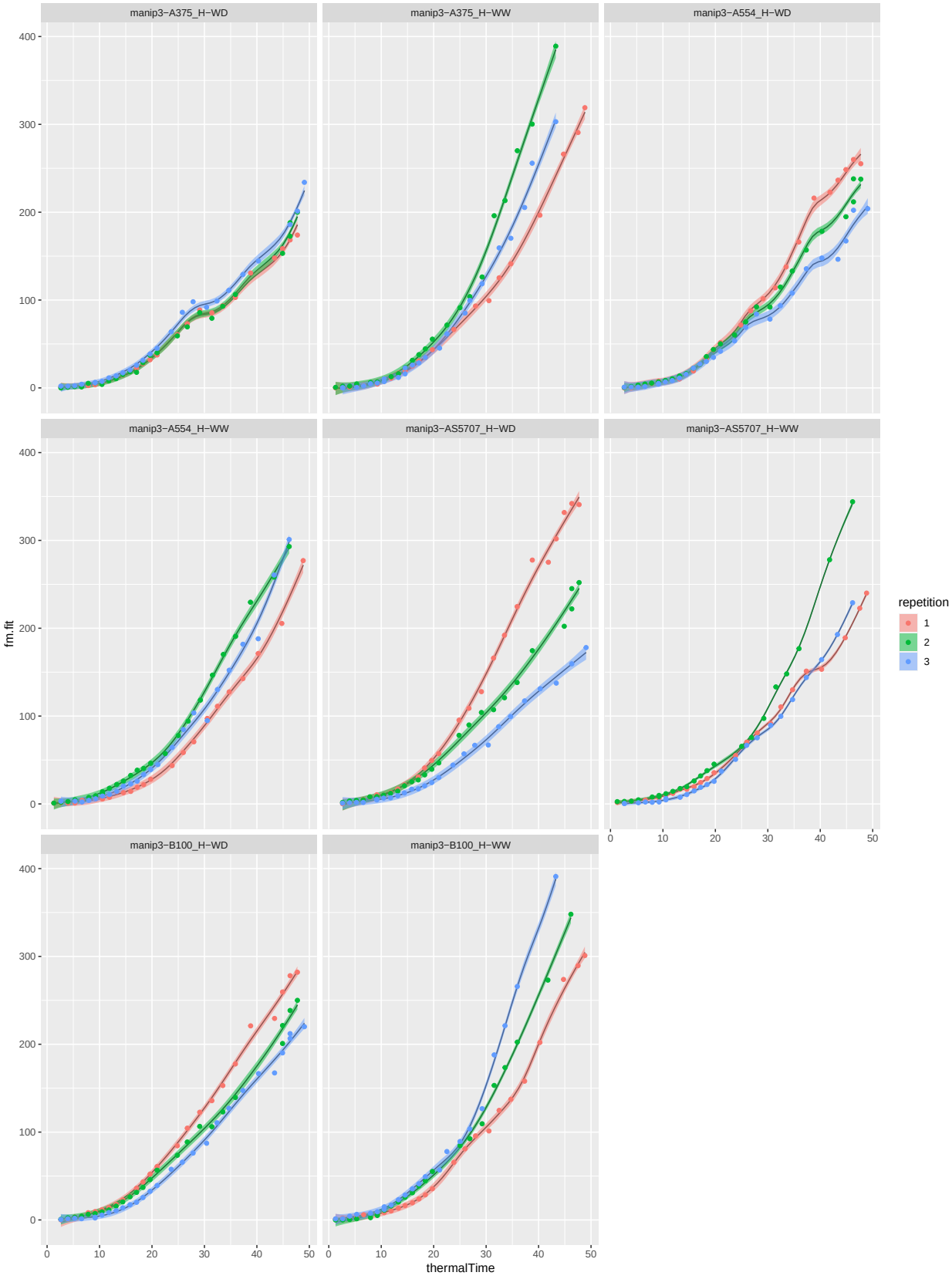
```
  #-------------------------------------------------
  # You can export these two datasets
  # suppress the comments
  #-------------------------------------------------
  #write.table(outlierbio,paste0(myreport,"outlier_gss_biovolume.csv"),
  #   row.names = FALSE,sep="\t")
  #write.table(klbio,paste0(myreport,"KLprojection_gss_biovolume.csv"),
  #   row.names = FALSE,sep="\t")
```

I take a threshold of 0.05 for this example. We can take a more conservative threshold like 0.01 or 0.02 to

detect more outlier curves...

```
# plot of the smoothing splines by genotype-scenario
for(i in seq(1,length(unique(mydata[,"Genosce"])),by=12)){
  myvec<-seq(i,i+11,1)
  myvec<-myvec[myvec<=length(unique(mydata[,"Genosce"]))]
  print(plotGSS(datain=mydata,modelin=resbio[[1]],trait="biovolume",
                myvec=myvec,lgrid=50))
  cat("\n\n")
}
```


manip3−11430_H−WD
manip3−11430_H−WW
manip3−A3_H−WD
manip3−A3_H−WW
manip3−A310_H−WD
manip3−A310_H−WW
manip3−A347−WD
manip3−A347−WW
manip3−A347_H−WD
manip3−A347_H−WW
manip3−A374_H−WD
manip3−A374_H−WW
fm.fit
thermalTime
repetition
1
2
3


manip3−A375_H−WD
manip3−A375_H−WW
manip3−A554_H−WD
manip3−A554_H−WW
manip3−AS5707_H−WD
manip3−AS5707_H−WW
manip3−B100_H−WD
manip3−B100_H−WW
fm.fit
thermalTime
repetition
1
2
3

Session info

```
## R version 4.0.2 (2020-06-22)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 18363)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=French_France.1252  LC_CTYPE=French_France.1252
## [3] LC_MONETARY=French_France.1252 LC_NUMERIC=C
## [5] LC_TIME=French_France.1252
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] gss_2.2-2            locfit_1.5-9.4       ggplot2_3.3.2
## [4] tidyr_1.1.0          openSilexStatR_1.1.0 dplyr_1.0.0
## [7] lubridate_1.7.9
##
## loaded via a namespace (and not attached):
##   [1] colorspace_1.4-1   deldir_0.1-28      ellipsis_0.3.1
##   [4] class_7.3-17       leaflet_2.0.3      rgdal_1.5-12
##   [7] evd_2.3-3          rprojroot_1.3-2    fs_1.4.2
##  [10] rstudioapi_0.11    farver_2.0.3       remotes_2.2.0
##  [13] fansi_0.4.1        codetools_0.2-16   splines_4.0.2
##  [16] knitr_1.29         pkgload_1.1.0      spam_2.5-1
##  [19] compiler_4.0.2     backports_1.1.8    assertthat_0.2.1
##  [22] Matrix_1.2-18      cli_2.0.2          htmltools_0.5.0
##  [25] prettyunits_1.1.1  tools_4.0.2        dotCall64_1.0-0
##  [28] coda_0.19-3        gtable_0.3.0       glue_1.4.1
##  [31] CARBayesdata_2.1   maps_3.3.0         gmodels_2.18.1
##  [34] Rcpp_1.0.5         raster_3.3-13      vctrs_0.3.2
##  [37] spdep_1.1-5        gdata_2.18.0       nlme_3.1-148
##  [40] crosstalk_1.1.0.1  xfun_0.16          stringr_1.4.0
##  [43] ps_1.3.3           testthat_2.3.2     lifecycle_0.2.0
##  [46] gtools_3.8.2       devtools_2.3.1     LearnBayes_2.15.1
##  [49] MASS_7.3-51.6      scales_1.1.1       expm_0.999-5
##  [52] RColorBrewer_1.1-2 fields_10.3        yaml_2.2.1
##  [55] memoise_1.1.0      gridExtra_2.3      truncdist_1.0-2
##  [58] reshape_0.8.8      stringi_1.4.6      SpATS_1.0-11
##  [61] desc_1.2.0         e1071_1.7-3        boot_1.3-25
##  [64] pkgbuild_1.1.0     truncnorm_1.0-8    spData_0.3.8
##  [67] rlang_0.4.7        pkgconfig_2.0.3    matrixStats_0.56.0
##  [70] evaluate_0.14      lattice_0.20-41    purrr_0.3.4
##  [73] sf_0.9-5           htmlwidgets_1.5.1  labeling_0.3
##  [76] processx_3.4.3     tidyselect_1.1.0   GGally_2.0.0
##  [79] plyr_1.8.6         magrittr_1.5       R6_2.4.1
##  [82] generics_0.0.2     DBI_1.1.0          pillar_1.4.6
##  [85] foreign_0.8-80     withr_2.2.0        units_0.6-7
##  [88] shapefiles_0.7     sp_1.4-2           tibble_3.0.3
##  [91] crayon_1.3.4       CARBayesST_3.1     KernSmooth_2.23-17
##  [94] rmarkdown_2.3      usethis_1.6.1      grid_4.0.2
```

```
##  [97] data.table_1.13.0  callr_3.4.3        matrixcalc_1.0-3
## [100] digest_0.6.25      classInt_0.4-3     stats4_4.0.2
## [103] munsell_0.5.0      sessioninfo_1.1.1
```

References

1. R Development Core Team (2015). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org.
2. Chong Gu (2014). Smoothing Spline ANOVA Models: R Package gss. Journal of Statistical Software, 58(5), 1-25. URL http://www.jstatsoft.org/v58/i05/.