

Package compilation and basic run

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Compilation

- structure
 - **tests** : removed all other folders and files except testthat from the package otherwise warnings about RDS files
 - **data** : removed remifentanil example from data folder
- **roxygen** documentation
 - warnings for ggplot (no visible global function definition)
 - added import command for pnorm (found in distribution plot) and median (found nowhere, so suspect it's the name median used in the ggplot plots, but added it all the same)
- **package size**: still 5.9 Mb so much too large for CRAN
 - the 3 simulated data files for warfarin and viral load data are all around 5Mb, consider making them available only on bookdown/website
- necessary files
 - added a DESCRIPTION file
 - added a CHANGES file
- for compilation:
 - removed NAMESPACE
 - removed man pages
- Compilation steps from Build menu
 - Document => create NAMESPACE, DESCRIPTION (update collate directive), create man pages
 - Check => update documentation, create NAMESPACE
- **FINAL COMPILATION FOR CRAN**
 - removed documentation (too large)
 - removed simwarfarineBase
 - still over 5Mo but seems to be ok
- CRAN pre-test doesn't pass :-/
 - added importFrom for ggplot functions, also for gridExtra (grid.arrange) and grid
 - 'solved' problem by adding a dependency on rlang
 - * partially fixed with rlang
 - * workaround by defining global variables so check won't complain about them, but we need to use the .data systematically in ggplot aes() => **Romain TODO**
- **March 2021**
 - mail Fu (15/03): added again the option to save the output in autonpde (probably removed by Romain :-/)

```
# Reduce size of viral load simulation data (to 500 simulations) for CRAN
if(FALSE) {
  cmd<-paste("mv ", file.path(workDir,"npde","data","simvirload.tab")," ", file.path(workDir,"keep","da
  system(cmd)
  tab<-read.table(file.path(workDir,"npde","data","simvirload.tab"), header=TRUE)
  tab1<-tab[1:(dim(tab)[1]/2),]
```

```

    write.table(tab1, file.path(workDir,"npde","data","simvirload.tab"), quote=FALSE, row.names=FALSE, col.names=FALSE)
  }

  setwd(file.path(workDir,"npde"))
  system("rm man/*")
  cmd<-paste("cp ", file.path(workDir,"latexDoc","userguide_3_1.pdf")," ", file.path(workDir,"userguide_npde.pdf"))
  system(cmd)
  devtools::document()

```

```
## Updating npde documentation
```

```
## Loading npde
```

```
## Loading required package: gridExtra
```

```
## Loading required package: ggplot2
```

```
## Loading required package: grid
```

```
## Writing NAMESPACE
```

```
## Writing NAMESPACE
```

```
## Writing NpdeSimData-class.Rd
```

```
## Writing extract-methods.Rd
```

```
## Writing NpdeData-class.Rd
```

```
## Writing read.Rd
```

```
## Writing show.Rd
```

```
## Writing npdeData.Rd
```

```
## Writing npdeSimData.Rd
```

```
## Writing print.NpdeData.Rd
```

```
## Writing showall.Rd
```

```
## Writing summary.NpdeData.Rd
```

```
## Writing subset.NpdeData.Rd
```

```
## Writing NpdeRes-class.Rd
```

```
## Writing kurtosis.Rd
```

```
## Writing skewness.Rd
```

```
## Writing gof.test.Rd
```

```
## Writing NpdeObject-class.Rd
```

```
## Writing dist.pred.sim.Rd
```

```
## Writing computenpde.Rd
```

```
## Writing npde.decorrelation.method.Rd
```

```
## Writing computepd.Rd
```

```
## Writing compute.ploq.Rd
```

```
## Writing autonpde.Rd
```

```
## Writing pdemenu.Rd
```

```
## Writing npde.main.Rd
```

```
## Writing npde.save.Rd
```

```
## Writing npde.graphs.Rd
```

```
## Writing npde-package.Rd
```

```
## Writing theopp.Rd
```

```
## Writing simtheopp.Rd
```

```
## Writing warfarin.Rd
```

```
## Writing virload.Rd
```

```
## Writing npde.cens.method.Rd
```

```
## Writing npdeControl.Rd
```

```
## Writing set.plotoptions.Rd
```

```
## Writing replace.plotoptions.Rd
```

```
## Writing npde.binning.Rd
## Writing npde.plot.covariate.Rd
## Writing npde.plot.dist.Rd
## Writing npde.plot.loq.Rd
## Writing plot.NpdeData.Rd
## Writing plot.NpdeRes.Rd
## Writing plot.NpdeObject.Rd
## Writing npde.plot.select.Rd
## Writing default.npde.plots.Rd
## Writing npde.plot.splitcov.Rd
## Writing npde.plot.npde.Rd
## Writing npde.plot.data.Rd
## Writing npde.plot.default.Rd
## Writing npde.plot.scatterplot.Rd
```

```
roxygenise()
```

```
## Loading npde
```

```
## Writing NAMESPACE
```

```
## Writing NAMESPACE
```

```
setwd(workDir)
```

```
system("R CMD build npde")
```

```
system("R CMD check --as-cran --run-donttest npde_3.1.tar.gz")
```

Après correction, la compilation du package passe sans erreurs et avec 2 notes restantes.

- **notes**
 - previous version archived
 - package size too large (recommended size less than 5Mb): reduce nb of simulations for warfarin ?
 - ggplot variables (rien à faire pour ça)
- **warnings** corrigés
 - jeux de données non documentés: removed remifentanyl, added virload documentation (used to be a specific man page, reintegrated them into roxygen format in npde.R like warfarin)
 - duplicated alias: fixed !

Warnings

- ggplot warnings

Undefined global functions or variables:

```
.x X2.5. X50. X97.5. Y0.025 Y0.025.1 Y0.5 Y0.5.1 Y0.975 Y0.975.1 aes
annotation_logticks category coord_cartesian coord_flip element_blank
element_line element_rect element_text expand_limits facet_wrap
geom_bar geom_boxplot geom_crossbar geom_hline geom_line geom_point
geom_ribbon ggplot ggtitle gpar grid.arrange group grp guides labs
lower name obs.inf obs.median obs.sup pinf.lower pinf.median
pinf.upper pmid.lower pmid.median pmid.upper psup.lower psup.median
psup.upper scale_fill_manual scale_x_continuous scale_x_discrete
scale_x_log10 scale_y_continuous scale_y_log10 textGrob theme upper
value x x1 x2 x_area_0.25 x_area_0.5 x_area_0.975 xcent y y1 y2
y_area_0.25 y_area_0.5 y_area_0.975
```

- Warnings in first compilation (solved)

W checking Rd metadata ...

```

Rd files with duplicated alias 'aux.npdeplot.computepi':
  'npde.plot.default.Rd' 'npde.plot.scatterplot.Rd'
Rd files with duplicated alias 'compute.bands':
  'npde.plot.default.Rd' 'npde.plot.scatterplot.Rd'
Rd files with duplicated alias 'compute.bands.true':
  'npde.plot.default.Rd' 'npde.plot.scatterplot.Rd'
Rd files with duplicated alias 'npde':
  'npde-package.Rd' 'npde.Rd'
checking Rd line widths ...
checking Rd cross-references ...
W checking for missing documentation entries (346ms)
Undocumented code objects:
  'remifent' 'simremifent' 'simremifent_base' 'simvirload' 'virload'
  'virload20' 'virload50' 'virloadMDV20'
Undocumented data sets:
  'remifent' 'simremifent' 'simremifent_base' 'simvirload' 'virload'
  'virload20' 'virload50' 'virloadMDV20'
All user-level objects in a package should have documentation entries.
See chapter 'Writing R documentation files' in the 'Writing R
Extensions' manual.

```

Install package in development mode

```

dev_mode() # development mode

## Dev mode: ON

install.packages(pkgs=file.path(workDir,"npde_3.1.tar.gz"),repos=NULL)

## Installing package into '/home/eco/R-dev'
## (as 'lib' is unspecified)

library(npde)
library(ggplot2)
library(gridExtra)
library(mclust)

## Package 'mclust' version 5.4.6
## Type 'citation("mclust")' for citing this R package in publications.

library(testthat)

##
## Attaching package: 'testthat'

## The following object is masked from 'package:devtools':
##
##   test_file

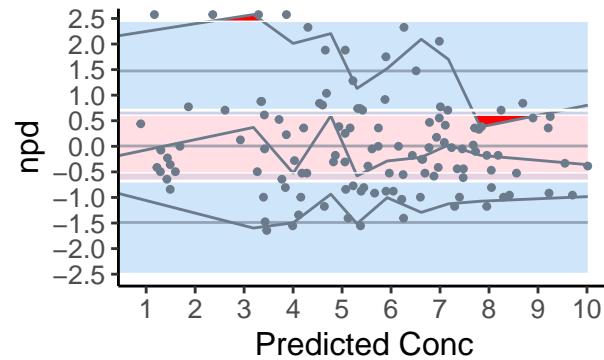
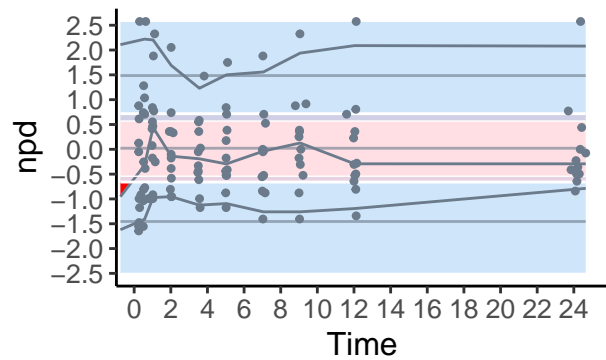
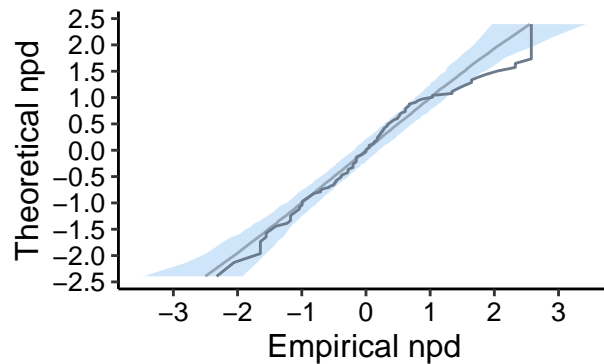
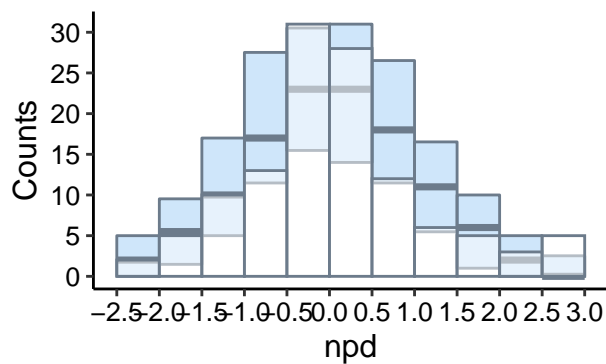
library(grid)

```

Theophylline

```
## -----
```

```
## Distribution of npde :
##      nb of obs: 120
##      mean= 0.0668   (SE= 0.095 )
##      variance= 1.074   (SE= 0.14 )
##      skewness= 0.511
##      kurtosis= 0.2912
## -----
## Statistical tests (adjusted p-values):
##      t-test          : 1
##      Fisher variance test : 1
##      SW test of normality : 0.00819 **
##      Global test      : 0.00819 **
## ---
## Signif. codes: '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
## -----
```



```
##      ypred ycomp  pd      ydobs      npde
## 1      NaN   NaN   NaN        NA        NA
## 2  2.923864  2.84  0.55 -0.05124648  0.1256613
## 3  4.682299  6.57  0.85  1.96398150  2.0537489
## 4  6.264357 10.50  0.99  2.56602650  2.3263479
## 5  6.986255  9.66  0.98  0.41616411  0.5244005
## 6  6.511039  8.58  0.93  0.28430866  0.2533471
```

Viral load, base plots

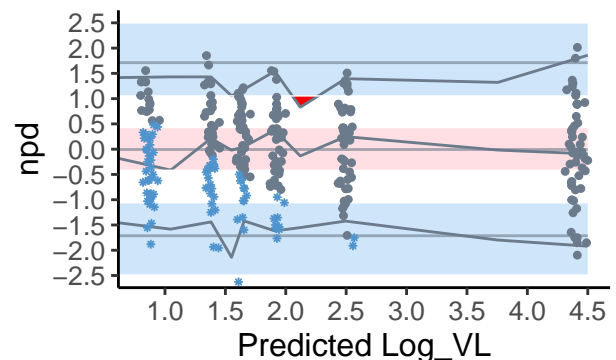
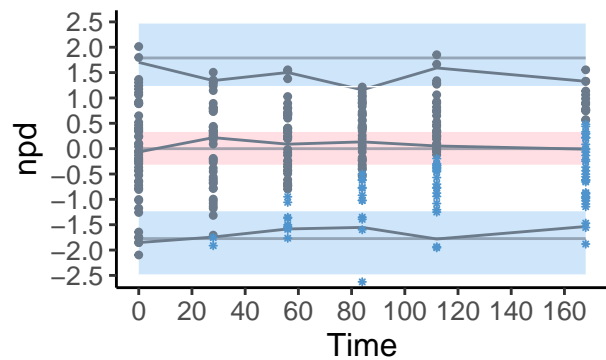
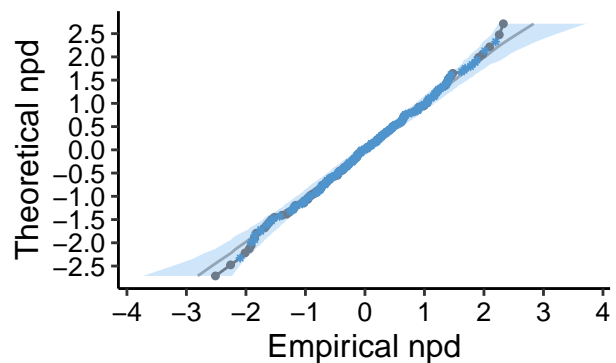
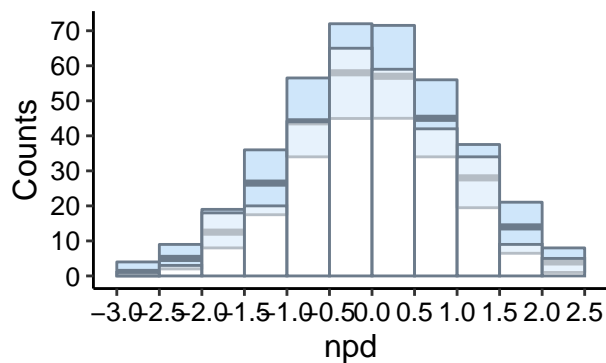
```
## -----
## Distribution of npde :
##      nb of obs: 300
```

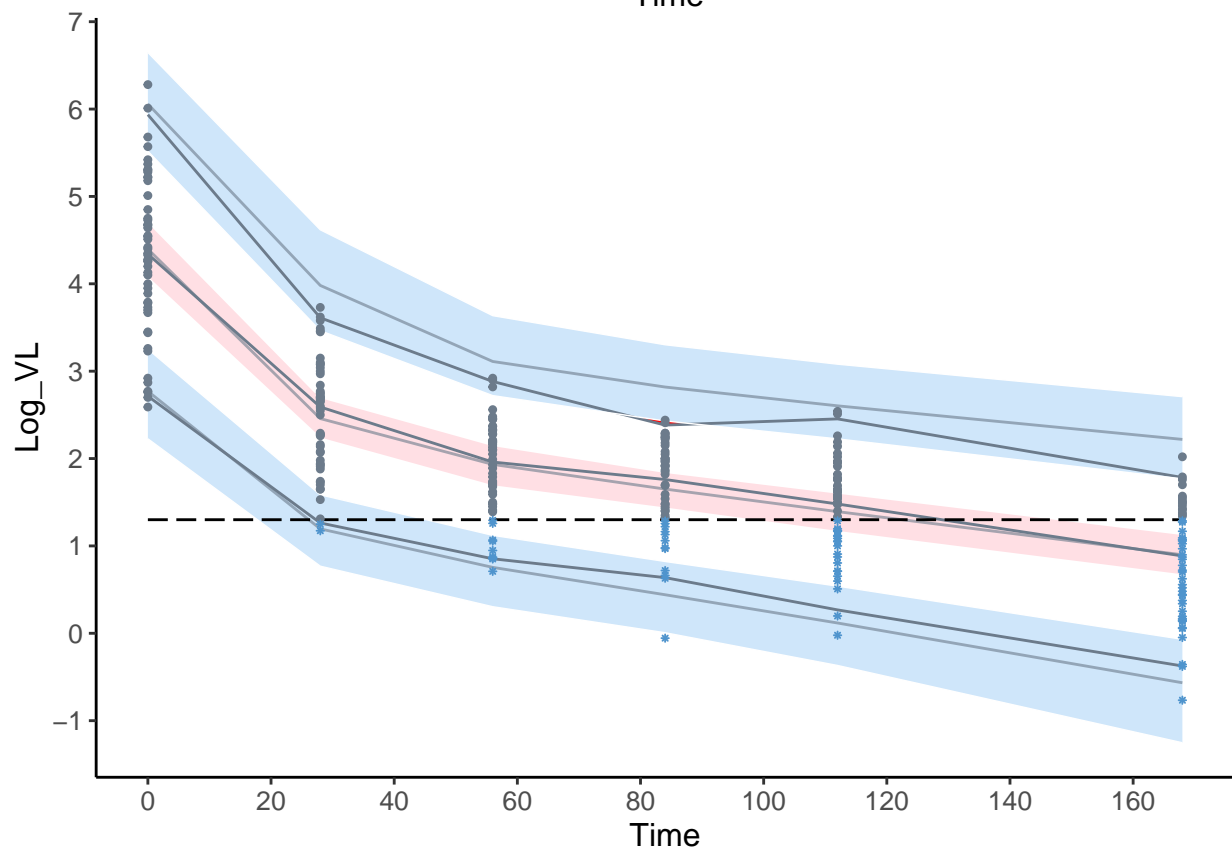
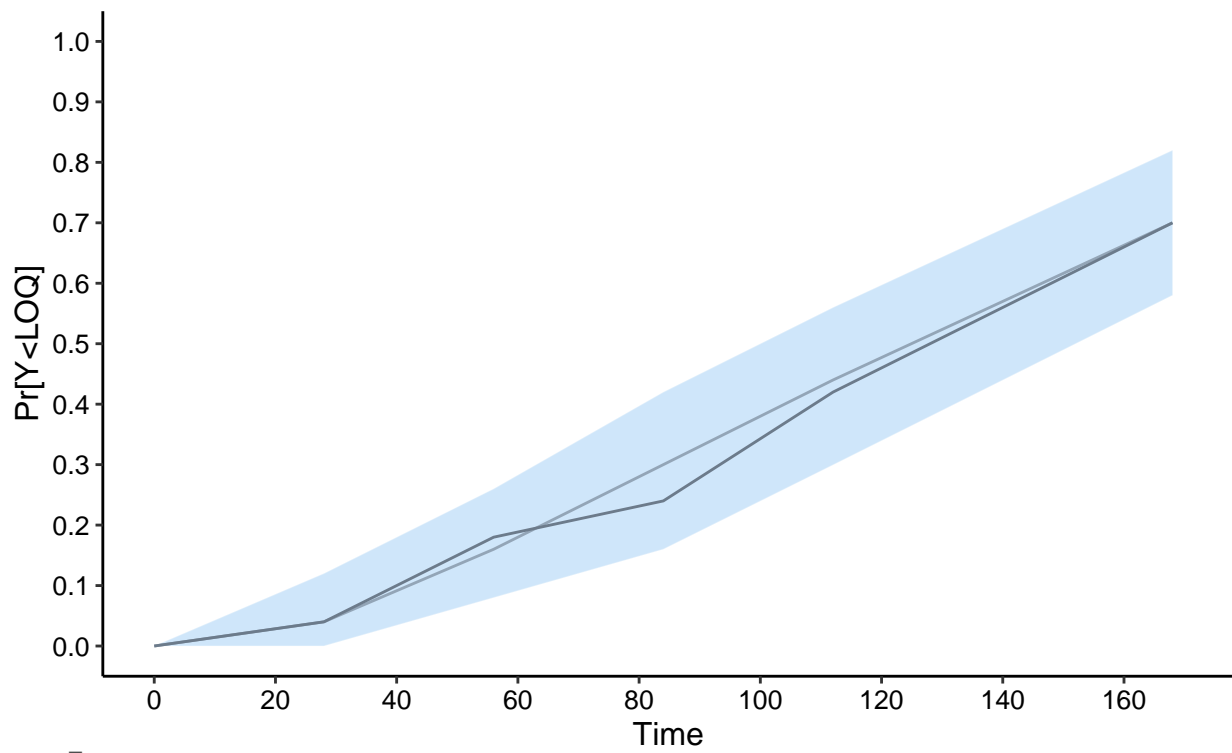
```

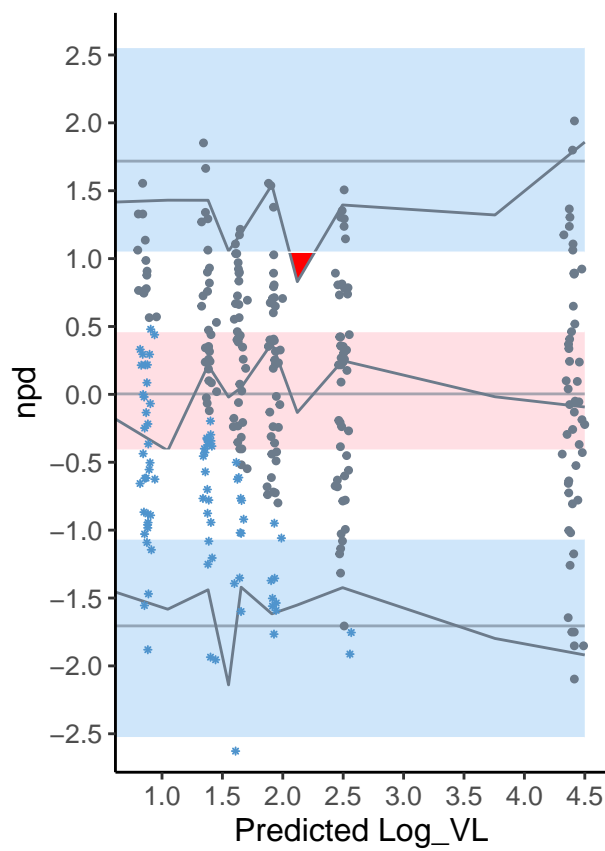
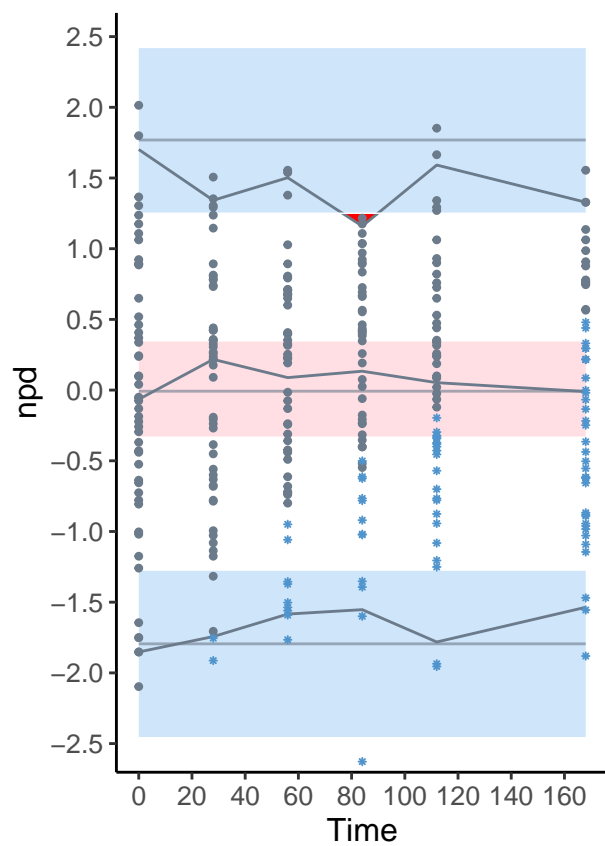
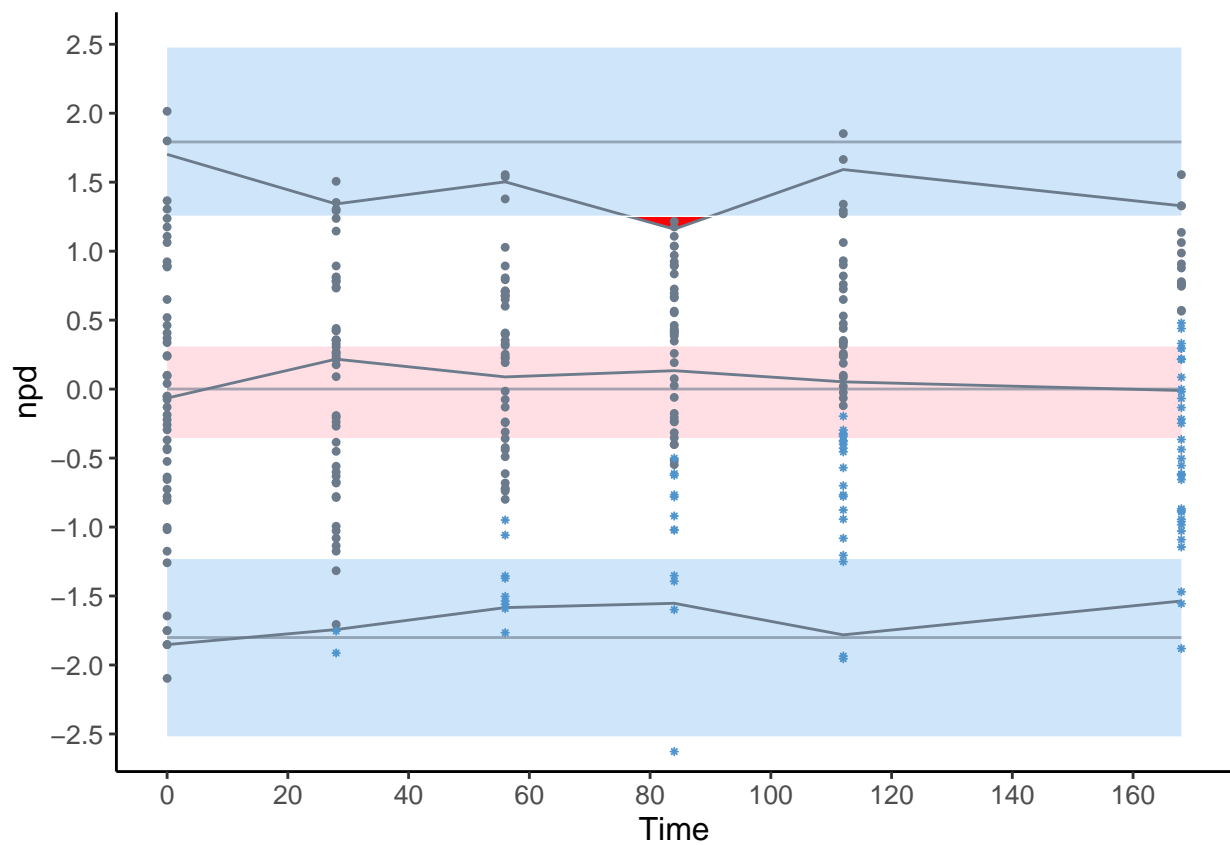
##          mean= 0.008611   (SE= 0.054 )
##        variance= 0.8858   (SE= 0.072 )
##        skewness= -0.03732
##        kurtosis= -0.2811
## -----
## Statistical tests (adjusted p-values):
##   t-test           : 1
##   Fisher variance test : 0.462
##   SW test of normality : 1
##   Global test       : 0.462
## ---
## Signif. codes: '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
## -----

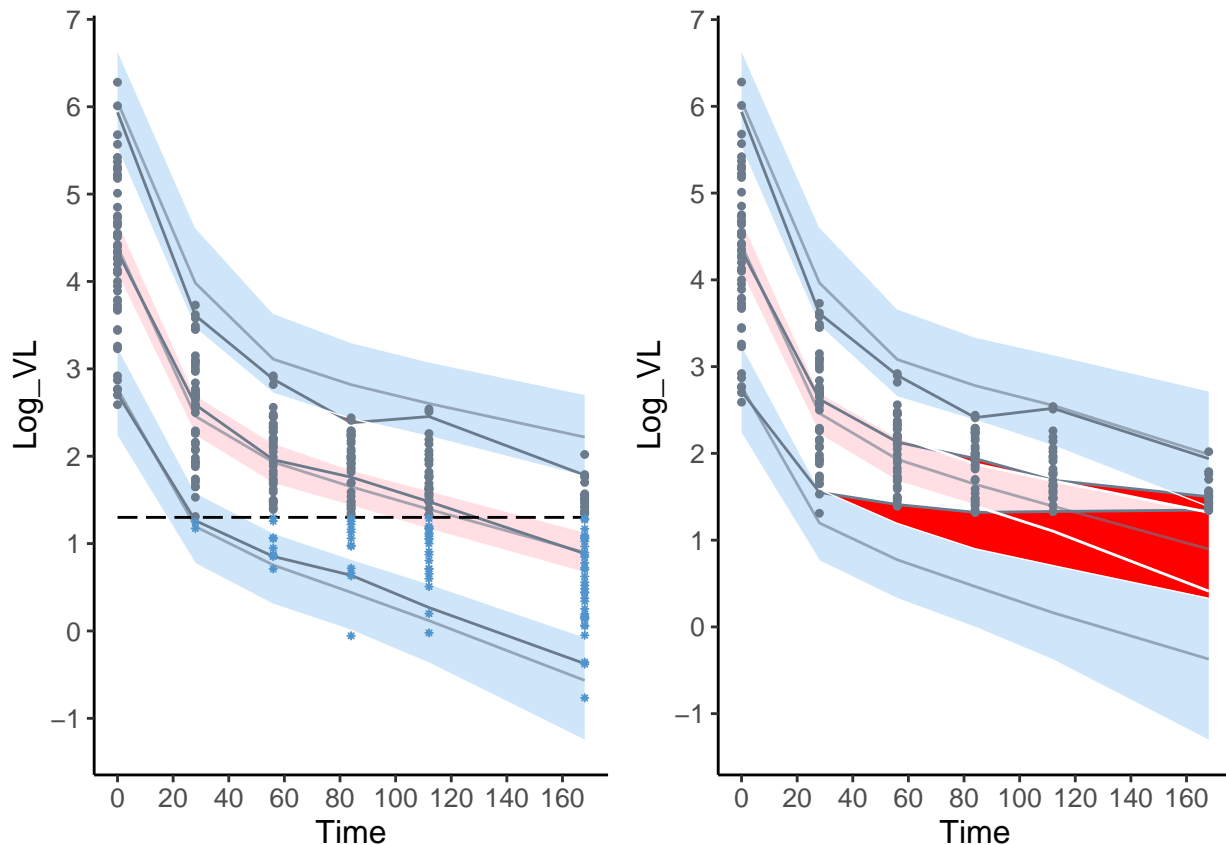
## -----
## Distribution of npde :
##   nb of obs: 221
##   mean= 0.09917   (SE= 0.062 )
##   variance= 0.8611 (SE= 0.082 )
##   skewness= -0.1174
##   kurtosis= -0.1955
## -----
## Statistical tests (adjusted p-values):
##   t-test           : 0.341
##   Fisher variance test : 0.402
##   SW test of normality : 1
##   Global test       : 0.341
## ---
## Signif. codes: '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
## -----

```









End of file, deactivating development mode

```
## Dev mode: OFF
```

Bugs to sort

Sort out covariate plots

There were two functions with almost the same name - `npde.plot.covariates`: regular plots split by covariates, only for `x`, `pred`, `ecdf` => renamed to **`npde.plot.splitcov`** and added options `hist` and `qqplot` - do we need those subplots, or maybe just simplify call to function (use `covsplit` and capture arguments instead of using `which.plot`) - `npde.plot.covariate`: covariate plots as in Brendel => kept as is

plot.NpdeRes (dans `plotNpde-methods.R`)

- **Romain TODO:** la fonction devrait prendre un objet `NpdeRes` et pas un objet `NpdeObject` (`NpdeRes` n'a pas d'element data, c'est juste le slot `res` d'un element `NpdeObject` !!!)
 - il faut lui donner des defaults pour `xlab`, `ylab` (et la possibilite de passer outre en passant des arguments en ...)
 - normalement il doit y avoir l'equivalent de `xobs` dans le dataframe `res` de l'objet
 - pas sure qu'on ait `not.miss` mais dans ce cas le reconstruire (a tester +++)
 - il n'y a pas de liste `plot.opt` donc prendre des defaults dans `set.default.options()`
- faire un `testthat` pour verifier que cette fonction marche par elle-meme (use `testthat` for class to generate an object `npdeData` and plot it)

`plot.NpdeData` (dans `plotNpde-methods.R`)

- **Romain TODO:** faire un `testthat` pour vérifier que la fonction et les options passent (use `testthat` for class to generate an object `npdeData` and plot it)