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, co
}

setwd(file.path(workDir,"npde"))
system("rm man/*")
cmd<-paste("cp ", file.path(workDir,"latexDoc","userguide_3_0.pdf")," ", file.path(workDir,"userguide_n
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.decorr.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")
```

Apres 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 a faire pour ça)
- **warnings** corriges
  - jeux de donnees non documentes: removed remifentanil, 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'
```

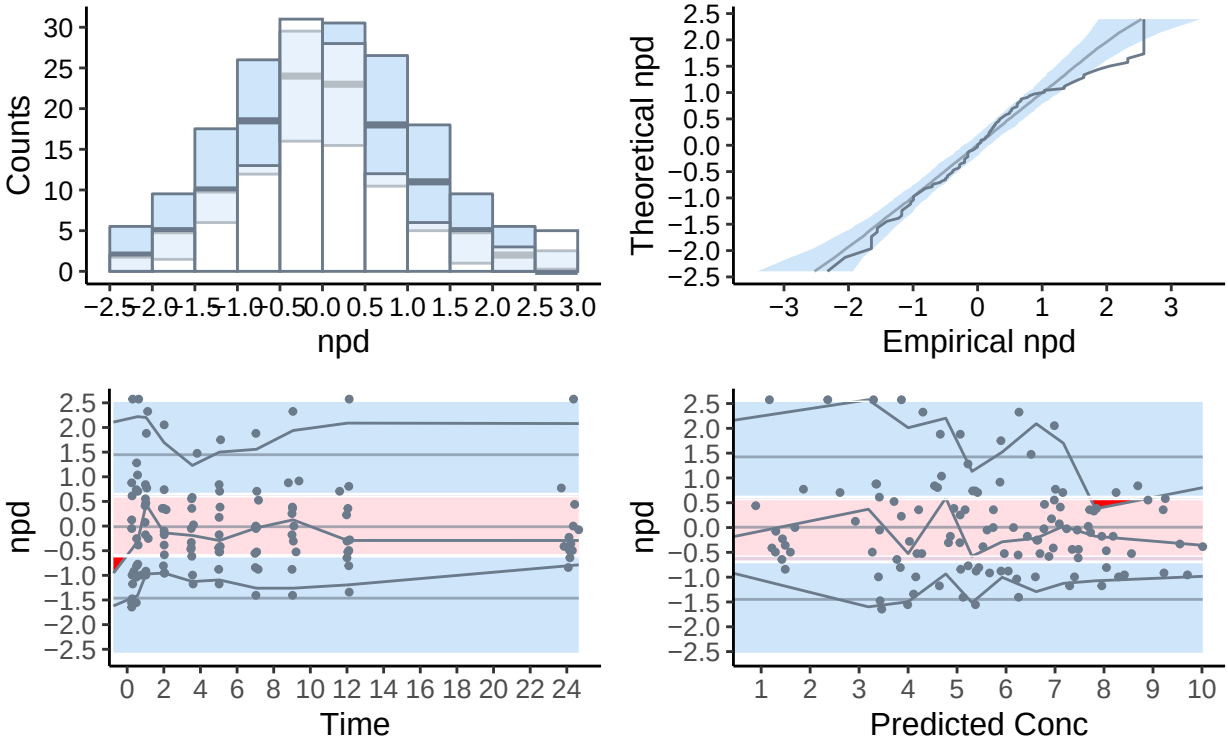
```
## The following object is masked from 'package:devtools':
##
##     test_file
```

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

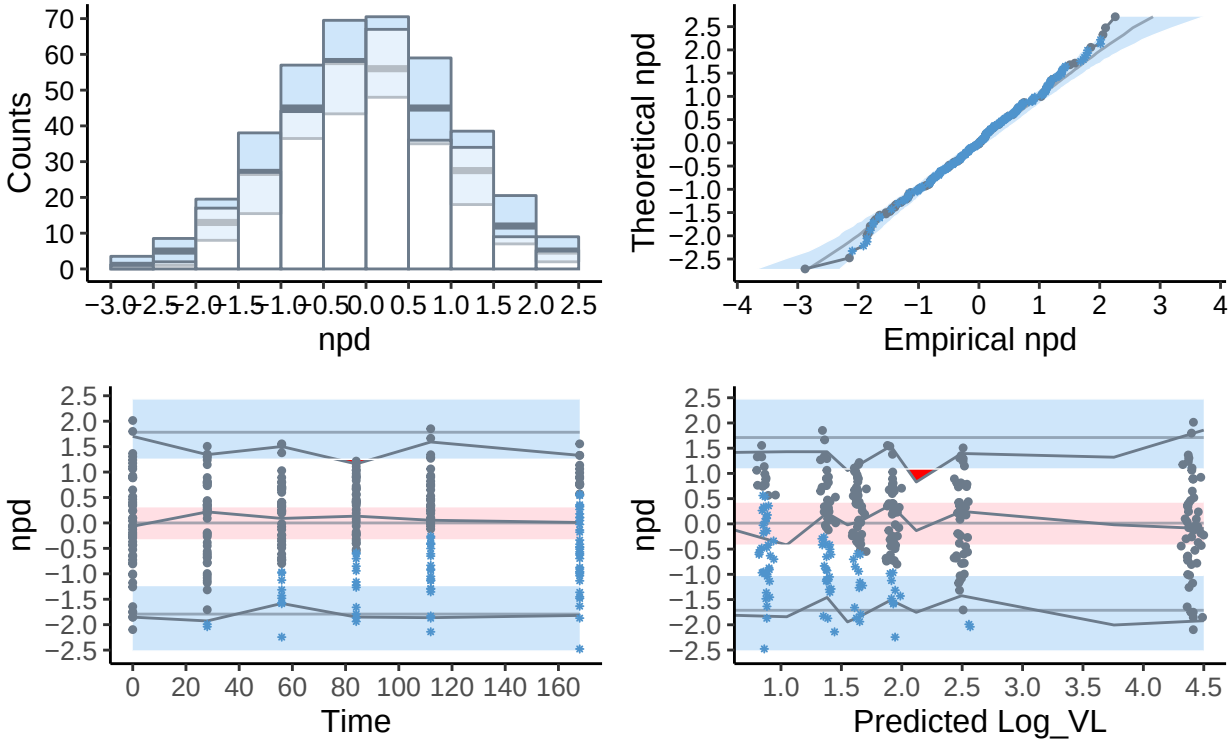


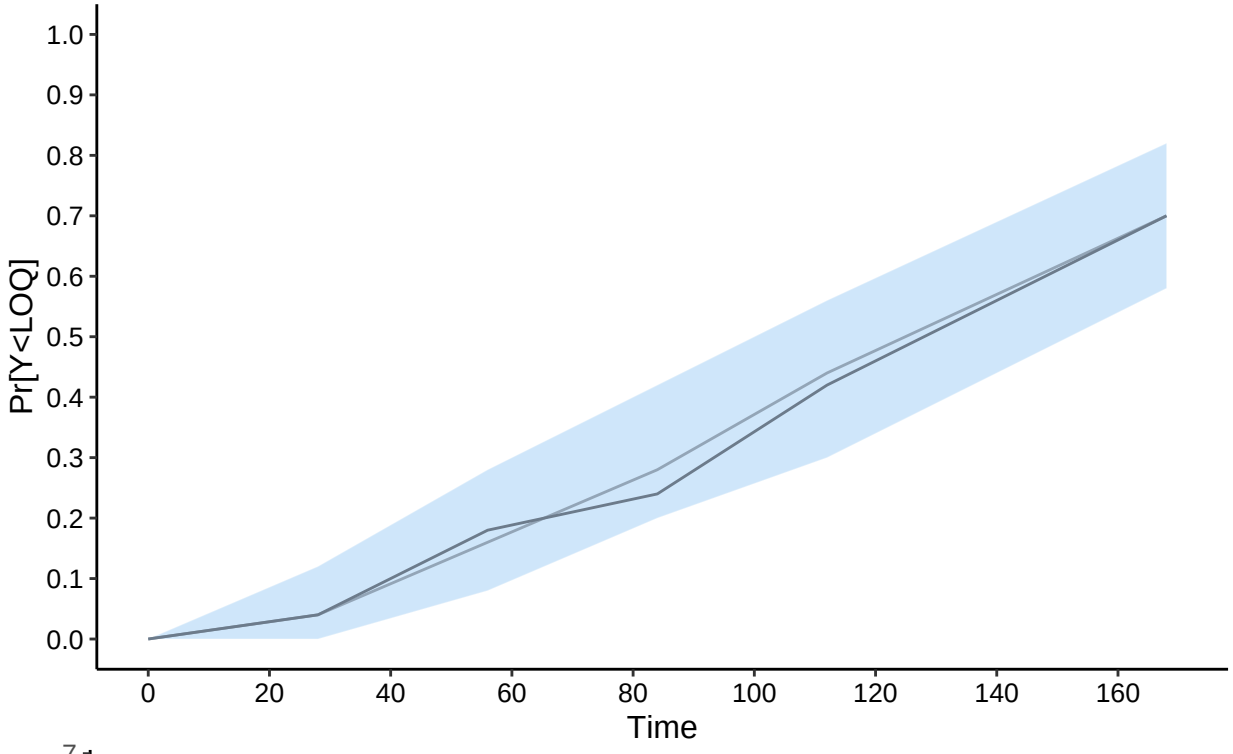

```
##      ypred ycomp   pd       ydobs       npde
## 1      NaN   NaN  NaN          NA         NA
## 2 2.923864  2.84 0.55 -0.05124648 0.1256613
## 3 4.682299  6.57 0.85  1.96398150 2.0537489
## 4 6.264357 10.50 0.99  2.56602650 2.3263479
## 5 6.986255  9.66 0.98  0.41616411 0.5244005
## 6 6.511039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

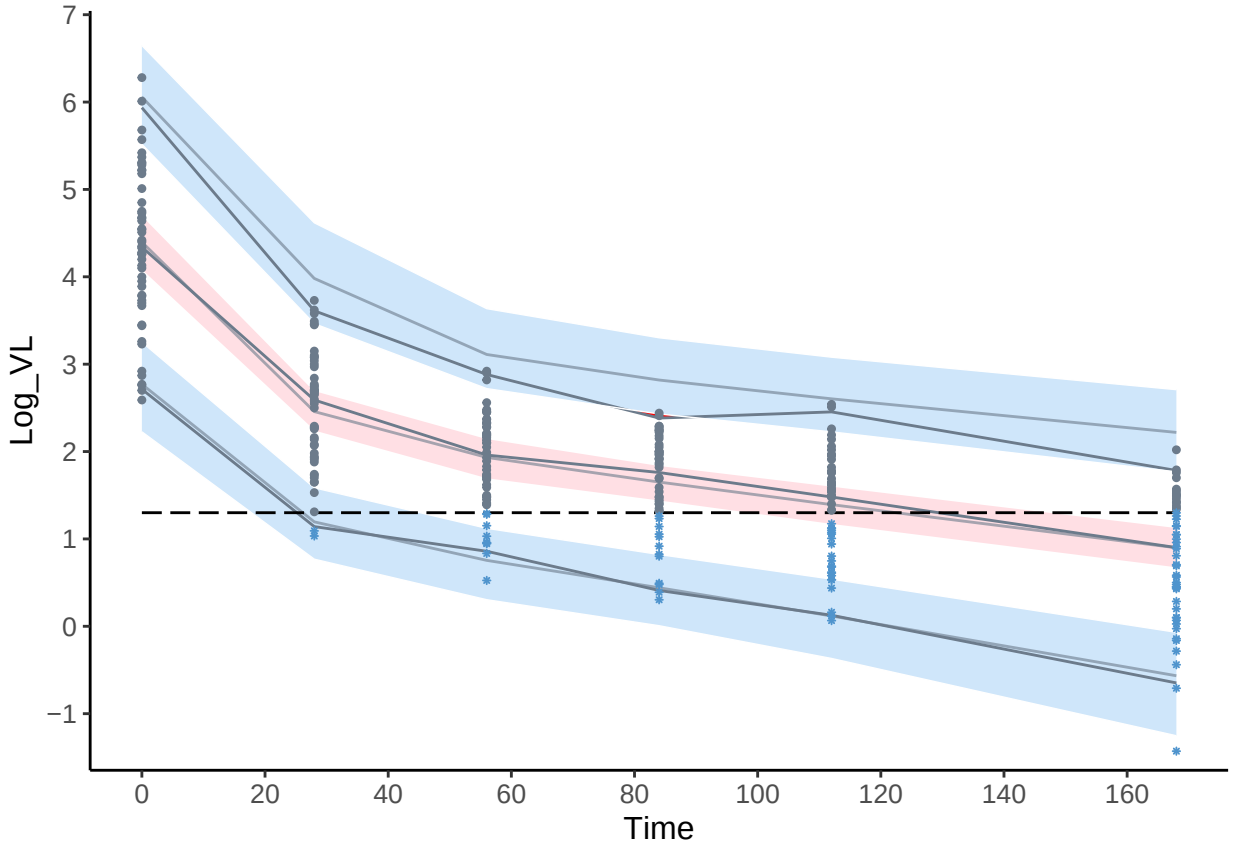
Viral load, base plots

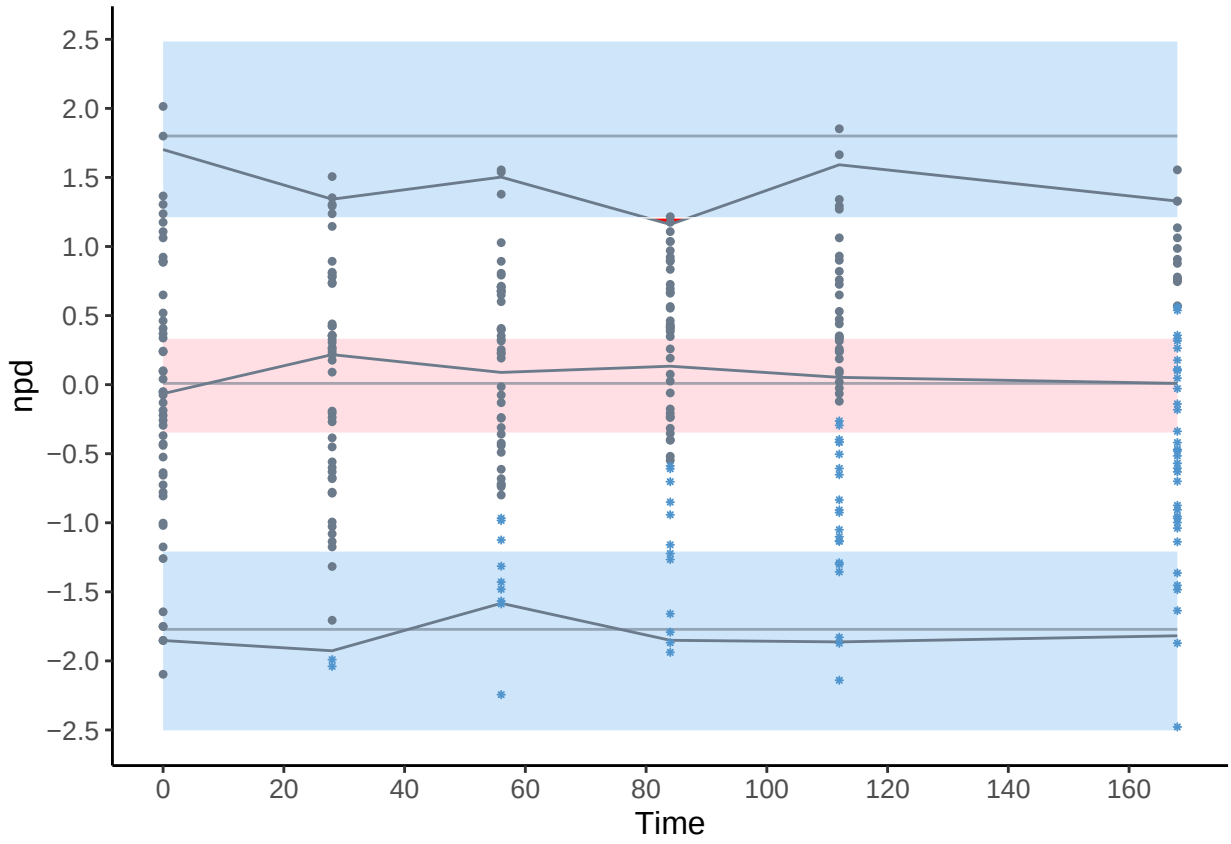
```
## ------------------------------------------------
## Distribution of npde :
##       nb of obs: 300
```

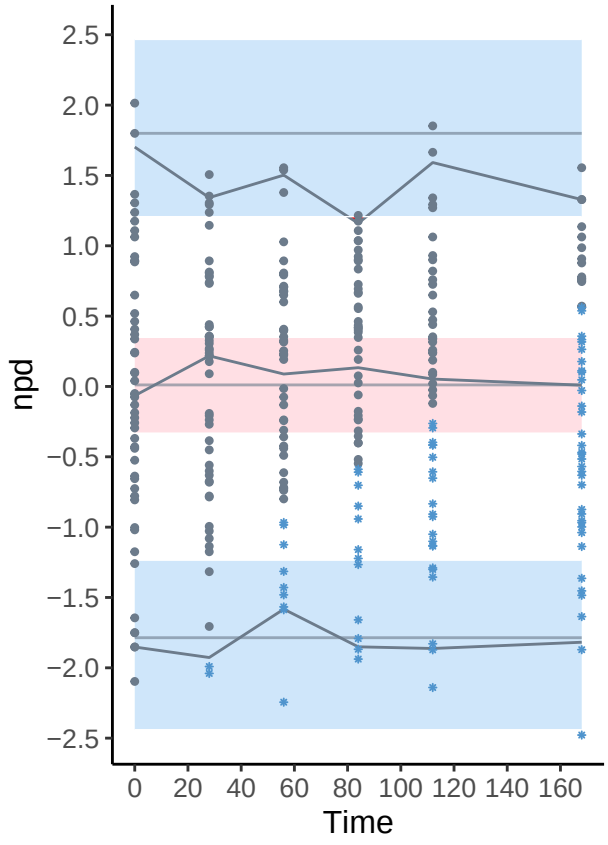
```
##            mean= -0.03396   (SE= 0.054 )
##        variance= 0.8688   (SE= 0.071 )
##        skewness= -0.06031
##        kurtosis= -0.2824
## ----------------------------------------------
## Statistical tests (adjusted p-values):
##   t-test                : 1
##   Fisher variance test  : 0.295
##   SW test of normality  : 1
##   Global test           : 0.295
## ---
## 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
## ----------------------------------------------
```

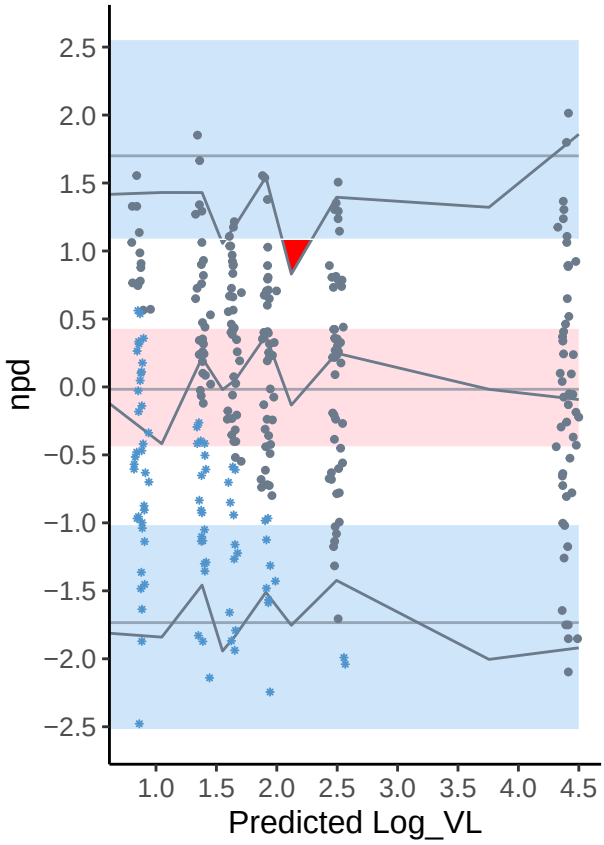


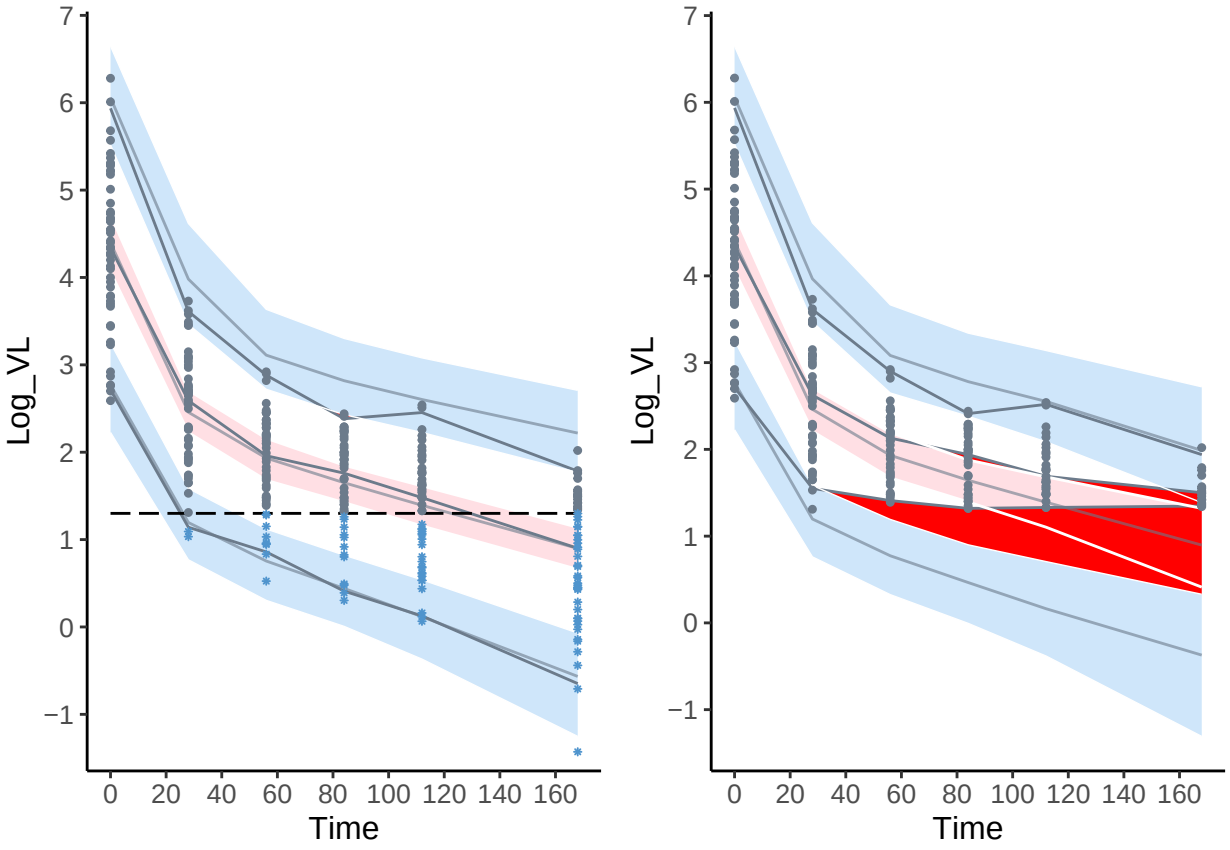

Pr[Y<LOQ]
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0
20
40
60
80
100
120
140
160
Time


Log_VL
7
6
5
4
3
2
1
0
−1
0
20
40
60
80
100
120
140
160
Time


npd
Time
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
0
20
40
60
80
100
120
140
160


npd
Time
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
0
20
40
60
80
100
120
140
160


npd
Predicted Log_VL
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5



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 defauts pour xlab, ylab (et la possiblite 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 defauts 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 veeifier que la fonction et les options passent (use testthat for class to generate an object npdeData and plot it)