

# Package compilation and basic run - current version 3.4

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## Compilation

First creation date: **02/02/2021**

- 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 :-/ )
- **June 2023**
  - fixed scatterplot when only one X-value (removed interpolation in this case as was causing the plot to fail)
  - note: the case when this happens within covsplit is **not fixed**

```

# 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
}

cmd<-paste("rm -r ",file.path(compilDir,"*"),sep="")
system(cmd)
dir.create(compilDir)

## Warning in dir.create(compilDir): '/home/eco/work/npde/compileNpde' existe déjà
dir.create(file.path(compilDir,"npde"))
dir.create(file.path(compilDir,"npde","inst"))
# File too large
if(FALSE) {
  cmd<-paste("cp ", file.path(workDir,"latexDoc","userguide_3_3.pdf")," ", file.path(compilDir,"inst","
  system(cmd)
}

cmd<-paste("cp -rp ",file.path(workDir,"npde","R")," ", file.path(compilDir,"npde"),sep="")
system(cmd)
cmd<-paste("cp -rp ",file.path(workDir,"data")," ", file.path(compilDir,"npde"),sep="")
system(cmd)
for(ifile in c("CHANGES","DESCRIPTION")) {
  cmd<-paste("cp ",file.path(workDir,"keep",ifile)," ", file.path(compilDir,"npde"),sep="")
  system(cmd)
}
for(ifile in c("CITATION")) {
  cmd<-paste("cp ",file.path(workDir,"keep",ifile)," ", file.path(compilDir,"npde","inst"),sep="")
  system(cmd)
}
# cmd<-paste("cp ",file.path(workDir,"LICENSE")," ", file.path(compilDir,"inst"),sep="")
# system(cmd)

setwd(compilDir)
system("R CMD build npde")
system("R CMD check --as-cran --run-donttest npde_3.4.tar.gz")

```

**npde 3.1** 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 !

**npde 3.2, 3.3**

- notes
  - time to run examples Examples with CPU or elapsed time > 5s user system elapsed  
npde.cens.method 7.51 0.019 7.605

## Warnings

- ggplot warnings
  - solved in npde 3.0 by adding global variables (horrible)
    - \* in 3.3, tried to add `.data$` to all the ggplot functions
  - can't remove the `.x` because of scales

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)

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’

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
```

```
## v Dev mode: ON
```

```
install.packages(pkgs=file.path(compilDir,"npde_3.4.tar.gz"),repos=NULL)
```

```
## Installation du package dans '/home/eco/R-dev'
```

```
## (car 'lib' n'est pas spécifié)
```

```

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

## Package 'mclust' version 6.0.0
## Type 'citation("mclust")' for citing this R package in publications.
library(testthat)

##
## Attachement du package : 'testthat'
##
## L'objet suivant est masqué depuis 'package:devtools':
##
##      test_file
library(grid)

```

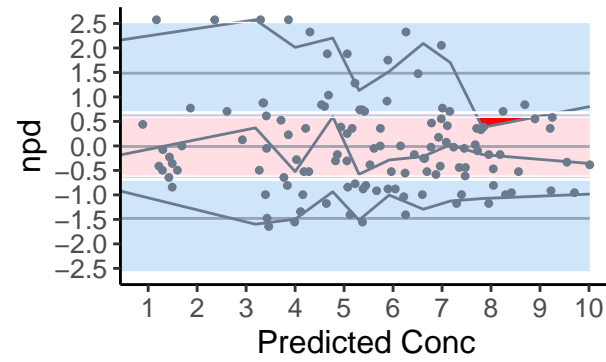
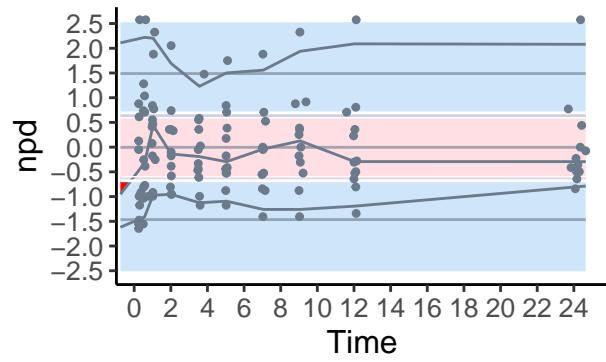
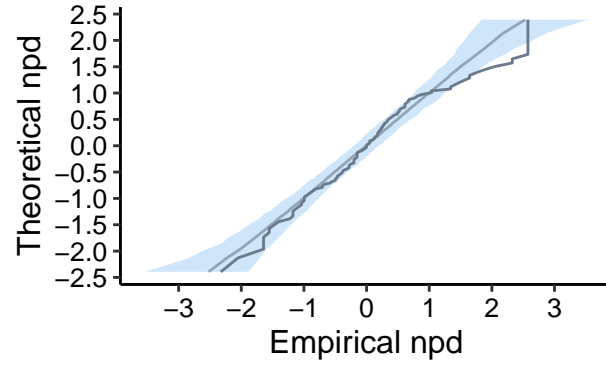
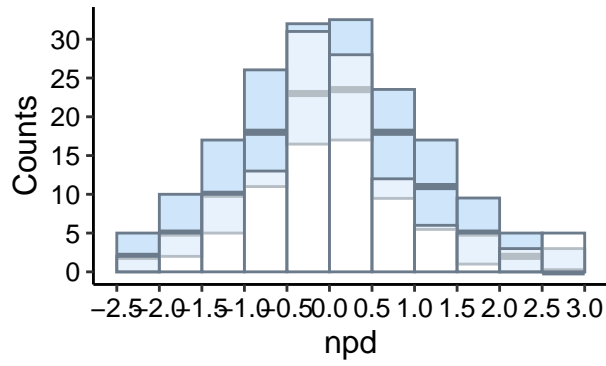
## Theophylline

- computation of npde and npd
- default plots

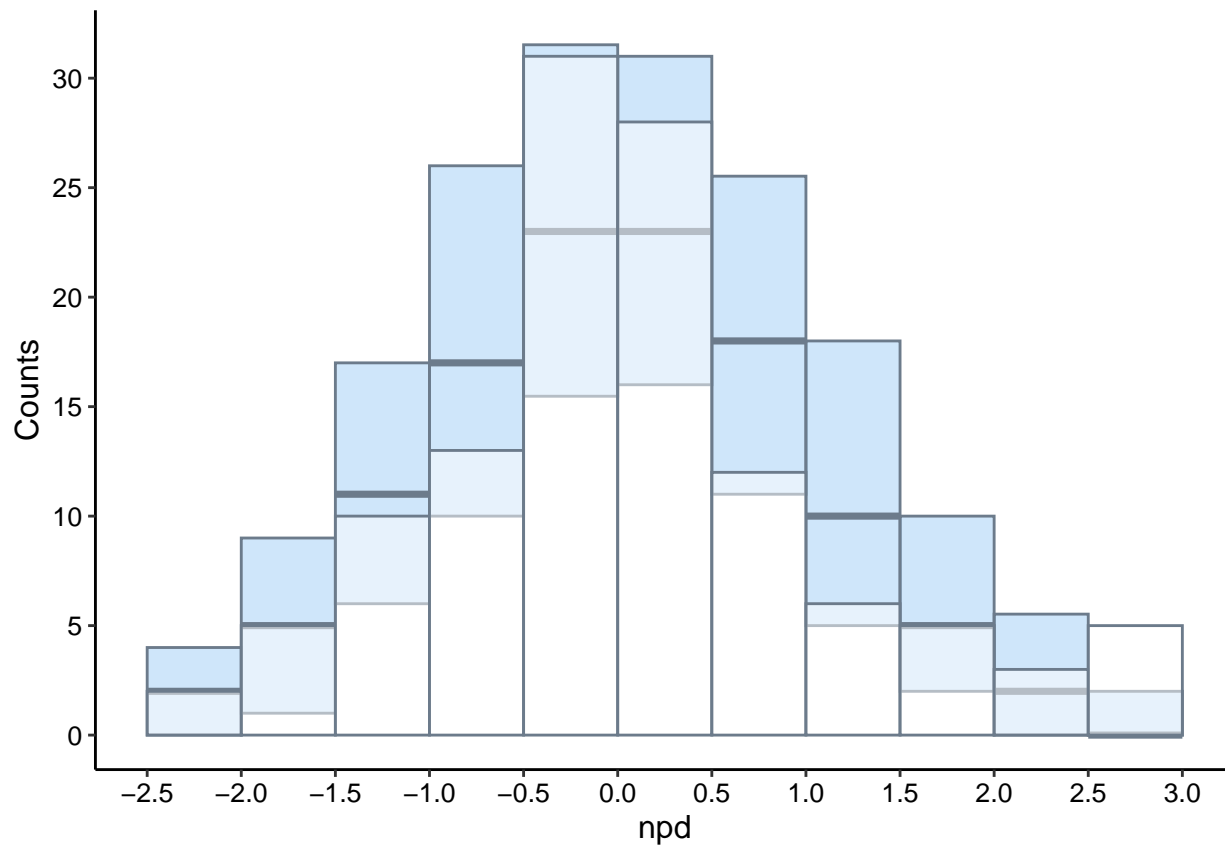
```

## -----
## 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
## -----

```



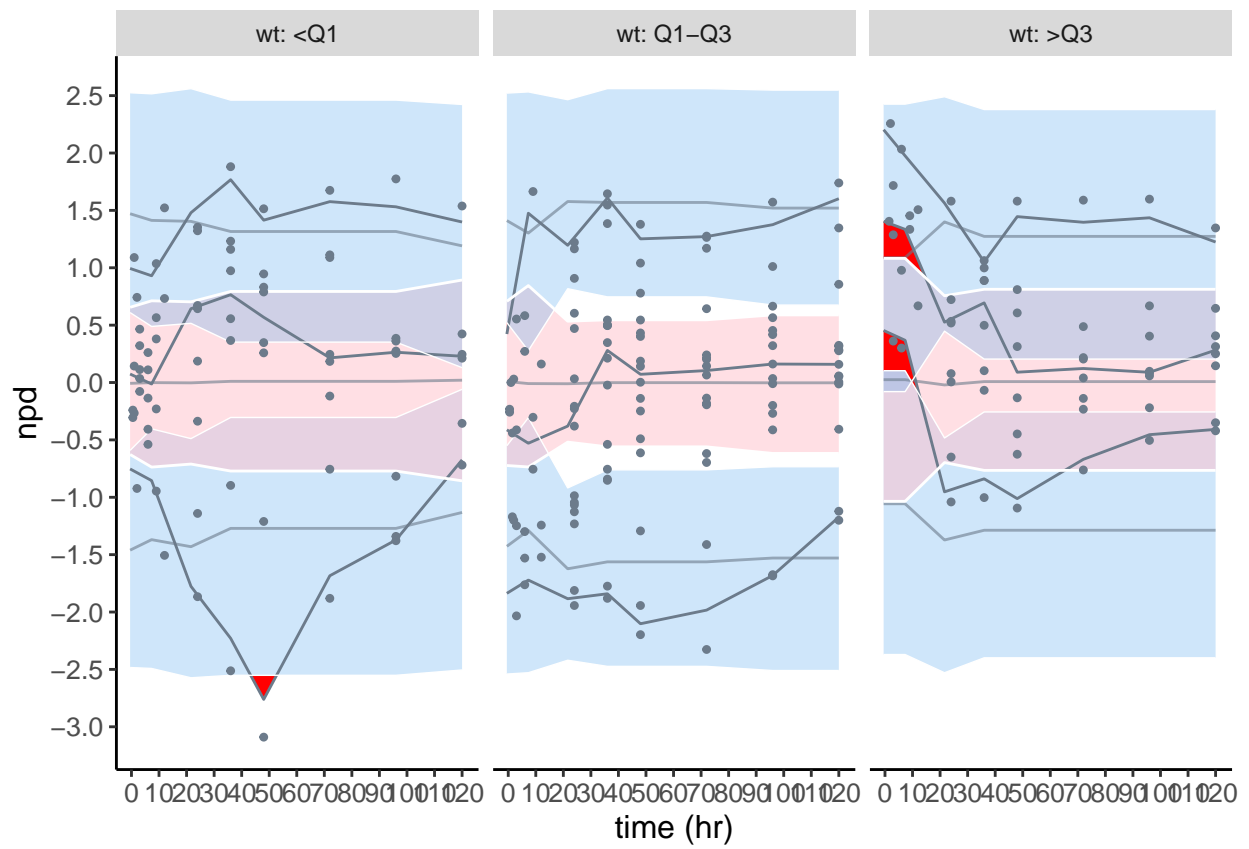
##	ypred	ycomp	pd	ydobs	npde
## 1	NaN	NaN	NaN	NA	NA
## 2	2.923864	2.84	0.55	-0.05124648	0.1256613
## 3	4.682299	6.57	0.85	1.96398150	2.0537489
## 4	6.264357	10.50	0.99	2.56602650	2.3263479
## 5	6.986255	9.66	0.98	0.41616411	0.5244005
## 6	6.511039	8.58	0.93	0.28430866	0.2533471



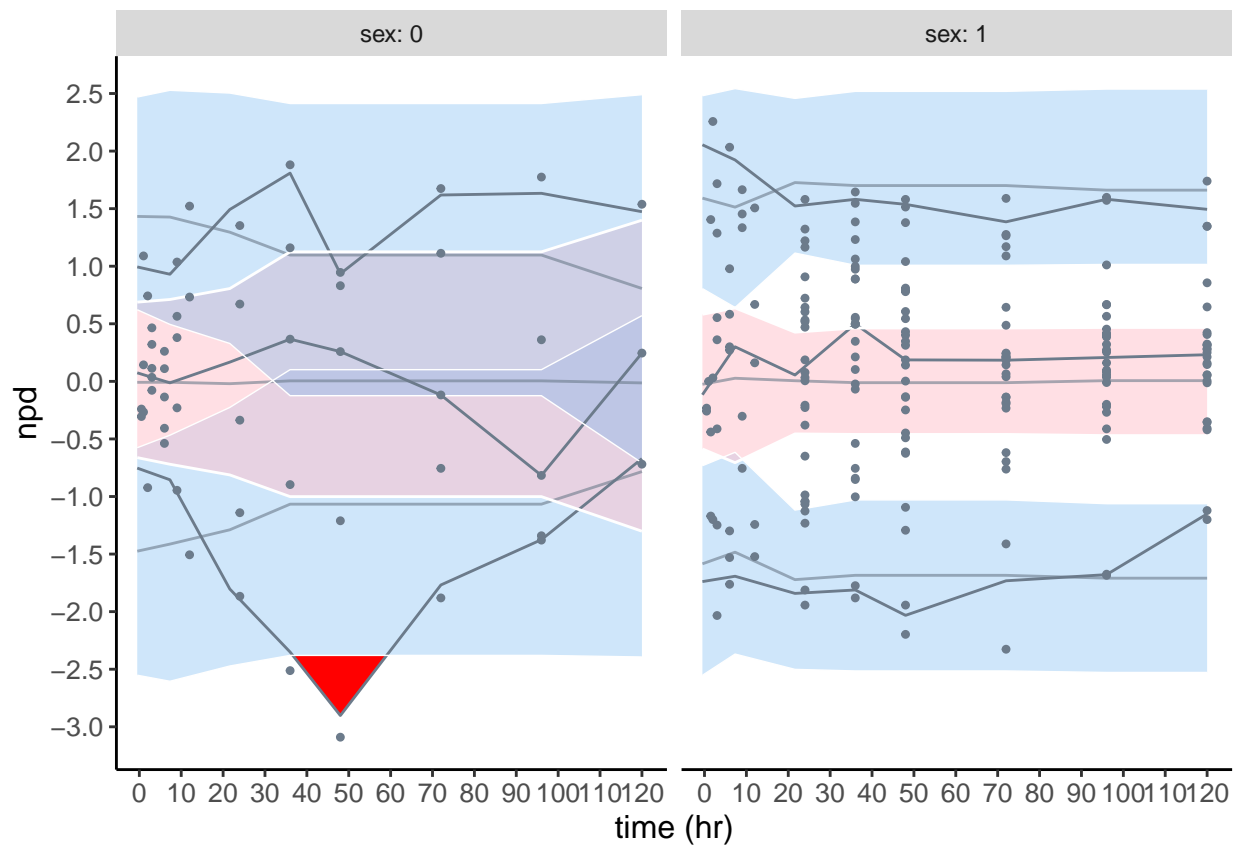
## Warfarin

- covariate plots
- reference profiles

```
## -----
## Distribution of npde :
##      nb of obs: 247
##           mean= 0.02928   (SE= 0.059 )
##           variance= 0.8549   (SE= 0.077 )
##           skewness= -0.07211
##           kurtosis= -0.4172
## -----
## Statistical tests (adjusted p-values):
##      t-test           : 1
##      Fisher variance test : 0.288
##      SW test of normality : 1
##      Global test       : 0.288
## ---
## Signif. codes: '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
## -----
## [[1]]
```

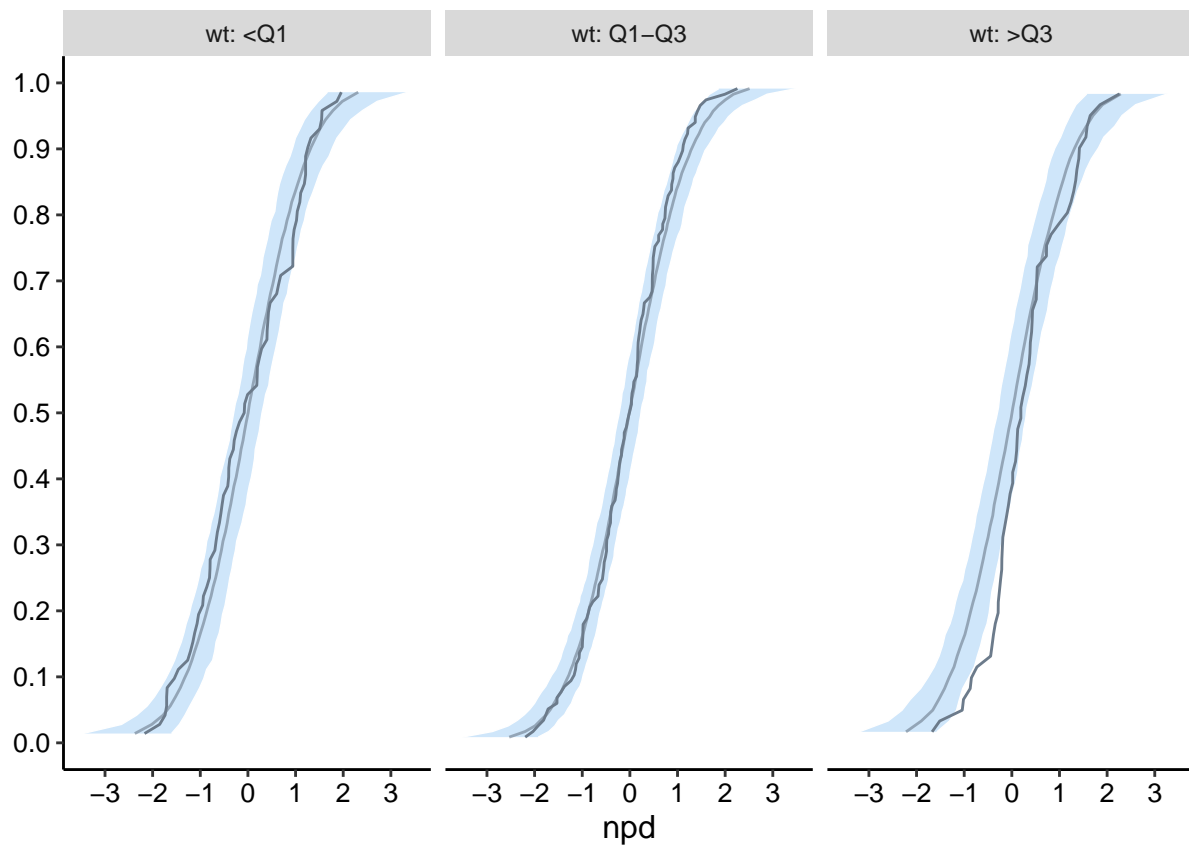


##  
## [[2]]

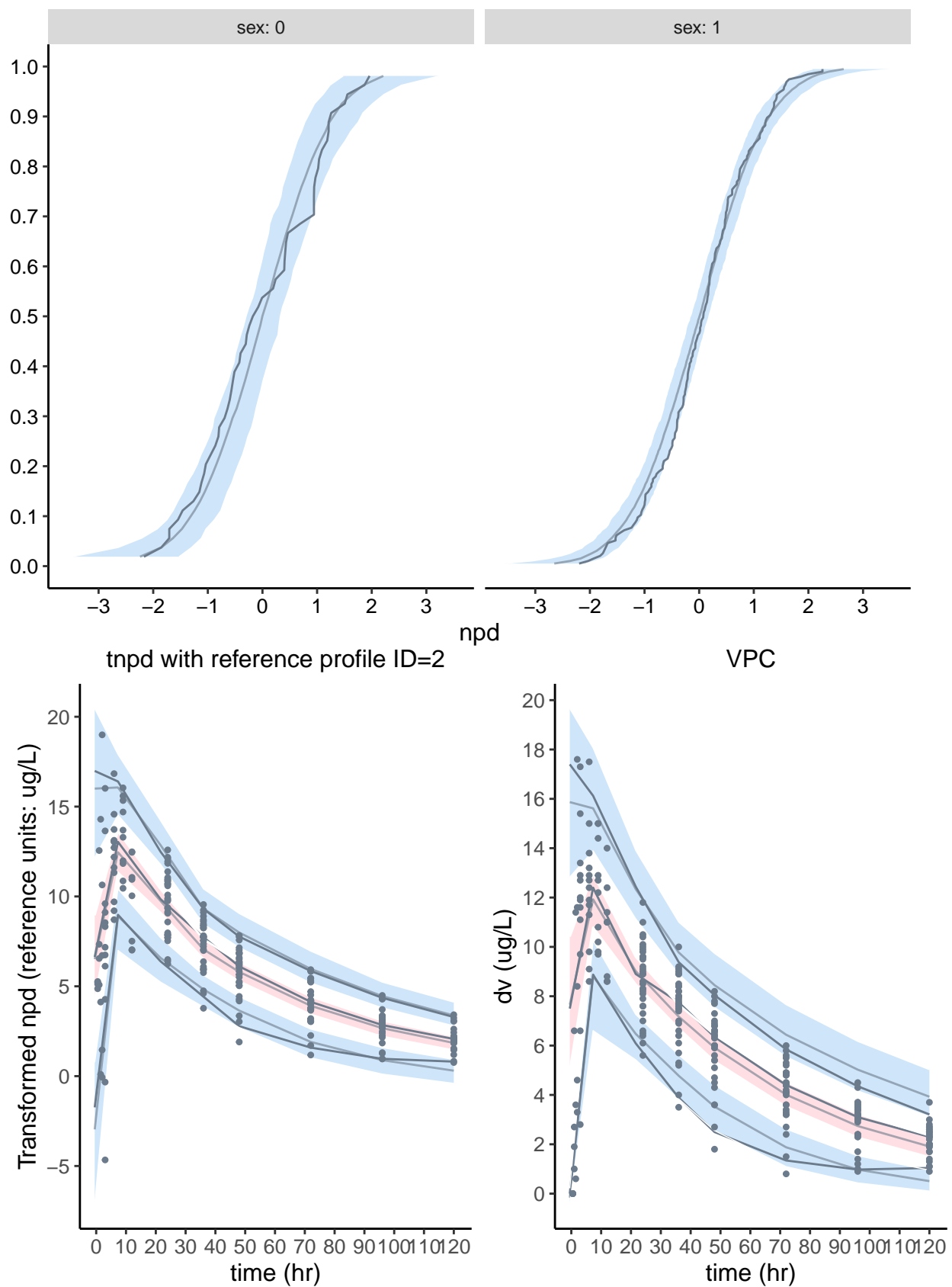


## [[1]]





```
##
## [[2]]
```



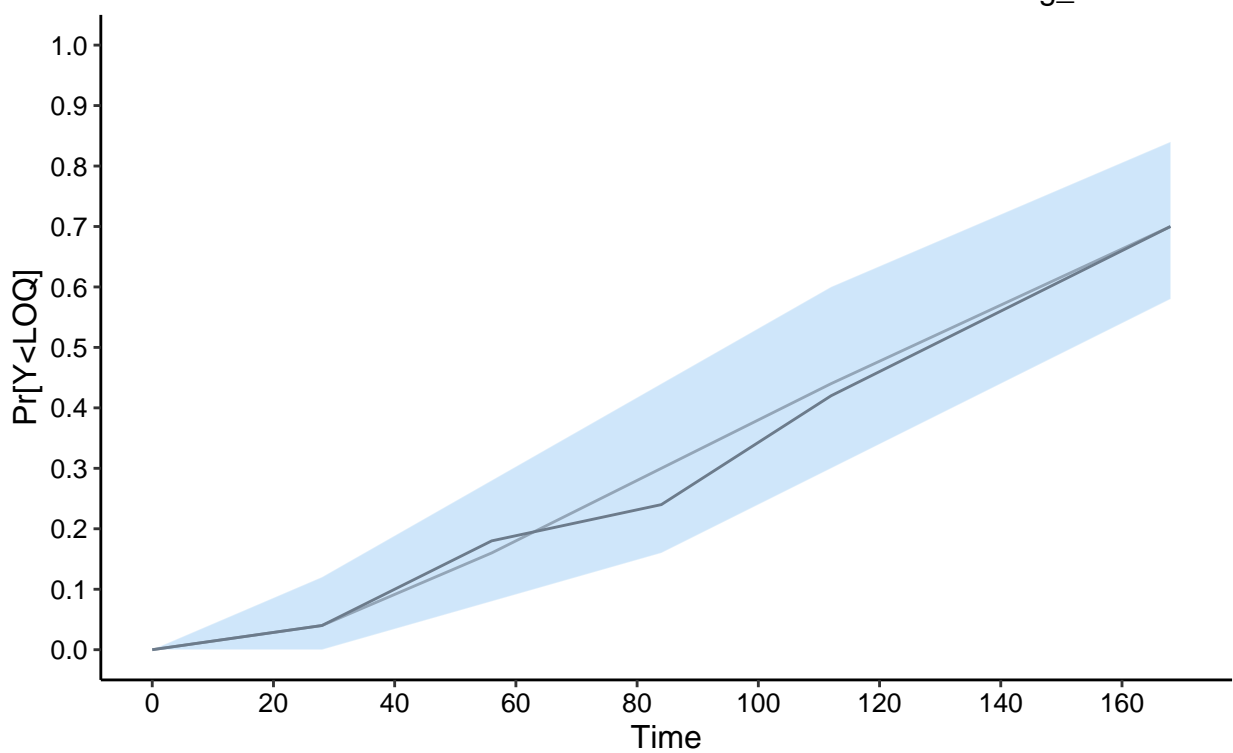
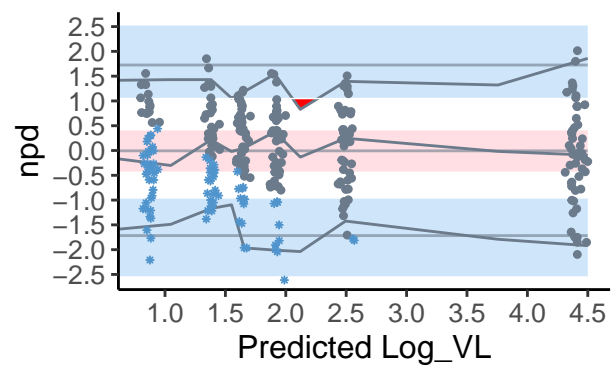
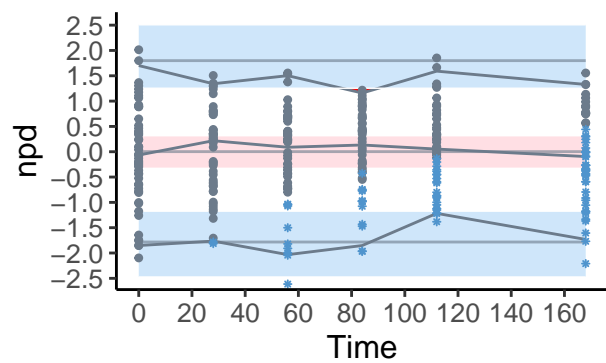
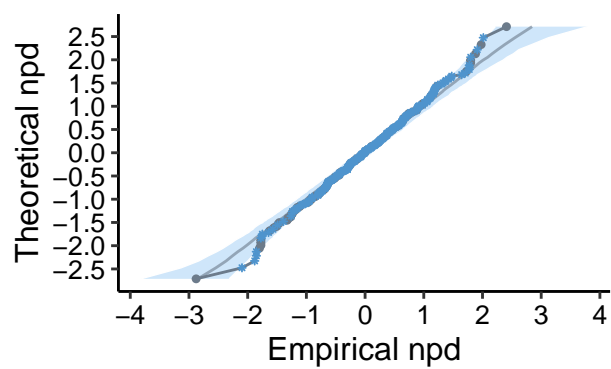
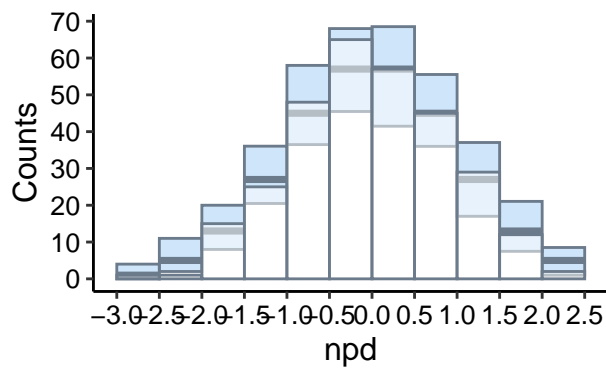
# Viral load, base plots

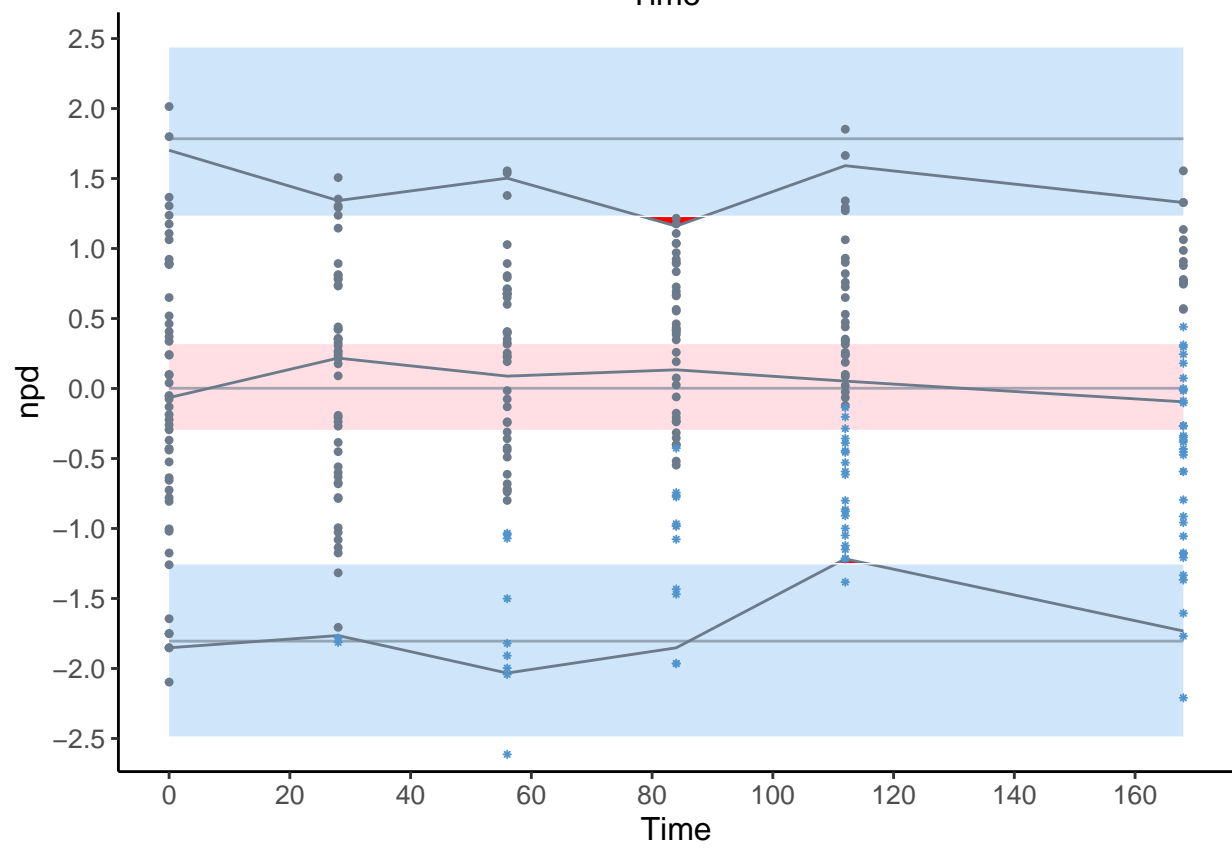
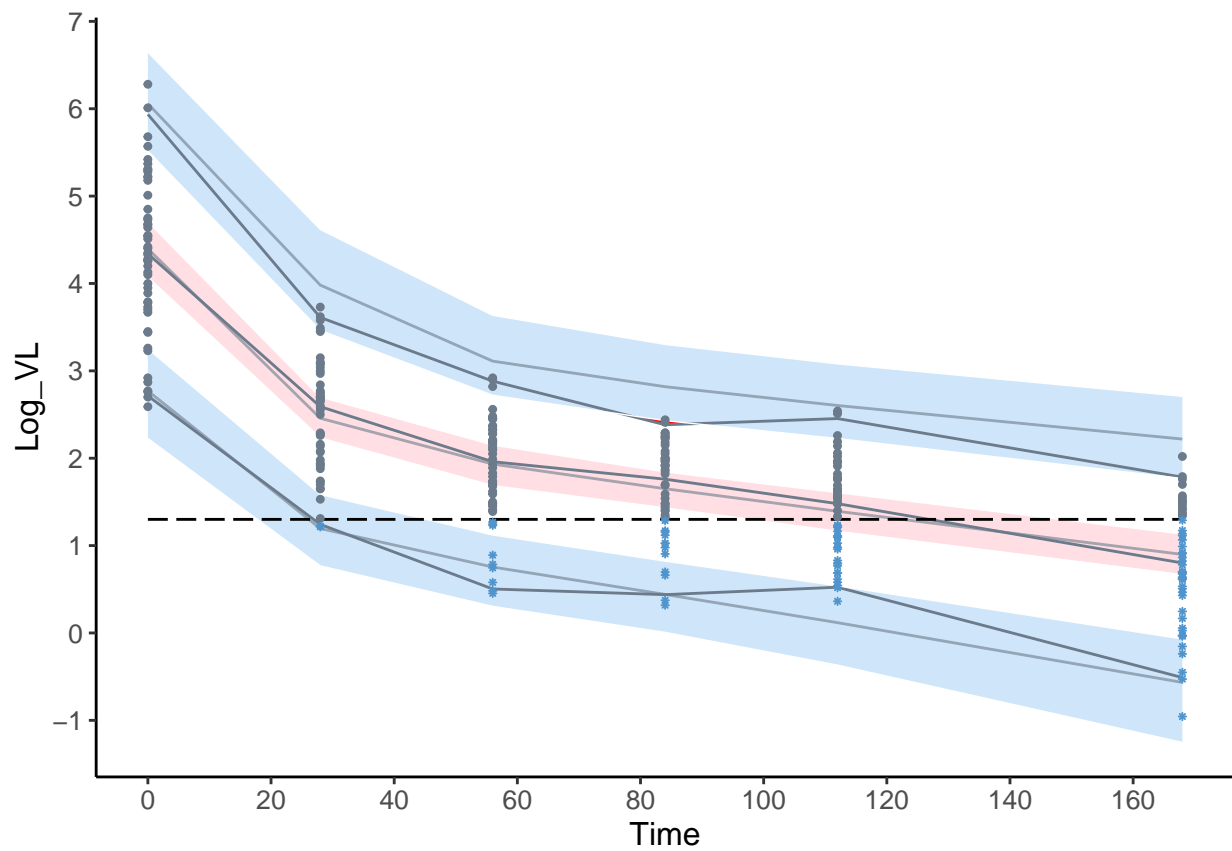
```

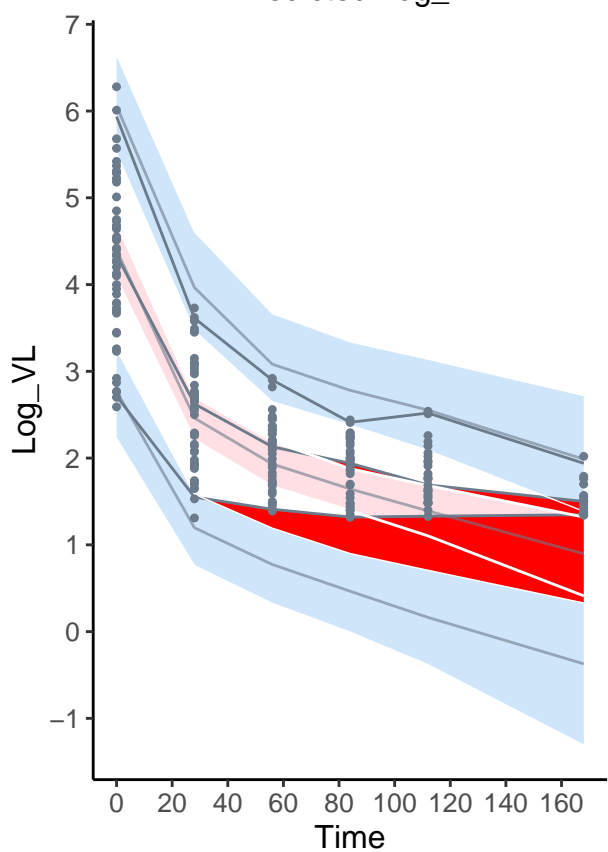
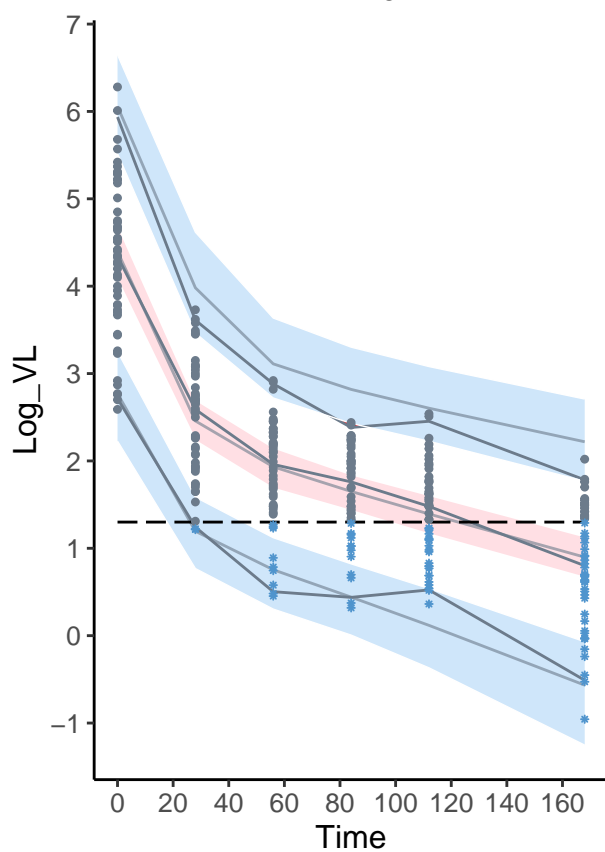
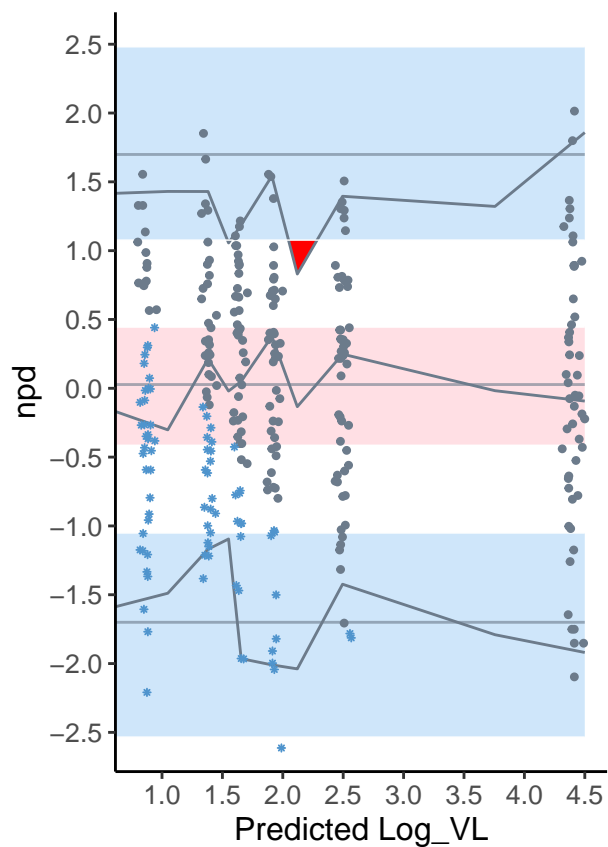
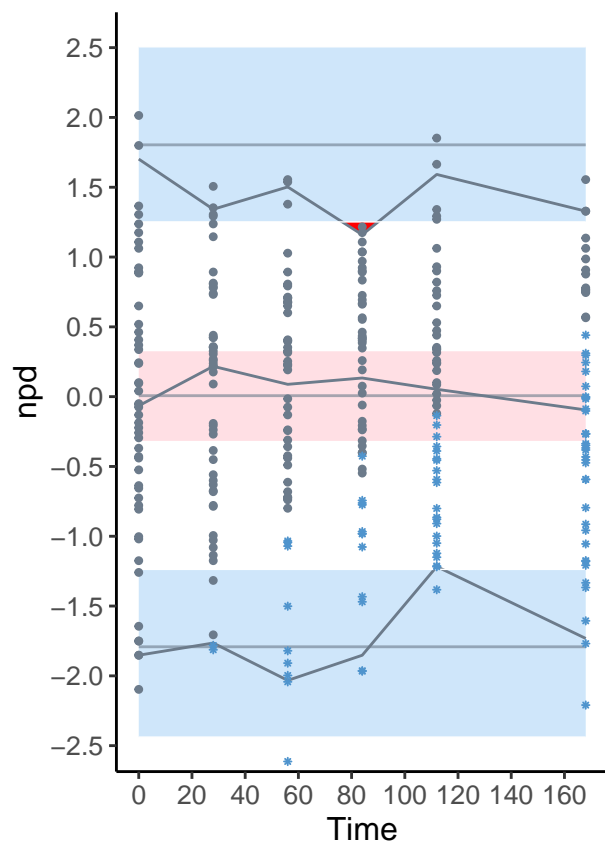
## -----
## Distribution of npde :
##      nb of obs: 300
##      mean= -0.008692   (SE= 0.052 )
##      variance= 0.824   (SE= 0.067 )
##      skewness= -0.04594
##      kurtosis= -0.244
## -----
## Statistical tests (adjusted p-values):
##      t-test           : 1
##      Fisher variance test : 0.0704 .
##      SW test of normality : 1
##      Global test       : 0.0704 .
## ---
## 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

```
## v 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 veeifier que la fonction et les options passent (use `testthat` for class to generate an object `npdeData` and plot it)