Supplementary material AAPS J

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07/04/2021

Loading libraries

```
knitr::opts_chunk$set(echo = TRUE)
# Libraries
library(gridExtra)
library(ggplot2)
library(grid)
library(devtools)

## Loading required package: usethis
library(mclust)

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

Install package in development mode

This is a snapshot of the version of npde released at the time of the revision of the paper submitted to AAPS Journal (version 3.1, April 2021). We use development mode to avoid messing up any existing installation of npde.

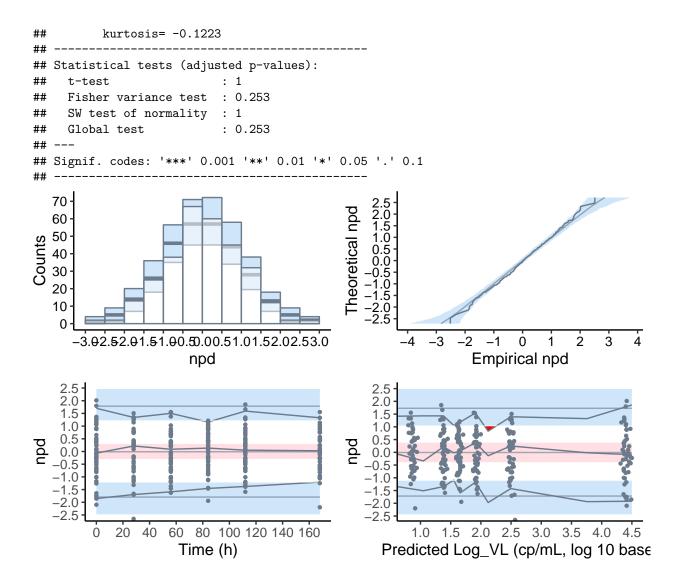
```
dev_mode() # development mode

## Dev mode: ON
install.packages(pkgs="/home/eco/work/npde/npde30/npde_3.1.tar.gz",repos=NULL)

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

Diagnostic plots for viral load example

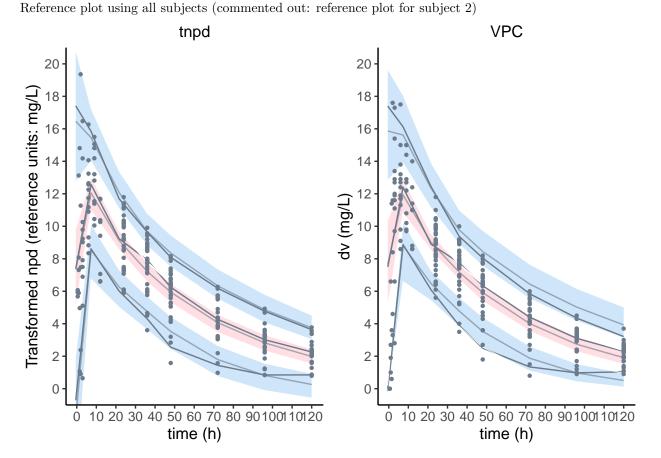
Default diagnostic plots for npd for the viral load example used in the paper



npd for the warfarin example in the documentation

Running the example:

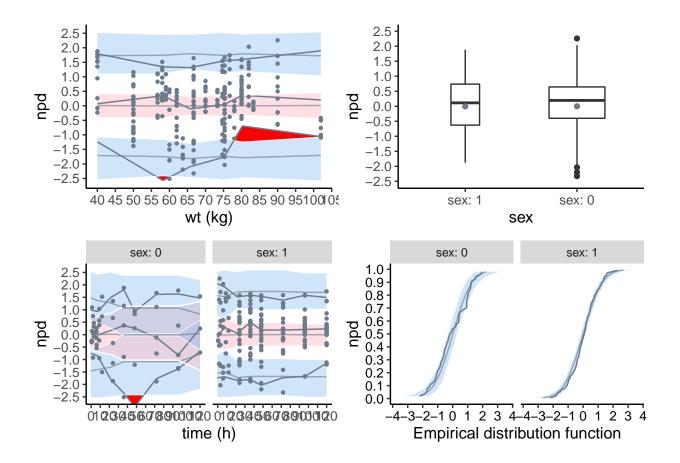
```
## Distribution of npde :
##
         nb of obs: 247
##
              mean = 0.02928
                               (SE = 0.059)
                              (SE= 0.077)
##
          variance= 0.8549
##
          skewness= -0.07211
##
          kurtosis = -0.4172
##
## Statistical tests (adjusted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



The code below shows several diagnostic plots for covariates:

- plots of npd versus covariates
 - we can also plot the distribution of eg npd versus the categories as boxplots
- $\bullet\,$ plots like scatter plots or distribution plots can be split over categories of covariates
 - we show this for weight (wt) and for sex

Warning: Removed 2 rows containing non-finite values (stat_boxplot).



End of code

Exit development mode.

dev_mode() # development mode

Dev mode: OFF