Package 'ggPMX'

May 8, 2026

Title 'ggplot2' Based Tool to Facilitate Diagnostic Plots for NLME Models

Description At Novartis, we aimed at standardizing the set of diagnostic plots used for modeling activities in order to reduce the overall effort required for generating such plots.
For this, we developed a guidance that proposes an adequate set of diagnostics and a toolbox, called 'ggPMX' to execute them. 'ggPMX' is a toolbox that can generate all diagnostic plots at a quality sufficient
for publication and submissions using few lines of code. This package focuses on plots recommended by ISoP
<doi:10.1002/psp4.12161>. While not required, you can get/install the 'R' 'lixoftConnectors' package in the 'Monolix' installation, as described at the following url
<https://monolixsuite.slp-software.com/r-functions/2024R1/installation-and-initialization>.
When 'lixoftConnectors' is available, 'R' can use 'Monolix' directly to create the required Chart Data instead of exporting it from the 'Monolix' gui.

Version 1.3.2

URL https://github.com/ggPMXdevelopment/ggPMX

BugReports https://github.com/ggPMXdevelopment/ggPMX/issues

Depends R (>= 3.5)

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Contents

`abbrev` *Give the whole abbreviation definition*

Description

Give the whole abbreviation definition

Usage

```
abbrev(param)
```

Arguments

param	abbreviation term

Value

character abbreviation definition

Examples

```
abbrev("VPC")
```

---

add_draft *Add draft layer annotation*

Description

This function adds the word draft to certain graphics.

Usage

```
add_draft(
  label = "DRAFT",
  size = 10,
  colour = "grey50",
  x = Inf,
  y = -Inf,
  ...
)
```

Arguments

label	draft layer default to DRAFT
size	size of the annotation
colour	color of the annotation default to grey50
x	numeric x coordinate of the draft label
y	numeric y coordinate of the draft label
...	extra parameters to geom text used to annotate the draft

Value

ggplot2 annotation

check_shrink *Performs checks of names in shrink list*

Description

Performs checks of names in shrink list

Usage

```
check_shrink(shrink_list)
```

Arguments

shrink_list	list list of shrink arguments

distrib *creates a graphic distribution object*

Description

creates a graphic distribution object

Usage

```
distrib(
  labels,
  is.shrink,
  type = c("box", "hist"),
  is.jitter = FALSE,
  jitter = NULL,
  facets = NULL,
  histogram = NULL,
  shrink = NULL,
  dname = NULL,
  ...
)
```

Arguments

labels	list of texts/titles used within the plot
is.shrink	logical if TRUE add shrinkage layer
type	box for boxplot or histogram
is.jitter	logical if TRUE add jitter operator for points
jitter	list set jitter parameter

facets	list set the facet setting in case of histogram plot
histogram	list histogram graphical parameters
shrink	pmxShrinkClass shrinkage graphical parameter or list coercible into one
dname	name of dataset to be used
...	others graphics arguments passed to pmx_gpar internal object.

Details

labels is a list that contains:

- **title:** plot title default "EBE distribution"
- **subtitle:** plot subtitle default empty
- **x:** x axis label default to "Etas"
- **y:** y axis label default to empty
- **legend:** legend title default to "random Effect"

shrink is a list that contains:

- **fun:** shrinkage function can be sd or var
- **size:** shrinkage text size
- **color:** shrinkage text color
- **vjust:** shrinkage position vertical adjustment

Value

distrib object

See Also

Other plot_pmx: eta_cov(), eta_pairs(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

---

eta_cov

This creates an ETA covariance matrix which can be used to define the co-relation between the parameters and its shrinkage..

Description

This creates an ETA covariance matrix which can be used to define the co-relation between the parameters and its shrinkage..

Usage

```
eta_cov(
  labels,
  type = c("cats", "conts"),
  dname = NULL,
  show.correl = TRUE,
  correl = NULL,
  facets = NULL,
  point = NULL,
  covariates = NULL,
  is.strat.color = FALSE,
  ...
)
```

Arguments

labels	list of texts/titles used within the plot
type	box for cats or conts
dname	name of dataset to be used
show.correl	logical if TRUE add correlation to the plot
correl	list correl geom text graphical parameter
facets	list facetting graphical parameter
point	list geom point graphical parameter
covariates	pmxCOVObject pmx_cov
is.strat.color	logical if 'TRUE' use a different color for the spline stratification.
...	others graphics arguments passed to pmx_gpar internal object.

Details

labels is a list that contains:

- **title:** plot title default "EBE vs. covariates"
- **x:** x axis label default to "Etas"
- **y:** y axis label default to empty

Value

eta_cov object

See Also

Other plot_pmx: distrib(), eta_pairs(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

`eta_cov_plot` *Eta Covariates plots*

Description

Eta Covariates plots

Relationships between (ETA) and categorical covariates

Relationships between (ETA) and continuous covariates

Usage

```
dummy(
  dname,
  show.correl,
  correl,
  point,
  facets,
  covariates,
  filter,
  strat.facet,
  strat.color,
  trans,
  pmxgpar,
  labels,
  axis.title,
  axis.text,
  ranges,
  is.smooth,
  smooth,
  is.band,
  band,
  is.draft,
  draft,
  is.identity_line,
  identity_line,
  scale_x_log10,
  scale_y_log10,
  color.scales
)

pmx_plot_eta_cats(ctr, ...)

pmx_plot_eta_conts(ctr, ...)
```

Arguments

`dname`	`character` name of dataset to be used

show.correl	logical if TRUE add correlation to the plot
correl	list correl geom text graphical parameter
point	list geom point graphical parameter
facets	list facetting graphical parameter
covariates	list of selected covariates and custom labels, e.g. pmx_cov(values = list("SEX"), labels = list("Sex")) list pmxCOVObject pmx_cov
	pmx_update parameters
filter	expression filter which will be applied to plotting data.
strat.facet	formula optional stratification parameter by facetting. This split plot by strats(each strat in a facet)
strat.color	character optional stratification parameter by grouping. This will split the plot by group (color) of strat.
trans	character define the transformation to apply on x or y or both variables
pmxgpar	a object of class pmx_gpar possibly the output of the
	pmx_gpar: Shared basic graphics parameters
labels	list list containing plot and/or axis labels: title, subtitle, x , y
axis.title	list containing element_text attributes to customize the axis title. (similar to ggplot2 axis.title theme)
axis.text	list containing element_text attributes to customize the axis text (similar to ggplot2 axis.text theme)
ranges	list limits of x/y ranges
is.smooth	logical if set to TRUE add smooth layer
smooth	list geom_smooth graphical/smoothing fun parameters
is.band	logical if TRUE add horizontal band
band	list horizontal band parameters. geom_hline graphical parameters.
is.draft	logical if TRUE add draft layer
draft	list draft layer parameters. geom_text graphical parameters.
is.identity_line	logical if TRUE add an identity line
identity_line	listgeom_abline graphical parameters.
scale_x_log10	logical if TRUE use log10 scale for x axis.
scale_y_log10	logical if TRUE use log10 scale for y axis.
color.scales	list define scales parameter in case of strat.color pmx_settings
ctr	pmx controller
...	others graphics parameters passed :

- pmx_gpar internal function to customize shared graphical parameters
- eta_cov generic object for eta/covariates plots.
- pmx_update function.

eta_cov parameters

Value

ggplot2 object

ggplot2 object

ggplot2 object

Examples

```
# basic use  ---------------------------------------

ctr <- theophylline()
ctr %>% pmx_plot_eta_cats
ctr %>% pmx_plot_eta_conts

# update graphical parameter  ----------------------

## plot selected covariates
ctr %>% pmx_plot_eta_cats(
  covariates = pmx_cov(values = list("SEX"))
  )


## update labels
ctr %>% pmx_plot_eta_cats(
  labels = list(title = "New eta cats title")
)

## remove draft
ctr %>% pmx_plot_eta_cats(is.draft = FALSE)

## change text color line
ctr %>% pmx_plot_eta_conts(
  correl=list(colour="magenta")
  )

## set covariates custom labels

ctr %>% pmx_plot_eta_conts(
  covariates=pmx_cov(values=list("WT0","AGE0"),
                     labels=list("Weight","Age"))
)

## set effects and covaraites custom labels


ctr <- theophylline( settings = pmx_settings(
  effects=list( levels=c("ka", "V", "Cl"),
                labels=c("Concentration","Volume","Clearance")
  )
)
```

```
)
ctr %>% pmx_plot_eta_conts(
  covariates=pmx_cov(values=list("WT0","AGE0"),
                     labels=list("Weight","Age"))
)
```

`eta_distribution_plot` *Eta distribution plots*

Description

Eta distribution plots

Eta Distribution boxplot

Eta Distribution histogram plot

Usage

```
eta_distribution_plot(
  jitter,
  type,
  dname,
  is.shrink,
  shrink,
  is.jitter,
  histogram,
  filter,
  strat.facet,
  facets,
  strat.color,
  trans,
  pmxgpar,
  labels,
  axis.title,
  axis.text,
  ranges,
  is.smooth,
  smooth,
  is.band,
  band,
  is.draft,
  draft,
  is.identity_line,
```

```
  identity_line,
  scale_x_log10,
  scale_y_log10,
  color.scales,
  ...
)

pmx_plot_eta_box(ctr, ...)

pmx_plot_eta_hist(ctr, ...)
```

Arguments

jitter	list set jitter parameter
type	box for boxplot or histogram
dname	name of dataset to be used
is.shrink	logical if TRUE add shrinkage layer
shrink	list parameters to control shrinkage, must contain "fun"
is.jitter	logical if TRUE add jitter operator for points
histogram	list histogram graphical parameters
	pmx_update parameters
filter	expression filter which will be applied to plotting data.
strat.facet	formula optional stratification parameter by facetting. This split plot by strats(each strat in a facet)
facets	list facet_wrap parameters.
strat.color	character optional stratification parameter by grouping. This will split the plot by group (color) of strat.
trans	character define the transformation to apply on x or y or both variables
pmxgpar	a object of class pmx_gpar possibly the output of the
	pmx_gpar: Shared basic graphics parameters
labels	list list containing plot and/or axis labels: title, subtitle, x , y
axis.title	list containing element_text attributes to customize the axis title. (similar to ggplot2 axis.title theme)
axis.text	list containing element_text attributes to customize the axis text (similar to ggplot2 axis.text theme)
ranges	list limits of x/y ranges
is.smooth	logical if set to TRUE add smooth layer
smooth	list geom_smooth graphical/smoothing fun parameters
is.band	logical if TRUE add horizontal band
band	list horizontal band parameters. geom_hline graphical parameters.
is.draft	logical if TRUE add draft layer
draft	list draft layer parameters. geom_text graphical parameters.

`is.identity_line`
: `logical` if TRUE add an identity line

`identity_line`
: `list`geom_abline graphical parameters.

`scale_x_log10`
: `logical` if TRUE use log10 scale for x axis.

`scale_y_log10`
: `logical` if TRUE use log10 scale for y axis.

`color.scales`
: `list` define scales parameter in case of strat.color `pmx_settings`

`...`
: others graphics parameters passed :

- `pmx_gpar` internal function to customize shared graphical parameters
- `distrib` generic object for distribution plots (histogram/boxplot).
- `pmx_update` function.

distrib parameters

`ctr`
: pmx controller

Value

ggplot2 object

Examples

```
# *************** basic use ***************** ------

ctr <- theophylline()
## boxplot variation
p <- ctr %>% pmx_plot_eta_box()
## histogram variation
p <- ctr %>% pmx_plot_eta_hist()

# update graphical parameter  ----------------------

## add jitter
ctr %>%
  pmx_plot_eta_hist(is.jitter = TRUE, jitter = list(alpha = 0.4, color = "red"))

## remove shrinkage
ctr %>%
  pmx_plot_eta_hist(is.shrink = FALSE)

## update histogram graphical parameters
ctr %>%
  pmx_plot_eta_hist(
    histogram = list(
      color = NA,
      position = "fill",
      binwidth = 1 / 100
    )
  )
```

```
# stratification  ---------------------------------

## categorical stratification color parameter
ctr %>% pmx_plot_eta_hist(is.jitter = TRUE, strat.facet = ~STUD, strat.color = ~SEX)

## categorical stratification facetting
ctr %>% pmx_plot_eta_hist(strat.facet = ~SEX)

## using formula categorical stratification facetting
ctr %>% pmx_plot_eta_hist(
  strat.facet = STUD ~ SEX,
  shrink = pmx_shrink(hjust = 0.5)
)

# subsetting  -------------------------------------

## select a set of random effect
ctr %>% pmx_plot_eta_hist(filter = EFFECT %in% c("ka", "Cl"))
## filter and stratify by facets
ctr %>% pmx_plot_eta_hist(
  filter = EFFECT %in% c("ka", "Cl"), strat.facet = ~SEX
)
ctr %>% pmx_plot_eta_hist(
  filter = EFFECT %in% c("ka", "Cl"), strat.facet = ~SEX
)
```

`eta_pairs` *This creates an eta correlation which defines the relationship between parameters*

Description

This creates an eta correlation which defines the relationship between parameters

Usage

```
eta_pairs(
  is.title,
  title,
  dname = NULL,
  type.eta = c("mode", "mean"),
  text_color = "black",
  is.shrink = TRUE,
  is.smooth = TRUE,
  smooth = NULL,
  point = NULL,
  shrink = NULL,
  is.hline = FALSE,
```

```
  hline = NULL,
  is.vreference_line = FALSE,
  vreference_line = list(colour = "orange", linetype = "longdash"),
  ...
)
```

Arguments

is.title	logical if TRUE then a title is used for the plot
title	character the plot title
dname	name of dataset to be used
type.eta	character type of eat can be 'mode' or 'mean'.'mode' by default
text_color	color of the correlation text in the upper matrix
is.shrink	logical if TRUE add shrinkage to the plot
is.smooth	logical if TRUE add smoothing to lower matrix plots
smooth	list geom_smooth graphical parameters
point	list geom_point graphical parameter
shrink	pmxShrinkClass shrinkage graphical parameter or list coercible into one
is.hline	logical if TRUE add horizontal line to lower matrix plots
hline	list geom_hline graphical parameters
is.vreference_line	logical if TRUE add the +- 1.96 lines
vreference_line	list geom_hline graphical parameters for the reference lines
...	others graphics arguments passed to pmx_gpar internal object.

Value

ecorrel object

See Also

Other plot_pmx: distrib(), eta_cov(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

eval_sym_parent_env *Try to evaluate a symbol in the parent frame (on error return the symbol)*

Description

Try to evaluate a symbol in the parent frame (on error return the symbol)

Usage

```
eval_sym_parent_env(x)
```

Arguments

x	any object

Value

evaluated symbol or the symbol in case of evaluation error

getPmxOption *Get ggPMX Option*

Description

Get ggPMX Option

Usage

```
getPmxOption(name, default = NULL)
```

Arguments

name	Name of an option to get.
default	Value to be returned if the option is not currently set.

Value

value of the option or NULL

Examples

```
## Not run:
pmxOptions(myOption = 10)
getPmxOption("myOption")

## End(Not run)
```

get_abbrev *Get abbreviation definition by key*

Description

Get abbreviation definition by key

Usage

```
get_abbrev(ctr, param)
```

Arguments

ctr	pmxClass controller
param	abbreviation term

Value

character abbreviation definition

get_cats *Get category covariates*

Description

Get category covariates

Usage

```
get_cats(ctr)
```

Arguments

ctr	the controller object

Value

a charcater vector

See Also

Other pmxclass: get_conts(), get_covariates(), get_data(), get_occ(), get_plot(), get_plot_config(), get_strats(), plot_names(), plots(), pmx_update(), set_data(), set_plot()

get_conts *Get continuous covariates*

Description

Get continuous covariates

Usage

```
get_conts(ctr)
```

Arguments

ctr	the controller object

Value

a charcater vector

See Also

Other pmxclass: get_cats(), get_covariates(), get_data(), get_occ(), get_plot(), get_plot_config(), get_strats(), plot_names(), plots(), pmx_update(), set_data(), set_plot()

get_covariates *Get covariates variables*

Description

Get covariates variables

Usage

```
get_covariates(ctr)
```

Arguments

ctr	the controller object

Value

a charcater vector

See Also

Other pmxclass: get_cats(), get_conts(), get_data(), get_occ(), get_plot(), get_plot_config(), get_strats(), plot_names(), plots(), pmx_update(), set_data(), set_plot()

get_data *Get controller data set*

Description

Get controller data set

Usage

```
get_data(
  ctr,
  data_set = c("estimates", "predictions", "eta", "finegrid", "input", "sim",
    "individual")
)
```

Arguments

ctr	the controller object
data_set	the data set name

Value

a data.table of the named data set if available.

See Also

Other pmxclass: get_cats(), get_conts(), get_covariates(), get_occ(), get_plot(), get_plot_config(), get_strats(), plot_names(), plots(), pmx_update(), set_data(), set_plot()

get_occ *Get controller occasional covariates*

Description

Get controller occasional covariates

Usage

```
get_occ(ctr)
```

Arguments

ctr	the controller object

Value

a charcater vector

See Also

Other pmxclass: get_cats(), get_conts(), get_covariates(), get_data(), get_plot(), get_plot_config(), get_strats(), plot_names(), plots(), pmx_update(), set_data(), set_plot()

`get_plot` *Get plot object*

Description

Get plot object

Usage

```
get_plot(ctr, nplot, which_pages = "all")
```

Arguments

`ctr`	`pmxClass` controller object
`nplot`	character the plot name
`which_pages`	integer vector (can be length 1), set page number in case of multi pages plot, or character "all" to plot all pages.

Value

ggplot object

See Also

Other pmxclass: get_cats(), get_conts(), get_covariates(), get_data(), get_occ(), get_plot_config(), get_strats(), plot_names(), plots(), pmx_update(), set_data(), set_plot()

Examples

```
library(ggPMX)
ctr <- theophylline()
p1 <- ctr %>% get_plot("iwres_ipred")
## get all pages or some pages
p2 <- ctr %>% get_plot("individual")
## returns one page of individual plot
p2 <- ctr %>% get_plot("individual", which_pages = 1)
p3 <- ctr %>% get_plot("individual", which_pages = c(1, 3))
## get distribution plot
pdistri <- ctr %>% get_plot("eta_hist")
```

get_plot_config *Get the plot config by name*

Description

Get the plot config by name

Usage

```
get_plot_config(ctr, pname)
```

Arguments

ctr	the controller object
pname	the plot name

Value

the config object

See Also

Other pmxclass: get_cats(), get_conts(), get_covariates(), get_data(), get_occ(), get_plot(), get_strats(), plot_names(), plots(), pmx_update(), set_data(), set_plot()

Examples

```
ctr <- theophylline()
ctr %>% set_plot("IND", pname = "indiv1")
ctr %>% get_plot_config("distr1")
```

get_strats *Get extra stratification variables*

Description

Get extra stratification variables

Usage

```
get_strats(ctr)
```

Arguments

ctr	the controller object

Value

a charcater vector

See Also

Other pmxclass: get_cats(), get_conts(), get_covariates(), get_data(), get_occ(), get_plot(), get_plot_config(), plot_names(), plots(), pmx_update(), set_data(), set_plot()

`gtable_remove_grobs` *Remove named elements from gtable*

Description

Remove named elements from gtable

Usage

```
gtable_remove_grobs(table, names, ...)
```

Arguments

`table`	The table from which grobs should be removed
`names`	A character vector of the grob names (as listed in `table$layout`) that should be removed
`...`	Other parameters passed through to `gtable_filter`.

Value

table The table with removed grobs

`individual` *This function can be used to obtain individual prediction and compare with observed data and population prediction for each individual separately*

Description

This function can be used to obtain individual prediction and compare with observed data and population prediction for each individual separately

Usage

```
individual(
  labels,
  facets = NULL,
  dname = NULL,
  ipred_line = NULL,
  pred_line = NULL,
  point = NULL,
  bloq = NULL,
  is.legend,
  use.finegrid,
  ...
)
```

Arguments

labels	plot texts. labels, axis,
facets	list facets settings nrow/ncol
dname	name of dataset to be used
ipred_line	list some pred line geom properties aesthetics
pred_line	list some ipred line geom properties aesthetics
point	list some point geom properties aesthetics
bloq	pmxBLOQ object created by pmx_bloq
is.legend	logical if TRUE add a legend
use.finegrid	logical if FALSE use predictions data set
...	others graphics arguments passed to pmx_gpar internal object.

Value

individual fit object

See Also

plot_pmx.individual

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

input_finegrid *Merge input and fingrid data sets*

Description

Merge input and fingrid data sets

Usage

```
input_finegrid(input, finegrid)
```

Arguments

input	data.table input data set
finegrid	data.table finegrid data set

Value

data.table

is.pmx_gpar *Check if an object is a pmx_gpar class*

Description

Check if an object is a pmx_gpar class

Usage

```
is.pmx_gpar(x)
```

Arguments

x	pmx_gpar object

Value

logical returns TRUE if it is a pmx_gpar object

load_config *Obtain the data source config*

Description

Obtain the data source config

Usage

```
load_config(x, sys = c("mlx", "nm", "mlx18"))
```

Arguments

x	the config name.
sys	can be mlx,nm,...

Value

a list :data configuration object

load_data_set *Load data set*

Description

Load data set

Usage

```
load_data_set(x, path, sys, ...)
```

Arguments

x	data set config
path	character path to the directory
sys	`character` mlx or nm
...	extra parameter passed to special readers

Value

data.table

load_source *Load all/or some source data set*

Description

Load all/or some source data set

Usage

```
load_source(sys, path, dconf, ...)
```

Arguments

sys	type cane mlx/nom
path	character directory path containing all sources.
dconf	configuration object
...	any extra parameters for readers

Value

list of data.table

l_left_join *Merge 2 lists*

Description

left join , the first list is updated by the seond one

Usage

```
l_left_join(base_list, overlay_list, recursive = TRUE)
```

Arguments

base_list	list to update
overlay_list	list used to update the first list
recursive	logical if TRUE do the merge in depth

Value

list

n_pages *Determine the number of pages in a paginated facet plot*

Description

This is a simple helper that returns the number of pages it takes to plot all panels when using facet_wrap_paginate . It partially builds the plot so depending on the complexity of your plot it might take some time to calculate...

Usage

```
n_pages(plot)
```

Arguments

plot	A ggplot object using either facet_wrap_paginate or facet_grid_paginate

Value

If the plot uses using either facet_wrap_paginate or facet_grid_paginate it returns the total number of pages. Otherwise it returns NULL

param_table *Creates parameter kable*

Description

Creates parameter kable

Usage

```
param_table(ctr, fun, return_table = FALSE, scientific = FALSE, digits = 2)
```

Arguments

ctr	Generated controller from e.g. pmx_mlx for Monolix.
fun	character can be "sd" or "var" for shrinkage computation, see pmx_comp_shrink
return_table	If TRUE, returns the same table as in get_data('estimates') otherwise it returns a kable
scientific	logical set to TRUE to get scientific notation of parameter values, or FALSE otherwise
digits	integer the number of significant digits to use when rounding parameter values

Value

Returns a kable with the parameter estimates from get_data('estimates')

Examples

```
#ctr <- theophylline()
#my_params <- ctr %>% param_table(fun = "var")
```

---

parse_mlxtran *Parse MONOLIX mlxtran file*

Description

Parse MONOLIX mlxtran file

Usage

```
parse_mlxtran(file_name)
```

Arguments

file_name	absolute path to mlxtran file

Value

list key/values to initialize ggPMX controller

---

pk_occ *Creates pmx controller using monlix data having Occasional variable*

Description

Creates pmx controller using monlix data having Occasional variable

Usage

```
pk_occ()
```

Value

pmx controller

Examples

```
## Not run:
pk_occ()

## End(Not run)
```

pk_pd *Creates pkpd pmx controller using package internal data*

Description

Creates pkpd pmx controller using package internal data

Usage

```
pk_pd(code = "3")
```

Arguments

code	can be 3 or 4

plots *Get plots description*

Description

Get plots description

Usage

```
plots(ctr)
```

Arguments

ctr	pmxClass controller object

Value

data.frame of plots

See Also

Other pmxclass: get_cats(), get_conts(), get_covariates(), get_data(), get_occ(), get_plot(), get_plot_config(), get_strats(), plot_names(), pmx_update(), set_data(), set_plot()

plot_names *Get plot names*

Description

Get plot names

Usage

```
plot_names(ctr)
```

Arguments

ctr	pmxClass controller object

Value

list of plot names

See Also

Other pmxclass: get_cats(), get_conts(), get_covariates(), get_data(), get_occ(), get_plot(), get_plot_config(), get_strats(), plots(), pmx_update(), set_data(), set_plot()

plot_pmx *This is a generic plot method that produces all plots by default described in pmx model evaluation guidance.*

Description

This is a generic plot method that produces all plots by default described in pmx model evaluation guidance.

Usage

```
plot_pmx(x, dx, ...)

## S3 method for class 'pmx_vpc'
plot_pmx(x, dx, ...)
```

Arguments

x	object to plot
dx	data.table , plot source data
...	extra argument (not used)

See Also

pmx_gpar.

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), individual(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

---

plot_pmx.distrib *Plot EBE distribution*

Description

Plot EBE distribution

Usage

```
## S3 method for class 'distrib'
plot_pmx(x, dx, ...)
```

Arguments

x	distribution object
dx	data set
...	not used for the moment

Value

ggplot2 plot

See Also

distrib

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), individual(), plot_pmx(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

plot_pmx.eta_cov *This plots an ETA covariance matrix which can be used to define the co-relation between the parameters and its shrinkage*

Description

This plots an ETA covariance matrix which can be used to define the co-relation between the parameters and its shrinkage

Usage

```
## S3 method for class 'eta_cov'
plot_pmx(x, dx, ...)
```

Arguments

x	eta_cov object
dx	data set
...	not used for the moment

Value

ggplot2 plot

See Also

eta_cov

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

plot_pmx.eta_pairs *Plot random effect correlation plot*

Description

Plot random effect correlation plot

Usage

```
## S3 method for class 'eta_pairs'
plot_pmx(x, dx, ...)
```

Arguments

x	distribution object
dx	data set
...	not used for the moment

Value

ggpairs plot

See Also

distrib

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

---

plot_pmx.individual *This function can be used to plot individual prediction and compare with observed data and population prediction for each individual separately*

Description

This function can be used to plot individual prediction and compare with observed data and population prediction for each individual separately

Usage

```
## S3 method for class 'individual'
plot_pmx(x, dx, ...)
```

Arguments

x	individual object
dx	data set
...	not used for the moment

Value

a list of ggplot2

See Also

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

plot_pmx.pmx_dens *This function plots EBE versus covariates using qq plots*

Description

This function plots EBE versus covariates using qq plots

Usage

```
## S3 method for class 'pmx_dens'
plot_pmx(x, dx, ...)
```

Arguments

x	eta_cov object
dx	data set
...	not used for the moment

Value

ggplot2 plot

See Also

eta_cov

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

plot_pmx.pmx_gpar *The ggPMX base plot function*

Description

This function should be called internally by other plots to set general settings like , smoothing, add band, labelling, theming,...

Usage

```
## S3 method for class 'pmx_gpar'
plot_pmx(x, dx, ...)
```

Arguments

x	object of pmx_gpar type
dx	plot
...	ignored parameters

Value

ggplot2 object

See Also

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq(), plot_pmx.residual()

---

plot_pmx.pmx_param_history

S3 method for plots of class pmx_param_history

Description

S3 method for plots of class pmx_param_history

Usage

```
## S3 method for class 'pmx_param_history'
plot_pmx(x, dx, ...)
```

Arguments

x	pmx_param_history object
dx	data set
...	not used

Value

ggplot2 plot

See Also

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_qq(), plot_pmx.residual()

plot_pmx.pmx_qq *This function plot EBE versus covariates using qq plots*

Description

This function plot EBE versus covariates using qq plots

Usage

```
## S3 method for class 'pmx_qq'
plot_pmx(x, dx, ...)
```

Arguments

x	pmx_qq object
dx	data set
...	not used for the moment

Value

ggplot2 plot

See Also

eta_cov

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.residual()

plot_pmx.residual *This function plots residual for each observed value by finding the difference between observed and predicted points. It also fits a distribution to the residual value.*

Description

This function plots residual for each observed value by finding the difference between observed and predicted points. It also fits a distribution to the residual value.

Usage

```
## S3 method for class 'residual'
plot_pmx(x, dx, ...)
```

Arguments

x	residual object
dx	data set
...	not used for the moment

Value

ggplot2 object

See Also

residual

Other plot_pmx: distrib(), eta_cov(), eta_pairs(), individual(), plot_pmx(), plot_pmx.distrib(), plot_pmx.eta_cov(), plot_pmx.eta_pairs(), plot_pmx.individual(), plot_pmx.pmx_dens(), plot_pmx.pmx_gpar(), plot_pmx.pmx_param_history(), plot_pmx.pmx_qq()

---

plot_shrink *Plot shrink in eta matric*

Description

Plot shrink in eta matric

Usage

```
plot_shrink(x, shrink.dx, shrink)
```

Arguments

x	pmx_gpar object
shrink.dx	data.table of shrinkage
shrink	pmxShrinkClass shrinkage graphical parameter or list coercible into one

Value

ggplot2 object

pmx *Create a pmx object*

Description

Create a pmx object from a data source

Usage

```
pmx(
  config,
  sys = "mlx",
  directory,
  input,
  dv,
  dvid,
  cats = NULL,
  conts = NULL,
  occ = NULL,
  strats = NULL,
  settings = NULL,
  endpoint = NULL,
  sim = NULL,
  bloq = NULL,
  id = NULL,
  time = NULL,
  sim_blq = NULL
)

pmx_mlx(
  config,
  directory,
  input,
  dv,
  dvid,
  cats,
  conts,
  occ,
  strats,
  settings,
  endpoint,
  sim,
  bloq,
  id,
  time,
  sim_blq
)
```

```
pmx_mlxtran(
  file_name,
  config = "standing",
  call = FALSE,
  endpoint,
  version = -1,
  ...
)
```

Arguments

config	Can be either : The complete path for the configuration file, the name of configuration within the built-in list of configurations, or a configuration object.
sys	the system name can "mlx" (for Monolix 2016) or "mlx18" (for Monolix 2018/19 and later)
directory	character modelling output directory.
input	character complete path to the modelling input file
dv	character the name of measurable variable used in the input modelling file
dvid	*[Optional]* character observation type parameter. This is mandatory in case of multiple endpoint (PKPD).
cats	*[Optional]*character vector of categorical covariates
conts	*[Optional]*character vector of continuous covariates
occ	*[Optional]*character occasional covariate variable name
strats	*[Optional]*character extra stratification variables
settings	*[Optional]*pmxSettingsClass pmx_settings shared between all plots
endpoint	pmxEndpointClass or integer or charcater default to NULL of the endpoint code. pmx_endpoint
sim	pmxSimClass default to NULL. pmx_sim used for VPC, e.g.: sim = pmx_sim(file=vpc_file, irun="rep",idv="TIME")
bloq	pmxBLOQClass default to NULL. pmx_bloq specify bloq, within controller: e.g. bloq=pmx_bloq(cens = "BLOQ_name", limit = "LIMIT_name")
id	*[Optional]* character the name of Indvidual variable used in the input modelling file
time	*[Optional]* character Time variable.
sim_blq	logical if TRUE uses sim_blq values for plotting. Only for Monolix 2018 and later.
file_name	character mlxtran file path.
call	logical if TRUE the result is the parameters parsed
version	integer Non-negative integer. Non-obligatory option, if you don't use a wildcard in the file_name. Otherwise you MUST provide version and wildcard will be substituted with "version", which represents the mlxtran model version.
...	extra arguments passed to pmx_mlx.

Details

pmx_mlx is a wrapper to mlx for the MONOLIX system (sys="mlx")

pmx_mlxtran parses mlxtran file and guess pmx_mlx arguments. In case of multi endpoint the first endpoint is selected. You can though set the endpoint through the same argument. When you set call=TRUE,no controller is created but only the parameters parsed by mlxtran. This can be very helpful, in case you would like to customize parameters (adding settings vi pmx_settings, chnag eth edefault endpoint.)

Value

pmxClass controller object.

Examples

```
## Example to create the controller using theophylline data
theophylline <- file.path(system.file(package = "ggPMX"), "testdata",
                          "theophylline")
WORK_DIR <- file.path(theophylline, "Monolix")
input_file <- file.path(theophylline, "data_pk.csv")

## using only mandatory variables
ctr <- pmx(
  sys="mlx",
  config = "standing",
  directory = WORK_DIR,
  input = input_file,
  dv = "Y",
  dvid ="DVID"
)
## Using covariates
ctr <- pmx(
  sys="mlx",
  config = "standing",
  directory = WORK_DIR,
  input = input_file,
  dv = "Y",
  dvid ="DVID",
  cats=c("SEX"),
  conts=c("WT0","AGE0"),
  strats="STUD"
)
## using settings parameter
ctr <- pmx(
  sys="mlx",
  config = "standing",
  directory = WORK_DIR,
  input = input_file,
  dv = "Y",
  dvid ="DVID",
  settings=list(is.draft=FALSE)
```

```
)

## using mlxtran file
mlxtran_file <-
  file.path(system.file(package = "ggPMX"),
    "testdata","1_popPK_model","project.mlxtran")
pmx_mlxtran(mlxtran_file)

## mlxtran , call =TRUE to get the pmx_mlx argument parsed by  pmx_mlxtran
params <- pmx_mlxtran(mlxtran_file,call=TRUE)

str(params)
# $ directory: chr results_pathile
# $ input    : chr observation file path
# $ dv       : chr "DV"
# $ cats     : chr [1:4] "SEX" "RACE" "DISE" "ILOW"
# $ conts    : chr [1:4] "AGE0" "WT0" "HT0" "TRT"
# $ occ      : chr "ISS"
# $ dvid     : chr "YTYPE"
# $ endpoint :List of 5
# ..$ code     : chr "1"
# ..$ label    : chr ""
# ..$ unit     : chr ""
# ..$ file.code: chr "1"
# ..$ trans    : NULL
# ..- attr(*, "class")= chr "pmxEndpointClass"
# $ config   : chr "standing"
```

`pmxOptions` *This function can be used to set ggPMX options*

Description

`getPmxOption` retrieves the value of a ggPMX option. `ggPMXOptions` sets the value of ggPMX options; it can also be used to return a list of all currently-set ggPMX options.

Usage

```
pmxOptions(...)
```

Arguments

`...`	Options to set, with the form `name = value`.

Details

There is a global option set, which is available by default.

Value

list with options that were set by the user

Options used in ggPMX

- **template_dir:** path to template directory

Examples

```
## Not run:
pmxOptions(template_dir = PATH_TO_CUSTOM_CONFIGURATION)

## End(Not run)
```

---

pmx_bloq *Creates BLOQ object attributes*

Description

Creates BLOQ object attributes

Usage

```
pmx_bloq(
  cens = "CENS",
  limit = "LIMIT",
  colour = "pink",
  size = 2,
  linewidth = 1,
  alpha = 0.9,
  show = TRUE,
  ...
)
```

Arguments

cens	character the censoring column name
limit	character the limit column name (optional)
colour	character the color of the geom
size	numeric the size of the geom when using geom_point()
linewidth	numeric the line width of the segment when using geom_segment()
alpha	numeric the alpha of the geom
show	logical if FALSE remove all censory observations
...	any other graphical parameter

Details

To define that a measurement is censored, the observation data set should include a CENSORING column (default to 'CENS') and put 1 for lower limit or -1 for upper limit.
Optionally, data set can contain have a limit column (default to 'LIMIT') column to set the other limit.

`pmx_comp_shrink` *Compute Shrinkage*

Description

Compute Shrinkage

Usage

```
pmx_comp_shrink(
  ctr,
  fun = c("var", "sd"),
  strat.facet,
  strat.color,
  filter,
  ...
)
```

Arguments

`ctr`	`pmxClass` controller object
`fun`	`character` can be sd or var , var by default
`strat.facet`	`formula` optional stratification parameter
`strat.color`	`character` optional stratification parameter
`filter`	optional filter which will be applied to plotting data
`...`	others parameters not used for the moment

Value

`data.table`

pmx_config *This function can be used to define the pmx configuration used in plots. e.g. Monolix/Nonmem*

Description

This function can be used to define the pmx configuration used in plots. e.g. Monolix/Nonmem

Usage

```
pmx_config(sys = "mlx", inputs, plots, ...)
```

Arguments

sys	charcarter system used , monolix,nonmem,...
inputs	charcater path to the inputs settings file (yaml format)
plots	charcater path to the inputs settings file (yaml format)
...	extra arguments not used

Details

To create a controller user can create a pmxConfig object using
- either an input template file
- or a plot template file
- or both.

By default the 'standing' configuration will be used.

Value

pmxConfig object

Examples

```
# *************** Create a controller using custom plot configuration ***************** ------

library(ggPMX)
theophylline <- file.path(
  system.file(package = "ggPMX"), "testdata",
  "theophylline"
)
WORK_DIR <- file.path(theophylline, "Monolix")
input_file <- file.path(theophylline, "data_pk.csv")


# create a controller with a custom plots template
ctr <-  pmx_mlx(
  config = pmx_config(
    plots=file.path( system.file(package = "ggPMX"),"examples/plots.yaml"),
```

```
    inputs = system.file(package = "ggPMX","examples/custom_inputs.yaml")
  ),
  directory = WORK_DIR,
  input = input_file,
  dv = "Y",
  dvid = "DVID",
  cats = c("SEX"),
  conts = c("WT0", "AGE0"),
  strats = "STUD"
)

## get the list of plots
ctr %>% plots
ctr %>% get_plot("custom_res_time")
ctr %>% get_plot("custom_npde_time")
```

---

pmx_copy *Creates a deep copy of the controller*

Description

Creates a deep copy of the controller

Usage

```
pmx_copy(ctr, keep_globals = FALSE, ...)
```

Arguments

ctr	pmxClass object
keep_globals	logical if TRUE we keep the global parameters changed by pmx_settings
...	extra parameters passed to pmx_settings

Details

The controller is an 'R6' object, it behaves like a reference object. Some functions (methods) can have a side effect on the controller and modify it internally. Technically speaking we talk about chaining not piping here. However , using pmx_copy user can work on a copy of the controller.

By default the copy does not keep global parameters set using pmx_settings.

Value

an object of pmxClass

Examples

```
ctr <- theophylline()
cctr <- ctr %>% pmx_copy()
## Any change in the ctr has no side effect in the ctr and vice versa
```

---

pmx_cov *Select/Map covariates using human labels*

Description

Select/Map covariates using human labels

Usage

```
pmx_cov(values, labels = NULL)
```

Arguments

values	list of covariates to use to create the plot
labels	list of covariates facets labels

Details

In case of ‘pmx_plot_eta_cats‘ and ‘pmx_plot_eta_conts‘ you can customize the covariates and covaraites labels using ‘pmx_cov‘.

Value

pmxCOVObject object

---

pmx_dens *Creates a density plot object*

Description

Creates a density plot object

Usage

```
pmx_dens(
  x,
  labels,
  dname = NULL,
  xlim = 3,
  var_line = NULL,
  snd_line = NULL,
  vline = NULL,
  is.legend = TRUE,
  ...
)
```

Arguments

x	character variable name to sample
labels	list of texts/titles used within the plot
dname	name of dataset to be used
xlim	numeric x axis limits
var_line	list variable density graphics parameters
snd_line	list normal density graphics parameters
vline	list vertical line graphics parameters
is.legend	logical whether to add a legend (defaults TRUE)
...	others graphics arguments passed to pmx_gpar internal object.

Details

labels is a list that contains:

- **title:** plot title default "IWRES density plot"
- **x:** x axis label default to "Etas"
- **y:** y axis label default to empty

var_line is a list that contains:

- **linetype:** default to 1
- **color:** default to black
- **linewidth:** default to 1

snd_line is a list that contains:

- **linetype:** default to 2
- **color:** default to black
- **linewidth:** default to 1

vline is a list that contains:

- **linetype:** default to 3
- **color:** default to black
- **linewidth:** default to 1

Value

list with options for density plot object

`pmx_endpoint` *Creates pmx endpoint object*

Description

Creates pmx endpoint object

Usage

```
pmx_endpoint(code, label = "", unit = "", file.code = code, trans = NULL)
```

Arguments

`code`	`character` endpoint code : used to filter observations DVID==code.
`label`	`character` endpoint label: used to set title and axis labels
`unit`	`character` endpoint unit : used to set title and axis labels
`file.code`	`character` endpoint file code : used to set predictions and finegrid files extensions in case using code parameter is not enough.
`trans`	`list` Transformation parameter not used yet.

Details

In case of multiple endpoints, pkpd case for example, we need to pass endpoint to the pmx call. Internally , ggPMX will filter the observations data set to keep only rows satisfying `DVID==code`. The code is also used to find the right predictions and or fingrid files. ggPMX use the configuration file to fine the path of the predictions file (like the single endpoint case) and then filter the right file using the code parameter.
For example:

- predictions{code}.txt for mlx16
- predictions{code}.txt and y{code}_residual for mlx18

For some tricky examples the code parameter is not enough to find the files. In that case the `file.code` parameter is used to distinguish the endpoint files.

Examples

```
## Use file.code parameter
pk_pd_path <- file.path(system.file(package = "ggPMX"), "testdata","pk_pd")

WORK_DIR <- file.path(pk_pd_path, "RESULTS")

ep <- pmx_endpoint(
  code="4",
  file.code="2"
)

input_file <- file.path(pk_pd_path, "pk_pd.csv")

ctr <- pmx_mlx(
  config = "standing",
  directory = WORK_DIR,
  input = input_file,
  dv = "dv",
  dvid = "dvid",
  cats = "sex",
  conts = "wt",
  endpoint = ep
 )

## using mlxtran

ep <- pmx_endpoint(
  code="3",
 file.code="1"
)

mlxtran_file <- file.path(pk_pd_path, "pk_pd.mlxtran")
ctr <- pmx_mlxtran(mlxtran_file,endpoint=ep)
```

`pmx_filter` *filter data in a pmx controller*

Description

filter data in a pmx controller

Usage

```
pmx_filter(
  ctr,
  data_set = c("estimates", "predictions", "eta", "finegrid", "shrink", "input",
    "individual", "sim_blq"),
  pmx_exp
)
```

Arguments

ctr	A controller. An object of 'pmxClass'
data_set	A data_set within the controller to apply a filter to.
pmx_exp	A filter expression

Value

Returns a pmx controller with a filtered data set.

Examples

```
## example of global filter
ctr <- theophylline()
ctr %>% pmx_filter(data_set = "prediction", ID == 5 & TIME < 2)
ctr %>% get_data("prediction")
```

---

pmx_get_configs *Get List of built-in configurations*

Description

Get List of built-in configurations

Usage

```
pmx_get_configs(sys = "mlx")
```

Arguments

sys	can be mlx, by default all configurations will be listed

Value

names of the config

Examples

```
pmx_get_configs()
```

pmx_gpar *Handling pmx Graphical parameters*

Description

Handling pmx Graphical parameters

Usage

```
pmx_gpar(
  is.title,
  labels,
  axis.title,
  which_pages,
  print,
  axis.text,
  ranges,
  is.smooth,
  smooth,
  is.band,
  band,
  is.draft,
  draft,
  discrete,
  is.identity_line,
  identity_line,
  smooth_with_bloq,
  scale_x_log10,
  scale_y_log10,
  color.scales,
  is.legend,
  legend.position
)
```

Arguments

is.title	logical if TRUE then a title is used for the plot
labels	list of labels, like title, subtitle, x , y
axis.title	list or element_text (same as ggplot2 axis.title theme)
which_pages	page(s) to display; if "all" display all pages, if 1 display first page, if c(1,2) display first and second pages
print	if TRUE the ouptut will be a print not a ggplot2. This is useful for rmarkdwon output to avoid verbose list index print.
axis.text	list or element_text (same as ggplot2 axis.text theme)
ranges	limits of x/y ranges

is.smooth	logical if set to TRUE add smooth layer
smooth	smooth layer parameters
is.band	logical if TRUE add horizontal band
band	horizontal band parameters
is.draft	logical if TRUE add draft layer
draft	draft layer parameters
discrete	logical if TRUE x axis is discrete(FALSE by default)
is.identity_line	logical if TRUE add y=x line
identity_line	list y=x aes properties
smooth_with_bloq	logical if TRUE perform spline in plots with BLOQ data
scale_x_log10	logical if TRUE add scale_x_log10 layer
scale_y_log10	logical if TRUE add scale_y_log10 layer
color.scales	list define scales parameter in case of strat.color pmx_settings
is.legend	logical if TRUE x axis is discrete(FALSE by default)
legend.position	charcater legend position it takes the same value as the equivalent ggplot2 parameter

Details

This object contains all general graphic settings. It used internally by all pmx_plot(generic function) to set the default behavior.

Value

An object of class "pmx_gpar".

---

pmx_list_nm_tables *List NONMEM output tables*

Description

List NONMEM output tables file names from a nm_model object.

Usage

```
pmx_list_nm_tables(nm_model = NULL)
```

Arguments

nm_model	An nm_model object generated with pmx_read_nm_model.

See Also

pmx_read_nm_model, pmx_read_nm_tables

Examples

```
## Not run:
pmx_read_nm_model(file = 'run001.lst') %>%
  pmx_list_nm_tables()

## End(Not run)
```

`pmx_manual_nm_import` *Manually define nonmem tables to be imported*

Description

Manually provide names of the table files to be imported.

Usage

```
pmx_manual_nm_import(
  tab_names = c("sdtab", "mutab", "patab", "catab", "cotab", "mytab", "extra", "xptab",
     "cwtab"),
  tab_suffix = "",
  sim_suffix = "sim"
)
```

Arguments

`tab_names`	Provide the name of the tables to import e.g. 'sdtab', 'patab', 'cotab', 'catab' for NONMEM.
`tab_suffix`	Default is '', but can be changed to any character string to be used as suffix in the table names.
`sim_suffix`	Default is 'sim', but can be changed to any character string to be used as suffix in the simulation table names e.g. sdtab001sim.

pmx_nlmixr *Creates pmx controller from an nlimxr fit object*

Description

Creates pmx controller from an nlimxr fit object

Usage

```
pmx_nlmixr(fit, dvid, conts, cats, strats, endpoint, settings, vpc = FALSE)
```

Arguments

fit	nlmixr object
dvid	*[Optional]* character observation type parameter.
conts	*[Optional]*character vector of continuous covariates
cats	*[Optional]*character vector of categorical covariates
strats	*[Optional]*character extra stratification variables
endpoint	pmxEndpointClass or integer or charcater defalut to NULL of the endpoint code. pmx_endpoint
settings	*[Optional]*pmxSettingsClass pmx_settings
vpc	*[Optional]* logical a boolean indiacting if vpc should be calculated (by default TRUE)

Value

pmxClass controller object.

pmx_nm *Creates pmx controller from NONMEM model outputs*

Description

Creates pmx controller from NONMEM model outputs

Usage

```
pmx_nm(
  file = NULL,
  directory = ".",
  runno = NULL,
  ext = ".lst",
  table_suffix = "",
  sim_suffix = "sim",
  simfile = NULL,
  prefix = "run",
 table_names = c("sdtab", "mutab", "patab", "catab", "cotab", "mytab", "extra", "xptab",
    "cwtab"),
  dvid = "DVID",
  pred = "PRED",
  time = "TIME",
  dv = "DV",
  conts,
  cats,
  npde,
  iwres,
  ipred,
  endpoint,
  strats = "",
  settings = pmx_settings(),
  vpc = TRUE,
  bloq = NULL,
  obs = FALSE,
  quiet = FALSE
)
```

Arguments

file	A character vector of path to the files or a nm_table_list object created with pmx_list_nm_tables.
directory	directory of the model files.
runno	run number which is used for generating the model file name, or used for alternative import of NONMEM-output tables.
ext	Extension to be used to generate model file name. Should be one of'.lst' (default), '.out', '.res', '.mod' or '.ctl' for NONMEM.
table_suffix	suffix of the output tables, standard is "" (no suffix).
sim_suffix	suffix of the simulation output tables, standard is "sim" (e.g. stdab1sim).
simfile	Useful if the simulation is peformed post-hoc and an additional simulation model file is generated e.g. "simulation.lst"; similar to "file" see above.
prefix	Prefix to be used to generate model file name. Used in combination with runno and ext.

table_names	contains the names of the NONMEM-output tables e.g. "sdtab", "patab", "cotab", "catab".
dvid	*[Optional]* character observation type parameter, mandatory in case of multiple endpoint (PKPD). Standard = "DVID"
pred	*[Optional]* character specifing variable name of the population prediction (standard ggPMX nomenclautre = "PRED")
time	*[Optional]* character specifing variable name of time (standard ggPMX nomenclautre = "TIME")
dv	character the name of measurable variable used in the input modelling file (standard ggPMX nomenclautre = "DV")
conts	*[Optional]* character vector of continuous covariates (automatically detected if "cotab" is provided)
cats	*[Optional]* character vector of categorical covariates (automatically detected if "catab" is provided)
npde	*[Optional]* character specifing variable name of the normalized population predictor (standard ggPMX nomenclautre = "NPDE")
iwres	*[Optional]* character specifing variable name of the individual weighted residuals (standard ggPMX nomenclautre = "IWRES")
ipred	*[Optional]* character specifing variable name of the individual population prediction (standard ggPMX nomenclautre = "IPRED")
endpoint	*[Optional]* pmxEndpointClass or integer or charcater default to NULL of the endpoint code. pmx_endpoint
strats	*[Optional]* character extra stratification variables
settings	pmxSettingsClass pmx_settings shared between all plots
vpc	logical a boolean indiacting if vpc should be calculated, simulation tables are required for VPC generation (by default TRUE)
bloq	pmxBLOQClass default to NULL. pmx_bloq specify bloq, within controller: e.g. bloq=pmx_bloq(cens = "BLOQ_name", limit = "LIMIT_name")
obs	logical if set to TRUE will filter dataset according to "MDV", default is FALSE
quiet	Logical, if FALSE messages are printed to the console.

Value

pmxClass controller object.

Author(s)

The ggPMX NONMEM reader (pmx_nm) is strongly based on NONMEM reading functions of the xpose package (v.0.4.11) (Thanks to Benjamin Guiastrennec) To avoid conflicts with the xpose package, the necessary xpose-based functions have been renamed with a "pmx_" prefix. If the user wants to use individual functions e.g. "read_nm_tables" please use the xpose-package

Examples

```
## using only runnumber
# ctr <- pmx_nm(
#  directory=model_dir,
#  runno = "001"
#)

## using a model file (e.g. run001.lst)
#ctr <- pmx_nm(
#  directory=model_dir,
#  file = "run001.lst"
#)

## if simulation was performed post-hoc, an additional simulation file can be loaded for VPC
#ctr <- pmx_nm(
#  directory=model_dir,
#  file = "run001.lst",
#  simfile = "simulation.ctl"
#)

## loading with individual table(s)-names
#ctr <- pmx_nm(directory = model_dir,
#              runno = 3,
#              table_names = "xptab")
```

`pmx_plot` *Generic pmx plot*

Description

Generic pmx plot

Usage

```
pmx_plot(ctr, pname, ...)
```

Arguments

`ctr`	`pmxClass` pmx controller
`pname`	plot name
`...`	others graphics parameters passed : • `pmx_gpar` internal function to customize shared graphical parameters • `pmx_qq` quantile-quantile plot object • `pmx_update` function.

Value

ggplot2 object

pmx_plot_cats *Generic pmx stratified plot*

Description

Generic pmx stratified plot

Usage

```
pmx_plot_cats(ctr, pname, cats, chunk = "", print = TRUE, ...)
```

Arguments

ctr	pmxClass pmx controller
pname	plot name
cats	list of categorical variables. By default all of them
chunk	chunk name
print	logical if TRUE print plots otherwise the list of plots is returned
...	others graphics parameters passed : • pmx_gpar internal function to customize shared graphical parameters • pmx_qq quantile-quantile plot object • pmx_update function.

Value

ggplot2 object(s)

pmx_plot_eta_matrix *Eta matrix plot*

Description

Eta matrix plot

Usage

```
pmx_plot_eta_matrix(
  ctr,
  title,
  dname,
  type.eta,
  text_color,
  is.shrink,
```

```
  shrink,
  point,
  is.smooth,
  smooth,
  is.hline,
  hline,
  is.vreference_line,
  vreference_line,
  filter,
  strat.facet,
  facets,
  strat.color,
  trans,
  pmxgpar,
  labels,
  axis.title,
  axis.text,
  ranges,
  is.band,
  band,
  is.draft,
  draft,
  is.identity_line,
  identity_line,
  scale_x_log10,
  scale_y_log10,
  color.scales,
  ...
)
```

Arguments

ctr	pmx controller
title	character the plot title
dname	name of dataset to be used
type.eta	character type of eat can be 'mode' or 'mean'.'mode' by default
text_color	color of the correlation text in the upper matrix
is.shrink	logical if TRUE add shrinkage to the plot
shrink	pmxShrinkClass shrinkage graphical parameter or list coercible into one
point	list geom_point graphical parameter
is.smooth	logical if TRUE add smoothing to lower matrix plots
smooth	list geom_smooth graphical parameters
is.hline	logical if TRUE add horizontal line to lower matrix plots
hline	list geom_hline graphical parameters
is.vreference_line	logical if TRUE add reference line to diag plots

vreference_line
: list geom_vline graphical parameters

pmx_update parameters

filter
: expression filter which will be applied to plotting data.

strat.facet
: formula optional stratification parameter by facetting. This split plot by strats(each strat in a facet)

facets
: list facet_wrap parameters.

strat.color
: character optional stratification parameter by grouping. This will split the plot by group (color) of strat.

trans
: character define the transformation to apply on x or y or both variables

pmxgpar
: a object of class pmx_gpar possibly the output of the

pmx_gpar: Shared basic graphics parameters

labels
: list list containing plot and/or axis labels: title, subtitle, x , y

axis.title
: list containing element_text attributes to customize the axis title. (similar to ggplot2 axis.title theme)

axis.text
: list containing element_text attributes to customize the axis text (similar to ggplot2 axis.text theme)

ranges
: list limits of x/y ranges

is.band
: logical if TRUE add horizontal band

band
: list horizontal band parameters. geom_hline graphical parameters.

is.draft
: logical if TRUE add draft layer

draft
: list draft layer parameters. geom_text graphical parameters.

is.identity_line
: logical if TRUE add an identity line

identity_line
: listgeom_abline graphical parameters.

scale_x_log10
: logical if TRUE use log10 scale for x axis.

scale_y_log10
: logical if TRUE use log10 scale for y axis.

color.scales
: list define scales parameter in case of strat.color pmx_settings

...
: others graphics parameters passed :

- pmx_gpar internal function to customize shared graphical parameters
- eta_pairs ggPMX internal function for eta matrix plot.
- pmx_update function.

eta_pairs parameters

Value

ggplot2 object

Examples

```
# basic use  ---------------------------------------

ctr <- theophylline()
p <- ctr %>% pmx_plot_eta_matrix

# update graphical parameter  ----------------------

## update labels
ctr %>% pmx_plot_eta_matrix(
  labels = list(title = "Eta matrix new title")
)

## remove draft
ctr %>% pmx_plot_eta_matrix(is.draft = FALSE)

## change text color line
ctr %>% pmx_plot_eta_matrix(
  text_color="red",
  shrink=pmx_shrink(mapping=aes(color="magenta"))
  )

## custom point aes and static parameters
## we can customize any geom_point parameter
ctr %>% pmx_plot_eta_matrix(
  point = list(color = "blue", shape = 4)
)



# stratification  ----------------------------------

## IGNORE continuous stratification
ctr %>% pmx_plot_eta_matrix(strat.color = "WT0")
## IGNORE  categorical stratification
ctr %>% pmx_plot_eta_matrix(strat.facet = ~SEX)

# subsetting  --------------------------------------

## we can use any expression involving the data
ctr %>% pmx_plot_eta_matrix(filter = EFFECT%in%  c("Cl","ka"))
```

`pmx_plot_individual` *Individual plot*

Description

Individual plot

Usage

```
pmx_plot_individual(
  ctr,
  which_pages = 1L,
  print = FALSE,
  dname,
  pred_line,
  ipred_line,
  point,
  is.legend,
  use.finegrid,
  bloq,
  filter,
  strat.facet,
  facets,
  strat.color,
  trans,
  pmxgpar,
  labels,
  axis.title,
  axis.text,
  ranges,
  is.smooth,
  smooth,
  is.band,
  band,
  is.draft,
  draft,
  is.identity_line,
  identity_line,
  scale_x_log10,
  scale_y_log10,
  color.scales,
  ...
)
```

Arguments

ctr	pmx controller
which_pages	integer page(s) to display, or character "all" to display all pages (argument previously called npage, now deprecated)
print	logical if TRUE the ouptut will be a print not a ggplot2. This is useful for rmarkdwon output to avoid verbose list index print.
dname	character name of dataset to be used. User can create his own dataset using set_data and pass it as dname to be plotted.
pred_line	list some ipred line geom properties aesthetics
ipred_line	list some pred line geom properties aesthetics

point	list some point geom properties aesthetics
is.legend	logical if TRUE add a legend
use.finegrid	logical if FALSE use predictions data set
bloq	pmxBLOQ object created by pmx_bloq.
	pmx_update parameters
filter	expression filter which will be applied to plotting data.
strat.facet	formula optional stratification parameter by facetting. This split plot by strats(each strat in a facet)
facets	list facet_wrap parameters.
strat.color	character optional stratification parameter by grouping. This will split the plot by group (color) of strat.
trans	character define the transformation to apply on x or y or both variables
pmxgpar	a object of class pmx_gpar possibly the output of the
	pmx_gpar: Shared basic graphics parameters
labels	list list containing plot and/or axis labels: title, subtitle, x , y
axis.title	list containing element_text attributes to customize the axis title. (similar to ggplot2 axis.title theme)
axis.text	list containing element_text attributes to customize the axis text (similar to ggplot2 axis.text theme)
ranges	list limits of x/y ranges
is.smooth	logical if set to TRUE add smooth layer
smooth	list geom_smooth graphical/smoothing fun parameters
is.band	logical if TRUE add horizontal band
band	list horizontal band parameters. geom_hline graphical parameters.
is.draft	logical if TRUE add draft layer
draft	list draft layer parameters. geom_text graphical parameters.
is.identity_line	logical if TRUE add an identity line
identity_line	listgeom_abline graphical parameters.
scale_x_log10	logical if TRUE use log10 scale for x axis.
scale_y_log10	logical if TRUE use log10 scale for y axis.
color.scales	list define scales parameter in case of strat.color pmx_settings
...	others graphics parameters passed : • pmx_gpar internal function to customize shared graphical parameters • individual generic object for individual plots. • pmx_update function.
	individual parameters

Value

ggplot2 or list of ggplot2 objects

Examples

```
# basic use  ---------------------------------------

ctr <- theophylline()
ctr %>% pmx_plot_individual(which_pages = 1)
## multiple pages
ctr %>% pmx_plot_individual(which_pages = c(1, 3))
## change faceting
ctr %>% pmx_plot_individual(facets = list(nrow = 5, ncol = 5), which_pages = 2)


# update graphical parameter  ----------------------

## update labels
ctr %>% pmx_plot_individual(
  labels = list(title = "Custom individual plot")
)

## remove draft
ctr %>% pmx_plot_individual(is.draft = FALSE)

## Customize ipred_line with any geom_line parameter
ctr %>% pmx_plot_individual(
  pred_line = list(color = "red", linetype = 20, alpha = 0.5)
)

## Customize ipred_line with any geom_line parameter
ctr %>% pmx_plot_individual(
  ipred_line = list(size = 5)
)


## Customize any geom_point parameter
ctr %>% pmx_plot_individual(
  point = list(aes(alpha = DV), color = "green", shape = 4)
)


## legend

p <- ctr %>% pmx_plot_individual(
  is.legend=TRUE,
  point=list(shape=20),
  pred_line=list(linetype=6)
)

# # stratification  ----------------------------------
#
# ## continuous stratification
ctr %>% pmx_plot_individual(strat.color = "WT0")

# # subsetting  --------------------------------------
```

```
#
# ## we can use any expression involving the data
# ## filter and stratify
ctr %>% pmx_plot_individual(
  filter = SEX == 1, strat.facet = ~SEX,
  facets = list(nrow = 5, ncol = 5))

# # transformation  -------------------------------------
#
# ## apply a log transformation in y
ctr %>% pmx_plot_individual(trans = "log10_y")
# ## apply a custonm trsnformation to normalize axis between 0 and 1

## get a list of parameter
p <- ctr %>% pmx_plot_individual(
  which_pages="all",
  point=list(shape=4,color='blue',size=10),
  facets = list(nrow = 5, ncol = 5),
  labels = list(title = "My individuals",x='my time',y='PD data')
)
```

---

pmx_plot_iwres_dens *IWRES density plot*

Description

IWRES density plot

Usage

```
pmx_plot_iwres_dens(
  ctr,
  sim_blq,
  dname,
  xlim,
  var_line,
  snd_line,
  vline,
  filter,
  strat.facet,
  facets,
  strat.color,
  trans,
  pmxgpar,
  labels,
  axis.title,
  axis.text,
```

```
  ranges,
  is.smooth,
  smooth,
  is.band,
  band,
  is.draft,
  draft,
  is.identity_line,
  identity_line,
  scale_x_log10,
  scale_y_log10,
  color.scales,
  ...
)
```

Arguments

ctr	pmx controller
sim_blq	logical if TRUE uses sim_blq as dataset for plotting instead of predictions.
dname	character name of dataset to be used. User can create his own dataset using set_data and pass it as dname to be plotted.
xlim	numeric x axis limits
var_line	list variable denstiy graphics parameters
snd_line	list normal denstiy graphics parameters
vline	list vertical line graphics parameters
	pmx_update parameters
filter	expression filter which will be applied to plotting data.
strat.facet	formula optional stratification parameter by facetting. This split plot by strats(each strat in a facet)
facets	list facet_wrap parameters.
strat.color	character optional stratification parameter by grouping. This will split the plot by group (color) of strat.
trans	character define the transformation to apply on x or y or both variables
pmxgpar	a object of class pmx_gpar possibly the output of the
	pmx_gpar: Shared basic graphics parameters
labels	list list containing plot and/or axis labels: title, subtitle, x , y
axis.title	list containing element_text attributes to customize the axis title. (similar to ggplot2 axis.title theme)
axis.text	list containing element_text attributes to customize the axis text (similar to ggplot2 axis.text theme)
ranges	list limits of x/y ranges
is.smooth	logical if set to TRUE add smooth layer
smooth	list geom_smooth graphical/smoothing fun parameters

is.band	logical if TRUE add horizontal band
band	list horizontal band parameters. geom_hline graphical parameters.
is.draft	logical if TRUE add draft layer
draft	list draft layer parameters. geom_text graphical parameters.
is.identity_line	logical if TRUE add an identity line
identity_line	listgeom_abline graphical parameters.
scale_x_log10	logical if TRUE use log10 scale for x axis.
scale_y_log10	logical if TRUE use log10 scale for y axis.
color.scales	list define scales parameter in case of strat.color pmx_settings
...	others graphics parameters passed :

- pmx_gpar internal function to customize shared graphical parameters
- pmx_dens pmx density object.
- pmx_update function.

pmx_dens parameters

Value

ggplot2 or list of ggplot2 objects

---

pmx_plot_saem_convergence

SAEM Convergence Plot

Description

This plot displays the sequence of estimates for population parameters computed after each iteration of the SAEM algorithm. The purpose is to check the convergence of the algorithm. In addition, a convergence indicator gives the estimation for -2 x log-likelihood along the iterations.

Usage

```
pmx_plot_saem_convergence(ctr, ...)
```

Arguments

ctr	pmxClass controller.
...	additional parameters (not used).

Value

A ggplot object showing SAEM convergence plot.

pmx_plot_vpc *VPC plot*

Description

VPC plot

Usage

```
pmx_plot_vpc(
  ctr,
  type,
  idv,
  obs,
  pi,
  ci,
  rug,
  bin,
  is.legend,
  sim_blq,
  dname,
  filter,
  strat.facet,
  facets,
  strat.color,
  trans,
  pmxgpar,
  labels,
  axis.title,
  axis.text,
  ranges,
  is.smooth,
  smooth,
  is.band,
  band,
  is.draft,
  draft,
  is.identity_line,
  identity_line,
  scale_x_log10,
  scale_y_log10,
  color.scales,
  is.footnote,
  ...
)
```

Arguments

ctr	pmx controller
type	charcater can be either percentile or scatter
idv	chracater individual variable
obs	pmx_vpc_obs object observation layer pmx_vpc_obs
pi	pmx_vpc_pi object percentile layer pmx_vpc_pi
ci	pmx_vpc_ci object confidence interval layer pmx_vpc_ci
rug	pmx_vpc_rug object rug layer pmx_vpc_rug. Note: consider not using a rug layer when bin[["within_strat"]]=TRUE, since the rugs plotted will not reflect the bins.
bin	pmx_vpc_bin object pmx_vpc_bin specify within pmx_plot_vpc() e.g.: bin = pmx_vpc_bin(style = "kmeans", n = 10)
is.legend	logical if TRUE add legend
sim_blq	logical if TRUE uses sim_blq values for plotting. Only for Monolix 2018 and later.
dname	added for compatibility with other ggPMX plots
	pmx_update parameters
filter	expression filter which will be applied to plotting data.
strat.facet	formula optional stratification parameter by facetting. This split plot by strats(each strat in a facet)
facets	list facet_wrap parameters.
strat.color	character optional stratification parameter by grouping. This will split the plot by group (color) of strat.
trans	character define the transformation to apply on x or y or both variables
pmxgpar	a object of class pmx_gpar possibly the output of the
	pmx_gpar: Shared basic graphics parameters
labels	list list containing plot and/or axis labels: title, subtitle, x , y
axis.title	list containing element_text attributes to customize the axis title. (similar to ggplot2 axis.title theme)
axis.text	list containing element_text attributes to customize the axis text (similar to ggplot2 axis.text theme)
ranges	list limits of x/y ranges
is.smooth	logical if set to TRUE add smooth layer
smooth	list geom_smooth graphical/smoothing fun parameters
is.band	logical if TRUE add horizontal band
band	list horizontal band parameters. geom_hline graphical parameters.
is.draft	logical if TRUE add draft layer
draft	list draft layer parameters. geom_text graphical parameters.
is.identity_line	logical if TRUE add an identity line

identity_line	listgeom_abline graphical parameters.
scale_x_log10	logical if TRUE use log10 scale for x axis.
scale_y_log10	logical if TRUE use log10 scale for y axis.
color.scales	list define scales parameter in case of strat.color pmx_settings
is.footnote	logical if TRUE add footnote
...	others graphics parameters passed : • pmx_gpar internal function to customize shared graphical parameters • pmx_vpc pmx vpc object. • pmx_update function. **pmx_vpc parameters**

Details

You can use pmx_vpc_bin to set the bin parameters. In case of stratification, binning can be different for each strat level (case within_strat equal to FALSE).

Value

ggplot2 or list of ggplot2 objects

See Also

Other vpc: pmx_vpc(), pmx_vpc_bin(), pmx_vpc_ci(), pmx_vpc_obs(), pmx_vpc_pi(), pmx_vpc_rug()

Examples

```
library(ggPMX)

theo_path <- file.path(
  system.file(package = "ggPMX"), "testdata",
  "theophylline"
)
WORK_DIR <- file.path(theo_path, "Monolix")
input_file <- file.path(theo_path, "data_pk.csv")
vpc_file <- file.path(theo_path, "sim.csv")

ctr <- pmx_mlx(
  config = "standing",
  directory = WORK_DIR,
  input = input_file,
  dv = "Y",
  dvid = "dvid",
  cats = c("SEX"),
  conts = c("WT0", "AGE0"),
  strats = "STUD",
  settings = pmx_settings(
    use.labels=TRUE,
    cats.labels=list(
      SEX=c("0"="Male","1"="Female")
```

```
    )
  ),
  sim = pmx_sim(
    file = vpc_file,
    irun ="rep",
    idv="TIME"
  )
)


ctr %>% pmx_plot_vpc(
  strat.facet=~SEX,
  facets=list(nrow=2),
  type="percentile",
  is.draft = FALSE,
  pi = pmx_vpc_pi(interval = c(0.1,0.9),
              median=list(color="green"),
              extreme= list(color="green")),
  obs = pmx_vpc_obs(color="blue",shape=18,size=2),
  ci = pmx_vpc_ci(interval = c(0.1,0.9),
              median=list(fill="pink")),
  bin=pmx_vpc_bin("kmeans",n=5)
)

ctr %>%
  pmx_plot_vpc(bin= pmx_vpc_bin(
     style = "fixed",
     fixedBreaks=c(-10,2, 5, 10,15,50))
  )

# example with legend

ctr %>% pmx_plot_vpc(
  is.legend = TRUE,
  pi = pmx_vpc_pi(interval=c(0.02,0.98),median = list(linetype="dotted")),
  ci = pmx_vpc_ci(interval = c(0.05,0.95),median=list(fill="red"))
)
```

---

pmx_qq *This function creates a qq plot object*

Description

This function creates a qq plot object

Usage

```
pmx_qq(
```

```
  x,
  labels,
  dname = NULL,
  point = NULL,
  xmax = TRUE,
  facets = NULL,
  is.reference_line = NULL,
  reference_line = NULL,
  is.shrink = NULL,
  shrink = NULL,
  is.hline = NULL,
  hline = NULL,
  is.vline = NULL,
  vline = NULL,
  ...
)
```

Arguments

x	character variable name to sample
labels	list of texts/titles used within the plot
dname	name of dataset to be used
point	list geom_point attributes color, shape,...
xmax	logical if FALSE do not use max(aes(x)) as limits default to TRUE
facets	list
is.reference_line	logical if TRUE add reference line to the plot
reference_line	list geom_line attributes. Used only for pmx_plot_eta_qq
is.shrink	logical if TRUE add shrinkage to the plot
shrink	pmxShrinkClass shrinkage graphical parameter or list coercible into one
is.hline	logical if TRUE add horizontal line y=0 (TRUE by default)
hline	geom hline graphical parameters
is.vline	logical if TRUE add vertical line x=0 (TRUE by default)
vline	geom vline graphical parameters
...	others graphics arguments passed to pmx_gpar internal object.

Details

labels is a list that contains:

- **title:** plot title default "EBE vs. covariates"
- **x:** x axis label default to "Etas"
- **y:** y axis label default to empty

point is a list that contains:

- **shape:** default to 1
- **color:** default to black
- **size:** default to 1

Value

pmx_qq object

---

pmx_qq_plot *Quantile-quantile plots*

Description

Quantile-quantile plots

Quantile-quantile plot of IWRES

Quantile-quantile plot of eta variables

Quantile-quantile plot of NPDE

Quantile-quantile plot of NPD

Quantile-quantile plot of CWRES

Usage

```
pmx_qq_plot(
  dname,
  point,
  is.reference_line,
  reference_line,
  is.shrink,
  shrink,
  is.hline,
  hline,
  is.vline,
  vline,
  filter,
  strat.facet,
  facets,
  strat.color,
  trans,
  pmxgpar,
  labels,
  axis.title,
  axis.text,
  ranges,
  is.smooth,
  smooth,
```

```
  is.band,
  band,
  is.draft,
  draft,
  is.identity_line,
  identity_line,
  scale_x_log10,
  scale_y_log10,
  color.scales,
  ...
)

pmx_plot_iwres_qq(ctr, ...)

pmx_plot_eta_qq(ctr, ...)

pmx_plot_npde_qq(ctr, ...)

pmx_plot_npd_qq(ctr, ...)

pmx_plot_cwres_qq(ctr, ...)
```

Arguments

dname	name of dataset to be used
point	list geom_point parameters.
is.reference_line	logical if TRUE add reference line to the plot
reference_line	list geom_abline parameters.
is.shrink	logical if TRUE add shrinkage to the plot
shrink	pmxShrinkClass shrinkage graphical parameter or list coercible into one
is.hline	logical if TRUE add horizontal line y=0 (TRUE by default)
hline	list geom hline graphical parameters
is.vline	logical if TRUE add vertical line x=0 (TRUE by default)
vline	list geom vline graphical parameters
	pmx_update parameters
filter	expression filter which will be applied to plotting data.
strat.facet	formula optional stratification parameter by facetting. This split plot by strats(each strat in a facet)
facets	list facet_wrap parameters.
strat.color	character optional stratification parameter by grouping. This will split the plot by group (color) of strat.
trans	character define the transformation to apply on x or y or both variables
pmxgpar	an object of class pmx_gpar

labels	list list containing plot and/or axis labels: title, subtitle, x , y
axis.title	list containing element_text attributes to customize the axis title. (similar to ggplot2 axis.title theme)
axis.text	list containing element_text attributes to customize the axis text (similar to ggplot2 axis.text theme)
ranges	list limits of x/y ranges
is.smooth	logical if set to TRUE add smooth layer
smooth	list geom_smooth graphical/smoothing fun parameters
is.band	logical if TRUE add horizontal band
band	list horizontal band parameters. geom_hline graphical parameters.
is.draft	logical if TRUE add draft layer
draft	list draft layer parameters. geom_text graphical parameters.
is.identity_line	logical if TRUE add an identity line
identity_line	listgeom_abline graphical parameters.
scale_x_log10	logical if TRUE use log10 scale for x axis.
scale_y_log10	logical if TRUE use log10 scale for y axis.
color.scales	list define scales parameter in case of strat.color pmx_settings
...	others graphics parameters passed : • pmx_gpar internal function to customize shared graphical parameters • pmx_qq quantile-quantile plot object. • pmx_update function.
	pmx_qq parameters
ctr	pmx controller

Value

ggplot2 object

Examples

```
# *************** basic use ***************** ------

ctr <- theophylline()
ctr %>% pmx_plot_eta_qq
ctr %>% pmx_plot_npde_qq
ctr %>% pmx_plot_iwres_qq

# update graphical parameter  ----------------------

## add reference line
ctr %>% pmx_plot_npde_qq(reference_line=list(color="blue"))
```

```
## remove reference line
ctr %>% pmx_plot_eta_qq(reference_line=NULL)


# stratification  ---------------------------------

## categorical stratification color parameter
ctr %>% pmx_plot_iwres_qq(strat.facet=~STUD,strat.color="SEX")
## categorical stratification facetting
ctr %>% pmx_plot_eta_qq(strat.facet = ~SEX)

## do not use symmetric axis
ctr %>% pmx_plot_npde_qq(xmax=FALSE,reference_line=list())
```

`pmx_read_nm_files` *NONMEM output file import function*

Description

Quickly import NONMEM output files into R.

Usage

```
pmx_read_nm_files(
  runno = NULL,
  prefix = "run",
  ext = c(".ext", ".cor", ".cov", ".phi", ".grd", ".shk"),
  file = NULL,
  dir = NULL,
  quiet = FALSE
)
```

Arguments

`runno`	Run number to be evaluated.
`prefix`	Prefix of the model file names.
`ext`	A vector of the file extension to import. By default '.ext', '.cor', '.cov', '.phi', '.grd', '.shk' files are listed.
`file`	Names of the model output file to be imported. Alternative argument to `prefix`, `runno` and `ext`.
`dir`	Location of the model files.
`quiet`	Logical, if `FALSE` messages are printed to the console.

Examples

```
## Not run:
# Using the `file` argument to import a model file:
ext_file <- pmx_read_nm_files(file = 'run001.ext', dir = 'models')

# Using the `runno` argument to import a model file:
ext_file <- pmx_read_nm_files(runno = '001', ext = '.ext', dir = 'models')

## End(Not run)
```

---

pmx_read_nm_model *NONMEM model file parser*

Description

Parse NONMEM model files in R format

Usage

```
pmx_read_nm_model(
  runno = NULL,
  prefix = "run",
  ext = ".lst",
  file = NULL,
  dir = NULL
)
```

Arguments

runno	run number which is used for generating the model file name
prefix	Prefix to be used to generate model file name. Used in combination with runno and ext.
ext	Extension to be used to generate model file name. Should be one of'.lst' (default), '.out', '.res', '.mod' or '.ctl' for NONMEM.
file	A character vector of path to the files or a nm_table_list object created with list_nm_tables.
dir	directory of the model files.

Value

A tibble of class model containing the following columns:

- **problem**: a numeric identifier for the $PROBLEM associated with the code.
- **level**: a unique numeric identifier to each subroutine block associated with the code.

- **subroutine**: a character identifier named after the 3 first letters of the subroutine name e.g. '$THETA' and '$TABLE' will become 'the' and 'tab' respectively. In addition all output from the .lst is labeled 'lst', the general nonmem output e.g. NM-TRAN messages are labelled 'oth'. With priors thp, tpv, omp, opd, sip, spd abbreviations are given to the THETAP, THETAPV, OMEGAP, etc.
- **code**: the code without comments or subroutine names e.g. '$THETA 0.5 ; TVCL' will return '0.5'.
- **comment**: the last comment of a record e.g. '0.5 ; Clearance (L/h) ; TVCL' will return 'TVCL'.

See Also

pmx_read_nm_tables

Examples

```
## Not run:
# Using the `file` argument to import a model file:
nm_model <- pmx_read_nm_model(file = 'run001.lst', dir = 'models')

# Using the `runno` argument to import a model file:
nm_model <- pmx_read_nm_model(runno = '001', ext = '.lst', dir = 'models')

## End(Not run)
```

---

pmx_read_nm_tables *NONMEM output table import function*

Description

Quickly import NONMEM output tables into R. This function automatically detects the optimal settings to import the tables from nonmem. It is based on the read_nm_tables function of xpose. Slight adjustment were made for purposes of pmx_nm()

Usage

```
pmx_read_nm_tables(
  file = NULL,
  dir = NULL,
  combined = TRUE,
  rm_duplicates = TRUE,
  quiet = FALSE,
  simtab = NULL,
  ziptab = TRUE,
  user_mode = TRUE,
  ...
)
```

Arguments

file	A character vector of path to the files or a nm_table_list object created with list_nm_tables.
dir	Location of the model files.
combined	Logical value indicating whether multiple tables should be combined into a single one. If the number of rows does not match an error will be returned.
rm_duplicates	Logical value indicating whether duplicated columns should be removed.
quiet	Logical, if FALSE messages are printed to the console.
simtab	If TRUE only reads in simulation tables, if FALSE only reads estimation tables. Default NULL reads all tables.
ziptab	If TRUE search for the tables that have been compressed and renamed ??<file>.zip'.
user_mode	Adjustment to the original code: usermode is set to "usermode = TRUE" in order to improve this function for purposes of pmx_nm() (nonmem_reader.R), In order to use this function seperatly, the use of the original function in the xpose package is advised.
...	Additional arguments to be passed to the read_table or read_csv functions.

Table format requirement

When using pmx_read_nm_tables with the combined argument set to FALSE an ID column must be present in all data tables. When combined is set to TRUE instead an ID column must be present in at least one table for each problem and for each 'firstonly' category. ID columns are required to properly combine/merge tables and removing NA records. If the ID column is missing from a table and combined = FALSE pmx_read_nm_tables will return the following warning: Unknown variables: `ID`. While the data is returned beware that NA records might be left in the data and the output should be checked carefully. If combined = TRUE pmx_read_nm_tables is more strict and will return the following warning instead: Dropped `<tablenames>` due to missing required `ID` column..

Examples

```
## Not run:

# Adjustment to the original code: usermode is set to "usermode = TRUE"
# in order to improve this function for purposes of pmx_nm() (nonmem_reader.R)
# In order to use this function seperatly, the use of the original function in
# the xpose package is advised.

# Import tables manually and return them as a list of individual tables
nm_tables <- pmx_read_nm_tables(file = c('sdtab001', 'patab001'),
                            dir = 'models', combined = FALSE)

# Import tables manually and return them as a single merged table
nm_tables <- pmx_read_nm_tables(file = c('sdtab001', 'patab001'),
                            dir = 'models', combined = TRUE)


## End(Not run)
```

pmx_register_plot *Register plot (Jun2025, Alex: I believe it doesn't work at all)*

Description

Register plot (Jun2025, Alex: I believe it doesn't work at all)

Usage

```
pmx_register_plot(ctr, pp, pname = NULL)
```

Arguments

ctr	pmxClass controller
pp	ggplot2 plot
pname	character plot nme

pmx_report *Generates ggpmX report from a pre-defined template*

Description

Generates ggpmX report from a pre-defined template

Usage

```
pmx_report(
  contr,
  name,
  save_dir,
  plots_subdir = "ggpmx_GOF",
  output = c("all", "plots", "report"),
  template = "standing",
  footnote = output == "all",
  edit = FALSE,
  format = NULL,
  title,
  ...
)
```

Arguments

contr	pmxClass controller
name	character The report name
save_dir	Output directory. A directory to write the results files to
plots_subdir	Output folder name, ggpmx_GOF by default
output	character the result type, can be a standalone directory of plots or a report document as defined in the template (pdf, docx,..) ,or both
template	character ggPMX predefined template or the path to a custom rmarkdown template. Use pmx_report_template to get the list of available templates
footnote	logical TRUE to add a footnote to the generated plots. The default footnote is to add the path where the plot is saved.
edit	logical TRUE to edit the template immediately
format	character The output document format. By default, a word report is generated. User can specify one or more formats from c("word","pdf","html","all"). format "all" to generate all formats.
title	character report title (optional)
...	extra parameters depending in the template used

Details

pmx_report uses pre-defined template .Rmd to generate the report. The idea is to pass the controller as a report argument using knitr params artifact.

Examples

```
library(ggPMX)
# you probably want to create the report in your own directory
# But using a temp directory allows for easy cleanup

## case1: generate a single report
withr::with_tempdir({
  ctr <- theophylline()
  ctr %>% pmx_report(
    name = "my_report",
    save_dir = getwd(),
    output="report"
  )
})


## case2: generate standalone plots
withr::with_tempdir({
  ctr <- theophylline()
```

```
  ctr %>% pmx_report(
    name = "my_report",
    save_dir = getwd(),
    output="plots"
  )
})


## case3: generate both : reports + plots
## by default add footnote
## Note, you can force footnote to FALSE using footnote parameter
withr::with_tempdir({
  ctr <- theophylline()
  ctr %>% pmx_report(
    name="my_report",
    save_dir=getwd(),
    output="all"
  )
})


## case4 : generate standalone plots with footnotes
withr::with_tempdir({
  ctr <- theophylline()
  ctr %>% pmx_report(
    name="my_report",
    save_dir=getwd(),
    footnote=TRUE,
    output="plots"
  )
})


##  case6: dynamic edit
## uncomment to run
# ctr <- theophylline()
# ctr %>% pmx_report(
#   save_dir = file.path(getwd(),"case6"),
#   name="my_report",
#   output="report",
#   edit = TRUE)


## case7 : generate individual plots report
## ctr <- theophylline()
## ctr %>% pmx_report(
##   name="report2",
##   save_dir = getwd(),
##   template="individual",
##   format="all",
##   which_pages=1:2
## )
```

pmx_report_template *Gets build-in report templates*

Description

Gets build-in report templates

Usage

```
pmx_report_template()
```

Value

list of templates names

Examples

```
pmx_report_template()
```

pmx_settings *Create controller global settings*

Description

Create controller global settings

Usage

```
pmx_settings(
  is.draft = TRUE,
  use.abbrev = TRUE,
  color.scales = NULL,
  cats.labels = NULL,
  use.labels = FALSE,
  use.titles = FALSE,
  effects = NULL,
  ...
)
```

Arguments

is.draft	logical if FALSE any plot is without draft annotation
use.abbrev	logical if FALSE use full description from abbreviation mapping for axis names
color.scales	list list containing elements of scale_color_manual
cats.labels	list list of named vectors for each factor
use.labels	logical if TRUE replace factor named by cats.labels
use.titles	logical FALSE to generate plots without titles
effects	list list of effects levels and labels
...	extra parameter not used yet

Value

pmxSettingsClass object

Examples

```
library(ggPMX)
library(ggplot2)
ctr <- theophylline(
  settings=
    pmx_settings(
      color.scales=list(
        "Study",
        labels=c("Study 1","Study 2"),
        values=c("1"="lightyellow","2"="lightblue")),
      cats.labels=list(
        SEX=c("0"="M","1"="F"),
        STUD=c("1"="Study 1","2"="Study 2")
      ),
      use.abbrev=TRUE,
      is.draft=TRUE,
      use.labels=TRUE
    )
)



ctr %>%
  pmx_plot_npde_time(strat.color="STUD",strat.facet=~SEX)
#
#
ctr  %>%
  pmx_plot_eta_box(strat.color="STUD", strat.facet =~SEX)

ctr  %>%  pmx_plot_eta_hist
```

pmx_shrink *Create shrinkage parameter object*

Description

Create shrinkage parameter object

Usage

```
pmx_shrink(
  fun = c("var", "sd"),
  size = 1,
  color = "green",
  vjust = 1.5,
  hjust = 0.5,
  ...
)
```

Arguments

fun	list shrinkage function can be sd or var
size	numeric shrinkage text size
color	character shrinkage text color
vjust	numeric shrinkage position vertical adjustment
hjust	numeric shrinkage position horizontal adjustment
...	any other parameter

Value

pmxShrinkClass object (list)

pmx_sim *Create simulation object*

Description

Create simulation object

Usage

```
pmx_sim(file, data, irun, idv)
```

Arguments

file	character path to the simulation file
data	data.table simulation data
irun	character name of the simulation column
idv	character name of the ind. variable

Examples

```
library(ggPMX)

theo_path <- file.path(
  system.file(package = "ggPMX"), "testdata",
  "theophylline"
)
WORK_DIR <- file.path(theo_path, "Monolix")
input_file <- file.path(theo_path, "data_pk.csv")
vpc_file <- file.path(theo_path, "sim.csv")

ctr <- pmx_mlx(
  config = "standing",
  directory = WORK_DIR,
  input = input_file,
  dv = "Y",
  dvid = "dvid",
  cats = c("SEX"),
  conts = c("WT0", "AGE0"),
  strats = "STUD",
  settings = pmx_settings(
    use.labels=TRUE,
    cats.labels=list(
      SEX=c("0"="Male","1"="Female")
    )
  ),
  sim = pmx_sim(
    file = vpc_file,
    irun ="rep",
    idv="TIME"
  )
)


ctr %>% pmx_plot_vpc(
  strat.facet=~SEX,
  facets=list(nrow=2),
  type="percentile",
  is.draft = FALSE,
  pi = pmx_vpc_pi(interval = c(0.1,0.9),
              median=list(color="green"),
              extreme= list(color="green")),
  obs = pmx_vpc_obs(color="blue",shape=18,size=2),
  ci = pmx_vpc_ci(interval = c(0.1,0.9),
```

```
              median=list(fill="pink")),
  bin=pmx_vpc_bin("kmeans",n=5)
)

ctr %>%
  pmx_plot_vpc(bin= pmx_vpc_bin(
     style = "fixed",
     fixedBreaks=c(-10,2, 5, 10,15,50))
  )

# example with legend

ctr %>% pmx_plot_vpc(
  is.legend = TRUE,
  pi = pmx_vpc_pi(interval=c(0.02,0.98),median = list(linetype="dotted")),
  ci = pmx_vpc_ci(interval = c(0.05,0.95),median=list(fill="red"))
)
```

`pmx_theme` *Define ggPMX theme*

Description

This theme is a simple wrapper gdoc theme from ggthems package.

Usage

```
pmx_theme(...)
```

Arguments

`...`	can contain any valid argument of ggplot2 `theme` object.

Value

ggplot2 theme object

pmx_update *Update plot object*

Description

Update plot object

Usage

```
pmx_update(
  ctr,
  pname,
  strat.color = NULL,
  strat.facet = NULL,
  color.scales = NULL,
  filter = NULL,
  trans = NULL,
  ...,
  pmxgpar = NULL
)
```

Arguments

ctr	pmxClass controller object
pname	character the plot name to update
strat.color	character optional stratification parameter
strat.facet	formula optional stratification parameter
color.scales	list can be used with strat.color to set scale_color_manual pmx_gpar function.
filter	optional filter which will be applied to plotting data
trans	character define the transformation to apply on x or y or both variables
...	others graphical parameters given to set the plot
pmxgpar	a object of class pmx_gpar possibly the output of the

Details

trans is a transformation that user can apply to x, or y coordinates. The transformation is applied to the data before the plotting. This gives more felxiblilty to the user and also conserves all static positions like annotations (draft specially)

For example:

var_x apply variance to x coordinates the variance function

var_xy apply variance to both This mechanism is applied internally to scale log.

Value

controller object with the plot updated

See Also

Other pmxclass: get_cats(), get_conts(), get_covariates(), get_data(), get_occ(), get_plot(), get_plot_config(), get_strats(), plot_names(), plots(), set_data(), set_plot()

---

pmx_vpc *Creates vpc object*

Description

Creates vpc object

Usage

```
pmx_vpc(
  type = c("percentile", "scatter"),
  idv = "TIME",
  obs = pmx_vpc_obs(),
  pi = pmx_vpc_pi(),
  ci = pmx_vpc_ci(),
  rug = pmx_vpc_rug(),
  bin = pmx_vpc_bin(),
  labels = NULL,
  facets = NULL,
  is.legend = TRUE,
  is.footnote = TRUE,
  dname = NULL,
  ...
)
```

Arguments

type	charcater can be either percentile or scatter
idv	chracater individual variable
obs	pmx_vpc_obs object observation layer pmx_vpc_obs
pi	pmx_vpc_pi object percentile layer pmx_vpc_pi
ci	pmx_vpc_ci object confidence interval layer pmx_vpc_ci
rug	pmx_vpc_rug object rug layer pmx_vpc_rug
bin	pmx_vpc_bin object pmx_vpc_bin
labels	list define title and axis labels
facets	is a list of parameters passed to facet_wrap in case of startification
is.legend	logical if TRUE add legend
is.footnote	logical if TRUE add footnote
dname	added for compatibility with other ggPMX plots
...	extra parameters passed to base graphical parameters

Value

list with parameters of the vpc object

See Also

Other vpc: pmx_plot_vpc(), pmx_vpc_bin(), pmx_vpc_ci(), pmx_vpc_obs(), pmx_vpc_pi(), pmx_vpc_rug()

`pmx_vpc_bin` *Creates vpc bins*

Description

Creates vpc bins

Usage

```
pmx_vpc_bin(style, within_strat = TRUE, seed = 42, ...)
```

Arguments

`style`	`character` style chosen on of the: "fixed", "sd", "equal", "pretty", "quantile", "kmeans", "hclust" or "jenks"
`within_strat`	`logical` if TRUE compute the bining for each strat level. By default t is false and bining are equal for all stratifications levels.
`seed`	`integer` used in `set.seed` call to ensure reproducibility if style is "kmeans". Set to NULL if this is not desired.
`...`	other classInt::classIntervals parameters excpet `style` and `n`

Details

This is a wrapper to the bin based VPC

Value

list with options for ‘pmx_vpc_bin‘ object

See Also

Other vpc: pmx_plot_vpc(), pmx_vpc(), pmx_vpc_ci(), pmx_vpc_obs(), pmx_vpc_pi(), pmx_vpc_rug()

pmx_vpc_ci *Sets vpc confidence interval layer*

Description

Sets vpc confidence interval layer

Usage

```
pmx_vpc_ci(
  show = c("all", "median"),
  interval = c(0.025, 0.975),
  method = c("ribbon", "rectangle"),
  median = list(fill = "red", alpha = 0.3),
  extreme = list(fill = "#3388cc", alpha = 0.3)
)
```

Arguments

show	charcater how areas are displayed: • **show="all"** areas will be displayed for each of the 3 percentiles. • **show="median"** Show only median area.
interval	numeric quantiles values default to c(.05,.95)
method	charcater which areas are displayed: • **method="ribbon"** areas are ribbons. • **method="rectangle"** areas are horizontal rectangles.
median	list containing: • **fill** character Color of the area representing the CI for the median. Default: "#3388cc". • **alpha** numeric Transparency of the area representing the PI for the median. Default=0.3.
extreme	list containing: • **fill** character Color of the area representing the CI for the extreme percentiles. Default: "#3388cc". • **alpha** numeric Transparency of the area representing the PI for the extreme percentiles. Default=0.3.

Value

list with options for Confidence Interval layer

See Also

Other vpc: pmx_plot_vpc(), pmx_vpc(), pmx_vpc_bin(), pmx_vpc_obs(), pmx_vpc_pi(), pmx_vpc_rug()

pmx_vpc_obs *Sets vpc observation layer*

Description

Sets vpc observation layer

Usage

```
pmx_vpc_obs(show = TRUE, color = "#000000", size = 1, alpha = 0.7, shape = 1)
```

Arguments

show	logical if TRUE show observation points
color	character Color of the observed endpoint values. Default: "#000000".
size	numeric Size of the observed endpoint values. Default: 1.
alpha	numeric Transparency of the observed endpoint values. Default: 0.7.
shape	numeric Shape of the observed endpoint values. Default: 1.

Value

list with options for ggplot2 layer with observations

See Also

Other vpc: pmx_plot_vpc(), pmx_vpc(), pmx_vpc_bin(), pmx_vpc_ci(), pmx_vpc_pi(), pmx_vpc_rug()

pmx_vpc_pi *Sets vpc percentile layer*

Description

Sets vpc percentile layer

Usage

```
pmx_vpc_pi(
  show = c("all", "median", "area"),
  interval = c(0.05, 0.95),
 median = list(color = "#000000", linewidth = 1, alpha = 0.7, linetype = "solid"),
 extreme = list(color = "#000000", linewidth = 1, alpha = 0.7, linetype = "dashed"),
  area = list(fill = "blue", alpha = 0.1)
)
```

Arguments

show	charcater how lines are displayed: • **show=all** lines will be displayed for each of the 3 percentiles. with a shaded area. • **show=median** Show only median line. • **show=area** Show only median line and the shaded area
interval	numeric quantiles values default to c(.05,.95)
median	list containing: • **color** charcater Color of the median percentile line. Default: "#000000". • **linewidth** numeric Thickness of the median percentile line. Default: 1. • **alpha** numeric Transparency of the median percentile line. Default: 0.7. • **linetype** charcater Linetype of the median percentile line. Default: "solid".
extreme	list containing: • **color** charcater Color of the median percentile line. Default: "#000000". • **linewidth** numeric Thickness of the median percentile line. Default: 1. • **alpha** numeric Transparency of the median percentile line. Default: 0.7. • **linetype** charcater Linetype of the median percentile line. Default: "solid"
area	list containing: • **fill** charcater Color of the shaded area. Default: "blue". • **alpha** numeric Transparency of the shaded area. Default: 0.1.

Value

list with options for Prediction Interval layer

See Also

Other vpc: pmx_plot_vpc(), pmx_vpc(), pmx_vpc_bin(), pmx_vpc_ci(), pmx_vpc_obs(), pmx_vpc_rug()

---

pmx_vpc_rug *Sets vpc rug layer*

Description

Sets vpc rug layer

Usage

```
pmx_vpc_rug(show = TRUE, color = "#000000", linewidth = 1, alpha = 0.7, size)
```

Arguments

show	logical If TRUE show bin separators
color	character Color of the rug. Default: "#000000".
linewidth	numeric Thickness of the rug. Default: 1.
alpha	numeric Transparency of the rug. Default: 0.7.
size	numeric Depreciated thickness of the rug. Default: 1.

Details

When the vpc confidence interval layer method is rectangles we don't show rug separators.

Value

list with options for the rug layer

See Also

Other vpc: pmx_plot_vpc(), pmx_vpc(), pmx_vpc_bin(), pmx_vpc_ci(), pmx_vpc_obs(), pmx_vpc_pi()

---

print.abbreviation *S3 print abbreviation*

Description

S3 print abbreviation

Usage

```
## S3 method for class 'abbreviation'
print(x, ...)
```

Arguments

x	object of class configs
...	pass additional options (not used presently)

Value

print abbreviation

`print.configs` *This function can be used to print configuration of the defined object using S3 method.*

Description

This function can be used to print configuration of the defined object using S3 method.

Usage

```
## S3 method for class 'configs'
print(x, ...)
```

Arguments

`x`	object of class configs
`...`	pass additional options (not used presently)

Value

print result

`print.pmxClass` *Print pmxClass object*

Description

Print pmxClass object

Usage

```
## S3 method for class 'pmxClass'
print(x, ...)
```

Arguments

`x`	pmxClass object
`...`	additinal arguments to pass to print

Value

print object to screen

print.pmxConfig *S3 method print pmxConfig object*

Description

S3 method print pmxConfig object

Usage

```
## S3 method for class 'pmxConfig'
print(x, ...)
```

Arguments

x	pmxConfig object
...	addtional arguments to pass to print (unused currently)

Value

invisible object

print.pmx_gpar *Print pmx_gpar object*

Description

Print pmx_gpar object

Usage

```
## S3 method for class 'pmx_gpar'
print(x, ...)
```

Arguments

x	pmx_gpar object
...	argument passed to print (to satisfy generic)

Value

a character description of graphical parameters

`read_extfile` *Reads .ext files generated by NONMEM*

Description

Reads .ext files generated by NONMEM

Usage

```
read_extfile(
  run = NA_real_,
  project = getwd(),
  file = paste0(run, ".ext"),
  path = NULL,
  read_fun = c("data.table", "read.table"),
  quiet
)
```

Arguments

`run`	run a run number or run identifier
`project`	project the NONMEM project directory
`file`	file the 'ext' file name
`path`	path full path and file name for 'ext' file
`read_fun`	read_fun function to read the 'ext' file
`quiet`	Logical, if `FALSE` messages are printed to the console.

Value

A list with param, omega, and sigma in a format ready to be used.

Author(s)

This function is based on read_nmext from mrgsolve, Original Author: Kyle T Baron. This function has some changes to the original code: Addition of param, "quiet", (option of pmx_msg function, from xpose package) (Line: 27) The code was slightly adjusted to check for multiple tables and also extract SE (ITERATION == 1000000001) (Line: 44-58, Line: 86-96, respectively) The output was also slightly adjusted to fit ggPMX output (df and df2) (Line: 105,106) as_bmat was replaced by bmat_like to create the diagonal matrix (Line 116:142)

Examples

```
#project <- system.file("nonmem", package = "mrgsolve")
#est <- read_nmext(1005, project = project)
```

read_input *Read Modelling input data*

Description

Read Modelling input data

Usage

```
read_input(
  ipath,
  dv,
  dvid,
  cats = "",
  conts = "",
  strats = "",
  occ = "",
  endpoint = NULL,
  id = NULL,
  time = NULL
)
```

Arguments

ipath	full path of the input file
dv	character the name of measurable variable used in the input modelling file
dvid	character observation type parameter
cats	*[Optional]*character vector of categorical covariates
conts	*[Optional]*character vector of continuous covariates
strats	*[Optional]*character extra stratification variables
occ	*[Optional]*character inter individual occasion variables
endpoint	integer null in case of a single endpoint otherwise the index of endpoints.
id	character the name of identifier variable used in the input modelling file.
time	character the name of time variable used in the input modelling file

Value

data.table well formatted containing modelling input data

read_mlx_ind_est *Read MONOLIX individual parameters*

Description

Read MONOLIX individual parameters

Usage

```
read_mlx_ind_est(path, x, ...)
```

Arguments

path	character path to the file
x	dataset object
...	extra parameter not used

Value

data.table object

read_mlx_par_est *Read MONOLIX parameter estimation file*

Description

Read MONOLIX parameter estimation file

Usage

```
read_mlx_par_est(path, x, ...)
```

Arguments

path	character path to the file
x	dataset object
...	extra parameter not used

Value

data.table object

read_mlx_pred *Read MONOLIX model predictions*

Description

Read MONOLIX model predictions

Usage

```
read_mlx_pred(path, x, ...)
```

Arguments

path	character path to the file
x	dataset object
...	extra parameter not used

Value

data.table object

read_mlx_saem_conv *Read MONOLIX SAEM convergence file*

Description

Read MONOLIX SAEM convergence file

Usage

```
read_mlx_saem_conv(path, ...)
```

Arguments

path	string specifying data path folder
...	extra parameter not used

Value

data.table object

`residual` *This function create a residual for each observed value and also generates a residual distribution*

Description

This function create a residual for each observed value and also generates a residual distribution

Usage

```
residual(
  x,
  y,
  labels = NULL,
  point = NULL,
  is.hline = FALSE,
  hline = NULL,
  dname = NULL,
  facets = NULL,
  bloq = NULL,
  square_plot = TRUE,
  ...
)
```

Arguments

`x`	x axis aesthetics
`y`	y axis aesthetics
`labels`	list that contain title,subtitle, axis labels
`point`	geom point graphical parameters
`is.hline`	logical if TRUE add horizontal line y=0 (TRUE by default)
`hline`	geom hline graphical parameters
`dname`	name of dataset to be used
`facets`	`list` wrap facetting in case of strat.facet
`bloq`	`pmxBLOQ` object created by `pmx_bloq`
`square_plot`	square dv_pred plot (TRUE by default)
`...`	others graphics arguments passed to `pmx_gpar` internal object.

Details

Some parameters are a list of parameters :

point is a list that contains:

- **shape:** default to 1

- **color:** default to black
- **size:** default to 1

labels is a list that contains:

- **title:** plot title default to AES_X versus AES_Y
- **subtitle:** plot subtitle default empty
- **x:** x axis label default to AES_X
- **y:** y axis label default to AES_Y

Value

a residual object

See Also

`plot_pmx.residual`

`residual_scatter` *Scatter residual plots*

Description

Scatter residual plots

DV vs PRED plot

DV vs IPRED plot

IWRES vs IPRED plot

|IWRES| vs IPRED plot

|IWRES| vs TIME plot

IWRES vs TIME plot

NPDE vs TIME plot

NPDE vs PRED plot

NPD vs TIME plot

NPD vs EPRED plot

NPD vs PRED plot

CWRES vs TIME plot

CWRES vs CPRED plot

CWRES vs PRED plot

Usage

```
residual_scatter(
  sim_blq,
  point,
  is.hline,
  hline,
  dname,
  bloq,
  filter,
  strat.facet,
  facets,
  strat.color,
  trans,
  pmxgpar,
  labels,
  axis.title,
  axis.text,
  ranges,
  is.smooth,
  smooth,
  is.band,
  band,
  is.draft,
  draft,
  is.identity_line,
  identity_line,
  scale_x_log10,
  scale_y_log10,
  color.scales,
  ...
)

pmx_plot_dv_pred(ctr, ...)

pmx_plot_dv_ipred(ctr, ...)

pmx_plot_iwres_ipred(ctr, ...)

pmx_plot_abs_iwres_ipred(ctr, ...)

pmx_plot_abs_iwres_time(ctr, ...)

pmx_plot_iwres_time(ctr, ...)

pmx_plot_npde_time(ctr, ...)

pmx_plot_npde_pred(ctr, ...)
```

```
pmx_plot_npd_time(ctr, ...)

pmx_plot_npd_epred(ctr, ...)

pmx_plot_npd_pred(ctr, ...)

pmx_plot_cwres_time(ctr, ...)

pmx_plot_cwres_cpred(ctr, ...)

pmx_plot_cwres_pred(ctr, ...)
```

Arguments

sim_blq	logical if TRUE uses sim_blq values for plotting. Only for Monolix 2018 and later.
point	list geom_point graphical parameters.
is.hline	logical if TRUE add horizontal line y=0 (TRUE by default).
hline	list geom_hline graphical parameters.
dname	character name of dataset to be used. User can create his own dataset using set_data and pass it as dname to be plotted.
bloq	pmxBLOQ object created by pmx_bloq.
	pmx_update parameters
filter	expression filter which will be applied to plotting data.
strat.facet	formula optional stratification parameter by facetting. This split plot by strats(each strat in a facet)
facets	list facet_wrap parameters.
strat.color	character optional stratification parameter by grouping. This will split the plot by group (color) of strat.
trans	character define the transformation to apply on x or y or both variables
pmxgpar	a object of class pmx_gpar possibly the output of the
	pmx_gpar: Shared basic graphics parameters
labels	list list containing plot and/or axis labels: title, subtitle, x , y
axis.title	list containing element_text attributes to customize the axis title. (similar to ggplot2 axis.title theme)
axis.text	list containing element_text attributes to customize the axis text (similar to ggplot2 axis.text theme)
ranges	list limits of x/y ranges
is.smooth	logical if set to TRUE add smooth layer
smooth	list geom_smooth graphical/smoothing fun parameters
is.band	logical if TRUE add horizontal band
band	list horizontal band parameters. geom_hline graphical parameters.

is.draft	logical if TRUE add draft layer
draft	list draft layer parameters. geom_text graphical parameters.
is.identity_line	logical if TRUE add an identity line
identity_line	listgeom_abline graphical parameters.
scale_x_log10	logical if TRUE use log10 scale for x axis.
scale_y_log10	logical if TRUE use log10 scale for y axis.
color.scales	list define scales parameter in case of strat.color pmx_settings
...	others graphics parameters passed : • pmx_gpar internal function to customize shared graphical parameters • residual generic object for all residual (scatter) plots . • pmx_update function. • aess can be used to change time variable within the plot (e.g. aess = list(x="TADQBW")) **residual parameters**
ctr	pmx controller

Value

ggplot2 object

Examples

```
# NOTES ######################
# examples are availables for all residual plots:
# - pmx_plot_abs_iwres_ipred
# - pmx_plot_dv_ipred
# - pmx_plot_dv_pred
# - pmx_plot_iwres_ipred
# - pmx_plot_iwres_time
# - pmx_plot_npde_time


# basic use  ----------------------------------------

ctr <- theophylline()
p <- ctr %>% pmx_plot_dv_pred()
## p is a ggplot2 object you can add any layer here
p + ggplot2::theme_minimal()

# update graphical parameter  ----------------------

## update labels
ctr %>% pmx_plot_dv_pred(
  labels = list(title = "DV versus PRED new title")
)

## remove draft
ctr %>% pmx_plot_dv_pred(is.draft = FALSE)
```

```
## remove horizontal line
ctr %>% pmx_plot_dv_pred(is.hline = FALSE)

## custom point aes and static parameters
## we can customize any geom_point parameter
ctr %>% pmx_plot_dv_pred(
  point = list(aes(alpha = DV), color = "green", shape = 4)
)



# stratification  ---------------------------------

## continuous stratification
ctr %>% pmx_plot_dv_pred(strat.color = ~WT0)
## categorical stratification
ctr %>% pmx_plot_dv_pred(strat.facet = ~SEX)
## using formula notation
ctr %>% pmx_plot_dv_pred(strat.facet = STUD~SEX)

# subsetting  -------------------------------------

## we can use any expression involving the data
ctr %>% pmx_plot_dv_pred(filter = DV > mean(DV) & PRED < median(PRED))
## filter and stratify
ctr %>% pmx_plot_dv_pred(filter = SEX == 1, strat.facet = ~SEX)


# transformation  ---------------------------------

## apply a log transformation in y
ctr %>% pmx_plot_dv_pred(trans = "log10_y")
```

`set_abbrev` *update or add a new abbreviation*

Description

update or add a new abbreviation

Usage

```
set_abbrev(ctr, ...)
```

Arguments

`ctr`	`pmxClass` controller object
`...`	Options to set or add, with the form `name = value`.

Examples

```
ctr <- theophylline()
ctr %>% set_abbrev("new_param" = "new value")
ctr %>% get_abbrev("new_param")
```

`set_data` *Set a controller data set*

Description

Set a controller data set

Usage

```
set_data(ctr, ..., envir = parent.frame())
```

Arguments

`ctr`	the controller object
`...`	a named list parameters (see example)
`envir`	the `environment` in which `expr` is to be evaluated. May also be `NULL`, a list, a data frame, a pairlist or an integer as specified to `sys.call`.

Details

This function can be used to set an existing data set or to create a new one. The basic idea is to change the built-in data set (change the factor level names, change some rows values or apply any other data set operation) and use the new data set using the dname parameter of pmx_plot family functions.

See Also

Other pmxclass: `get_cats()`, `get_conts()`, `get_covariates()`, `get_data()`, `get_occ()`, `get_plot()`, `get_plot_config()`, `get_strats()`, `plot_names()`, `plots()`, `pmx_update()`, `set_plot()`

Examples

```
ctr <- theophylline()
dx <- ctr %>% get_data("eta")
dx <- dx[, EFFECT := factor(
  EFFECT,
  levels = c("ka", "V", "Cl"),
  labels = c("Concentration", "Volume", "Clearance")
)]
## update existing data set
ctr %>% set_data(eta = dx)
## or create a new data set
```

```
ctr %>% set_data(eta_long = dx)
```

`set_plot` *Create a new plot of the desired type*

Description

Create a new plot of the desired type

Usage

```
set_plot(
  ctr,
 ptype = c("IND", "DIS", "SCATTER", "ETA_PAIRS", "ETA_COV", "PMX_QQ", "VPC", "PMX_DENS",
    "PARAM_HISTORY"),
  pname,
  use.defaults = TRUE,
  filter = NULL,
  strat.color = NULL,
  strat.facet = NULL,
  color.scales = NULL,
  trans = NULL,
  ...
)
```

Arguments

`ctr`	`pmxClass` controller object
`ptype`	plot type can be: • "IND" Individual plot type: `individual` • "DIS" Distribution plot type : `distrib` • "SCATTER" Residual plot type :`residual`
`pname`	plot name, if missing it will be created using function aestetics
`use.defaults`	`logical` if FALSE do not use defaults defined in yaml init files
`filter`	optional filter which will be applied to plotting data
`strat.color`	`character`
`strat.facet`	`formula` define categorical stratification as formula
`color.scales`	`list` can be used with strat.color to set scale_color_manual
`trans`	`list` transformation operator
`...`	other plot parameters to configure `pmx_gpar`.

Value

invisible ctr object

See Also

Other pmxclass: get_cats(), get_conts(), get_covariates(), get_data(), get_occ(), get_plot(), get_plot_config(), get_strats(), plot_names(), plots(), pmx_update(), set_data()

`theophylline` *Creates pmx controller using theophylline data*

Description

Creates pmx controller using theophylline data

Usage

```
theophylline(settings = NULL, ...)
```

Arguments

settings	pmxSettings object
...	other parameters of pmx_mlx like endpoint

Value

pmx controller

Examples

```
## Not run:
theophylline()

## End(Not run)
```

`wrap_formula` *merge facets formula with new formula*

Description

merge facets formula with new formula

Usage

```
wrap_formula(x, origin = "lfacet")
```

Arguments

x	formula object
origin	the origin formula default to ~lfacets

Value

formula object

`[.pmx_gpar` *Method for subsetting "pmx_gpar" objects*

Description

Method for subsetting "pmx_gpar" objects

Usage

```
## S3 method for class 'pmx_gpar'
x[index, ...]
```

Arguments

x	pmx_gpar object
index	can be character/integer of element
...	other parameter (not used just for generic)

Value

if exists the parameter description

Index