

Package ‘mapbayr’

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Title MAP-Bayesian Estimation of PK Parameters

Version 0.10.2

Description Performs maximum a posteriori Bayesian estimation of individual pharmacokinetic parameters from a model defined in 'mrgsolve', typically for model-based therapeutic drug monitoring. Internally computes an objective function value from model and data, performs optimization and returns predictions in a convenient format. The performance of the package was described by Le Louedec et al (2021) <[doi:10.1002/psp4.12689](https://doi.org/10.1002/psp4.12689)>.

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BugReports <https://github.com/FelicienLL/mapbayr/issues>

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add_covariates	<i>Add covariate columns to a dataset</i>
----------------	---

Description

The `add_covariates()` function adds an one or several covariate columns to a dataset provided as a proper data.frame or within a 'mrgsolve' model. Used in combination with `adm_rows()` and `obs_rows()`, it helps the creation of datasets in the proper format for simulations with 'mrgsolve' or parameter estimation with 'mapbayr', as explained in [data_helpers](#).

Usage

```
add_covariates(x, ...)

## S3 method for class 'data.frame'
add_covariates(x, ..., covariates = list(), AOLA = FALSE, TOLA = FALSE)

## S3 method for class 'mrgmod'
add_covariates(x, ..., covariates = list(), AOLA = NULL, TOLA = NULL)
```

Arguments

x	either a data.frame or a 'mrgsolve' model object
...	covariates values to add to the data. For each variable, supply a vector of length 1 or with the same number of rows. Ignored if covariates argument is used.
covariates	Covariates passed as a single list of variables. Overrides ...
AOLA, TOLA	a logical. Should the "Amount Of Last Administration" and "Time Of Last Administration" variables be added into the dataset? Default if FALSE if x is a dataset, TRUE if x is a 'mrgsolve' model where AOLA and TOLA are defined as covariates

Value

a data.frame, or a 'mrgsolve' model with a dataset in the @args\$data slot (accessible with [get_data\(\)](#)).

See Also

[data_helpers](#)

Examples

```
# Cannot start from scratch
## Not run:
add_covariates(BW = 90, SEX = 0)

## End(Not run)

library(magrittr)
adm_rows(time = c(0, 24, 48), cmt = 1, amt = c(100, 200, 300)) %>%
  add_covariates(BW = c(90, 85, 80), SEX = 0)

# If covariates are stored in a list, use `covariates = `
adm_rows(time = c(0, 24, 48), cmt = 1, amt = c(100, 200, 300)) %>%
  add_covariates(covariates = list(BW = c(90, 85, 80), SEX = 0))

# Missing values are filled with the "next observation carried backward" rule
adm_rows(time = c(0, 24, 48), cmt = 1, amt = c(100, 200, 300)) %>%
  add_covariates(BW = c(90, 85, 80), SEX = 0) %>%
  obs_rows(time = 36, DV = .0123, cmt = 2)
# Always verify the output in case of time-varying covariates
```

```
# Possibility to add Time and Amount of last administration as covariates
adm_rows(time = c(0, 24, 48), amt = c(100, 200, 300), cmt = 1) %>%
  obs_rows(time = c(8, 16, 32, 40), cmt = 2, DV = runif(4)) %>%
  add_covariates(TOLA = TRUE, AOLA = TRUE) %>%
  obs_rows(time = 72, cmt = 2, DV = .123) # AOLA/TOLA re-updated afterwards

# Automatic inclusion of `TOLA`/`AOLA` if they are covariates of the model
library(mrgsolve)
model <- mcode("model", "
$PARAM @annotated @covariates
TOLA : 0 : Time Last Adm
AOLA : 0 : Amount Last Adm
", compile = FALSE)

model %>%
  adm_rows(time = c(0, 24, 48), amt = c(100, 200, 300), cmt = 1) %>%
  add_covariates() %>%
  get_data()
```

adm_rows

Add administration lines to a dataset

Description

The `adm_rows()` function adds an one or several administration lines to a dataset provided as a proper data.frame or within a 'mrgsolve' model. Used in combination with `obs_rows()` and `add_covariates()`, it helps the creation of datasets in the proper format for simulations with 'mrgsolve' or parameter estimation with 'mapbayr', as explained in [data_helpers](#).

Usage

```
adm_rows(x, ...)

## S3 method for class 'data.frame'
adm_rows(
  x,
  ID = NULL,
  time = NULL,
  evid = 1L,
  cmt,
  amt,
  mdv = 1L,
  addl = NULL,
  ss = NULL,
  ii = NULL,
  rate = NULL,
  .datehour = NULL,
  ...
)
```

```
)

## S3 method for class 'missing'
adm_rows(...)

## S3 method for class 'mrgmod'
adm_rows(x, cmt = adm_cmt(x), rate = NULL, ...)
```

Arguments

x	either a data.frame or a 'mrgsolve' model object
...	additional columns or arguments for mrgsolve::ev()
ID	subject ID (default is 1)
time	event time. Default is 0 if no previous events. Mind consistency with .datehour.
evid	event identification (default is 1 for administration, 0 for observation)
cmt	compartment (no default, except if [ADM] was tagged in the \$CMT block in model code. See examples.)
amt	dose amount (for administration records only)
mdv	missing dependent value (default is 1 for administration records)
addl	additional dose (optional)
ss	steady-state (optional, is this dose the last of an infinity of administration? Yes, 1, or no, 0)
ii	inter-dose interval (optional, use it with ss and addl)
rate	rate of administration (optional, set to -2 if you model zero-order infusion. See examples.)
.datehour	a object of class POSIXct, a number or a character vector that can be passed to parse_datehour() . Using .datehour will update the value of time in the dataset, with units in hours. Mind consistency with the time argument.

Value

a data.frame, or a 'mrgsolve' model with a dataset in the @args\$data slot (accessible with [get_data\(\)](#)).

See Also

[data_helpers](#)

Examples

```
# Create a dataset from scratch
adm_rows(amt = 100, cmt = 1)

# Pipe-friendly addition of administration record to a pre-existing dataset
library(magrittr)
adm_rows(amt = 100, cmt = 1) %>%
  adm_rows(time = 3, amt = 200, cmt = 1, addl = 3, ii = 1)
```

```

# Inform times using the `.datehour` argument:
adm_rows(.datehour = "2020-01-01 11:11", amt = 100, cmt = 1) %>%
  adm_rows(.datehour = "2020-01-02 22:22", amt = 200, cmt = 1) %>%
  adm_rows(time = 48, amt = 300, cmt = 1)

# Start from a 'mrgsolve' model
library(mrgsolve)
house() %>%
  adm_rows(amt = 100, cmt = 1) %>%
  adm_rows(time = 3, amt = 200, cmt = 1, addl = 3, ii = 1) %>%
  mrgsim(delta = 1)

# Default administration compartments
# Set default administration compartments in the code with `[ADM]`
model <- mcode("model", "
$CMT @annotated
DEPOT : Depot [ADM]
CENTR : Central
", compile = FALSE)
adm_cmt(model)

# Thus, no need to manually specify `cmt = 1` anymore.
model %>%
  adm_rows(amt = 100) %>%
  adm_rows(time = 3, amt = 200, addl = 3, ii = 1) %>%
  get_data()

# Automatic lines duplication if multiple depot compartments
# Automatic `rate = -2` increment if model with 0-order absorption
model <- mcode("model", "
$PARAM DUR = 1.0
$CMT @annotated
DEPOT : Depot [ADM]
CENTR : Central [ADM]
$MAIN
D_CENTR = DUR ;
", compile = FALSE)
adm_cmt(model)

model %>%
  adm_rows(amt = 100) %>%
  adm_rows(time = 3, amt = 200, addl = 3, ii = 1) %>%
  get_data()

```

as.data.frame.mapbayests

Return the mapbay_tab as a data.frame

Description

Return the mapbay_tab as a data.frame

Usage

```
## S3 method for class 'mapbayests'  
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

x A mapbayests object.
row.names, optional, ...
 passed to as.data.frame

Value

a data.frame (the mapbay_tab from estimation)

augment

Compute full PK profile prediction from mapbayr estimates.

Description

Compute full PK profile prediction from mapbayr estimates.

Usage

```
augment(x, ...)
```

Arguments

x object to augment
... additional arguments

Value

an augmented object (depending on the object passed).

augment.mapbayests	<i>Compute full PK profile prediction from mapbayr estimates.</i>
--------------------	---

Description

Compute full PK profile prediction from mapbayr estimates.

Usage

```
## S3 method for class 'mapbayests'
augment(
  x,
  data = NULL,
  start = NULL,
  end = NULL,
  delta = NULL,
  ci = FALSE,
  ci_width = 90,
  ci_method = "delta",
  ci_sims = 500,
  ...
)
```

Arguments

x	A mapbayests object.
data	dataset to pass to mrgsolve for simulation (default is dataset used for estimation)
start, end, delta	start, end and delta of simulation time passed to mrgsim() (see details)
ci	a logical. If TRUE, compute a confidence interval around the prediction (default is FALSE)
ci_width	a number between 0 and 100, width of the confidence interval (default is "90" for a 90%CI)
ci_method	method to compute the confidence interval. Can be "delta" (the default) to use the Delta approximation. Alternatively "simulations" for a more accurate approach, but also more time-consuming.
ci_sims	number of replicates to simulate in order to derive the confidence interval (default is 500)
...	additional arguments passed to mrgsim()

Details

This function is called in the background by plot() in order to simulate the full PK profile, and return a mapbayests object with an additional aug_tab data.frame inside. The latter is used with by the plot method. The time grid, for each PK profile (i.e. patient) is defaulted with the minimum time

in the dataset for start and the maximum time in the dataset +20% for end. delta is a power of 10 (e.g. 0.1, 1, 10 etc...), automatically chosen to render visually appealing graphs with a reasonable computing time (about 200 time points). Additional arguments can be passed to `mrgsim()` through Note that `recsort` is set to 3 (see `mrgsolve` documentation for more details).

Value

a `mapbayests` object, augmented of an `aug_tab` data.frame.

Examples

```
#x is the result of `mapbayest()`.
#Default plot is returned by:
# plot(x)
#Argument passed to `plot()` are passed to `augment()` in the background:
# plot(x, end = 240, ci = TRUE)
#Save the augmented object if simulation time is long
# x2 <- augment(x, ci = TRUE, ci_method = "simulations", ci_sims = 10000) %>%
# plot(x2)
```

check_mapbayr_model	<i>Check if model is valid for 'mapbayr'</i>
---------------------	--

Description

Checks that the model respects points related exclusively to 'mapbayr'. Useful at the time you wish to convert a "regular" 'mrgsolve' model you used for simulation into a model to perform MAP-Bayesian estimation. Note that some elements cannot be checked:

- In \$MAIN block, make sure that you added ETA1, ETA2... in the code. For instance: `double CL = TVCL * exp(ETA(1) + ETA1) ;`.
- In \$OMEGA block, make sure the order of the (diagonal) values is the same as for ETAs in \$PARAM. For instance, if ETA1 corresponds to clearance, the first value in \$OMEGA must be the variance of clearance.
- In \$SIGMA block, make sure the order is respected: proportional error first, and additive error secondly.

Usage

```
check_mapbayr_model(x, check_compile = TRUE)
```

Arguments

x	model file
check_compile	check if model is compiled

Value

TRUE (invisibly) if checks are passed, errors otherwise.

Examples

```
library(mapbayr)
library(mrgsolve)
## Not run: check_mapbayr_model(house())
```

compute_ofv	<i>Compute the objective function value</i>
-------------	---

Description

Compute the objective function value

Usage

```
compute_ofv(
  eta,
  qmod,
  sigma,
  omega_inv,
  all_cmt,
  log_transformation,
  lambda = 1,
  idvaliddata,
  idDV,
  idcmt,
  idblq = NULL,
  idlloq = NULL,
  ...
)

do_compute_ofv(eta, argofv, ...)
```

Arguments

eta	a named vector/list of parameters
qmod, sigma, log_transformation, omega_inv, all_cmt, lambda	generated by preprocess.ofv.fix
idvaliddata, idDV, idcmt	generated by preprocess.ofv.id
idblq, idlloq	optionally generated by preprocess.ofv.id
...	for compatibility (not used)
argofv	above mentioned arguments as a list

Details

This function is called iteratively by the optimization function. Arguments should not be passed directly, but generated by the pre-processing functions (see [preprocess.ofv](#)).

Value

a single numeric value (the objective function value)

data_helpers

Data helpers: functions to build the dataset

Description

Use [adm_rows\(\)](#), [obs_rows\(\)](#) and [add_covariates\(\)](#) to create or modify a dataset from scratch, from a pre-existing dataset, or from a dataset stored into a 'mrgsolve' model.

Details

Instead of importing a '.csv' file, or painfully build a data set with a call to `data.frame()` and mind how to format the data, you can pass information about:

- administrations with [adm_rows\(\)](#),
- observations with [obs_rows\(\)](#),
- covariates with [add_covariates\(\)](#),

all being called jointly with a pipe (`%>%` or `|>`). These functions can be used to create or modify a dataset as a proper `data.frame`, or to create or modify a dataset within a 'mrgsolve' model (`@args$data` slot). The latter is particularly useful in order to:

- automatically use default administration and observation compartments,
- automatically duplicate rows if there are several depot compartments,
- automatically set `rate = -2` if model has zero-order absorption pathways,
- automatically duplicate rows if concentrations of Parent drug and Metabolite are observed together,
- automatically add "Amount Of Last Administration" and "Time Of Last Administration" variables if these are covariates,
- subsequently call `mrgsim()` or `mapbayest()`.

Details

- mbrest() is now [mapbayest\(\)](#)
- adm_lines() is now [adm_rows\(\)](#)
- obs_lines() is now [obs_rows\(\)](#)

do_mapbayr_sim

*Simulate with mapbayr***Description**

A wrapper around [mrgsolve::mrgsim\(\)](#) for results generated from [mapbayest\(\)](#). Exported for the purpose of utility but might be prone to changes.

Usage

```
do_mapbayr_sim(
  x,
  data,
  recsort = 3,
  output = "df",
  ...,
  eta = NULL,
  nrep = NULL,
  new_omega = NULL,
  new_sigma = NULL
)
```

Arguments

x	the model object
data	NMTRAN-like data set
recsort	record sorting flag. Defaulted to 3. See mrgsolve::mrgsim() .
output	type of object returned. Defaulted to "df" for a data.frame. See mrgsolve::mrgsim() .
...	passed to mrgsolve::mrgsim() .
eta	a matrix of individual point estimates of ETA. Most likely obtained with get_eta() .
nrep	number of replicates. If used, the original "ID" in the data will be replaced by unique identifiers.
new_omega, new_sigma	New "omega" and "sigma" matrices to use instead of those defined in "\$OMEGA" and "\$SIGMA".

Value

An output from [mrgsolve::mrgsim\(\)](#).

Examples

```
library(mrgsolve)
mod <- exmodel(1, exdata = FALSE)
dat <- exdata(ID = c(1,2))

# Classic framework
set.seed(123)
do_mapbayr_sim(x = mod, data = dat, Request = "DV")

# No random effect
do_mapbayr_sim(x = zero_re(mod), data = dat)
do_mapbayr_sim(x = mod, data = dat, new_omega = "zero_re")

# New random effects
## New omega matrix
do_mapbayr_sim(x = mod, data = dat, new_omega = dmat(0.1, 0.03, 0.01), nrep = 10)

## Matrix with "eta" as mean and "new_omega" as variance covariance matrix
etamat <- get_eta(est001, output = "num")[1:2,]

do_mapbayr_sim(
  x = mod, data = dat, nrep = 10,
  eta = etamat, new_omega = dmat(0.1, 0.03, 0.01)
)
```

est001

Estimation object

Description

An example of mapbayests object, corresponding to the parameter estimation of the 8 subjects from model 1. Note that the model object within is not associated to a shared object, which make some features unavailable. This object can be re-generated by executing `est001 <- mapbayest(exmodel(ID = 1:8))`

Usage

```
est001
```

Format

An object of class mapbayests of length 9.

See Also

[mapbayest](#)

eta	<i>Generate a vector of "ETA"</i>
-----	-----------------------------------

Description

Generate a vector of "ETA" values. If `x` is a `mrgsolve` model, these will be extracted from values defined in `$PARAM`. Otherwise, any numeric values passed to `x` and `...` as vector(s) or list(s) will be coerced as a single vector. Alternatively, if `x` and `...` are missing, generate a vector of ETA equal to `val` of length `n`.

Usage

```
eta(x, ..., n, val = 0)
```

Arguments

<code>x</code>	either a <code>mrgsolve</code> model object, or a numeric
<code>...</code>	additional numeric(s)
<code>n, val</code>	generate a sequence of <code>val</code> of length <code>n</code>

Value

a single named vector of numeric

Examples

```
# Extract ETA from the model
mod <- exmodel()
eta(mod)

# Coerce numeric values
eta(0.1, 0.2, c(0.3, 0.4), list(0.5, 0.6))
eta(rnorm(4))

# Generate a sequence from scratch
eta(n = 3)
eta(n = 3, val = 0.001)
```

exmodel_exdata	<i>Example model and data</i>
----------------	-------------------------------

Description

A collection of example models and corresponding data to test and explore mapbayr.

Usage

```
exmodel(
  num = 1,
  add_exdata = TRUE,
  cache = TRUE,
  quiet = getOption("mrgsolve_mread_quiet", TRUE),
  ...,
  ID = 1,
  clean_data = TRUE
)

exdata(num = 1, ID = 1, clean_data = TRUE)
```

Arguments

num	model number (see details)
add_exdata	should data be automatically loaded with the model
cache	read the model with <code>mrgsolve::mread_cache()</code>
quiet	don't print messages when compiling
...	passed to <code>mrgsolve::mread()</code> or <code>mrgsolve::mread_cache()</code>
ID	individual number to include in the data (from 1 to 8)
clean_data	remove useless columns and rows from the original data

Details

Available models are:

- 1: Base model. A simple monocompartmental PK model with inter-individual variability on absorption constant (KA), volume of distribution (VC) and clearance (CL). The residual error model is proportional.
- 6: Complex absorption model. Dual 0- and 1st orders absorption phenomena.
- 301: Time-varying covariates. A continuous covariate (body weight "BW") and a categorical one (sex "SEX") influence the clearance parameter. In the corresponding dataset, the values randomly changes from one record to another within a single individual.
- 401: Metabolite. The PK model of both a parent drug and its metabolite.

An example dataset of eight (simulated) individuals is available for each model. Individuals differ in terms of sampling times (sparse or rich) and dosing regimen (single or multiple dosing).

Model code and data files are stored at the location given by `system.file("exmodel", package = "mapbayr")`.

These models and data were created for the validation study of mapbayr published in [CPT:Pharmacometrics & System Pharmacology](#). More models and full datasets can be accessed [in a dedicated repository](#)

Value

`exmodel()` reads and compiles code, and returns a (mrgmod) model object. `exdata()` returns a data.frame.

Source

<https://github.com/FelicienLL/mapbayr-CPTPSP-2021>

Examples

```
# Models can be loaded with data (the default), ready for parameter estimation
est <- mapbayest(exmodel())

# Number of subjects in dataset can be chosen up to 8 individuals
exdata(301, ID = c(5,8))
```

filter.mrgmod	<i>Filter a dataset within a mrgmod</i>
---------------	---

Description

Filter a dataset within a mrgmod

Usage

```
## S3 method for class 'mrgmod'
filter(.data, ..., .preserve = FALSE)
```

Arguments

```
.data          a mrgmod
..., .preserve additional arguments for dplyr::filter()
```

Value

a mrgmod

Examples

```
library(magrittr)
mod <- mrgsolve::mcode("mod", "$CMT F00", compile = FALSE)
mod %>%
  adm_rows(amt = c(100, 200, 300), cmt = 1) %>%
  filter(amt != 200) %>%
  get_data()
```

get_x	<i>Get content from object</i>
-------	--------------------------------

Description

Helpful functions to get content from a mrgmod object (i.e. data) or from a mapbayests object (data, eta, cov, param, phi).

Usage

```
get_data(x, ...)

## S3 method for class 'mrgmod'
get_data(x, ...)

## S3 method for class 'mapbayests'
get_data(x, ..., output = "df")

get_eta(x, ...)

## S3 method for class 'mapbayests'
get_eta(x, ..., output = NULL)

get_cov(x, ...)

## S3 method for class 'mapbayests'
get_cov(x, ..., simplify = TRUE)

get_param(x, ...)

## S3 method for class 'mapbayests'
get_param(x, ..., output = NULL, keep_ID = NULL, keep_names = NULL)

get_phi(x, ...)

## S3 method for class 'mapbayests'
get_phi(x, ...)
```

Arguments

x	mapbayests object
...	not used
output	either a data.frame ("df") or a vector of numeric ("num"). Default to "num" if only one ID
simplify	a logical. If TRUE (the default) and only one ID, one matrix is returned instead of a list of length 1
keep_ID	a logical. By default, the ID variable is dropped if one ID in data.
keep_names	a logical. By default, names are dropped if one parameter is requested, and output is not a data frame.

Value

the class of the object returned depends on the function, and on their arguments. Typically, a data.frame or a vector if the output can be reduced to one line.

Examples

```
# From a model object (mrgmod)
mod <- exmodel(ID = 1:2, cache = FALSE, capture = "CL")
get_data(mod)

# From an estimation object (mapbayests)
est <- mapbayest(mod)
get_data(est)
get_data(est, output = "list")

get_eta(est)
get_eta(est, output = "list")

get_cov(est)

get_param(est)

get_phi(est)
```

hist.mapbayests

Plot posterior distribution of bayesian estimates

Description

Plot posterior distribution of bayesian estimates

Usage

```
## S3 method for class 'mapbayests'
hist(x, select_eta = x$arg.optim$select_eta, shk = c("sd", "var", NA), ...)
```

Arguments

<code>x</code>	A mapbayests object.
<code>select_eta</code>	a vector of numeric values, the numbers of the ETAs to show (default are estimated ETAs).
<code>shk</code>	method to compute the shrinkage if multiple subjects are analyzed. Possible values are "sd" (based on the ratio of standard deviation like in 'NONMEM'), "var" (based on the ratio of variances like 'Monolix'), or NA (do not show the shrinkage)
<code>...</code>	additional arguments (not used)

Details

Use this function to plot the results of the estimations, in the form of histograms with the *a priori* distribution in the background. For every parameter, the inter-individual variability is displayed, as well as the percentile of the patient in the corresponding distribution (if n = 1 patient). For additional modifications, you can add extra `+function(...)` in order to modify the plot as a regular ggplot2 object.

Value

a ggplot object.

Examples

```
est <- mapbayest(exmodel(ID = 1))

# Default Method
h <- hist(est)

# Can be modified with `ggplot2`
h +
  ggplot2::labs(title = "Awesome estimations")

# Select the ETAs
hist(est, select_eta = c(1,3))
```

mapbayest

Estimate parameters (maximum a posteriori)

Description

The main function of the mapbayr package. Performs a *maximum a posteriori* Bayesian estimation of parameters, from a mrgsolve model object and a dataset containing information about administrations and observed concentrations.

Usage

```
mapbayest(
  x,
  data = NULL,
  method = c("L-BFGS-B", "newuoa"),
  hessian = stats::optimHess,
  select_eta = NULL,
  lambda = 1,
  lloq = NULL,
  force_initial_eta = NULL,
  quantile_bound = 0.001,
  control = list(),
  check = TRUE,
  verbose = TRUE,
  progress = TRUE,
  reset = 50,
  output = NULL,
  ...
)
```

Arguments

x	the model object
data	NMTRAN-like data set
method	optimization method; the default is "L-BFGS-B" (from <code>stats::optim()</code>), alternatively "newuoa" for <code>minqa::newuoa()</code>
hessian	function used to compute the Hessian and variance-covariance matrix with (default is <code>stats::optimHess</code> , alternatively use <code>nlmixr::nlmixrHess</code>)
select_eta	a vector of numeric values, the numbers of the ETAs to be estimated (default is NULL, all ETAs non-equal to zero)
lambda	a numeric value, the weight applied to the model prior (default is 1)
lloq	a numeric value, the lower limit of quantification. If not NULL, LLOQ and BLQ (below limit of quantification) variables will be added to the data. The related records will be censored with the M3 method. Ignored if LLOQ already in the data.
force_initial_eta	a vector of numeric values to start the estimation from (default to 0 for "L-BFGS-B")
quantile_bound	a numeric value representing the quantile of the normal distribution admitted to define the bounds for L-BFGS-B (default is 0.001, i.e. 0.1%)
control	a list passed to the optimizer (see <code>stats::optim()</code> or <code>minqa::newuoa()</code> documentation)
check	check model code for mapbayr specification (a logical, default is TRUE)
verbose	print a message whenever optimization is reset (a logical, default is TRUE)
progress	print a progress bar (a logical, default is TRUE)

reset	maximum allowed reset of the optimizer with new initial eta values if numerical difficulties, or with new bounds (L-BFGS-B) if estimate equal to a bound. (a numeric, default is 50)
output	if NULL (the default) a mapbayests object is returned; if df a <i>mapbay_tab</i> dataframe is returned
...	for compatibility (not used)

Value

a mapbayests object. Basically a list containing:

- model: the model object
- arg.ofv.optim, arg.ofv.fix, arg.ofv.id: arguments passed to the optimization function. Useful for debugging but not relevant for a basic usage. Access to the data with `get_data(x)`
- opt.value: the original output of the optimization function
- final_eta: a list of individual vectors of final estimates. Access it with `x$final_eta` or `get_eta(x)`.
- covariance: a list of individual variance-covariance matrix of estimation. Access it with `x$covariance` or `get_cov(x)`.
- mapbay_tab: an output table containing the results of your estimations (data, IPRED, PRED, covariates, captured items, ETA etc...). Access it with `x$mapbay_tab`, `as.data.frame(x)` or `as_tibble(x)`.
- information: run times and package versions.

See Also

[hist.mapbayests](#)
[plot.mapbayests](#)
[use_posterior](#)

Examples

```
# First, code a model
code1 <- "$PARAM ETA1 = 0, ETA2 = 0,
KA = 0.5, TVCL = 1.1, TVV = 23.3
$OMEGA 0.41 0.32
$SIGMA 0.04 0
$CMT DEPOT CENT
$PK
double CL=TVCL*exp(ETA1+ETA(1));
double V=TVV*exp(ETA2+ETA(2)) ;
$error
double DV=CENT/V*(1+EPS(1))+EPS(2);
$PKMODEL ncmt = 1, depot = TRUE
$CAPTURE DV CL
"

my_model <- mrgsolve::mcode("my_model", code1)
```

```
# Then, import your data
my_data <- data.frame(ID = 1, TIME = c(0, 1.1, 5.2, 12.3), EVID = c(1,0,0,0), AMT = c(500, 0,0,0),
  CMT = c(1,2,2,2), DV = c(0, 15.1, 29.5, 22.3))
print(my_data)

# And estimate
my_est <- mapbayest(x = my_model, data = my_data)
print(my_est)
# see also plot(my_est) and hist(my_est)

# Use your estimation
get_eta(my_est)
get_param(my_est)
as.data.frame(my_est)
use_posterior(my_est)
```

mapbayr_plot

Make mapbayr plot

Description

Make mapbayr plot

Usage

```
mapbayr_plot(
  aug_tab,
  obs_tab = NULL,
  PREDICTION = c("IPRED", "PRED"),
  MODEL_color = NULL
)
```

Arguments

aug_tab	a table of predictions, generated by <code>augment(x)</code> and available at <code>x\$aug_tab</code>
obs_tab	a table of observations
PREDICTION	plot either "IPRED", "PRED" or both.
MODEL_color	a vector of strings interpretable as colors, with names that correspond to a value in <code>aug_tab\$MODEL</code>

Value

a ggplot object

Examples

```

aug <- data.frame(
  ID = 1, name = factor("DV"), cmt = 2, time = rep(c(0,8,16,24), each = 2),
  type = rep(c("PRED", "IPRED"), 4), value = c(0,0, 1, 2, 4, 8, 2, 4)
)

obs <- data.frame(
  ID = 1, time = c(6, 20), evid = 0,
  mdv = c(0,1), DV = c(0.5, 5), cmt = 2
)

mapbayr_plot(aug, obs)
mapbayr_plot(aug, obs, PREDICTION = "IPRED")

aug2 <- dplyr::bind_rows(
  FOO = aug,
  BAZ = dplyr::mutate(aug, value = value * 2),
  BAR = dplyr::mutate(aug, value = value * 3),
  .id = "MODEL"
)

mapbayr_plot(aug2, obs)
mapbayr_plot(aug2, obs, PREDICTION = "IPRED")
mapbayr_plot(aug2, obs, PREDICTION = "IPRED", MODEL_color = c(FOO = "black"))

```

mapbayr_vpc

Visual Predicted Checks

Description

Visual Predicted Checks

Usage

```

mapbayr_vpc(
  x,
  data = NULL,
  nrep = 500,
  pcvpc = TRUE,
  idv = "time",
  stratify_on = NULL,
  start = NULL,
  end = NULL,
  delta = 1,
  ...
)

```

Arguments

x	the model object
data	NMTRAN-like data set
nrep	a numeric, the number of replicates for stochastic simulations. Default is 500.
pcvpc	a logical, if TRUE (the default) will output "prediction-corrected VPC" (see Details).
idv	a character indicating the variable used as independent variable. Default is "time", alternatively use "tad" to automatically compute the time after last dose.
stratify_on	a character (vector) indicating the variables of the data used to stratify the results. Variables must be numeric (as they are passed to <code>mrgsolve::carry_out()</code>)
start, end, delta, ...	passed to <code>mrgsolve::mrgsim()</code>

Details

- Prediction-corrected VPC

By default, VPC are prediction corrected (Bergstrand et al (2011) [doi:10.1208/s122480119255z](https://doi.org/10.1208/s122480119255z)). This correction is advised if several levels of doses or covariates are in the dataset for instance. Note that the implemented correction formula does not take into account the 'lower bound' term (*lbij*), nor the log-transformed variables.

Value

a ggplot object, results of the VPC. The median and the 50%, 80% and 90% prediction intervals of the simulated distributions are reported.

Examples

```
library(mrgsolve)
library(magrittr)
# Define a model. Adding variability to house model because default is 0.
mod <- house() %>%
  omat(dmat(rep(0.2,4)))

# Creating dataset for the example
# Same concentration, but different dose (ID 2) and covariate (ID 3)
data <- adm_rows(ID = 1, amt = 1000, cmt = 1, addl = 6, ii = 12) %>%
  obs_rows(DV = 50, cmt = 2, time = 7 * 12) %>%
  adm_rows(ID = 2, time = 0, amt = 2000, cmt = 1, addl = 6, ii = 12) %>%
  obs_rows(DV = 50, cmt = 2, time = 7 * 12) %>%
  adm_rows(ID = 3, time = 0, amt = 1000, cmt = 1, addl = 6, ii = 12) %>%
  obs_rows(DV = 50, cmt = 2, time = 7 * 12) %>%
  add_covariates(SEX = c(0,0,0,0,1,1))

mapbayr_vpc(mod, data, nrep = 30) # prediction-corrected by default
mapbayr_vpc(mod, data, idv = "tad", start = 72, nrep = 30)
mapbayr_vpc(mod, data, pcvpc = FALSE, nrep = 30)
mapbayr_vpc(mod, data, stratify_on = "SEX", nrep = 30)
```

model_averaging

Average predictions from multiple models

Description

Model Averaging consists in analyzing the same data with different models and to average their predictions. In order to perform weighted means of clearance predictions, (or concentrations, or any metric of interest), it is necessary to compute the "weight" of each estimation. It is informed by the likelihood of estimation. Two weighting scheme are currently implemented, one based on the log-likelihood ("LL", the default), the other on the Akaike criterion ("AIC"). The method was previously described by Uster et al (2021) [doi:10.1002/cpt.2065](https://doi.org/10.1002/cpt.2065).

Usage

```
model_averaging(
  ...,
  output_function = as.data.frame,
  scheme = c("LL", "AIC"),
  estlist = NULL
)

compute_weights(..., scheme = c("LL", "AIC"), estlist = NULL)

do_model_averaging(list_of_tabs, weights_matrix)
```

Arguments

...	estimation objects generated with <code>mapbayest()</code> , from which the weights will be computed
output_function	a unique function that takes any estimation object and returns a table with controlled variables, dimensions and attributes.
scheme	scheme weight, either "LL" or "AIC"
estlist	a list of estimation objects. Overrides ...
list_of_tabs, weights_matrix	respectively outputs of the output_function and <code>compute_weights()</code>

Value

- `model_averaging()` and `do_model_averaging()`: a data.frame of the same dimensions and attributes as the outputs
- `compute_weights()`: a matrix with IDs as rows and estimation weights as columns

Examples

```

library(magrittr)

# Three different models: A, B, and C.
modA <- exmodel(1, add_exdata = FALSE)
modB <- mrgsolve::param(modA, TVCL = 2, TVVC = 30)
modC <- mrgsolve::param(modA, TVCL = 10)

# A common dataset that has 2 patients (ID 2 & 9)
data <- adm_rows(ID = 2, time = 0, amt = 200, addl = 3, ii = 24, cmt = 1) %>%
  obs_rows(ID = 2, time = 84, DV = 1.5, cmt = 2) %>%
  adm_rows(ID = 9, time = 0, amt = 100, addl = 3, ii = 24, cmt = 1) %>%
  obs_rows(ID = 9, time = 96, DV = 1, cmt = 2)

# Three different estimation objects: A, B and C.
estA <- mapbayest(modA, data)
as.data.frame(estA)
plot(estA) # Fit is pretty good

estB <- mapbayest(modB, data)
as.data.frame(estB)
plot(estB) # Excellent fit

estC <- mapbayest(modC, data)
as.data.frame(estC)
plot(estC) # Fit is worst

# Model averaging
model_averaging(A = estA, B = estB, C = estC)
# Weighted average of the table returned by as.data.frame(est))

# Internally, it first computes the "weight" of each model such as:
W <- compute_weights(A = estA, B = estB, C = estC)

# Then multiply the prediction table with each weight such as:
do_model_averaging(
  list_of_tabs = list(
    A = as.data.frame(estA),
    B = as.data.frame(estB),
    C = as.data.frame(estC)
  ),
  weights_matrix = W
)

# If you do not want to perform an average of the full table, you can specify
# a function that takes the estimation object as an input and returns
# value(s) of interest: a single prediction, a clearance value, a full
# table of augmented predictions... as long as the structure of the final
# object is the same whatever the model.

reframe <- function(est){
  # From any estimation object, return a table with ID, time and predictions

```

```

  as.data.frame(est)[,c("ID", "time", "DV", "IPRED")]
}

model_averaging(A = estA, B = estB, C = estC, output_function = reframe)

# Make a plot that compares predictions
List_aug_tab <- lapply(
  X = list(A = estA, B = estB, C = estC),
  FUN = function(x) augment(x)$aug_tab
)
List_aug_tab$.AVERAGE <- do_model_averaging(List_aug_tab, W)

mapbayr_plot(
  aug_tab = dplyr::bind_rows(List_aug_tab, .id = "MODEL"),
  obs_tab = data,
  PREDICTION = "IPRED",
  MODEL_color = c(.AVERAGE = "black")
)

```

obs_rows

Add observation lines to a dataset

Description

The `obs_rows()` function adds an one or several observation lines to a dataset provided as a proper `data.frame` or within a 'mrgsolve' model. Used in combination with `adm_rows()` and `add_covariates()`, it helps the creation of datasets in the proper format for simulations with 'mrgsolve' or parameter estimation with 'mapbayr', as explained in [data_helpers](#).

Usage

```

obs_rows(x, ...)

## S3 method for class 'data.frame'
obs_rows(
  x,
  ID = NULL,
  time = NULL,
  evid = 0L,
  cmt,
  DV = NA_real_,
  mdv = NULL,
  .datehour = NULL,
  ...
)

## S3 method for class 'missing'
obs_rows(...)

```

```
## S3 method for class 'mrgmod'
obs_rows(x, cmt = NULL, DV = NA_real_, DVmet = NULL, ...)
```

Arguments

x	either a data.frame or a 'mrgsolve' model object
...	additional columns
ID	subject ID (default is 1)
time	event time. Default is 0 if no previous events. Mind consistency with .datehour.
evid	event identification (default is 1 for administration, 0 for observation)
cmt	compartment (no default, except if [OBS] was tagged in the \$CMT block in model code. See examples.)
DV	dependent value, i.e. observed concentration.
mdv	missing dependent value (default is 0 a non-missing concentration value to take into account for parameter estimation, 1 otherwise)
.datehour	a object of class POSIXct, a number or a character vector that can be passed to parse_datehour() . Using .datehour will update the value of time in the dataset, with units in hours. Mind consistency with the time argument.
DVmet	second observation at the same time (e.g. a metabolite, "DVmet") observed jointly with parent drug ("DV"). Works only if x is a 'mrgsolve' model where two [OBS] compartments were defined (see examples)

Value

a data.frame, or a 'mrgsolve' model with a dataset in the @args\$data slot (accessible with [get_data\(\)](#)).

See Also

[data_helpers](#)

Examples

```
# Create a dataset from scratch
obs_rows(time = 12, DV = 0.12, cmt = 2)

# Pipe-friendly addition of observation record to a pre-existing dataset
library(magrittr)
obs_rows(time = 12, DV = 0.12, cmt = 2) %>%
  obs_rows(time = c(24, 36, 48), DV = c(0.34, 0.56, 0.78), mdv = c(0, 1, 0), cmt = 2)

# Inform times using the `.datehour` argument:
obs_rows(.datehour = "2020-01-01 11:11", DV = 0.12, cmt = 1) %>%
  obs_rows(.datehour = "2020-01-02 22:22", DV = 0.34, cmt = 1) %>%
  obs_rows(time = 48, DV = 0.56, cmt = 1)

# Start from a 'mrgsolve' model
library(mrgsolve)
```

```

house() %>%
  obs_rows(time = 12, DV = 0.12, cmt = 2) %>%
  obs_rows(time = c(24, 36, 48), DV = c(0.34, 0.56, 0.78), mdv = c(0, 1, 0), cmt = 2) %>%
  mrgsim()

# Default observation compartments
# Set default observation compartments in the code with `[OBS]`
model <- mcode("model", "
$CMT @annotated
DEPOT : Depot
CENTR : Central [OBS]
", compile = FALSE)
obs_cmt(model)

# Thus, no need to manually specify `cmt = 2` anymore.
model %>%
  obs_rows(time = 12, DV = 0.12) %>%
  obs_rows(time = c(24, 36, 48), DV = c(0.34, 0.56, 0.78), mdv = c(0, 1, 0)) %>%
  get_data()

# Automatic lines duplication if parent + metabolite defined in the model
model <- mcode("model", "
$CMT @annotated
DEPOT : Depot
CENTR : Central [OBS]
PERIPH : Periph
METABO : Metabo [OBS]
", compile = FALSE)
obs_cmt(model)

model %>%
  obs_rows(time = 12, DV = 0.12, DVmet = 120) %>%
  obs_rows(
    time = c(24, 36, 48), DV = c(0.34, 0.56, 0.78),
    mdv = c(0, 1, 0), DVmet = c(340, 560, 780)
  ) %>%
  get_data()

```

parse_datehour

Parse value to "POSIXct"

Description

A wrapper around functions of lubridate, mainly in order to transform characters into a date-time ("POSIXct") format.

Usage

```

parse_datehour(
  x,

```

```

    orders = getOption("mapbayr.datehour", default = c("Ymd HMS", "Ymd HM", "dmY HMS",
    "dmY HM"))
  )

```

Arguments

x a numeric or a character.

orders format specification for x, passed to `lubridate::parse_date_time()`

Value

a POSIXct

Examples

```

# POSIXct are returned as is.
parse_datehour(x = as.POSIXct("2022-02-02 22:22:22", tz = "UTC"))

# Numerics are passed to `lubridate::as_datetime()`.
parse_datehour(1643840542)

# Characters are passed to `lubridate::parse_date_time()`.
# The format used will be the one defined in `orders`
parse_datehour(x = "2022-02-02 22:22:22", orders = "Ymd HMS")
parse_datehour(x = "02-02-2022 22:22", orders = "dmY HM")

# By default, the following formats will be subsequently tried:
# "Ymd HMS", "Ymd HM", "dmY HMS", "dmY HM"

# Alternatively, set a format through `options(mapbayr.datehour)`.
# Convenient for the use `.datehour` in `adm_rows()` and `obs_rows()`.

# Following format will return NA:
adm_rows(.datehour = "22:22 02-02-2022", amt = 100, cmt = 1)

options(mapbayr.datehour = "HM dmY")
adm_rows(.datehour = "22:22 02-02-2022", amt = 100, cmt = 1)
options(mapbayr.datehour = NULL)

```

plot.mapbayests

Plot predictions from mapbayests object

Description

Plot predictions from mapbayests object

Usage

```
## S3 method for class 'mapbayests'
plot(x, ..., PREDICTION = c("IPRED", "PRED"))
```

Arguments

<code>x</code>	A mapbayests object.
<code>...</code>	additional arguments (passed to augment.mapbayests)
<code>PREDICTION</code>	plot either "IPRED", "PRED" or both.

Details

Use this function to plot the results of the estimations, in the form of concentration vs time profiles for every patient of the data set. For additional modifications, you can:

- see [augment.mapbayests](#) to modify the simulation output.
- add extra `+function(...)` in order to modify the plot as a regular ggplot2 object.

Value

a ggplot object.

Examples

```
est <- mapbayest(exmodel(ID = 1))
plot(est, end = 48) +
  ggplot2::labs(title = "Awesome prediction")
```

```
preprocess.ofv
```

Preprocess model and data for ofv computation

Description

Functions to generate arguments passed to [compute_ofv](#). Arguments that are fixed between individuals are created once (`preprocess.ofv.fix`), while others are specific of each individual (`preprocess.ofv.id`).

Usage

```
preprocess.ofv.fix(x, data, select_eta = seq_along(eta(x)), lambda = 1)

preprocess.ofv.id(x, iddata)
```

Arguments

<code>x</code>	the model object
<code>data, iddata</code>	NMTRAN-like data set. <code>iddata</code> is likely a dataset of one individual
<code>select_eta</code>	numbers of the ETAs taken into account. Set the dimensions of the inversed OMEGA matrix
<code>lambda</code>	a numeric value, the weight applied to the model prior (default is 1)

Value

A list of arguments used to compute the objective function value.

The following arguments are fixed between individuals:

- `qmod`: model object, modified to simulate without random effects and with controlled outputs
- `sigma`: a single matrix object
- `log_transformation`: a logical, whether predictions need to be log-transformed for ofv computation
- `omega_inv`: a single matrix object
- `all_cmt`: a vector of compartment numbers where observations can be expected

The following arguments differs between individuals:

- `idvaliddata`: a matrix, individual data set (with administrations and covariates), validated with [valid_data_set](#)
- `idDV`: a vector of (possibly log-transformed) observations
- `idcmt`: a vector of compartments where observations belong to
- `idblq, idlloq`: optional, a logical and numerical vector indicating if the observation is below the lower limit of quantification, and the LLOQ value, respectively

Examples

```
mod <- exmodel(add_exdata = FALSE, compile = FALSE)
dat <- exdata(ID = c(1,4))

preprocess.ofv.fix(x = mod, data = dat)
preprocess.ofv.id(x = mod, iddata = dat[dat$ID == 1,])
preprocess.ofv.id(x = mod, iddata = dat[dat$ID == 4,])
```

```
preprocess.optim
```

Pre-process: arguments for optimization function

Description

Pre-process: arguments for optimization function

Usage

```
preprocess.optim(
  x,
  method = c("L-BFGS-B", "newuoa"),
  select_eta = NULL,
  control = list(),
  force_initial_eta = NULL,
  quantile_bound = 0.001
)
```

Arguments

<code>x</code>	the model object
<code>method</code>	optimization method; the default is "L-BFGS-B" (from <code>stat::optim()</code>), alternatively "newuoa" for <code>minqa::newuoa()</code>
<code>select_eta</code>	a vector of numeric values, the numbers of the ETAs to be estimated (default is NULL, all ETAs non-equal to zero)
<code>control</code>	a list passed to the optimizer (see <code>stats::optim()</code> or <code>minqa::newuoa()</code> documentation)
<code>force_initial_eta</code>	a vector of numeric values to start the estimation from (default to 0 for "L-BFGS-B")
<code>quantile_bound</code>	a numeric value representing the quantile of the normal distribution admitted to define the bounds for L-BFGS-B (default is 0.001, i.e. 0.1%)

Value

a list of named arguments passed to optimizer (i.e. `arg.optim`)

print.mapbayests	<i>Print a mapbayests object</i>
------------------	----------------------------------

Description

Print a mapbayests object

Usage

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

Arguments

x	A mapbayests object.
...	additional arguments

Value

print the results of the estimation to the console, and returns it invisibly.

use_posterior	<i>Use posterior estimation</i>
---------------	---------------------------------

Description

Use posterior estimation

Usage

```
use_posterior(  
  x,  
  update_omega = FALSE,  
  update_cov = TRUE,  
  update_eta = TRUE,  
  .zero_re = NULL,  
  simplify = TRUE  
)
```

Arguments

<code>x</code>	A <code>mapbayests</code> object.
<code>update_omega</code>	Update the OMEGA matrix with the variance-covariance matrix of estimation (a logical, default is FALSE).
<code>update_cov</code>	Update the values of covariates with the individual values (a logical, default is TRUE).
<code>update_eta</code>	Update the values of ETA with the final estimates (a logical, default is TRUE).
<code>.zero_re</code>	Set all elements of the OMEGA or SIGMA matrix to zero. Default is "both" if <code>update_omega</code> is FALSE, "sigma" otherwise. (possible values are "both", "sigma", "omega", "none")
<code>simplify</code>	a logical. If TRUE (the default) and only one ID, one <code>mrgmod</code> is returned instead of a list of length 1

Details

This function takes the results of an estimation (i.e. a `mapbayests` object) and return a modified `mrgmod` in order to perform *a posteriori* simulations. Modifications are:

- If `update_eta` is TRUE, the values of ETA are updated to the estimated values (instead of 0) in `$PARAM`.
- If `update_cov` is TRUE, the covariates values are updated to the values of the individual (instead of default model values) in `$PARAM`.
- If `update_omega` is TRUE, the values of OMEGA are updated with the variance-covariance matrix of estimation (i.e. an approximation of the *a posteriori* distribution) instead of the inter-individual variability (i.e. the *a priori* distribution). Use this command in order to derive a confidence interval of concentrations that reflects the uncertainty about parameter estimation when a large number of profiles are simulated. Note that if inter-individual variability was initially defined in multiple `$OMEGA` blocks in the model, they will be collapsed to a single full matrix (this is irreversible).
- Depending on the values of `.zero_re`, the elements of `$OMEGA` or `$SIGMA` can be set to zero, whether you want to simulate one profile, or several in order to derive confidence/prediction intervals. It does not handle time-varying covariates: only the first value will be used as the individual value.

Value

a `mrgmod`, or a list of `mrgmod` if there is more than 1 ID

Examples

```
library(magrittr)
est <- mapbayest(exmodel())
est %>%
  use_posterior() %>%
  mrgsolve::ev(amt = 50000) %>%
  mrgsolve::mrgsim()
```

vs_nonmem

*Compare results to NONMEM .phi***Description**

Compare results to NONMEM .phi

Usage

```
read_nmphi(x)

merge_phi(mapbayr_phi, nonmem_phi)

plot_phi(merged_phi, only_ETA = TRUE)

summarise_phi(
  merged_phi,
  group,
  only_ETA = TRUE,
  levels = c(Excellent = 0, Acceptable = 0.001, Discordant = 0.1)
)

bar_phi(summarised_phi, xaxis = NULL, facet = NULL)
```

Arguments

x	full path to a .phi file generated by NONMEM
mapbayr_phi	results of mapbayr estimations, in the form of a tibble data.frame, typically obtained from get_phi()
nonmem_phi	results of NONMEM estimations, in the form of a tibble data.frame, typically obtained from read_nmphi()
merged_phi	merged results of estimations, typically obtained from merge_phi()
only_ETA	filter the data with type=="ETA" (a logical, default is TRUE)
group	one or multiple variables to group_by()
levels	a named vector of length 3 in order to classify the absolute differences. Default cut-offs are 0.1% and 10% in the parameters space.
summarised_phi	summarized results of estimations, typically obtained from summarise_phi()
xaxis	optional. A character value, that correspond to a variable in data, passed to the x-axis to plot multiple bars side-by-side.
facet	a formula, that will be passed to ggplot2::facet_wrap()

Details

These functions were made to easily compare the results of mapbayr to NONMEM. For instance, it could be useful in the case of the transposition of a pre-existing NONMEM model into mapbayr. For this, you need to code your model in both mapbayr and NONMEM, and perform the MAP-Bayesian estimation on the **same dataset**. Ideally, the latter contains a substantial number of patients. NONMEM returns the estimations results into a .phi file.

Use `read_nmphi()` to parse the NONMEM .phi file into a convenient tibble data.frame with the columns:

- SUBJECT_NO, ID: Subject identification.
- ETA1, ETA2, ..., ETAn: Point estimates of eta.
- ETC1_1, ETC2_1, ETC2_2, ..., ETCn_n: Variance-covariance matrix of estimation.
- OBJ: objective function value

Use `get_phi()` to access to the estimations of mapbayr with the same "phi" format.

Use `merge_phi()` to combine mapbayr and NONMEM "phi files" into a single long-form data.frame with the columns:

- SUBJECT_NO, ID: Subject identification.
- variable name and its type: ETA (point estimate), VARIANCE (on-diagonal element of the matrix), COVARIANCE (off-diagonal), and OBJ.
- mapbayr and nonmem: corresponding values
- adiff: absolute difference between mapbayr and nonmem values.

Use `plot_phi()` to graphically represent adiff vs variable. Alternatively, the table returned by `merge_phi()` is easy to play with in order to derive performance statistics or the graphical plot of your choice.

Use `summarise_phi()` to classify the estimation as "Excellent", "Acceptable" or "Discordant", over the whole dataset or by group.

Use `bar_phi()` to graphically represent the proportion of the aforementioned classification as bar plot.

Value

- `read_nmphi`: a tibble data.frame with a format close to the original .phi file
- `merge_phi`: a long-form tibble data.frame with results of mapbayr and NONMEM
- `summarise_phi`: a summarized tibble data.frame classifying the performance of mapbayr and NONMEM
- `plot_phi`, `bar_phi`: a ggplot2 object

Examples

```
library(mapbayr)
nmphi <- read_nmphi(system.file("nm001", "run001.phi", package = "mapbayr"))
mapbayrphi <- get_phi(est001)
```

```
merged <- merge_phi(mapbayrphi, nmphi)
plot_phi(merged)

summarised <- summarise_phi(merged)
bar_phi(summarised)

# Analyse the results of multiple runs simultaneously

#Example dataset that represents 3 runs
merge3 <- dplyr::bind_rows(merged, merged, merged, .id = "RUN")
merge3$adiff <- 10 ^ runif(nrow(merge3), -8, 0)

summarised3 <- summarise_phi(merge3, group = RUN)
bar_phi(summarised3, xaxis = "RUN")
```

x_cmt

*Read compartment options in a model***Description**

Read compartment options in a model

Usage

```
adm_cmt(x)
```

```
obs_cmt(x)
```

Arguments

x model object

Details

In a mrgsolve model, it is possible to specify options in \$CMT. If [ADM] or [OBS] are set, mapbayr will interpret these as default administration and observation compartments, respectively.

Value

a vector of compartment identified as default "administration" or "observation" compartments.

Examples

```
#Administration: Both 1st and 0- order
model <- exmodel(6, compile = FALSE)
mrgsolve::see(model)
adm_cmt(model)
```

```
#Observation: Both parent drug and metabolite
model <- exmodel(401, compile = FALSE)
mrgsolve::see(model)
obs_cmt(model)
```

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