Package 'breathtestcore'

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Title Core Functions to Read and Fit 13c Time Series from Breath Tests

Version 0.8.4

Description Reads several formats of 13C data (IRIS/Wagner, BreathID) and CSV. Creates artificial sample data for testing. Fits Maes/Ghoos, Bluck-Coward self-correcting formula using 'nls', 'nlme'. Methods to fit breath test curves with Bayesian Stan methods are refactored to package 'breathteststan'. For a Shiny GUI, see package 'dmenne/breathtestshiny' on github.

License GPL-3

URL https://github.com/dmenne/breathtestcore

BugReports https://github.com/dmenne/breathtestcore/issues

Depends R (>= 4.0.0)

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AIC.breathtestnlmefit *S3 AIC method for breathtestnlmefit*

Description

Extract AIC from a model fitted with nlme_fit

Usage

```
## S3 method for class 'breathtestnlmefit'
AIC(object, ...)
```

Arguments

object	of class breathtestnlmefit
...	not used

augment.breathtestfit *Augmented prediction for breathtest fit*

Description

Broom method augment to compute predicted values from the results of class breathttestfit as generated by nls_fit or nlme_fit.

Usage

```
## S3 method for class 'breathtestfit'
augment(x, by = NULL, minute = NULL, dose = 100, ...)
```

Arguments

x	Object of class breathttestfit
by	When by is NULL, predictions for the original data values are returned. When by is a positive number, it is used as a step size for a sequence of minutes from 0 to the maximum value of minute in data set.
minute	When a vector is passed, this overrides settings in by, and predictions are calculated at the requested minute values.
dose	13C acetate or octanoate dose
...	other parameters passed to methods

Value

When by is NULL, returns one row for each original observation pdr, and column fitted. If new data are given, i.e. when one of parameter by or minute is not null, only column fitted is added.

See Also

augment

Examples

```
library(broom)
# Generate simulated data
data = cleanup_data(simulate_breathtest_data(n_records = 3)$data)
# Fit using the curves individually
fit = nls_fit(data)
# Predict values at t=60 and t=120
augment(fit, minute = c(60, 120))
```

---

breathtest_data *Data structure with PDR data and descriptors for breath test records*

Description

Generates structure of class breathtest_data with required fields and optional fields. Optional fields by default are NA. This structure is used internally as an intermediate when reading in external file formats. All read_xxx functions return this structure, or a list of this structure (e.g. read_breathid_xml), and any converter to a new format should do the same to be used with cleanup_data. To support a new format with, also update breathtest_read_function which returns the most likely function to read the file by reading a few lines in it.

Usage

```
breathtest_data(
  patient_id,
  name = NA,
  first_name = NA,
  initials = NA,
  dob = NA,
  birth_year = NA,
  gender = NA,
  study = NA,
  pat_study_id = NA,
  file_name,
  device = "generic",
  substrate,
  record_date,
  start_time = record_date,
  end_time = record_date,
  test_no,
  dose = 100,
  height = 180,
```

```
  weight = 75,
  t50 = NA,
  gec = NA,
  tlag = NA,
  data = data
)
```

Arguments

patient_id	required, string or number for unique identification
name	optional
first_name	optional
initials	optional, 2 characters, 1 number
dob	optional date of birth (not to be confused with "delta over baseline")
birth_year	optional
gender	optional `m` or `f`
study	optional name of study; can be used in population fit
pat_study_id	optional; patient number within study_ does not need to be globally unique
file_name	required; file where data were read from, or other unique string_ when data are read again, this string is tested and record is skipped when same filename is already in database, therefore uniqueness is important_ when some record does not turn up in database after repeated reading, check if a record with the same file name is already there, and rename the file to avoid collisions_
device	breath_id or iris; default "generic"
substrate	should contain string "ace" or "oct" or "okt", case insensitive_ will be replaced by "acetate" or "octanoate". If empty, "ocatanoate" is assumed.
record_date	required record date_
start_time	optional
end_time	optional
test_no	required integer; unique test number converted to integer if factor
dose	optional, default 100 mg
height	optional, in cm; when pdr must be calculated, default values are used; see dob_to_pdr
weight	optional, in kg
t50	optional, only present if device computes this value
gec	optional, only present if device computes this value
tlag	optional, only present if device computes this value
data	data frame with at least 5 rows and columns `minute` or `time` and one or both of dob or pdr. If pdr is missing, and height, weight and substrate are given, computes pdr via function dob_to_pdr. When height and weight are missing, defaults 180 cm and 75 kg are used instead.

Examples

```
# Read a file with known format
iris_csv_file = btcore_file("IrisCSV.TXT")
iris_csv_data = read_iris_csv(iris_csv_file)
# Note that many filds are NA
str(iris_csv_data)
# Convert to a format that can be fed to one of the fit functions
iris_df = cleanup_data(iris_csv_data)
# Individual curve fit
coef(nls_fit(iris_df))
```

`breathtest_read_function`

Snoop method to read breath test file

Description

Reads the first line of a file, and returns the best matching function to read the breath test data in it. To automatically read the file with the inferred file type, use `read_any_breathtest`. For Excel files, only the first sheet is read.

Usage

```
breathtest_read_function(filename = NULL, text = NULL)
```

Arguments

`filename`	breath test data file from Iris/Wagner (extended or CSV), BreathID
`text`	as alternative to filename, pass the text of the file directly. This parameter is not used for Excel files.

Value

Function to read the file or the text; NULL if no matching function was found

Examples

```
file = btcore_file("IrisCSV.TXT")
# Get function to read this file. Returns \code{\link{read_iris_csv}}.
read_fun = breathtest_read_function(file)
str(read_fun(file))
# or, simple (returns a list!)
str(read_any_breathtest(file), 1 )
```

btcore_file *Path to example breath test data file*

Description

Path to example breath test data file

Usage

```
btcore_file(filename = NULL, full.names = FALSE)
```

Arguments

filename	example file in extdata directory without path. Case sensitive on Unix. When filename is missing, returns the names of the available sample files.
full.names	When filename is NULL, return full path names

Value

full filename to example file to use in read_xxx

Examples

```
head(btcore_file())
filename = btcore_file("IrisMulti.TXT")
data = read_iris(filename)
```

cleanup_data *Transforms 13C breath data into a clean format for fitting*

Description

Accepts various data formats of ungrouped or grouped 13C breath test time series, and transforms these into a data frame that can be used by all fitting functions, e.g. nls_fit. If in doubt, pass data frame through cleanup_data before forwarding it to a fitting function. If the function cannot repair the format, it gives better error messages than the xxx_fit functions.

Usage

```
cleanup_data(data, ...)
```

Arguments

`data`

- A data frame, array or tibble with at least two numeric columns with optional names `minute` and `pdr` to fit a single 13C record.
- A data frame or tibble with three columns named `patient_id`, `minute` and `pdr`.
- A matrix that can be converted to one of the above.
- A list of data frames/tibbles that are concatenated. When the list has named elements, the names are converted to group labels. When the list elements are not named, group name `A` is used for all items.
- A structure of class `breathtest_data`, as imported from a file with `read_any_breathtest`
- A list of class `breathtest_data_list` as generated from read function such as `read_breathid_xml`

`...` optional.

use_filename_as_patient_id Always use filename instead of patient name. Use this when patient id are not unique.

Value

A tibble with 4 columns. Column `patient_id` is created with a dummy entry of `pat_a` if no patient_id was present in the input data set. A column `group` is required in the input data if the patients are from different treatment groups or within-subject repeats, e.g. in crossover design. A dummy group name "A" is added if no group column was available in the input data set. If `group` is present, this is a hint to the analysis functions to do post-hoc breakdown or use it as a grouping variable in population-based methods. A patient can have records in multiple groups, for example in a cross-over designs.

Columns `minute` and `pdr` are the same as given on input, but negative minute values are removed, and an entry at 0 minutes is shifted to 0.01 minutes because most fit methods cannot handle the singularity at t=0.

An error is raised if dummy columns `patient_id` and `group` cannot be added in a unique way, i.e. when multiple values for a given minute cannot be disambiguated.

Comments are persistent; multiple comments are concatenated with newline separators.

Examples

```
options(digits = 4)
# Full manual
minute = seq(0,30, by = 10)
data1 = data.frame(minute,
   pdr = exp_beta(minute, dose = 100, m = 30,  k = 0.01, beta = 2))
# Two columns with data at t = 0
data1
# Four columns with data at t = 0.01
cleanup_data(data1)

# Results from simulate_breathtest_data can be passed directly to cleanup_data
cleanup_data(simulate_breathtest_data(3))
# .. which implicitly does
```

```
cleanup_data(simulate_breathtest_data(3)$data)

# Use simulated data
data2 = list(
  Z = simulate_breathtest_data(seed = 10)$data,
  Y = simulate_breathtest_data(seed = 11)$data)
d = cleanup_data(data2)
str(d)
unique(d$patient_id)
unique(d$group)
# "Z" "Y"

# Mix multiple input formats
f1 = btcore_file("350_20043_0_GER.txt")
f2 = btcore_file("IrisMulti.TXT")
f3 = btcore_file("IrisCSV.TXT")
# With a named list, the name is used as a group parameter
data = list(A = read_breathid(f1), B = read_iris(f2), C = read_iris_csv(f3))
d = cleanup_data(data)
str(d)
unique(d$patient_id)
# "350_20043_0_GER" "1871960"         "123456"
# File name is used as patient name if none is available
unique(d$group)
# "A" "B" "C"
```

`coef.breathtestfit` *S3 coef and summary for breathtestfit*

Description

Function `coef` extracts the estimates such as t50, tlag, from fitted 13C beta exponential models. The result is the same as `fit$coef`, but without column `stat`, which always is `"estimate"` for `nls_fit` and `nlme_fit`.

The `summary` method only extracts `t50` by the Maes/Ghoos method

Usage

```
## S3 method for class 'breathtestfit'
coef(object, ...)
```

Arguments

`object`	of class `breathtestfit`, as returned by `nls_fit` or `nlme_fit`
`...`	other parameters passed to methods

Examples

```
# Generate simulated data
data = cleanup_data(simulate_breathtest_data())
# Fit with the population method
fit = nlme_fit(data)
# All coefficients in the long form
coef(fit)
# Access coefficients directly
fit$coef
# Only t50 by Maes/Ghoos
# Can also be used with stan fit (slow!)
## Not run:
if (require("breathteststan")) {
  fit = stan_fit(data, iter = 300, chain = 1)
  coef(fit)
  # We get quantiles here in key/value format
  unique(fit$coef$stat)
}

## End(Not run)
```

`coef_by_group` *Tabulates per-group breath test parameters*

Description

Given a fit to 13C breath test curves, computes absolute values and their confidence intervals of parameters, e.g. of the half emptying time `t50`. Generic S3 method for class breathtestfit.

Usage

```
coef_by_group(fit, ...)
```

Arguments

`fit`	Object of class `breathtestfit`, for example from `nlme_fit`, `nls_fit` or `stan_fit`
`...`	Not used

Value

A `tibble` of class `coef_by_group` with columns

parameter Parameter of fit, e.g. `beta,k,m,t50`

method Method used to compute parameter. `exp_beta` refers to primary fit parameters `beta,k,m`. `maes_ghoos` uses the method from Maes B D, Ghoos Y F, Rutgeerts P J, Hiele M I, Geypens B and Vantrappen G 1994 Dig. Dis. Sci. 39 S104-6. `bluck_coward` is the self-correcting method from Bluck L J C and Coward W A 2006

group Grouping parameter of the fit, e.g. `patient,normal,liquid,solid`

estimate Parameter estimate

conf.low, conf.high Lower and upper 95 estimate.

diff_group Letters a, b, c indicate that parameter would be in mutually significantly different groups. Letter combinations like ab or abc indicated that this parameter is not significantly different from the given other groups in a Tukey-corrected pairwise test.

Examples

```
library(dplyr)
data("usz_13c")
data = usz_13c %>%
  dplyr::filter( patient_id %in%
   c("norm_001", "norm_002", "norm_003", "norm_004", "pat_001", "pat_002","pat_003")) %>%
  cleanup_data()
fit = nls_fit(data)
coef_by_group(fit)

fit = nlme_fit(data)
coef_by_group(fit)
```

`coef_diff_by_group` *Tabulates breath test parameter differences of groups*

Description

Given a fit to 13C breath test curves, computes between-group confidence intervals and p-values, for examples of the half emptying time `t50`, with correction for multiple testing.

Usage

```
coef_diff_by_group(fit, mcp_group = "Tukey", reference_group = NULL, ...)
```

Arguments

`fit`	Object of class `breathtestfit`, for example from `nlme_fit`, `nls_fit`
`mcp_group`	"Tukey" (default) for all pairwise comparisons, "Dunnett" for comparisons relative to the reference group.
`reference_group`	Used as the first group and as reference group for `mcp_group == "Dunnett"`
`...`	Not used

Value

A tibble of class coef_diff_by_group with columns

parameter Parameter of fit, e.g. beta,k,m,t50

method Method used to compute parameter. exp_beta refers to primary fit parameters beta,k,m. maes_ghoos uses the method from Maes B D, Ghoos Y F, Rutgeerts P J, Hiele M I, Geypens B and Vantrappen G 1994 Dig. Dis. Sci. 39 S104-6. bluck_coward is the self-correcting method from Bluck L J C and Coward W A 2006

groups Which pairwise difference, e.g solid -liquid

estimate Estimate of the difference

conf.low, conf.high Lower and upper 95 A comparison is significantly different from zero when both estimates have the same sign.

p.value p-value of the difference against 0, corrected for multiple testing

Examples

```
library(dplyr)
data("usz_13c")
data = usz_13c %>%
  dplyr::filter( patient_id %in%
   c("norm_001", "norm_002", "norm_003", "norm_004", "pat_001", "pat_002","pat_003")) %>%
  cleanup_data()
fit = nls_fit(data)
coef_diff_by_group(fit)

fit = nlme_fit(data)
coef_diff_by_group(fit)

# TODO: Add example for Stan fit typecast to class \code{breathtestfit} to compute
# confidence intervals instead of credible intervals
```

---

cum_exp_beta *Cumulative exponential beta function*

Description

Equation (2), page 4 from Bluck, "Recent advances in the interpretation of the 13C octanoate breath test for gastric emptying"

Usage

```
cum_exp_beta(minute, dose, cf)
```

Arguments

minute	time in minutes
dose	in mg
cf	named vector of coefficients; only k and beta are required. Note that k is measured in 1/min (e_g_ 0_01/min), while often it is quoted as 1/h (e_g_ 0_6/h).

Value

Vector of predicted cumulative pdr

See Also

exp_beta

---

dob_to_pdr *Convert breath test DOB data to PDR data*

Description

Convert DOB (delta-over-baseline) to PDR for 13C breath test. This is equation (4) in Sanaka, Yamamoto, Tsutsumi, Abe, Kuyama (2005) Wagner-Nelson method for analysing the atypical double-peaked excretion curve in the [13c]-octanoate gastric emptying breath test in humans. Clinical and experimental pharmacology and physiology 32, 590-594.

Usage

```
dob_to_pdr(
  dob,
  weight = 75,
  height = 180,
  mw = 167,
  purity_percent = 99.1,
  mg_substrate = 100
)
```

Arguments

dob	Delta-over-baseline vector in 0/00
weight	Body weight in kg; assumed 75 kg if missing
height	Body height in cm; assume 180 cm if missing
mw	Molecular weight, 83.023388 g/mol for acetate, 167 g/mol for octanoate. Can also be given as string "acetate" or "octanoate".
purity_percent	Purity in percent
mg_substrate	Substrate in mg

Value

PDR percent dose/h

Note

I have no idea where the factor 10 in equation (4) comes from, possibly from percent(PDR)/and DOB(0/00). In Kim and Camillieri, Stable isotope breath test and gastric emptying, page 207, a factor of 0.1123 instead of 0.01123 is used, without the factor 10. Which one is correct?

Examples

```
filename = btcore_file("350_20049_0_GERWithWeight.txt")
bid = read_breathid(filename)
bid$data$pdr1 = dob_to_pdr(bid$data$dob, weight=bid$weight, height=bid$height)

plot(bid$data$minute, bid$data$pdr1, main="points: from breath_id; line: computed",
type="l")
points(bid$data$minute, bid$data$pdr,col="red",type="p",pch=16)
#
# Check how far our computed pdr is from the stored pdr
var(bid$data$pdr1-bid$data$pdr)
```

---

exp_beta *Exponential beta function for 13C breath data*

Description

Function to fit PDR time series data to exponential-beta function as given in:

Maes, B. D., B. J. Geypens, Y. F. Ghoos, M. I. Hiele, and P. J. Rutgeerts. 1998. 13C-Octanoic Acid Breath Test for Gastric Emptying Rate of Solids. Gastroenterology 114(4): 856-50

Sanaka M, Nakada K (2010) Stable isotope breath test for assessing gastric emptying: A comprehensive review. J. Smooth Muscle Research 46(6): 267-280

Bluck L J C and Coward W A 2006 Measurement of gastric emptying by the C-13-octanoate breath test — rationalization with scintigraphy Physiol. Meas. 27 279?89

For a review, see

Bluck LJC (2009) Recent advances in the interpretation of the 13C octanoate breath test for gastric emptying. Journal of Breath Research, 3 1-8

Usage

```
exp_beta(minute, dose, m, k, beta)
```

Arguments

minute	vector of time values in minutes
dose	in mg
m	efficiency
k	time constant
beta	form factor

Details

The function is defined as

```
exp_beta = function(minute,dose,m,k,beta) {
     m*dose*k*beta*(1-exp(-k*minute))^(beta-1)*exp(-k*minute)
}
```

At minute == 0, the function behaves like a polynomial with degree (beta-1).

Value

Values and gradients of estimated PDR for use with `nls` and `nlme`

See Also

In the example below, data and fit are plotted with standard R graphics. The S3 method `plot.breathtestfit` provides `ggplot2` graphics.

Examples

```
start = list(m=20,k=1/100,beta=2)

# fit to real data set and show different t50 results
sample_file = btcore_file("350_20043_0_GER.txt")
# minute 0 must be removed to avoid singularity
breath_id = read_breathid(sample_file)
data = subset(breath_id$data, minute >0)
sample_nls = nls(pdr~exp_beta(minute, 100, m, k, beta), data = data, start = start)
data$pdr_fit_bluck=predict(sample_nls)
plot(data$minute, data$pdr, pch=16, cex=0.7, xlab="time (min)", ylab="PDR",
  main="t50 with different methods")
lines(data$minute,data$pdr_fit_bluck, col="blue")
t50 = t50_bluck_coward(coef(sample_nls))
t50_maes_ghoos = t50_maes_ghoos(coef(sample_nls))
t50scint = t50_maes_ghoos_scintigraphy(coef(sample_nls))
abline(v = t50, col = "red")
abline(v = t50_maes_ghoos, col = "darkgreen", lty = 2)
abline(v = breath_id$t50, col = "black", lty = 4)
abline(v = t50scint, col = "gray", lty = 3)
text(t50, 0, "Self-corrected Bluck/Coward", col = "red", adj = -0.01)
text(breath_id$t50, 0.5,"From BreathID device",col = "black", adj=-0.01)
text(t50scint, 1," Maes/Ghoos scintigraphic", col = "gray", adj = -0.01)
text(t50_maes_ghoos,1.5, "Classic Maes/Ghoos", col = "darkgreen", adj = -0.01)

# simulated data set
dose = 100
set.seed(4711)
# do not use minute 0, this gives singular gradients
# if required, shift minute = 0 by a small positive amount, e.g. 0.1
# create simulated data
pdr  = data.frame(minute=seq(2, 200, by = 10))
```

```
pdr$pdr =
  exp_beta(pdr$minute, 100, start$m, start$k, start$beta) + rnorm(nrow(pdr), 0, 1)
par(mfrow = c(1, 2))
# plot raw data
plot(pdr$minute, pdr$pdr, pch=16, cex=0.5, xlab = "time (min)",ylab = "PDR")
# compute fit
pdr_nls = nls(pdr~exp_beta(minute, 100, m, k, beta), data = pdr, start = start)
# compute prediction
pdr$pd_rfit = predict(pdr_nls)
lines(pdr$minute, pdr$pd_rfit, col="red", lwd=2)

# plot cumulative
plot(pdr$minute, cum_exp_beta(pdr$minute,100,coef(pdr_nls)), type="l",
     xlab = "time (min)", ylab = "cumulative PDR")
# show t50
t50 = t50_bluck_coward(coef(pdr_nls))
tlag = tlag_bluck_coward(coef(pdr_nls))
abline(v = t50, col = "gray")
abline(v = tlag,col = "green")
abline(h = 50, col = "gray")


# create simulated data from several patients
pdr1 = data.frame(patient = as.factor(letters[1:10]))
pdr1$m = start$m*(1 + rnorm(nrow(pdr1), 0, 0.1))
pdr1$k = start$k*(1 + rnorm(nrow(pdr1), 0, 0.3))
pdr1$beta = start$beta*(1 + rnorm(nrow(pdr1), 0, 0.1))
pdr1  = merge(pdr1, expand.grid(minute = seq(2, 200, by = 10),
   patient = letters[1:10]))
pdr1 = pdr1[order(pdr1$patient, pdr1$minute), ]

# simulated case: for patient a, only data up to 50 minutes are available
pdr1 = pdr1[!(pdr1$patient == "a" & pdr1$minute > 50),]
set.seed(4711)
pdr1$pdr =
  with(pdr1, exp_beta(minute, 100, m, k, beta) + rnorm(nrow(pdr1), 0, 1))

# compute nls fit for patient a only: fails
# the following line will produce an error message

pdr_nls = try(nls(pdr~exp_beta(minute, 100, m, k, beta), data=pdr1, start=start,
                  subset = patient=="a"))
stopifnot(class(pdr_nls) == "try-error")

# use nlme to fit the whole set with one truncated record
suppressPackageStartupMessages(library(nlme))
pdr_nlme = nlme(pdr~exp_beta(minute,100,m,k,beta), data = pdr1,
                fixed = m+k+beta~1,
                random = m+k+beta~1,
                groups = ~patient,
                start = c(m = 20, k = 1/100, beta = 2))
coef(pdr_nlme)
pred_data = expand.grid(minute = seq(0, 400, 10), patient = letters[1:10])
```

```
pred_data$pdr = predict(pdr_nlme, newdata = pred_data)
suppressPackageStartupMessages(library(ggplot2))
ggplot() +
  geom_point(data = pdr1, aes(x = minute, y = pdr, color = "red")) +
  geom_line(data = pred_data, aes(x = minute, y = pdr), color = "black", size=1) +
  ggtitle("Short patient record 'a' gives a good fit with many missing data using nlme.\n
          Borrowing strength from nlme in action!")+
  facet_wrap(~patient) +
  theme(legend.position="none")
```

`extract_id` *Extracts an ID from string IRIS CSV file*

Description

First tries to extract only digits, separating these by underscore when there are multiple blocks. If this give a non-valid id, returns the whole string without spaces and periods, hoping it makes sense. For internal use, but should be overridden for exotic IDs

Usage

```
extract_id(id)
```

Arguments

`id`	One item from column Identifikation, e.g. "KEK-ZH-Nr.2013-1234"

Examples

```
extract_id
```

`nlme_fit` *Mixed-model nlme fit to 13C Breath Data*

Description

Fits exponential beta curves to 13C breath test series data using a mixed-model population approach. See https://menne-biomed.de/blog/breath-test-stan for a comparison between single curve, mixed-model population and Bayesian methods.

Usage

```
nlme_fit(
  data,
  dose = 100,
  start = list(m = 30, k = 1/100, beta = 2),
  sample_minutes = 15
)
```

Arguments

data	Data frame or tibble as created by cleanup_data, with mandatory columns patient_id,group,minute and pdr. It is recommended to run all data through cleanup_data to insert dummy columns for patient_id and group if the data are distinct, and report an error if not. At least 2 records are required for a population fit, but 10 or more are recommended to obtain a stable result.
dose	Dose of acetate or octanoate. Currently, only one common dose for all records is supported. The dose only affects parameter m of the fit; all important t50-parameters are unaffected by the dose.
start	Optional start values. In most case, the default values are good enough to achieve convergence, but slightly different values for beta (between 1 and 2.5) can save a non-convergent run.
sample_minutes	When the mean sampling interval is < sampleMinutes, data are subsampled using a spline algorithm by function subsample_data. See the graphical output of plot.breathtestfit for an example where too densely sampled data of one patients were subsampled for the fit.

Value

A list of class ("breathtestnlmefit" "breathtestfit") with elements

coef Estimated parameters in a key-value format with columns patient_id,group,parameter,stat,method and value. Parameter stat currently always has value "estimate". Confidence intervals will be added later, so do not take for granted that all parameters are estimates. Has an attribute AIC which can be retrieved by the S3-function AIC.

data The data effectively fitted. If points are to closely sampled in the input, e.g. with BreathId devices, data are subsampled before fitting.

See Also

Base methods coef,plot,print; methods from package broom: tidy,augment.

Examples

```
d = simulate_breathtest_data(n_records = 3, noise = 0.7, seed = 4712)
data = cleanup_data(d$data)
fit = nlme_fit(data)
plot(fit) # calls plot.breathtestfit
options(digits = 3)
library(dplyr)
cf = coef(fit)
# The coefficients are in long key-value format
cf
# AIC can be extracted
AIC(fit)
# Reformat the coefficients to wide format and compare
# with the expected coefficients from the simulation
# in d$record.
cf %>%
```

```
  filter(grepl("m|k|beta", parameter )) %>%
  select(-method, -group) %>%
  tidyr::spread(parameter, value) %>%
  inner_join(d$record, by = "patient_id") %>%
  select(patient_id, m_in = m.y, m_out = m.x,
         beta_in = beta.y, beta_out = beta.x,
         k_in = k.y, k_out = k.x)
```

`nls_fit` *Individual curve fit with nls to 13C breath test data*

Description

Fits individual exponential beta curves to 13C breath test time series

Usage

```
nls_fit(data, dose = 100, start = list(m = 50, k = 1/100, beta = 2))
```

Arguments

`data`	Data frame or tibble as created by `cleanup_data`, with mandatory columns `patient_id,group,minute` and `pdr`. It is recommended to run all data through `cleanup_data` which will insert dummy columns for `patient_id` and `minute` if the data are distinct, and report an error if not.
`dose`	Dose of acetate or octanoate. Currently, only one common dose for all records is supported.
`start`	Optional start values `patient_id` and `group`.

Value

A list of class ("breathtestnlsfit" "breathtestfit") with elements

coef Estimated parameters in a key-value format with columns `patient_id,group,parameter,stat,method` and `value`. Parameter `stat` always has value `"estimate"`. Confidence intervals might be added later, so do not take for granted all parameters are estimates.

data Input data; `nls_fit` does not decimate the data. If you have large data sets where subsampling might be required to achieve faster convergence, using `nls_fit` anyway is only relevant to show how NOT to do it. Use `nlme_fit` or `stan_fit` instead.

See Also

Base methods `coef,plot,print`; methods from package `broom: tidy,augment`.

Examples

```
d = simulate_breathtest_data(n_records = 3, noise = 0.2, seed = 4711)
data = cleanup_data(d$data)
fit = nls_fit(data)
plot(fit) # calls plot.breathtestfit
options(digits = 2)
cf = coef(fit)
library(dplyr)
cf %>%
  filter(grepl("m|k|beta", parameter )) %>%
  select(-method, -group) %>%
  tidyr::spread(parameter, value) %>%
  inner_join(d$record, by = "patient_id") %>%
  select(patient_id, m_in = m.y, m_out = m.x,
         beta_in = beta.y, beta_out = beta.x,
         k_in = k.y, k_out = k.x)
```

---

null_fit *Convert data to class breathtestfit*

Description

Does not change the data set, but returns a class suitable for plotting raw data with `plot.breathtestfit`. See `read_any_breathtest` for an example.

Usage

```
null_fit(data, ...)
```

Arguments

`data`	Data frame or tibble as created by `cleanup_data`, with mandatory columns `patient_id`,`group`,`minute` and `pdr`.
`...`	Not used

Value

A list of classes `breathtestnullfit`,`breathtestfit` with element `data` which contains the unmodified data.

`plot.breathtestfit` *S3 plot method for breathtestfit*

Description

Plots 13C data and fits.

Usage

```
## S3 method for class 'breathtestfit'
plot(
  x,
  inc = 5,
  method_t50 = "maes_ghoos",
  line_size = 1,
  point_size = NULL,
  ...
)
```

Arguments

`x`	object of class `breathtestfit`, as returned by `nls_fit`, `nlme_fit`, `null_fit` or `stan_fit`; stan_fit is in package `breathteststan`,
`inc`	Increment for fitted curve plot in minutes
`method_t50`	Method for t50: "`maes_ghoos`", "`bluck_coward`" or "`maes_ghoos_scintigraphy`"
`line_size`	optional line width; can improve look for printouts
`point_size`	optional point size; determined dynamically when NULL
`...`	other parameters passed to methods. Not used

Examples

```
data = list(
  A = simulate_breathtest_data(n_records = 6, seed = 100),
  B = simulate_breathtest_data(n_records = 4, seed = 187)
)
# cleanup_data combines the list into a data frame
x = nls_fit(cleanup_data(data))
plot(x)
```

read_any_breathtest *Read breathtest files of any format*

Description

Uses breathtest_read_function to determine the file type and reads it if it has a valid format.

Usage

```
read_any_breathtest(files)
```

Arguments

files	A single filename, a list or a character vector of filenames.

Value

A list of breathtest_data, even if only one file was passed. The list can be passed to cleanup_data to extract one concatenated data frame for processing with nls_fit, nlme_fit, null_fit (no processing) or stan_fit in separate package breathteststan.

Examples

```
files = c(
  group_a = btcore_file("IrisCSV.TXT"),
  group_a = btcore_file("350_20043_0_GER.txt"),
  group_b = btcore_file("IrisMulti.TXT"),
  group_b = btcore_file("NewBreathID_01.xml")
 )
 bt = read_any_breathtest(files)
 str(bt, 1)
 # Passing through cleanup_data gives a data frame/tibble
 bt_df = cleanup_data(bt)
 str(bt_df)
 # If you want data only, use null_fit()
 plot(null_fit(bt_df))
 # Plot population fit with decimated data
 plot(nlme_fit(bt_df))
```

read_breathid *Read BreathID file*

Description

Reads 13c data from a BreathID file, and returns a structure of class breathtest_data.

Usage

```
read_breathid(filename = NULL, text = NULL)
```

Arguments

filename	name of txt-file to be read
text	alternatively, text can be given as string

Value

Structure of class breathtest_data

Examples

```
filename = btcore_file("350_20043_0_GER.txt")
# Show first lines
cat(readLines(filename, n = 10), sep="\n")
#
bid = read_breathid(filename)
str(bid)
```

---

read_breathid_xml *Read new BreathID/Examens XML file*

Description

Reads 13c data from an XML BreathID file, and returns a structure of class breathtest_data_list, which is a list with elements of class breathtest_data.

Usage

```
read_breathid_xml(filename = NULL, text = NULL)
```

Arguments

filename	name of xml-file to be read
text	alternatively, text can be given as string

Value

List of class breathtest_data_list of structures of class breathtest_data; an XML file can contain multiple data sets.

Examples

```
filename = btcore_file("NewBreathID_01.xml")
# Show first lines
cat(readLines(filename, n = 10), sep="\n")
bid = read_breathid_xml(filename)
# List with length 1
str(bid, 1)
filename = btcore_file("NewBreathID_multiple.xml")
bids = read_breathid_xml(filename)
str(bids, 1) # 3 elements - the others in the file have no data
# Create hook function to deselect first record
choose_record = function(records) {
  r  = rep(TRUE, length(records))
  r[1] = FALSE
  r
}
options(breathtestcore.choose_record = choose_record)
bids = read_breathid_xml(filename)
str(bids, 1) # 2 elements, first deselected
```

---

read_breathtest_excel *Reads breathtest data in Excel format*

Description

Can read several formats of data sets in Excel, from 2 (`minute,pdr` or `dob` for 1 record) to 4 columns (`patient_id,group,minute,pdr` or `dob`). Conversion from dob to pdf is done for assuming 180 cm height and 75 kg weight. See the example below with several sheets for supported formats

Usage

```
read_breathtest_excel(filename, sheet = 1)
```

Arguments

`filename`	Name of Excel-file to be read
`sheet`	Name or number of Excel file to be read. When used with `read_any_breathtest`, the first sheet is always read. You must call `read_breathtest_excel` explicitly to read other worksheets, as shown in the example below.

Value

Different from the other readXXX function, this returns a list with a data frame, not a structure of `breathtest_data`. Pass result through `cleanup_data` to make it compatible with other formats.

Examples

```
filename = btcore_file("ExcelSamples.xlsx")
sheets = readxl::excel_sheets(filename)
# First 4 lines of each sheet
for (sheet in sheets) {
  cat("\nSheet ", sheet,"\n")
  ex = readxl::read_excel(filename, sheet = sheet, n_max = 4)
  print(ex)
}
# To get consistently formatted data from a sheet
bt_data = read_breathtest_excel(filename, sheets[6])
# 3 columns
str(bt_data)
bt_cleaned = cleanup_data(bt_data)
# 4 columns standard format
str(bt_cleaned)
```

`read_iris` *Read 13C data from IRIS/Wagner Analysen*

Description

Reads composite files with 13C data from IRIS/Wagner Analysen. The composite files start as follows:

```
"Testergebnis"
"Nummer","1330"
"Datum","10.10.2013"
"Testart"
```

Usage

```
read_iris(filename = NULL, text = NULL)
```

Arguments

`filename`	name of IRIS/Wagner file in composite format
`text`	alternatively, text can be given as string

Value

List of class `breathtest_data` with `file_name`,`patient_name`,`patient_first_name`,`test`,`identifikation`, and data frame `data` with `time` and dob

Examples

```
filename = btcore_file("IrisMulti.TXT")
cat(readLines(filename, n = 10), sep="\n")
#
iris_data = read_iris(filename)
str(iris_data)
```

`read_iris_csv` *Read 13C data from IRIS/Wagner Analysen in CSV Format*

Description

Reads 13C data from IRIS/Wagner Analysen in CSV Format The CSV files start as follows:

```
"Name","Vorname","Test","Identifikation"
```

This format does not have information about the substrate (acetate, octanoate), the dose and body weight and height. The following defaults are used: `substrate = acetate,dose = 100,weight = 75,height = 180`.

Usage

```
read_iris_csv(filename = NULL, text = NULL)
```

Arguments

`filename`	Name of IRIS/Wagner file in CSV format
`text`	alternatively, text can be given as string

Value

List of class `breath_test_data` with `file name,patient name,patient first name,test,identifikation`, and data frame `data` with `time` and dob

Examples

```
filename = btcore_file("IrisCSV.TXT")
cat(readLines(filename, n = 3), sep="\n")
#
iris_data = read_iris_csv(filename)
str(iris_data)
```

sigma.breathtestnlmefit

S3 method to extract the fit's residual standard deviation

Description

Functions for `nls` and `nlme` are available; additional functions for Stan-based fits are defined in package `breathteststan`.

Usage

```
## S3 method for class 'breathtestnlmefit'
sigma(object, ...)
```

Arguments

`object`	Result of class `breathtestfit`
`...`	Not used

Value

A numeric value giving the standard deviation of the residuals.

simulate_breathtest_data

Simulate 13C breath time series data

Description

Generates simulated breath test data, optionally with errors. If none of the three standard deviations `m_std,k_std,beta_std` is given, an empirical covariance matrix from USZ breath test data is used. If any of the standard deviations is given, default values for the others will be used.

Usage

```
simulate_breathtest_data(
  n_records = 10,
  m_mean = 40,
  m_std = NULL,
  k_mean = 0.01,
  k_std = NULL,
  beta_mean = 2,
  beta_std = NULL,
  noise = 1,
  cov = NULL,
```

```
  student_t_df = NULL,
  missing = 0,
  seed = NULL,
  dose = 100,
  first_minute = 5,
  step_minute = 15,
  max_minute = 155
)
```

Arguments

`n_records`	Number of records
`m_mean, m_std`	Mean and between-record standard deviation of parameter m giving metabolized fraction.
`k_mean, k_std`	Mean and between-record standard deviation of parameter k, in units of 1/minutes.
`beta_mean, beta_std`	Mean and between-record standard deviations of lag parameter beta
`noise`	Standard deviation of normal noise when `student_t_df = NULL`; scaling of noise when student_t_df >= 2.
`cov`	Covariance matrix, default NULL, i.e. not used. If given, overrides standard deviation settings.
`student_t_df`	When NULL (default), Gaussian noise is added; when >= 2, Student_t distributed noise is added, which generates more realistic outliers. Values from 2 to 5 are useful, when higher values are used the result comes close to that of Gaussian noise. Values below 2 are truncated to 2.
`missing`	When 0 (default), all curves have the same number of data points. When > 0, this is the fraction of points that were removed randomly to simulate missing
`seed`	Optional seed; not set if seed = NULL (default)
`dose`	Octanoate/acetate dose, almost always 100 mg, which is also the default
`first_minute`	First sampling time. Do not use 0 here, some algorithms do not converge when data near 0 are passed.
`step_minute`	Inter-sample interval for breath test
`max_minute`	Maximal time in minutes.

Value

A list of class simulated_breathtest_data with 2 elements:

record Data frame with columns `patient_id(chr),m,k,beta,t50` giving the effective parameters for the individual patient record.

data Data frame with columns `patient_id(chr),minute(dbl),pdr(dbl)` giving the time series and grouping parameters.

A comment is attached to the return value that can be used as a title for plotting.

Examples

```
library(ggplot2)
pdr = simulate_breathtest_data(n_records = 4, seed = 4711, missing = 0.3,
       student_t_df = 2, noise = 1.5) # Strong outliers
#
str(pdr, 1)
#
pdr$record # The "correct" parameters
#
# Explicit plotting
ggplot(pdr$data, aes(x = minute, y = pdr)) + geom_point() +
  facet_wrap(~patient_id) + ggtitle(comment(pdr$data))
#
# Or use cleanup_data and null_fit for S3 plotting
plot(null_fit(cleanup_data(pdr$data)))
```

---

subsample_data *Decimate densely sampled 13C time series*

Description

When data of a record are more closely spaced than `sample_minutes`, these are spline-subsampled to `sample_minutes`. In the region of the initial slope, i.e. the initial fifth of the time, the record is sampled more densely. Too dense sampling leads to non-convergent `nlme` fits and to long runs with Stan-based fits. The function is used internally by function `link{nlme_fit}` in package `breathtestcore` and is exported for use by package `breathteststan`.

Usage

```
subsample_data(data, sample_minutes)
```

Arguments

`data`	Data frame with columns `patient_id,group,minute,pdr`.
`sample_minutes`	Required average density. When points are more closely spaced, data are subsampled. No upsampling occurs when data are more sparse.

---

t50_bluck_coward *Bluck-Coward self-corrected half-emptying time*

Description

Uses Newton's method to solve the self-corrected Bluck-Coward equation for 1/2 to compute the half-emptying time t_50.

See also equation G(n,t) in

Bluck LJC, Jackson S, Vlasakakis G, Mander A (2011) Bayesian hierarchical methods to interpret the 13C-octanoic acid breath test for gastric emptying. Digestion 83_96-107, page 98.

Usage

```
t50_bluck_coward(cf)
```

Arguments

cf	Named vector of coefficients; only k and beta are required. In this package, k is measured in units of 1/min (e.g. 0.01/min), in publications it is often quoted as 1/h (e.g. 0.6/h).

Value

Time where value is 1/2 of the maximum, i.e. t_50 or t_1/2 in minutes; in the publication by Bluck et al, the parameter is called t_1/2(in).

See Also

exp_beta

Examples

```
# From table 3 and 4 in Bluck et al.; values for \code{k} and \code{beta}
# (nls, bayesian) are entered and checked against the tabulated values of
# t_{1/2(in)}.
# Most errors are small, but there are some outliers; errors in paper table?
# Parameters and Bluck et al. results:
# table 3 of Bluck et al.
cf3 = data.frame(
          method = rep(c("nls", "bayesian")),
          group = rep(c("lean", "obese"),each=2),
          k =    c(0.576,0.606,0.529,0.608),
          beta = c(5.24, 5.79, 5.95, 7.54),
          t12 =  c(3.67, 3.63, 4.23, 3.99),
          t12in = c(2.076, 2.110, 2.422, 2.466),
          tlag = c(2.88, 2.88, 3.34, 3.26),
          tlagin = c(1.632, 1.724, 1.92, 2.101)
)
cf3 = dplyr::mutate(cf3,
          t50_maes_ghoos = t50_maes_ghoos(cf3),
          t50_bluck_coward = t50_bluck_coward(cf3),
          tlag_maes_ghoos = tlag_maes_ghoos(cf3),
          tlag_bluck_coward = tlag_bluck_coward(cf3),
          err_t50_maes_ghoos = round(100*(t50_maes_ghoos-t12)/t12, 2),
          err_t50_bluck_coward =
            round(100*(t50_bluck_coward-t12in)/t12in, 2),
          err_lag_maes = round(100*(tlag_maes_ghoos-tlag)/tlag,2),
          err_lag_bluck_coward =
            round(100*(tlag_bluck_coward-tlagin)/tlagin,2)
)
cf3
# table 4
# there are large differences for mj3, both using the bayesian (26%)
```

```
# and the nls method (16%).  The other data are within the expected limits
cf4 = data.frame(
          method = rep(c("nls", "bayesian"),each=3),
          group = rep(c("mj1",   "mj2",   "mj3")),
          k = c(0.585,  0.437,  0.380,  0.588,  0.418,  0.361),
          beta=c(4.35,  4.08,  4.44,  4.49, 4.30, 4.29),
          t12 = c(3.39, 4.25, 4.82, 3.40, 4.61, 5.09),
          t12in = c(1.77, 2.16, 2.19, 1.81, 2.34, 2.43),
          tlag = c(2.56, 3.17, 3.39, 2.58, 3.40, 3.62),
          tlagin = c(1.30, 1.53, 1.33, 1.35, 1.65, 1.57)
)
cf4 = dplyr::mutate(cf4,
          t50_maes_ghoos = t50_maes_ghoos(cf4),
          t50_bluck_coward = t50_bluck_coward(cf4),
          tlag_maes_ghoos = tlag_maes_ghoos(cf4),
          tlag_bluck_coward = tlag_bluck_coward(cf4),
          err_t50_maes_ghoos = unlist(round(100*(t50_maes_ghoos-t12)/t12)),
          err_t50_bluck_coward =
            round(100*(t50_bluck_coward-t12in)/t12in,2),
          err_lag_maes = round(100*(tlag_maes_ghoos-tlag)/tlag,2),
          err_lag_bluck_coward =
            round(100*(tlag_bluck_coward-tlagin)/tlagin,2)
)
cf4
```

`t50_maes_ghoos` *Half-emptying time by Maes/Ghoos method*

Description

Half-emptying time t50 as determined from the fit of a beta exponential function. In the Maes/Ghoos model, it is defined as the time when the area under curve (AUC) is 50% of the AUC from 0 to infinity.

Maes B D, Ghoos Y F, Rutgeerts P J, Hiele M I, Geypens B and Vantrappen G 1994 Dig. Dis. Sci. 39 S104-6.

Usage

```
t50_maes_ghoos(cf)
```

Arguments

`cf`	named vector of coefficients; only `k` and `beta` are required note that `k` is measured in 1/min (e.g. 0.01/min), usually it is quoted as 1/h (e.g. 0.6/h).

Value

Time in minutes when area under curve is 50% of the AUC to infinity. In the Maes/Ghoos model, this is used as a surrogate for gastric emptying half time `t50`.

See Also

exp_beta, and t50_bluck_coward for an example.

Examples

```
# Integral from 0 to infinity is 100 at dose 100 mg
integrate(exp_beta, 0, Inf, beta = 1.5, k = 0.01, m = 1, dose = 100)
t50_mg = t50_maes_ghoos(c(beta = 1.5, k = 0.01, dose = 100))
t50_mg
# Integral to half-emptying time \code{t50_maes_ghoos} is 50
integrate(exp_beta, 0, t50_mg, beta = 1.5, k = 0.01, m = 1, dose = 100)
```

---

t50_maes_ghoos_scintigraphy

Half-emptying time t50 from Maes/Ghoos fit with scintigraphic correction

---

Description

Half-emptying time t50 in minutes from beta exponential function fit, with linear and rather arbitrary correction for scintigraphic values. This is given for comparison with published data only; there is little justification to use it, even if it is closer to real gastric emptying times as determined by MRI or scintigraphy. Ghoos YF, Maes BD, Geypens BJ, Mys G, Hiele MI, Rutgeerts PJ, Vantrappen G. Measurement of gastric emptying rate of solids by means of a carbon-labeled octanoic acid breath test. Gastroenterology. 1993;104:1640-1647.

Usage

```
t50_maes_ghoos_scintigraphy(cf)
```

Arguments

cf	named vector of coefficients; only k and beta are required

Value

Time where value is 1/2 of maximum, i.e. t50 in minutes.

See Also

exp_beta, and t50_bluck_coward for an example.

`tidy.breathtestfit` *Broom-style tidying methods for breathtestfit*

Description

Broom-method `tidy` to streamline the results of class `breathttestfit` as generated by `nls_fit` or `nlme_fit`. Returns the fit coefficients and half-emptying time t50 with the Maes/Ghoos method; additional parameters should be extracted with `coef`.

Usage

```
## S3 method for class 'breathtestfit'
tidy(x, ...)
```

Arguments

`x`	Object of class `breathttestfit`
`...`	other parameters passed to methods

Value

A tibble/data frame with columns

patient_id Patient Id (character)

group Treatment or patient group (character)

m Fraction metabolized

k Time constant (1/minutes)

beta The so-called lag parameters, no dimension

t50 Emptying half time in minutes as calculated following Maes/Ghoos

See Also

`tidy`

Examples

```
library(broom)
# Generate simulated data
data = cleanup_data(simulate_breathtest_data()$data)
# Fit with the population method
fit = nlme_fit(data)
# Output coefficients
tidy(fit)
# All coefficients in the long form
coef(fit)
```

tlag_bluck_coward *Lag phase for Bluck-Coward self-correcting fit*

Description

This parameter is probably not very useful, as it can be negative

Usage

```
tlag_bluck_coward(cf)
```

Arguments

cf	named vector of coefficients; only k and beta are required. Note that in this package, k is measured in 1/min (e.g. 0.01/min), while in the literature is is often quoted as 1/h (e.g. 0.6/h).

Value

Lag phase in minutes (time t at which the maximum in the rate of change of g(t) occurs)

See Also

exp_beta, and t50_bluck_coward for an example.

tlag_maes_ghoos *So-called lag time from Maes/Ghoos fit*

Description

Computes tlag from uncorrected fit to the beta exponential function. The name tlag is a misnomer; it simply is the maximum of the PDR curve, so in papers by Bluck et al. it is renamed to t_max.

Maes B D, Ghoos Y F, Rutgeerts P J, Hiele M I, Geypens B and Vantrappen G 1994 Dig. Dis. Sci. 39 S104-6.

Usage

```
tlag_maes_ghoos(cf)
```

Arguments

cf	named vector of coefficients; only k and beta are required k is measured in 1/min (e.g. 0.01/min).

Value

Lag time as defined from Maes/Ghoos fit

See Also

exp_beta, and t50_bluck_coward for an example.

---

usz_13c *Zurich sample set of 13C breath test data*

Description

13C time series PDR data from normals and random patients from the division of Gastroenterology and Hepatology, University Hospital Zurich. Most breath samples from normals were collected with bags and analyzed by IRIS/Wagner infrared spectroscopy. Patient samples were recorded with the continuous monitoring system BreathID.

patient_id Patient identifier, starting with `norm` for normals (healthy volunteers) and `pat` for patients. Note that for normals there are two records for each subject, so only the combination of patient_id and group is a unique identifier of the time series record.

group `liquid_normal` for normals and liquid meal, `solid_normal` normals and solid meal, and `patient` for patients from the University Hospital of Zurich.

minute Time in minutes

pdr PDR as computed by breathtest device or from dob via function dob_to_pdr

Usage

```
data(usz_13c)
```

Format

A data frame with 15574 rows and 4 variables

Examples

```
data(usz_13c)
## Not run:
str(usz_13c)
# Plot all records; this needs some time
pdf(file.path(tempdir(), "usz_13c.pdf"), height= 30)
# null_fit makes data plotable without fitting a model
plot(null_fit(usz_13c))
dev.off()

## End(Not run)
# Plot a subset
suppressPackageStartupMessages(library(dplyr))
```

```
usz_part =  usz_13c  %>%
  filter(patient_id %in% c("norm_001","norm_002", "pat_001", "pat_002"))
plot(null_fit(usz_part))
```

---

usz_13c_a *Exotic 13C breath test data*

Description

13C time series PDR data from three different groups in a randomized (= not-crossover) design. This are unpublished data from Gastroenterology and Hepatology, University Hospital Zurich.

Data are formatted as described in usz_13c. These time series present a challenge for algorithms.

Usage

```
data(usz_13c_a)
```

Examples

```
library(dplyr)
library(ggplot2)
data(usz_13c_a)
d = usz_13c_a %>%
  cleanup_data() %>% # recommended to test for validity
  nlme_fit()
plot(d)
```

---

usz_13c_d *13C breath test data with MRI emptying for comparison*

Description

13C time series PDR data from normals and three different meals in a cross-over design from the division of Gastroenterology and Hepatology, University Hospital Zurich. See Kuyumcu et al., Gastric secretion does not affect....

Data are formatted as described in usz_13c. In addition, half emptying times from MRI measurements are attached to the data as attribute mri_t50. The example below shows how to analyze the data and present half emptying times from MRI and 13C in diagrams.

Usage

```
data(usz_13c_d)
```

Examples

```
library(dplyr)
library(ggplot2)
data(usz_13c_d)
mri_t50 = attr(usz_13c_d, "mri_t50")
d = usz_13c_d %>%
  cleanup_data() %>% # recommended to test for validity
  nlme_fit()
plot(d) +
  geom_vline(data = mri_t50, aes(xintercept = t50), linetype = 2)

# Maes-Ghoos t50
dd = mri_t50 %>%
  inner_join(
    coef(d) %>% filter(parameter=="t50", method == "maes_ghoos"),
    by = c("patient_id", "group")) %>%
  mutate(
    t50_maes_ghoos = value
 )

ggplot(dd, aes(x=t50, y = t50_maes_ghoos, color = group)) +
  geom_point() +
  facet_wrap(~group) +
  geom_abline(slope = 1, intercept = 0) +
  xlim(45,205) +
  ylim(45,205)

# Bluck-Coward t50
dd = mri_t50 %>%
  inner_join(
    coef(d) %>% filter(parameter=="t50", method == "bluck_coward"),
    by = c("patient_id", "group")) %>%
  mutate(
    t50_bluck_coward = value
 )

ggplot(dd, aes(x=t50, y = t50_bluck_coward, color = group)) +
  geom_point() +
  facet_wrap(~group) +
  geom_abline(slope = 1, intercept = 0) +
  xlim(0,205) +
  ylim(0,205)
```

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