Package ‘breathteststan’

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**Type** Package

**Title** Stan-Based Fit to Gastric Emptying Curves

**Version** 0.8.4

**Description** 
Stan-based curve-fitting function for use with package 'breathtestcore' by the same author. Stan functions are refactored here for easier testing.

**License** GPL (>= 3)

**Encoding** UTF-8

**ByteCompile** true

**Depends** R (>= 4.0.0), methods, Rcpp (>= 1.0.6)

**Imports** dplyr, purrr, rstan (>= 2.21.2), rstantools (>= 2.1.1), stringr, tidyr

**Suggests** ggplot2, shinystan, igraph, bayesplot, testthat, covr, knitr, rmarkdown, RcppParallel (>= 5.0.1), breathtestcore(>= 0.8.1)

**LinkingTo** StanHeaders, rstan, BH (>= 1.72), Rcpp, RcppEigen, RcppParallel (>= 5.0.1)

**URL** https://github.com/dmenne/breathteststan

**BugReports** https://github.com/dmenne/breathteststan/issues

**NeedsCompilation** yes

**RoxygenNote** 7.1.2.9000

**Biarch** FALSE

**SystemRequirements** GNU make

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**Repository** CRAN

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sigma.breathteststanfit

S3 method to extract the residual standard deviation

Description

Functions for S3 method defined in breathtestcore for stan_fit and stan_group fit.

Usage

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

Arguments

object A Stan-based fit

... Not used

Value

A numeric value giving the sigma (= average residual standard deviation) term from the Stan fit.

stan_fit

Bayesian Stan fit to 13C Breath Data

Description

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

stan_fit(
  data,
  dose = 100,
  sample_minutes = 15,
  student_t_df = 10,
  chains = 2,
  iter = 1000,
  model = "breath_test_1",
  seed = 4711
)

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. Since the Bayesian method is stabilized by priors, it is possible to fit single curves.
dose  Dose of acetate or octanoate. Currently, only one common dose for all records is supported.
sample_minutes  If mean sampling interval is < sampleMinutes, data are subsampled using a spline algorithm
student_t_df  When student_t_df < 10, the student distribution is used to model the residuals. Recommended values to model typical outliers are from 3 to 6. When student_t_df >= 10, the normal distribution is used.
chains  Number of chains for Stan
iter  Number of iterations for each Stan chain
model  Name of model; use names(stanmodels) for other models.
seed  Optional seed for rstan

Value

A list of classes "breathestanfit" and "breathestfit" with elements

- coef Estimated parameters as data frame in a key-value format with columns patient_id, group, parameter, method and value. Has an attribute AIC.
- data The effectively analyzed data. If density of points is too high, e.g. with BreathId devices, data are subsampled before fitting.
- stan_fit The Stan fit for use with shinystan::launch_shiny or extraction of chains.

See Also

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

library(breathtestcore)
suppressPackageStartupMessages(library(dplyr))
d = breathtestcore::simulate_breathtest_data(n_records = 3) # default 3 records
data = breathtestcore::cleanup_data(d$data)
# Use more than 80 iterations and 4 chains for serious fits
fit = stan_fit(data, chains = 1, iter = 80)
plot(fit) # calls plot.breathtestfit
# Extract coefficients and compare these with those
# used to generate the data
options(digits = 2)
cf = coef(fit)
cf %>%
  filter(grepl("m|k|beta", parameter )) %>%
  select(-method, -group) %>%
  tidy::spread(parameter, value) %>%
  inner_join(d$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)
# For a detailed analysis of the fit, use the shinystan library
library(shinystan)
# launch_shinystan(fit$stan_fit)

# The following plots are somewhat degenerate because
# of the few iterations in stan_fit
suppressPackageStartupMessages(library(rstan))
stan_plot(fit$stan_fit, pars = c("beta[1]","beta[2]","beta[3]"))
stan_plot(fit$stan_fit, pars = c("k[1]","k[2]","k[3]"))
stan_plot(fit$stan_fit, pars = c("m[1]","m[2]","m[3]"))
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