

Package ‘breathteststan’

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Type Package

Title Stan-Based Fit to Gastric Emptying Curves

Version 0.6.0.0

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

LazyData true

ByteCompile true

Depends R (>= 3.5.0), methods, Rcpp (>= 0.12.18)

Imports dplyr, purrr, rstan (>= 2.18.1), rstantools (>= 2.0.0),
stringr, tibble, tidyr

Suggests ggplot2, shinystan, bayesplot, testthat, covr, knitr,
rmarkdown, breathtestcore(>= 0.4.1.0)

LinkingTo StanHeaders (>= 2.18.0), rstan (>= 2.18.1), BH (>=
1.66.0-1), Rcpp (>= 0.12.18), RcppEigen (>= 0.3.3.4.0)

URL <https://github.com/dmenne/breathteststan>

BugReports <https://github.com/dmenne/breathteststan/issues>

NeedsCompilation yes

SystemRequirements GNU make

RoxygenNote 7.1.0

Biarch true

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sigma.breathteststanfit	<i>S3 method to extract the residual standard deviation</i>
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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	<i>Bayesian Stan fit to 13C Breath Data</i>
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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 <code>patient_id</code> , <code>group</code> , <code>minute</code> and <code>pdr</code> . It is recommended to run all data through cleanup_data which will insert dummy columns for <code>patient_id</code> and <code>minute</code> 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 $<$ <code>sampleMinutes</code> , data are subsampled using a spline algorithm
student_t_df	When <code>student_t_df</code> $<$ 10, the student distribution is used to model the residuals. Recommended values to model typical outliers are from 3 to 6. When <code>student_t_df</code> \geq 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 <code>names(stanmodels)</code> for other models.
seed	Optional seed for rstan

Value

A list of classes "breathteststanfit" and "breathtestfit" 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$data)
# Use more than 80 iterations and 4 chains for serious fits
fit = stan_fit(data, chains = 1, iter = 80)
plot(fit) # calls plot.breathtestfit
# Extract coefficients and compare these with those
# used to generate the data
options(digits = 2)
cf = coef(fit)
cf %>%
  filter(grepl("m|k|beta", parameter)) %>%
  select(-method, -group) %>%
  tidyr::spread(parameter, value) %>%
  inner_join(d$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)
# 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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