Package ‘breathteststan’

March 22, 2020

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,
markdown, 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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\textbf{R topics documented:}

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\section*{sigma.breathteststanfit}

\emph{S3 method to extract the residual standard deviation}

\section*{Description}

Functions for S3 method defined in breathtestcore for \texttt{stan_fit} and \texttt{stan_group fit}.

\section*{Usage}

\begin{verbatim}
## S3 method for class 'breathteststanfit'
sigma(object, ...)
\end{verbatim}

\section*{Arguments}

\begin{itemize}
\item \texttt{object} \hspace{1cm} A Stan-based fit
\item \texttt{...} \hspace{1cm} Not used
\end{itemize}

\section*{Value}

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

\section*{stan_fit}

\emph{Bayesian Stan fit to 13C Breath Data}

\section*{Description}

Fits exponential beta curves to 13C breath test series data using Bayesian Stan methods. See \url{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 "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

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