Package 'rater'

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Title Statistical Models of Repeated Categorical Rating Data

Version 1.2.0

Description Fit statistical models based on the Dawid-Skene model - Dawid and Skene (1979) <doi:10.2307/2346806> - to repeated categorical rating data. Full Bayesian inference for these models is supported through the Stan modelling language. 'rater' also allows the user to extract and plot key parameters of these models.

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URL https://jeffreypullin.github.io/rater/, https://github.com/jeffreypullin/rater

BugReports https://github.com/jeffreypullin/rater/issues

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`rater-package` *The 'rater' package.*

Description

Fit statistical models based on the Dawid-Skene model to repeated categorical rating data. Full Bayesian inference for these models is supported through the Stan modelling language. rater also allows the user to extract and plot key parameters of these models.

References

Stan Development Team (2018). RStan: the R interface to Stan. R package version 2.18.2. http://mc-stan.org

anesthesia *Anaesthetist ratings for patient suitability for surgery*

Description

The data consist of ratings, on a 4-point scale, made by four anaesthetists of patients' pre-operative health. The ratings were based on the anaesthetists assessments of a standard form completed for all of the patients. There are 45 patients (items) and four anaesthetists (raters) in total. The first anaesthetist assessed the forms a total of three times, spaced several weeks apart. The other anaesthetists each assessed the forms once. The data is in 'long' format.

Usage

```
anesthesia
```

Format

A `data.frame` with 315 rows and 3 columns:

item The item index - which item is being rated

rater The rater index - which rater is doing the rating

rating The rating given

References

Dawid, A. P., and A. M. Skene. "Maximum Likelihood Estimation of Observer Error-Rates Using the EM Algorithm." Applied Statistics 28, no. 1 (1979): 20.

as_mcmc.list *Convert a rater_fit object to a coda* `mcmc.list` *object.*

Description

Convert a rater_fit object to a coda `mcmc.list` object.

Usage

```
as_mcmc.list(fit)
```

Arguments

`fit`	A rater_fit object.

Value

A coda mcmc.list object.

Examples

```
# Fit a model using MCMC (the default).
mcmc_fit <- rater(anesthesia, "dawid_skene")

# Convert it to an mcmc.list
rater_mcmc_list <- as_mcmc.list(mcmc_fit)
```

`caries` *Dentist ratings of whether caries are healthy or not based on X-rays*

Description

It consists of binary ratings, made by 5 dentists, of whether a given tooth was healthy (sound) or had caries, also known as cavities. The ratings were performed using X-ray only, which was thought to be more error-prone than visual/tactile assessment of each tooth. In total 3,689 ratings were made. This data is in 'grouped' format. Each row is one of the 'pattern' with the final columns being a tally of how many times that pattern occurs in the dataset.

Usage

```
caries
```

Format

A `data.frame` with 6 columns and 32 rows.

rater_1 The rating of the dentist 1

rater_2 The rating of the dentist 2

rater_3 The rating of the dentist 3

rater_4 The rating of the dentist 4

rater_5 The rating of the dentist 5

n The number of times the rating pattern appears in the dataset

References

Espeland, Mark A., and Stanley L. Handelman. "Using Latent Class Models to Characterize and Assess Relative Error in Discrete Measurements." Biometrics 45, no. 2 (1989): 587–99.

`class_probabilities` *Extract latent class probabilities from a rater fit object*

Description

Extract latent class probabilities from a rater fit object

Usage

```
class_probabilities(fit, ...)

## S3 method for class 'mcmc_fit'
class_probabilities(fit, ...)

## S3 method for class 'optim_fit'
class_probabilities(fit, ...)
```

Arguments

`fit`	A rater fit object.
`...`	Extra arguments.

Details

The latent class probabilities are obtained by marginalising out the latent class and then calculating, for each draw of pi and theta, the conditional probability of the latent class given the other parameters and the data. Averaging these conditional probabilities gives the (unconditional) latent class probabilities retuned by this function.

Value

A I * K matrix where each element is the probably of item i being of class k. (I is the number of items and K the number of classes).

Examples

```
fit <- rater(anesthesia, "dawid_skene")
class_probabilities(fit)
```

get_stanfit *Get the underlying* stanfit *object from a* rater_fit *object.*

Description

Get the underlying stanfit object from a rater_fit object.

Usage

```
get_stanfit(fit)
```

Arguments

fit	A rater_fit object.

Value

A stanfit object from rstan.

Examples

```
fit <- rater(anesthesia, "dawid_skene", verbose = FALSE)

stan_fit <- get_stanfit(fit)
stan_fit
```

loo.rater_fit *Compute the PSIS LOO CV - a measure of model fit - of a rater fit object.*

Description

Compute the PSIS LOO CV - a measure of model fit - of a rater fit object.

Usage

```
## S3 method for class 'rater_fit'
loo(x, ..., cores = getOption("mc.cores", 1))
```

Arguments

x	A `rater_fit` object. All model types are currently supported except the basic Dawid-Skene model fit with grouped data.
...	Other arguments passed.
cores	The number of cores to use when calling the underlying functions. By default the value of the `mc.cores` option.

Details

This function is somewhat experimental; model comparison is always difficult and choosing between variants of the Dawid-Skene model should be largely guided by considerations of data size and what is known about the characteristics of the raters. loo is, however, one of the leading methods for Bayesian model comparison and should provide a helpful guide in many situations.

When calculating loo we always use the relative effective sample size, calculated using `loo::relaive_eff` to improve the estimates of the PSIS effective sample sizes and Monte Carlo error.

For further information about the details of loo and PSIS please consult the provided references.

Value

A loo object.

References

Vehtari, A., Gelman, A., and Gabry, J. (2017a). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 (journal version, preprint arXiv:1507.04544).

Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. preprint arXiv:1507.02646

Examples

```
fit_ds <- rater(anesthesia, "dawid_skene", verbose = FALSE, chains = 1)
fit_ccds <- rater(anesthesia, "class_conditional_dawid_skene",
                  verbose = FALSE, chains = 1)

loo_ds <- loo(fit_ds)
loo_ccds <- loo(fit_ccds)

# To compare the loos easily we can use the loo_compare function from the
# loo package:
library(loo)

loo_compare(loo_ds, loo_ccds)

# The documentation of the loo package contains more information about how
# the output should be interpreted.
```

`mcmc_diagnostics` *Retrieve MCMC convergence diagnostics for a rater fit*

Description

Retrieve MCMC convergence diagnostics for a rater fit

Usage

```
mcmc_diagnostics(fit, pars = c("pi", "theta"))
```

Arguments

`fit`	An rater `mcmc_fit` object.
`pars`	A character vector of parameter names to return. By default `c("pi", "theta")`.

Details

MCMC diagnostics cannot be calculate for the z due to the marginalisation used to fit the models.

These MCMC diagnostics are intended as basic sanity check of the quality of the MCMC samples returned. Users who want more in depth diagnostics should consider using `as_mcmc.list()` to convert the samples to a `coda::mcmc.list()` object, or `get_stanfit()` to extract the underlying stanfit object.

Value

A matrix where the columns represent different diagnostics and the rows are different parameters. Currently the first column contains the Rhat statistic and the second bulk effective samples size. The rownames contain the parameter names.

References

Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2019). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC. *arXiv preprint* `arXiv:1903.08008`.

See Also

`rstan::Rhat()`, `rstan::ess_bulk()` `as_mcmc.list()`, `get_stanfit()`.

Examples

```
fit <- rater(anesthesia, "dawid_skene")

# Calculate the diagnostics for all parameters.
mcmc_diagnostics(fit)

# Calculate the diagnostics just for the pi parameter.
mcmc_diagnostics(fit, pars = "pi")
```

`models` *Probabilistic models of repeated categorical rating*

Description

Functions to set up models and change their prior parameters for use in `rater()`.

Usage

```
dawid_skene(alpha = NULL, beta = NULL)

hier_dawid_skene(alpha = NULL)

class_conditional_dawid_skene(alpha = NULL, beta_1 = NULL, beta_2 = NULL)
```

Arguments

`alpha`	prior parameter for pi
`beta`	prior parameter for theta. This can either be a K * K matrix, in which case it is interpreted as the prior parameter of all of the J raters, or a J by K by K array in which case it is the fully specified prior parameter for all raters. (Here K is the number of categories in the data and J is the number of raters in the data.)
`beta_1`	First on diagonal prior probability parameter
`beta_2`	Second on diagonal prior probability parameter for theta

Value

a rater model object that can be passed to `rater()`.

Examples

```
# Model with default prior parameters:
default_m <- dawid_skene()

# Changing alpha:
set_alpha_m <- dawid_skene(alpha = c(2, 2, 2))

# Changing beta, single matrix:
# (See details for how this is interpreted.)
beta_mat <- matrix(1, nrow = 4, ncol = 4)
diag(beta_mat) <- 4
beta_mat_m <- dawid_skene()

# The above is equivalent (when the model is fit - see details) to:
beta_array <- array(NA, dim = c(2, 4, 4))
for (i in 1:2) {
  beta_array[i, , ] <- beta_mat
}
beta_array_m <- dawid_skene(beta = beta_array)

# But you can also specify an array where each slice is different.
# (Again, see details for how this is interpreted.)
beta_array[1, , ] <- matrix(1, nrow = 4, ncol = 4)
beta_array_m <- dawid_skene(beta = beta_array)

# Default:
hier_dawid_skene()

# Changing alpha
hier_dawid_skene(alpha = c(2, 2))

# Default:
class_conditional_dawid_skene()

# Not default:
class_conditional_dawid_skene(
  alpha = c(2, 2),
  beta_1 = c(4, 4),
  beta_2 = c(2, 2)
)
```

---

plot.rater_fit *Plot a* rater_fit *object*

Description

Plot a rater_fit object

Usage

```
## S3 method for class 'rater_fit'
plot(x, pars = "theta", prob = 0.9, rater_index = NULL, item_index = NULL, ...)
```

Arguments

x	An object of class rater_fit.
pars	A length one character vector specifying the parameter to plot. By default "theta".
prob	The coverage of the credible intervals shown in the "pi" plot. If not plotting pi this argument will be ignored. By default 0.9.
rater_index	The indexes of the raters shown in the "theta plot. If not plotting theta this argument will be ignored. By default NULL which means that all raters will be plotted.
item_index	The indexes of the items shown in the class probabilities plot. If not plotting the class probabilities this argument will be ignored. By default NULL which means that all items will be plotted. This argument is particularly useful to focus the subset of items with substantial uncertiuanlty in their class assignments.
...	Other arguments.

Details

The use of pars to refer to only one parameter is for backwards compatibility and consistency with the rest of the interface.

Value

A ggplot2 object.

Examples

```
fit <- rater(anesthesia, "dawid_skene")

# By default will just plot the theta plot
plot(fit)

# Select which parameter to plot.
plot(fit, pars = "pi")
```

`point_estimate` *Extract point estimates of parameters from a fit object*

Description

Extract point estimates of parameters from a fit object

Usage

```
point_estimate(fit, pars = c("pi", "theta", "z"), ...)
```

Arguments

`fit`	A rater fit object
`pars`	A character vector of parameter names to return. By default `c("pi", "theta", "z")`.
`...`	Extra arguments

Details

If the passed fit object was fit using MCMC then the posterior means are returned. If it was fit through optimisation the maximum a priori (MAP) estimates are returned. The z parameter returned is the value of class probabilities which is largest. To return the full posterior distributions of the latent class use `class_probabilities()`.

For the class conditional model the 'full' theta parameterisation (i.e. appearing to have the same number of parameters as the standard Dawid-Skene model) is calculated and returned. This is designed to allow easier comparison with the full Dawid-Skene model.

Value

A named list of the parameter estimates.

See Also

`class_probabilities()`

Examples

```
# A model fit using MCMC.
mcmc_fit <- rater(anesthesia, "dawid_skene")

# This will return the posterior mean (except for z)
post_mean_estimate <- point_estimate(mcmc_fit)

# A model fit using optimisation.
optim_fit <- rater(anesthesia, dawid_skene(), method = "optim")
```

```
# This will output MAP estimates of the parameters.
map_estimate <- point_estimate(optim_fit)
```

`posterior_interval.mcmc_fit` *Extract posterior intervals for parameters of the model*

Description

Extract posterior intervals for parameters of the model

Usage

```
## S3 method for class 'mcmc_fit'
posterior_interval(object, prob = 0.9, pars = c("pi", "theta"), ...)
```

Arguments

`object`	A rater `mcmc_fit` object.
`prob`	A single probability. The size of the credible interval returned. By default `0.9`.
`pars`	The parameters to calculate the intervals for
`...`	Other arguments.

Details

Posterior intervals can only be calculated for models fit with MCMC. In addition, posterior intervals are not meaningful for the latent class (and indeed cannot be calculated). The *full* posterior distribution of the latent class can be extracted using class_probabilities

For the class conditional model the 'full' theta parameterisation (i.e. appearing to have the same number of parameters as the standard Dawid-Skene model) is calculated and returned. This is designed to allow easier comparison with the full Dawid-Skene model.

Value

A matrix with 2 columns. The first column is the lower bound of of the credible interval and the second is the upper bound. Each row corresponds to one individuals parameters. The rownames are the parameter names.

Examples

```
fit <- rater(anesthesia, "dawid_skene", verbose = FALSE, chains = 1)

intervals <- posterior_interval(fit)
head(intervals)
```

`posterior_interval.optim_fit`
Extract posterior intervals for parameters of the model

Description

Extract posterior intervals for parameters of the model

Usage

```
## S3 method for class 'optim_fit'
posterior_interval(object, prob = 0.9, pars = c("pi", "theta"), ...)
```

Arguments

`object`	A rater optim_fit object
`prob`	A probability
`pars`	The parameters to calculate the intervals for
`...`	Other arguments

`posterior_predict.rater_fit`
Draw from the posterior predictive distribution

Description

Draw from the posterior predictive distribution

Usage

```
## S3 method for class 'rater_fit'
posterior_predict(object, new_data, seed = NULL, ...)
```

Arguments

object	A rater_fit object.
new_data	New data for the model to be fit to. The must be in the form used in rater() except without the 'rating' column.
seed	An optional random seed to use.
...	Other arguments.

Details

The number of raters implied by the entries in the rater column must match the number of raters in the fitted model.

Due to technical issues drawing from the posterior predictive distribution of the hierarchical Dawid-Skene model is currently not supported.

Value

The passed new_data augmented with a column 'z' containing the latent class of each item and 'rating' containing the simulated rating.

Examples

```
fit <- rater(anesthesia, "dawid_skene", verbose = FALSE)
new_data <- data.frame(item = rep(1:2, each = 5), rater = rep(1:5, 2))

predictions <- posterior_predict(fit, new_data)
predictions
```

---

posterior_samples *Extract posterior samples from a rater fit object*

Description

Extract posterior samples from a rater fit object

Usage

```
posterior_samples(fit, pars = c("pi", "theta"))
```

Arguments

fit	A rater fit object.
pars	A character vector of parameter names to return. By default c("pi", "theta").

Details

Posterior samples can only be returned for models fitting using MCMC not optimisation. In addition, posterior samples cannot be returned for the latent class due to the marginalisation technique used internally.

For the class conditional model the 'full' theta parameterisation (i.e. appearing to have the same number of parameters as the standard Dawid-Skene model) is calculated and returned. This is designed to allow easier comparison with the full Dawid-Skene model.

Value

A named list of the posterior samples for each parameters. For each parameter the samples are in the form returned by `rstan::extract()`.

Examples

```
fit <- rater(anesthesia, "dawid_skene")

samples <- posterior_samples(fit)

# Look at first 6 samples for each of the pi parameters
head(samples$pi)

# Look at the first 6 samples for the theta[1, 1, 1] parameter
head(samples$theta[, 1, 1, 1])

# Only get the samples for the pi parameter:
pi_samples <- posterior_samples(fit, pars = "pi")
```

---

print.mcmc_fit *Print a* mcmc_fit *object*

Description

Print a mcmc_fit object

Usage

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

Arguments

x	An object of class mcmc_fit.
...	Other arguments.

Examples

```
# Suppress sampling output.
mcmc_fit <- rater(anesthesia, "dawid_skene", verbose = FALSE)
print(mcmc_fit)
```

`print.optim_fit` *Print a* `optim_fit` *object*

Description

Print a `optim_fit` object

Usage

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

Arguments

`x`	An object of class `optim_fit`.
`...`	Other arguments.

Examples

```
optim_fit <- rater(anesthesia, "dawid_skene", method = "optim")
print(optim_fit)
```

print.rater_model *Print a* rater_model *object.*

Description

Print a rater_model object.

Usage

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

Arguments

x	A rater_model object.
...	Other arguments

Examples

```
mod <- dawid_skene()
print(mod)
```

prior_summary.rater_fit *Provide a summary of the priors specified in a* rater_fit *object.*

Description

Provide a summary of the priors specified in a rater_fit object.

Usage

```
## S3 method for class 'rater_fit'
prior_summary(object, ...)
```

Arguments

object	A rater_fit object.
...	Other arguments.

Examples

```
# Fit a model using MCMC (the default).
fit <- rater(anesthesia, "dawid_skene", verbose = FALSE)

# Summarise the priors (and model) specified in the fit.
prior_summary(fit)
```

`rater` *Fit statistical models to repeated categorical rating data using Stan*

Description

This functions allows the user to fit statistical models of noisy categorical rating, based on the Dawid-Skene model, using Bayesian inference. A variety of data formats and models are supported. Inference is done using Stan, allowing models to be fit efficiently, using both optimisation and Markov Chain Monte Carlo (MCMC).

Usage

```
rater(
  data,
  model,
  method = "mcmc",
  data_format = "long",
  inits = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

`data`	A 2D data object: data.frame, matrix, tibble etc. with data in either long or grouped format.
`model`	Model to fit to data - must be rater_model or a character string - the name of the model. If the character string is used, the prior parameters will be set to their default values.
`method`	A length 1 character vector, either `"mcmc"` or `"optim"`. This will be fitting method used by Stan. By default `"mcmc"`
`data_format`	A length 1 character vector, `"long"`, `"wide"` and `"grouped"`. The format that the passed data is in. Defaults to `"long"`. See `vignette("data-formats")` for details.
`inits`	The initialization points of the fitting algorithm

verbose	Should rater() produce information about the progress of the chains while using the MCMC algorithm. Defaults to TRUE
...	Extra parameters which are passed to the Stan fitting interface.

Details

The default MCMC algorithm used by Stan is No U Turn Sampling (NUTS) and the default optimisation method is LGFGS. For MCMC 4 chains are run be default with 2000 iterations in total each.

Value

An object of class rater_fit containing the fitted parameters.

See Also

rstan::sampling(), rstan::optimizing()

Examples

```
# Fit a model using MCMC (the default).
mcmc_fit <- rater(anesthesia, "dawid_skene")

# Fit a model using optimisation.
optim_fit <- rater(anesthesia, dawid_skene(), method = "optim")

# Fit a model using passing data grouped data.
grouped_fit <- rater(caries, dawid_skene(), data_format = "grouped")
```

---

summary.mcmc_fit *Summarise a* mcmc_fit *object*

Description

Summarise a mcmc_fit object

Usage

```
## S3 method for class 'mcmc_fit'
summary(object, n_pars = 8, ...)
```

Arguments

object	An object of class mcmc_fit.
n_pars	The number of pi/theta parameters and z 'items' to display.
...	Other arguments passed to function.

Details

For the class conditional model the 'full' theta parameterisation (i.e. appearing to have the same number of parameters as the standard Dawid-Skene model) is calculated and returned. This is designed to allow easier comparison with the full Dawid-Skene model.

Examples

```
fit <- rater(anesthesia, "dawid_skene", verbose = FALSE)

summary(fit)
```

---

summary.optim_fit *Summarise an* optim_fit *object*

Description

Summarise an optim_fit object

Usage

```
## S3 method for class 'optim_fit'
summary(object, n_pars = 8, ...)
```

Arguments

object	An object of class optim_fit.
n_pars	The number of pi/theta parameters and z 'items' to display.
...	Other arguments passed to function.

Details

For the class conditional model the 'full' theta parameterisation (i.e. appearing to have the same number of parameters as the standard Dawid-Skene model) is calculated and returned. This is designed to allow easier comparison with the full Dawid-Skene model.

Examples

```
fit <- rater(anesthesia, "dawid_skene", method = "optim")

summary(fit)
```

`summary.rater_model` *Summarise a* `rater_model`.

Description

Summarise a `rater_model`.

Usage

```
## S3 method for class 'rater_model'
summary(object, ...)
```

Arguments

`object`	A `rater_model` object.
`...`	Other arguments.

Examples

```
mod <- dawid_skene()
summary(mod)
```

`waic.rater_fit` *Compute the WAIC - a measure of model fit - of a rater fit object.*

Description

Compute the WAIC - a measure of model fit - of a rater fit object.

Usage

```
## S3 method for class 'rater_fit'
waic(x, ...)
```

Arguments

x	A rater_fit object. All model types are currently supported except the basic Dawid-Skene model fit with grouped data.
...	Other arguments passed.

Details

This function provides provides an additional method for model comparison, on top of the loo() function. In general we recommend that loo() is preferred: see the documentation of the loo package for details. Also, note the comments regarding model selection the the details section of loo().

Value

A waic/loo object.

References

Watanabe, S. (2010). Asymptotic equivalence of Bayes cross validation and widely application information criterion in singular learning theory. *Journal of Machine Learning Research* 11, 3571-3594.

Vehtari, A., Gelman, A., and Gabry, J. (2017a). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 (journal version, preprint arXiv:1507.04544).

Examples

```
fit_ds <- rater(anesthesia, "dawid_skene", verbose = FALSE, chains = 1)
fit_ccds <- rater(anesthesia, "class_conditional_dawid_skene",
                  verbose = FALSE, chains = 1)

waic(fit_ds)
waic(fit_ccds)
```

---

wide_to_long *Convert wide data to the long format*

Description

Convert wide data to the long format

Usage

```
wide_to_long(data)
```

Arguments

`data`	Data in a wide format. Must be 2D data object which can be converted to a data.frame

Details

Wide data refers to a way of laying out categorical rating data where each item is one row and each column represents the ratings of each rater. Elements of the data can be `NA`, indicating that an item wasn't rated by a rater. Wide data cannot represent the same rater rating an item multiple times.

Currently any column names of the data are ignored and the raters are labelled by their column position (1 indexed, left to right). Only numeric ratings are currently supported.

Value

The data converted into long format. A data.frame with three columns item, rater and rating.

Examples

```
wide_data <- data.frame(dater_1 = c(3, 2, 2), rater_2 = c(4, 2, 2))
wide_data

long_data <- wide_to_long(wide_data)
long_data
```

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