Package ‘tidybayes’

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Title Tidy Data and ‘Geoms’ for Bayesian Models

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Description
Compose data for and extract, manipulate, and visualize posterior draws from Bayesian models (‘JAGS’, ‘Stan’, ‘rstanarm’, ‘brms’, ‘MCMCglmm’, ‘coda’, ...) in a tidy data format. Functions are provided to help extract tidy data frames of draws from Bayesian models and that generate point summaries and intervals in a tidy format. In addition, ‘ggplot2’ geoms and 'stats' are provided for common visualization primitives like points with multiple uncertainty intervals, eye plots (intervals plus densities), and fit curves with multiple, arbitrary uncertainty bands.

Depends R (>= 3.5.0)

Imports methods, ggdist (>= 3.0.0), dplyr (>= 0.8.0), tidyr (>= 1.0.0), ggplot2 (>= 3.3.5), coda, rlang (>= 0.3.0), arrayhelpers, tidyselect, tibble, magrittr, posterior (>= 1.0.1), withr, vctrs

Suggests knitr, testthat, purrr (>= 0.2.3), forcats, vdiffr (>= 1.0.0), svglite, rstan (>= 2.17.0), rstantools (>= 2.1.0), runjags, rjags, jagsUI, rstanarm (>= 2.19.2), emmeans, broom (>= 0.4.3), dotwhisker, MCMCglmm, bayesplot, modelr, brms (>= 2.16.0), cowplot, covr, gdtools, rmarkdown, ggforce, bindrcpp, RColorBrewer, gganimate, gifski, png, pkgdown, distributional, transformr

License GPL (>= 3)

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BugReports https://github.com/mjskay/tidybayes/issues/new

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Collate 「ggdist-curve_interval.R」「ggdist-cut_cdf_qi.R」
「ggdist-geom_slabinterval.R」「ggdist-geom_dotsinterval.R」
「ggdist-geom_interval.R」「ggdist-geom_lineribbon.R」
「ggdist-geom_pointinterval.R」「ggdist-lkjcorr_marginal.R」
「ggdist-parse_dist.R」「ggdist-scales.R」
「ggdist-stat_slabinterval.R」「ggdist-stat_dist_slabinterval.R」
「ggdist-stat_sample_slabinterval.R」
「ggdist-stat_dotsinterval.R」「ggdist-stat_pointinterval.R」
「ggdist-stat_interval.R」「ggdist-stat_lineribbon.R」
「ggdist-student_t.R」「ggdist-theme_ggdist.R」
「ggdist-tidy_format_translators.R」「tidybayes-package.R」
「add_draws.R」「combine_chains.R」「compare_levels.R」
「compose_data.R」「density_bins.R」「emmeans_comparison.R」
「gather_emmeans_draws.R」「gather_pairs.R」「gather_rvars.R」
「point_interval.R」「predict_curve.R」「predicted_draws.R」
「predicted_rvars.R」「recover_types.R」「residual_draws.R」
「sample_draws.R」「spread_draws.R」「spread_rvars.R」
「summarise_draws.R」「testthat.R」「tidy_draws.R」
「tidybayes-models.R」「ungather_draws.R」「unspread_draws.R」
「util.R」「x_at_y.R」「deprecated.R」

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**Description**

Tidybayes is an R package that aims to make it easy to integrate popular Bayesian modeling methods into a tidy data + ggplot workflow.

**Details**

Tidy data frames (one observation per row) are particularly convenient for use in a variety of R data manipulation and visualization packages (Wickham 2014). However, when using Bayesian modeling functions like JAGS or Stan in R, we often have to translate this data into a form the model understands, and then after running the model, translate the resulting sample (or predictions) into a more tidy format for use with other R functions. tidybayes aims to simplify these two common (often tedious) operations. It also provides a variety of ggplot geometries aimed at making the visualization of model output easier.

For a comprehensive overview of the package, see vignette("tidybayes"). For overviews aimed at the rstanarm and brms packages, see vignette("tidy-rstanarm") and vignette("tidy-brms"). For an overview of the majority of geoms in the ggdist/tidybayes family, see vignette("slabinterval", package = "ggdist").

For a list of supported models, see tidybayes-models.

**References**

Add draws to a data frame in tidy format

Description

Add draws from a matrix of draws (usually draws from a predictive distribution) to a data frame in tidy format. This is a generic version of `add_predicted_draws()` that can be used with model types that have their own prediction functions that are not yet supported by tidybayes.

Usage

```r
add_draws(data, draws, value = ".value")
```

Arguments

- `data`: Data frame to add draws to, with M rows.
- `draws`: N by M matrix of draws, with M columns corresponding to the M rows in `data`, and N draws in each column.
- `value`: The name of the output column; default ".value".

Details

Given a data frame with M rows and an N by M matrix of N draws, adds a `.row`, `.draw`, and `.value` column (or another name if `value` is set) to `data`, and expands `data` into a long-format dataframe of draws.

- `add_epred_draws(df,m)` is roughly equivalent to `add_draws(df,posterior_epred(m,newdata = df))`, except that `add_epred_draws` standardizes argument names and values across packages and has additional features for some model types (like handling ordinal responses and distributional parameters in brms).
- `add_predicted_draws(df,m)` is roughly equivalent to `add_draws(df,posterior_predict(m,newdata = df))`, except that `add_predicted_draws` standardizes argument names and values across packages.

Value

A data frame (actually, a tibble) with a `.row` column (a factor grouping rows from the input data), a `.draw` column (a unique index corresponding to each draw from the distribution), and a column with its name specified by the `value` argument (default is `.value`) containing the values of draws from draws. The data frame is grouped by all rows in `data` plus the `.row` column.

Author(s)

Matthew Kay

See Also

`add_predicted_draws()`, `add_draws()`
Examples

```r
library(ggplot2)
library(dplyr)
library(brms)
library(modelr)

theme_set(theme_light())

m_mpg = brm(mpg ~ hp * cyl, data = mtcars,
# 1 chain / few iterations just so example runs quickly
# do not use in practice
  chains = 1, iter = 500)

# plot posterior predictive intervals
mtcars %>%
  group_by(cyl) %>%
  data_grid(hp = seq_range(hp, n = 101)) %>%
# the line below is roughly equivalent to add_epred_draws(m_mpg), except
# that it does not standardize arguments across model types.
  add_draws(posterior_epred(m_mpg, newdata = .)) %>%
  ggplot(aes(x = hp, y = mpg, color = ordered(cyl))) +
  stat_lineribbon(aes(y = .value), alpha = 0.25) +
  geom_point(data = mtcars) +
  scale_fill_brewer(palette = "Greys")
```

---

**add_epred_draws**

*Add draws from the posterior fit, predictions, or residuals of a model to a data frame*

**Description**

Given a data frame and a model, adds draws from the linear/link-level predictor, the expectation of the posterior predictive, the posterior predictive, or the residuals of a model to the data frame in a long format.

**Usage**

```r
add_epred_draws(
  newdata,
  object,
  ...,
  value = ".epred",
  ndraws = NULL,
```
seed = NULL,
re_formula = NULL,
category = ".category",
dpar = NULL
)

epred_draws(
  object,
  newdata,
  ..., 
  value = ".epred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  category = ".category",
  dpar = NULL
)

## Default S3 method:
epred_draws(
  object,
  newdata,
  ..., 
  value = ".epred",
  seed = NULL,
  category = NULL
)

## S3 method for class 'stanreg'
epred_draws(
  object,
  newdata,
  ..., 
  value = ".epred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  category = ".category",
  dpar = NULL
)

## S3 method for class 'brmsfit'
epred_draws(
  object,
  newdata,
  ..., 
  value = ".epred",
  ndraws = NULL,
add_epred_draws

    seed = NULL,
    re_formula = NULL,
    category = ".category",
    dpar = NULL
)

add_linpred_draws(
    newdata,
    object,
    ..., 
    value = ".linpred",
    ndraws = NULL,
    seed = NULL,
    re_formula = NULL,
    category = ".category",
    dpar = NULL,
    n
)

linpred_draws(
    object,
    newdata,
    ..., 
    value = ".linpred",
    ndraws = NULL,
    seed = NULL,
    re_formula = NULL,
    category = ".category",
    dpar = NULL,
    n,
    scale
)

## Default S3 method:
linpred_draws(
    object,
    newdata,
    ..., 
    value = ".linpred",
    seed = NULL,
    category = NULL
)

## S3 method for class 'stanreg'
linpred_draws(
    object,
    newdata,
    ..., 

add_epred_draws

value = ".linpred",
ndraws = NULL,
seed = NULL,
re_formula = NULL,
category = ".category",
dpar = NULL
)

## S3 method for class 'brmsfit'
linpred_draws(
  object,
  newdata,
  ..., 
  value = ".linpred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  category = ".category",
dpar = NULL
)

add_predicted_draws(
  newdata,
  object,
  ..., 
  value = ".prediction",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  category = ".category",
  n
)

predicted_draws(
  object,
  newdata,
  ..., 
  value = ".prediction",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  category = ".category",
  n,
prediction
)

## Default S3 method:
predicted_draws(
add_epred_draws

object,
newdata,
..., 
value = ".prediction",
seed = NULL,
category = ".category"
)

## S3 method for class 'stanreg'
predicted_draws(
  object,
  newdata,
  ..., 
  value = ".prediction",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  category = ".category"
)

## S3 method for class 'brmsfit'
predicted_draws(
  object,
  newdata,
  ..., 
  value = ".prediction",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  category = ".category"
)

add_residual_draws(
  newdata,
  object,
  ..., 
  value = ".residual",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  category = ".category",
  n
)

residual_draws(
  object,
  newdata,
  ..., 
  
)
value = ".residual",
ndraws = NULL,
seed = NULL,
re_formula = NULL,
category = ".category",
n,
residual
)

## Default S3 method:
residual_draws(object, newdata, ...)

## S3 method for class 'brmsfit'
residual_draws(  
  object,
  newdata,
  ...,  
  value = ".residual",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  category = ".category"
)

**Arguments**

- **newdata** Data frame to generate predictions from.
- **object** A supported Bayesian model fit that can provide fits and predictions. Supported models are listed in the second section of tidybayes-models: Models Supporting Prediction. While other functions in this package (like spread_draws()) support a wider range of models, to work with add_epred_draws(), add_predicted_draws(), etc. a model must provide an interface for generating predictions, thus more generic Bayesian modeling interfaces like runjags and rstan are not directly supported for these functions (only wrappers around those languages that provide predictions, like rstanarm and brm, are supported here).
- **...** Additional arguments passed to the underlying prediction method for the type of model given.
- **value** The name of the output column:
  - for [add_]epred_draws(), defaults to ".epred".
  - for [add_]predicted_draws(), defaults to ".prediction".
  - for [add_]linpred_draws(), defaults to ".linpred".
  - for [add_]residual_draws(), defaults to ".residual"
- **ndraws** The number of draws to return, or NULL to return all draws.
- **seed** A seed to use when subsampling draws (i.e. when ndraws is not NULL).
- **re_formula** formula containing group-level effects to be considered in the prediction. If NULL (default), include all group-level effects; if NA, include no group-level effects. Some model types (such as brms::brmsfit and rstanarm::stanreg-objects)
allow marginalizing over grouping factors by specifying new levels of a factor in newdata. In the case of `brms::brm()`, you must also pass `allow_new_levels = TRUE` here to include new levels (see `brms::posterior_predict()`).

category
For some ordinal, multinomial, and multivariate models (notably, `brms::brm()` models but not `rstanarm::stan_polr()` models), multiple sets of rows will be returned per input row for `epred_draws()` or `predicted_draws()`, depending on the model type. For ordinal/multinomial models, these rows correspond to different categories of the response variable. For multivariate models, these correspond to different response variables. The category argument specifies the name of the column to put the category names (or variable names) into in the resulting data frame. The default name of this column (".category") reflects the fact that this functionality was originally used only for ordinal models and has been re-used for multivariate models. The fact that multiple rows per response are returned only for some model types reflects the fact that tidybayes takes the approach of tidying whatever output is given to us, and the output from different modeling functions differs on this point. See vignette("tidy-brms") and vignette("tidy-rstanarm") for examples of dealing with output from ordinal models using both approaches.

dpar
For `add_epred_draws()` and `add_linpred_draws()`: Should distributional regression parameters be included in the output? Valid only for models that support distributional regression parameters, such as submodels for variance parameters (as in `brms::brm()`). If TRUE, distributional regression parameters are included in the output as additional columns named after each parameter (alternative names can be provided using a list or named vector, e.g. `c(sigma.hat = "sigma")` would output the "sigma" parameter from a model as a column named "sigma.hat"). If NULL or FALSE (the default), distributional regression parameters are not included.

n
(Deprecated). Use `ndraws`.

scale
(Deprecated). Use the appropriate function (`epred_draws()` or `linpred_draws()`) depending on what type of distribution you want. For `linpred_draws()`, you may want the `transform` argument. See `rstanarm::posterior_linpred()` or `brms::posterior_linpred()`.

Details
`add_epred_draws()` adds draws from expectation of the posterior predictive distribution to the data. It corresponds to `rstanarm::posterior_epred()` or `brms::posterior_epred()`.

`add_predicted_draws()` adds draws from posterior predictive distribution to the data. It corresponds to `rstanarm::posterior_predict()` or `brms::posterior_predict()`.

`add_linpred_draws()` adds draws from (possibly transformed) posterior linear predictors (or "link-level" predictors) to the data. It corresponds to `rstanarm::posterior_linpred()` or `brms::posterior_linpred()`.

`add_residual_draws()` adds draws from residuals to the data. It corresponds to `brms::residuals.brmsfit()`.

The corresponding functions without `add_` as a prefix are alternate spellings with the opposite order of the first two arguments: e.g. `add_predicted_draws()` and `predicted_draws()`. This facilitates use in data processing pipelines that start either with a data frame or a model.
Given equal choice between the two, the spellings prefixed with add_ are preferred.

Value

A data frame (actually, a tibble) with a .row column (a factor grouping rows from the input newdata), .chain column (the chain each draw came from, or NA if the model does not provide chain information), .iteration column (the iteration the draw came from, or NA if the model does not provide iteration information), and a .draw column (a unique index corresponding to each draw from the distribution). In addition, epred_draws includes a column with its name specified by the epred argument (default ".epred"); linpred_draws includes a column with its name specified by the linpred argument (default ".linpred"), and predicted_draws contains a column with its name specified by the .prediction argument (default ".prediction"). For convenience, the resulting data frame comes grouped by the original input rows.

Author(s)

Matthew Kay

See Also

add_draws() for the variant of these functions for use with packages that do not have explicit support for these functions yet. See spread_draws() for manipulating posteriors directly.

Examples

```r
library(ggplot2)
library(dplyr)
library(brms)
library(modelr)

theme_set(theme_light())

m_mpg = brm(mpg ~ hp * cyl, data = mtcars,
  # 1 chain / few iterations just so example runs quickly
  # do not use in practice
  chains = 1, iter = 500)

# draw 100 lines from the posterior means and overplot them
mtcars %>%
  group_by(cyl) %>%
  data_grid(hp = seq_range(hp, n = 101)) %>%
  # NOTE: only use ndraws here when making spaghetti plots; for
  # plotting intervals it is always best to use all draws (omit ndraws)
  add_epred_draws(m_mpg, ndraws = 100) %>%
  ggplot(aes(x = hp, y = mpg, color = ordered(cyl))) +
  geom_line(aes(y = .epred, group = paste(cyl, .draw)), alpha = 0.25) +
  geom_point(data = mtcars)

# plot posterior predictive intervals
```
mtcars %>%
group_by(cyl) %>%
data_grid(hp = seq_range(hp, n = 101)) %>%
add_predicted_draws(m_mpg) %>%
ggplot(aes(x = hp, y = mpg, color = ordered(cyl))) +
stat_lineribbon(aes(y = .prediction), .width = c(.99, .95, .8, .5), alpha = 0.25) +
geom_point(data = mtcars) +
scale_fill_brewer(palette = "Greys")

---

**add_epred_rvars**

Add *rvars* for the linear predictor, posterior expectation, posterior predictive, or residuals of a model to a data frame

**Description**

Given a data frame and a model, adds *rvars* of draws from the linear/link-level predictor, the expectation of the posterior predictive, or the posterior predictive to the data frame.

**Usage**

```r
add_epred_rvars(
  newdata,
  object,
  ...,  
  value = ".epred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  dpar = NULL,
  columns_to = NULL
)

epred_rvars(
  object,
  newdata,
  ...,  
  value = "epred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  dpar = NULL,
  columns_to = NULL
)
```

---

## Default S3 method:
add_epred_rvars

epred_rvars(
  object,
  newdata,
  ..., 
  value = ".epred",
  seed = NULL,
  dpar = NULL,
  columns_to = NULL
)

## S3 method for class 'stanreg'
epred_rvars(
  object,
  newdata,
  ..., 
  value = ".epred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  dpar = NULL,
  columns_to = NULL
)

## S3 method for class 'brmsfit'
epred_rvars(
  object,
  newdata,
  ..., 
  value = ".epred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  dpar = NULL,
  columns_to = NULL
)

add_linpred_rvars(
  newdata,
  object,
  ..., 
  value = ".linpred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  dpar = NULL,
  columns_to = NULL
)
linpred_rvars(
  object,
  newdata,
  ..., 
  value = ".linpred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  dpar = NULL,
  columns_to = NULL
)

## Default S3 method:
linpred_rvars(
  object,
  newdata,
  ..., 
  value = ".linpred",
  seed = NULL,
  dpar = NULL,
  columns_to = NULL
)

## S3 method for class 'stanreg'
linpred_rvars(
  object,
  newdata,
  ..., 
  value = ".linpred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  dpar = NULL,
  columns_to = NULL
)

## S3 method for class 'brmsfit'
linpred_rvars(
  object,
  newdata,
  ..., 
  value = ".linpred",
  ndraws = NULL,
  seed = NULL,
  re_formula = NULL,
  dpar = NULL,
  columns_to = NULL
)
add_predicted_rvars(
    newdata,
    object,
    ..., 
    value = ".prediction",
    ndraws = NULL,
    seed = NULL,
    re_formula = NULL,
    columns_to = NULL
)

predicted_rvars(
    object,
    newdata,
    ..., 
    value = ".prediction",
    ndraws = NULL,
    seed = NULL,
    re_formula = NULL,
    columns_to = NULL
)

## Default S3 method:
predicted_rvars(
    object,
    newdata,
    ..., 
    value = ".prediction",
    seed = NULL,
    columns_to = NULL
)

## S3 method for class 'stanreg'
predicted_rvars(
    object,
    newdata,
    ..., 
    value = ".prediction",
    ndraws = NULL,
    seed = NULL,
    re_formula = NULL,
    columns_to = NULL
)

## S3 method for class 'brmsfit'
predicted_rvars(
    object,
add_epred_rvars

newdata,
..., 
value = ".prediction",
ndraws = NULL,
seed = NULL,
re_formula = NULL,
columns_to = NULL
)

Arguments

newdata Data frame to generate predictions from.
object A supported Bayesian model fit that can provide fits and predictions. Supported
models are listed in the second section of tidybayes-models: Models Supporting
Prediction. While other functions in this package (like spread_rvars()) sup-
port a wider range of models, to work with add_epred_rvars(), add_predicted_rvars(),
etc. a model must provide an interface for generating predictions, thus more
generic Bayesian modeling interfaces like runjags and rstan are not directly
supported for these functions (only wrappers around those languages that pro-
vide predictions, like rstanarm and brm, are supported here).
...
Additional arguments passed to the underlying prediction method for the type
of model given.
value The name of the output column:
  • for [add_]epred_rvars(), defaults to ".epred".
  • for [add_]predicted_rvars(), defaults to ".prediction".
  • for [add_]linpred_rvars(), defaults to ".linpred".
ndraws The number of draws to return, or NULL to return all draws.
seed A seed to use when subsampling draws (i.e. when ndraws is not NULL).
re_formula formula containing group-level effects to be considered in the prediction. If
NULL (default), include all group-level effects; if NA, include no group-level ef-
ects. Some model types (such as brms::brmsfit and rstanarm::stanreg-objects)
allow marginalizing over grouping factors by specifying new levels of a factor in
newdata. In the case of brms::brm(), you must also pass allow_new_levels = TRUE here to include new levels (see brms::posterior_predict()).
dpar For add_epred_rvars() and add_linpred_rvars(): Should distributional re-
gression parameters be included in the output? Valid only for models that sup-
port distributional regression parameters, such as submodels for variance pa-
rameters (as in brms::brm()). If TRUE, distributional regression parameters are
included in the output as additional columns named after each parameter (alter-
native names can be provided using a list or named vector, e.g. c(sigma.hat = "sigma") would output the "sigma" parameter from a model as a column
named "sigma.hat"). If NULL or FALSE (the default), distributional regression
parameters are not included.
columns_to For some models, such as ordinal, multinomial, and multivariate models (not-
ably, brms::brm() models but not rstanarm::stan_polr() models), the col-
umn of predictions in the resulting data frame may include nested columns. For
add_epred_rvars

example, for ordinal/multinomial models, these columns correspond to different
categories of the response variable. It may be more convenient to turn these
nested columns into rows in the output; if this is desired, set columns_to to a
string representing the name of a column you would like the column names
to be placed in. In this case, a .row column will also be added to the result
indicating which rows of the output correspond to the same row in newdata.

See vignette("tidy-posterior") for examples of dealing with output ordinal models.

Details

add_epred_rvars() adds rvars containing draws from the expectation of the posterior predictive
distribution to the data. It corresponds to rstanarm::posterior_epred() or brms::posterior_epred().

add_predicted_rvars() adds rvars containing draws from the posterior predictive distribution to
the data. It corresponds to rstanarm::posterior_predict() or brms::posterior_predict().

add_linpred_rvars() adds rvars containing draws from the (possibly transformed) posterior linear
predictors (or "link-level" predictors) to the data. It corresponds to rstanarm::posterior_linpred() or
brms::posterior_linpred().

The corresponding functions without add_ as a prefix are alternate spellings with the opposite order
of the first two arguments: e.g. add_predicted_rvars() and predicted_rvars(). This facilitates
use in data processing pipelines that start either with a data frame or a model.

Given equal choice between the two, the spellings prefixed with add_ are preferred.

Value

A data frame (actually, a tibble) equal to the input newdata with additional columns added containing rvars representing the requested predictions or fits.

Author(s)

Matthew Kay

See Also

add_predicted_draws() for the analogous functions that use a long-data-frame-of-draws format
instead of a data-frame-of-rvars format. See spread_rvars() for manipulating posteriors directly.

Examples

library(ggplot2)
library(dplyr)
library(posterior)
library(brms)
library(modelr)

theme_set(theme_light())
m_mpg = brm(mpg ~ hp * cyl, data = mtcars, family = lognormal(),
# 1 chain / few iterations just so example runs quickly
# do not use in practice
chains = 1, iter = 500)

# Look at mean predictions for some cars (epred) and compare to
# the exponeniated mu parameter of the lognormal distribution (linpred).
# Notice how they are NOT the same. This is because exp(mu) for a
# lognormal distribution is equal to its median, not its mean.
mtcars %>%
  select(hp, cyl, mpg) %>%
  add_epred_rvars(m_mpg) %>%
  add_linpred_rvars(m_mpg, value = "mu") %>%
  mutate(expmu = exp(mu), .epred - expmu)

# plot intervals around conditional means (epred_rvars)
mtcars %>%
  group_by(cyl)
  data_grid(hp = seq_range(hp, n = 101)) %>%
  add_epred_rvars(m_mpg) %>%
  ggplot(aes(x = hp, color = ordered(cyl), fill = ordered(cyl))) +
  stat_dist_lineribbon(aes(dist = .epred), .width = c(.95, .8, .5), alpha = 1/3) +
  geom_point(aes(y = mpg), data = mtcars) +
  scale_color_brewer(palette = "Dark2") +
  scale_fill_brewer(palette = "Set2")

# plot posterior predictive intervals (predicted_rvars)
mtcars %>%
  group_by(cyl)
  data_grid(hp = seq_range(hp, n = 101)) %>%
  add_predicted_rvars(m_mpg) %>%
  ggplot(aes(x = hp, color = ordered(cyl), fill = ordered(cyl))) +
  stat_dist_lineribbon(aes(dist = .prediction), .width = c(.95, .8, .5), alpha = 1/3) +
  geom_point(aes(y = mpg), data = mtcars) +
  scale_color_brewer(palette = "Dark2") +
  scale_fill_brewer(palette = "Set2")

---

**combine_chains**

Combine the chain and iteration columns of tidy data frames of draws

**Description**

Combines the chain and iteration columns of a tidy data frame of draws from a Bayesian model fit into a new column that can uniquely identify each draw. Generally speaking **not needed for pure tidybayes code**, as tidybayes functions now automatically include a .draw column, but can be useful when interacting with packages that do not provide such a column.
Usage

```
combine_chains(data, chain = .chain, iteration = .iteration, into = ".draw")
```

Arguments

data: Tidy data frame of draws with columns representing the chain and iteration of each draw.

chain: Bare name of column in data indicating the chain of each row. The default (\texttt{.chain}) is the same as used by other functions in \texttt{tidybayes}.

iteration: Bare name of column in data indicating the iteration of each row. The default (\texttt{.iteration}) is the same as used by other functions in \texttt{tidybayes}.

into: Name (as a character vector) of the column to combine chains into. The default, \texttt{NULL}, replaces the chain column with NAs and writes the combined chain iteration numbers into \texttt{iteration}. If provided, \texttt{chain} and \texttt{iteration} will not be modified, and the combined iteration number will be written into a new column named \texttt{into}.

Value

A data frame of tidy draws with a combined iteration column

Author(s)

Matthew Kay

See Also

\texttt{emmeans::emmeans()}

Examples

```
library(magrittr)
library(coda)

data(line, package = "coda")

# The \texttt{\textbackslash{}line} posterior has two chains with 200 iterations each:
line %>%
tidy_draws() %>%
summary()

# combine_chains combines the chain and iteration column into the \texttt{.draw} column.
line %>%
tidy_draws() %>%
combine_chains() %>%
summary()
```
**compare_levels**  
*Compare the value of draws of some variable from a Bayesian model for different levels of a factor*

**Description**

Given posterior draws from a Bayesian model in long format (e.g. as returned by `spread_draws()`), compare the value of a variable in those draws across different paired combinations of levels of a factor.

**Usage**

```r
compare_levels(
  data, 
  variable, 
  by, 
  fun = `~`, 
  comparison = "default", 
  draw_indices = c(".chain", ".iteration", ".draw"), 
  ignore_groups = ".row"
)
```

**Arguments**

- **data**: Long-format data.frame of draws such as returned by `spread_draws()` or `gather_draws()`. If `data` is a grouped data frame, comparisons will be made within groups (if one of the groups in the data frame is the by column, that specific group will be ignored, as it is not possible to make comparisons both within some variable and across it simultaneously).

- **variable**: Bare (unquoted) name of a column in data representing the variable to compare across levels. Can be a numeric variable (as in long-data-frame-of-draws format) or a `posterior::rvar`.

- **by**: Bare (unquoted) name of a column in data that is a factor or ordered. The value of `variable` will be compared across pairs of levels of this factor.

- **fun**: Binary function to use for comparison. For each pair of levels of `by` we are comparing (as determined by `comparison`), compute the result of this function.

- **comparison**: One of (a) the comparison types ordered, control, pairwise, or default (may also be given as strings, e.g. "ordered"), see Details; (b) a user-specified function that takes a factor and returns a list of pairs of names of levels to compare (as strings) and/or unevaluated expressions containing representing the comparisons to make; or (c) a list of pairs of names of levels to compare (as strings) and/or unevaluated expressions representing the comparisons to make, e.g.: `list(c("a","b"),c("b","c"))` or `exprs(a - b, b - c)`, both of which would compare level "a" against "b" and level "b" against "c". Note that the unevaluated expression syntax ignores the `fun` argument, can include
any other functions desired (e.g. variable transformations), and can even include more than two levels or other columns in data. Types (b) and (c) may use named lists, in which case the provided names are used in the output variable column instead converting the unevaluated expression to a string. You can also use `emmeans_comparison()` to generate a comparison function based on contrast methods from the emmeans package.

**draw_indices**  
Character vector of column names in `data` that should be treated as indices when making the comparison (i.e. values of `variable` within each level of `by` will be compared at each unique combination of levels of `draw_indices`). Columns in `draw_indices` not found in `data` are ignored. The default is `c(".chain",".iteration",".draw")`, which are the same names used for chain/iteration/draw indices returned by `spread_draws()` or `gather_draws()`: thus if you are using `compare_levels` with `spread_draws()` or `gather_draws()` you generally should not need to change this value.

**ignore_groups**  
Character vector of names of groups to ignore by default in the input grouping. This is primarily provided to make it easier to pipe output of `add_epred_draws()` into this function, as that function provides a ".row" output column that is grouped, but which is virtually never desired to group by when using `compare_levels`.

**Details**

This function simplifies conducting comparisons across levels of some variable in a tidy data frame of draws. It applies `fun` to all values of `variable` for each pair of levels of `by` as selected by `comparison`. By default, all pairwise comparisons are generated if `by` is an unordered factor and ordered comparisons are made if `by` is ordered.

The included comparison types are:

- **ordered**: compare each level i with level i - 1; e.g. `fun(i,i -1)`
- **pairwise**: compare each level of `by` with every other level.
- **control**: compare each level of `by` with the first level of `by`. If you wish to compare with a different level, you can first apply `relevel()` to `by` to set the control (reference) level.
- **default**: use ordered if `is.ordered(by)` and pairwise otherwise.

**Value**

A data frame with the same columns as `data`, except that the `by` column contains a symbolic representation of the comparison of pairs of levels of `by` in `data`, and `variable` contains the result of that comparison.

**Author(s)**

Matthew Kay

**See Also**

`emmeans_comparison()` to use emmeans-style contrast methods with `compare_levels()`.
Examples

```r
library(dplyr)
library(ggplot2)

data(RankCorr, package = "ggdist")

# Let's do all pairwise comparisons of b[i,1]:
RankCorr %>%
  spread_draws(b[i,j]) %>%
  filter(j == 1) %>%
  compare_levels(b, by = i) %>%
  median_qi()

# Or let's plot all comparisons against the first level (control):
RankCorr %>%
  spread_draws(b[i,j]) %>%
  filter(j == 1) %>%
  compare_levels(b, by = i, comparison = control) %>%
  ggplot(aes(x = b, y = i)) +
  stat_halfeye()

# Or let's plot comparisons of all levels of j within # all levels of i
RankCorr %>%
  spread_draws(b[i,j]) %>%
  group_by(i) %>%
  compare_levels(b, by = j) %>%
  ggplot(aes(x = b, y = j)) +
  stat_halfeye() +
  facet_grid(cols = vars(i))
```

**compose_data**

**Compose data for input into a Bayesian model**

**Description**

Compose data into a list suitable to be passed into a Bayesian model (JAGS, BUGS, Stan, etc).

**Usage**

```r
compose_data(..., .n_name = n_prefix("n"))
```

**Arguments**

... Data to be composed into a list suitable for being passed into Stan, JAGS, etc. Named arguments will have their name used as the name argument to as_data_list when translated; unnamed arguments that are not lists or data
frames will have their bare value (passed through `make.names`) used as the name argument to `as_data_list`. Each argument is evaluated using `eval_tidy` in an environment that includes all list items composed so far.

`.n_name` A function that is used to form dimension index variables (a variable whose value is number of levels in a factor or the length of a data frame in ...). For example, if a data frame with 20 rows and a factor "foo" (having 3 levels) is passed to `compose_data`, the list returned by `compose_data` will include an element named `.n_name("foo")`, which by default would be "n_foo", containing the value 3, and a column named "n" containing the value 20. See `n_prefix()`.

### Details

This function recursively translates each argument into list elements using `as_data_list()`, merging all resulting lists together. By default this means that:

- numerics are included as-is.
- logicals are translated into numeric using `as.numeric()`.
- factors are translated into numeric using `as.numeric()`, and an additional element named `.n_name(argument_name)` is added with the number of levels in the factor. The default `.n_name` function prefixes "n_" before the factor name; e.g. a factor named foo will have an element named n_foo added containing the number of levels in foo.
- character vectors are converted into factors then translated into numeric in the same manner as factors are.
- lists are translated by translating all elements of the list (recursively) and adding them to the result.
- data.frames are translated by translating every column of the data.frame and adding them to the result. A variable named "n" (or `.n_name(argument_name)` if the data.frame is passed as a named argument `argument_name`) is also added containing the number of rows in the data frame.
- NULL values are dropped. Setting a named argument to NULL can be used to drop that item from the resulting list (if an unwanted element was added to the list by a previous argument, such as a column from a data frame that is not needed in the model).
- all other types are dropped (and a warning given)

As in functions like `mutate()`, each expression is evaluated in an environment containing the data list built up so far.

For example, this means that if the first argument to `compose_data` is a data frame, subsequent arguments can include direct references to columns from that data frame. This allows you, for example, to easily use `x_at_y()` to generate indices for nested models.

If you wish to add support for additional types not described above, provide an implementation of `as_data_list()` for the type. See the implementations of `as_data_list.numeric`, `as_data_list.logical`, etc for examples.

### Value

A list where each element is a translated variable as described above.
data_list

Author(s)
Matthew Kay

See Also
x_at_y(), spread_draws(), gather_draws().

Examples

library(magrittr)

df = data.frame(
  plot = factor(paste0("p", rep(1:8, times = 2))),
  site = factor(paste0("s", rep(1:4, each = 2, times = 2)))
)

# without changing `.n_name`, compose_data() will prefix indices
# with "n" by default
df %>%
  compose_data()

# you can use n_prefix() to define a different prefix (e.g. "N"):
df %>%
  compose_data(.n_name = n_prefix("N"))

# If you have nesting, you may want a nested index, which can be generated using x_at_y()
# Here, site[p] will give the site for plot p
df %>%
  compose_data(site = x_at_y(site, plot))

---

data_list

Data lists for input into Bayesian models

Description
Functions used by compose_data() to create lists of data suitable for input into a Bayesian modeling function. These functions typically should not be called directly (instead use compose_data()), but are exposed for the rare cases in which you may need to provide your own conversion routines for a data type not already supported (see Details).

Usage
data_list(...)

as_data_list(object, name = "", ...)  
## Default S3 method:
as_data_list(object, name = "", ...)  
## S3 method for class 'numeric'
as_data_list(object, name = "", scalar_as_array = FALSE, ...)  
## S3 method for class 'logical'
as_data_list(object, name = "", ...)  
## S3 method for class 'factor'
as_data_list(object, name = "", .n_name = n_prefix("n"), ...)  
## S3 method for class 'character'
as_data_list(object, name = "", ...)  
## S3 method for class 'list'
as_data_list(object, name = "", ...)  
## S3 method for class 'data.frame'
as_data_list(object, name = "", .n_name = n_prefix("n"), ...)  
## S3 method for class 'data_list'
as_data_list(object, name = "", ...)  

Arguments

...  
Additional arguments passed to other implementations of as_data_list, or for data_list, passed to list().

object  
The object to convert (see Details).

name  
The name of the element in the returned list corresponding to this object.

scalar_as_array  
If TRUE, returns single scalars as an 1-dimensional array with one element. This is used by as_data_list.data.frame to ensure that columns from a data frame with only one row are still returned as arrays instead of scalars.

.n_name  
A function that is used to form variables storing the number of rows in data frames or the number of levels in factors in ...). For example, if a factor with name = "foo" (having three levels) is passed in, the list returned will include an element named .n_name("foo"), which by default would be "n_foo", containing the value 3.

Details

data_list creates a list with class c("data_list","list") instead of c("list"), but largely otherwise acts like the list() function.

as_data_list recursively translates its first argument into list elements, concatenating all resulting lists together. By default this means that:

- numerics are included as-is.
- logicals are translated into numeric using as.numeric().
- factors are translated into numeric using `as.numeric()`, and an additional element named `.n_name(name)` is added with the number of levels in the factor.
- character vectors are converted into factors then translated into numeric in the same manner as factors are.
- lists are translated by translating all elements of the list (recursively) and adding them to the result.
- data.frames are translated by translating every column of the data.frame and adding them to the result. A variable named "n" (or `.n_name(name)` if name is not "") is also added containing the number of rows in the data frame.
- all other types are dropped (and a warning given)

If you wish to add support for additional types not described above, provide an implementation of `as_data_list()` for the type. See the implementations of `as_data_list.numeric`, `as_data_list.logical`, etc for examples.

**Value**

An object of class `c("data_list","list")`, where each element is a translated variable as described above.

**Author(s)**

Matthew Kay

**See Also**

`compose_data()`.

**Examples**

```r
# Typically these functions should not be used directly.
# See the compose_data function for examples of how to translate
# data in lists for input to Bayesian modeling functions.
```

---

**Description**

Generates a data frame of bins representing the kernel density (or histogram) of a vector, suitable for use in generating predictive distributions for visualization. These functions were originally designed for use with the now-deprecated `predict_curve()`, and may be deprecated in the future.
Usage

density_bins(x, n = 101, ...)

histogram_bins(x, n = 30, breaks = n, ...)

Arguments

x
A numeric vector

n
Number of bins

... Additional arguments passed to density() or hist().

breaks Used to set bins for histogram_bins. Can be number of bins (by default it is set to the value of n) or a method for setting bins. See the breaks argument of hist().

Details

These functions are simple wrappers to density() and hist() that compute density estimates and return their results in a consistent format: a data frame of bins suitable for use with the now-deprecated predict_curve().

density_bins computes a kernel density estimate using density().
histogram_bins computes a density histogram using hist().

Value

A data frame representing bins and their densities with the following columns:

mid Bin midpoint
lower Lower endpoint of each bin
upper Upper endpoint of each bin
density Density estimate of the bin

Author(s)

Matthew Kay

See Also

See add_predicted_draws() and stat_lineribbon() for a better approach. These functions may be deprecated in the future.

Examples

library(ggplot2)
library(dplyr)
library(brms)
emmeans_comparison

Use emmeans contrast methods with compare_levels

Description

Convert emmeans contrast methods into comparison functions suitable for use with compare_levels().

Usage

emmeans_comparison(method, ...)

Arguments

method

An emmeans-style contrast method. One of: (1) a string specifying the name of an emmeans contrast method, like "pairwise", "trt.vs.ctrl", "eff"; or (2) an emmeans-style contrast function itself, like emmeans::pairwise.emmc, emmeans::trt.vs.ctrl.emmc, etc, or a custom function that takes a vector of factor levels and returns a contrast matrix.

...  

Arguments passed on to the contrast method.

Details

Given an emmeans contrast method name as a string (e.g., "pairwise", "trt.vs.ctrl", etc) or an emmeans-style contrast function (e.g., emmeans::pairwise.emmc, emmeans::trt.vs.ctrl.emmc, etc), emmeans_comparison() returns a new function that can be used in the comparison argument to compare_levels() to compute those contrasts.
Value

A function that takes a single argument, `var`, containing a variable to generate contrasts for (e.g., a factor or a character vector) and returns a function that generates a list of named unevaluated expressions representing different contrasts of that variable. This function is suitable to be used as the comparison argument in `compare_levels()`.

Author(s)

Matthew Kay

See Also

`compare_levels()`, `emmeans::contrast-methods`. See `gather_emmeans_draws()` for a different approach to using `emmeans` with `tidybayes`.

Examples

```r
library(dplyr)
library(ggplot2)

data(RankCorr, package = "ggdist")

# emmeans contrast methods return matrices. E.g. the "eff" comparison
# compares each level to the average of all levels:
emmeans:::eff.emmc(c("a","b","c","d"))

# tidybayes::compare_levels() can't use a contrast matrix like this
# directly; it takes arbitrary expressions of factor levels. But
# we can use `emmeans_comparision` to generate the equivalent expressions:
emmeans_comparision("eff") %>% c("a","b","c","d")

# We can use the "eff" comparison type with `compare_levels()` as follows:
RankCorr %>%
  spread_draws(b[i,j]) %>%
  filter(j == 1) %>%
  compare_levels(b, by = i, comparison = emmeans_comparision("eff")) %>%
  median_qi()
```

**gather_draws**

Extract draws of variables in a Bayesian model fit into a tidy data format

Description

Extract draws from a Bayesian model for one or more variables (possibly with named dimensions) into one of two types of long-format data frames.
**gather_draws**

Usage

```r
gather_draws(
  model,
  ..., 
  regex = FALSE, 
  sep = "[, ]",
  ndraws = NULL, 
  seed = NULL, 
  n
)
```

```r
spread_draws(
  model,
  ..., 
  regex = FALSE, 
  sep = "[, ]",
  ndraws = NULL, 
  seed = NULL, 
  n
)
```

Arguments

- **model**: A supported Bayesian model fit. Tidybayes supports a variety of model objects; for a full list of supported models, see tidybayes-models.
- **...**: Expressions in the form of `variable_name[dimension_1,dimension_2,...]` | wide_dimension. See Details.
- **regex**: If TRUE, variable names are treated as regular expressions and all column matching the regular expression and number of dimensions are included in the output. Default FALSE.
- **sep**: Separator used to separate dimensions in variable names, as a regular expression.
- **ndraws**: The number of draws to return, or NULL to return all draws.
- **seed**: A seed to use when subsampling draws (i.e. when ndraws is not NULL).
- **n** (Deprecated). Use ndraws.

Details

Imagine a JAGS or Stan fit named `model`. The model may contain a variable named `b[i,v]` (in the JAGS or Stan language) with dimension `i` in 1:100 and dimension `v` in 1:3. However, the default format for draws returned from JAGS or Stan in R will not reflect this indexing structure, instead they will have multiple columns with names like "b[1,1]", "b[2,1]", etc.

`spread_draws` and `gather_draws` provide a straightforward syntax to translate these columns back into properly-indexed variables in two different tidy data frame formats, optionally recovering dimension types (e.g. factor levels) as it does so.

`spread_draws` and `gather_draws` return data frames already grouped by all dimensions used on the variables you specify.
The difference between `spread_draws` is that names of variables in the model will be spread across the data frame as column names, whereas `gather_draws` will gather variables into a single column named ".variable" and place values of variables into a column named ".value". To use naming schemes from other packages (such as `broom`), consider passing results through functions like `to_broom_names()` or `to_ggmcmc_names()`.

For example, `spread_draws(model,a[i],b[i,v])` might return a grouped data frame (grouped by i and v), with:

- column ".chain": the chain number. NA if not applicable to the model type; this is typically only applicable to MCMC algorithms.
- column ".iteration": the iteration number. Guaranteed to be unique within-chain only. NA if not applicable to the model type; this is typically only applicable to MCMC algorithms.
- column ".draw": a unique number for each draw from the posterior. Order is not guaranteed to be meaningful.
- column "i": value in 1:5
- column "v": value in 1:10
- column "a": value of "a[i]" for draw ".draw"
- column "b": value of "b[i,v]" for draw ".draw"

`gather_draws(model,a[i],b[i,v])` on the same model would return a grouped data frame (grouped by i and v), with:

- column ".chain": the chain number
- column ".iteration": the iteration number
- column ".draw": the draw number
- column "i": value in 1:5
- column "v": value in 1:10, or NA if ".variable" is "a".
- column ".variable": value in c("a","b").
- column ".value": value of "a[i]" (when ".variable" is "a") or "b[i,v]" (when ".variable" is "b") for draw ".draw"

`spread_draws` and `gather_draws` can use type information applied to the model object by `recover_types()` to convert columns back into their original types. This is particularly helpful if some of the dimensions in your model were originally factors. For example, if the v dimension in the original data frame data was a factor with levels c("a","b","c"), then we could use `recover_types` before `spread_draws`:

```r
model %>%
  recover_types(data)
  spread_draws(model, b[i,v])
```

Which would return the same data frame as above, except the "v" column would be a value in c("a","b","c") instead of 1:3.

For variables that do not share the same subscripts (or share some but not all subscripts), we can supply their specifications separately. For example, if we have a variable d[i] with the same i subscript as b[i,v], and a variable x with no subscripts, we could do this:
spread_draws(model, x, d[i], b[i,v])

Which is roughly equivalent to this:

```r
spread_draws(model, x) %>%
  inner_join(spread_draws(model, d[i])) %>%
  inner_join(spread_draws(model, b[i,v])) %>%
  group_by(i,v)
```

Similarly, this:

```r
gather_draws(model, x, d[i], b[i,v])
```

Is roughly equivalent to this:

```r
bind_rows(
  gather_draws(model, x),
  gather_draws(model, d[i]),
  gather_draws(model, b[i,v])
)
```

The `c()` and `cbind` functions can be used to combine multiple variable names that have the same dimensions. For example, if we have several variables with the same subscripts `i` and `v`, we could do either of these:

```r
spread_draws(model, c(w, x, y, z)[i,v])
spread_draws(model, cbind(w, x, y, z)[i,v]) # equivalent
```

Each of which is roughly equivalent to this:

```r
spread_draws(model, w[i,v], x[i,v], y[i,v], z[i,v])
```

Besides being more compact, the `c()`-style syntax is currently also faster (though that may change). Dimensions can be omitted from the resulting data frame by leaving their names blank; e.g. `spread_draws(model, b[,v])` will omit the first dimension of `b` from the output. This is useful if a dimension is known to contain all the same value in a given model.

The shorthand `..` can be used to specify one column that should be put into a wide format and whose names will be the base variable name, plus a dot `(".")`, plus the value of the dimension at `..`. For example:

```r
spread_draws(model, b[i,..])
```

would return a grouped data frame (grouped by `i`), with:

- column `".chain"`: the chain number
- column `".iteration"`: the iteration number
- column `".draw"`: the draw number
- column `"i"`: value in 1:20
• column "b.1": value of "b[i,1]" for draw ".draw"
• column "b.2": value of "b[i,2]" for draw ".draw"
• column "b.3": value of "b[i,3]" for draw ".draw"

An optional clause in the form | wide_dimension can also be used to put the data frame into a wide format based on wide_dimension. For example, this:

spread_draws(model, b[i,v] | v)

is roughly equivalent to this:

spread_draws(model, b[i,v]) %>% spread(v,b)

The main difference between using the | syntax instead of the .. syntax is that the | syntax respects prototypes applied to dimensions with recover_types(), and thus can be used to get columns with nicer names. For example:

model %>% recover_types(data) %>% spread_draws(b[i,v] | v)

would return a grouped data frame (grouped by i), with:

• column ".chain": the chain number
• column ".iteration": the iteration number
• column ".draw": the draw number
• column "i": value in 1:20
• column "a": value of "b[i,1]" for draw ".draw"
• column "b": value of "b[i,2]" for draw ".draw"
• column "c": value of "b[i,3]" for draw ".draw"

The shorthand . can be used to specify columns that should be nested into vectors, matrices, or n-dimensional arrays (depending on how many dimensions are specified with .).

For example, spread_draws(model, a[.],b[.,.]) might return a data frame, with:

• column ".chain": the chain number.
• column ".iteration": the iteration number.
• column ".draw": a unique number for each draw from the posterior.
• column "a": a list column of vectors.
• column "b": a list column of matrices.

Ragged arrays are turned into non-ragged arrays with missing entries given the value NA.

Finally, variable names can be regular expressions by setting regex = TRUE; e.g.:

spread_draws(model, \b_.*\[i], regex = TRUE)

Would return a tidy data frame with variables starting with b_ and having one dimension.
**gather_emmeans_draws**

Extract a tidy data frame of draws of posterior distributions of "estimated marginal means" (emmeans/lsmeans) from a Bayesian model fit.

**Value**

A data frame.

**Author(s)**

Matthew Kay

**See Also**

*spread_rvars*, *recover_types*, *compose_data*.

**Examples**

```r
library(dplyr)
library(ggplot2)

data(RankCorr, package = "ggdist")

RankCorr %>%
  spread_draws(b[i, j])

RankCorr %>%
  spread_draws(b[i, j], tau[i], u_tau[i])

RankCorr %>%
  gather_draws(b[i, j], tau[i], u_tau[i])

RankCorr %>%
  gather_draws(tau[i], typical_r) %>%
  median_qi()
```

**Description**

Extract draws from the result of a call to `emmeans::emmeans` (formerly `lsmeans`) or `emmeans::ref_grid` applied to a Bayesian model.
Usage

gather_emmeans_draws(object, value = ".value", ...)  

## Default S3 method:
gather_emmeans_draws(object, value = ".value", ...)  

## S3 method for class 'emm_list'
gather_emmeans_draws(object, value = ".value", grid = ".grid", ...)  

Arguments

- **object**: An `emmGrid` object such as returned by `emmeans::ref_grid()` or `emmeans::emmeans()`.
- **value**: The name of the output column to use to contain the values of draws. Defaults to ".value".
- **grid**: If `object` is an `emmeans::emm_list()`, the name of the output column to use to contain the name of the reference grid that a given row corresponds to. Defaults to ".grid".
- **...**: Additional arguments passed to the underlying method for the type of object given.

Details

`emmeans::emmeans()` provides a convenient syntax for generating draws from "estimated marginal means" from a model, and can be applied to various Bayesian models, like `rstanarm::stanreg-objects` and `MCMCglmm::MCMCglmm()`. Given a `emmeans::ref_grid()` object as returned by functions like `emmeans::ref_grid()` or `emmeans::emmeans()` applied to a Bayesian model, `gather_emmeans_draws` returns a tidy format data frame of draws from the marginal posterior distributions generated by `emmeans::emmeans()`.

Value

A tidy data frame of draws. The columns of the reference grid are returned as-is, with an additional column called `.value` (by default) containing marginal draws. The resulting data frame is grouped by the columns from the reference grid to make use of summary functions like `point_interval()` straightforward.

If `object` is an `emmeans::emm_list()`, which contains estimates from different reference grids, an additional column with the default name of ".grid" is added to indicate the reference grid for each row in the output. The name of this column is controlled by the `grid` argument.

Author(s)

Matthew Kay

See Also

`emmeans::emmeans()`
Examples

library(dplyr)
library(magrittr)
library(brms)
library(emmeans)

# Here's an example dataset with a categorical predictor ('condition') with several levels:
set.seed(5)
n = 10
n_condition = 5
ABC = tibble(
  condition = rep(c("A","B","C","D","E"), n),
  response = rnorm(n * 5, c(0,1,2,1,-1), 0.5)
)

m = brm(response ~ condition, data = ABC,
  # 1 chain / few iterations just so example runs quickly
  # do not use in practice
  chains = 1, iter = 500)

# Once we've fit the model, we can use emmeans() (and functions
# from that package) to get whatever marginal distributions we want.
# For example, we can get marginal means by condition:
  m %>%
  emmeans(~ condition) %>%
  gather_emmeans_draws() %>%
  median_qi()

# or we could get pairwise differences:
  m %>%
  emmeans(~ condition) %>%
  contrast(method = "pairwise") %>%
  gather_emmeans_draws() %>%
  median_qi()

# see the documentation of emmeans() for more examples of types of
# contrasts supported by that package.

gather_pairs

Gather pairwise combinations of values from key/value columns in a
long-format data frame
Description

Fast method for producing combinations of values in a value column for different levels of a key column, assuming long-format (tidy) data with an equal number of values per key. Among other things, this is useful for producing scatter-plot matrices.

Usage

gather_pairs(
  data,  
  key,  
  value,  
  row = ".row",  
  col = ".col",  
  x = ".x",  
  y = ".y",  
  triangle = c("lower only", "upper only", "lower", "upper", "both only", "both")
)

Arguments

data Tidy data frame.
key Bare name of column in data containing the key .
value Bare name of column in data containing the value.
row Character vector giving the name of the output column identifying rows in the matrix of pairs (takes values of key).
col Character vector giving the name of the output column identifying columns in the matrix of pairs (takes values of key).
x Character vector giving the name of the output column with x values in the matrix of pairs (takes values of value).
y Character vector giving the name of the output column with y values in the matrix of pairs (takes values of value).
triangle Should the upper or lower triangle of the matrix of all possible combinations be returned? The default, "lower only", returns the lower triangle without the diagonal; "lower" returns the lower triangle with the diagonal ("upper" and "upper only" operate analogously), "both" returns the full set of possible combinations, and "both only" returns all combinations except the diagonal.

This method is particularly useful for constructing scatterplot matrices. See examples below.

Value

A tidy data frame of combinations of values in key and value, with columns row and col (default names ".row" and ".col") containing values from key, and columns y and x (default names ".y" and ".x") containing values from value.
**gather_pairs**

*Author(s)*

Matthew Kay

*See Also*

`emmeans::emmeans()`

*Examples*

```r
library(ggplot2)
library(dplyr)

t_a = rnorm(100)
t_b = rnorm(100, t_a * 2)
t_c = rnorm(100)

df = rbind(
  data.frame(g = "a", t = t_a),
  data.frame(g = "b", t = t_b),
  data.frame(g = "c", t = t_c)
)

df %>%
  gather_pairs(g, t, row = "g_row", col = "g_col", x = "t_x", y = "t_y") %>%
  ggplot(aes(t_x, t_y)) +
  geom_point() +
  facet_grid(vars(g_row), vars(g_col))

df %>%
  gather_pairs(g, t, triangle = "upper") %>%
  ggplot(aes(.x, .y)) +
  geom_point() +
  facet_grid(vars(.row), vars(.col))

df %>%
  gather_pairs(g, t, triangle = "both") %>%
  ggplot(aes(.x, .y)) +
  geom_point() +
  facet_grid(vars(.row), vars(.col))

data(line, package = "coda")

line %>%
  tidy_draws() %>%
  gather_variables() %>%
  gather_pairs(.variable, .value) %>%
  ggplot(aes(.x, .y)) +
  geom_point(alpha = .25) +
  facet_grid(vars(.row), vars(.col))
```
line %>%
tidy_draws() %>%
gather_variables() %>%
gather_pairs(.variable, .value) %>%
geom_density_2d(alpha = 0.5) +
facet_grid(vars(.row), vars(.col))

---

**gather_rvars**

Extract draws from a Bayesian model into tidy data frames of random variables

**Description**

Extract draws from a Bayesian model for one or more variables (possibly with named dimensions) into one of two types of long-format data frames of posterior::rvar objects.

**Usage**

```r
gather_rvars(model, ..., ndraws = NULL, seed = NULL)
spread_rvars(model, ..., ndraws = NULL, seed = NULL)
```

**Arguments**

- `model` A supported Bayesian model fit. Tidybayes supports a variety of model objects; for a full list of supported models, see tidybayes-models.
- `...` Expressions in the form of `variable_name[dimension_1,dimension_2,...]`. See Details.
- `ndraws` The number of draws to return, or NULL to return all draws.
- `seed` A seed to use when subsampling draws (i.e. when `ndraws` is not NULL).

**Details**

Imagine a JAGS or Stan fit named `model`. The model may contain a variable named `b[i,v]` (in the JAGS or Stan language) with dimension `i` in 1:100 and dimension `v` in 1:3. However, the default format for draws returned from JAGS or Stan in R will not reflect this indexing structure, instead they will have multiple columns with names like "b[1,1]", "b[2,1]", etc.

`spread_rvars` and `gather_rvars` provide a straightforward syntax to translate these columns back into properly-indexed *rvars* in two different tidy data frame formats, optionally recovering dimension types (e.g. factor levels) as it does so.

`spread_rvars` will spread names of variables in the model across the data frame as column names, whereas `gather_rvars` will gather variable names into a single column named ".variable" and place values of variables into a column named ".value". To use naming schemes from other
packages (such as broom), consider passing results through functions like to_broom_names() or to_ggmcmc_names().

For example, spread_rvars(model, a[i], b[i,v]) might return a data frame with:

- column "i": value in 1:5
- column "v": value in 1:10
- column "a": rvar containing draws from "a[i]"
- column "b": rvar containing draws from "b[i,v]"

gather_rvars(model, a[i], b[i,v]) on the same model would return a data frame with:

- column "i": value in 1:5
- column "v": value in 1:10, or NA on rows where ".variable" is "a".
- column ".variable": value in c("a","b").
- column ".value": rvar containing draws from "a[i]" (when ".variable" is "a") or "b[i,v]" (when ".variable" is "b")

spread_rvars and gather_rvars can use type information applied to the model object by recover_types() to convert columns back into their original types. This is particularly helpful if some of the dimensions in your model were originally factors. For example, if the v dimension in the original data frame data was a factor with levels c("a","b","c"), then we could use recover_types before spread_rvars:

model %>%
  recover_types(data)
  spread_rvars(model, b[i,v])

Which would return the same data frame as above, except the "v" column would be a value in c("a","b","c") instead of 1:3.

For variables that do not share the same subscripts (or share some but not all subscripts), we can supply their specifications separately. For example, if we have a variable d[i] with the same i subscript as b[i,v], and a variable x with no subscripts, we could do this:

spread_rvars(model, x, d[i], b[i,v])

Which is roughly equivalent to this:

spread_rvars(model, x) %>%
  inner_join(spread_rvars(model, d[i])) %>%
  inner_join(spread_rvars(model, b[i,v]))

Similarly, this:

gather_rvars(model, x, d[i], b[i,v])

Is roughly equivalent to this:
bind_rows(
    gather_rvars(model, x),
    gather_rvars(model, d[i]),
    gather_rvars(model, b[i,v])
)

The `c` and `cbind` functions can be used to combine multiple variable names that have the same dimensions. For example, if we have several variables with the same subscripts `i` and `v`, we could do either of these:

```r
spread_rvars(model, c(w, x, y, z)[i,v])
spread_rvars(model, cbind(w, x, y, z)[i,v]) # equivalent
```

Each of which is roughly equivalent to this:

```r
spread_rvars(model, w[i,v], x[i,v], y[i,v], z[i,v])
```

Besides being more compact, the `c()`-style syntax is currently also slightly faster (though that may change).

Dimensions can be left nested in the resulting `rvar` objects by leaving their names blank; e.g. `spread_rvars(model, b[i,])` will place the first index (`i`) into rows of the data frame but leave the second index nested in the `b` column (see Examples below).

**Value**

A data frame.

**Author(s)**

Matthew Kay

**See Also**

`spread_draws()`, `recover_types()`, `compose_data()`. See also `posterior::rvar()` and `posterior::as_draws_rvars()` the functions that power `spread_rvars` and `gather_rvars`.

**Examples**

```r
library(dplyr)

data(RankCorr, package = "ggdist")

RankCorr %>%
    spread_rvars(b[i, j])

# leaving an index out nests the index in the column containing the rvar
RankCorr %>%


```r
spread_rvars(b[i, ])
RankCorr %>%
  spread_rvars(b[i, j], tau[i], u_tau[i])
```

# gather_rvars places variables and values in a longer format data frame

```r
RankCorr %>%
  gather_rvars(b[i, j], tau[i], typical_r)
```

---

### Description

Given a data frame such as might be returned by `tidy_draws()` or `spread_draws()`, gather variables and their values from that data frame into a "variable" and "value" column.

### Usage

```r
gather_variables(data, exclude = c(".chain", ".iteration", ".draw", ".row"))
```

### Arguments

- **data**
  A data frame with variable names spread across columns, such as one returned by `tidy_draws()` or `spread_draws()`.

- **exclude**
  A character vector of names of columns to be excluded from the gather. Default ignores several meta-data column names used in tidybayes.

### Details

This function gathers every column except grouping columns and those matching the expression exclude into key/value columns "variable" and "value".

Imagine a data frame `data` as returned by `spread_draws(fit, a[i], b[i,v]), like this:

- column ".chain": the chain number
- column ".iteration": the iteration number
- column ".draw": the draw number
- column "i": value in 1:5
- column "v": value in 1:10
- column "a": value of "a[i]" for draw number ".draw"
- column "b": value of "b[i,v]" for draw number ".draw"

`gather_variables(data)` on that data frame would return a grouped data frame (grouped by i and v), with:
gather_variables

- column ".chain": the chain number
- column ".iteration": the iteration number
- column ".draw": the draw number
- column "i": value in 1:5
- column "v": value in 1:10
- column ".variable": value in c("a", "b").
- column ".value": value of "a[i]" (when ".variable" is "a"); repeated for every value of "v" or "b[i,v]" (when ".variable" is "b") for draw number ".draw"

In this example, this call:

gather_variables(data)

Is roughly equivalent to:

data %>%
gather(.variable, .value, -c(.chain, .iteration, .draw, i, v)) %>%
group_by(.variable, .add = TRUE)

Value

A data frame.

Author(s)
Matthew Kay

See Also

spread_draws(), tidy_draws().

Examples

library(dplyr)

data(RankCorr, package = "ggdist")

RankCorr %>%
  spread_draws(b[i,v], tau[i]) %>%
  gather_variables() %>%
  median_qi()

# the first three lines below are roughly equivalent to ggmcnc::ggs(RankCorr)
RankCorr %>%
tidy_draws() %>%
gather_variables() %>%
median_qi()
get_variables

Get the names of the variables in a fitted Bayesian model

Description

Get a character vector of the names of the variables in a variety of fitted Bayesian model types. All models supported by tidy_draws() are supported.

Usage

get_variables(model)

## Default S3 method:
get_variables(model)

## S3 method for class 'mcmc'
get_variables(model)

## S3 method for class 'mcmc.list'
get_variables(model)

Arguments

model A supported Bayesian model fit. Tidybayes supports a variety of model objects; for a full list of supported models, see tidybayes-models.

Details

This function is often useful for inspecting a model interactively in order to construct calls to spread_draws() or gather_draws() in order to extract draws from models in a tidy format.

Value

A character vector of variable names in the fitted model.

Author(s)

Matthew Kay

See Also

spread_draws(), gather_draws().
Examples

```r
data(line, package = "coda")
get_variables(line)

data(RankCorr, package = "ggdist")
get_variables(RankCorr)
```

---

**nest_rvars**  
*Nest and unnest rvar columns in data frames*

---

**Description**

Converts between data-frame-of-`rvar`s format and long-data-frame-of-draws formats by nesting or unnesting all columns containing `posterior::rvar` objects.

**Usage**

```r
nest_rvars(data)
unnest_rvars(data)
```

**Arguments**

- **data**  
  A data frame to nest or unnest.
  - For `nest_rvars()`, the data frame should be in long-data-frame-of-draws format; i.e. it should contain a `.draw` column (and optionally `.chain` and `.iteration` columns) indexing draws. It should be a grouped by any columns that are not intended to be nested.
  - For `unnest_rvars()`, the data frame should have at least one column that is an `rvar`; all `rvar` columns will be unnested.

**Value**

For `nest_rvars()`, returns a data frame without `.chain`, `.iteration`, and `.draw` columns, where all non-grouped columns have been converted to `rvars`.

For `unnest_rvars()`, returns a data frame with `.chain`, `.iteration`, and `.draw` columns added, where every `rvar` column in the input has been converted to (one or more) columns containing draws from those `rvars` in long format. The result is grouped by all non-`rvar` columns in the input; this ensures that `nest_rvars(unnest_rvars(x))` returns `x`. 
Examples

```r
library(dplyr)

data(RankCorr, package = "ggdist")

# here's a data frame with some rvars
rvar_df = RankCorr %>%
  spread_rvars(b[i,], tau[i])
rvar_df

# we can unnest it into long format.
# note how the result is grouped by all non-rvar input columns,
# and nested indices in `b` are converted into columns.
draws_df = rvar_df %>%
  unnest_rvars()
draws_df

# calling nest_rvars() again on the result of unnest_rvars()
# recovers the original data frame
nest_rvars(draws_df)
```

---

**n_prefix**  
Prefix function generator for composing dimension index columns

**Description**

Generates a function for generating names of index columns for factors in `compose_data()` by prefixing a character vector to the original column name.

**Usage**

`n_prefix(prefix)`

**Arguments**

- `prefix`  
  Character vector to be prepended to column names by `compose_data()` to create index columns. Typically something like "n" (that is the default used in the `.n_name` argument of `compose_data()`).

  Returns a function. The function returned takes a character vector, `name` and returns `paste0(prefix,"_",name)`, unless `name` is empty, in which case it will return `prefix`.  

  `n_prefix("n")` is the default method that `compose_data()` uses to generate column names for variables storing the number of levels in a factor. Under this method, given a data frame `df` with a factor column "foo" containing 5 levels, the results of `compose_data(df)` will include an element named "n" (the result of `n_prefix("n")("")`) equal to the number of rows in `df` and an
element named "n_foo" (the result of n_prefix("n")("foo")) equal to the number of levels in df$foo.

See Also

The .n_name argument of compose_data().

Examples

library(magrittr)

df = data.frame(
  plot = factor(paste0("p", rep(1:8, times = 2))),
  site = factor(paste0("s", rep(1:4, each = 2, times = 2)))
)

# without changing `.n_name`, compose_data() will prefix indices
# with "n" by default
df %>%
  compose_data()

# you can use n_prefix() to define a different prefix (e.g. "N"):
df %>%
  compose_data(.n_name = n_prefix("N"))

---

**predict_curve**  
*Deprecated: Prediction curves for arbitrary functions of posteriors*

**Description**

Deprecated function for generating prediction curves (or a density for a prediction curve).

**Usage**

```r
predict_curve(data, formula, summary = median, ...)
predict_curve_density(
  data,
  formula,
  summary = function(...) density_bins(..., n = n),
  n = 50,
  ...
)
```
**Arguments**

- `data`: A data.frame, tbl_df or grouped_df representing posteriors from a Bayesian model as might be obtained through `spread_draws()`. Grouped data frames as returned by `group_by()` are supported.

- `formula`: A formula specifying the prediction curve. The left-hand side of the formula should be a name representing the name of the column that will hold the predicted response in the returned data frame. The right-hand side is an expression that may include numeric columns from `data` and variables passed into this function in `...`.

- `summary`: The function to apply to summarize each predicted response. Useful functions (if you just want a curve) might be `median()`, `mean()`, or `Mode()`. If you want predictive distribution at each point on the curve, try `density_bins()` or `histogram_bins()`.

- `...`: Variables defining the curve. The right-hand side of `formula` is evaluated for every combination of values of variables in `...`.

- `n`: For `predict_curve_density`, the number of bins to use to represent the distribution at each point on the curve.

**Details**

This function is deprecated. Use `modelr::data_grid()` combined with `point_interval()` or `dplyr::do()` and `density_bins()` instead.

The function generates a predictive curve given posterior draws (`data`), an expression (`formula`), and a set of variables defining the curve (`. ...`). For every group in `data` (if it is a grouped data frame—see `group_by()`; otherwise the entire data frame is taken at once), and for each combination of values in `. ...`, the right-hand side of `formula` is evaluated and its results passed to the `summary` function. This allows a predictive curve to be generated, given (e.g.) some samples of coefficients in `data` and a set of predictors defining the space of the curve in `. ...`.

Given a summary function like `median()` or `mean()`, this function will produce the median (resp. mean) prediction at each point on the curve.

Given a summary function like `density_bins()`, this function will produce a predictive distribution for each point on the curve. `predict_curve_density` is a shorthand for such a call, with a convenient argument for adjusting the number of bins per point on the curve.

**Value**

If `formula` is in the form `lhs ~ rhs` and `summary` is a function that returns a single value, such as `median` or `mode`, then `predict_curve` returns a data.frame with a column for each group in `data` (if it was grouped), a column for each variable in `. ...`, and a column named `lhs` with the value of `summary(rhs)` evaluated for every group in `data` and combination of variables in `. ...`.

If `summary` is a function that returns a data.frame, such as `density_bins()`, `predict_curve` has the same set of columns as above, except that in place of the `lhs` column is a set of columns named `lhs.x` for every column named `x` returned by `summary`. For example, `density_bins()` returns a data frame with the columns mid, lower, upper, and density, so the data frame returned by `predict_curve` with `summary = density_bins()` will have columns `lhs.mid`, `lhs.lower`, `lhs.upper`, and `lhs.density` in place of `lhs`. 
**Author(s)**
Matthew Kay

**See Also**
See `density_bins()`.

**Examples**

```r
# Deprecated; see examples for density_bins
```

---

**recover_types**

Decorate a model fit or sample with data types recovered from the input data

**Description**

Decorate a Bayesian model fit or a sample from it with types for variable and dimension data types. Meant to be used before calling `spread_draws()` or `gather_draws()` so that the values returned by those functions are translated back into useful data types.

**Usage**

```r
recover_types(model, ...)
```

**Arguments**

- `model` A supported Bayesian model fit. Tidybayes supports a variety of model objects; for a full list of supported models, see `tidybayes-models`.
- `...` Lists (or data frames) providing data prototypes used to convert columns returned by `spread_draws()` and `gather_draws()` back into useful data types. See Details.

**Details**

Each argument in ... specifies a list or data.frame. The model is decorated with a list of constructors that can convert a numeric column into the data types in the lists in ... Then, when `spread_draws()` or `gather_draws()` is called on the decorated model, each list entry with the same name as the variable or a dimension in `variable_spec` is a used as a prototype for that variable or dimension — i.e., its type is taken to be the expected type of that variable or dimension. Those types are used to translate numeric values of variables back into useful values (for example, levels of a factor).

The most common use of `recover_types` is to automatically translate dimensions of a variable that correspond to levels of a factor in the original data back into levels of that factor. The simplest way to do this is to pass in the data frame from which the original data came.

Supported types of prototypes are factor, ordered, and logical. For example:
• if `prototypes$v` is a factor, the v column in the returned draws is translated into a factor using `factor(v, labels=levels(prototypes$v), ordered=is.ordered(prototypes$v))`.
• if `prototypes$v` is a logical, the v column is translated into a logical using `as.logical(v)`.

Additional data types can be supported by providing a custom implementation of the generic function `as_constructor`.

### Value
A decorated version of `model`.

### Author(s)
Matthew Kay

### See Also
`spread_draws()`, `gather_draws()`, `compose_data()`.

### Examples

```r
library(dplyr)
library(magrittr)
library(rstan)

# Here's an example dataset with a categorical predictor ('condition') with several levels:
set.seed(5)
n = 10
n_condition = 5
ABC = tibble(
  condition = rep(c("A","B","C","D","E"), n),
  response = rnorm(n * 5, c(0,1,2,1,-1), 0.5)
)

# We'll fit the following model to it:
stan_code = "
data {
  int<lower=1> n;
  int<lower=1> n_condition;
  int<lower=1, upper=n_condition> condition[n];
  real response[n];
}
parameters {
  real overall_mean;
  vector[n_condition] condition_zoffset;
  real<lower=0> response_sd;
  real<lower=0> condition_mean_sd;
}
transformed parameters {
```
vector[n_condition] condition_mean;
  condition_mean = overall_mean + condition_zoffset * condition_mean_sd;
}
model {
  response_sd ~ cauchy(0, 1); // => half-cauchy(0, 1)
  condition_mean_sd ~ cauchy(0, 1); // => half-cauchy(0, 1)
  overall_mean ~ normal(0, 5);
  //=> condition_mean ~ normal(overall_mean, condition_mean_sd)
  condition_zoffset ~ normal(0, 1);
  for (i in 1:n) {
    response[i] ~ normal(condition_mean[condition[i]], response_sd);
  }
}

m = stan(model_code = stan_code, data = compose_data(ABC), control = list(adapt_delta=0.99),
  # 1 chain / few iterations just so example runs quickly
  # do not use in practice
  chains = 1, iter = 500)

# without using recover_types(), the `condition` column returned by spread_draws()
# will be an integer:
m %>%
spread_draws(condition_mean[condition]) %>%
median_qi()

# If we apply recover_types() first, subsequent calls to other tidybayes functions will
# automatically back-convert factors so that they are labeled with their original levels
# (assuming the same name is used)
m %>% recover_types(ABC)

# now the `condition` column with be a factor with levels "A", "B", "C", ...
m %>%
spread_draws(condition_mean[condition]) %>%
median_qi()

---

**sample_draws**

Sample draws from a tidy-format data frame of draws

**Description**

Given a tidy-format data frame of draws with a column indexing each draw, subsample the data frame to a given size based on a column indexing draws, ensuring that rows in sub-groups of a grouped data frame are sampled from the same draws.
Usage

sample_draws(data, ndraws, draw = ".draw", seed = NULL)

Arguments

data Data frame to sample from
ndraws The number of draws to return, or NULL to return all draws.
draw The name of the column indexing the draws; default ".draw".
seed A seed to use when subsampling draws (i.e. when ndraws is not NULL).

Details

sample_draws() makes it easier to sub-sample a grouped, tidy-format data frame of draws. On a grouped data frame, the naive approach of using filter with the .draw column will give incorrect results as it will select a different sample within each group. sample_draws() ensures the same sample is selected within each group.

Author(s)

Matthew Kay

Examples

library(ggplot2)
library(dplyr)
library(brms)
library(modelr)
theme_set(theme_light())

m_mpg = brm(mpg ~ hp * cyl, data = mtcars,
    # 1 chain / few iterations just so example runs quickly
    # do not use in practice
    chains = 1, iter = 500)

# draw 100 fit lines from the posterior and overplot them
mtcars %>%
    group_by(cyl) %>%
data_grid(hp = seq_range(hp, n = 101)) %>%
    add_epred_draws(m_mpg) %>%
    # NOTE: only use sample_draws here when making spaghetti plots; for
    # plotting intervals it is always best to use all draws
    sample_draws(100) %>%
ggplot(aes(x = hp, y = mpg, color = ordered(cyl))) +
ggplot2::geom_line(aes(y = .epred, group = paste(cyl, .draw)), alpha = 0.25) +
ggplot2::geom_point(data = mtcars)
summarise_draws.grouped_df

Summaries of draws in grouped_df objects

Description
An implementation of posterior::summarise_draws() for grouped data frames (dplyr::grouped_df objects) such as returned by dplyr::group_by() and the various grouped-data-aware functions in tidybayes, such as spread_draws(), gather_draws(), add_epred_draws(), and add_predicted_draws(). This function provides a quick way to get a variety of summary statistics and diagnostics on draws.

Usage
## S3 method for class 'grouped_df'
summarise_draws(.x, ...)

Arguments
.x
A grouped data frame (dplyr::grouped_df object) such as returned by dplyr::group_by() where the data frame in each group (ignoring grouping columns) has the structure of a posterior::draws_df() object: ".chain", ".iteration", and ".draw" columns, with the remaining (non-grouping) columns being draws from variables.

... Name-value pairs of summary or diagnostic functions. The provided names will be used as the names of the columns in the result unless the function returns a named vector, in which case the latter names are used. The functions can be specified in any format supported by as_function(). See Examples.

Details
While posterior::summarise_draws() can operate on tidy data frames of draws in the posterior::draws_df() format, that format does not support grouping columns. This provides an implementation of summarise_draws() that does support grouped data tables, essentially applying posterior::summarise_draws() to every sub-table of .x implied by the groups defined on the data frame.

See posterior::summarise_draws() for more details on the summary statistics and diagnostics you can use with this function. If you just want point summaries and intervals (not diagnostics), particularly for plotting, see point_interval(), which returns long-format data tables more suitable for that purpose (especially if you want to plot multiple uncertainty levels).

Value
A data frame (actually, a tibble) with all grouping columns from .x, a "variable" column containing variable names from .x, and the remaining columns containing summary statistics and diagnostics.
Author(s)

Matthew Kay

See Also

posterior::summarise_draws(), point_interval()

Examples

```r
library(posterior)
library(dplyr)

d = posterior::example_draws()

# The default posterior::summarise_draws() summarises all variables without
# splitting out indices:
summarise_draws(d)

# The grouped_df implementation of summarise_draws() in tidybayes can handle
# output from spread_draws(), which is a grouped data table with the indices
# (here, ‘i’) left as columns:
d %>%
  spread_draws(theta[i]) %>%
  summarise_draws()

# Summary functions can also be provided, as in posterior::summarise_draws():
d %>%
  spread_draws(theta[i]) %>%
  summarise_draws(median, mad, rhat, ess_tail)
```

Description

Deprecated functions, arguments, and column names and their alternatives are listed below. Many of the deprecations are due to a naming scheme overhaul in tidybayes version 1.0 (see Deprecated Functions and Deprecated Arguments and Column Names below) or due to the deprecation of horizontal shortcut geoms and stats in tidybayes 2.1 (see Deprecated Horizontal Shortcut Geoms and Stats).

Deprecated Functions

Several deprecated versions of functions use slightly different output formats (e.g., they use names like term and estimate where new functions use .variable and .value; or they set .iteration even when iteration information is not available — new functions always set .draw but may not set
.iteration), so be careful when upgrading to new function names. See Deprecation Arguments and Column Names, below, for more information.

Functions deprecated in tidybayes 3.0:

- fitted_draws and add_fitted_draws are deprecated because their names were confusing: it was unclear to many users if these functions returned draws from the posterior predictive, the mean of the posterior predictive, or the linear predictor (and depending on model type it might have been either of the latter). Use epred_draws()/add_epred_draws() if you want the expectation of the posterior predictive and use linpred_draws()/add_linpred_draws() if you want the linear predictor.

Functions deprecated in tidybayes 1.0:

- spread_samples, extract_samples, and tidy_samples are deprecated names for spread_draws(). The spread/gather terminology better distinguishes the resulting data frame format, and draws is more correct terminology than samples for describing multiple realizations from a posterior distribution.
- gather_samples is a deprecated name for gather_draws(), reflecting a package-wide move to using draws instead of samples for describing multiple realizations from a distribution.
- unspread_samples is a deprecated name for unspread_draws(), reflecting a package-wide move to using draws instead of samples for describing multiple realizations from a distribution.
- ungather_samples is a deprecated name for ungather_draws(), reflecting a package-wide move to using draws instead of samples for describing multiple realizations from a distribution.
- fitted_samples/add_fitted_samples are deprecated names for fitted_draws/add_fitted_draws, reflecting a package-wide move to using draws instead of samples for describing multiple realizations from a distribution. (though see the note above about the deprecation of fitted_draws in favor of epred_draws() and linpred_draws()).
- predicted_samples/add_predicted_samples are deprecated names for predicted_draws()/add_predicted_draws(), reflecting a package-wide move to using draws instead of samples for describing multiple realizations from a distribution.
- gather_lsmeans_samples and gather_emmeans_samples are deprecated aliases for gather_emmeans_draws(). The new name (estimated marginal means) is more appropriate for Bayesian models than the old name (least-squares means), and reflects the naming of the newer emmeans package. It also reflects a package-wide move to using draws instead of samples for describing multiple realizations from a distribution.
- as_sample_tibble and as_sample_data_frame are deprecated aliases for tidy_draws(). The original intent of as_sample_tibble was to be used primarily internally (hence its less user-friendly name); however, increasingly I have come across use cases of tidy_draws that warrant a more user-friendly name. It also reflects a package-wide move to using draws instead of samples for describing multiple realizations from a distribution.
- ggeye is deprecated: for a package whose goal is flexible and customizable visualization, monolithic functions are inflexible and do not sufficiently capitalize on users’ existing knowledge of ggplot; instead, I think it is more flexible to design geoms and stats that can used within a complete ggplot workflow. stat_eye() offers a horizontal eye plot geom that can be used instead of ggeye.
• See the sections below for additional deprecated functions, including horizontal geoms, stats, and point_intervals

Deprecated Eye Geom Spellings

gemue, gemeyeh, and gemeyehalfe are deprecated spellings of `stat_eye()` and `stat_halfeye()` from before name standardization of stats and geoms. Use those functions instead.

Deprecated Horizontal Shortcut Geoms and Stats

Due to the introduction of automatic orientation detection in tidybayes 2.1, shortcut geoms and stats (which end in h) are no longer necessary, and are deprecated. In most cases, these can simply be replaced with the same geom without the h suffix and they will remain horizontal; e.g. `stat_halfeye(...) can simply be replaced with `stat_halfeye(...). If automatic orientation detection fails, override it with the orientation parameter; e.g. `stat_halfeye(orientation = "horizontal")

These deprecated stats and geoms include:

• `stat_eyeh / stat_dist_eyeh`
• `stat_halfeyeh / stat_dist_halfeyeh`
• `geom_slabh / stat_slabh / stat_dist_slabh`
• `geom_intervalh / stat_intervalh / stat_dist_intervalh`
• `geom_pointintervalh / stat_pointintervalh / stat_dist_pointintervalh`
• `stat_gradientintervalh / stat_dist_gradientintervalh`
• `stat_cdfintervalh / stat_dist_cdfintervalh`
• `stat_ccdfintervalh / stat_dist_ccdfintervalh`
• `geom_dotsintervalh / stat_dotsintervalh / stat_dist_dotsintervalh`
• `stat_histintervalh`

Deprecated Horizontal Point/Interval Functions

These functions ending in h (e.g., `point_intervalh`, `median_qih`) used to be needed for use with `ggstance::stat_summaryh`, but are no longer necessary because `ggplot2::stat_summary()` supports automatic orientation detection, so they have been deprecated. They behave identically to the corresponding function without the h, except that when passed a vector, they return a data frame with x/xmin/xmax instead of y/ymin/ymax.

• `point_intervalh`
• `mean_qih / median_qih / mode_qih`
• `mean_hdie / median_hdie / mode_hdie`
• `mean_hdiecih / median_hdiecih / mode_hdiecih`
Deprecation of Arguments and Column Names

Arguments deprecated in tidybayes 3.0 are:

- The `n` argument is now called `ndraws` in `predicted_draws()`, `linpred_draws()`, etc. This prevents some bugs due to partial matching of argument names where `n` might be mistaken for `newdata`.
- The `value` argument in `linpred_draws()` is now spelled `linpred` and defaults to `".linpred"` in the same way that the `predicted_draws()` and `epred_draws()` functions work.
- The `scale` argument in `linpred_draws()` is no longer allowed (use `transform` instead) as this naming scheme only made sense when `linpred_draws()` was an alias for `fitted_draws()`, which it no longer is (see note above about the deprecation of `fitted_draws()`).

Versions of tidybayes before version 1.0 used a different naming scheme for several arguments and output columns.

Arguments and column names deprecated in tidybayes 1.0 are:

- `term` is now `.variable`
- `estimate` is now `.value`
- `pred` is now `.prediction`
- `conf.low` is now `.lower`
- `conf.high` is now `.upper`
- `.prob` is now `.width`
- The `.draw` column was added, and should be used instead of `.chain` and `.iteration` to uniquely identify draws when you do not care about chains. (.chain and .iteration are still provided for identifying draws within chains, if desired).

To translate to/from the old naming scheme in output, use `to_broom_names()` and `from_broom_names()`.

Many of these names were updated in version 1.0 in order to make terminology more consistent and in order to satisfy these criteria:

- Ignore compatibility with broom names on the assumption an adapter function can be created.
- Use names that could be compatible with frequentist approaches (hence `.width` instead of `.prob`).
- Always precede with "." to avoid collisions with variable names in models.
- No abbreviations (remembering if something is abbreviated or not can be a pain).
- No two-word names (multi-word names can always be standardized on and used in documentation, but I think data frame output should be succinct).
- Names should be nouns (I made an exception for lower/upper because they are common).

Author(s)

Matthew Kay
Description

Tidybayes supports two classes of models and sample formats: Models/formats that provide prediction functions, and those that do not.

All Supported Models/Sample Formats

All supported models/formats support the base tidybayes sample extraction functions, such as `tidy_draws()`, `spread_draws()`, `gather_draws()`, `spread_rvars()`, and `gather_rvars()`. These models/formats include:

- **rstan** models
- **cmdstanr** models
- **brms::brm()** models
- **rstanarm** models
- **runjags::runjags()** models
- **rjags::jags.model()** models, if sampled using **rjags::coda.samples()**
- **jagsUI::jags()** models
- **MCMCglmm::MCMCglmm()** models
- **coda::mcmc()** and **coda::mcmc.list()** objects, which are output by several model types.
- **posterior::draws** objects
- Any object with an implementation of **posterior::as_draws_df()** or **posterior::as_draws()**. For a list of those available in your environment, run `methods(as_draws_df)` or `methods(as_draws)`
- Any object with an implementation of **coda::as.mcmc.list()**. For a list of those available in your environment, run `methods(as.mcmc.list)`

If you install the **tidybayes.rethinking** package, models from the **rethinking** package are also supported.

Models Supporting Prediction

In addition, the following models support fit and prediction extraction functions, such as **add_epred_draws()**, **add_predicted_draws()**, **add_linpred_draws()**, **add_epred_rvars()**, **add_predicted_rvars()**, and **add_linpred_rvars()**:

- **brms::brm()** models
- **rstanarm** models
- any package with implementations of **rstantools::posterior_epred()**, **rstantools::posterior_predict()**, or **rstantools::posterior_linpred()** that include an argument called `newdata` which takes a data frame of predictors.
If your model type is not in the above list, you may still be able to use the \texttt{add_draws()} function to turn matrices of predictive draws (or fit draws) into tidy data frames. Or, you can wrap output from a prediction function in \texttt{posterior::rvar()} and add it to a data frame so long as that output is a matrix with draws as rows.

If you install the \texttt{tidybayes.rethinking} package, models from the \texttt{rethinking} package are also supported.

### Extending tidybayes

To include basic support for new models, one need only implement the \texttt{tidy_draws()} generic function for that model. Alternatively, objects that support \texttt{posterior::as_draws()} or \texttt{coda::as.mcmc.list()} will automatically be supported by \texttt{tidy_draws()}.

To include support for estimation and prediction, one must either implement the \texttt{epred_draws()}, \texttt{predicted_draws()}, and \texttt{linpred_draws()} functions or their correspond functions from \texttt{rstantools::posterior_epred()}, \texttt{rstantools::posterior_predict()}, and \texttt{rstantools::posterior_linpred()}. If you take the latter approach, you should include \texttt{newdata} and \texttt{n.draws} arguments that work as documented in \texttt{predicted_draws()}.

---

#### tidy_draws

Get a sample of posterior draws from a model as a tibble

**Description**

Extract draws from a Bayesian fit into a wide-format data frame with a .chain, .iteration, and .draw column, as well as all variables as columns. This function does not parse indices from variable names (e.g. for variable names like "x[1]"; see \texttt{spread_draws()} or \texttt{gather_draws()} for functions that parse variable indices.

**Usage**

\begin{verbatim}
tidy_draws(model, ...)  

## Default S3 method:  
tidy_draws(model, ...)  

## S3 method for class 'draws'  
tidy_draws(model, ...)  

## S3 method for class 'data.frame'  
tidy_draws(model, ...)  

## S3 method for class 'mcmc.list'  
tidy_draws(model, ...)  

## S3 method for class 'stanfit'  
tidy_draws(model, ...)  
\end{verbatim}
# tidy_draws

## S3 method for class 'stanreg'
tidy_draws(model, ...)

## S3 method for class 'runjags'
tidy_draws(model, ...)

## S3 method for class 'jagsUI'
tidy_draws(model, ...)

## S3 method for class 'brmsfit'
tidy_draws(model, ...)

## S3 method for class 'CmdStanFit'
tidy_draws(model, ...)

## S3 method for class 'CmdStanMCMC'
tidy_draws(model, ...)

## S3 method for class 'matrix'
tidy_draws(model, ...)

## S3 method for class 'MCMCglmm'
tidy_draws(model, ...)

### Arguments

- **model**
  - A supported Bayesian model fit. Tidybayes supports a variety of model objects; for a full list of supported models, see tidybayes-models.

- **...**
  - Further arguments passed to other methods (mostly unused).

### Details

This function can be useful for quick glances at models (especially combined with `gather_variables()` and `median_qi()`), and for models with parameters without indices in their names (like "x[1]"). `spread_draws()` and `gather_draws()`, which do parse variable name indices, call this function internally if their input is not already a tidy data frame.

To provide support for new models in tidybayes, you must provide an implementation of this function or an implementation of `coda::as.mcmc.list()` (tidy_draws should work on any model with an implementation of `coda::as.mcmc.list()`)

`tidy_draws()` can be applied to a data frame that is already a tidy-format data frame of draws, provided it has one row per draw. In other words, it can be applied to data frames that have the same format it returns, and it will return the same data frame back, while checking to ensure the `.chain`, `.iteration`, and `.draw` columns are all integers (converting if possible) and that the `.draw` column is unique. This allows you to pass already-tidy-format data frames into other tidybayes functions, like `spread_draws()` or `gather_draws()`. This functionality can be useful if the tidying step is expensive: you can tidy once, possibly subsetting to some particular variables of interest, then call
spread_draws() or gather_draws() repeatedly to extract variables and indices from the already-tidied data frame.

Value

A data frame (actually, a tibble) with a .chain column, .iteration column, .draw column, and one column for every variable in model.

Author(s)

Matthew Kay

See Also

spread_draws() or gather_draws(), which use this function internally and provides a friendly interface for extracting tidy data frames from model fits.

Examples

library(magrittr)
data(line, package = "coda")

line %>%
  tidy_draws()

---

ungather_draws

Turn tidy data frames of variables from a Bayesian model back into untidy data

Description

Inverse operations of spread_draws() and gather_draws(), giving results that look like tidy_draws().

Usage

ungather_draws(
data,
  ...,
  variable = ".variable",
  value = ".value",
  draw_indices = c(".chain", ".iteration", ".draw"),
  drop_indices = FALSE
)

unspread_draws(
data, 
..., 
draw_indices = c(".chain", ".iteration", ".draw"), 
drop_indices = FALSE
)

Arguments

data A tidy data frame of draws, such as one output by spread_draws or gather_draws.
...
Expressions in the form of variable_name[dimension_1,dimension_2,...]. See spread_draws().
variable The name of the column in data that contains the names of variables from the model.
value The name of the column in data that contains draws from the variables.
draw_indices Character vector of column names in data that should be treated as indices of draws. The default is c(".chain", ".iteration", ".draw"), which are the same names used for chain, iteration, and draw indices returned by spread_draws() or gather_draws().
drop_indices Drop the columns specified by draw_indices from the resulting data frame. Default FALSE.

Details

These functions take symbolic specifications of variable names and dimensions in the same format as spread_draws() and gather_draws() and invert the tidy data frame back into a data frame whose column names are variables with dimensions in them.

Value

A data frame.

Author(s)

Matthew Kay

See Also

spread_draws(), gather_draws(), tidy_draws().

Examples

library(dplyr)
data(RankCorr, package = "ggdist")

# We can use unspread_draws to allow us to manipulate draws with tidybayes
# and then transform the draws into a form we can use with packages like bayesplot.
# Here we subset b[i,j] to just values of i in 1:2 and j == 1, then plot with bayesplot
x_at_y

Generate lookup vectors for composing nested indices

Description
Generates a lookup vector such that x_at_y(x,y)[y] == x. Particularly useful for generating lookup tables for nested indices in conjunction with compose_data().

Usage
x_at_y(x, y, missing = NA)

Arguments
x        Values in the resulting lookup vector. There should be only one unique value of x for every corresponding value of y.
y        Keys in the resulting lookup vector. Should be factors or integers.
missing        Missing levels from y will be filled in with this value in the resulting lookup vector. Default NA.

Details
x_at_y(x,y) returns a vector k such that k[y] == x. It also fills in missing values in y: if y is an integer, k will contain entries for all values from 1 to max(y); if y is a factor, k will contain entries for all values from 1 to nlevels(y). Missing values are replaced with missing (default NA).

Author(s)
Matthew Kay

See Also
compose_data().

RankCorr %>%
  spread_draws(b[i,j]) %>%
  filter(i %in% 1:2, j == 1) %>%
  unspread_draws(b[i,j], drop_indices = TRUE) %>%
  bayesplot::mcmc_areas()

# As another example, we could use compare_levels to plot all pairwise comparisons
# of b[1,j] for j in 1:3
RankCorr %>%
  spread_draws(b[i,j]) %>%
  filter(i == 1, j %in% 1:3) %>%
  compare_levels(b, by = j) %>%
  unspread_draws(b[j], drop_indices = TRUE) %>%
  bayesplot::mcmc_areas()

x_at_y

Generate lookup vectors for composing nested indices

Description
Generates a lookup vector such that x_at_y(x,y)[y] == x. Particularly useful for generating lookup tables for nested indices in conjunction with compose_data().

Usage
x_at_y(x, y, missing = NA)

Arguments
x        Values in the resulting lookup vector. There should be only one unique value of x for every corresponding value of y.
y        Keys in the resulting lookup vector. Should be factors or integers.
missing        Missing levels from y will be filled in with this value in the resulting lookup vector. Default NA.

Details
x_at_y(x,y) returns a vector k such that k[y] == x. It also fills in missing values in y: if y is an integer, k will contain entries for all values from 1 to max(y); if y is a factor, k will contain entries for all values from 1 to nlevels(y). Missing values are replaced with missing (default NA).

Author(s)
Matthew Kay

See Also
compose_data().
Examples

library(magrittr)

df = data.frame(
    plot = factor(paste0("p", rep(1:8, times = 2))),
    site = factor(paste0("s", rep(1:4, each = 2, times = 2)))
)

# turns site into a nested index: site[p] gives the site for plot p
df %>%
    compose_data(site = x_at_y(site, plot))
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