

Package ‘broom’

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Type Package

Title Convert Statistical Analysis Objects into Tidy Tibbles

Version 0.5.1

Description Summarizes key information about statistical objects in tidy tibbles. This makes it easy to report results, create plots and consistently work with large numbers of models at once. Broom provides three verbs that each provide different types of information about a model. `tidy()` summarizes information about model components such as coefficients of a regression. `glance()` reports information about an entire model, such as goodness of fit measures like AIC and BIC. `augment()` adds information about individual observations to a dataset, such as fitted values or influence measures.

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URL <http://github.com/tidyverse/broom>

BugReports <http://github.com/tidyverse/broom/issues>

Depends R (>= 3.1)

Imports backports, dplyr, generics (>= 0.0.2), methods, nlme, purrr, reshape2, stringr, tibble, tidyr

Suggests AER, akima, AUC, bbmle, betareg, biglm, binGroup, boot, brms, btergm, car, caret, coda, covr, e1071, emmeans, ergm, gam (>= 1.15), gamlss, gamlss.data, gamlss.dist, geepack, ggplot2, glmnet, gmm, Hmisc, irlba, joineRML, Kendall, knitr, ks, Lahman, lavaan, lfe, lme4, lmodel2, lmtest, lsmeans, maps, mapprobs, MASS, Matrix, mclust, mgcv, muhaz, multcomp, network, nnet, orcutt (>= 2.2), ordinal, plm, plyr, poLCA, psych, quantreg, rgeos, rmarkdown, robust, rsample, rstan, rstanarm, sp, speedglm, statnet.common, survey, survival, testthat, tseries, xergm, zoo

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| | |
|-------------------|--|
| argument_glossary | <i>Allowed argument names in tidiers</i> |
|-------------------|--|

Description

Allowed argument names in tidiers

Usage

argument_glossary

Format

A tibble with 3 variables:

method One of "glance", "augment" or "tidy".

argument Character name of allowed argument name.

description Character description of argument use.

Examples

```
argument_glossary
```

| | |
|-----------------|---|
| augment.betareg | <i>Augment data with information from a(n) betareg object</i> |
|-----------------|---|

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to augment via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases augment tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'betareg'
augment(x, data = stats::model.frame(x),
        newdata = NULL, type.predict, type.residuals, ...)
```

Arguments

| | |
|-------------------|--|
| <code>x</code> | A betareg object produced by a call to <code>betareg::betareg()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. Augment will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |

| | |
|----------------|---|
| newdata | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create <code>x</code> . Defaults to <code>NULL</code> , indicating that nothing has been passed to <code>newdata</code> . If <code>newdata</code> is specified, the <code>data</code> argument will be ignored. |
| type.predict | Character indicating type of prediction to use. Passed to the <code>type</code> argument of the <code>stats::predict()</code> generic. Allowed arguments vary with model class, so be sure to read the <code>predict.my_class</code> documentation. |
| type.residuals | Character indicating type of residuals to use. Passed to the <code>type</code> argument of <code>stats::residuals()</code> generic. Allowed arguments vary with model class, so be sure to read the <code>residuals.my_class</code> documentation. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

`augment` returns the original data, along with new columns describing each observation:

| | |
|----------------------|---|
| <code>.fitted</code> | Fitted values of model |
| <code>.resid</code> | Residuals |
| <code>.cooks</code> | Cooks distance, <code>cooks.distance()</code> |

See Also

`augment()`, `betareg::betareg()`

| | |
|----------------------------|---|
| <code>augment.coxph</code> | <i>Augment data with information from a(n) coxph object</i> |
|----------------------------|---|

Description

`Augment` accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

`Augment` will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default data arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'coxph'
augment(x, data = NULL, newdata = NULL,
        type.predict = "lp", type.residuals = "martingale", ...)
```

Arguments

| | |
|-----------------------------|---|
| <code>x</code> | A <code>coxph</code> object returned from <code>survival::coxph()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. <code>augment</code> will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| <code>newdata</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create <code>x</code> . Defaults to <code>NULL</code> , indicating that nothing has been passed to <code>newdata</code> . If <code>newdata</code> is specified, the <code>data</code> argument will be ignored. |
| <code>type.predict</code> | Character indicating type of prediction to use. Passed to the <code>type</code> argument of the <code>stats::predict()</code> generic. Allowed arguments vary with model class, so be sure to read the <code>predict.my_class</code> documentation. |
| <code>type.residuals</code> | Character indicating type of residuals to use. Passed to the <code>type</code> argument of <code>stats::residuals()</code> generic. Allowed arguments vary with model class, so be sure to read the <code>residuals.my_class</code> documentation. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Details

When the modeling was performed with `na.action = "na.omit"` (as is the typical default), rows with NA in the initial data are omitted entirely from the augmented data frame. When the

modeling was performed with `na.action = "na.exclude"`, one should provide the original data as a second argument, at which point the augmented data will contain those rows (typically with NAs in place of the new columns). If the original data is not provided to `augment()` and `na.action = "na.exclude"`, a warning is raised and the incomplete rows are dropped.

Value

A `tibble::tibble` with the passed data and additional columns:

| | |
|----------------------|--|
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of fitted values |
| <code>.resid</code> | Residuals (not present if <code>newdata</code> specified.) |

See Also

[na.action](#)

[augment\(\)](#), [survival::coxph\(\)](#)

Other `coxph` tidiers: [glance.coxph](#), [tidy.coxph](#)

Other survival tidiers: [augment.survreg](#), [glance.aareg](#), [glance.cch](#), [glance.coxph](#), [glance.pyears](#), [glance.survdiff](#), [glance.survexp](#), [glance.survfit](#), [glance.survreg](#), [tidy.aareg](#), [tidy.cch](#), [tidy.coxph](#), [tidy.pyears](#), [tidy.survdiff](#), [tidy.survexp](#), [tidy.survfit](#), [tidy.survreg](#)

`augment.decomposed.ts` *Augment data with information from a(n) decomposed.ts object*

Description

`Augment` accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

`Augment` will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many `augment` methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model

formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'decomposed.ts'
augment(x, ...)
```

Arguments

| | |
|------------------|--|
| <code>x</code> | A <code>decomposed.ts</code> object returned from <code>stats::decompose()</code> . |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble` with one row for each observation in the original times series:

| | |
|-------------------------|--|
| <code>.seasonal</code> | The seasonal component of the decomposition. |
| <code>.trend</code> | The trend component of the decomposition. |
| <code>.remainder</code> | The remainder, or "random" component of the decomposition. |
| <code>.weight</code> | The final robust weights (stl only). |
| <code>.seasadj</code> | The seasonally adjusted (or "deseasonalised") series. |

See Also

`augment()`, `stats::decompose()`

Other decompose tidiers: `augment.stl`

Examples

```
# Time series of temperatures in Nottingham, 1920-1939:
nottem

# Perform seasonal decomposition on the data with both decompose
# and stl:
d1 <- stats::decompose(nottem)
d2 <- stats::stl(nottem, s.window = "periodic", robust = TRUE)
```

```

# Compare the original series to its decompositions.

cbind(broom::tidy(nottem), broom::augment(d1),
      broom::augment(d2))

# Visually compare seasonal decompositions in tidy data frames.

library(tibble)
library(dplyr)
library(tidyr)
library(ggplot2)

decomps <- tibble(
  # Turn the ts objects into data frames.
  series = list(as.data.frame(nottem), as.data.frame(nottem)),
  # Add the models in, one for each row.
  decomp = c("decompose", "stl"),
  model = list(d1, d2)
) %>%
  rowwise() %>%
  # Pull out the fitted data using broom::augment.
  mutate(augment = list(broom::augment(model))) %>%
  ungroup() %>%
  # Unnest the data frames into a tidy arrangement of
  # the series next to its seasonal decomposition, grouped
  # by the method (stl or decompose).
  group_by(decomp) %>%
  unnest(series, augment) %>%
  mutate(index = 1:n()) %>%
  ungroup() %>%
  select(decomp, index, x, adjusted = .seasadj)

ggplot(decomps) +
  geom_line(aes(x = index, y = x), colour = "black") +
  geom_line(aes(x = index, y = adjusted, colour = decomp,
               group = decomp))

```

 augment.factanal

Augment data with information from a(n) factanal object

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to augment via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object.

Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default data arguments, so that `augment(fit)` will return the augmented training data. In these cases augment tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'factanal'
augment(x, data, ...)
```

Arguments

| | |
|-------------------|---|
| <code>x</code> | A <code>factanal</code> object created by <code>stats::factanal()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. Augment will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

When `data` is not supplied `augment.factanal` returns one row for each observation, with a factor score column added for each factor `X`, (`.fsX`). This is because `factanal()`, unlike other stats methods like `lm()`, does not retain the original data.

When `data` is supplied, `augment.factanal` returns one row for each observation, with a factor score column added for each factor `X`, (`.fsX`).

See Also

[augment\(\)](#), [stats::factanal\(\)](#)

Other factanal tidiers: [glance.factanal](#), [tidy.factanal](#)

augment.felm

Augment data with information from a(n) felm object

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many `augment` methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'felm'
augment(x, data = NULL, ...)
```

Arguments

| | |
|-------------------|--|
| <code>x</code> | A <code>felm</code> object returned from <code>lfe::felm()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. Augment will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble()` containing the data passed to `augment`, and **additional** columns:

| | |
|----------------------|---|
| <code>.fitted</code> | The predicted response for that observation. |
| <code>.resid</code> | The residual for a particular point. Present only when data has been passed to <code>augment</code> via the <code>data</code> argument. |

See Also

`augment()`, `lfe::felm()`

Other `felm` tidiers: `tidy.felm`

augment.glm

Augment a(n) glm object

Description

This `augment` method wraps `augment.lm()`.

Usage

```
## S3 method for class 'glm'
augment(x, ...)
```

Arguments

| | |
|----------------|---|
| <code>x</code> | A <code>glm</code> object returned from <code>stats::glm()</code> . |
| ... | Arguments passed on to <code>augment.lm</code> |
| data | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. <code>Augment</code> will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| newdata | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create <code>x</code> . Defaults to <code>NULL</code> , indicating that nothing has been passed to <code>newdata</code> . If <code>newdata</code> is specified, the <code>data</code> argument will be ignored. |

type.predict Type of predictions to use when `x` is a `glm` object. Passed to `stats::predict.glm()`.

type.residuals Type of residuals to use when `x` is a `glm` object. Passed to `stats::residuals.glm()`.

x An `lm` object created by `stats::lm()`.

Value

When `newdata` is not supplied `augment.lm` returns one row for each observation, with seven columns added to the original data:

| | |
|-------------------------|--|
| <code>.hat</code> | Diagonal of the hat matrix |
| <code>.sigma</code> | Estimate of residual standard deviation when corresponding observation is dropped from model |
| <code>.cooks</code> | Cooks distance, <code>cooks.distance()</code> |
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of fitted values |
| <code>.resid</code> | Residuals |
| <code>.std.resid</code> | Standardised residuals |

Some unusual `lm` objects, such as `r1m` from MASS, may omit `.cooks` and `.std.resid`. `gam` from `mgcv` omits `.sigma`.

When `newdata` is supplied, returns one row for each observation, with three columns added to the new data:

| | |
|----------------------|--|
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of fitted values |
| <code>.resid</code> | Residuals of fitted values on the new data |

See Also

`augment()`, `augment.lm()`

`stats::glm()`

Other `lm` tidiers: `augment.lm`, `glance.glm`, `glance.lm`, `tidy.glm`, `tidy.lm`

| | |
|----------------|-----------------------------------|
| augment.glmRob | <i>Augment a(n) glmRob object</i> |
|----------------|-----------------------------------|

Description

This augment method wraps [augment.lm\(\)](#).

Usage

```
## S3 method for class 'glmRob'
augment(x, ...)
```

Arguments

| | |
|-----------------------|--|
| x | A glmRob object returned from robust::glmRob() . |
| ... | Arguments passed on to augment.lm |
| data | A data.frame() or tibble::tibble() containing the original data that was used to produce the object x. Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the data argument. Augment will report information such as influence and cooks distance for data passed to the data argument. These measures are only defined for the original training data. |
| newdata | A data.frame() or tibble::tibble() containing all the original predictors used to create x. Defaults to NULL, indicating that nothing has been passed to newdata. If newdata is specified, the data argument will be ignored. |
| type.predict | Type of predictions to use when x is a glm object. Passed to stats::predict.glm() . |
| type.residuals | Type of residuals to use when x is a glm object. Passed to stats::residuals.glm() . |
| x | An lm object created by stats::lm() . |

Details

For tidiers for robust models from the MASS package see [tidy.rlm\(\)](#).

Value

When newdata is not supplied `augment.lm` returns one row for each observation, with seven columns added to the original data:

| | |
|--------|--|
| .hat | Diagonal of the hat matrix |
| .sigma | Estimate of residual standard deviation when corresponding observation is dropped from model |
| .cooks | Cooks distance, cooks.distance() |

| | |
|-------------------------|----------------------------------|
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of fitted values |
| <code>.resid</code> | Residuals |
| <code>.std.resid</code> | Standardised residuals |

Some unusual `lm` objects, such as `rlm` from MASS, may omit `.cooks` and `.std.resid`. `gam` from `mgcv` omits `.sigma`.

When `newdata` is supplied, returns one row for each observation, with three columns added to the new data:

| | |
|----------------------|--|
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of fitted values |
| <code>.resid</code> | Residuals of fitted values on the new data |

See Also

[augment\(\)](#), [augment.lm\(\)](#)

[robust::glmRob\(\)](#)

Other robust tidiers: [augment.lmRob](#), [glance.glmRob](#), [glance.lmRob](#), [tidy.glmRob](#), [tidy.lmRob](#)

`augment.htest`

Augment data with information from a(n) htest object

Description

`augment` accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

`augment` will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many `augment` methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a [tibble::tibble](#) with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that [splines::ns\(\)](#), [stats::poly\(\)](#) and

`survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'htest'
augment(x, ...)
```

Arguments

`x` An `htest` objected, such as those created by `stats::cor.test()`, `stats::t.test()`, `stats::wilcox.test()`, `stats::chisq.test()`, etc.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Details

See `stats::chisq.test()` for more details on how residuals are computed.

Value

Errors unless `x` is a chi-squared test. If `x` is a chi-squared test, for each cell of the tested table returns columns:

| | |
|-------------------------|---|
| <code>.observed</code> | Observed count |
| <code>.prop</code> | Proportion of the total |
| <code>.row.prop</code> | Row proportion (2 dimensions table only) |
| <code>.col.prop</code> | Column proportion (2 dimensions table only) |
| <code>.expected</code> | Expected count under the null hypothesis |
| <code>.residuals</code> | Pearson residual |
| <code>.stdres</code> | Standardized residual |

See Also

`augment()`, `stats::chisq.test()`

Other `htest` tidiers: `tidy.htest`, `tidy.pairwise.htest`, `tidy.power.htest`

augment.ivreg

Augment data with information from a(n) ivreg object

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to augment via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default data arguments, so that `augment(fit)` will return the augmented training data. In these cases augment tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'ivreg'
augment(x, data = model.frame(x), newdata, ...)
```

Arguments

| | |
|----------------------|--|
| <code>x</code> | An ivreg object created by a call to <code>AER::ivreg()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. Augment will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| <code>newdata</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create <code>x</code> . Defaults to <code>NULL</code> , indicating that nothing has been passed to <code>newdata</code> . If <code>newdata</code> is specified, the <code>data</code> argument will be ignored. |

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble()` containing the data passed to `augment`, and **additional** columns:

| | |
|----------------------|---|
| <code>.fitted</code> | The predicted response for that observation. |
| <code>.resid</code> | The residual for a particular point. Present only when data has been passed to <code>augment</code> via the <code>data</code> argument. |

See Also

`augment()`, `AER::ivreg()`

Other ivreg tidiers: `glance.ivreg`, `tidy.ivreg`

Examples

```
library(AER)

data("CigarettesSW", package = "AER")
ivr <- ivreg(
  log(packs) ~ income | population,
  data = CigarettesSW,
  subset = year == "1995"
)

summary(ivr)

tidy(ivr)
tidy(ivr, conf.int = TRUE)
tidy(ivr, conf.int = TRUE, exponentiate = TRUE)

augment(ivr)

glance(ivr)
```

augment.kmeans

Augment data with information from a(n) kmeans object

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to augment via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default data arguments, so that `augment(fit)` will return the augmented training data. In these cases augment tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'kmeans'
augment(x, data, ...)
```

Arguments

| | |
|-------------------|--|
| <code>x</code> | A kmeans object created by <code>stats::kmeans()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. Augment will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be |

used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

The original data as a `tibble::tibble` with one extra column:

`.cluster` The cluster assigned by the k-means algorithm

See Also

`augment()`, `stats::kmeans()`

Other kmeans tidiers: `glance.kmeans`, `tidy.kmeans`

`augment.lm`

Augment data with information from a(n) lm object

Description

`Augment` accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

`Augment` will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many `augment` methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'lm'
augment(x, data = stats::model.frame(x), newdata,
        type.predict, type.residuals, ...)
```

Arguments

| | |
|----------------|---|
| x | An lm object created by <code>stats::lm()</code> . |
| data | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object x. Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the data argument. Augment will report information such as influence and cooks distance for data passed to the data argument. These measures are only defined for the original training data. |
| newdata | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create x. Defaults to NULL, indicating that nothing has been passed to newdata. If newdata is specified, the data argument will be ignored. |
| type.predict | Type of predictions to use when x is a glm object. Passed to <code>stats::predict.glm()</code> . |
| type.residuals | Type of residuals to use when x is a glm object. Passed to <code>stats::residuals.glm()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a newdata argument, it will use the default value for the data argument. |

Details

When the modeling was performed with `na.action = "na.omit"` (as is the typical default), rows with NA in the initial data are omitted entirely from the augmented data frame. When the modeling was performed with `na.action = "na.exclude"`, one should provide the original data as a second argument, at which point the augmented data will contain those rows (typically with NAs in place of the new columns). If the original data is not provided to `augment()` and `na.action = "na.exclude"`, a warning is raised and the incomplete rows are dropped.

Value

When newdata is not supplied `augment.lm` returns one row for each observation, with seven columns added to the original data:

| | |
|----------------------|--|
| <code>.hat</code> | Diagonal of the hat matrix |
| <code>.sigma</code> | Estimate of residual standard deviation when corresponding observation is dropped from model |
| <code>.cooks</code> | Cooks distance, <code>cooks.distance()</code> |
| <code>.fitted</code> | Fitted values of model |

| | |
|------------|----------------------------------|
| .se.fit | Standard errors of fitted values |
| .resid | Residuals |
| .std.resid | Standardised residuals |

Some unusual `lm` objects, such as `rlm` from MASS, may omit `.cooks` and `.std.resid`. `gam` from `mgcv` omits `.sigma`.

When `newdata` is supplied, returns one row for each observation, with three columns added to the new data:

| | |
|---------|--|
| .fitted | Fitted values of model |
| .se.fit | Standard errors of fitted values |
| .resid | Residuals of fitted values on the new data |

See Also

[na.action](#)

[augment\(\)](#), [stats::predict.lm\(\)](#)

Other `lm` tidiers: [augment.glm](#), [glance.glm](#), [glance.lm](#), [tidy.glm](#), [tidy.lm](#)

| | |
|----------------------------|----------------------------------|
| <code>augment.lmRob</code> | <i>Augment a(n) lmRob object</i> |
|----------------------------|----------------------------------|

Description

This `augment` method wraps [augment.lm\(\)](#).

Usage

```
## S3 method for class 'lmRob'
augment(x, ...)
```

Arguments

| | |
|------------------|---|
| <code>x</code> | A <code>lmRob</code> object returned from robust::lmRob() . |
| <code>...</code> | Arguments passed on to <code>augment.lm</code> |

data A [data.frame\(\)](#) or [tibble::tibble\(\)](#) containing the original data that was used to produce the object `x`. Defaults to `stats::model.frame(x)` so that `augment(my_fit)` returns the augmented original data. **Do not** pass new data to the `data` argument. `Augment` will report information such as influence and cooks distance for data passed to the `data` argument. These measures are only defined for the original training data.

newdata A [data.frame\(\)](#) or [tibble::tibble\(\)](#) containing all the original predictors used to create `x`. Defaults to `NULL`, indicating that nothing has been passed to `newdata`. If `newdata` is specified, the `data` argument will be ignored.

type.predict Type of predictions to use when `x` is a `glm` object. Passed to `stats::predict.glm()`.

type.residuals Type of residuals to use when `x` is a `glm` object. Passed to `stats::residuals.glm()`.

x An `lm` object created by `stats::lm()`.

Details

For tidiers for robust models from the **MASS** package see `tidy.rlm()`.

Value

When `newdata` is not supplied `augment.lm` returns one row for each observation, with seven columns added to the original data:

| | |
|-------------------------|--|
| <code>.hat</code> | Diagonal of the hat matrix |
| <code>.sigma</code> | Estimate of residual standard deviation when corresponding observation is dropped from model |
| <code>.cooks</code> | Cooks distance, <code>cooks.distance()</code> |
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of fitted values |
| <code>.resid</code> | Residuals |
| <code>.std.resid</code> | Standardised residuals |

Some unusual `lm` objects, such as `rlm` from **MASS**, may omit `.cooks` and `.std.resid`. `gam` from **mgcv** omits `.sigma`.

When `newdata` is supplied, returns one row for each observation, with three columns added to the new data:

| | |
|----------------------|--|
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of fitted values |
| <code>.resid</code> | Residuals of fitted values on the new data |

See Also

`augment()`, `augment.lm()`

`robust::lmRob()`

Other robust tidiers: `augment.glmRob`, `glance.glmRob`, `glance.lmRob`, `tidy.glmRob`, `tidy.lmRob`

| | |
|---------------|-------------------------------|
| augment.loess | <i>Tidy a(n) loess object</i> |
|---------------|-------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'loess'
augment(x, data = stats::model.frame(x), newdata, ...)
```

Arguments

| | |
|---------|--|
| x | A loess objects returned by <code>stats::loess()</code> . |
| data | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object x. Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the data argument. Augment will report information such as influence and cooks distance for data passed to the data argument. These measures are only defined for the original training data. |
| newdata | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create x. Defaults to NULL, indicating that nothing has been passed to newdata. If newdata is specified, the data argument will be ignored. |
| ... | Arguments passed on to <code>stats::predict.loess</code> |

object an object fitted by loess.

newdata an optional data frame in which to look for variables with which to predict, or a matrix or vector containing exactly the variables needs for prediction. If missing, the original data points are used.

se should standard errors be computed?

na.action function determining what should be done with missing values in data frame newdata. The default is to predict NA.

Details

When the modeling was performed with `na.action = "na.omit"` (as is the typical default), rows with NA in the initial data are omitted entirely from the augmented data frame. When the modeling was performed with `na.action = "na.exclude"`, one should provide the original data as a second argument, at which point the augmented data will contain those rows (typically with NAs in place of the new columns). If the original data is not provided to `augment()` and `na.action = "na.exclude"`, a warning is raised and the incomplete rows are dropped.

Value

When `newdata` is not supplied `augment.loess` returns one row for each observation with three columns added to the original data:

| | |
|----------------------|--------------------------------------|
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of the fitted values |
| <code>.resid</code> | Residuals of the fitted values |

When `newdata` is supplied `augment.loess` returns one row for each observation with one additional column:

| | |
|----------------------|--------------------------------------|
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of the fitted values |

See Also

[na.action](#)

`augment()`, `stats::loess()`, `stats::predict.loess()`

Examples

```
lo <- loess(mpg ~ wt, mtcars)
augment(lo)

# with all columns of original data
augment(lo, mtcars)

# with a new dataset
augment(lo, newdata = head(mtcars))
```

augment.Mclust

Augment data with information from a(n) Mclust object

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether data or newdata is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default data arguments, so that `augment(fit)` will return the augmented training data. In these cases augment tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'Mclust'
augment(x, data, ...)
```

Arguments

| | |
|-------------------|---|
| <code>x</code> | An Mclust object return from <code>mclust::Mclust()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. Augment will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble` of the original data with two extra columns:

| | |
|---------------------------|--|
| <code>.class</code> | The class assigned by the Mclust algorithm |
| <code>.uncertainty</code> | The uncertainty associated with the classification. If a point has a probability of 0.9 of being in its assigned class under the model, then the uncertainty is 0.1. |

See Also

`augment()`, `mclust::Mclust()`

Other mclust tidiers: `tidy.Mclust`

augment.mjoint *Augment data with information from a(n) mjoint object*

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many `augment` methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'mjoint'
augment(x, data = x$data, ...)
```

Arguments

`x` An `mjoint` object returned from `joineRML::mjoint()`.

`data` A `data.frame()` or `tibble::tibble()` containing the original data that was used to produce the object `x`. Defaults to `stats::model.frame(x)` so that `augment(my_fit)` returns the augmented original data. **Do not** pass new data to the `data` argument. Augment will report information such as influence and cooks distance for data passed to the `data` argument. These measures are only defined for the original training data.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Details

See `joineRML::fitted.mjoint()` and `joineRML::residuals.mjoint()` for more information on the difference between population-level and individual-level fitted values and residuals.

If fitting a joint model with a single longitudinal process, make sure you are using a named list to define the formula for the fixed and random effects of the longitudinal submodel.

Value

A `tibble::tibble()` with one row for each original observation with addition columns:

| | |
|--------------------------|---|
| <code>.fitted_j_0</code> | population-level fitted values for the j-th longitudinal process |
| <code>.fitted_j_1</code> | individuals-level fitted values for the j-th longitudinal process |
| <code>.resid_j_0</code> | population-level residuals for the j-th longitudinal process |
| <code>.resid_j_1</code> | individual-level residuals for the j-th longitudinal process |

| | |
|---------------------------|------------------------------|
| <code>augment.nlrq</code> | <i>Tidy a(n) nlrq object</i> |
|---------------------------|------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'nlrq'
augment(x, ...)
```

Arguments

| | |
|----------------|--|
| <code>x</code> | A <code>nlrq</code> object returned from <code>quantreg::nlrq()</code> . |
| ... | Arguments passed on to <code>augment.nls</code> |

- data** A `data.frame()` or `tibble::tibble()` containing the original data that was used to produce the object `x`. Defaults to `stats::model.frame(x)` so that `augment(my_fit)` returns the augmented original data. **Do not** pass new data to the `data` argument. Augment will report information such as influence and cooks distance for data passed to the `data` argument. These measures are only defined for the original training data.
- newdata** A `data.frame()` or `tibble::tibble()` containing all the original predictors used to create `x`. Defaults to `NULL`, indicating that nothing has been passed to `newdata`. If `newdata` is specified, the `data` argument will be ignored.
- x** An `nls` object returned from `stats::nls()`.

Value

A `tibble::tibble()` containing the data passed to `augment`, and **additional** columns:

| | |
|----------------------|---|
| <code>.fitted</code> | The predicted response for that observation. |
| <code>.resid</code> | The residual for a particular point. Present only when data has been passed to <code>augment</code> via the <code>data</code> argument. |

See Also

`augment()`, `quantreg::nlrq()`

Other `quantreg` tidiers: `augment.rqs`, `augment.rq`, `glance.nlrq`, `glance.rq`, `tidy.nlrq`, `tidy.rqs`, `tidy.rq`

augment.nls

Augment data with information from a(n) nls object

Description

`Augment` accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

`Augment` will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many `augment` methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'nls'
augment(x, data = NULL, newdata = NULL, ...)
```

Arguments

| | |
|----------------------|---|
| <code>x</code> | An <code>nls</code> object returned from <code>stats::nls()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. Augment will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| <code>newdata</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create <code>x</code> . Defaults to <code>NULL</code> , indicating that nothing has been passed to <code>newdata</code> . If <code>newdata</code> is specified, the <code>data</code> argument will be ignored. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble()` containing the data passed to `augment`, and **additional** columns:

| | |
|----------------------|---|
| <code>.fitted</code> | The predicted response for that observation. |
| <code>.resid</code> | The residual for a particular point. Present only when data has been passed to <code>augment</code> via the <code>data</code> argument. |

See Also

`tidy`, `stats::nls()`, `stats::predict.nls()`

Other `nls` tidiers: `glance.nls`, `tidy.nls`

augment.plm

Augment data with information from a(n) plm object

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to augment via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases augment tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'plm'
augment(x, data = model.frame(x), ...)
```

Arguments

| | |
|-------------------|--|
| <code>x</code> | A <code>plm</code> object returned by <code>plm::plm()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. Augment will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be |

used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble()` containing the data passed to `augment`, and **additional** columns:

| | |
|----------------------|---|
| <code>.fitted</code> | The predicted response for that observation. |
| <code>.resid</code> | The residual for a particular point. Present only when data has been passed to <code>augment</code> via the <code>data</code> argument. |

See Also

`augment()`, `plm::plm()`

Other plm tidiers: `glance.plm`, `tidy.plm`

augment.poLCA

Augment data with information from a(n) poLCA object

Description

`Augment` accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

`Augment` will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many `augment` methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'poLCA'
augment(x, data = NULL, ...)
```

Arguments

`x` A poLCA object returned from `poLCA::poLCA()`.

`data` The original dataset used to fit the latent class model, as a tibble or data. If not given, uses manifest variables in `x$y` and, if applicable, covariates in `x$x`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with one row for each original observation, with additional columns:

| | |
|---------------------------|--|
| <code>.class</code> | Predicted class, using modal assignment |
| <code>.probability</code> | Posterior probability of predicted class |

If the `data` argument is given, those columns are included in the output (only rows for which predictions could be made). Otherwise, the `y` element of the poLCA object, which contains the manifest variables used to fit the model, are used, along with any covariates, if present, in `x`.

Note that while the probability of all the classes (not just the predicted modal class) can be found in the posterior element, these are not included in the augmented output.

See Also

`augment()`, `poLCA::poLCA()`

Other poLCA tidiers: `glance.poLCA`, `tidy.poLCA`

`augment.prcomp`

Augment data with information from a(n) prcomp object

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object.

Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'pcomp'
augment(x, data = NULL, newdata, ...)
```

Arguments

| | |
|----------------------|---|
| <code>x</code> | A <code>pcomp</code> object returned by <code>stats::pcomp()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. Augment will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| <code>newdata</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create <code>x</code> . Defaults to <code>NULL</code> , indicating that nothing has been passed to <code>newdata</code> . If <code>newdata</code> is specified, the <code>data</code> argument will be ignored. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble` containing the original data along with additional columns containing each observation's projection into PCA space.

See Also

[stats::prcomp\(\)](#), [svd_tidiers](#)

Other svd tidiers: [tidy.prcomp](#), [tidy_irlba](#), [tidy_svd](#)

augment.rlm

Augment a(n) rlm object

Description

This augment method wraps [augment.lm\(\)](#).

Usage

```
## S3 method for class 'rlm'
augment(x, ...)
```

Arguments

x An rlm object returned by [MASS::rlm\(\)](#).

... Arguments passed on to [augment.lm](#)

data A [data.frame\(\)](#) or [tibble::tibble\(\)](#) containing the original data that was used to produce the object x. Defaults to [stats::model.frame\(x\)](#) so that [augment\(my_fit\)](#) returns the augmented original data. **Do not** pass new data to the data argument. Augment will report information such as influence and cooks distance for data passed to the data argument. These measures are only defined for the original training data.

newdata A [data.frame\(\)](#) or [tibble::tibble\(\)](#) containing all the original predictors used to create x. Defaults to NULL, indicating that nothing has been passed to newdata. If newdata is specified, the data argument will be ignored.

type.predict Type of predictions to use when x is a glm object. Passed to [stats::predict.glm\(\)](#).

type.residuals Type of residuals to use when x is a glm object. Passed to [stats::residuals.glm\(\)](#).

x An lm object created by [stats::lm\(\)](#).

Details

For tidiers for models from the **robust** package see [tidy.lmRob\(\)](#) and [tidy.glmRob\(\)](#).

Value

When `newdata` is not supplied `augment.lm` returns one row for each observation, with seven columns added to the original data:

| | |
|-------------------------|--|
| <code>.hat</code> | Diagonal of the hat matrix |
| <code>.sigma</code> | Estimate of residual standard deviation when corresponding observation is dropped from model |
| <code>.cooks</code> | Cooks distance, <code>cooks.distance()</code> |
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of fitted values |
| <code>.resid</code> | Residuals |
| <code>.std.resid</code> | Standardised residuals |

Some unusual `lm` objects, such as `rlm` from MASS, may omit `.cooks` and `.std.resid`. `gam` from `mgcv` omits `.sigma`.

When `newdata` is supplied, returns one row for each observation, with three columns added to the new data:

| | |
|----------------------|--|
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of fitted values |
| <code>.resid</code> | Residuals of fitted values on the new data |

See Also

[augment\(\)](#), [augment.lm\(\)](#)

[MASS::rlm\(\)](#)

Other `rlm` tidiers: [glance.rlm](#), [tidy.rlm](#)

`augment.rq`

Augment data with information from a(n) rq object

Description

`Augment` accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

`Augment` will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default data arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'rq'
augment(x, data = model.frame(x), newdata = NULL, ...)
```

Arguments

| | |
|----------------------|---|
| <code>x</code> | An <code>rq</code> object returned from <code>quantreg::rq()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. <code>augment</code> will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| <code>newdata</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create <code>x</code> . Defaults to <code>NULL</code> , indicating that nothing has been passed to <code>newdata</code> . If <code>newdata</code> is specified, the <code>data</code> argument will be ignored. |
| <code>...</code> | Arguments passed on to <code>quantreg::predict.rq</code> |

object object of class `rq` or `rqs` or `rq.process` produced by `rq`

newdata An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.

interval type of interval desired: default is 'none', when set to 'confidence' the function returns a matrix predictions with point predictions for each of the 'newdata' points as well as lower and upper confidence limits.

level coverage probability for the 'confidence' intervals.

type For `predict.rq`, the method for 'confidence' intervals, if desired. If 'percentile' then one of the bootstrap methods is used to generate percentile intervals for each prediction, if 'direct' then a version of the Portnoy and Zhou (1998) method is used, and otherwise an estimated covariance matrix for the parameter estimates is used. Further arguments to determine the choice of bootstrap method or covariance matrix estimate can be passed via the `...` argument. For `predict.rqs` and `predict.rq.process` when `stepfun = TRUE`, `type` is "Qhat", "Fhat" or "fhat" depending on whether the user would like to have estimates of the conditional quantile, distribution or density functions respectively. As noted below the two former

estimates can be monotonized with the function `rearrange`. When the "fhat" option is invoked, a list of conditional density functions is returned based on Silverman's adaptive kernel method as implemented in `akj` and `approxfun`.

na.action function determining what should be done with missing values in 'newdata'. The default is to predict 'NA'.

Value

A `tibble::tibble` with one row per observation and columns:

| | |
|----------------------|-------------------------------|
| <code>.resid</code> | Residuals |
| <code>.fitted</code> | Fitted quantiles of the model |
| <code>.tau</code> | Quantile estimated |

Depending on the arguments passed on to `predict.rq` via `...`, a confidence interval is also calculated on the fitted values resulting in columns:

| | |
|-------------------------|---------------------------------|
| <code>.conf.low</code> | Lower confidence interval value |
| <code>.conf.high</code> | Upper confidence interval value |

`predict.rq` does not provide confidence intervals when `newdata` is provided.

See Also

`augment`, `quantreg::rq()`, `quantreg::predict.rq()`

Other `quantreg` tidiers: `augment.nlrq`, `augment.rqs`, `glance.nlrq`, `glance.rq`, `tidy.nlrq`, `tidy.rqs`, `tidy.rq`

`augment.rqs`

Augment data with information from a(n) rqs object

Description

`Augment` accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

`Augment` will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default data arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'rqs'
augment(x, data = model.frame(x), newdata, ...)
```

Arguments

| | |
|----------------------|--|
| <code>x</code> | An <code>rqs</code> object returned from <code>quantreg::rq()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. <code>Augment</code> will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |
| <code>newdata</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create <code>x</code> . Defaults to <code>NULL</code> , indicating that nothing has been passed to <code>newdata</code> . If <code>newdata</code> is specified, the <code>data</code> argument will be ignored. |
| <code>...</code> | Arguments passed on to <code>quantreg::predict.rqs</code> object object of class <code>rq</code> or <code>rqs</code> or <code>rq.process</code> produced by <code>rq</code> newdata An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used. type For <code>predict.rq</code> , the method for 'confidence' intervals, if desired. If 'percentile' then one of the bootstrap methods is used to generate percentile intervals for each prediction, if 'direct' then a version of the Portnoy and Zhou (1998) method is used, and otherwise an estimated covariance matrix for the parameter estimates is used. Further arguments to determine the choice of bootstrap method or covariance matrix estimate can be passed via the <code>...</code> argument. For <code>predict.rqs</code> and <code>predict.rq.process</code> when <code>stepfun = TRUE</code> , <code>type</code> is "Qhat", "Fhat" or "fhat" depending on whether the user would like to have estimates of the conditional quantile, distribution or density functions respectively. As noted below the two former estimates can be monotonized with the function <code>rearrange</code> . When the "fhat" option is invoked, a list of conditional density functions is returned based on Silverman's adaptive kernel method as implemented in <code>akj</code> and <code>approxfun</code> . |

stepfun If 'TRUE' return stepfunctions otherwise return matrix of predictions. these functions can be estimates of either the conditional quantile or distribution functions depending upon the type argument. When stepfun = FALSE a matrix of point estimates of the conditional quantile function at the points specified by the newdata argument.

na.action function determining what should be done with missing values in 'newdata'. The default is to predict 'NA'.

Value

A `tibble::tibble` with one row per obseration and columns:

| | |
|----------------------|-------------------------------|
| <code>.resid</code> | Residuals |
| <code>.fitted</code> | Fitted quantiles of the model |
| <code>.tau</code> | Quantile estimated |

Depending on the arguments passed on to `predict.rqs` via `...`, a confidence interval is also calculated on the fitted values resulting in columns:

| | |
|-------------------------|---------------------------------|
| <code>.conf.low</code> | Lower confidence interval value |
| <code>.conf.high</code> | Upper confidence interval value |

`predict.rqs` does not provide confidence intervals when `newdata` is provided.

See Also

`augment`, `quantreg::rq()`, `quantreg::predict.rqs()`

Other `quantreg` tidiers: `augment.nlrq`, `augment.rq`, `glance.nlrq`, `glance.rq`, `tidy.nlrq`, `tidy.rqs`, `tidy.rq`

`augment.smooth.spline` *Tidy a(n) smooth.spline object*

Description

`Tidy` summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what `tidy` considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'smooth.spline'
augment(x, data = x$data, ...)
```

Arguments

| | |
|------|--|
| x | A <code>smooth.spline</code> object returned from <code>stats::smooth.spline()</code> . |
| data | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object x. Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the data argument. Augment will report information such as influence and cooks distance for data passed to the data argument. These measures are only defined for the original training data. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble()` containing the data passed to `augment`, and **additional** columns:

| | |
|----------------------|--|
| <code>.fitted</code> | The predicted response for that observation. |
| <code>.resid</code> | The residual for a particular point. Present only when data has been passed to <code>augment</code> via the data argument. |

See Also

`augment()`, `stats::smooth.spline()`, `stats::predict.smooth.spline()`

Other smoothing spline tidiers: `glance.smooth.spline`

Examples

```
spl <- smooth.spline(mtcars$wt, mtcars$mpg, df = 4)
augment(spl, mtcars)
augment(spl) # calls original columns x and y

library(ggplot2)
ggplot(augment(spl, mtcars), aes(wt, mpg)) +
  geom_point() + geom_line(aes(y = .fitted))
```

augment.speedlm

Augment data with information from a(n) speedlm object

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many `augment` methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'speedlm'
augment(x, data = model.frame(x), newdata = data,
  ...)
```

Arguments

| | |
|-------------------|--|
| <code>x</code> | A <code>speedlm</code> object returned from <code>speedglm::speedlm()</code> . |
| <code>data</code> | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object <code>x</code> . Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the <code>data</code> argument. Augment will report information such as influence and cooks distance for data passed to the <code>data</code> argument. These measures are only defined for the original training data. |

`newdata` A `data.frame()` or `tibble::tibble()` containing all the original predictors used to create `x`. Defaults to `NULL`, indicating that nothing has been passed to `newdata`. If `newdata` is specified, the `data` argument will be ignored.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` containing the original data and one additional column `.fitted`.

See Also

`speedglm::speedlm()`

Other `speedlm` tidiers: `glance.speedlm`, `tidy.speedlm`

`augment.stl`

Augment data with information from a(n) stl object

Description

`Augment` accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to `augment` data that was not used during model fitting. This still requires that all columns used to fit the model are present.

`Augment` will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many `augment` methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a `tibble`. At this time, `tibbles` do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a `tibble`, or fitting the original model on data in a `tibble`.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'stl'
augment(x, weights = TRUE, ...)
```

Arguments

`x` An `stl` object returned from `stats::stl()`.

`weights` Logical indicating whether or not to include the robust weights in the output.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with one row for each observation in the original times series:

| | |
|-------------------------|--|
| <code>.seasonal</code> | The seasonal component of the decomposition. |
| <code>.trend</code> | The trend component of the decomposition. |
| <code>.remainder</code> | The remainder, or "random" component of the decomposition. |
| <code>.weight</code> | The final robust weights, if requested. |
| <code>.seasadj</code> | The seasonally adjusted (or "deseasonalised") series. |

See Also

`augment()`, `stats::stl()`

Other decompose tidiers: `augment.decomposed.ts`

`augment.survreg`

Augment data with information from a(n) survreg object

Description

Augment accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to augment data that was not used during model fitting. This still requires that all columns used to fit the model are present.

Augment will often behavior different depending on whether data or newdata is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many augment methods provide default data arguments, so that `augment(fit)` will return the augmented training data. In these cases augment tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'survreg'
augment(x, data = NULL, newdata = NULL,
        type.predict = "response", type.residuals = "response", ...)
```

Arguments

| | |
|----------------|---|
| x | An survreg object returned from <code>survival::survreg()</code> . |
| data | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing the original data that was used to produce the object x. Defaults to <code>stats::model.frame(x)</code> so that <code>augment(my_fit)</code> returns the augmented original data. Do not pass new data to the data argument. Augment will report information such as influence and cooks distance for data passed to the data argument. These measures are only defined for the original training data. |
| newdata | A <code>data.frame()</code> or <code>tibble::tibble()</code> containing all the original predictors used to create x. Defaults to NULL, indicating that nothing has been passed to newdata. If newdata is specified, the data argument will be ignored. |
| type.predict | Character indicating type of prediction to use. Passed to the type argument of the <code>stats::predict()</code> generic. Allowed arguments vary with model class, so be sure to read the <code>predict.my_class</code> documentation. |
| type.residuals | Character indicating type of residuals to use. Passed to the type argument of <code>stats::residuals()</code> generic. Allowed arguments vary with model class, so be sure to read the <code>residuals.my_class</code> documentation. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a newdata argument, it will use the default value for the data argument. |

Details

When the modeling was performed with `na.action = "na.omit"` (as is the typical default), rows with NA in the initial data are omitted entirely from the augmented data frame. When the modeling was performed with `na.action = "na.exclude"`, one should provide the original data as a second argument, at which point the augmented data will contain those rows (typically with NAs in place of the new columns). If the original data is not provided to `augment()` and `na.action = "na.exclude"`, a warning is raised and the incomplete rows are dropped.

Value

A `tibble::tibble` with the passed data and additional columns:

| | |
|----------------------|----------------------------------|
| <code>.fitted</code> | Fitted values of model |
| <code>.se.fit</code> | Standard errors of fitted values |
| <code>.resid</code> | Residuals |

See Also

[na.action](#)

[augment\(\)](#), [survival::survreg\(\)](#)

Other survreg tidiers: [glance.survreg](#), [tidy.survreg](#)

Other survival tidiers: [augment.coxph](#), [glance.aareg](#), [glance.cch](#), [glance.coxph](#), [glance.pyears](#), [glance.survdiff](#), [glance.survexp](#), [glance.survfit](#), [glance.survreg](#), [tidy.aareg](#), [tidy.cch](#), [tidy.coxph](#), [tidy.pyears](#), [tidy.survdiff](#), [tidy.survexp](#), [tidy.survfit](#), [tidy.survreg](#)

| | |
|------------------------------|--|
| <code>augment_columns</code> | <i>add fitted values, residuals, and other common outputs to an augment call</i> |
|------------------------------|--|

Description

Add fitted values, residuals, and other common outputs to the value returned from `augment`.

Usage

```
augment_columns(x, data, newdata, type, type.predict = type,
  type.residuals = type, se.fit = TRUE, ...)
```

Arguments

| | |
|---------------------------|---|
| <code>x</code> | a model |
| <code>data</code> | original data onto which columns should be added |
| <code>newdata</code> | new data to predict on, optional |
| <code>type</code> | Type of prediction and residuals to compute |
| <code>type.predict</code> | Type of prediction to compute; by default same as <code>type</code> |

`type.residuals` Type of residuals to compute; by default same as `type`
`se.fit` Value to pass to `predict`'s `se.fit`, or `NULL` for no value
`...` extra arguments (not used)

Details

In the case that a residuals or influence generic is not implemented for the model, fail quietly.

bootstrap *Set up bootstrap replicates of a dplyr operation*

Description

The `bootstrap()` function is deprecated and will be removed from an upcoming release of broom. For tidy resampling, please use the `rsample` package instead.

Usage

```
bootstrap(df, m, by_group = FALSE)
```

Arguments

`df` a data frame
`m` number of bootstrap replicates to perform
`by_group` If `TRUE`, then bootstrap within each group if `df` is a grouped `tbl`.

Details

This code originates from Hadley Wickham (with a few small corrections) here:
<https://github.com/hadley/dplyr/issues/269>

Examples

```
## Not run:
library(dplyr)
mtcars %>% bootstrap(10) %>% do(tidy(lm(mpg ~ wt, .)))

## End(Not run)
```

brms_tidiers

*Tidying methods for a brms model***Description**

brms tidiers will soon be deprecated in broom and there is no ongoing development of these functions at this time. brms tidiers are being developed in the broom.mixed package, which is not yet on CRAN.

Usage

```
## S3 method for class 'brmsfit'
tidy(x, parameters = NA, par_type = c("all",
  "non-varying", "varying", "hierarchical"), robust = FALSE,
  intervals = TRUE, prob = 0.9, ...)
```

Arguments

| | |
|------------|--|
| x | Fitted model object from the brms package. See <code>brms::brmsfit-class()</code> . |
| parameters | Names of parameters for which a summary should be returned, as given by a character vector or regular expressions. If NA (the default) summarized parameters are specified by the par_type argument. |
| par_type | One of "all", "non-varying", "varying", or "hierarchical" (can be abbreviated). See the Value section for details. |
| robust | Whether to use median and median absolute deviation rather than mean and standard deviation. |
| intervals | If TRUE columns for the lower and upper bounds of posterior uncertainty intervals are included. |
| prob | Defines the range of the posterior uncertainty intervals, such that $100 * \text{prob}\%$ of the parameter's posterior distribution lies within the corresponding interval. Only used if intervals = TRUE. |
| ... | Extra arguments, not used |

Details

These methods tidy the estimates from `brms::brmsfit()` (fitted model objects from the **brms** package) into a summary.

Value

All tidying methods return a data.frame without rownames. The structure depends on the method chosen.

When parameters = NA, the par_type argument is used to determine which parameters to summarize.

Generally, tidy.brmsfit returns one row for each coefficient, with at least three columns:

| | |
|-----------|---|
| term | The name of the model parameter. |
| estimate | A point estimate of the coefficient (mean or median). |
| std.error | A standard error for the point estimate (sd or mad). |

When `par_type = "non-varying"`, only population-level effects are returned.

When `par_type = "varying"`, only group-level effects are returned. In this case, two additional columns are added:

| | |
|-------|---|
| group | The name of the grouping factor. |
| level | The name of the level of the grouping factor. |

Specifying `par_type = "hierarchical"` selects the standard deviations and correlations of the group-level parameters.

If `intervals = TRUE`, columns for the lower and upper bounds of the posterior intervals computed.

See Also

[brms::brms\(\)](#), [brms::brmsfit\(\)](#)

Examples

```
## Not run:
library(brms)
fit <- brm(mpg ~ wt + (1|cyl) + (1+wt|gear), data = mtcars,
          iter = 500, chains = 2)
tidy(fit)
tidy(fit, parameters = "^sd_", intervals = FALSE)
tidy(fit, par_type = "non-varying")
tidy(fit, par_type = "varying")
tidy(fit, par_type = "hierarchical", robust = TRUE)

## End(Not run)
```

broom

Convert Statistical Objects into Tidy Tibbles

Description

Convert statistical analysis objects from R into tidy tibbles, so that they can more easily be combined, reshaped and otherwise processed with tools like `dplyr`, `tidyr` and `ggplot2`. The package provides three S3 generics: `tidy`, which summarizes a model's statistical findings such as coefficients of a regression; `augment`, which adds columns to the original data such as predictions, residuals and cluster assignments; and `glance`, which provides a one-row summary of model-level statistics.

| | |
|-----------------|---|
| column_glossary | <i>Allowed column names in tidied tibbles</i> |
|-----------------|---|

Description

Allowed column names in tidied tibbles

Usage

```
column_glossary
```

Format

A tibble with 4 variables:

method One of "glance", "augment" or "tidy".

column Character name of allowed output column.

description Character description of expected column contents.

used_by A list of character vectors detailing the *classes* that use the column when tidied. For example `c("Arima", "betareg")`.

Examples

```
column_glossary
```

| | |
|--------------|---|
| confint_tidy | <i>Calculate confidence interval as a tidy data frame</i> |
|--------------|---|

Description

Return a confidence interval as a tidy data frame. This directly wraps the `confint()` function, but ensures it follows broom conventions: column names of `conf.low` and `conf.high`, and no row names.

Usage

```
confint_tidy(x, conf.level = 0.95, func = stats::confint, ...)
```

Arguments

| | |
|-------------------------|--|
| <code>x</code> | a model object for which <code>confint()</code> can be calculated |
| <code>conf.level</code> | confidence level |
| <code>func</code> | A function to compute a confidence interval for <code>x</code> . Calling <code>func(x, level = conf.level, ...)</code> must return an object coercable to a tibble. This dataframe like object should have to columns corresponding the lower and upper bounds on the confidence interval. |
| <code>...</code> | extra arguments passed on to <code>confint</code> |

Details

confint_tidy

Value

A tibble with two columns: `conf.low` and `conf.high`.

See Also

[confint](#)

data.frame_tidiers *Tidiers for data.frame objects*

Description

Data frame tidiers are deprecated and will be removed from an upcoming release of broom.

Usage

```
## S3 method for class 'data.frame'
tidy(x, ..., na.rm = TRUE, trim = 0.1)
```

```
## S3 method for class 'data.frame'
glance(x, ...)
```

Arguments

| | |
|--------------------|--|
| <code>x</code> | A data.frame |
| <code>...</code> | Additional arguments for other methods. |
| <code>na.rm</code> | a logical value indicating whether NA values should be stripped before the computation proceeds. |
| <code>trim</code> | the fraction (0 to 0.5) of observations to be trimmed from each end of <code>x</code> before the mean is computed. Passed to the <code>trim</code> argument of <code>mean()</code> |
| <code>data</code> | data, not used |

Details

These perform tidy summaries of data.frame objects. `tidy` produces summary statistics about each column, while `glance` simply reports the number of rows and columns. Note that `augment.data.frame` will throw an error.

Value

`tidy.data.frame` produces a data frame with one row per original column, containing summary statistics of each:

| | |
|-----------------------|---|
| <code>column</code> | name of original column |
| <code>n</code> | Number of valid (non-NA) values |
| <code>mean</code> | mean |
| <code>sd</code> | standard deviation |
| <code>median</code> | median |
| <code>trimmed</code> | trimmed mean, with trim defaulting to .1 |
| <code>mad</code> | median absolute deviation (from the median) |
| <code>min</code> | minimum value |
| <code>max</code> | maximum value |
| <code>range</code> | range |
| <code>skew</code> | skew |
| <code>kurtosis</code> | kurtosis |
| <code>se</code> | standard error |

`glance` returns a one-row data.frame with

| | |
|---------------------------|---|
| <code>nrow</code> | number of rows |
| <code>ncol</code> | number of columns |
| <code>complete.obs</code> | number of rows that have no missing values |
| <code>na.fraction</code> | fraction of values across all rows and columns that are missing |

Author(s)

David Robinson, Benjamin Nutter

Source

Skew and Kurtosis functions are adapted from implementations in the `moments` package: Lukasz Komsta and Frederick Novomestky (2015). `moments`: Moments, cumulants, skewness, kurtosis and related tests. R package version 0.14.
<https://CRAN.R-project.org/package=moments>

Examples

```
## Not run:  
td <- tidy(mtcars)  
td  
  
glance(mtcars)  
  
library(ggplot2)
```

```
# compare mean and standard deviation
ggplot(td, aes(mean, sd)) + geom_point() +
  geom_text(aes(label = column), hjust = 1, vjust = 1) +
  scale_x_log10() + scale_y_log10() + geom_abline()

## End(Not run)
```

durbinWatsonTest_tidiers

Tidy/glance a(n) durbinWatsonTest object

Description

For models that have only a single component, the `tidy()` and `glance()` methods are identical. Please see the documentation for both of those methods.

Usage

```
## S3 method for class 'durbinWatsonTest'
tidy(x, ...)

## S3 method for class 'durbinWatsonTest'
glance(x, ...)
```

Arguments

| | |
|------------------|--|
| <code>x</code> | An object of class <code>durbinWatsonTest</code> created by a call to <code>car::durbinWatsonTest()</code> . |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|------------------------------|--|
| <code>statistic</code> | Test statistic for Durbin-Watson test. |
| <code>p.value</code> | P-value of test statistic. |
| <code>autocorrelation</code> | Residual autocorrelations. |
| <code>method</code> | Always "Durbin-Watson Test". |
| <code>alternative</code> | Alternative hypothesis (character). |

See Also

[tidy\(\)](#), [glance\(\)](#), [car::durbinWatsonTest\(\)](#)

Examples

```
dw <- car::durbinWatsonTest(lm(mpg ~ wt, data = mtcars))
tidy(dw)
glance(dw) # same output for all durbinWatsonTests
```

| | |
|-----------------|--|
| emmeans_tidiers | <i>Tidy estimated marginal means (least-squares means) objects from the emmeans and lsmeans packages</i> |
|-----------------|--|

Description

Tidiers for estimated marginal means objects, which report the predicted means for factors or factor combinations in a linear model. This covers three classes: `emmGrid`, `lsmobj`, and `ref.grid`. (The first class is from the `emmeans` package, and is the successor to the latter two classes, which have slightly different purposes within the `lsmeans` package but have similar output).

Usage

```
## S3 method for class 'lsmobj'
tidy(x, conf.level = 0.95, ...)

## S3 method for class 'ref.grid'
tidy(x, ...)

## S3 method for class 'emmGrid'
tidy(x, ...)
```

Arguments

| | |
|-------------------------|---|
| <code>x</code> | "emmGrid", "lsmobj", or "ref.grid" object |
| <code>conf.level</code> | Level of confidence interval, used only for <code>emmGrid</code> and <code>lsmobj</code> objects |
| <code>...</code> | Additional arguments passed to emmeans::summary.emmGrid() or lsmeans::summary.ref.grid() . Cautionary note: misspecified arguments may be silently ignored! |

Details

There are a large number of arguments that can be passed on to [emmeans::summary.emmGrid\(\)](#) or [lsmeans::summary.ref.grid\(\)](#). By broom convention, we use `conf.level` to pass the `level` argument.


```

by_price
tidy(by_price)

ggplot(tidy(by_price), aes(price2, estimate, color = day)) +
  geom_line() +
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high))
}

```

| | |
|---------------|--|
| finish_glance | <i>Add logLik, AIC, BIC, and other common measurements to a glance of a prediction</i> |
|---------------|--|

Description

A helper function for several functions in the glance generic. Methods such as logLik, AIC, and BIC are defined for many prediction objects, such as lm, glm, and nls. This is a helper function that adds them to a glance data.frame can be performed. If any of them cannot be computed, it fails quietly.

Usage

```
finish_glance(ret, x)
```

Arguments

| | |
|-----|--|
| ret | a one-row data frame (a partially complete glance) |
| x | the prediction model |

Details

In one special case, deviance for objects of the lmerMod class from lme4 is computed with deviance(x, REML=FALSE).

Value

a one-row data frame with additional columns added, such as

| | |
|-------------|--------------------------------|
| logLik | log likelihoods |
| AIC | Akaike Information Criterion |
| BIC | Bayesian Information Criterion |
| deviance | deviance |
| df.residual | residual degrees of freedom |

Each of these are produced by the corresponding generics

| | |
|----------------|--|
| fix_data_frame | <i>Ensure an object is a data frame, with rownames moved into a column</i> |
|----------------|--|

Description

Ensure an object is a data frame, with rownames moved into a column

Usage

```
fix_data_frame(x, newnames = NULL, newcol = "term")
```

Arguments

| | |
|----------|--|
| x | a data.frame or matrix |
| newnames | new column names, not including the rownames |
| newcol | the name of the new rownames column |

Value

a data.frame, with rownames moved into a column and new column names assigned

| | |
|--------------|------------------------------------|
| glance.aareg | <i>Glance at a(n) aareg object</i> |
|--------------|------------------------------------|

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'aareg'
glance(x, ...)
```

Arguments

`x` An aareg object returned from `survival::aareg()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|------------------------|---|
| <code>statistic</code> | chi-squared statistic |
| <code>p.value</code> | p-value based on chi-squared statistic |
| <code>df</code> | degrees of freedom used by coefficients |

See Also

`glance()`, `survival::aareg()`

Other aareg tidiers: `tidy.aareg`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.cch`, `glance.coxph`, `glance.pyears`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `glance.survreg`, `tidy.aareg`, `tidy.cch`, `tidy.coxph`, `tidy.pyears`, `tidy.survdiff`, `tidy.survexp`, `tidy.survfit`, `tidy.survreg`

`glance.Arima`

Glance at a(n) Arima object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'Arima'
glance(x, ...)
```

Arguments

`x` An object of class `Arima` created by `stats::arima()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|---------------------|--|
| <code>sigma</code> | the square root of the estimated residual variance |
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |

See Also

`stats::arima()`

Other Arima tidiers: `tidy.Arima`

| | |
|-----------------------------|--------------------------------------|
| <code>glance.betareg</code> | <i>Glance at a(n) betareg object</i> |
|-----------------------------|--------------------------------------|

Description

`Glance` accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

`Glance` never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

`Glance` does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'betareg'
glance(x, ...)
```

Arguments

`x` A betareg object produced by a call to `betareg::betareg()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

`glance` returns a one-row tibble with columns:

| | |
|-------------------------------|---|
| <code>pseudo.r.squared</code> | the deviance of the null model |
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |
| <code>df.residual</code> | residual degrees of freedom |
| <code>df.null</code> | degrees of freedom under the null |

See Also

`glance()`, `betareg::betareg()`

Examples

```
library(betareg)

data("GasolineYield", package = "betareg")

mod <- betareg(yield ~ batch + temp, data = GasolineYield)

mod
tidy(mod)
tidy(mod, conf.int = TRUE)
tidy(mod, conf.int = TRUE, conf.level = .99)

augment(mod)

glance(mod)
```

| | |
|--------------|------------------------------------|
| glance.biglm | <i>Glance at a(n) biglm object</i> |
|--------------|------------------------------------|

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'biglm'
glance(x, ...)
```

Arguments

| | |
|-----|---|
| x | A biglm object created by a call to <code>biglm::biglm()</code> or <code>biglm::bigglm()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

`glance.biglm` returns a one-row data frame, with columns

| | |
|--------------------------|--|
| <code>r.squared</code> | The percent of variance explained by the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>deviance</code> | deviance |
| <code>df.residual</code> | residual degrees of freedom |

See Also

`glance()`, `biglm::biglm()`, `biglm::bigglm()`

Other biglm tidiers: `tidy.biglm`

| | |
|------------------|--|
| glance.binDesign | <i>Glance at a(n) binDesign object</i> |
|------------------|--|

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'binDesign'
glance(x, ...)
```

Arguments

| | |
|------------------|--|
| <code>x</code> | A <code>binGroup::binDesign</code> object. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|----------------------------|---|
| <code>power</code> | Power achieved by the analysis. |
| <code>n</code> | Sample size used to achieve this power. |
| <code>power.reached</code> | Whether the desired power was reached. |
| <code>maxit</code> | Number of iterations performed. |

See Also

`glance()`, `binGroup::binDesign()`

Other bingroup tidiers: `tidy.binDesign`, `tidy.binWidth`

Examples

```
if (require("binGroup", quietly = TRUE)) {
  des <- binDesign(nmax = 300, delta = 0.06,
                  p.hyp = 0.1, power = .8)

  glance(des)
  tidy(des)

  # the ggplot2 equivalent of plot(des)
  library(ggplot2)
  ggplot(tidy(des), aes(n, power)) +
    geom_line()
}
```

glance.cch

Glance at a(n) cch object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'cch'
glance(x, ...)
```

Arguments

| | |
|-----|--|
| x | An cch object returned from <code>survival::cch()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|---------|------------------------|
| score | score |
| rscore | rscore |
| p.value | p-value from Wald test |
| iter | number of iterations |
| n | number of predictions |
| nevent | number of events |

See Also

`glance()`, `survival::cch()`

Other cch tidiers: `glance.survfit`, `tidy.cch`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.aareg`, `glance.coxph`, `glance.pyyears`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `glance.survreg`, `tidy.aareg`, `tidy.cch`, `tidy.coxph`, `tidy.pyyears`, `tidy.survdiff`, `tidy.survexp`, `tidy.survfit`, `tidy.survreg`

| | |
|---------------------------|------------------------------------|
| <code>glance.coxph</code> | <i>Glance at a(n) coxph object</i> |
|---------------------------|------------------------------------|

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'coxph'
glance(x, ...)
```

Arguments

`x` A coxph object returned from `survival::coxph()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A one-row `tibble::tibble` with columns: TODO.

See Also

`glance()`, `survival::coxph()`

Other coxph tidiers: `augment.coxph`, `tidy.coxph`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.aareg`, `glance.cch`, `glance.pyears`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `glance.survreg`, `tidy.aareg`, `tidy.cch`, `tidy.coxph`, `tidy.pyears`, `tidy.survdiff`, `tidy.survexp`, `tidy.survfit`, `tidy.survreg`

`glance.cv.glmnet`

Glance at a(n) cv.glmnet object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'cv.glmnet'
glance(x, ...)
```

Arguments

`x` A `cv.glmnet` object returned from `glmnet::cv.glmnet()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with one-row with columns:

`lambda.min` The value of the penalization parameter `lambda` that achieved minimum loss as estimated by cross validation.

`lambda.1se` The value of the penalization parameter `lambda` that results in the sparsest model while remaining within one standard error of the minimum loss.

See Also

`glance()`, `glmnet::cv.glmnet()`

Other `glmnet` tidiers: `glance.glmnet`, `tidy.cv.glmnet`, `tidy.glmnet`

`glance.ergm`

Glance at a(n) ergm object

Description

`Glance` accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

`Glance` never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

`Glance` does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'ergm'
glance(x, deviance = FALSE, mcmc = FALSE, ...)
```

Arguments

| | |
|-----------------------|--|
| <code>x</code> | An ergm object returned from a call to <code>ergm::ergm()</code> . |
| <code>deviance</code> | Logical indicating whether or not to report null and residual deviance for the model, as well as degrees of freedom. Defaults to FALSE. |
| <code>mcmc</code> | Logical indicating whether or not to report MCMC interval, burn-in and sample size used to estimate the model. Defaults to FALSE. |
| <code>...</code> | Additional arguments to pass to <code>ergm::summary.ergm()</code> . Cautionary note: Mispecified arguments may be silently ignored. |

Value

`glance.ergm` returns a one-row data.frame with the columns

| | |
|---------------------------|---|
| <code>independence</code> | Whether the model assumed dyadic independence |
| <code>iterations</code> | The number of iterations performed before convergence |
| <code>logLik</code> | If applicable, the log-likelihood associated with the model |
| <code>AIC</code> | The Akaike Information Criterion |
| <code>BIC</code> | The Bayesian Information Criterion |

If `deviance = TRUE`, and if the model supports it, the data frame will also contain the columns

| | |
|--------------------------------|---|
| <code>null.deviance</code> | The null deviance of the model |
| <code>df.null</code> | The degrees of freedom of the null deviance |
| <code>residual.deviance</code> | The residual deviance of the model |
| <code>df.residual</code> | The degrees of freedom of the residual deviance |

Last, if `mcmc = TRUE`, the data frame will also contain the columns

| | |
|------------------------------|---|
| <code>MCMC.interval</code> | The interval used during MCMC estimation |
| <code>MCMC.burnin</code> | The burn-in period of the MCMC estimation |
| <code>MCMC.samplesize</code> | The sample size used during MCMC estimation |

See Also

`glance()`, `ergm::ergm()`, `ergm::summary.ergm()`

Other ergm tidiers: `tidy.ergm`

| | |
|-----------------|---------------------------------------|
| glance.factanal | <i>Glance at a(n) factanal object</i> |
|-----------------|---------------------------------------|

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'factanal'
glance(x, ...)
```

Arguments

| | |
|-----|--|
| x | A factanal object created by <code>stats::factanal()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|----------------|--|
| n.factors | The number of fitted factors |
| total.variance | Total cumulative proportion of variance accounted for by all factors |
| statistic | Significance-test statistic |
| p.value | p-value from the significance test, describing whether the covariance matrix estimated from the factors is significantly different from the observed covariance matrix |
| df | Degrees of freedom used by the factor analysis |
| n | Sample size used in the analysis |
| method | The estimation method; always Maximum Likelihood, "mle" |
| converged | Whether the factor analysis converged |

See Also

[glance\(\)](#), [stats::factanal\(\)](#)

Other factanal tidiers: [augment.factanal](#), [tidy.factanal](#)

glance.felm

Glance at a(n) felm object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'felm'
glance(x, ...)
```

Arguments

`x` A `felm` object returned from `lfe::felm()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|----------------------------|---|
| <code>r.squared</code> | The percent of variance explained by the model |
| <code>adj.r.squared</code> | <code>r.squared</code> adjusted based on the degrees of freedom |
| <code>sigma</code> | The square root of the estimated residual variance |
| <code>statistic</code> | F-statistic |
| <code>p.value</code> | p-value from the F test |
| <code>df</code> | Degrees of freedom used by the coefficients |
| <code>df.residual</code> | residual degrees of freedom |

| | |
|-----------------|---------------------------------------|
| glance.fitdistr | <i>Glance at a(n) fitdistr object</i> |
|-----------------|---------------------------------------|

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'fitdistr'
glance(x, ...)
```

Arguments

| | |
|-----|---|
| x | A fitdistr object returned by <code>MASS::fitdistr()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|--------|---|
| n | Number of observations used in estimation |
| logLik | log-likelihood of estimated data |
| AIC | Akaike Information Criterion |
| BIC | Bayesian Information Criterion |

See Also

`tidy()`, `MASS::fitdistr()`

Other fitdistr tidiers: `tidy.fitdistr`

glance.Gam

Glance at a(n) Gam object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'Gam'
glance(x, ...)
```

Arguments

`x` A Gam object returned from a call to `gam::gam()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Details

Glance at gam objects created by calls to `mgcv::gam()` with `glance.gam()`.

Value

A one-row `tibble::tibble` with columns:

| | |
|--------------------------|---|
| <code>logLik</code> | Log-likelihood of the model. |
| <code>AIC</code> | Akaike's Information Criterion for the model. |
| <code>BIC</code> | Bayesian Information Criterion for the model. |
| <code>deviance</code> | Deviance of the model. |
| <code>df.residual</code> | Residual degrees of freedom for the model. |

See Also

[glance\(\)](#), [gam::gam\(\)](#)

Other gam tidiers: [tidy.Gam](#)

glance.gam

Glance at a(n) gam object

Description

Glance accepts a model object and returns a [tibble::tibble\(\)](#) with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'gam'
glance(x, ...)
```

Arguments

| | |
|-----|---|
| x | A gam object returned from a call to mgcv::gam() . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an augment() method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Details

To glance Gam objects created by calls to [gam::gam\(\)](#), see [glance.Gam\(\)](#).

Value

A one-row [tibble::tibble](#) with columns:

| | |
|-------------|---|
| logLik | Log-likelihood of the model. |
| AIC | Akaike's Information Criterion for the model. |
| BIC | Bayesian Information Criterion for the model. |
| deviance | Deviance of the model. |
| df.residual | Residual degrees of freedom for the model. |

See Also

[glance\(\)](#), [mgcv::gam\(\)](#), [glance.Gam\(\)](#)

Other mgcv tidiers: [tidy.gam](#)

glance.garch

Tidy a(n) garch object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'garch'
glance(x, test = c("box-ljung-test", "jarque-bera-test"),
  ...)
```

Arguments

| | |
|------|---|
| x | A garch object returned by tseries::garch() . |
| test | Character specification of which hypothesis test to use. The garch function reports 2 hypothesis tests: Jarque-Bera to residuals and Box-Ljung to squared residuals. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an augment() method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row [tibble::tibble](#) with columns:

| | |
|-----------|--|
| statistic | Test statistic used to compute the p-value |
| p.value | P-value |
| parameter | Parameter field in the htest, typically degrees of freedom |
| method | Method used to compute the statistic as a string |
| logLik | the data's log-likelihood under the model |
| AIC | the Akaike Information Criterion |
| BIC | the Bayesian Information Criterion |

See Also

`glance()`, `tseries::garch()`, []
 Other garch tidiers: `tidy.garch`

glance.glm

*Glance at a(n) glm object***Description**

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'glm'
glance(x, ...)
```

Arguments

`x` A glm object returned from `stats::glm()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|----------------------------|--|
| <code>null.deviance</code> | the deviance of the null model |
| <code>df.null</code> | the residual degrees of freedom for the null model |
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |
| <code>deviance</code> | deviance |
| <code>df.residual</code> | residual degrees of freedom |

See Also

`stats::glm()`

Other lm tidiers: `augment.glm`, `augment.lm`, `glance.lm`, `tidy.glm`, `tidy.lm`

Examples

```
g <- glm(am ~ mpg, mtcars, family = "binomial")
glance(g)
```

glance.glmnet

Glance at a(n) glmnet object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'glmnet'
glance(x, ...)
```

Arguments

`x` A `glmnet` object returned from `glmnet::glmnet()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|----------------------|---|
| <code>nulldev</code> | null deviance |
| <code>npasses</code> | total passes over the data across all lambda values |

See Also

[glance\(\)](#), [glmnet::glmnet\(\)](#)

Other glmnet tidiers: [glance.cv.glmnet](#), [tidy.cv.glmnet](#), [tidy.glmnet](#)

`glance.glmRob`

Glance at a(n) glmRob object

Description

Glance accepts a model object and returns a [tibble::tibble\(\)](#) with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'glmRob'
glance(x, ...)
```

Arguments

`x` A `glmRob` object returned from [robust::glmRob\(\)](#).

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an [augment\(\)](#) method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A one-row [tibble::tibble](#) with columns:

| | |
|----------------------------|---------------------------------------|
| <code>deviance</code> | Robust deviance |
| <code>null.deviance</code> | Deviance under the null model |
| <code>df.residual</code> | Number of residual degrees of freedom |

See Also

[robust::glmRob\(\)](#)

Other robust tidiers: [augment.glmRob](#), [augment.lmRob](#), [glance.lmRob](#), [tidy.glmRob](#), [tidy.lmRob](#)

glance.gmm

Glance at a(n) gmm object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'gmm'
glance(x, ...)
```

Arguments

`x` A gmm object returned from `gmm::gmm()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|--------------------------|--|
| <code>df</code> | Degrees of freedom |
| <code>statistic</code> | Statistic from J-test for $E(g)=0$ |
| <code>p.value</code> | P-value from J-test |
| <code>df.residual</code> | Residual degrees of freedom, if included in <code>x</code> . |

See Also

`glance()`, `gmm::gmm()`

Other gmm tidiers: `tidy.gmm`

| | |
|--------------|------------------------------------|
| glance.ivreg | <i>Glance at a(n) ivreg object</i> |
|--------------|------------------------------------|

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'ivreg'
glance(x, diagnostics = FALSE, ...)
```

Arguments

| | |
|-------------|--|
| x | An ivreg object created by a call to <code>AER::ivreg()</code> . |
| diagnostics | Logical indicating whether to include statistics and p-values for Sargan, Wu-Hausman and weak instrument tests. Defaults to FALSE. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row tibble with columns

| | |
|---------------|--|
| r.squared | The percent of variance explained by the model |
| adj.r.squared | r.squared adjusted based on the degrees of freedom |
| sigma | The square root of the estimated residual variance |
| statistic | Wald test statistic |
| p.value | p-value from the Wald test |
| df | Degrees of freedom used by the coefficients |
| df.residual | residual degrees of freedom |

If `diagnostics = TRUE`, will also return the following columns:

```
statistic.Sargan      Statistic for Sargan test
p.value.Sargan       P-value for Sargan test
statistic.Wu.Hausman Statistic for Wu-Hausman test
p.value.Wu.Hausman   P-value for Wu-Hausman test
statistic.weakinst   Statistic for Wu-Hausman test
p.value.weakinst     P-value for weak instruments test
```

See Also

[glance\(\)](#), [AER::ivreg\(\)](#)

Other ivreg tidiers: [augment.ivreg](#), [tidy.ivreg](#)

Examples

```
library(AER)

data("CigarettesSW", package = "AER")
ivr <- ivreg(
  log(packs) ~ income | population,
  data = CigarettesSW,
  subset = year == "1995"
)

summary(ivr)

tidy(ivr)
tidy(ivr, conf.int = TRUE)
tidy(ivr, conf.int = TRUE, exponentiate = TRUE)

augment(ivr)

glance(ivr)
```

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'kmeans'
glance(x, ...)
```

Arguments

| | |
|------------------|--|
| <code>x</code> | A kmeans object created by <code>stats::kmeans()</code> . |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|---------------------------|--|
| <code>totss</code> | The total sum of squares |
| <code>tot.withinss</code> | The total within-cluster sum of squares |
| <code>betweenss</code> | The total between-cluster sum of squares |
| <code>iter</code> | The number of (outer) iterations |

See Also

`glance()`, `stats::kmeans()`

Other kmeans tidiers: `augment.kmeans`, `tidy.kmeans`

glance.lavaan *Glance at a(n) lavaan object*

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'lavaan'
glance(x, ...)
```

Arguments

`x` A lavaan object, such as those return from `lavaan::cfa()`, and `lavaan::sem()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|------------------------------|---|
| <code>chisq</code> | Model chi squared |
| <code>npar</code> | Number of parameters in the model |
| <code>rmsea</code> | Root mean square error of approximation |
| <code>rmsea.conf.high</code> | 95 percent upper bound on RMSEA |
| <code>srmr</code> | Standardised root mean residual |
| <code>agfi</code> | Adjusted goodness of fit |
| <code>cfi</code> | Comparative fit index |
| <code>tli</code> | Tucker Lewis index |
| <code>aic</code> | Akaike information criterion |

| | |
|----------------|---|
| bic | Bayesian information criterion |
| ngroups | Number of groups in model |
| nobs | Number of observations included |
| norig | Number of observation in the original dataset |
| nexcluded | Number of excluded observations |
| converged | Logical - Did the model converge |
| estimator | Estimator used |
| missing_method | Method for eliminating missing data |

For further recommendations on reporting SEM and CFA models see Schreiber, J. B. (2017). Update to core reporting practices in structural equation modeling. *Research in Social and Administrative Pharmacy*, 13(3), 634-643. <https://doi.org/10.1016/j.sapharm.2016.06.006>

See Also

[glance\(\)](#), [lavaan::cfa\(\)](#), [lavaan::sem\(\)](#), [lavaan::fitmeasures\(\)](#)

Other lavaan tidiers: [tidy.lavaan](#)

Examples

```
if (require("lavaan", quietly = TRUE)) {
  library(lavaan)

  cfa.fit <- cfa(
    'F =~ x1 + x2 + x3 + x4 + x5',
    data = HolzingerSwineford1939, group = "school"
  )
  glance(cfa.fit)
}
```

glance.lm

Glance at a(n) lm object

Description

Glance accepts a model object and returns a [tibble::tibble\(\)](#) with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'lm'
glance(x, ...)

## S3 method for class 'summary.lm'
glance(x, ...)
```

Arguments

`x` An `lm` object created by `stats::lm()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|----------------------------|--|
| <code>r.squared</code> | The percent of variance explained by the model |
| <code>adj.r.squared</code> | <code>r.squared</code> adjusted based on the degrees of freedom |
| <code>sigma</code> | The square root of the estimated residual variance |
| <code>statistic</code> | F-statistic |
| <code>p.value</code> | p-value from the F test, describing whether the full regression is significant |
| <code>df</code> | Degrees of freedom used by the coefficients |
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |
| <code>deviance</code> | deviance |
| <code>df.residual</code> | residual degrees of freedom |

See Also

[glance\(\)](#)

Other `lm` tidiers: [augment.glm](#), [augment.lm](#), [glance.glm](#), [tidy.glm](#), [tidy.lm](#)

| | |
|----------------|--------------------------------------|
| glance.lmodel2 | <i>Glance at a(n) lmodel2 object</i> |
|----------------|--------------------------------------|

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'lmodel2'
glance(x, ...)
```

Arguments

| | |
|-----|---|
| x | A lmodel2 object returned by <code>lmodel2::lmodel2()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|-----------|---|
| r.squared | OLS R-squared |
| p.value | OLS parametric p-value |
| theta | Angle between OLS lines $lm(y \sim x)$ and $lm(x \sim y)$ |
| H | H statistic for computing confidence interval of major axis slope |

See Also

`glance()`, `lmodel2::lmodel2()`

Other lmodel2 tidiers: `tidy.lmodel2`

glance.lmRob

Glance at a(n) lmRob object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'lmRob'
glance(x, ...)
```

Arguments

`x` A `lmRob` object returned from `robust::lmRob()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|--------------------------|---------------------------------------|
| <code>r.squared</code> | R-squared |
| <code>deviance</code> | Robust deviance |
| <code>sigma</code> | Residual scale estimate |
| <code>df.residual</code> | Number of residual degrees of freedom |

See Also

`robust::lmRob()`

Other robust tidiers: `augment.glmRob`, `augment.lmRob`, `glance.glmRob`, `tidy.glmRob`, `tidy.lmRob`

| | |
|---------------|-------------------------------------|
| glance.Mclust | <i>Glance at a(n) Mclust object</i> |
|---------------|-------------------------------------|

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'Mclust'
glance(x, ...)
```

Arguments

| | |
|-----|--|
| x | An Mclust object return from <code>mclust::Mclust()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|--------|--|
| model | A character string denoting the model at which the optimal BIC occurs |
| n | The number of observations in the data |
| G | The optimal number of mixture components |
| BIC | The optimal BIC value |
| logLik | The log-likelihood corresponding to the optimal BIC |
| df | The number of estimated parameters |
| hypvol | If the other model contains a noise component, the value of the hypervolume parameter. Otherwise NA. |

glance.mjoint

Glance at a(n) mjoint object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'mjoint'
glance(x, ...)
```

Arguments

`x` An `mjoint` object returned from `joineRML::mjoint()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|-----------------------|--|
| <code>sigma2_j</code> | the square root of the estimated residual variance for the <code>j</code> -th longitudinal process |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |
| <code>logLik</code> | the data's log-likelihood under the model |

See Also

`glance()`, `joineRML::mjoint()`

Other `mjoint` tidiers: `tidy.mjoint`

| | |
|--------------|------------------------------------|
| glance.muhaz | <i>Glance at a(n) muhaz object</i> |
|--------------|------------------------------------|

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'muhaz'
glance(x, ...)
```

Arguments

| | |
|-----|--|
| x | A muhaz object returned by <code>muhaz::muhaz()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|------------|--|
| nobs | Number of observations used for estimation |
| min.time | The minimum observed event or censoring time |
| max.time | The maximum observed event or censoring time |
| min.hazard | Minimal estimated hazard |
| max.hazard | Maximal estimated hazard |

See Also

`glance()`, `muhaz::muhaz()`

Other muhaz tidiers: `tidy.muhaz`

glance.multinom *Glance at a(n) multinom object*

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'multinom'
glance(x, ...)
```

Arguments

| | |
|------------------|--|
| <code>x</code> | A <code>multinom</code> object returned from <code>nnet::multinom()</code> . |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|-----------------------|----------------------------------|
| <code>edf</code> | The effective degrees of freedom |
| <code>deviance</code> | deviance |
| <code>AIC</code> | the Akaike Information Criterion |

See Also

`glance()`, `nnet::multinom()`

Other `multinom` tidiers: `tidy.multinom`

glance.nlrq

*Glance at a(n) nlrq object***Description**

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'nlrq'
glance(x, ...)
```

Arguments

| | |
|------------------|---|
| <code>x</code> | A <code>nlrq</code> object returned from <code>quantreg::nlrq()</code> . |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A one-row `tibble::tibble()` with columns:

| | |
|--------------------------|---|
| <code>tau</code> | quantile |
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |
| <code>df.residual</code> | residual degrees of freedom |

See Also

`glance()`, `quantreg::nlrq()`

Other `quantreg` tidiers: `augment.nlrq`, `augment.rqs`, `augment.rq`, `glance.rq`, `tidy.nlrq`, `tidy.rqs`, `tidy.rq`

glance.nls

Glance at a(n) nls object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'nls'
glance(x, ...)
```

Arguments

`x` An nls object returned from `stats::nls()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|--------------------------|--|
| <code>sigma</code> | the square root of the estimated residual variance |
| <code>isConv</code> | whether the fit successfully converged |
| <code>finTol</code> | the achieved convergence tolerance |
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |
| <code>deviance</code> | deviance |
| <code>df.residual</code> | residual degrees of freedom |

See Also

[tidy](#), [stats::nls\(\)](#)

Other nls tidiers: [augment.nls](#), [tidy.nls](#)

glance.orcutt

Glance at a(n) orcutt object

Description

Glance accepts a model object and returns a [tibble::tibble\(\)](#) with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'orcutt'
glance(x, ...)
```

Arguments

`x` An orcutt object returned from [orcutt::cochrane.orcutt\(\)](#).

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an [augment\(\)](#) method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A one-row [tibble::tibble](#) with columns:

| | |
|---------------------------------|---|
| <code>r.squared</code> | R-squared |
| <code>adj.r.squared</code> | Adjusted R-squared |
| <code>rho</code> | Spearman's rho autocorrelation |
| <code>number.interaction</code> | Number of interactions |
| <code>dw.original</code> | Durbin-Watson statistic of original fit |

`p.value.original` P-value of original Durbin-Watson statistic
`dw.transformed` Durbin-Watson statistic of transformed fit
`p.value.transformed` P-value of autocorrelation after transformation

See Also

[glance\(\)](#), [orcutt::cochrane.orcutt\(\)](#)

Other orcutt tidiers: [tidy.orcutt](#)

glance.plm

Glance at a(n) plm object

Description

Glance accepts a model object and returns a [tibble::tibble\(\)](#) with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'plm'
glance(x, ...)
```

Arguments

`x` A `plm` object returned by [plm::plm\(\)](#).
`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an [augment\(\)](#) method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|----------------------------|--|
| <code>r.squared</code> | The percent of variance explained by the model |
| <code>adj.r.squared</code> | <code>r.squared</code> adjusted based on the degrees of freedom |
| <code>statistic</code> | F-statistic |
| <code>p.value</code> | p-value from the F test, describing whether the full regression is significant |
| <code>deviance</code> | deviance |
| <code>df.residual</code> | residual degrees of freedom |

See Also

`glance()`, `plm::plm()`

Other plm tidiers: `augment.plm`, `tidy.plm`

`glance.poLCA`

Augment data with information from a(n) poLCA object

Description

`Augment` accepts a model object and a dataset and adds information about each observation in the dataset. Most commonly, this includes predicted values in the `.fitted` column, residuals in the `.resid` column, and standard errors for the fitted values in a `.se.fit` column. New columns always begin with a `.` prefix to avoid overwriting columns in the original dataset.

Users may pass data to `augment` via either the `data` argument or the `newdata` argument. If the user passes data to the `data` argument, it **must** be exactly the data that was used to fit the model object. Pass datasets to `newdata` to `augment` data that was not used during model fitting. This still requires that all columns used to fit the model are present.

`Augment` will often behavior different depending on whether `data` or `newdata` is specified. This is because there is often information associated with training observations (such as influences or related) measures that is not meaningfully defined for new observations.

For convenience, many `augment` methods provide default `data` arguments, so that `augment(fit)` will return the augmented training data. In these cases `augment` tries to reconstruct the original data based on the model object, with some varying degrees of success.

The augmented dataset is always returned as a `tibble::tibble` with the **same number of rows** as the passed dataset. This means that the passed data must be coercible to a tibble. At this time, tibbles do not support matrix-columns. This means you should not specify a matrix of covariates in a model formula during the original model fitting process, and that `splines::ns()`, `stats::poly()` and `survival::Surv()` objects are not supported in input data. If you encounter errors, try explicitly passing a tibble, or fitting the original model on data in a tibble.

We are in the process of defining behaviors for models fit with various `na.action` arguments, but make no guarantees about behavior when data is missing at this time.

Usage

```
## S3 method for class 'poLCA'
glance(x, ...)
```

Arguments

`x` A poLCA object returned from `poLCA: :poLCA()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|--------------------------|---|
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |
| <code>g.squared</code> | The likelihood ratio/deviance statistic |
| <code>chi.squared</code> | The Pearson Chi-Square goodness of fit statistic for multiway tables |
| <code>df</code> | Number of parameters estimated, and therefore degrees of freedom used |
| <code>df.residual</code> | Number of residual degrees of freedom left |

See Also

`glance()`, `poLCA: :poLCA()`

Other poLCA tidiers: `augment.poLCA`, `tidy.poLCA`

`glance.pyyears`

Glance at a(n) pyyears object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'pyears'
glance(x, ...)
```

Arguments

`x` A pyears object returned from `survival::pyears()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|-----------------------|--|
| <code>total</code> | total number of person-years tabulated |
| <code>offtable</code> | total number of person-years off table |

See Also

`glance()`, `survival::pyears()`

Other pyears tidiers: `tidy.pyears`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.aareg`, `glance.cch`, `glance.coxph`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `glance.survreg`, `tidy.aareg`, `tidy.cch`, `tidy.coxph`, `tidy.pyears`, `tidy.survdiff`, `tidy.survexp`, `tidy.survfit`, `tidy.survreg`

`glance.ridgelm`

Glance at a(n) ridgelm object

Description

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'ridgelm'
glance(x, ...)
```

Arguments

`x` A `ridgelm` object returned from `MASS::lm.ridge()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Details

This is similar to the output of `select.ridgelm`, but it is returned rather than printed.

Value

A one-row `tibble::tibble` with columns:

| | |
|------------------------|---|
| <code>kHKB</code> | modified HKB estimate of the ridge constant |
| <code>kLW</code> | modified L-W estimate of the ridge constant |
| <code>lambdaGCV</code> | choice of lambda that minimizes GCV |

See Also

`glance()`, `MASS::select.ridgelm()`, `MASS::lm.ridge()`

Other `ridgelm` tidiers: `tidy.ridgelm`

`glance.rlm`

Glance at a(n) rlm object

Description

`Glance` accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

`Glance` never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

`Glance` does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'rlm'
glance(x, ...)
```

Arguments

`x` An `rlm` object returned by `MASS::rlm()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Details

For tidiers for models from the **robust** package see `tidy.lmRob()` and `tidy.glmRob()`.

Value

A one-row `tibble::tibble` with columns:

| | |
|------------------------|--|
| <code>sigma</code> | The square root of the estimated residual variance |
| <code>converged</code> | whether the IWLS converged |
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |
| <code>deviance</code> | deviance |

See Also

`glance()`, `MASS::rlm()`

Other `rlm` tidiers: `augment.rlm`, `tidy.rlm`

Examples

```
library(MASS)

r <- rlm(stack.loss ~ ., stackloss)
tidy(r)
augment(r)
glance(r)
```

glance.rq

*Glance at a(n) rq object***Description**

Glance accepts a model object and returns a `tibble::tibble()` with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'rq'
glance(x, ...)
```

Arguments

`x` An rq object returned from `quantreg::rq()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Details

Only models with a single tau value may be passed. For multiple values, please use a `purrr::map()` workflow instead, e.g.

```
taus %>%
  map(function(tau_val) rq(y ~ x, tau = tau_val)) %>%
  map_dfr(glance)
```

Value

A one-row `tibble::tibble` with columns:

| | |
|---------------------|---|
| <code>tau</code> | quantile estimated |
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |

| | |
|-------------|------------------------------------|
| BIC | the Bayesian Information Criterion |
| df.residual | residual degrees of freedom |

See Also

[glance\(\)](#), [quantreg::rq\(\)](#)

Other quantreg tidiers: [augment.nlqr](#), [augment.rqs](#), [augment.rq](#), [glance.nlqr](#), [tidy.nlqr](#), [tidy.rqs](#), [tidy.rq](#)

`glance.smooth.spline` *Tidy a(n) smooth.spline object*

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'smooth.spline'
glance(x, ...)
```

Arguments

| | |
|------------------|--|
| <code>x</code> | A <code>smooth.spline</code> object returned from stats::smooth.spline() . |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an augment() method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A one-row [tibble::tibble](#) with columns:

| | |
|-----------------------|---|
| <code>spar</code> | smoothing parameter |
| <code>lambda</code> | choice of lambda corresponding to <code>spar</code> |
| <code>df</code> | equivalent degrees of freedom |
| <code>crit</code> | minimized criterion |
| <code>pen.crit</code> | penalized criterion |
| <code>cv.crit</code> | cross-validation score |

See Also

[augment\(\)](#), [stats::smooth.spline\(\)](#)

Other smoothing spline tidiers: [augment.smooth.spline](#)

glance.speedlm

Glance at a(n) speedlm object

Description

Glance accepts a model object and returns a [tibble::tibble\(\)](#) with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'speedlm'
glance(x, ...)
```

Arguments

| | |
|-----|---|
| x | A speedlm object returned from speedglm::speedlm() . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an augment() method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row [tibble::tibble](#) with columns:

| | |
|---------------|--|
| r.squared | The percent of variance explained by the model |
| adj.r.squared | r.squared adjusted based on the degrees of freedom |
| statistic | F-statistic |
| p.value | p-value from the F test, describing whether the full regression is significant |
| df | Degrees of freedom used by the coefficients |
| logLik | the data's log-likelihood under the model |

| | |
|-------------|------------------------------------|
| AIC | the Akaike Information Criterion |
| BIC | the Bayesian Information Criterion |
| deviance | deviance |
| df.residual | residual degrees of freedom |

See Also

[speedglm::speedlm\(\)](#)

Other speedlm tidiers: [augment.speedlm](#), [tidy.speedlm](#)

| | |
|-----------------|---------------------------------------|
| glance.survdiff | <i>Glance at a(n) survdiff object</i> |
|-----------------|---------------------------------------|

Description

Glance accepts a model object and returns a [tibble::tibble\(\)](#) with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'survdiff'
glance(x, ...)
```

Arguments

| | |
|-----|--|
| x | An survdiff object returned from survival::survdiff() . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an augment() method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A one-row [tibble::tibble](#) with columns:

| | |
|-----------|-----------------------------|
| statistic | value of the test statistic |
| df | degrees of freedom |
| p.value | p-value |

See Also

[glance\(\)](#), [survival::survdiff\(\)](#)

Other survdiff tidiers: [tidy.survdiff](#)

Other survival tidiers: [augment.coxph](#), [augment.survreg](#), [glance.aareg](#), [glance.cch](#), [glance.coxph](#), [glance.pyears](#), [glance.survexp](#), [glance.survfit](#), [glance.survreg](#), [tidy.aareg](#), [tidy.cch](#), [tidy.coxph](#), [tidy.pyears](#), [tidy.survdiff](#), [tidy.survexp](#), [tidy.survfit](#), [tidy.survreg](#)

glance.survexp

Glance at a(n) survexp object

Description

Glance accepts a model object and returns a [tibble::tibble\(\)](#) with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'survexp'
glance(x, ...)
```

Arguments

| | |
|-----|--|
| x | An survexp object returned from survival::survexp() . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an augment() method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A one-row [tibble::tibble](#) with columns:

| | |
|------------|-------------------------------------|
| n.max | maximum number of subjects at risk |
| n.start | starting number of subjects at risk |
| timepoints | number of timepoints |

See Also

[glance\(\)](#), [survival::survexp\(\)](#)

Other survexp tidiers: [tidy.survexp](#)

Other survival tidiers: [augment.coxph](#), [augment.survreg](#), [glance.aareg](#), [glance.cch](#), [glance.coxph](#), [glance.pyears](#), [glance.survdiff](#), [glance.survfit](#), [glance.survreg](#), [tidy.aareg](#), [tidy.cch](#), [tidy.coxph](#), [tidy.pyears](#), [tidy.survdiff](#), [tidy.survexp](#), [tidy.survfit](#), [tidy.survreg](#)

glance.survfit

Glance at a(n) survfit object

Description

Glance accepts a model object and returns a [tibble::tibble\(\)](#) with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'survfit'
glance(x, ...)
```

Arguments

`x` An survfit object returned from [survival::survfit\(\)](#).

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an [augment\(\)](#) method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A one-row [tibble::tibble](#) with columns:

| | |
|----------------------|------------------------|
| <code>records</code> | number of observations |
| <code>n.max</code> | <code>n.max</code> |
| <code>n.start</code> | <code>n.start</code> |

| | |
|-----------------|--|
| events | number of events |
| rmean | Restricted mean (see survival::print.survfit()) |
| rmean.std.error | Restricted mean standard error |
| median | median survival |
| conf.low | lower end of confidence interval on median |
| conf.high | upper end of confidence interval on median |

See Also

[glance\(\)](#), [survival::survfit\(\)](#)

Other cch tidiers: [glance.cch](#), [tidy.cch](#)

Other survival tidiers: [augment.coxph](#), [augment.survreg](#), [glance.aareg](#), [glance.cch](#), [glance.coxph](#), [glance.pyears](#), [glance.survdiff](#), [glance.survexp](#), [glance.survreg](#), [tidy.aareg](#), [tidy.cch](#), [tidy.coxph](#), [tidy.pyears](#), [tidy.survdiff](#), [tidy.survexp](#), [tidy.survfit](#), [tidy.survreg](#)

| | |
|-----------------------------|--------------------------------------|
| <code>glance.survreg</code> | <i>Glance at a(n) survreg object</i> |
|-----------------------------|--------------------------------------|

Description

Glance accepts a model object and returns a [tibble::tibble\(\)](#) with exactly one row of model summaries. The summaries are typically goodness of fit measures, p-values for hypothesis tests on residuals, or model convergence information.

Glance never returns information from the original call to the modelling function. This includes the name of the modelling function or any arguments passed to the modelling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropriate methods and gathers the results together. Sometimes a goodness of fit measure will be undefined. In these cases the measure will be reported as NA.

Usage

```
## S3 method for class 'survreg'
glance(x, ...)
```

Arguments

| | |
|-----|---|
| x | An survreg object returned from survival::survreg() . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an augment() method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|--------------------------|--------------------------------|
| <code>iter</code> | number of iterations |
| <code>df</code> | degrees of freedom |
| <code>statistic</code> | chi-squared statistic |
| <code>p.value</code> | p-value from chi-squared test |
| <code>logLik</code> | log likelihood |
| <code>AIC</code> | Akaike information criterion |
| <code>BIC</code> | Bayesian information criterion |
| <code>df.residual</code> | residual degrees of freedom |

See Also

`glance()`, `survival::survreg()`

Other survreg tidiers: `augment.survreg`, `tidy.survreg`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.aareg`, `glance.cch`, `glance.coxph`, `glance.pyears`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `tidy.aareg`, `tidy.cch`, `tidy.coxph`, `tidy.pyears`, `tidy.survdiff`, `tidy.survexp`, `tidy.survfit`, `tidy.survreg`

`glance_optim`

Tidy a(n) optim object masquerading as list

Description

Broom tidies a number of lists that are effectively S3 objects without a class attribute. For example, `stats::optim()`, `svd()` and `akima::interp()` produce consistent output, but because they do not have a class attribute, they cannot be handled by S3 dispatch.

These functions look at the elements of a list and determine if there is an appropriate tidying method to apply to the list. Those tidiers are themselves implemented as functions of the form `tidy_<function>` or `glance_<function>` and are not exported (but they are documented!).

If no appropriate tidying method is found, throws an error.

Usage

```
glance_optim(x, ...)
```

Arguments

`x` A list returned from `stats::optim()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A one-row `tibble::tibble` with columns:

| | |
|-----------------------------|---|
| <code>value</code> | minimized or maximized output value |
| <code>function.count</code> | number of calls to <code>fn</code> |
| <code>gradient.count</code> | number of calls to <code>gr</code> |
| <code>convergence</code> | convergence code representing the error state |

See Also

`glance()`, `optim()`

Other list tidiers: `list_tidiers`, `tidy_irlba`, `tidy_optim`, `tidy_svd`, `tidy_xyz`

| | |
|-------------------------|--|
| <code>insert_NAs</code> | <i>insert a row of NAs into a data frame wherever another data frame has NAs</i> |
|-------------------------|--|

Description

insert a row of NAs into a data frame wherever another data frame has NAs

Usage

```
insert_NAs(x, original)
```

Arguments

| | |
|-----------------------|--|
| <code>x</code> | data frame that has one row for each non-NA row in <code>original</code> |
| <code>original</code> | data frame with NAs |

| | |
|--------------|--|
| list_tidiers | <i>Tidying methods for lists / returned values that are not S3 objects</i> |
|--------------|--|

Description

Broom tidies a number of lists that are effectively S3 objects without a class attribute. For example, `stats::optim()`, `svd()` and `akima::interp()` produce consistent output, but because they do not have a class attribute, they cannot be handled by S3 dispatch.

Usage

```
## S3 method for class 'list'
tidy(x, ...)

## S3 method for class 'list'
glance(x, ...)
```

Arguments

`x` A list, potentially representing an object that can be tidied.
`...` Additionally arguments passed to the tidying function.

Details

These functions look at the elements of a list and determine if there is an appropriate tidying method to apply to the list. Those tidiers are themselves implemented as functions of the form `tidy_<function>` or `glance_<function>` and are not exported (but they are documented!).

If no appropriate tidying method is found, throws an error.

See Also

Other list tidiers: [glance_optim](#), [tidy_irlba](#), [tidy_optim](#), [tidy_svd](#), [tidy_xyz](#)

| | |
|--------------|---|
| lme4_tidiers | <i>Tidying methods for mixed effects models</i> |
|--------------|---|

Description

lme4 tidiers will soon be deprecated in broom and there is no ongoing development of these functions at this time. lme4 tidiers are being developed in the `broom.mixed` package, which is not yet on CRAN.

Usage

```
## S3 method for class 'merMod'
tidy(x, effects = c("ran_pars", "fixed"),
     scales = NULL, ran_prefix = NULL, conf.int = FALSE,
     conf.level = 0.95, conf.method = "Wald", ...)

## S3 method for class 'merMod'
augment(x, data = stats::model.frame(x), newdata, ...)

## S3 method for class 'merMod'
glance(x, ...)
```

Arguments

| | |
|--------------------------|---|
| <code>x</code> | An object of class <code>merMod</code> , such as those from <code>lmer</code> , <code>glmer</code> , or <code>nlmer</code> |
| <code>effects</code> | A character vector including one or more of "fixed" (fixed-effect parameters), "ran_pars" (variances and covariances or standard deviations and correlations of random effect terms) or "ran_modes" (conditional modes/BLUPs/latent variable estimates) |
| <code>scales</code> | scales on which to report the variables: for random effects, the choices are "sd-cor" (standard deviations and correlations: the default if <code>scales</code> is <code>NULL</code>) or "vcov" (variances and covariances). <code>NA</code> means no transformation, appropriate e.g. for fixed effects; inverse-link transformations (exponentiation or logistic) are not yet implemented, but may be in the future. |
| <code>ran_prefix</code> | a length-2 character vector specifying the strings to use as prefixes for self- (variance/standard deviation) and cross- (covariance/correlation) random effects terms |
| <code>conf.int</code> | whether to include a confidence interval |
| <code>conf.level</code> | confidence level for CI |
| <code>conf.method</code> | method for computing confidence intervals (see <code>lme4::confint.merMod</code>) |
| <code>...</code> | extra arguments (not used) |
| <code>data</code> | original data this was fitted on; if not given this will attempt to be reconstructed |
| <code>newdata</code> | new data to be used for prediction; optional |

Details

These methods tidy the coefficients of mixed effects models, particularly responses of the `merMod` class

When the modeling was performed with `na.action = "na.omit"` (as is the typical default), rows with `NA` in the initial data are omitted entirely from the augmented data frame. When the modeling was performed with `na.action = "na.exclude"`, one should provide the original data as a second argument, at which point the augmented data will contain those rows (typically with `NA`s in place of the new columns). If the original data is not provided to `augment()` and `na.action = "na.exclude"`, a warning is raised and the incomplete rows are dropped.

Value

All tidying methods return a `data.frame` without rownames. The structure depends on the method chosen.

`tidy` returns one row for each estimated effect, either with groups depending on the effects parameter. It contains the columns

| | |
|------------------------|--|
| <code>group</code> | the group within which the random effect is being estimated: "fixed" for fixed effects |
| <code>level</code> | level within group (NA except for modes) |
| <code>term</code> | term being estimated |
| <code>estimate</code> | estimated coefficient |
| <code>std.error</code> | standard error |
| <code>statistic</code> | t- or Z-statistic (NA for modes) |
| <code>p.value</code> | P-value computed from t-statistic (may be missing/NA) |

`augment` returns one row for each original observation, with columns (each prepended by a `.`) added. Included are the columns

| | |
|----------------------|---|
| <code>.fitted</code> | predicted values |
| <code>.resid</code> | residuals |
| <code>.fixed</code> | predicted values with no random effects |

Also added for "merMod" objects, but not for "mer" objects, are values from the response object within the model (of type `lmResp`, `glmResp`, `nlsResp`, etc). These include `".mu"`, `".offset"`, `".sqrtXwt"`, `".sqrttrwt"`,

`glance` returns one row with the columns

| | |
|-----------------------|--|
| <code>sigma</code> | the square root of the estimated residual variance |
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |
| <code>deviance</code> | deviance |

See Also

[na.action](#)

Examples

```
## Not run:
if (require("lme4")) {
  # example regressions are from lme4 documentation
  lmm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
  tidy(lmm1)
  tidy(lmm1, effects = "fixed")
  tidy(lmm1, effects = "fixed", conf.int=TRUE)
  tidy(lmm1, effects = "fixed", conf.int=TRUE, conf.method="profile")
}
```

```

tidy(lmm1, effects = "ran_modes", conf.int=TRUE)
head(augment(lmm1, sleepstudy))
glance(lmm1)

glmm1 <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
              data = cbpp, family = binomial)
tidy(glmm1)
tidy(glmm1, effects = "fixed")
head(augment(glmm1, cbpp))
glance(glmm1)

startvec <- c(Asym = 200, xmid = 725, scal = 350)
nm1 <- nlmr(circumference ~ SSlogis(age, Asym, xmid, scal) ~ Asym|Tree,
           Orange, start = startvec)
tidy(nm1)
tidy(nm1, effects = "fixed")
head(augment(nm1, Orange))
glance(nm1)
}

## End(Not run)

```

matrix_tidiers

Tidiers for matrix objects

Description

Matrix tidiers are deprecated and will be removed from an upcoming release of broom.

Usage

```

## S3 method for class 'matrix'
tidy(x, ...)

## S3 method for class 'matrix'
glance(x, ...)

```

Arguments

| | |
|-----|---------------------------|
| x | A matrix |
| ... | extra arguments, not used |

Details

These perform tidying operations on matrix objects. `tidy` turns the matrix into a `data.frame` while bringing rownames, if they exist, in as a column called `.rownames` (since results of tidying operations never contain rownames). `glance` simply reports the number of rows and columns. Note that no `augment` method exists for matrices.

Value

`tidy.matrix` returns the original matrix converted into a `data.frame`, except that it incorporates rownames (if they exist) into a column called `.rownames`.

`glance` returns a one-row `data.frame` with

| | |
|---------------------------|---|
| <code>nrow</code> | number of rows |
| <code>ncol</code> | number of columns |
| <code>complete.obs</code> | number of rows that have no missing values |
| <code>na.fraction</code> | fraction of values across all rows and columns that are missing |

Examples

```
## Not run:
mat <- as.matrix(mtcars)
tidy(mat)
glance(mat)

## End(Not run)
```

mcmc_tidiers

Tidying methods for MCMC (Stan, JAGS, etc.) fits

Description

MCMC tidiers will soon be deprecated in broom and there is no ongoing development of these functions at this time. MCMC tidiers are being developed in the broom.mixed package, which is not yet on CRAN.

Usage

```
tidyMCMC(x, pars, estimate.method = "mean", conf.int = FALSE,
  conf.level = 0.95, conf.method = "quantile", droppars = "lp__",
  rhat = FALSE, ess = FALSE, ...)

## S3 method for class 'rjags'
tidy(x, pars, estimate.method = "mean",
  conf.int = FALSE, conf.level = 0.95, conf.method = "quantile", ...)

## S3 method for class 'stanfit'
tidy(x, pars, estimate.method = "mean",
  conf.int = FALSE, conf.level = 0.95, conf.method = "quantile",
  droppars = "lp__", rhat = FALSE, ess = FALSE, ...)
```

Arguments

| | |
|------------------------------|---|
| <code>x</code> | an object of class "stanfit" |
| <code>pars</code> | (character) specification of which parameters to include |
| <code>estimate.method</code> | method for computing point estimate ("mean" or "median") |
| <code>conf.int</code> | (logical) include confidence interval? |
| <code>conf.level</code> | probability level for CI |
| <code>conf.method</code> | method for computing confidence intervals ("quantile" or "HPDinterval") |
| <code>droppars</code> | Parameters not to include in the output (such as log-probability information) |
| <code>rhat, ess</code> | (logical) include Rhat and/or effective sample size estimates? |
| <code>...</code> | unused |

Examples

```
## Not run:

# Using example from "RStan Getting Started"
# https://github.com/stan-dev/rstan/wiki/RStan-Getting-Started

model_file <- system.file("extdata", "8schools.stan", package = "broom")

schools_dat <- list(J = 8,
                   y = c(28, 8, -3, 7, -1, 1, 18, 12),
                   sigma = c(15, 10, 16, 11, 9, 11, 10, 18))

if (requireNamespace("rstan", quietly = TRUE)) {
  set.seed(2015)
  rstan_example <- stan(file = model_file, data = schools_dat,
                      iter = 100, chains = 2)
}

## End(Not run)

if (requireNamespace("rstan", quietly = TRUE)) {
  # the object from the above code was saved as rstan_example.rda
  infile <- system.file("extdata", "rstan_example.rda", package = "broom")
  load(infile)

  tidy(rstan_example)
  tidy(rstan_example, conf.int = TRUE, pars = "theta")

  td_mean <- tidy(rstan_example, conf.int = TRUE)
  td_median <- tidy(rstan_example, conf.int = TRUE, estimate.method = "median")

  library(dplyr)
  library(ggplot2)
  tds <- rbind(mutate(td_mean, method = "mean"),
```

```

mutate(td_median, method = "median"))

ggplot(tds, aes(estimate, term)) +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high)) +
  geom_point(aes(color = method))
}

```

Description

nlme tidiers will soon be deprecated in broom and there is no ongoing development of these functions at this time. nlme tidiers are being developed in the broom.mixed package, which is not yet on CRAN.

Usage

```

## S3 method for class 'lme'
tidy(x, effects = "random", ...)

## S3 method for class 'lme'
augment(x, data = x$data, newdata, ...)

## S3 method for class 'lme'
glance(x, ...)

```

Arguments

| | |
|---------|--|
| x | An object of class lme, such as those from lme or nlme |
| effects | Either "random" (default) or "fixed" |
| ... | extra arguments (not used) |
| data | original data this was fitted on; if not given this will attempt to be reconstructed |
| newdata | new data to be used for prediction; optional |

Details

These methods tidy the coefficients of mixed effects models of the lme class from functions of the nlme package.

When the modeling was performed with `na.action = "na.omit"` (as is the typical default), rows with NA in the initial data are omitted entirely from the augmented data frame. When the modeling was performed with `na.action = "na.exclude"`, one should provide the original data as a second argument, at which point the augmented data will contain those rows (typically with NAs in place of the new columns). If the original data is not provided to `augment()` and `na.action = "na.exclude"`, a warning is raised and the incomplete rows are dropped.

Value

All tidying methods return a `data.frame` without rownames. The structure depends on the method chosen.

`tidy` returns one row for each estimated effect, either random or fixed depending on the `effects` parameter. If `effects = "random"`, it contains the columns

| | |
|-----------------------|---|
| <code>group</code> | the group within which the random effect is being estimated |
| <code>level</code> | level within group |
| <code>term</code> | term being estimated |
| <code>estimate</code> | estimated coefficient |

If `effects="fixed"`, `tidy` returns the columns

| | |
|------------------------|-----------------------------------|
| <code>term</code> | fixed term being estimated |
| <code>estimate</code> | estimate of fixed effect |
| <code>std.error</code> | standard error |
| <code>statistic</code> | t-statistic |
| <code>p.value</code> | P-value computed from t-statistic |

`augment` returns one row for each original observation, with columns (each prepended by a `.`) added. Included are the columns

| | |
|----------------------|---|
| <code>.fitted</code> | predicted values |
| <code>.resid</code> | residuals |
| <code>.fixed</code> | predicted values with no random effects |

`glance` returns one row with the columns

| | |
|-----------------------|---|
| <code>sigma</code> | the square root of the estimated residual variance |
| <code>logLik</code> | the data's log-likelihood under the model |
| <code>AIC</code> | the Akaike Information Criterion |
| <code>BIC</code> | the Bayesian Information Criterion |
| <code>deviance</code> | returned as NA. To quote Brian Ripley on R-help: McCullagh & Nelder (1989) would be the authoritative reference, but the 1982 first edition manages to use 'deviance' in three separate senses on one page. |

See Also

[na.action](#)

Examples

```
## Not run:
if (require("nlme") & require("lme4")) {
  # example regressions are from lme4 documentation, but used for nlme
  lmm1 <- lme(Reaction ~ Days, random=~ Days|Subject, sleepstudy)
  tidy(lmm1)
  tidy(lmm1, effects = "fixed")
  head(augment(lmm1, sleepstudy))
  glance(lmm1)

  startvec <- c(Asym = 200, xmid = 725, scal = 350)
  nm1 <- nlme(circumference ~ SSlogis(age, Asym, xmid, scal),
             data = Orange,
             fixed = Asym + xmid + scal ~1,
             random = Asym ~1,
             start = startvec)

  tidy(nm1)
  tidy(nm1, effects = "fixed")
  head(augment(nm1, Orange))
  glance(nm1)
}

## End(Not run)
```

null_tidiers

Tidiers for NULL inputs

Description

`tidy(NULL)`, `glance(NULL)` and `augment(NULL)` all return an empty `tibble::tibble`. This empty tibble can be treated a tibble with zero rows, making it convenient to combine with other tibbles using functions like `purrr::map_df()` on lists of potentially NULL objects.

Usage

```
## S3 method for class 'NULL'
tidy(x, ...)
```

```
## S3 method for class 'NULL'
glance(x, ...)
```

```
## S3 method for class 'NULL'
augment(x, ...)
```

Arguments

x The value NULL.
 ... Additional arguments (not used).

Value

An empty `tibble::tibble`.

See Also

[tibble::tibble](#)

| | |
|--------------------|---|
| rowwise_df_tidiers | <i>Tidying methods for rowwise_dfs from dplyr, for tidying each row and recombining the results</i> |
|--------------------|---|

Description

Rowwise tidiers are deprecated and will be removed from an upcoming version of broom. We strongly recommend moving to a nest-map-unnest workflow over a rowwise-do workflow. See the vignettes for examples.

Usage

```
## S3 method for class 'rowwise_df'
tidy(x, object, ...)

## S3 method for class 'rowwise_df'
tidy_(x, object, ...)

## S3 method for class 'rowwise_df'
augment(x, object, ...)

## S3 method for class 'rowwise_df'
augment_(x, object, ...)

## S3 method for class 'rowwise_df'
glance(x, object, ...)

## S3 method for class 'rowwise_df'
glance_(x, object, ...)

## S3 method for class 'tbl_df'
tidy(x, ...)

## S3 method for class 'tbl_df'
```



```
augment(x, ...)

## S3 method for class 'tbl_df'
glance(x, ...)
```

Arguments

| | |
|--------|--|
| x | a rowwise_df |
| object | the column name of the column containing the models to be tidied. For tidy, augment, and glance it should be the bare name; for _ methods it should be quoted. |
| ... | additional arguments to pass on to the respective tidying method |

Details

These tidy, augment and glance methods are for performing tidying on each row of a rowwise data frame created by dplyr's group_by and do operations. They first group a rowwise data frame based on all columns that are not lists, then perform the tidying operation on the specified column. This greatly shortens a common idiom of extracting tidy/augment/glance outputs after a do statement.

Note that this functionality is not currently implemented for data.tables, since the result of the do operation is difficult to distinguish from a regular data.table.

Value

A "grouped_df", where the non-list columns of the original are used as grouping columns alongside the tidied outputs.

Examples

```
library(dplyr)
regressions <- mtcars %>%
  group_by(cyl) %>%
  do(mod = lm(mpg ~ wt, .))

regressions

regressions %>% tidy(mod)
regressions %>% augment(mod)
regressions %>% glance(mod)

# we can provide additional arguments to the tidying function
regressions %>% tidy(mod, conf.int = TRUE)

# we can also include the original dataset as a "data" argument
# to augment:
regressions <- mtcars %>%
  group_by(cyl) %>%
  do(mod = lm(mpg ~ wt, .), original = (..))
```

```
# this allows all the original columns to be included:
regressions %>% augment(mod) # doesn't include all original
regressions %>% augment(mod, data = original) # includes all original
```

rstanarm_tidiers

Tidying methods for an rstanarm model

Description

rstanarm tidiers will soon be deprecated in broom and there is no ongoing development of these functions at this time.

Usage

```
## S3 method for class 'stanreg'
tidy(x, parameters = "non-varying",
     intervals = FALSE, prob = 0.9, ...)
```

```
## S3 method for class 'stanreg'
glance(x, looic = FALSE, ...)
```

Arguments

| | |
|------------|---|
| x | Fitted model object from the rstanarm package. See rstanarm::stanreg-objects() . |
| parameters | One or more of "non-varying", "varying", "hierarchical", "auxiliary" (can be abbreviated). See the Value section for details. |
| intervals | If TRUE columns for the lower and upper bounds of the 100*prob% posterior uncertainty intervals are included. See rstanarm::posterior_interval() for details. |
| prob | See rstanarm::posterior_interval() . |
| ... | For glance, if looic=TRUE, optional arguments to rstanarm::loo.stanreg() . |
| looic | Should the LOO Information Criterion (and related info) be included? See rstanarm::loo.stanreg() for details. Note: for models fit to very large datasets this can be a slow computation. |

Details

These methods tidy the estimates from [rstanarm::stanreg-objects\(\)](#) (fitted model objects from the **rstanarm** package) into a summary.

Value

All tidying methods return a `data.frame` without rownames. The structure depends on the method chosen.

When `parameters="non-varying"` (the default), `tidy.stanreg` returns one row for each coefficient, with three columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the corresponding term in the model. |
| <code>estimate</code> | A point estimate of the coefficient (posterior median). |
| <code>std.error</code> | A standard error for the point estimate based on <code>stats::mad()</code> . See the <i>Uncertainty estimates</i> section in <code>rstanarm::print.stanreg()</code> for more details. |

For models with group-specific parameters (e.g., models fit with `rstanarm::stan_glmer()`), setting `parameters="varying"` selects the group-level parameters instead of the non-varying regression coefficients. Additional columns are added indicating the level and group. Specifying `parameters="hierarchical"` selects the standard deviations and (for certain models) correlations of the group-level parameters.

Setting `parameters="auxiliary"` will select parameters other than those included by the other options. The particular parameters depend on which **rstanarm** modeling function was used to fit the model. For example, for models fit using `rstanarm::stan_glm.nb()` the overdispersion parameter is included if `parameters="aux"`, for `rstanarm::stan_lm()` the auxiliary parameters include the residual SD, R^2 , and $\log(\text{fit_ratio})$, etc.

If `intervals=TRUE`, columns for the lower and upper values of the posterior intervals computed with `rstanarm::posterior_interval()` are also included.

`glance` returns one row with the columns

| | |
|------------------------|--|
| <code>algorithm</code> | The algorithm used to fit the model. |
| <code>pss</code> | The posterior sample size (except for models fit using optimization). |
| <code>nobs</code> | The number of observations used to fit the model. |
| <code>sigma</code> | The square root of the estimated residual variance, if applicable. If not applicable (e.g., for binomial GLMs), <code>sigma</code> will be given the value 1 in the returned object. |

If `looic=TRUE`, then the following additional columns are also included:

| | |
|-----------------------|---|
| <code>looic</code> | The LOO Information Criterion. |
| <code>elpd_loo</code> | The expected log predictive density ($\text{elpd_loo} = -2 * \text{looic}$). |
| <code>p_loo</code> | The effective number of parameters. |

See Also

[rstanarm::summary.stanreg\(\)](#)

Examples

```
## Not run:
fit <- stan_glmmer(mpg ~ wt + (1|cyl) + (1+wt|gear), data = mtcars,
                  iter = 300, chains = 2)
# non-varying ("population") parameters
tidy(fit, intervals = TRUE, prob = 0.5)

# hierarchical sd & correlation parameters
tidy(fit, parameters = "hierarchical")

# group-specific deviations from "population" parameters
tidy(fit, parameters = "varying")

# glance method
glance(fit)
glance(fit, looic = TRUE, cores = 1)

## End(Not run)
```

sparse_tidiers

Tidy a sparseMatrix object from the Matrix package

Description

sparseMatrix tidiers are deprecated and will be removed from an upcoming version of broom.

Usage

```
## S3 method for class 'dgTMatrix'
tidy(x, ...)

## S3 method for class 'dgCMatrix'
tidy(x, ...)

## S3 method for class 'sparseMatrix'
tidy(x, ...)
```

Arguments

| | |
|-----|---------------------------|
| x | A Matrix object |
| ... | Extra arguments, not used |

Details

Tidy a sparseMatrix object from the Matrix package into a three-column data frame, row, column, and value (with zeros missing). If there are row names or column names, use those, otherwise use indices

`sp_tidiers`*Tidy a(n) SpatialPolygonsDataFrame object*

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Note that the `sf` package now defines tidy spatial objects and is the recommend approach to spatial data. `sp tidiers` are likely to be deprecated in the near future in favor of `sf::st_as_sf()`. Development of `sp tidiers` has halted in broom.

Usage

```
## S3 method for class 'SpatialPolygonsDataFrame'  
tidy(x, region = NULL, ...)
```

```
## S3 method for class 'SpatialPolygons'  
tidy(x, ...)
```

```
## S3 method for class 'Polygons'  
tidy(x, ...)
```

```
## S3 method for class 'Polygon'  
tidy(x, ...)
```

```
## S3 method for class 'SpatialLinesDataFrame'  
tidy(x, ...)
```

```
## S3 method for class 'Lines'  
tidy(x, ...)
```

```
## S3 method for class 'Line'  
tidy(x, ...)
```

Arguments

| | |
|---------------------|--|
| <code>x</code> | A <code>SpatialPolygonsDataFrame</code> , <code>SpatialPolygons</code> , <code>Polygons</code> , <code>Polygon</code> , <code>SpatialLinesDataFrame</code> , <code>Lines</code> or <code>Line</code> object. |
| <code>region</code> | name of variable used to split up regions |
| <code>...</code> | not used by this method |

| | |
|-----------------|---|
| summary_tidiers | <i>Tidy/glance a(n) summaryDefault object</i> |
|-----------------|---|

Description

For models that have only a single component, the `tidy()` and `glance()` methods are identical. Please see the documentation for both of those methods.

Usage

```
## S3 method for class 'summaryDefault'
tidy(x, ...)

## S3 method for class 'summaryDefault'
glance(x, ...)
```

Arguments

| | |
|------------------|---|
| <code>x</code> | A <code>summaryDefault</code> object, created by calling <code>summary()</code> on a vector. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|----------------------|---|
| <code>minimum</code> | Minimum value in original vector. |
| <code>q1</code> | First quartile of original vector. |
| <code>median</code> | Median of original vector. |
| <code>mean</code> | Mean of original vector. |
| <code>q3</code> | Third quartile of original vector. |
| <code>maximum</code> | Maximum value in original vector. |
| <code>na</code> | Number of NA values in original vector. Column present only when original vector had at least one NA entry. |

See Also

`tidy()`, `summary()`

Examples

```
v <- rnorm(1000)
s <- summary(v)
s

tidy(s)
glance(s)

v2 <- c(v, NA)
tidy(summary(v2))
```

tidy.aareg

Tidy a(n) aareg object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'aareg'
tidy(x, ...)
```

Arguments

| | |
|-----|---|
| x | An aareg object returned from <code>survival::aareg()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble` with one row for each coefficient and columns:

| | |
|-----------|--------------------------------|
| term | name of coefficient |
| estimate | estimate of the slope |
| statistic | test statistic for coefficient |
| std.error | standard error of statistic |

| | |
|-----------|---|
| robust.se | robust version of standard error estimate (only when x was called with dfbeta = TRUE) |
| z | z score |
| p.value | p-value |

See Also

[tidy\(\)](#), [survival::aareg\(\)](#)

Other aareg tidiers: [glance.aareg](#)

Other survival tidiers: [augment.coxph](#), [augment.survreg](#), [glance.aareg](#), [glance.cch](#), [glance.coxph](#), [glance.pyyears](#), [glance.survdiff](#), [glance.survexp](#), [glance.survfit](#), [glance.survreg](#), [tidy.cch](#), [tidy.coxph](#), [tidy.pyyears](#), [tidy.survdiff](#), [tidy.survexp](#), [tidy.survfit](#), [tidy.survreg](#)

Examples

```
library(survival)

afit <- aareg(
  Surv(time, status) ~ age + sex + ph.ecog,
  data = lung,
  dfbeta = TRUE
)

tidy(afit)
```

tidy.acf

Tidy a(n) acf object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'acf'
tidy(x, ...)
```

Arguments

x An acf object created by [stats::acf\(\)](#), [stats::pacf\(\)](#) or [stats::ccf\(\)](#).

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with columns:

| | |
|-----|------------------------|
| lag | lag values |
| acf | calculated correlation |

See Also

`tidy()`, `stats::acf()`, `stats::pacf()`, `stats::ccf()`

Other time series tidiers: `tidy.spec`, `tidy.ts`, `tidy.zoo`

Examples

```
tidy(acf(lh, plot = FALSE))
tidy(ccf(mdeaths, fdeaths, plot = FALSE))
tidy(pacf(lh, plot = FALSE))
```

tidy.anova

Tidy a(n) anova object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'anova'
tidy(x, ...)
```

Arguments

`x` An anova objects, such as those created by `stats::anova()` or `car::Anova()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Details

The term column of an ANOVA table can come with leading or trailing whitespace, which this tidying method trims.

Value

A `tibble::tibble` with columns

| | |
|------------------------|---|
| <code>term</code> | Term within the model, or "Residuals" |
| <code>df</code> | Degrees of freedom used by this term in the model |
| <code>sumsq</code> | Sum of squares explained by this term |
| <code>meansq</code> | Mean of sum of squares among degrees of freedom |
| <code>statistic</code> | F statistic |
| <code>p.value</code> | P-value from F test |

See Also

`tidy()`, `stats::anova()`, `car::Anova()`

Other anova tidiers: `tidy.TukeyHSD`, `tidy.aovlist`, `tidy.aov`, `tidy.manova`

Examples

```
a <- a <- aov(mpg ~ wt + qsec + disp, mtcars)
tidy(a)
```

| | |
|----------|-----------------------------|
| tidy.aov | <i>Tidy a(n) aov object</i> |
|----------|-----------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'aov'
tidy(x, ...)
```

Arguments

| | |
|-----|--|
| x | An aov objects, such as those created by <code>stats::aov()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Details

The term column of an ANOVA table can come with leading or trailing whitespace, which this tidying method trims.

Value

A `tibble::tibble` with columns

| | |
|-----------|---|
| term | Term within the model, or "Residuals" |
| df | Degrees of freedom used by this term in the model |
| sumsq | Sum of squares explained by this term |
| meansq | Mean of sum of squares among degrees of freedom |
| statistic | F statistic |
| p.value | P-value from F test |

See Also

`tidy()`, `stats::aov()`

Other anova tidiers: `tidy.TukeyHSD`, `tidy.anova`, `tidy.aovlist`, `tidy.manova`

Examples

```
a <- aov(mpg ~ wt + qsec + disp, mtcars)
tidy(a)
```

| | |
|--------------|---------------------------------|
| tidy.aovlist | <i>Tidy a(n) aovlist object</i> |
|--------------|---------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'aovlist'
tidy(x, ...)
```

Arguments

| | |
|-----|--|
| x | An aovlist objects, such as those created by <code>stats::aov()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Details

The term column of an ANOVA table can come with leading or trailing whitespace, which this tidying method trims.

Value

A `tibble::tibble` with columns

| | |
|-----------|---|
| term | Term within the model, or "Residuals" |
| df | Degrees of freedom used by this term in the model |
| sumsq | Sum of squares explained by this term |
| meansq | Mean of sum of squares among degrees of freedom |
| statistic | F statistic |
| p.value | P-value from F test |
| stratum | The error stratum |

See Also

`tidy()`, `stats::aov()`

Other anova tidiers: `tidy.TukeyHSD`, `tidy.anova`, `tidy.aov`, `tidy.manova`

Examples

```
a <- aov(mpg ~ wt + qsec + Error(displ / am), mtcars)
tidy(a)
```

tidy.Arima

Tidy a(n) Arima object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'Arima'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

| | |
|-------------------------|--|
| <code>x</code> | An object of class Arima created by <code>stats::arima()</code> . |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble` with one row for each coefficient and columns:

| | |
|------------------------|--|
| <code>term</code> | The term in the nonlinear model being estimated and tested |
| <code>estimate</code> | The estimated coefficient |
| <code>std.error</code> | The standard error from the linear model |

If `conf.int = TRUE`, also returns

| | |
|------------------------|---------------------------------|
| <code>conf.low</code> | low end of confidence interval |
| <code>conf.high</code> | high end of confidence interval |

See Also

`stats::arima()`

Other Arima tidiers: `glance.Arima`

Examples

```
fit <- arima(lh, order = c(1, 0, 0))
tidy(fit)
glance(fit)
```

| | |
|---------------------------|---------------------------------|
| <code>tidy.betareg</code> | <i>Tidy a(n) betareg object</i> |
|---------------------------|---------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'betareg'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

| | |
|-------------------------|--|
| <code>x</code> | A betareg object produced by a call to <code>betareg::betareg()</code> . |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

In addition to the standard columns, the returned tibble has an additional column `component`. `component` indicates whether a particular term was used to model either the "mean" or "precision". Here the precision is the inverse of the variance, often referred to as ϕ . At least one term will have been used to model ϕ .

See Also

`tidy()`, `betareg::betareg()`

Examples

```
library(betareg)

data("GasolineYield", package = "betareg")

mod <- betareg(yield ~ batch + temp, data = GasolineYield)
```

```

mod
tidy(mod)
tidy(mod, conf.int = TRUE)
tidy(mod, conf.int = TRUE, conf.level = .99)

augment(mod)

glance(mod)

```

tidy.biglm

Tidy a(n) biglm object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'biglm'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = FALSE, quick = FALSE, ...)

```

Arguments

| | |
|--------------|--|
| x | A biglm object created by a call to <code>biglm::biglm()</code> or <code>biglm::bigglm()</code> . |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| conf.level | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| exponentiate | Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE. |
| quick | Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to FALSE. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

See Also

`tidy()`, `biglm::biglm()`, `biglm::bigglm()`

Other biglm tidiers: `glance.biglm`

Examples

```
if (require("biglm", quietly = TRUE)) {
  bfit <- biglm(mpg ~ wt + disp, mtcars)
  tidy(bfit)
  tidy(bfit, conf.int = TRUE)
  tidy(bfit, conf.int = TRUE, conf.level = .9)

  glance(bfit)

  # bigglm: logistic regression
  bgfit <- bigglm(am ~ mpg, mtcars, family = binomial())
  tidy(bgfit)
  tidy(bgfit, exponentiate = TRUE)
  tidy(bgfit, conf.int = TRUE)
  tidy(bgfit, conf.int = TRUE, conf.level = .9)
  tidy(bgfit, conf.int = TRUE, conf.level = .9, exponentiate = TRUE)

  glance(bgfit)
}
```

| | |
|----------------|-----------------------------------|
| tidy.binDesign | <i>Tidy a(n) binDesign object</i> |
|----------------|-----------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'binDesign'
tidy(x, ...)
```

Arguments

| | |
|-----|--|
| x | A <code>binGroup::binDesign()</code> object. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|-------|--------------------------------------|
| n | Number of trials in given iteration. |
| power | Power achieved for given value of n. |

See Also

`tidy()`, `binGroup::binDesign()`

Other bingroup tidiers: `glance.binDesign`, `tidy.binWidth`

Examples

```
if (require("binGroup", quietly = TRUE)) {
  des <- binDesign(nmax = 300, delta = 0.06,
                  p.hyp = 0.1, power = .8)

  glance(des)
  tidy(des)
}
```

```

# the ggplot2 equivalent of plot(des)
library(ggplot2)
ggplot(tidy(des), aes(n, power)) +
  geom_line()
}

```

tidy.binWidth

Tidy a(n) binWidth object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'binWidth'
tidy(x, ...)

```

Arguments

| | |
|-----|--|
| x | A <code>binGroup::binWidth()</code> object. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A one-row `tibble::tibble` with columns:

| | |
|-------------|--|
| ci.width | Expected width of confidence interval. |
| alternative | Alternative hypothesis. |
| p | True proportion. |
| n | Total sample size. |

See Also

`tidy()`, `binGroup::binWidth()`

Other bingroup tidiers: `glance.binDesign`, `tidy.binDesign`

Examples

```

if (require("binGroup", quietly = TRUE)) {
  bw <- binWidth(100, .1)
  bw
  tidy(bw)

  library(dplyr)
  d <- expand.grid(n = seq(100, 800, 100),
                 p = .5,
                 method = c("CP", "Blaker", "Score", "Wald"),
                 stringsAsFactors = FALSE) %>%
    group_by(n, p, method) %>%
    do(tidy(binWidth(.$n, .$p, method = .$method)))

  library(ggplot2)
  ggplot(d, aes(n, ci.width, color = method)) +
    geom_line() +
    xlab("Total Observations") +
    ylab("Expected CI Width")
}

```

tidy.boot

Tidy a(n) boot object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'boot'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     conf.method = "perc", ...)

```

Arguments

| | |
|-------------|---|
| x | A <code>boot::boot()</code> object. |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| conf.level | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| conf.method | Passed to the type argument of <code>boot::boot.ci()</code> . Defaults to "perc". |

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with one row per bootstrapped statistic and columns:

| | |
|------------------------|---|
| <code>term</code> | Name of the computed statistic, if present. |
| <code>statistic</code> | Original value of the statistic. |
| <code>bias</code> | Bias of the statistic. |
| <code>std.error</code> | Standard error of the statistic. |

If weights were provided to the `boot` function, an `estimate` column is included showing the weighted bootstrap estimate, and the standard error is of that estimate.

If there are no original statistics in the "boot" object, such as with a call to `tsboot` with `orig.t = FALSE`, the `original` and `statistic` columns are omitted, and only `estimate` and `std.error` columns shown.

See Also

[tidy\(\)](#), [boot::boot\(\)](#), [boot::tsboot\(\)](#), [boot::boot.ci\(\)](#), [rsample::bootstraps\(\)](#)

Examples

```
if (require("boot")) {
  clotting <- data.frame(
    u = c(5,10,15,20,30,40,60,80,100),
    lot1 = c(118,58,42,35,27,25,21,19,18),
    lot2 = c(69,35,26,21,18,16,13,12,12))

  g1 <- glm(lot2 ~ log(u), data = clotting, family = Gamma)

  bootfun <- function(d, i) {
    coef(update(g1, data= d[i,]))
  }
  bootres <- boot(clotting, bootfun, R = 999)
  tidy(g1, conf.int=TRUE)
  tidy(bootres, conf.int=TRUE)
}
```

tidy.btergm

*Tidy a(n) btergm object***Description**

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

This method tidies the coefficients of a bootstrapped temporal exponential random graph model estimated with the **xergm**. It simply returns the coefficients and their confidence intervals.

Usage

```
## S3 method for class 'btergm'
tidy(x, conf.level = 0.95, exponentiate = FALSE,
     quick = FALSE, ...)
```

Arguments

| | |
|--------------|--|
| x | A <code>btergm:btergm()</code> object. |
| conf.level | Confidence level for confidence intervals. Defaults to 0.95. |
| exponentiate | Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE. |
| quick | Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to FALSE. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble` with one row per term in the random graph model and columns:

| | |
|-----------|---|
| term | The term in the model being estimated and tested. |
| estimate | The estimated value of the coefficient. |
| conf.low | The lower bound of the confidence interval. |
| conf.high | The lower bound of the confidence interval. |

See Also

[tidy\(\)](#), [btergm::btergm\(\)](#)

Examples

```
if (require("xergm")) {
  set.seed(1)
  # Using the same simulated example as the xergm package
  # Create 10 random networks with 10 actors
  networks <- list()
  for(i in 1:10){
    mat <- matrix(rbinom(100, 1, .25), nrow = 10, ncol = 10)
    diag(mat) <- 0
    nw <- network::network(mat)
    networks[[i]] <- nw
  }
  # Create 10 matrices as covariates
  covariates <- list()
  for (i in 1:10) {
    mat <- matrix(rnorm(100), nrow = 10, ncol = 10)
    covariates[[i]] <- mat
  }
  # Fit a model where the propensity to form ties depends
  # on the edge covariates, controlling for the number of
  # in-stars
  suppressWarnings(btfit <- btergm(networks ~ edges + istar(2) +
    edgescov(covariates), R = 100))

  # Show terms, coefficient estimates and errors
  tidy(btfit)

  # Show coefficients as odds ratios with a 99% CI
  tidy(btfit, exponentiate = TRUE, conf.level = 0.99)
}
```

tidy.cch

Tidy a(n) cch object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'cch'
tidy(x, conf.level = 0.95, ...)
```

Arguments

| | |
|------------|--|
| x | An cch object returned from <code>survival::cch()</code> . |
| conf.level | confidence level for CI |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.lvel = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|-----------|---|
| term | The name of the regression term. |
| estimate | The estimated value of the regression term. |
| std.error | The standard error of the regression term. |
| statistic | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| p.value | The two-sided p-value associated with the observed statistic. |
| conf.low | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| conf.high | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

See Also

`tidy()`, `survival::cch()`

Other cch tidiers: `glance.cch`, `glance.survfit`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.aareg`, `glance.cch`, `glance.coxph`, `glance.pyears`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `glance.survreg`, `tidy.aareg`, `tidy.coxph`, `tidy.pyears`, `tidy.survdiff`, `tidy.survexp`, `tidy.survfit`, `tidy.survreg`

Examples

```
library(survival)

# examples come from cch documentation
subcoh <- nwtco$in.subcohort
```



```

selccoh <- with(nwtco, rel==1|subcoh==1)
ccoh.data <- nwtco[selccoh,]
ccoh.data$subcohort <- subcoh[selccoh]
## central-lab histology
ccoh.data$histol <- factor(ccoh.data$histol, labels=c("FH", "UH"))
## tumour stage
ccoh.data$stage <- factor(ccoh.data$stage, labels=c("I", "II", "III", "IV"))
ccoh.data$age <- ccoh.data$age/12 # Age in years

fit.ccP <- cch(Surv(edrel, rel) ~ stage + histol + age, data = ccoh.data,
              subcoh = ~subcohort, id= ~seqno, cohort.size = 4028)

tidy(fit.ccP)

# coefficient plot
library(ggplot2)
ggplot(tidy(fit.ccP), aes(x = estimate, y = term)) +
  geom_point() +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high), height = 0) +
  geom_vline(xintercept = 0)

```

tidy.cld

Tidy a(n) cld object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'cld'
tidy(x, ...)
```

Arguments

x A cld object created by calling `multcomp::cld()` on a `glht`, `confint.glht()` or `summary.glht()` object.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

See Also

[tidy\(\)](#), [multcomp::cld\(\)](#), [multcomp::summary.glht\(\)](#), [multcomp::confint.glht\(\)](#), [multcomp::glht\(\)](#)
 Other multcomp tidiers: [tidy.confint.glht](#), [tidy.glht](#), [tidy.summary.glht](#)

 tidy.coefstest

Tidy a(n) coefstest object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'coefstest'
tidy(x, ...)
```

Arguments

`x` A `coefstest` object returned from [lmtest::coefstest\(\)](#).
`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an [augment\(\)](#) method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with one row for each coefficient and columns:

| | |
|------------------------|---|
| <code>term</code> | The term in the linear model being estimated and tested |
| <code>estimate</code> | The estimated coefficient |
| <code>std.error</code> | The standard error |
| <code>statistic</code> | test statistic |
| <code>p.value</code> | p-value |

See Also

[tidy\(\)](#), [lmtest::coefstest\(\)](#)

Examples

```
if (require("lmtest", quietly = TRUE)) {
  data(Mandible)
  fm <- lm(length ~ age, data=Mandible, subset=(age <= 28))

  lmtest::coefstest(fm)
  tidy(coefstest(fm))
}
```

tidy.confint.glm *Tidy a(n) confint.glm object*

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'confint.glm'
tidy(x, ...)
```

Arguments

x A confint.glm object created by calling `multcomp::confint.glm()` on a glm object created with `multcomp::glm()`.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

See Also

`tidy()`, `multcomp::confint.glm()`, `multcomp::glm()`

Other multcomp tidiers: `tidy.cld`, `tidy.glm`, `tidy.summary.glm`

tidy.confusionMatrix *Tidy a(n) confusionMatrix object*

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'confusionMatrix'
tidy(x, by_class = TRUE, ...)
```

Arguments

| | |
|----------|--|
| x | An object of class confusionMatrix created by a call to <code>caret::confusionMatrix()</code> . |
| by_class | Logical indicating whether or not to show performance measures broken down by class. Defaults to TRUE. When <code>by_class = FALSE</code> only returns a tibble with accuracy and kappa statistics. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble` with one or more of the following columns:

| | |
|-----------|---|
| term | The name of a statistic from the confusion matrix |
| class | Which class the term is a measurement of |
| estimate | The value of the statistic |
| conf.low | Low end of 95 percent CI only applicable to accuracy |
| conf.high | High end of 95 percent CI only applicable to accuracy |
| p.value | P-value for accuracy and kappa statistics |

See Also

`tidy()`, `caret::confusionMatrix()`

Examples

```

if (requireNamespace("caret", quietly = TRUE)) {

  set.seed(27)

  two_class_sample1 <- as.factor(sample(letters[1:2], 100, TRUE))
  two_class_sample2 <- as.factor(sample(letters[1:2], 100, TRUE))

  two_class_cm <- caret::confusionMatrix(
    two_class_sample1,
    two_class_sample2
  )

  tidy(two_class_cm)
  tidy(two_class_cm, by_class = FALSE)

  # multiclass example

  six_class_sample1 <- as.factor(sample(letters[1:6], 100, TRUE))
  six_class_sample2 <- as.factor(sample(letters[1:6], 100, TRUE))

  six_class_cm <- caret::confusionMatrix(
    six_class_sample1,
    six_class_sample2
  )

  tidy(six_class_cm)
  tidy(six_class_cm, by_class = FALSE)
}

```

tidy.coxph

Tidy a(n) coxph object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'coxph'
tidy(x, exponentiate = FALSE, conf.int = TRUE,
     conf.level = 0.95, ...)

```

Arguments

| | |
|---------------------------|--|
| <code>x</code> | A coxph object returned from <code>survival::coxph()</code> . |
| <code>exponentiate</code> | Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE. |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble` with one row for each term and columns:

| | |
|------------------------|----------------------------|
| <code>estimate</code> | estimate of slope |
| <code>std.error</code> | standard error of estimate |
| <code>statistic</code> | test statistic |
| <code>p.value</code> | p-value |

See Also

`tidy()`, `survival::coxph()`

Other coxph tidiers: `augment.coxph`, `glance.coxph`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.aareg`, `glance.cch`, `glance.coxph`, `glance.pyears`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `glance.survreg`, `tidy.aareg`, `tidy.cch`, `tidy.pyears`, `tidy.survdiff`, `tidy.survexp`, `tidy.survfit`, `tidy.survreg`

Examples

```
library(survival)

cf1t <- coxph(Surv(time, status) ~ age + sex, lung)

tidy(cf1t)
tidy(cf1t, exponentiate = TRUE)

lp <- augment(cf1t, lung)
risks <- augment(cf1t, lung, type.predict = "risk")
```

```
expected <- augment(cfit, lung, type.predict = "expected")

glance(cfit)

# also works on clogit models
resp <- levels(logan$occupation)
n <- nrow(logan)
indx <- rep(1:n, length(resp))
logan2 <- data.frame(
  logan[indx,],
  id = indx,
  tocc = factor(rep(resp, each=n))
)

logan2$case <- (logan2$occupation == logan2$tocc)

c1 <- clogit(case ~ tocc + tocc:education + strata(id), logan2)
tidy(c1)
glance(c1)

library(ggplot2)

ggplot(lp, aes(age, .fitted, color = sex)) +
  geom_point()

ggplot(risks, aes(age, .fitted, color = sex)) +
  geom_point()

ggplot(expected, aes(time, .fitted, color = sex)) +
  geom_point()
```

tidy.cv.glmnet

Tidy a(n) cv.glmnet object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'cv.glmnet'
tidy(x, ...)
```

Arguments

`x` A `cv.glmnet` object returned from `glmnet::cv.glmnet()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A `tibble::tibble` with one-row for each value of the penalization parameter `lambda` in `x` and columns:

| | |
|------------------------|---|
| <code>lambda</code> | Value of the penalty parameter <code>lambda</code> . |
| <code>estimate</code> | Median loss across all cross-validation folds for a given <code>lambda</code> . |
| <code>std.error</code> | Standard error of the cross-validation estimated loss. |
| <code>conf.low</code> | lower bound on confidence interval for cross-validation estimated loss. |
| <code>conf.high</code> | Upper bound on confidence interval for cross-validation estimated loss. |
| <code>nzero</code> | Number of coefficients that are exactly zero for given <code>lambda</code> |
| <code>.</code> | |

See Also

[tidy\(\)](#), [glmnet::cv.glmnet\(\)](#)

Other `glmnet` tidiers: [glance.cv.glmnet](#), [glance.glmnet](#), [tidy.glmnet](#)

Examples

```
if (requireNamespace("glmnet", quietly = TRUE)) {
  library(glmnet)
  set.seed(27)

  nobs <- 100
  nvar <- 50
  real <- 5

  x <- matrix(rnorm(nobs * nvar), nobs, nvar)
  beta <- c(rnorm(real, 0, 1), rep(0, nvar - real))
  y <- c(t(beta) %*% t(x)) + rnorm(nvar, sd = 3)

  cvfit1 <- cv.glmnet(x,y)

  tidy(cvfit1)
  glance(cvfit1)
}
```



```

library(ggplot2)
tidied_cv <- tidy(cvfit1)
glance_cv <- glance(cvfit1)

# plot of MSE as a function of lambda
g <- ggplot(tidied_cv, aes(lambda, estimate)) + geom_line() + scale_x_log10()
g

# plot of MSE as a function of lambda with confidence ribbon
g <- g + geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = .25)
g

# plot of MSE as a function of lambda with confidence ribbon and choices
# of minimum lambda marked
g <- g + geom_vline(xintercept = glance_cv$lambda.min) +
  geom_vline(xintercept = glance_cv$lambda.1se, lty = 2)
g

# plot of number of zeros for each choice of lambda
ggplot(tidied_cv, aes(lambda, nzero)) + geom_line() + scale_x_log10()

# coefficient plot with min lambda shown
tidied <- tidy(cvfit1$glmnet.fit)
ggplot(tidied, aes(lambda, estimate, group = term)) + scale_x_log10() +
  geom_line() +
  geom_vline(xintercept = glance_cv$lambda.min) +
  geom_vline(xintercept = glance_cv$lambda.1se, lty = 2)
}

```

tidy.density

Tidy a(n) density object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'density'
tidy(x, ...)
```

Arguments

x A density object returned from `stats::density()`.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with two columns: points `x` where the density is estimated, and estimated density `y`.

See Also

`tidy()`, `stats::density()`

Other stats tidiers: `tidy.dist`, `tidy.ftable`

`tidy.dist`

Tidy a(n) dist object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'dist'
tidy(x, diagonal = attr(x, "Diag"), upper = attr(x,
  "Upper"), ...)
```

Arguments

`x` A `dist` object returned from `stats::dist()`.

`diagonal` Logical indicating whether or not to tidy the diagonal elements of the distance matrix. Defaults to whatever was based to the `diag` argument of `stats::dist()`.

`upper` Logical indicating whether or not to tidy the upper half of the distance matrix. Defaults to whatever was based to the `upper` argument of `stats::dist()`.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Details

If the distance matrix does not include an upper triangle and/or diagonal, the tidied version will not either.

Value

A `tibble::tibble` with one row for each pair of items in the distance matrix, with columns:

| | |
|-----------------------|------------------------|
| <code>item1</code> | First item |
| <code>item2</code> | Second item |
| <code>distance</code> | Distance between items |

See Also

`tidy()`, `stats::dist()`

Other stats tidiers: `tidy.density`, `tidy.ftable`

Examples

```
iris_dist <- dist(t(iris[, 1:4]))
iris_dist

tidy(iris_dist)
tidy(iris_dist, upper = TRUE)
tidy(iris_dist, diagonal = TRUE)
```

tidy.ergm

Tidy a(n) ergm object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

The methods should work with any model that conforms to the `ergm` class, such as those produced from weighted networks by the `ergm.count` package.

Usage

```
## S3 method for class 'ergm'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = FALSE, quick = FALSE, ...)
```

Arguments

| | |
|--------------|---|
| x | An ergm object returned from a call to <code>ergm::ergm()</code> . |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| conf.level | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| exponentiate | Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE. |
| quick | Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to FALSE. |
| ... | Additional arguments to pass to <code>ergm::summary.ergm()</code> . Cautionary note: Mispecified arguments may be silently ignored. |

Value

A `tibble::tibble` with one row for each coefficient in the exponential random graph model, with columns:

| | |
|------------|--|
| term | The term in the model being estimated and tested |
| estimate | The estimated coefficient |
| std.error | The standard error |
| mcmc.error | The MCMC error |
| p.value | The two-sided p-value |

If `conf.int = TRUE`, it also includes columns for `conf.low` and `conf.high`.

References

Hunter DR, Handcock MS, Butts CT, Goodreau SM, Morris M (2008b). **ergm**: A Package to Fit, Simulate and Diagnose Exponential-Family Models for Networks. *Journal of Statistical Software*, 24(3). <http://www.jstatsoft.org/v24/i03/>.

See Also

`tidy()`, `ergm::ergm()`, `ergm::control.ergm()`, `ergm::summary.ergm()`

Other ergm tidiers: `glance.ergm`

Examples

```
## Not run:
if (require("ergm")) {
  # Using the same example as the ergm package
  # Load the Florentine marriage network data
```

```

data(florentine)

# Fit a model where the propensity to form ties between
# families depends on the absolute difference in wealth
gest <- ergm(flomarriage ~ edges + absdiff("wealth"))

# Show terms, coefficient estimates and errors
tidy(gest)

# Show coefficients as odds ratios with a 99% CI
tidy(gest, exponentiate = TRUE, conf.int = TRUE, conf.level = 0.99)

# Take a look at likelihood measures and other
# control parameters used during MCMC estimation
glance(gest)
glance(gest, deviance = TRUE)
glance(gest, mcmc = TRUE)
}

## End(Not run)

```

tidy.factanal

Tidy a(n) factanal object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'factanal'
tidy(x, ...)

```

Arguments

x A factanal object created by `stats::factanal()`.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A `tibble::tibble` with one row for each variable used in the analysis and columns:

| | |
|------------|--|
| variable | The variable being estimated in the factor analysis |
| uniqueness | Proportion of residual, or unexplained variance |
| flX | Factor loading of term on factor X. There will be as many columns of this format as there were factors fitted. |

See Also

`tidy()`, `stats::factanal()`

Other factanal tidiers: `augment.factanal`, `glance.factanal`

Examples

```
mod <- factanal(mtcars, 3, scores = "regression")
```

```
glance(mod)
```

```
tidy(mod)
```

```
augment(mod)
```

```
augment(mod, mtcars)
```

tidy.felm

Tidy a(n) felm object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'felm'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     fe = FALSE, ...)
```

Arguments

| | |
|----------|---|
| x | A <code>felm</code> object returned from <code>lfe::felm()</code> . |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |

| | |
|-------------------------|---|
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| <code>fe</code> | Logical indicating whether or not to include estimates of fixed effects. Defaults to FALSE. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

If `fe = TRUE`, also includes rows for fixed effects estimates.

See Also

`tidy()`, `lfe::felm()`

Other `felm` tidiers: `augment.felm`

Examples

```
if (require("lfe", quietly = TRUE)) {
  library(lfe)

  N=1e2
  DT <- data.frame(
    id = sample(5, N, TRUE),
    v1 = sample(5, N, TRUE),
    v2 = sample(1e6, N, TRUE),
    v3 = sample(round(runif(100,max=100),4), N, TRUE),
```

```

    v4 = sample(round(runif(100,max=100),4), N, TRUE)
  )

  result_felm <- felm(v2~v3, DT)
  tidy(result_felm)
  augment(result_felm)
  result_felm <- felm(v2~v3|id+v1, DT)
  tidy(result_felm, fe = TRUE)
  augment(result_felm)
  v1<-DT$v1
  v2 <- DT$v2
  v3 <- DT$v3
  id <- DT$id
  result_felm <- felm(v2~v3|id+v1)
  tidy(result_felm)
  augment(result_felm)
  glance(result_felm)
}

```

tidy.fitdistr

Tidy a(n) fitdistr object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'fitdistr'
tidy(x, ...)

```

Arguments

| | |
|-----|--|
| x | A fitdistr object returned by <code>MASS::fitdistr()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble` with one row for estimated parameter, with columns:

| | |
|-----------|-----------------------------|
| term | The term that was estimated |
| estimate | Estimated value |
| std.error | Standard error of estimate |

See Also

`tidy()`, `MASS::fitdistr()`

Other fitdistr tidiers: `glance.fitdistr`

Examples

```
set.seed(2015)
x <- rnorm(100, 5, 2)

library(MASS)
fit <- fitdistr(x, dnorm, list(mean = 3, sd = 1))

tidy(fit)
glance(fit)
```

| | |
|-------------|--------------------------------|
| tidy.ftable | <i>Tidy a(n) ftable object</i> |
|-------------|--------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'ftable'
tidy(x, ...)
```

Arguments

x An ftable object returned from `stats::ftable()`.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

An `fable` contains a "flat" contingency table. This melts it into a `tibble::tibble` with one column for each variable, then a `Freq` column.

See Also

`tidy()`, `stats::ftable()`

Other stats tidiers: `tidy.density`, `tidy.dist`

Examples

```
tidy(ftable(Titanic, row.vars = 1:3))
```

tidy.Gam

Tidy a(n) Gam object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'Gam'
tidy(x, ...)
```

Arguments

`x` A Gam object returned from a call to `gam::gam()`.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Details

Tidy gam objects created by calls to `mgcv::gam()` with `tidy.gam()`.

Value

The tidied output of the parametric ANOVA for the GAM model as a `tibble::tibble` with one row for each term in the model.

See Also

`tidy()`, `gam::gam()`, `tidy.anova()`, `tidy.gam()`

Other gam tidiers: `glance.Gam`

Examples

```
library(gam)
g <- gam(mpg ~ s(hp, 4) + am + qsec, data = mtcars)

tidy(g)
glance(g)
```

tidy.gam

Tidy a(n) gam object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'gam'
tidy(x, parametric = FALSE, ...)
```

Arguments

`x` A gam object returned from a call to `mgcv::gam()`.

`parametric` Logical indicating if parametric or smooth terms should be tidied. Defaults to FALSE, meaning that smooth terms are tidied by default.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Details

To tidy Gam objects created by calls to `gam::gam()`, see `tidy.Gam()`.

See Also

`tidy()`, `mgcv::gam()`, `tidy.Gam()`

Other mgcv tidiers: `glance.gam`

Examples

```
g <- mgcv::gam(mpg ~ s(hp) + am + qsec, data = mtcars)

tidy(g)
tidy(g, parametric = TRUE)
glance(g)
```

tidy.gamlss

Tidy a(n) gamlss object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'gamlss'
tidy(x, quick = FALSE, ...)
```

Arguments

| | |
|-------|---|
| x | A <code>gamlss</code> object returned from <code>gamlss::gamlss()</code> . |
| quick | Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to FALSE. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble` with one row for each coefficient, containing columns

| | |
|-----------|--|
| parameter | Type of coefficient being estimated: mu, sigma, nu, or tau. |
| term | Name of term in the model. |
| estimate | Estimate coefficient of given term. |
| std.error | Standard error of given term. |
| statistic | T-statistic used to test hypothesis that coefficient equals zero. |
| p.value | Two sided p-value based on null hypothesis of coefficient equaling zero. |

Examples

```
library(gamlss)

g <- gamlss(
  y ~ pb(x),
  sigma.fo = ~ pb(x),
  family = BCT,
  data = abdom,
  method = mixed(1, 20)
)

tidy(g)
```

tidy.garch

Tidy a(n) garch object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'garch'
tidy(x, ...)
```

Arguments

`x` A garch object returned by `tseries::garch()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A `tibble::tibble` with one row for each coefficient and columns:

| | |
|------------------------|---|
| <code>term</code> | The term in the linear model being estimated and tested |
| <code>estimate</code> | The estimated coefficient |
| <code>std.error</code> | The standard error |
| <code>statistic</code> | test statistic |
| <code>p.value</code> | p-value |

See Also

`tidy()`, `tseries::garch()`

Other garch tidiers: `glance.garch`

Examples

```
library(tseries)

data(EuStockMarkets)
dax <- diff(log(EuStockMarkets))[, "DAX"]
dax.garch <- garch(dax)
dax.garch

tidy(dax.garch)
glance(dax.garch)
```

| | |
|-------------|--------------------------------|
| tidy.geeglm | <i>Tidy a(n) geeglm object</i> |
|-------------|--------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'geeglm'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = FALSE, quick = FALSE, ...)
```

Arguments

| | |
|--------------|---|
| x | A geeglm object returned from a call to <code>geepack::geeglm()</code> . |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| conf.level | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| exponentiate | Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE. |
| quick | Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to FALSE. |

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Details

If `conf.int = TRUE`, the confidence interval is computed with the an internal `confint.geeglm()` function.

If you have missing values in your model data, you may need to refit the model with `na.action = na.exclude` or deal with the missingness in the data beforehand.

Value

A `tibble::tibble` with one row for each coefficient, with five columns:

| | |
|------------------------|---|
| <code>term</code> | The term in the linear model being estimated and tested |
| <code>estimate</code> | The estimated coefficient |
| <code>std.error</code> | The standard error from the GEE model |
| <code>statistic</code> | Wald statistic |
| <code>p.value</code> | two-sided p-value |

If `conf.int = TRUE`, includes includes columns `conf.low` and `conf.high`, which are computed internally.

See Also

`tidy()`, `geepack::geeglm()`

Examples

```
if (requireNamespace("geepack", quietly = TRUE)) {
  library(geepack)
  data(state)

  ds <- data.frame(state.region, state.x77)

  geefit <- geeglm(Income ~ Frost + Murder, id = state.region,
                  data = ds, family = gaussian,
                  corstr = "exchangeable")

  tidy(geefit)
  tidy(geefit, quick = TRUE)
  tidy(geefit, conf.int = TRUE)
}
```

| | |
|-----------|------------------------------|
| tidy.glht | <i>Tidy a(n) glht object</i> |
|-----------|------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'glht'
tidy(x, ...)
```

Arguments

| | |
|-----|---|
| x | A glht object returned by <code>multcomp::glht()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

See Also

`tidy()`, `multcomp::glht()`

Other multcomp tidiers: `tidy.cld`, `tidy.confint.glht`, `tidy.summary.glht`

Examples

```
if (require("multcomp") && require("ggplot2")) {
  library(multcomp)
  library(ggplot2)

  amod <- aov(breaks ~ wool + tension, data = warpbreaks)
  wht <- glht(amod, linfct = mcp(tension = "Tukey"))

  tidy(wht)
  ggplot(wht, aes(lhs, estimate)) + geom_point()

  CI <- confint(wht)
  tidy(CI)
  ggplot(CI, aes(lhs, estimate, ymin = lwr, ymax = upr)) +
```

```

    geom_pointrange()

tidy(summary(wht))
ggplot(mapping = aes(lhs, estimate)) +
  geom_linerange(aes(ymin = lwr, ymax = upr), data = CI) +
  geom_point(aes(size = p), data = summary(wht)) +
  scale_size(trans = "reverse")

cld <- cld(wht)
tidy(cld)
}

```

tidy.glm

*Tidy a(n) glm object***Description**

This method wraps `tidy.lm()`.

Usage

```
## S3 method for class 'glm'
tidy(x, ...)
```

Arguments

`x` A `glm` object returned from `stats::glm()`.

`...` Arguments passed on to `tidy.lm`

`x` An `lm` object created by `stats::lm()`.

conf.int Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to `FALSE`.

conf.level The confidence level to use for the confidence interval if `conf.int = TRUE`. Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval.

quick Logical indicating if the only the `term` and `estimate` columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to `FALSE`.

exponentiate Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to `FALSE`.

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

`term` The name of the regression term.

| | |
|-----------|---|
| estimate | The estimated value of the regression term. |
| std.error | The standard error of the regression term. |
| statistic | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| p.value | The two-sided p-value associated with the observed statistic. |
| conf.low | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| conf.high | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

If the linear model is an `mlm` object (multiple linear model), there is an additional column:

| | |
|----------|--|
| response | Which response column the coefficients correspond to (typically Y1, Y2, etc) |
|----------|--|

See Also

[tidy\(\)](#), [tidy.lm\(\)](#)

[stats::glm\(\)](#)

Other lm tidiers: [augment.glm](#), [augment.lm](#), [glance.glm](#), [glance.lm](#), [tidy.lm](#)

| | |
|-------------|--------------------------------|
| tidy.glmnet | <i>Tidy a(n) glmnet object</i> |
|-------------|--------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'glmnet'
tidy(x, return_zeros = FALSE, ...)
```

Arguments

| | |
|--------------|---|
| x | A <code>glmnet</code> object returned from glmnet::glmnet() . |
| return_zeros | Logical indicating whether coefficients with value zero should be included in the results. Defaults to <code>FALSE</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an augment() method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Details

Note that while this representation of GLMs is much easier to plot and combine than the default structure, it is also much more memory-intensive. Do not use for large, sparse matrices.

No augment method is yet provided even though the model produces predictions, because the input data is not tidy (it is a matrix that may be very wide) and therefore combining predictions with it is not logical. Furthermore, predictions make sense only with a specific choice of lambda.

Value

A `tibble::tibble` with columns:

| | |
|-----------|---|
| term | coefficient name (V1...VN by default, along with "(Intercept)") |
| step | which step of lambda choices was used |
| estimate | estimate of coefficient |
| lambda | value of penalty parameter lambda |
| dev.ratio | fraction of null deviance explained at each value of lambda |

See Also

`tidy()`, `glmnet::glmnet()`

Other glmnet tidiers: `glance.cv.glmnet`, `glance.glmnet`, `tidy.cv.glmnet`

Examples

```
if (requireNamespace("glmnet", quietly = TRUE)) {
  library(glmnet)

  set.seed(2014)
  x <- matrix(rnorm(100*20),100,20)
  y <- rnorm(100)
  fit1 <- glmnet(x,y)

  tidy(fit1)
  glance(fit1)

  library(dplyr)
  library(ggplot2)

  tidied <- tidy(fit1) %>% filter(term != "(Intercept)")

  ggplot(tidied, aes(step, estimate, group = term)) + geom_line()
  ggplot(tidied, aes(lambda, estimate, group = term)) +
    geom_line() + scale_x_log10()

  ggplot(tidied, aes(lambda, dev.ratio)) + geom_line()

  # works for other types of regressions as well, such as logistic
```

```

g2 <- sample(1:2, 100, replace=TRUE)
fit2 <- glmnet(x, g2, family="binomial")
tidy(fit2)
}

```

tidy.glmRob

Tidy a(n) glmRob object

Description

This method wraps `tidy.lm()`.

Usage

```

## S3 method for class 'glmRob'
tidy(x, ...)

```

Arguments

`x` A `glmRob` object returned from `robust::glmRob()`.

`...` Arguments passed on to `tidy.lm`

x An `lm` object created by `stats::lm()`.

conf.int Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to `FALSE`.

conf.level The confidence level to use for the confidence interval if `conf.int = TRUE`. Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval.

quick Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to `FALSE`.

exponentiate Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to `FALSE`.

Details

For tidiers for robust models from the **MASS** package see `tidy.rlm()`.

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |

| | |
|-----------|---|
| statistic | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| p.value | The two-sided p-value associated with the observed statistic. |
| conf.low | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| conf.high | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

If the linear model is an `mlm` object (multiple linear model), there is an additional column:

| | |
|----------|--|
| response | Which response column the coefficients correspond to (typically Y1, Y2, etc) |
|----------|--|

See Also

[tidy\(\)](#), [tidy.lm\(\)](#)

[robust::glmRob\(\)](#)

Other robust tidiers: [augment.glmRob](#), [augment.lmRob](#), [glance.glmRob](#), [glance.lmRob](#), [tidy.lmRob](#)

Examples

```
library(robust)
m <- lmRob(mpg ~ wt, data = mtcars)

tidy(m)
augment(m)
glance(m)

gm <- glmRob(am ~ wt, data = mtcars, family = "binomial")
glance(gm)
```

tidy.gmm

Tidy a(n) gmm object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'gmm'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = FALSE, quick = FALSE, ...)
```

Arguments

| | |
|---------------------------|--|
| <code>x</code> | A gmm object returned from <code>gmm::gmm()</code> . |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| <code>exponentiate</code> | Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE. |
| <code>quick</code> | Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to FALSE. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

See Also

`tidy()`, `gmm::gmm()`

Other gmm tidiers: `glance.gmm`

Examples

```

if (requireNamespace("gmm", quietly = TRUE)) {

  library(gmm)

  # examples come from the "gmm" package
  ## CAPM test with GMM
  data(Finance)
  r <- Finance[1:300, 1:10]
  rm <- Finance[1:300, "rm"]
  rf <- Finance[1:300, "rf"]

  z <- as.matrix(r-rf)
  t <- nrow(z)
  zm <- rm-rf
  h <- matrix(zm, t, 1)
  res <- gmm(z ~ zm, x = h)

  # tidy result
  tidy(res)
  tidy(res, conf.int = TRUE)
  tidy(res, conf.int = TRUE, conf.level = .99)

  # coefficient plot
  library(ggplot2)
  library(dplyr)
  tidy(res, conf.int = TRUE) %>%
    mutate(variable = reorder(variable, estimate)) %>%
    ggplot(aes(estimate, variable)) +
    geom_point() +
    geom_errorbarh(aes(xmin = conf.low, xmax = conf.high)) +
    facet_wrap(~ term) +
    geom_vline(xintercept = 0, color = "red", lty = 2)

  # from a function instead of a matrix
  g <- function(theta, x) {
    e <- x[,2:11] - theta[1] - (x[,1] - theta[1]) %*% matrix(theta[2:11], 1, 10)
    gmat <- cbind(e, e*c(x[,1]))
    return(gmat) }

  x <- as.matrix(cbind(rm, r))
  res_black <- gmm(g, x = x, t0 = rep(0, 11))

  tidy(res_black)
  tidy(res_black, conf.int = TRUE)

  ## APT test with Fama-French factors and GMM

  f1 <- zm
  f2 <- Finance[1:300, "hml"] - rf
  f3 <- Finance[1:300, "smb"] - rf

```



```

h <- cbind(f1, f2, f3)
res2 <- gmm(z ~ f1 + f2 + f3, x = h)

td2 <- tidy(res2, conf.int = TRUE)
td2

# coefficient plot
td2 %>%
  mutate(variable = reorder(variable, estimate)) %>%
  ggplot(aes(estimate, variable)) +
  geom_point() +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high)) +
  facet_wrap(~ term) +
  geom_vline(xintercept = 0, color = "red", lty = 2)
}

```

tidy.htest

Tidy/glance a(n) htest object

Description

For models that have only a single component, the `tidy()` and `glance()` methods are identical. Please see the documentation for both of those methods.

Usage

```

## S3 method for class 'htest'
tidy(x, ...)

## S3 method for class 'htest'
glance(x, ...)

```

Arguments

- `x` An htest objected, such as those created by `stats::cor.test()`, `stats::t.test()`, `stats::wilcox.test()`, `stats::chisq.test()`, etc.
- `...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A one-row `tibble::tibble` with one or more of the following columns, depending on which hypothesis test was used.

| | |
|--------------------------|--|
| <code>estimate</code> | Estimate of the effect size |
| <code>statistic</code> | Test statistic used to compute the p-value |
| <code>p.value</code> | P-value |
| <code>parameter</code> | Parameter field in the htest, typically degrees of freedom |
| <code>conf.low</code> | Lower bound on a confidence interval |
| <code>conf.high</code> | Upper bound on a confidence interval |
| <code>estimate1</code> | Sometimes two estimates are computed, such as in a two-sample t-test |
| <code>estimate2</code> | Sometimes two estimates are computed, such as in a two-sample t-test |
| <code>method</code> | Method used to compute the statistic as a string |
| <code>alternative</code> | Alternative hypothesis as a string |

See Also

`tidy()`, `stats::cor.test()`, `stats::t.test()`, `stats::wilcox.test()`, `stats::chisq.test()`

Other htest tidiers: `augment.htest`, `tidy.pairwise.htest`, `tidy.power.htest`

Examples

```
tt <- t.test(rnorm(10))
tidy(tt)
glance(tt) # same output for all htests

tt <- t.test(mpg ~ am, data = mtcars)
tidy(tt)

wt <- wilcox.test(mpg ~ am, data = mtcars, conf.int = TRUE, exact = FALSE)
tidy(wt)

ct <- cor.test(mtcars$wt, mtcars$mpg)
tidy(ct)

chit <- chisq.test(xtabs(Freq ~ Sex + Class, data = as.data.frame(Titanic)))
tidy(chit)
augment(chit)
```

| | |
|------------|-------------------------------|
| tidy.ivreg | <i>Tidy a(n) ivreg object</i> |
|------------|-------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'ivreg'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = FALSE, ...)
```

Arguments

| | |
|--------------|--|
| x | An ivreg object created by a call to <code>AER::ivreg()</code> . |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| conf.level | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| exponentiate | Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|-----------|---|
| term | The name of the regression term. |
| estimate | The estimated value of the regression term. |
| std.error | The standard error of the regression term. |
| statistic | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| p.value | The two-sided p-value associated with the observed statistic. |

| | |
|-----------|--|
| conf.low | The low end of a confidence interval for the regression term. Included only if conf.int = TRUE. |
| conf.high | The high end of a confidence interval for the regression term. Included only if conf.int = TRUE. |

See Also

[tidy\(\)](#), [AER::ivreg\(\)](#)

Other ivreg tidiers: [augment.ivreg](#), [glance.ivreg](#)

Examples

```
library(AER)

data("CigarettesSW", package = "AER")
ivr <- ivreg(
  log(packs) ~ income | population,
  data = CigarettesSW,
  subset = year == "1995"
)

summary(ivr)

tidy(ivr)
tidy(ivr, conf.int = TRUE)
tidy(ivr, conf.int = TRUE, exponentiate = TRUE)

augment(ivr)

glance(ivr)
```

tidy.kappa

Tidy a(n) kappa object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'kappa'
tidy(x, ...)
```

Arguments

`x` A kappa object returned from `psych::cohen.kappa()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Details

Note that confidence level (alpha) for the confidence interval cannot be set in `tidy`. Instead you must set the `alpha` argument to `psych::cohen.kappa()` when creating the kappa object.

Value

A `tibble::tibble` with columns:

| | |
|------------------------|---|
| <code>type</code> | Either "weighted" or "unweighted" |
| <code>estimate</code> | The estimated value of kappa with this method |
| <code>conf.low</code> | Lower bound of confidence interval |
| <code>conf.high</code> | Upper bound of confidence interval |

See Also

`tidy()`, `psych::cohen.kappa()`

Examples

```
library(psych)

rater1 = 1:9
rater2 = c(1, 3, 1, 6, 1, 5, 5, 6, 7)
ck <- cohen.kappa(cbind(rater1, rater2))

tidy(ck)

# graph the confidence intervals
library(ggplot2)
ggplot(tidy(ck), aes(estimate, type)) +
  geom_point() +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high))
```

tidy.kde

*Tidy a(n) kde object***Description**

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'kde'
tidy(x, ...)
```

Arguments

`x` A kde object returned from `ks::kde()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with one row for each point in the estimated grid. The result contains one column (named `x1`, `x2`, etc) for each dimension, and an `estimate` column containing the estimated density.

See Also

`tidy()`, `ks::kde()`

Examples

```
if (requireNamespace("ks", quietly = TRUE)) {
  library(ks)

  dat <- replicate(2, rnorm(100))
  k <- kde(dat)

  td <- tidy(k)
  td
```

```

library(ggplot2)
ggplot(td, aes(x1, x2, fill = estimate)) +
  geom_tile() +
  theme_void()

# also works with 3 dimensions
dat3 <- replicate(3, rnorm(100))
k3 <- kde(dat3)

td3 <- tidy(k3)
td3
}

```

tidy.Kendall

Tidy a(n) Kendall object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'Kendall'
tidy(x, ...)
```

Arguments

x A Kendall object returned from a call to `Kendall::Kendall()`, `Kendall::MannKendall()`, or `Kendall::SeasonalMannKendall()`.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A `tibble::tibble` with one row and columns:

| | |
|----------------------------|--------------------------|
| <code>statistic</code> | Kendall's tau statistic. |
| <code>p.value</code> | two-sided p-value. |
| <code>kendall_score</code> | Kendall score. |

denominator The denominator, which is $\tau = \text{kendall_score} / \text{denominator}$.
 var_kendall_score Variance of the kendall_score.

See Also

[tidy\(\)](#), [Kendall::Kendall\(\)](#), [Kendall::MannKendall\(\)](#), [Kendall::SeasonalMannKendall\(\)](#)

Examples

```
library(Kendall)

A <- c(2.5,2.5,2.5,2.5,5,6.5,6.5,10,10,10,10,10,14,14,14,16,17)
B <- c(1,1,1,1,2,1,1,2,1,1,1,1,1,1,1,2,2,2)

f_res <- Kendall(A, B)
tidy(f_res)

s_res <- MannKendall(B)
tidy(s_res)

t_res <- SeasonalMannKendall(ts(A))
tidy(t_res)
```

| | |
|-------------|--------------------------------|
| tidy.kmeans | <i>Tidy a(n) kmeans object</i> |
|-------------|--------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'kmeans'
tidy(x, col.names = paste0("x", 1:ncol(x$centers)), ...)
```

Arguments

x A kmeans object created by [stats::kmeans\(\)](#).
 col.names Dimension names. Defaults to x1, x2, ...
 ... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed

using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Details

For examples, see the `kmeans` vignette.

Value

A `tibble::tibble` with one row per cluster, and columns:

| | |
|-----------------------|--|
| <code>size</code> | Number of points in cluster |
| <code>withinss</code> | The within-cluster sum of squares |
| <code>cluster</code> | A factor describing the cluster from 1:k |

See Also

`tidy()`, `stats::kmeans()`

Other `kmeans` tidiers: `augment.kmeans`, `glance.kmeans`

tidy.lavaan

Tidy a(n) lavaan object

Description

`Tidy` summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what `tidy` considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'lavaan'
tidy(x, conf.int = TRUE, conf.level = 0.95, ...)
```

Arguments

| | |
|-------------------------|---|
| <code>x</code> | A lavaan object, such as those return from <code>lavaan::cfa()</code> , and <code>lavaan::sem()</code> . |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to <code>FALSE</code> . |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| <code>...</code> | Additional arguments passed to <code>lavaan::parameterEstimates()</code> . Cautionary note: Misspecified arguments may be silently ignored. |

Value

A `tibble::tibble` with one row for each estimated parameter and columns:

| | |
|------------------------|---|
| <code>term</code> | The result of <code>paste(lhs, op, rhs)</code> |
| <code>op</code> | The operator in the model syntax (e.g. <code>~~</code> for covariances, or <code>~</code> for regression parameters) |
| <code>group</code> | The group (if specified) in the lavaan model |
| <code>estimate</code> | The parameter estimate (may be standardized) |
| <code>std.error</code> | |
| <code>statistic</code> | The z value returned by <code>lavaan::parameterEstimates()</code> |
| <code>p.value</code> | |
| <code>conf.low</code> | |
| <code>conf.high</code> | |
| <code>std.lv</code> | Standardized estimates based on the variances of the (continuous) latent variables only |
| <code>std.all</code> | Standardized estimates based on both the variances of both (continuous) observed and latent variables. |
| <code>std.nox</code> | Standardized estimates based on both the variances of both (continuous) observed and latent variables, but not the variances of exogenous covariates. |

See Also

`tidy()`, `lavaan::cfa()`, `lavaan::sem()`, `lavaan::parameterEstimates()`

Other lavaan tidiers: `glance.lavaan`

Examples

```
if (require("lavaan")) {
  library(lavaan)

  cfa.fit <- cfa('F =~ x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8 + x9',
    data = HolzingerSwineford1939, group = "school")
  tidy(cfa.fit)
}
```

| | |
|---------|----------------------------|
| tidy.lm | <i>Tidy a(n) lm object</i> |
|---------|----------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'lm'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = FALSE, quick = FALSE, ...)

## S3 method for class 'summary.lm'
tidy(x, ...)
```

Arguments

| | |
|--------------|--|
| x | An lm object created by <code>stats::lm()</code> . |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| conf.level | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| exponentiate | Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE. |
| quick | Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to FALSE. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Details

If you have missing values in your model data, you may need to refit the model with `na.action = na.exclude`.

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

If the linear model is an `mlm` object (multiple linear model), there is an additional column:

| | |
|-----------------------|--|
| <code>response</code> | Which response column the coefficients correspond to (typically Y1, Y2, etc) |
|-----------------------|--|

See Also

[tidy\(\)](#), [stats::summary.lm\(\)](#)

Other lm tidiers: [augment.glm](#), [augment.lm](#), [glance.glm](#), [glance.lm](#), [tidy.glm](#)

Examples

```
library(ggplot2)
library(dplyr)

mod <- lm(mpg ~ wt + qsec, data = mtcars)

tidy(mod)
glance(mod)

# coefficient plot
d <- tidy(mod) %>%
  mutate(
    low = estimate - std.error,
    high = estimate + std.error
  )

ggplot(d, aes(estimate, term, xmin = low, xmax = high, height = 0)) +
  geom_point() +
  geom_vline(xintercept = 0) +
  geom_errorbarh()

augment(mod)
augment(mod, mtcars)
```

```

# predict on new data
newdata <- mtcars %>% head(6) %>% mutate(wt = wt + 1)
augment(mod, newdata = newdata)

au <- augment(mod, data = mtcars)

ggplot(au, aes(.hat, .std.resid)) +
  geom_vline(size = 2, colour = "white", xintercept = 0) +
  geom_hline(size = 2, colour = "white", yintercept = 0) +
  geom_point() + geom_smooth(se = FALSE)

plot(mod, which = 6)
ggplot(au, aes(.hat, .cooks)) +
  geom_vline(xintercept = 0, colour = NA) +
  geom_abline(slope = seq(0, 3, by = 0.5), colour = "white") +
  geom_smooth(se = FALSE) +
  geom_point()

# column-wise models
a <- matrix(rnorm(20), nrow = 10)
b <- a + rnorm(length(a))
result <- lm(b ~ a)
tidy(result)

```

tidy.lmodel2

Tidy a(n) lmodel2 object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'lmodel2'
tidy(x, ...)

```

Arguments

x A `lmodel2` object returned by `lmodel2::lmodel2()`.

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Details

There are always only two terms in an `lmodel2`: "Intercept" and "Slope". These are computed by four methods: OLS (ordinary least squares), MA (major axis), SMA (standard major axis), and RMA (ranged major axis).

Value

A `tibble::tibble` within eight rows (one for each term estimated with each method) and columns:

| | |
|------------------------|--|
| <code>method</code> | Either OLS/MA/SMA/RMA |
| <code>term</code> | Either "Intercept" or "Slope" |
| <code>estimate</code> | Estimated coefficient |
| <code>conf.low</code> | Lower bound of 95% confidence interval |
| <code>conf.high</code> | Upper bound of 95% confidence interval |

See Also

[tidy\(\)](#), [lmodel2::lmodel2\(\)](#)

Other `lmodel2` tidiers: [glance.lmodel2](#)

Examples

```
if (require("lmodel2", quietly = TRUE)) {
  library(lmodel2)

  data(mod2ex2)
  Ex2.res <- lmodel2(Prey ~ Predators, data=mod2ex2, "relative", "relative", 99)
  Ex2.res

  tidy(Ex2.res)
  glance(Ex2.res)

  # this allows coefficient plots with ggplot2
  library(ggplot2)
  ggplot(tidy(Ex2.res), aes(estimate, term, color = method)) +
    geom_point() +
    geom_errorbarh(aes(xmin = conf.low, xmax = conf.high)) +
    geom_errorbarh(aes(xmin = conf.low, xmax = conf.high))
}
```

| | |
|------------|-------------------------------|
| tidy.lmRob | <i>Tidy a(n) lmRob object</i> |
|------------|-------------------------------|

Description

This method wraps `tidy.lm()`.

Usage

```
## S3 method for class 'lmRob'
tidy(x, ...)
```

Arguments

| | |
|---------------------|--|
| <code>x</code> | A <code>lmRob</code> object returned from <code>robust::lmRob()</code> . |
| <code>...</code> | Arguments passed on to <code>tidy.lm</code> |
| <code>x</code> | An <code>lm</code> object created by <code>stats::lm()</code> . |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to <code>FALSE</code> . |
| conf.level | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| quick | Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to <code>FALSE</code> . |
| exponentiate | Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to <code>FALSE</code> . |

Details

For tidiers for robust models from the **MASS** package see `tidy.rlm()`.

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

`conf.high` The high end of a confidence interval for the regression term. Included only if `conf.int = TRUE`.

If the linear model is an `mlm` object (multiple linear model), there is an additional column:

`response` Which response column the coefficients correspond to (typically Y1, Y2, etc)

See Also

[tidy\(\)](#), [tidy.lm\(\)](#)

[robust::lmRob\(\)](#)

Other robust tidiers: [augment.glmRob](#), [augment.lmRob](#), [glance.glmRob](#), [glance.lmRob](#), [tidy.glmRob](#)

Examples

```
library(robust)
m <- lmRob(mpg ~ wt, data = mtcars)

tidy(m)
augment(m)
glance(m)

gm <- glmRob(am ~ wt, data = mtcars, family = "binomial")
glance(gm)
```

| | |
|-------------|--------------------------------|
| tidy.manova | <i>Tidy a(n) manova object</i> |
|-------------|--------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'manova'
tidy(x, test = "Pillai", ...)
```


Arguments

| | |
|-------------------|---|
| <code>x</code> | A manova object return from <code>stats::manova()</code> . |
| <code>test</code> | One of "Pillai" (Pillai's trace), "Wilks" (Wilk's lambda), "Hotelling-Lawley" (Hotelling-Lawley trace) or "Roy" (Roy's greatest root) indicating which test statistic should be used. Defaults to "Pillai". |
| <code>...</code> | Arguments passed on to <code>stats::summary.manova</code> |
| | object An object of class "manova" or an aov object with multiple responses. |
| | test The name of the test statistic to be used. Partial matching is used so the name can be abbreviated. |
| | intercept logical. If TRUE, the intercept term is included in the table. |
| | tol tolerance to be used in deciding if the residuals are rank-deficient: see qr . |

Value

A `tibble::tibble` with columns:

```
\item{term}{Term in design}
\item{statistic}{Approximate F statistic}
\item{num.df}{Degrees of freedom}
\item{p.value}{P-value}
```

Depending on which test statistic is specified, one of the following columns is also included:

```
\item{pillai}{Pillai's trace}
\item{wilks}{Wilk's lambda}
\item{hl}{Hotelling-Lawley trace}
\item{roy}{Roy's greatest root}
```

See Also

[tidy\(\)](#), [stats::summary.manova\(\)](#)

Other anova tidiers: [tidy.TukeyHSD](#), [tidy.anova](#), [tidy.aovlist](#), [tidy.aov](#)

Examples

```
npk2 <- within(npk, foo <- rnorm(24))
m <- manova(cbind(yield, foo) ~ block + N * P * K, npk2)
tidy(m)
```

| | |
|----------|-----------------------------|
| tidy.map | <i>Tidy a(n) map object</i> |
|----------|-----------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'map'
tidy(x, ...)
```

Arguments

| | |
|-----|--|
| x | A map object returned from <code>maps::map()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

See Also

[tidy\(\)](#), [maps::map\(\)](#)

Examples

```
if (require("maps") && require("ggplot2")) {
  library(maps)
  library(ggplot2)

  ca <- map("county", "ca", plot = FALSE, fill = TRUE)
  tidy(ca)
  qplot(long, lat, data = ca, geom = "polygon", group = group)

  tx <- map("county", "texas", plot = FALSE, fill = TRUE)
  tidy(tx)
  qplot(long, lat, data = tx, geom = "polygon", group = group,
        colour = I("white"))
}
```

| | |
|-------------|--------------------------------|
| tidy.Mclust | <i>Tidy a(n) Mclust object</i> |
|-------------|--------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'Mclust'
tidy(x, ...)
```

Arguments

| | |
|-----|---|
| x | An Mclust object return from <code>mclust::Mclust()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble` with one row per component:

| | |
|------------|---|
| component | Cluster id as a factor. For a model k clusters, these will be <code>as.factor(1:k)</code> , or <code>as.factor(0:k)</code> if there's a noise term. |
| size | Number of observations assigned to component |
| proportion | The mixing proportion of each component |
| variance | In case of one-dimensional and spherical models, the variance for each component, omitted otherwise. NA for noise component |
| mean | The mean for each component. In case of 2+ dimensional models, a column with the mean is added for each dimension. NA for noise component |

See Also

`tidy()`, `mclust::Mclust()`

Other mclust tidiers: `augment.Mclust`

Examples

```

library(dplyr)
library(mclust)
set.seed(27)

centers <- tibble::tibble(
  cluster = factor(1:3),
  num_points = c(100, 150, 50), # number points in each cluster
  x1 = c(5, 0, -3), # x1 coordinate of cluster center
  x2 = c(-1, 1, -2) # x2 coordinate of cluster center
)

points <- centers %>%
  mutate(
    x1 = purrr::map2(num_points, x1, rnorm),
    x2 = purrr::map2(num_points, x2, rnorm)
  ) %>%
  select(-num_points, -cluster) %>%
  tidyr::unnest(x1, x2)

m <- mclust::Mclust(points)

tidy(m)
augment(m, points)
glance(m)

```

tidy.mjoint

Tidy a(n) mjoint object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'mjoint'
tidy(x, component = "survival", conf.int = FALSE,
     conf.level = 0.95, boot_se = NULL, ...)

```

Arguments

x An mjoint object returned from `joineRML::mjoint()`.

| | |
|------------|---|
| component | Character specifying whether to tidy the survival or the longitudinal component of the model. Must be either "survival" or "longitudinal". Defaults to "survival". |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| conf.level | The confidence level to use for the confidence interval if conf.int = TRUE. Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| boot_se | Optionally a bootSE object from <code>joineRML::bootSE()</code> . If specified, calculates confidence intervals via the bootstrap. Defaults to NULL, in which case standard errors are calculated from the empirical information matrix. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|-----------|---|
| term | The name of the regression term. |
| estimate | The estimated value of the regression term. |
| std.error | The standard error of the regression term. |
| statistic | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| p.value | The two-sided p-value associated with the observed statistic. |
| conf.low | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| conf.high | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

See Also

`tidy()`, `joineRML::mjoint()`, `joineRML::bootSE()`

Other mjoint tidiers: `glance.mjoint`

Examples

```
## Not run:
# Fit a joint model with bivariate longitudinal outcomes
library(joineRML)
data(heart.valve)
hvd <- heart.valve[!is.na(heart.valve$log.grad) &
```

```

      !is.na(heart.valve$log.lvmi) &
      heart.valve$num <= 50, ]
fit <- mjoint(
  formLongFixed = list(
    "grad" = log.grad ~ time + sex + hs,
    "lvmi" = log.lvmi ~ time + sex
  ),
  formLongRandom = list(
    "grad" = ~ 1 | num,
    "lvmi" = ~ time | num
  ),
  formSurv = Surv(fuyrs, status) ~ age,
  data = hvd,
  inits = list("gamma" = c(0.11, 1.51, 0.80)),
  timeVar = "time"
)

# Extract the survival fixed effects
tidy(fit)

# Extract the longitudinal fixed effects
tidy(fit, component = "longitudinal")

# Extract the survival fixed effects with confidence intervals
tidy(fit, ci = TRUE)

# Extract the survival fixed effects with confidence intervals based
# on bootstrapped standard errors
bSE <- bootSE(fit, nboot = 5, safe.boot = TRUE)
tidy(fit, boot_se = bSE, ci = TRUE)

# Augment original data with fitted longitudinal values and residuals
hvd2 <- augment(fit)

# Extract model statistics
glance(fit)

## End(Not run)

```

tidy.mle2

Tidy a(n) mle2 object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'mle2'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

| | |
|-------------------------|---|
| <code>x</code> | An <code>mle2</code> object created by a call to <code>bbmle::mle2()</code> . |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to <code>FALSE</code> . |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.lvel = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

See Also

`tidy()`, `bbmle::mle2()`, `tidy_optim()`

Examples

```
if (require("bbmle", quietly = TRUE)) {
  x <- 0:10
  y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
  d <- data.frame(x,y)

  fit <- mle2(y ~ dpois(lambda = ymean),
             start = list(ymean = mean(y)), data = d)

  tidy(fit)
}
```

tidy.muhaaz

Tidy a(n) muhaaz object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'muhaz'
tidy(x, ...)
```

Arguments

`x` A muhaz object returned by `muhaz::muhaz()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with two columns:

| | |
|-----------------------|--|
| <code>time</code> | The time at which the hazard rate was estimated. |
| <code>estimate</code> | The estimated hazard rate. |

See Also

`tidy()`, `muhaz::muhaz()`

Other muhaz tidiers: `glance.muhaz`

Examples

```
if (require("muhaz", quietly = TRUE)) {
  data(ovarian, package="survival")
  x <- muhaz::muhaz(ovarian$futime, ovarian$fustat)
  tidy(x)
  glance(x)
}
```

Description

These methods tidy the coefficients of multinomial logistic regression models generated by `multinom` of the `nnet` package.

Usage

```
## S3 method for class 'multinom'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = TRUE, ...)
```

Arguments

| | |
|---------------------------|--|
| <code>x</code> | A multinom object returned from <code>nnet::multinom()</code> . |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to <code>FALSE</code> . |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| <code>exponentiate</code> | Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to <code>FALSE</code> . |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

`tidy.multinom` returns one row for each coefficient at each level of the response variable, with six columns:

| | |
|------------------------|--|
| <code>y.value</code> | The response level |
| <code>term</code> | The term in the model being estimated and tested |
| <code>estimate</code> | The estimated coefficient |
| <code>std.error</code> | The standard error from the linear model |
| <code>statistic</code> | Wald z-statistic |
| <code>p.value</code> | two-sided p-value |

If `conf.int = TRUE`, also includes columns for `conf.low` and `conf.high`.

See Also

`tidy()`, `nnet::multinom()`

Other multinom tidiers: `glance.multinom`

Examples

```

if (require(nnet) & require(MASS)){
  library(nnet)
  library(MASS)

  example(birthwt)
  bwt.mu <- multinom(low ~ ., bwt)
  tidy(bwt.mu)
  glance(bwt.mu)

  #* This model is a truly terrible model
  #* but it should show you what the output looks
  #* like in a multinomial logistic regression

  fit.gear <- multinom(gear ~ mpg + factor(am), data = mtcars)
  tidy(fit.gear)
  glance(fit.gear)
}

```

tidy.nlrq

Tidy a(n) nlrq object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'nlrq'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)

```

Arguments

| | |
|------------|---|
| x | A nlrq object returned from <code>quantreg::nlrq()</code> . |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| conf.level | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be |

used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

See Also

`tidy()`, `quantreg::nlrq()`

Other quantreg tidiers: `augment.nlrq`, `augment.rqs`, `augment.rq`, `glance.nlrq`, `glance.rq`, `tidy.rqs`, `tidy.rq`

`tidy.nls`

Tidy a(n) nls object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'nls'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     quick = FALSE, ...)
```

Arguments

| | |
|-------------------------|--|
| <code>x</code> | An <code>nls</code> object returned from <code>stats::nls()</code> . |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to <code>FALSE</code> . |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| <code>quick</code> | Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to <code>FALSE</code> . |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

See Also

`tidy`, `stats::nls()`, `stats::summary.nls()`

Other nls tidiers: `augment.nls`, `glance.nls`

Examples

```
n <- nls(mpg ~ k * e ^ wt, data = mtcars, start = list(k = 1, e = 2))
```

```
tidy(n)
augment(n)
glance(n)
```

```
library(ggplot2)
ggplot(augment(n), aes(wt, mpg)) +
  geom_point() +
  geom_line(aes(y = .fitted))

newdata <- head(mtcars)
newdata$wt <- newdata$wt + 1
augment(n, newdata = newdata)
```

tidy.numeric

Tidy atomic vectors

Description

Vector tidiers are deprecated and will be removed from an upcoming release of broom.

Usage

```
## S3 method for class 'numeric'
tidy(x, ...)

## S3 method for class 'character'
tidy(x, ...)

## S3 method for class 'logical'
tidy(x, ...)
```

Arguments

| | |
|-----|--|
| x | An object of class "numeric", "integer", "character", or "logical". Most likely a named vector |
| ... | Extra arguments (not used) |

Details

Turn atomic vectors into data frames, where the names of the vector (if they exist) are a column and the values of the vector are a column.

Examples

```
## Not run:
x <- 1:5
names(x) <- letters[1:5]
tidy(x)

## End(Not run)
```

tidy.orcutt

*Tidy a(n) orcutt object***Description**

This method wraps `tidy.lm()`.

Usage

```
## S3 method for class 'orcutt'
tidy(x, ...)
```

Arguments

`x` An orcutt object returned from `orcutt::cochrane.orcutt()`.

`...` Arguments passed on to `tidy.lm`

`x` An `lm` object created by `stats::lm()`.

conf.int Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to `FALSE`.

conf.level The confidence level to use for the confidence interval if `conf.int = TRUE`. Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval.

quick Logical indicating if the only the `term` and `estimate` columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to `FALSE`.

exponentiate Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to `FALSE`.

Value

`tidy` returns the same information as `tidy.lm()`, though without confidence interval options.

See Also

`tidy()`, `tidy.lm()`

`orcutt::cochrane.orcutt()`

Other orcutt tidiers: `glance.orcutt`

Examples

```
reg <- lm(mpg ~ wt + qsec + disp, mtcars)
tidy(reg)

if (require("orcutt", quietly = TRUE)) {
```

```

co <- cochrane.orcutt(reg)
co

tidy(co)
glance(co)
}

```

tidy.pairwise.htest *Tidy a(n) pairwise.htest object*

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'pairwise.htest'
tidy(x, ...)

```

Arguments

| | |
|-----|--|
| x | A pairwise.htest object such as those returned from <code>stats::pairwise.t.test()</code> or <code>stats::pairwise.wilcox.test()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Details

Note that in one-sided tests, the alternative hypothesis of each test can be stated as "group1 is greater/less than group2".

Note also that the columns of `group1` and `group2` will always be a factor, even if the original input is (e.g.) numeric.

Value

A `tibble::tibble` with one row per group/group comparison and columns:

| | |
|---------|----------------------------------|
| group1 | First group being compared |
| group2 | Second group being compared |
| p.value | (Adjusted) p-value of comparison |

See Also

`stats::pairwise.t.test()`, `stats::pairwise.wilcox.test()`, `tidy()`

Other htest tidiers: `augment.htest`, `tidy.htest`, `tidy.power.htest`

Examples

```
attach(airquality)
Month <- factor(Month, labels = month.abb[5:9])
ptt <- pairwise.t.test(Ozone, Month)
tidy(ptt)

attach(iris)
ptt2 <- pairwise.t.test(Petal.Length, Species)
tidy(ptt2)

tidy(pairwise.t.test(Petal.Length, Species, alternative = "greater"))
tidy(pairwise.t.test(Petal.Length, Species, alternative = "less"))

tidy(pairwise.wilcox.test(Petal.Length, Species))
```

tidy.plm

Tidy a(n) plm object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'plm'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = FALSE, ...)
```

Arguments

| | |
|-------------------------|---|
| <code>x</code> | A <code>plm</code> object returned by <code>plm::plm()</code> . |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to <code>FALSE</code> . |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |

`exponentiate` Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

See Also

`tidy()`, `plm::plm()`, `tidy.lm()`

Other plm tidiers: `augment.plm`, `glance.plm`

Examples

```
library(plm)

data("Produc", package = "plm")
zz <- plm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp,
          data = Produc, index = c("state", "year"))

summary(zz)

tidy(zz)
tidy(zz, conf.int = TRUE)
tidy(zz, conf.int = TRUE, conf.level = .9)

augment(zz)
glance(zz)
```

tidy.poLCA

Tidy a(n) poLCA object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'poLCA'
tidy(x, ...)
```

Arguments

`x` A poLCA object returned from `poLCA: :poLCA()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A `tibble::tibble` with one row per variable-class-outcome combination, with columns:

| | |
|------------------------|--|
| <code>variable</code> | Manifest variable |
| <code>class</code> | Latent class ID, an integer |
| <code>outcome</code> | Outcome of manifest variable |
| <code>estimate</code> | Estimated class-conditional response probability |
| <code>std.error</code> | Standard error of estimated probability |

See Also

`tidy()`, `poLCA: :poLCA()`

Other poLCA tidiers: `augment.poLCA`, `glance.poLCA`

Examples

```

if (require("poLCA", quietly = TRUE)) {
  library(poLCA)
  library(dplyr)

  data(values)
  f <- cbind(A, B, C, D)~1
  M1 <- poLCA(f, values, nclass = 2, verbose = FALSE)

  M1
  tidy(M1)
  augment(M1)
  glance(M1)

  library(ggplot2)

  ggplot(tidy(M1), aes(factor(class), estimate, fill = factor(outcome))) +
    geom_bar(stat = "identity", width = 1) +
    facet_wrap(~ variable)

  set.seed(2016)
  # compare multiple
  mods <- tibble(nclass = 1:3) %>%
    group_by(nclass) %>%
    do(mod = poLCA(f, values, nclass = .$nclass, verbose = FALSE))

  # compare log-likelihood and/or AIC, BIC
  mods %>%
    glance(mod)

  ## Three-class model with a single covariate.

  data(election)
  f2a <- cbind(MORALG,CARESG,KNOWG,LEADG,DISHONG,INTELG,
              MORALB,CARESB,KNOWB,LEADB,DISHONB,INTELB)~PARTY
  nes2a <- poLCA(f2a, election, nclass = 3, nrep = 5, verbose = FALSE)

  td <- tidy(nes2a)
  td

  # show

  ggplot(td, aes(outcome, estimate, color = factor(class), group = class)) +
    geom_line() +
    facet_wrap(~ variable, nrow = 2) +
    theme(axis.text.x = element_text(angle = 90, hjust = 1))

  au <- augment(nes2a)
  au
  au %>%
    count(.class)

```

```

# if the original data is provided, it leads to NAs in new columns
# for rows that weren't predicted
au2 <- augment(nes2a, data = election)
au2
dim(au2)
}

```

tidy.polr

Tidying methods for ordinal logistic regression models

Description

These methods tidy the coefficients of ordinal logistic regression models generated by `ordinal::clm()` or `ordinal::clmm()` of the `ordinal` package, `MASS::polr()` of the `MASS` package, or `survey::svyolr()` of the `survey` package.

Usage

```

## S3 method for class 'polr'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = FALSE, quick = FALSE, ...)

## S3 method for class 'polr'
glance(x, ...)

## S3 method for class 'polr'
augment(x, data = stats::model.frame(x), newdata,
        type.predict = c("probs", "class"), ...)

## S3 method for class 'clm'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = FALSE, quick = FALSE, conf.type = c("profile",
     "Wald"), ...)

## S3 method for class 'clmm'
tidy(x, conf.int = FALSE, conf.level = 0.95,
     exponentiate = FALSE, quick = FALSE, conf.type = c("profile",
     "Wald"), ...)

## S3 method for class 'clm'
glance(x, ...)

## S3 method for class 'clmm'
glance(x, ...)

## S3 method for class 'clm'

```

```

augment(x, data = stats::model.frame(x), newdata,
  type.predict = c("prob", "class"), ...)

## S3 method for class 'svyolr'
tidy(x, conf.int = FALSE, conf.level = 0.95,
  exponentiate = FALSE, quick = FALSE, ...)

## S3 method for class 'svyolr'
glance(x, ...)

```

Arguments

| | |
|---------------------------|---|
| <code>x</code> | a model of class <code>clm</code> , <code>clmm</code> , <code>polr</code> or <code>svyolr</code> |
| <code>conf.int</code> | whether to include a confidence interval |
| <code>conf.level</code> | confidence level of the interval, used only if <code>conf.int=TRUE</code> |
| <code>exponentiate</code> | whether to exponentiate the coefficient estimates and confidence intervals (typical for ordinal logistic regression) |
| <code>quick</code> | whether to compute a smaller and faster version, containing only the term, estimate and <code>coefficient_type</code> columns |
| <code>...</code> | extra arguments |
| <code>data</code> | original data, defaults to the extracting it from the model |
| <code>newdata</code> | if provided, performs predictions on the new data |
| <code>type.predict</code> | type of prediction to compute for a CLM; passed on to <code>ordinal::predict.clm()</code> or <code>predict.polr</code> |
| <code>conf.type</code> | the type of confidence interval (see <code>ordinal::confint.clm()</code>) |

Value

`tidy.clm`, `tidy.clmm`, `tidy.polr` and `tidy.svyolr` return one row for each coefficient at each level of the response variable, with six columns:

| | |
|-------------------------------|--|
| <code>term</code> | term in the model |
| <code>estimate</code> | estimated coefficient |
| <code>std.error</code> | standard error |
| <code>statistic</code> | z-statistic |
| <code>p.value</code> | two-sided p-value |
| <code>coefficient_type</code> | type of coefficient, see <code>ordinal::clm()</code> |

If `conf.int=TRUE`, it also includes columns for `conf.low` and

`glance.clm`, `glance.clmm`, `glance.polr` and `glance.svyolr` return a one-row data.frame with the columns:

| | |
|---------------------|---|
| <code>edf</code> | the effective degrees of freedom |
| <code>logLik</code> | the data's log-likelihood under the model |

AIC the Akaike Information Criterion
 BIC the Bayesian Information Criterion
 df.residual residual degrees of freedom

`augment.clm` and `augment.polr` returns one row for each observation, with additional columns added to the original data:

`.fitted` fitted values of model
`.se.fit` standard errors of fitted values

`augment` is not supported for `ordinal::clmm()` and `survey::svyolr()` models.

All tidying methods return a data.frame without rownames. The structure depends on the method chosen.

Examples

```
if (require(ordinal)){
  clm_mod <- clm(rating ~ temp * contact, data = wine)
  tidy(clm_mod)
  tidy(clm_mod, conf.int = TRUE)
  tidy(clm_mod, conf.int = TRUE, conf.type = "Wald", exponentiate = TRUE)
  glance(clm_mod)
  augment(clm_mod)

  clm_mod2 <- clm(rating ~ temp, nominal = ~ contact, data = wine)
  tidy(clm_mod2)

  clmm_mod <- clmm(rating ~ temp + contact + (1 | judge), data = wine)
  tidy(clmm_mod)
  glance(clmm_mod)
}
if (require(MASS)) {
  polr_mod <- polr(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
  tidy(polr_mod, exponentiate = TRUE, conf.int = TRUE)
  glance(polr_mod)
  augment(polr_mod, type.predict = "class")
}
```

tidy.power.htest

Tidy a(n) power.htest object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'power.htest'
tidy(x, ...)
```

Arguments

`x` A `power.htest` object such as those returned from `stats::power.t.test()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A data frame with one row per parameter passed in, with columns `n`, `delta`, `sd`, `sig.level`, and `power`.

See Also

[stats::power.t.test\(\)](#)

Other `htest` tidiers: [augment.htest](#), [tidy.htest](#), [tidy.pairwise.htest](#)

Examples

```
ptt <- power.t.test(n = 2:30, delta = 1)
tidy(ptt)

library(ggplot2)

ggplot(tidy(ptt), aes(n, power)) +
  geom_line()
```

tidy.prcomp

Tidy a(n) prcomp object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'prcomp'
tidy(x, matrix = "u", ...)
```

Arguments

| | |
|--------|--|
| x | A prcomp object returned by <code>stats::prcomp()</code> . |
| matrix | Character specifying which component of the PCA should be tidied. <ul style="list-style-type: none"> • "u", "samples", or "x": returns information about the map from the original space into principle components space. • "v", "rotation", or "variables": returns information about the map from principle components space back into the original space. • "d" or "pcs": returns information about the eigenvalues will return information about |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Details

See <https://stats.stackexchange.com/questions/134282/relationship-between-svd-and-pca-how-to-use-svd-to-perform-pca> for information on how to interpret the various tidied matrices. Note that SVD is only equivalent to PCA on centered data.

Value

A `tibble::tibble` with columns depending on the component of PCA being tidied.

If `matrix` is "u", "samples", or "x" each row in the tidied output corresponds to the original data in PCA space. The columns are:

| | |
|-------|--|
| row | ID of the original observation (i.e. rowname from original data). |
| PC | Integer indicating a principle component. |
| value | The score of the observation for that particular principle component. That is, the location of the observation in PCA space. |

If `matrix` is "v", "rotation", or "variables", each row in the tidied output corresponds to information about the principle components in the original space. The columns are:

| | |
|-------|--|
| row | The variable labels (colnames) of the data set on which PCA was performed |
| PC | An integer vector indicating the principal component |
| value | The value of the eigenvector (axis score) on the indicated principal component |

If `matrix` is "d" or "pcs", the columns are:

| | |
|------------|--|
| PC | An integer vector indicating the principal component |
| std.dev | Standard deviation explained by this PC |
| percent | Percentage of variation explained |
| cumulative | Cumulative percentage of variation explained |

See Also

[stats::prcomp\(\)](#), [svd_tidiers](#)

Other svd tidiers: [augment.prcomp](#), [tidy_irlba](#), [tidy_svd](#)

Examples

```
pc <- prcomp(USArrests, scale = TRUE)

# information about rotation
tidy(pc)

# information about samples (states)
tidy(pc, "samples")

# information about PCs
tidy(pc, "pcs")

# state map
library(dplyr)
library(ggplot2)

pc %>%
  tidy(matrix = "samples") %>%
  mutate(region = tolower(row)) %>%
  inner_join(map_data("state"), by = "region") %>%
  ggplot(aes(long, lat, group = group, fill = value)) +
  geom_polygon() +
  facet_wrap(~ PC) +
  theme_void() +
  ggtitle("Principal components of arrest data")

au <- augment(pc, data = USArrests)
au

ggplot(au, aes(.fittedPC1, .fittedPC2)) +
  geom_point() +
  geom_text(aes(label = .rownames), vjust = 1, hjust = 1)
```

tidy.pyyears

*Tidy a(n) pyyears object***Description**

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'pyyears'
tidy(x, ...)
```

Arguments

`x` A pyyears object returned from `survival::pyyears()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A `tibble::tibble` with one row for each time point and columns:

| | |
|-----------------------|--|
| <code>pyyears</code> | person-years of exposure |
| <code>n</code> | number of subjects contributing time |
| <code>event</code> | observed number of events |
| <code>expected</code> | expected number of events (present only if a <code>ratetable</code> term is present) |

If the `data.frame = TRUE` argument is supplied to `pyyears`, this is simply the contents of `x$data`.

See Also

`tidy()`, `survival::pyyears()`

Other pyyears tidiers: `glance.pyyears`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.aareg`, `glance.cch`, `glance.coxph`, `glance.pyyears`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `glance.survreg`, `tidy.aareg`, `tidy.cch`, `tidy.coxph`, `tidy.survdiff`, `tidy.survexp`, `tidy.survfit`, `tidy.survreg`

Examples

```
library(survival)

temp.yr <- tcut(mgus$dxyr, 55:92, labels=as.character(55:91))
temp.age <- tcut(mgus$age, 34:101, labels=as.character(34:100))
ptime <- ifelse(is.na(mgus$pctime), mgus$futime, mgus$pctime)
pstat <- ifelse(is.na(mgus$pctime), 0, 1)
pfit <- pyears(Surv(ptime/365.25, pstat) ~ temp.yr + temp.age + sex, mgus,
              data.frame=TRUE)

tidy(pfit)
glance(pfit)

# if data.frame argument is not given, different information is present in
# output
pfit2 <- pyears(Surv(ptime/365.25, pstat) ~ temp.yr + temp.age + sex, mgus)
tidy(pfit2)
glance(pfit2)
```

tidy.rcorr

Tidy a(n) rcorr object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'rcorr'
tidy(x, diagonal = FALSE, ...)
```

Arguments

| | |
|----------|--|
| x | An rcorr object returned from <code>Hmisc::rcorr()</code> . |
| diagonal | Logical indicating whether or not to include diagonal elements of the correlation matrix, or the correlation of a column with itself. For the elements, estimate is always 1 and p.value is always NA. Defaults to FALSE. |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Details

Suppose the original data has columns A and B. In the correlation matrix from `rcorr` there may be entries for both the `cor(A, B)` and `cor(B, A)`. Only one of these pairs will ever be present in the tidy output.

Value

A `tibble::tibble` with one row for each unique pair of columns in the correlation matrix and columns:

| | |
|-----------------------|--|
| <code>column1</code> | Name or index of the first column being described |
| <code>column2</code> | Name or index of the second column being described |
| <code>estimate</code> | Estimate of Pearson's r or Spearman's ρ |
| <code>n</code> | Number of observations used to compute the correlation |
| <code>p.value</code> | P-value of correlation |

See Also

[tidy\(\)](#), [Hmisc::rcorr\(\)](#)

Examples

```
if (requireNamespace("Hmisc", quietly = TRUE)) {
  library(Hmisc)

  mat <- replicate(52, rnorm(100))
  # add some NAs
  mat[sample(length(mat), 2000)] <- NA
  # also column names
  colnames(mat) <- c(LETTERS, letters)

  rc <- rcorr(mat)

  td <- tidy(rc)
  td

  library(ggplot2)
  ggplot(td, aes(p.value)) +
    geom_histogram(binwidth = .1)

  ggplot(td, aes(estimate, p.value)) +
    geom_point() +
    scale_y_log10()
}
```

| | |
|--------------|---------------------------------|
| tidy.ridgelm | <i>Tidy a(n) ridgelm object</i> |
|--------------|---------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'ridgelm'
tidy(x, ...)
```

Arguments

| | |
|-----|---|
| x | A ridgelm object returned from <code>MASS::lm.ridge()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble` with one row for each combination of lambda and a term in the formula, with columns:

| | |
|----------|--|
| lambda | choice of lambda |
| GCV | generalized cross validation value for this lambda |
| term | the term in the ridge regression model being estimated |
| estimate | estimate of scaled coefficient using this lambda |
| scale | Scaling factor of estimated coefficient |

See Also

`tidy()`, `MASS::lm.ridge()`

Other ridgelm tidiers: `glance.ridgelm`

Examples

```

names(longley)[1] <- "y"
fit1 <- MASS::lm.ridge(y ~ ., longley)
tidy(fit1)

fit2 <- MASS::lm.ridge(y ~ ., longley, lambda = seq(0.001, .05, .001))
td2 <- tidy(fit2)
g2 <- glance(fit2)

# coefficient plot
library(ggplot2)
ggplot(td2, aes(lambda, estimate, color = term)) +
  geom_line()

# GCV plot
ggplot(td2, aes(lambda, GCV)) +
  geom_line()

# add line for the GCV minimizing estimate
ggplot(td2, aes(lambda, GCV)) +
  geom_line() +
  geom_vline(xintercept = g2$lambdaGCV, col = "red", lty = 2)

```

tidy.rlm

Tidy a(n) rlm object

Description

This method wraps `tidy.lm()`.

Usage

```

## S3 method for class 'rlm'
tidy(x, ...)

```

Arguments

| | |
|-------------------------|---|
| <code>x</code> | An <code>rlm</code> object returned by <code>MASS::rlm()</code> . |
| <code>...</code> | Arguments passed on to <code>tidy.lm</code> |
| <code>x</code> | An <code>lm</code> object created by <code>stats::lm()</code> . |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to <code>FALSE</code> . |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |

quick Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to FALSE.

exponentiate Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE.

Details

For tidiers for models from the **robust** package see [tidy.lmRob\(\)](#) and [tidy.glmRob\(\)](#).

Value

A [tibble::tibble\(\)](#) with one row for each term in the regression. The tibble has columns:

| | |
|-----------|---|
| term | The name of the regression term. |
| estimate | The estimated value of the regression term. |
| std.error | The standard error of the regression term. |
| statistic | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| p.value | The two-sided p-value associated with the observed statistic. |
| conf.low | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| conf.high | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

If the linear model is an `mlm` object (multiple linear model), there is an additional column:

| | |
|----------|--|
| response | Which response column the coefficients correspond to (typically Y1, Y2, etc) |
|----------|--|

See Also

[tidy\(\)](#), [tidy.lm\(\)](#)

[MASS::rlm\(\)](#)

Other rlm tidiers: [augment.rlm](#), [glance.rlm](#)

tidy.roc

Tidy a(n) roc object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'roc'
tidy(x, ...)
```

Arguments

`x` An roc object returned from a call to `AUC::roc()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble()` with three columns:

| | |
|---------------------|---|
| <code>cutoff</code> | The cutoff used for classification. Observations with predicted probabilities above this value were assigned class 1, and observations with predicted probabilities below this value were assigned class 0. |
| <code>tpr</code> | The true positive rate at the given cutoff. |
| <code>fpr</code> | The false positive rate at the given cutoff. |

See Also

`tidy()`, `AUC::roc()`

Examples

```
if (require("AUC", quietly = TRUE)) {
  data(churn)
  r <- roc(churn$predictions, churn$labels)

  td <- tidy(r)
  td

  library(ggplot2)

  ggplot(td, aes(fpr, tpr)) +
    geom_line()

  # compare the ROC curves for two prediction algorithms

  library(dplyr)
  library(tidyr)

  rocs <- churn %>%
```



```

gather(algorithm, value, -labels) %>%
nest(-algorithm) %>%
mutate(tidy_roc = purrr::map(data, ~tidy(roc(.x$value, .x$labels)))) %>%
unnest(tidy_roc)

ggplot(rocs, aes(fpr, tpr, color = algorithm)) +
  geom_line()
}

```

tidy.rq

*Tidy a(n) rq object***Description**

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'rq'
tidy(x, se.type = "rank", conf.int = TRUE,
     conf.level = 0.95, ...)

```

Arguments

| | |
|------------|---|
| x | An rq object returned from <code>quantreg::rq()</code> . |
| se.type | Character specifying the method to use to calculate standard errors. Passed to <code>quantreg::summary.rq()</code> se argument. Defaults to "rank". |
| conf.int | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| conf.level | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| ... | Additional arguments passed to <code>quantreg::summary.rq()</code> . |

Details

If `se.type = "rank"` confidence intervals are calculated by `summary.rq`. When only a single predictor is included in the model, no confidence intervals are calculated and the confidence limits are set to NA.

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

See Also

`tidy()`, `quantreg::rq()`

Other quantreg tidiers: `augment.nlrq`, `augment.rqs`, `augment.rq`, `glance.nlrq`, `glance.rq`, `tidy.nlrq`, `tidy.rqs`

tidy.rqs

Tidy a(n) rqs object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'rqs'
tidy(x, se.type = "rank", conf.int = TRUE,
     conf.level = 0.95, ...)
```

Arguments

| | |
|-------------------------|---|
| <code>x</code> | An rqs object returned from <code>quantreg::rq()</code> . |
| <code>se.type</code> | Character specifying the method to use to calculate standard errors. Passed to <code>quantreg::summary.rq()</code> <code>se</code> argument. Defaults to "rank". |
| <code>conf.int</code> | Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE. |
| <code>conf.level</code> | The confidence level to use for the confidence interval if <code>conf.int = TRUE</code> . Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval. |
| <code>...</code> | Additional arguments passed to <code>quantreg::summary.rqs()</code> |

Details

If `se.type = "rank"` confidence intervals are calculated by `summary.rq`. When only a single predictor is included in the model, no confidence intervals are calculated and the confidence limits are set to NA.

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

An additional quantile column indicating with quantile the coefficient corresponds to.

See Also

`tidy()`, `quantreg::rq()`

Other `quantreg` tidiers: `augment.nlrq`, `augment.rqs`, `augment.rq`, `glance.nlrq`, `glance.rq`, `tidy.nlrq`, `tidy.rq`

`tidy.spec`

Tidy a(n) spec object

Description

`Tidy` summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what `tidy` considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'spec'
tidy(x, ...)
```

Arguments

`x` A spec object created by `stats::spectrum()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with two columns: `freq` and `spec`.

See Also

`tidy()`, `stats::spectrum()`

Other time series tidiers: `tidy.acf`, `tidy.ts`, `tidy.zoo`

Examples

```
spc <- spectrum(lh)
tidy(spc)

library(ggplot2)
ggplot(tidy(spc), aes(freq, spec)) +
  geom_line()
```

`tidy.speedlm`

Tidy a(n) speedlm object

Description

This method wraps `tidy.lm()`.

Usage

```
## S3 method for class 'speedlm'
tidy(x, ...)
```

Arguments

- `x` A speedlm object returned from `speedglm::speedlm()`.
- `...` Arguments passed on to `tidy.lm`
- `x` An lm object created by `stats::lm()`.
- conf.int** Logical indicating whether or not to include a confidence interval in the tidied output. Defaults to FALSE.
- conf.level** The confidence level to use for the confidence interval if `conf.int = TRUE`. Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence interval.
- quick** Logical indicating if the only the term and estimate columns should be returned. Often useful to avoid time consuming covariance and standard error calculations. Defaults to FALSE.
- exponentiate** Logical indicating whether or not to exponentiate the the coefficient estimates. This is typical for logistic and multinomial regressions, but a bad idea if there is no log or logit link. Defaults to FALSE.

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|------------------------|---|
| <code>term</code> | The name of the regression term. |
| <code>estimate</code> | The estimated value of the regression term. |
| <code>std.error</code> | The standard error of the regression term. |
| <code>statistic</code> | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| <code>p.value</code> | The two-sided p-value associated with the observed statistic. |
| <code>conf.low</code> | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| <code>conf.high</code> | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

If the linear model is an `m lm` object (multiple linear model), there is an additional column:

| | |
|-----------------------|--|
| <code>response</code> | Which response column the coefficients correspond to (typically Y1, Y2, etc) |
|-----------------------|--|

See Also

`tidy()`, `tidy.lm()`

`speedglm::speedlm()`

Other speedlm tidiers: `augment.speedlm`, `glance.speedlm`

Examples

```
mod <- speedglm::speedlm(mpg ~ wt + qsec, data = mtcars)

tidy(mod)
glance(mod)
augment(mod)
```

tidy.summary.glm *Tidy a(n) summary.glm object*

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'summary.glm'
tidy(x, ...)
```

Arguments

| | |
|-----|--|
| x | A <code>summary.glm</code> object created by calling <code>multcomp::summary.glm()</code> on a <code>glm</code> object created with <code>multcomp::glm()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

See Also

`tidy()`, `multcomp::summary.glm()`, `multcomp::glm()`

Other multcomp tidiers: `tidy.cld`, `tidy.confint.glm`, `tidy.glm`

| | |
|---------------|----------------------------------|
| tidy.survdiff | <i>Tidy a(n) survdiff object</i> |
|---------------|----------------------------------|

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'survdiff'
tidy(x, ...)
```

Arguments

| | |
|-----|---|
| x | An survdiff object returned from <code>survival::survdiff()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble` with one row for each time point and columns:

| | |
|-----|---|
| ... | The initial columns correspond to the grouping factors on the right hand side of the model formula. |
| obs | weighted observed number of events in each group |
| exp | weighted expected number of events in each group |
| N | number of subjects in each group |

See Also

`tidy()`, `survival::survdiff()`

Other survdiff tidiers: `glance.survdiff`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.aareg`, `glance.cch`, `glance.coxph`, `glance.pyyears`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `glance.survreg`, `tidy.aareg`, `tidy.cch`, `tidy.coxph`, `tidy.pyyears`, `tidy.survexp`, `tidy.survfit`, `tidy.survreg`

Examples

```
library(survival)

s <- survdiff(
  Surv(time, status) ~ pat.karno + strata(inst),
  data = lung
)

tidy(s)
glance(s)
```

tidy.survexp

Tidy a(n) survexp object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'survexp'
tidy(x, ...)
```

Arguments

| | |
|-----|---|
| x | An survexp object returned from <code>survival::survexp()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble` with one row for each time point and columns:

| | |
|----------|-------------------------------|
| time | time point |
| estimate | estimated survival |
| n.risk | number of individuals at risk |

See Also

[tidy\(\)](#), [survival::survexp\(\)](#)

Other survexp tidiers: [glance.survexp](#)

Other survival tidiers: [augment.coxph](#), [augment.survreg](#), [glance.aareg](#), [glance.cch](#), [glance.coxph](#), [glance.pyears](#), [glance.survdiff](#), [glance.survexp](#), [glance.survfit](#), [glance.survreg](#), [tidy.aareg](#), [tidy.cch](#), [tidy.coxph](#), [tidy.pyears](#), [tidy.survdiff](#), [tidy.survfit](#), [tidy.survreg](#)

Examples

```
library(survival)
sexpfit <- survexp(
  futime ~ 1,
  rmap = list(
    sex = "male",
    year = accept.dt,
    age = (accept.dt - birth.dt)
  ),
  method = 'conditional',
  data = jasa
)

tidy(sexpfit)
glance(sexpfit)
```

tidy.survfit

Tidy a(n) survfit object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'survfit'
tidy(x, ...)
```

Arguments

x An survfit object returned from [survival::survfit\(\)](#).

... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with one row for each time point and columns:

| | |
|------------------------|---|
| <code>time</code> | timepoint |
| <code>n.risk</code> | number of subjects at risk at time t0 |
| <code>n.event</code> | number of events at time t |
| <code>n.censor</code> | number of censored events |
| <code>estimate</code> | estimate of survival or cumulative incidence rate when multistate |
| <code>std.error</code> | standard error of estimate |
| <code>conf.high</code> | upper end of confidence interval |
| <code>conf.low</code> | lower end of confidence interval |
| <code>state</code> | state if multistate survfit object inputted |
| <code>strata</code> | strata if stratified survfit object inputted |

See Also

`tidy()`, `survival::survfit()`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.aareg`, `glance.cch`, `glance.coxph`, `glance.pyears`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `glance.survreg`, `tidy.aareg`, `tidy.cch`, `tidy.coxph`, `tidy.pyears`, `tidy.survdiff`, `tidy.survexp`, `tidy.survreg`

Examples

```
library(survival)
cfits <- coxph(Surv(time, status) ~ age + sex, lung)
sfit <- survfit(cfits)

tidy(sfit)
glance(sfit)

library(ggplot2)
ggplot(tidy(sfit), aes(time, estimate)) + geom_line() +
  geom_ribbon(aes(ymin=conf.low, ymax=conf.high), alpha=.25)

# multi-state
fitCI <- survfit(Surv(stop, status * as.numeric(event), type = "mstate") ~ 1,
  data = mgus1, subset = (start == 0))
td_multi <- tidy(fitCI)
```

```

td_multi

ggplot(td_multi, aes(time, estimate, group = state)) +
  geom_line(aes(color = state)) +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = .25)

```

tidy.survreg

Tidy a(n) survreg object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```

## S3 method for class 'survreg'
tidy(x, conf.level = 0.95, ...)

```

Arguments

| | |
|------------|---|
| x | An survreg object returned from <code>survival::survreg()</code> . |
| conf.level | confidence level for CI |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble()` with one row for each term in the regression. The tibble has columns:

| | |
|-----------|---|
| term | The name of the regression term. |
| estimate | The estimated value of the regression term. |
| std.error | The standard error of the regression term. |
| statistic | The value of a statistic, almost always a T-statistic, to use in a hypothesis that the regression term is non-zero. |
| p.value | The two-sided p-value associated with the observed statistic. |
| conf.low | The low end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |
| conf.high | The high end of a confidence interval for the regression term. Included only if <code>conf.int = TRUE</code> . |

See Also

`tidy()`, `survival::survreg()`

Other survreg tidiers: `augment.survreg`, `glance.survreg`

Other survival tidiers: `augment.coxph`, `augment.survreg`, `glance.aareg`, `glance.cch`, `glance.coxph`, `glance.pyears`, `glance.survdiff`, `glance.survexp`, `glance.survfit`, `glance.survreg`, `tidy.aareg`, `tidy.cch`, `tidy.coxph`, `tidy.pyears`, `tidy.survdiff`, `tidy.survexp`, `tidy.survfit`

Examples

```
library(survival)

sr <- survreg(
  Surv(futime, fustat) ~ ecog.ps + rx,
  ovarian,
  dist = "exponential"
)

td <- tidy(sr)
augment(sr, ovarian)
glance(sr)

# coefficient plot
library(ggplot2)
ggplot(td, aes(estimate, term)) +
  geom_point() +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high), height = 0) +
  geom_vline(xintercept = 0)
```

tidy.table

Tidy a(n) table object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'table'
tidy(x, ...)
```

Arguments

`x` A [table](#) object.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Details

Directly calls `tibble::as_tibble()` on a `table` object, which does the same things as `as.data.frame.table()` but also gives the returned object `tibble::tibble` class.

Value

A `tibble::tibble` in long-form containing frequency information for the table in a `Freq` column. The result is much like what you get from `tidyr::gather()`.

See Also

[as_tibble.table\(\)](#)

Examples

```
tab <- with(airquality, table(Temp = cut(Temp, quantile(Temp)), Month))
tidy(tab)
```

tidy.ts

Tidy a(n) ts object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'ts'
tidy(x, ...)
```

Arguments

`x` A univariate or multivariate `ts` times series object.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with one row for each observation and columns:

| | |
|---------------------|--|
| <code>index</code> | Index (i.e. date or time) for the "ts" object. |
| <code>series</code> | Name of the series (multivariate "ts" objects only). |
| <code>value</code> | Value of the observation. |

See Also

`tidy()`, `stats::ts()`

Other time series tidiers: `tidy.acf`, `tidy.spec`, `tidy.zoo`

Examples

```
set.seed(678)

tidy(ts(1:10, frequency = 4, start = c(1959, 2)))

z <- ts(matrix(rnorm(300), 100, 3), start = c(1961, 1), frequency = 12)
colnames(z) <- c("Aa", "Bb", "Cc")
tidy(z)
```

`tidy.TukeyHSD`

Tidy a(n) TukeyHSD object

Description

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'TukeyHSD'
tidy(x, ...)
```

Arguments

`x` A TukeyHSD object return from `stats::TukeyHSD()`.

`...` Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in `...`, where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the data argument.

Value

A `tibble::tibble` with one row per comparison and columns:

| | |
|--------------------------|---|
| <code>term</code> | Term for which levels are being compared |
| <code>comparison</code> | Levels being compared, separated by - |
| <code>estimate</code> | Estimate of difference |
| <code>conf.low</code> | Low end of confidence interval of difference |
| <code>conf.high</code> | High end of confidence interval of difference |
| <code>adj.p.value</code> | P-value adjusted for multiple comparisons |

See Also

`tidy()`, `stats::TukeyHSD()`

Other anova tidiers: `tidy.anova`, `tidy.aovlist`, `tidy.aov`, `tidy.manova`

Examples

```
fm1 <- aov(breaks ~ wool + tension, data = warpbreaks)
thsd <- TukeyHSD(fm1, "tension", ordered = TRUE)
tidy(thsd)

# may include comparisons on multiple terms
fm2 <- aov(mpg ~ as.factor(gear) * as.factor(cyl), data = mtcars)
tidy(TukeyHSD(fm2))
```

tidy.zoo

*Tidy a(n) zoo object***Description**

Tidy summarizes information about the components of a model. A model component might be a single term in a regression, a single hypothesis, a cluster, or a class. Exactly what tidy considers to be a model component varies cross models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Usage

```
## S3 method for class 'zoo'
tidy(x, ...)
```

Arguments

| | |
|-----|--|
| x | A zoo object such as those created by <code>zoo::zoo()</code> . |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Value

A `tibble::tibble` with one row for each observation in the zoo time series and columns:

| | |
|--------|---|
| index | Index (usually date) for the zoo object |
| series | Name of the series |
| value | Value of the observation |

See Also

`tidy()`, `zoo::zoo()`

Other time series tidiers: `tidy.acf`, `tidy.spec`, `tidy.ts`

Examples

```
library(zoo)
library(ggplot2)

set.seed(1071)
```



```

# data generated as shown in the zoo vignette
Z.index <- as.Date(sample(12450:12500, 10))
Z.data <- matrix(rnorm(30), ncol = 3)
colnames(Z.data) <- c("Aa", "Bb", "Cc")
Z <- zoo(Z.data, Z.index)

tidy(Z)

ggplot(tidy(Z), aes(index, value, color = series)) +
  geom_line()

ggplot(tidy(Z), aes(index, value)) +
  geom_line() +
  facet_wrap(~ series, ncol = 1)

Zrolled <- rollmean(Z, 5)
ggplot(tidy(Zrolled), aes(index, value, color = series)) +
  geom_line()

```

tidy_irlba

Tidy a(n) irlba object masquerading as list

Description

Broom tidies a number of lists that are effectively S3 objects without a class attribute. For example, `stats::optim()`, `svd()` and `akima::interp()` produce consistent output, but because they do not have a class attribute, they cannot be handled by S3 dispatch.

These functions look at the elements of a list and determine if there is an appropriate tidying method to apply to the list. Those tidiers are themselves implemented as functions of the form `tidy_<function>` or `glance_<function>` and are not exported (but they are documented!).

If no appropriate tidying method is found, throws an error.

Usage

```
tidy_irlba(x, ...)
```

Arguments

`x` A list returned from `irlba::irlba()`.

`...` Arguments passed on to `tidy_svd`

`x` A list with components `u`, `d`, `v` returned by `svd()`.

matrix Character specifying which component of the PCA should be tidied.

- `"u"`, `"samples"`, or `"x"`: returns information about the map from the original space into principle components space.
- `"v"`, `"rotation"`, or `"variables"`: returns information about the map from principle components space back into the original space.
- `"d"` or `"pcs"`: returns information about the eigenvalues will return information about

Details

A very thin wrapper around `tidy_svd()`.

Value

A `tibble::tibble` with columns depending on the component of PCA being tidied.

If `matrix` is "u", "samples", or "x" each row in the tidied output corresponds to the original data in PCA space. The columns are:

| | |
|-------|--|
| row | ID of the original observation (i.e. rowname from original data). |
| PC | Integer indicating a principle component. |
| value | The score of the observation for that particular principle component. That is, the location of the observation in PCA space. |

If `matrix` is "v", "rotation", or "variables", each row in the tidied output corresponds to information about the principle components in the original space. The columns are:

| | |
|-------|--|
| row | The variable labels (colnames) of the data set on which PCA was performed |
| PC | An integer vector indicating the principal component |
| value | The value of the eigenvector (axis score) on the indicated principal component |

If `matrix` is "d" or "pcs", the columns are:

| | |
|------------|--|
| PC | An integer vector indicating the principal component |
| std.dev | Standard deviation explained by this PC |
| percent | Percentage of variation explained |
| cumulative | Cumulative percentage of variation explained |

See Also

`tidy()`, `irlba::irlba()`

Other list tidiers: `glance_optim`, `list_tidiers`, `tidy_optim`, `tidy_svd`, `tidy_xyz`

Other svd tidiers: `augment.prcomp`, `tidy.prcomp`, `tidy_svd`

`tidy_optim`*Tidy a(n) optim object masquerading as list*

Description

Broom tidies a number of lists that are effectively S3 objects without a class attribute. For example, `stats::optim()`, `svd()` and `akima::interp()` produce consistent output, but because they do not have a class attribute, they cannot be handled by S3 dispatch.

These functions look at the elements of a list and determine if there is an appropriate tidying method to apply to the list. Those tidiers are themselves implemented as functions of the form `tidy_<function>` or `glance_<function>` and are not exported (but they are documented!).

If no appropriate tidying method is found, throws an error.

Usage

```
tidy_optim(x, ...)
```

Arguments

| | |
|------------------|---|
| <code>x</code> | A list returned from <code>stats::optim()</code> . |
| <code>...</code> | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in <code>...</code> , where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the <code>data</code> argument. |

Value

A `tibble::tibble` with one row per parameter estimated by `optim` and columns:

| | |
|------------------------|--|
| <code>parameter</code> | name of the parameter, or <code>parameter1</code> , <code>parameter2</code> ... if the input vector is not named |
| <code>value</code> | parameter value that minimizes or maximizes the output |

See Also

`tidy()`, `stats::optim()`

Other list tidiers: `glance_optim`, `list_tidiers`, `tidy_irlba`, `tidy_svd`, `tidy_xyz`

Examples

```
func <- function(x) {
  (x[1] - 2)^2 + (x[2] - 3)^2 + (x[3] - 8)^2
}

o <- optim(c(1, 1, 1), func)

tidy(o)
glance(o)
```

tidy_svd

Tidy a(n) svd object masquerading as list

Description

Broom tidies a number of lists that are effectively S3 objects without a class attribute. For example, `stats::optim()`, `svd()` and `akima::interp()` produce consistent output, but because they do not have a class attribute, they cannot be handled by S3 dispatch.

These functions look at the elements of a list and determine if there is an appropriate tidying method to apply to the list. Those tidiers are themselves implemented as functions of the form `tidy_<function>` or `glance_<function>` and are not exported (but they are documented!).

If no appropriate tidying method is found, throws an error.

Usage

```
tidy_svd(x, matrix = "u", ...)
```

Arguments

| | |
|--------|--|
| x | A list with components u, d, v returned by <code>svd()</code> . |
| matrix | Character specifying which component of the PCA should be tidied. <ul style="list-style-type: none"> • "u", "samples", or "x": returns information about the map from the original space into principle components space. • "v", "rotation", or "variables": returns information about the map from principle components space back into the original space. • "d" or "pcs": returns information about the eigenvalues will return information about |
| ... | Additional arguments. Not used. Needed to match generic signature only. Cautionary note: Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be used. For example, if you pass <code>conf.level = 0.9</code> , all computation will proceed using <code>conf.level = 0.95</code> . Additionally, if you pass <code>newdata = my_tibble</code> to an <code>augment()</code> method that does not accept a <code>newdata</code> argument, it will use the default value for the data argument. |

Details

See <https://stats.stackexchange.com/questions/134282/relationship-between-svd-and-pca-how-to-use-svd-to-perform-pca> for information on how to interpret the various tidied matrices. Note that SVD is only equivalent to PCA on centered data.

Value

A `tibble::tibble` with columns depending on the component of PCA being tidied.

If `matrix` is "u", "samples", or "x" each row in the tidied output corresponds to the original data in PCA space. The columns are:

| | |
|-------|--|
| row | ID of the original observation (i.e. rowname from original data). |
| PC | Integer indicating a principle component. |
| value | The score of the observation for that particular principle component. That is, the location of the observation in PCA space. |

If `matrix` is "v", "rotation", or "variables", each row in the tidied output corresponds to information about the principle components in the original space. The columns are:

| | |
|-------|--|
| row | The variable labels (colnames) of the data set on which PCA was performed |
| PC | An integer vector indicating the principal component |
| value | The value of the eigenvector (axis score) on the indicated principal component |

If `matrix` is "d" or "pcs", the columns are:

| | |
|------------|--|
| PC | An integer vector indicating the principal component |
| std.dev | Standard deviation explained by this PC |
| percent | Percentage of variation explained |
| cumulative | Cumulative percentage of variation explained |

See Also

[svd\(\)](#)

Other svd tidiers: [augment.prcomp](#), [tidy.prcomp](#), [tidy_irlba](#)

Other list tidiers: [glance_optim](#), [list_tidiers](#), [tidy_irlba](#), [tidy_optim](#), [tidy_xyz](#)

Examples

```
mat <- scale(as.matrix(iris[, 1:4]))
s <- svd(mat)

tidy_u <- tidy(s, matrix = "u")
tidy_u

tidy_d <- tidy(s, matrix = "d")
tidy_d
```

```

tidy_v <- tidy(s, matrix = "v")
tidy_v

library(ggplot2)
library(dplyr)

ggplot(tidy_d, aes(PC, percent)) +
  geom_point() +
  ylab("% of variance explained")

tidy_u %>%
  mutate(Species = iris$Species[row]) %>%
  ggplot(aes(Species, value)) +
  geom_boxplot() +
  facet_wrap(~ PC, scale = "free_y")

```

tidy_xyz

Tidy a(n) xyz object masquerading as list

Description

Broom tidies a number of lists that are effectively S3 objects without a class attribute. For example, `stats::optim()`, `svd()` and `akima::interp()` produce consistent output, but because they do not have a class attribute, they cannot be handled by S3 dispatch.

These functions look at the elements of a list and determine if there is an appropriate tidying method to apply to the list. Those tidiers are themselves implemented as functions of the form `tidy_<function>` or `glance_<function>` and are not exported (but they are documented!).

If no appropriate tidying method is found, throws an error.

xyz lists (lists where x and y are vector of coordinates and z is a matrix of values) are typically used by functions such as `graphics::persp()` or `graphics::image()` and returned by interpolation functions such as `akima::interp()`.

Usage

```
tidy_xyz(x, ...)
```

Arguments

- x A list with component x, y and z, where x and y are vectors and z is a matrix. The length of x must equal the number of rows in z and the length of y must equal the number of columns in z.
- ... Additional arguments. Not used. Needed to match generic signature only. **Cautionary note:** Misspelled arguments will be absorbed in ..., where they will be ignored. If the misspelled argument has a default value, the default value will be

used. For example, if you pass `conf.level = 0.9`, all computation will proceed using `conf.level = 0.95`. Additionally, if you pass `newdata = my_tibble` to an `augment()` method that does not accept a `newdata` argument, it will use the default value for the `data` argument.

Value

A `tibble::tibble` with vector columns `x`, `y` and `z`.

See Also

`tidy()`, `graphics::persp()`, `graphics::image()`, `akima::interp()`

Other list tidiers: `glance_optim`, `list_tidiers`, `tidy_irlba`, `tidy_optim`, `tidy_svd`

Examples

```
A <- list(x = 1:5, y = 1:3, z = matrix(runif(5 * 3), nrow = 5))
image(A)
tidy(A)
```

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