Package 'broom'

September 26, 2024

Type Package

Title Convert Statistical Objects into Tidy Tibbles

Version 1.0.7

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 https://broom.tidymodels.org/, https://github.com/tidymodels/broom

BugReports https://github.com/tidymodels/broom/issues

Depends R (>= 3.5)

Imports backports, dplyr (>= 1.0.0), generics (>= 0.0.2), glue,
lifecycle, purrr, rlang, stringr, tibble (>= 3.0.0), tidyr (>=
1.0.0)

Suggests AER, AUC, bbmle, betareg (>= 3.2-1), biglm, binGroup, boot,
btergm (>= 1.10.6), car (>= 3.1-2), carData, caret, cluster,
cmprsk, coda, covr, drc, e1071, emmeans, epiR, ergm (>=
3.10.4), fixest (>= 0.9.0), gam (>= 1.15), gee, geepack,
ggplot2, glmnet, glmnetUtils, gmm, Hmisc, irlba, interp,
joineRML, Kendall, knitr, ks, Lahman, lavaan (>= 0.6.18),
leaps, lfe, lm.beta, lme4, lmodel2, lmtest (>= 0.9.38),
lsmeans, maps, margins, MASS, mclust, mediation, metafor, mfx,
mgcv, mlogit, modeldata, modeltests (>= 0.1.6), muhaz,
multcomp, network, nnet, orcutt (>= 2.2), ordinal, plm, poLCA,
psych, quantreg, rmarkdown, robust, robustbase, rsample,
sandwich, spdep (>= 1.1), spatialreg, speedglm, spelling,
survey, survival (>= 3.6-4), systemfit, testthat (>= 2.1.0),
tseries, vars, zoo

VignetteBuilder knitr

Config/Needs/website tidyverse/tidytemplate

Encoding UTF-8

RoxygenNote 7.3.2

Language en-US

Collate 'aaa-documentation-helper.R' 'null-and-default-tidiers.R'
'aer-tidiers.R' 'auc-tidiers.R' 'base-tidiers.R'
'bbmle-tidiers.R' 'betareg-tidiers.R' 'biglm-tidiers.R'
'bingroup-tidiers.R' 'boot-tidiers.R' 'broom-package.R'
'broom.R' 'btergm-tidiers.R' 'car-tidiers.R' 'caret-tidiers.R'
'cluster-tidiers.R' 'cmprsk-tidiers.R' 'data-frame-tidiers.R'
'deprecated-0-7-0.R' 'drc-tidiers.R' 'emmeans-tidiers.R'
'epiR-tidiers.R' 'ergm-tidiers.R' 'fixest-tidiers.R'
'gam-tidiers.R' 'geepack-tidiers.R'
'glmnet-cv-glmnet-tidiers.R' 'glmnet-glmnet-tidiers.R'
'gmm-tidiers.R' 'hmisc-tidiers.R' 'joinerml-tidiers.R'
'kendall-tidiers.R' 'ks-tidiers.R' 'lavaan-tidiers.R'
'leaps-tidiers.R' 'lfe-tidiers.R' 'list-irlba.R'
'list-optim-tidiers.R' 'list-svd-tidiers.R' 'list-tidiers.R'
'list-xyz-tidiers.R' 'lm-beta-tidiers.R' 'lmodel2-tidiers.R'
'lmtest-tidiers.R' 'maps-tidiers.R' 'margins-tidiers.R'
'mass-fitdistr-tidiers.R' 'mass-negbin-tidiers.R'
'mass-polr-tidiers.R' 'mass-ridgelm-tidiers.R'
'stats-lm-tidiers.R' 'mass-rlm-tidiers.R' 'mclust-tidiers.R'
'mediation-tidiers.R' 'metafor-tidiers.R' 'mfx-tidiers.R'
'mgcv-tidiers.R' 'mlogit-tidiers.R' 'muhaz-tidiers.R'
'multcomp-tidiers.R' 'nnet-tidiers.R' 'nobs.R'
'orcutt-tidiers.R' 'ordinal-clm-tidiers.R'
'ordinal-clmm-tidiers.R' 'plm-tidiers.R' 'polca-tidiers.R'
'psych-tidiers.R' 'stats-nls-tidiers.R'
'quantreg-nlrq-tidiers.R' 'quantreg-rq-tidiers.R'
'quantreg-rqs-tidiers.R' 'robust-glmrob-tidiers.R'
'robust-lmrob-tidiers.R' 'robustbase-glmrob-tidiers.R'
'robustbase-lmrob-tidiers.R' 'sp-tidiers.R' 'spdep-tidiers.R'
'speedglm-speedglm-tidiers.R' 'speedglm-speedlm-tidiers.R'
'stats-anova-tidiers.R' 'stats-arima-tidiers.R'
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'stats-mlm-tidiers.R' 'stats-prcomp-tidiers.R'
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'survival-aareg-tidiers.R' 'survival-cch-tidiers.R'
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'survival-survdiff-tidiers.R' 'survival-survexp-tidiers.R'
'survival-survfit-tidiers.R' 'survival-survreg-tidiers.R'
'systemfit-tidiers.R' 'tseries-tidiers.R' 'utilities.R'

'vars-tidiers.R' 'zoo-tidiers.R' 'zzz.R'

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-09-26 21:00:13 UTC

Contents

augment.betamfx   *Augment data with information from a(n) betamfx 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'betamfx'
augment(
  x,
  data = model.frame(x$fit),
  newdata = NULL,
  type.predict = c("response", "link", "precision", "variance", "quantile"),
  type.residuals = c("sweighted2", "deviance", "pearson", "response", "weighted",
    "sweighted"),
  ...
)
```

Arguments

x	A `betamfx` object.
data	A [base::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 [base::data.frame()](#) or [tibble::tibble()](#) containing all the original pre-
                     dictors 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
                     [betareg::predict.betareg()](#). Defaults to "response".

type.residuals   Character indicating type of residuals to use. Passed to the type argument of
                     [betareg::residuals.betareg()](#). Defaults to "sweighted2.

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                     tionary 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.lvel = 0.9, all computation will proceed
                     using conf.level = 0.95. Two exceptions here are:

                     • tidy() methods will warn when supplied an exponentiate argument if it
                       will be ignored.
                     • augment() methods will warn when supplied a newdata argument if it will
                       be ignored.

Details

This augment method wraps [augment.betareg()](#) for [mfx::betamfx()](#) objects.

Value

A [tibble::tibble()](#) with columns:

.cooksd   Cooks distance.

.fitted   Fitted or predicted value.

.resid   The difference between observed and fitted values.

See Also

[augment.betareg()](#), [mfx::betamfx()](#)

Other mfx tidiers: [augment.mfx()](#), [glance.betamfx()](#), [glance.mfx()](#), [tidy.betamfx()](#), [tidy.mfx()](#)

Examples

```
library(mfx)

# Simulate some data
set.seed(12345)
n <- 1000
x <- rnorm(n)

# Beta outcome
y <- rbeta(n, shape1 = plogis(1 + 0.5 * x), shape2 = (abs(0.2 * x)))
# Use Smithson and Verkuilen correction
y <- (y * (n - 1) + 0.5) / n
```

```
d <- data.frame(y, x)
mod_betamfx <- betamfx(y ~ x | x, data = d)

tidy(mod_betamfx, conf.int = TRUE)

# Compare with the naive model coefficients of the equivalent betareg call (not run)
# tidy(betamfx(y ~ x | x, data = d), conf.int = TRUE)

augment(mod_betamfx)
glance(mod_betamfx)
```

---

augment.betareg   *Augment data with information from a(n) betareg 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 = model.frame(x),
    newdata = NULL,
    type.predict,
    type.residuals,
    ...
)
```

Arguments

x	A betareg object produced by a call to `betareg::betareg()`.
data	A `base::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 `base::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	Character indicating type of prediction to use. Passed to the type argument of the `stats::predict()` generic. Allowed arguments vary with model class, so be sure to read the predict.my_class documentation.
type.residuals	Character indicating type of residuals to use. Passed to the type argument of `stats::residuals()` generic. Allowed arguments vary with model class, so be sure to read the residuals.my_class 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 `conf.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:
	• tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
	• augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

For additional details on Cook's distance, see `stats::cooks.distance()`.

Value

A `tibble::tibble()` with columns:

.cooksd	Cooks distance.
.fitted	Fitted or predicted value.
.resid	The difference between observed and fitted values.

See Also

augment(), betareg::betareg()

Examples

```
# load libraries for models and data
library(betareg)

# load dats
data("GasolineYield", package = "betareg")

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

mod

# summarize model fit with tidiers
tidy(mod)
tidy(mod, conf.int = TRUE)
tidy(mod, conf.int = TRUE, conf.level = .99)

augment(mod)

glance(mod)
```

---

augment.clm   *Augment data with information from a(n) clm 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 at least all predictor variable columns used to fit the model are present. If the original outcome
variable used to fit the model is not included in newdata, then no .resid column will be included
in the output.

Augment will often behave differently depending on whether data or newdata is given. This is be-
cause 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'clm'
augment(
  x,
  data = model.frame(x),
  newdata = NULL,
  type.predict = c("prob", "class"),
  ...
)
```

Arguments

x	A clm object returned from [ordinal::clm()](#).
data	A [base::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 [base::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	Which type of prediction to compute, either "prob" or "class", passed to [ordinal::predict.clm()](#). Defaults to "prob".
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

See Also

[tidy](#), [ordinal::clm()](#), [ordinal::predict.clm()](#)

Other ordinal tidiers: [augment.polr()](#), [glance.clm()](#), [glance.clmm()](#), [glance.polr()](#), [glance.svyolr()](#), [tidy.clm()](#), [tidy.clmm()](#), [tidy.polr()](#), [tidy.svyolr()](#)

Examples

```
# load libraries for models and data
library(ordinal)

# fit model
fit <- clm(rating ~ temp * contact, data = wine)

# summarize model fit with tidiers
tidy(fit)
tidy(fit, conf.int = TRUE, conf.level = 0.9)
tidy(fit, conf.int = TRUE, conf.type = "Wald", exponentiate = TRUE)

glance(fit)
augment(fit, type.predict = "prob")
augment(fit, type.predict = "class")

# ...and again with another model specification
fit2 <- clm(rating ~ temp, nominal = ~contact, data = wine)

tidy(fit2)
glance(fit2)
```

---

augment.coxph   *Augment data with information from a(n) coxph 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters

the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 = model.frame(x),
  newdata = NULL,
  type.predict = "lp",
  type.residuals = "martingale",
  ...
)
```

Arguments

x	A coxph object returned from [survival::coxph()](#).
data	A [base::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 [base::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	Character indicating type of prediction to use. Passed to the type argument of the [stats::predict()](#) generic. Allowed arguments vary with model class, so be sure to read the predict.my_class documentation.
type.residuals	Character indicating type of residuals to use. Passed to the type argument of [stats::residuals()](#) generic. Allowed arguments vary with model class, so be sure to read the residuals.my_class 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 conf.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

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 columns:

.fitted	Fitted or predicted value.
.resid	The difference between observed and fitted values.
.se.fit	Standard errors of fitted values.

See Also

stats::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()

Examples

```
# load libraries for models and data
library(survival)

# fit model
cfit <- coxph(Surv(time, status) ~ age + sex, lung)

# summarize model fit with tidiers
tidy(cfit)
tidy(cfit, exponentiate = TRUE)

lp <- augment(cfit, lung)
risks <- augment(cfit, 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)

cl <- clogit(case ~ tocc + tocc:education + strata(id), logan2)

tidy(cl)
glance(cl)

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()
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters

the model as part of a matrix of covariates, such as when the model formula uses `splines::ns()`, `stats::poly()`, or `survival::Surv()`, it is represented as a matrix column.

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

x	A decomposed.ts object returned from `stats::decompose()`.
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

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

.seasonal	The seasonal component of the decomposition.
.trend	The trend component of the decomposition.
.remainder	The remainder, or "random" component of the decomposition.
.weight	The final robust weights (`stl` only).
.seasadj	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 <- decompose(nottem)
d2 <- stl(nottem, s.window = "periodic", robust = TRUE)
```

```
# compare the original series to its decompositions.

cbind(
  tidy(nottem), augment(d1),
  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(c(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.drc   *Augment data with information from a(n) drc 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'drc'
augment(
  x,
  data = NULL,
  newdata = NULL,
  se_fit = FALSE,
  conf.int = FALSE,
  conf.level = 0.95,
  ...
)
```

Arguments

x	A drc object produced by a call to [drc::drm()](#).
data	A [base::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 [base::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.

se_fit   Logical indicating whether or not a .se.fit column should be added to the
                augmented output. For some models, this calculation can be somewhat time-
                consuming. Defaults to FALSE.

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.

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                tionary 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.lvel = 0.9, all computation will proceed
                using conf.level = 0.95. Two exceptions here are:

                  • tidy() methods will warn when supplied an exponentiate argument if it
                    will be ignored.
                  • augment() methods will warn when supplied a newdata argument if it will
                    be ignored.

Value

A [tibble::tibble()](#) with columns:

.cooksd   Cooks distance.
.fitted   Fitted or predicted value.
.lower   Lower bound on interval for fitted values.
.resid   The difference between observed and fitted values.
.se.fit   Standard errors of fitted values.
.upper   Upper bound on interval for fitted values.

See Also

[augment()](#), [drc::drm()](#)

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

Examples

```
# load libraries for models and data
library(drc)

# fit model
mod <- drm(dead / total ~ conc, type,
  weights = total, data = selenium, fct = LL.2(), type = "binomial"
)

# summarize model fit with tidiers
tidy(mod)
```

```
tidy(mod, conf.int = TRUE)

glance(mod)

augment(mod, selenium)
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [`splines::ns()`](#), [`stats::poly()`](#), or [`survival::Surv()`](#), it is represented as a matrix column.

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

x   A `factanal` object created by [`stats::factanal()`](#).

data   A [base::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. **Cau-
            tionary 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.lvel = 0.9, all computation will proceed
            using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it
  will be ignored.
- augment() methods will warn when supplied a newdata argument if it will
  be ignored.

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 [stats::factanal()](#), unlike other
stats methods like [stats::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 at least all predictor variable columns used to fit the model are present. If the original outcome
variable used to fit the model is not included in newdata, then no .resid column will be included
in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 = model.frame(x), ...)
```

Arguments

x	A `felm` object returned from [lfe::felm()](#).
data	A [base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an `exponentiate` argument if it will be ignored.
- augment() methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

.fitted	Fitted or predicted value.
.resid	The difference between observed and fitted values.

See Also

[augment()](#), [lfe::felm()](#)

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

Examples

```
# load libraries for models and data
library(lfe)

# use built-in `airquality` dataset
head(airquality)

# no FEs; same as lm()
est0 <- felm(Ozone ~ Temp + Wind + Solar.R, airquality)

# summarize model fit with tidiers
tidy(est0)
augment(est0)

# add month fixed effects
est1 <- felm(Ozone ~ Temp + Wind + Solar.R | Month, airquality)

# summarize model fit with tidiers
tidy(est1)
tidy(est1, fe = TRUE)
augment(est1)
glance(est1)

# the "se.type" argument can be used to switch out different standard errors
# types on the fly. In turn, this can be useful exploring the effect of
# different error structures on model inference.
tidy(est1, se.type = "iid")
tidy(est1, se.type = "robust")

# add clustered SEs (also by month)
est2 <- felm(Ozone ~ Temp + Wind + Solar.R | Month | 0 | Month, airquality)

# summarize model fit with tidiers
tidy(est2, conf.int = TRUE)
tidy(est2, conf.int = TRUE, se.type = "cluster")
tidy(est2, conf.int = TRUE, se.type = "robust")
tidy(est2, conf.int = TRUE, se.type = "iid")
```

---

augment.fixest   *Augment data with information from a(n) fixest 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'fixest'
augment(
  x,
  data = NULL,
  newdata = NULL,
  type.predict = c("link", "response"),
  type.residuals = c("response", "deviance", "pearson", "working"),
  ...
)
```

Arguments

x	A fixest object returned from any of the fixest estimators
data	A [base::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 [base::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	Passed to [predict.fixest](#) type argument. Defaults to "link" (like predict.glm).
type.residuals	Passed to [predict.fixest](#) type argument. Defaults to "response" (like residuals.lm, but unlike residuals.glm).

| ... | Additional arguments passed to summary and confint. Important arguments are se and cluster. Other arguments are dof, exact_dof, forceCovariance, and keepBounded. See summary.fixest. |

Value

A tibble::tibble() with columns:

| .fitted | Fitted or predicted value. |
| .resid | The difference between observed and fitted values. |

Note

Important note: fixest models do not include a copy of the input data, so you must provide it manually.

augment.fixest only works for fixest::feols(), fixest::feglm(), and fixest::femlm() models. It does not work with results from fixest::fenegbin(), fixest::feNmlm(), or fixest::fepois().

See Also

augment(), fixest::feglm(), fixest::femlm(), fixest::feols()

Other fixest tidiers: tidy.fixest()

Examples

```
# load libraries for models and data
library(fixest)

gravity <-
  feols(
    log(Euros) ~ log(dist_km) | Origin + Destination + Product + Year, trade
  )

tidy(gravity)
glance(gravity)
augment(gravity, trade)

# to get robust or clustered SEs, users can either:

# 1) specify the arguments directly in the `tidy()` call

tidy(gravity, conf.int = TRUE, cluster = c("Product", "Year"))

tidy(gravity, conf.int = TRUE, se = "threeway")

# 2) or, feed tidy() a summary.fixest object that has already accepted
# these arguments

gravity_summ <- summary(gravity, cluster = c("Product", "Year"))
```

```
tidy(gravity_summ, conf.int = TRUE)

# approach (1) is preferred.
```

---

augment.gam   *Augment data with information from a(n) gam 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'gam'
augment(
  x,
  data = model.frame(x),
  newdata = NULL,
  type.predict,
  type.residuals,
  ...
)
```

Arguments

x	A gam object returned from a call to `mgcv::gam()`.
data	A base::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 `base::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	Character indicating type of prediction to use. Passed to the type argument of the `stats::predict()` generic. Allowed arguments vary with model class, so be sure to read the predict.my_class documentation.
type.residuals	Character indicating type of residuals to use. Passed to the type argument of `stats::residuals()` generic. Allowed arguments vary with model class, so be sure to read the residuals.my_class 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 conf.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are: • tidy() methods will warn when supplied an exponentiate argument if it will be ignored. • augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

For additional details on Cook's distance, see `stats::cooks.distance()`.

Value

A `tibble::tibble()` with columns:

.cooksd	Cooks distance.
.fitted	Fitted or predicted value.
.hat	Diagonal of the hat matrix.
.resid	The difference between observed and fitted values.
.se.fit	Standard errors of fitted values.
.sigma	Estimated residual standard deviation when corresponding observation is dropped from model.

See Also

augment(), mgcv::gam()

Examples

```
# load libraries for models and data
library(mgcv)

# fit model
g <- gam(mpg ~ s(hp) + am + qsec, data = mtcars)

# summarize model fit with tidiers
tidy(g)
tidy(g, parametric = TRUE)
glance(g)
augment(g)
```

---

augment.glm   *Augment data with information from a(n) glm 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses splines::ns(), stats::poly(), or survival::Surv(), it is represented as a matrix column.

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 'glm'
augment(
  x,
  data = model.frame(x),
  newdata = NULL,
  type.predict = c("link", "response", "terms"),
  type.residuals = c("deviance", "pearson"),
  se_fit = FALSE,
  ...
)
```

Arguments

x	A glm object returned from `stats::glm()`.
data	A base::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 base::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	Passed to `stats::predict.glm()` type argument. Defaults to "link".
type.residuals	Passed to `stats::residuals.glm()` and to `stats::rstandard.glm()` type arguments. Defaults to "deviance".
se_fit	Logical indicating whether or not a .se.fit column should be added to the augmented output. For some models, this calculation can be somewhat time-consuming. 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

If the weights for any of the observations in the model are 0, then columns ".infl" and ".hat" in the result will be 0 for those observations.

A .resid column is not calculated when data is specified via the newdata argument.

Value

A [tibble::tibble()](#) with columns:

`.cooksd`	Cooks distance.
`.fitted`	Fitted or predicted value.
`.hat`	Diagonal of the hat matrix.
`.resid`	The difference between observed and fitted values.
`.se.fit`	Standard errors of fitted values.
`.sigma`	Estimated residual standard deviation when corresponding observation is dropped from model.
`.std.resid`	Standardised residuals.

See Also

[stats::glm()](#)

Other lm tidiers: [augment.lm()](#), [glance.glm()](#), [glance.lm()](#), [glance.summary.lm()](#), [glance.svyglm()](#), [tidy.glm()](#), [tidy.lm()](#), [tidy.lm.beta()](#), [tidy.mlm()](#), [tidy.summary.lm()](#)

---

augment.glmRob   *Augment data with information from a(n) glmRob 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'glmRob'
augment(x, ...)
```

Arguments

x	Unused.
...	Unused.

---

augment.glmrob   *Augment data with information from a(n) glmrob 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 at least all predictor variable columns used to fit the model are present. If the original outcome
variable used to fit the model is not included in newdata, then no .resid column will be included
in the output.

Augment will often behave differently depending on whether data or newdata is given. This is be-
cause 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 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. If a predictor enters
the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#),
[stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'glmrob'
augment(
  x,
  data = model.frame(x),
  newdata = NULL,
  type.predict = c("link", "response"),
```

```
  type.residuals = c("deviance", "pearson"),
  se_fit = FALSE,
  ...
)
```

Arguments

x	A glmrob object returned from [robustbase::glmrob()]().
data	A [base::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 [base::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	Character indicating type of prediction to use. Passed to the type argument of the [stats::predict()]() generic. Allowed arguments vary with model class, so be sure to read the predict.my_class documentation.
type.residuals	Character indicating type of residuals to use. Passed to the type argument of [stats::residuals()]() generic. Allowed arguments vary with model class, so be sure to read the residuals.my_class documentation.
se_fit	Logical indicating whether or not a .se.fit column should be added to the augmented output. For some models, this calculation can be somewhat time-consuming. 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

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

Value

A [tibble::tibble()]() with columns:

.fitted	Fitted or predicted value.
.resid	The difference between observed and fitted values.

See Also

robustbase::glmrob()

Other robustbase tidiers: augment.lmrob(), glance.lmrob(), tidy.glmrob(), tidy.lmrob()

Examples

```
if (requireNamespace("robustbase", quietly = TRUE)) {
  # load libraries for models and data
  library(robustbase)

  data(coleman)
  set.seed(0)

  m <- lmrob(Y ~ ., data = coleman)
  tidy(m)
  augment(m)
  glance(m)

  data(carrots)

  Rfit <- glmrob(cbind(success, total - success) ~ logdose + block,
    family = binomial, data = carrots, method = "Mqle",
    control = glmrobMqle.control(tcc = 1.2)
  )

  tidy(Rfit)
  augment(Rfit)
}
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

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

Value

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

.observed	Observed count.
.prop	Proportion of the total.
.row.prop	Row proportion (2 dimensions table only).
.col.prop	Column proportion (2 dimensions table only).
.expected	Expected count under the null hypothesis.
.resid	Pearson residuals.
.std.resid	Standardized residual.

See Also

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

Other htest tidiers: tidy.htest(), tidy.pairwise.htest(), tidy.power.htest()

Examples

```
tt <- t.test(rnorm(10))

tidy(tt)

# the glance output will be the same for each of the below tests
glance(tt)

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)
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 = NULL, ...)
```

Arguments

x
: An ivreg object created by a call to [AER::ivreg()](#).

data
: A [base::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 [base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

  - tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
  - augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

This tidier currently only supports ivreg-classed objects outputted by the AER package. The ivreg package also outputs objects of class ivreg, and will be supported in a later release.

Value

A [tibble::tibble()](#) with columns:

.fitted	Fitted or predicted value.
.resid	The difference between observed and fitted values.

See Also

[augment()](#), [AER::ivreg()](#)

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

Examples

```
# load libraries for models and data
library(AER)

# load data
data("CigarettesSW", package = "AER")

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

# summarize model fit with tidiers
tidy(ivr)
tidy(ivr, conf.int = TRUE)
tidy(ivr, conf.int = TRUE, instruments = TRUE)

augment(ivr)
augment(ivr, data = CigarettesSW)
augment(ivr, newdata = CigarettesSW)

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses splines::ns(), stats::poly(), or survival::Surv(), it is represented as a matrix column.

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

x	A kmeans object created by stats::kmeans().
data	A base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

.cluster	Cluster assignment.

See Also

augment(), stats::kmeans()

Other kmeans tidiers: glance.kmeans(), tidy.kmeans()

Examples

```
library(cluster)
library(modeldata)
library(dplyr)

data(hpc_data)

x <- hpc_data[, 2:5]

fit <- pam(x, k = 4)

tidy(fit)
glance(fit)
augment(fit, x)
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome
variable used to fit the model is not included in newdata, then no .resid column will be included
in the output.

Augment will often behave differently depending on whether data or newdata is given. This is be-
cause 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 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. If a predictor enters

the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](), [stats::poly()](), or [survival::Surv()](), it is represented as a matrix column.

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 = model.frame(x),
  newdata = NULL,
  se_fit = FALSE,
  interval = c("none", "confidence", "prediction"),
  conf.level = 0.95,
  ...
)
```

Arguments

x	An lm object created by [stats::lm()]().
data	A [base::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 [base::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.
se_fit	Logical indicating whether or not a .se.fit column should be added to the augmented output. For some models, this calculation can be somewhat time-consuming. Defaults to FALSE.
interval	Character indicating the type of confidence interval columns to be added to the augmented output. Passed on to predict() and defaults to "none".
conf.level	The confidence level to use for the interval created if interval is "confidence" or "prediction". Must be strictly greater than 0 and less than 1. Defaults to 0.95, which corresponds to a 95 percent confidence/prediction 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

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.

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

When newdata is supplied, only returns .fitted, .resid and .se.fit columns.

Value

A tibble::tibble() with columns:

.cooksd	Cooks distance.
.fitted	Fitted or predicted value.
.hat	Diagonal of the hat matrix.
.lower	Lower bound on interval for fitted values.
.resid	The difference between observed and fitted values.
.se.fit	Standard errors of fitted values.
.sigma	Estimated residual standard deviation when corresponding observation is dropped from model.
.std.resid	Standardised residuals.
.upper	Upper bound on interval for fitted values.

See Also

stats::na.action

augment(), stats::predict.lm()

Other lm tidiers: augment.glm(), glance.glm(), glance.lm(), glance.summary.lm(), glance.svyglm(), tidy.glm(), tidy.lm(), tidy.lm.beta(), tidy.mlm(), tidy.summary.lm()

Examples

```
library(ggplot2)
library(dplyr)

mod <- lm(mpg ~ wt + qsec, data = mtcars)

tidy(mod)
glance(mod)

# coefficient plot
d <- tidy(mod, conf.int = TRUE)
```

```
ggplot(d, aes(estimate, term, xmin = conf.low, xmax = conf.high, height = 0)) +
  geom_point() +
  geom_vline(xintercept = 0, lty = 4) +
  geom_errorbarh()

# aside: There are tidy() and glance() methods for lm.summary objects too.
# this can be useful when you want to conserve memory by converting large lm
# objects into their leaner summary.lm equivalents.
s <- summary(mod)
tidy(s, conf.int = TRUE)
glance(s)

augment(mod)
augment(mod, mtcars, interval = "confidence")

# predict on new data
newdata <- mtcars %>%
  head(6) %>%
  mutate(wt = wt + 1)
augment(mod, newdata = newdata)

# ggplot2 example where we also construct 95% prediction interval

# simpler bivariate model since we're plotting in 2D
mod2 <- lm(mpg ~ wt, data = mtcars)

au <- augment(mod2, newdata = newdata, interval = "prediction")

ggplot(au, aes(wt, mpg)) +
  geom_point() +
  geom_line(aes(y = .fitted)) +
  geom_ribbon(aes(ymin = .lower, ymax = .upper), col = NA, alpha = 0.3)

# predict on new data without outcome variable. Output does not include .resid
newdata <- newdata %>%
  select(-mpg)

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, .cooksd)) +
  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)
```

---

augment.lmRob   *Augment data with information from a(n) lmRob 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 at least all predictor variable columns used to fit the model are present. If the original outcome
variable used to fit the model is not included in newdata, then no .resid column will be included
in the output.

Augment will often behave differently depending on whether data or newdata is given. This is be-
cause 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 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. If a predictor enters
the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#),
[stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'lmRob'
augment(x, data = model.frame(x), newdata = NULL, ...)
```

Arguments

x	A lmRob object returned from robust::lmRob().
data	A base::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 base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

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

See Also

robust::lmRob()

Other robust tidiers: glance.glmRob(), glance.lmRob(), tidy.glmRob(), tidy.lmRob()

Examples

```
# load modeling library
library(robust)

# fit model
m <- lmRob(mpg ~ wt, data = mtcars)

# summarize model fit with tidiers
tidy(m)
augment(m)
glance(m)
```

---

augment.lmrob   *Augment data with information from a(n) lmrob 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'lmrob'
augment(x, data = model.frame(x), newdata = NULL, se_fit = FALSE, ...)
```

Arguments

x   A lmrob object returned from [robustbase::lmrob()](#).

data   A [base::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 [base::data.frame()](#) or [tibble::tibble()](#) containing all the original pre-
              dictors 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.

| se_fit | Logical indicating whether or not a .se.fit column should be added to the augmented output. For some models, this calculation can be somewhat time-consuming. 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are: |

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

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

Value

A tibble::tibble() with columns:

| .fitted | Fitted or predicted value. |
| .resid | The difference between observed and fitted values. |

See Also

robustbase::lmrob()

Other robustbase tidiers: augment.glmrob(), glance.lmrob(), tidy.glmrob(), tidy.lmrob()

Examples

```
if (requireNamespace("robustbase", quietly = TRUE)) {
  # load libraries for models and data
  library(robustbase)

  data(coleman)
  set.seed(0)

  m <- lmrob(Y ~ ., data = coleman)
  tidy(m)
  augment(m)
  glance(m)

  data(carrots)

  Rfit <- glmrob(cbind(success, total - success) ~ logdose + block,
    family = binomial, data = carrots, method = "Mqle",
    control = glmrobMqle.control(tcc = 1.2)
  )
```

```
  tidy(Rfit)
  augment(Rfit)
}
```

---

augment.loess   *Tidy a(n) loess 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 across 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 = model.frame(x), newdata = NULL, se_fit = FALSE, ...)
```

Arguments

x	A loess objects returned by [stats::loess()]().
data	A [base::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 [base::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.
se_fit	Logical indicating whether or not a .se.fit column should be added to the augmented output. For some models, this calculation can be somewhat time-consuming. 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

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.

Note that loess objects by default will not predict on data outside of a bounding hypercube defined by the training data unless the original loess object was fit with control = loess.control(surface = \"direct\")). See stats::predict.loess() for details.

Value

A tibble::tibble() with columns:

.fitted	Fitted or predicted value.
.resid	The difference between observed and fitted values.
.se.fit	Standard errors of fitted values.

See Also

stats::na.action

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

Examples

```
lo <- loess(
  mpg ~ hp + wt,
  mtcars,
  control = loess.control(surface = "direct")
)

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 = NULL, ...)
```

Arguments

x	An Mclust object return from [mclust::Mclust()](#).
data	A [base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

.class	Predicted class.
.uncertainty	The uncertainty associated with the classification. Equal to one minus the model class probability.

See Also

[augment()](#), [mclust::Mclust()](#)

Other mclust tidiers: [tidy.Mclust()](#)

Examples

```
# load library for models and data
library(mclust)

# load data manipulation libraries
library(dplyr)
library(tibble)
library(purrr)
library(tidyr)

set.seed(27)

centers <- tibble(
  cluster = factor(1:3),
  # number points in each cluster
  num_points = c(100, 150, 50),
  # x1 coordinate of cluster center
  x1 = c(5, 0, -3),
  # x2 coordinate of cluster center
  x2 = c(-1, 1, -2)
)

points <- centers %>%
  mutate(
    x1 = map2(num_points, x1, rnorm),
    x2 = map2(num_points, x2, rnorm)
  ) %>%
  select(-num_points, -cluster) %>%
  unnest(c(x1, x2))
```

```
# fit model
m <- Mclust(points)

# summarize model fit with tidiers
tidy(m)
augment(m, points)
glance(m)
```

---

augment.mfx   *Augment data with information from a(n) mfx 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 at least all predictor variable columns used to fit the model are present. If the original outcome
variable used to fit the model is not included in newdata, then no .resid column will be included
in the output.

Augment will often behave differently depending on whether data or newdata is given. This is be-
cause 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 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. If a predictor enters
the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#),
[stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'mfx'
augment(
  x,
  data = model.frame(x$fit),
  newdata = NULL,
  type.predict = c("link", "response", "terms"),
```

```
    type.residuals = c("deviance", "pearson"),
    se_fit = FALSE,
    ...
)

## S3 method for class 'logitmfx'
augment(
  x,
  data = model.frame(x$fit),
  newdata = NULL,
  type.predict = c("link", "response", "terms"),
  type.residuals = c("deviance", "pearson"),
  se_fit = FALSE,
  ...
)

## S3 method for class 'negbinmfx'
augment(
  x,
  data = model.frame(x$fit),
  newdata = NULL,
  type.predict = c("link", "response", "terms"),
  type.residuals = c("deviance", "pearson"),
  se_fit = FALSE,
  ...
)

## S3 method for class 'poissonmfx'
augment(
  x,
  data = model.frame(x$fit),
  newdata = NULL,
  type.predict = c("link", "response", "terms"),
  type.residuals = c("deviance", "pearson"),
  se_fit = FALSE,
  ...
)

## S3 method for class 'probitmfx'
augment(
  x,
  data = model.frame(x$fit),
  newdata = NULL,
  type.predict = c("link", "response", "terms"),
  type.residuals = c("deviance", "pearson"),
  se_fit = FALSE,
  ...
)
```

Arguments

x	A `logitmfx`, `negbinmfx`, `poissonmfx`, or `probitmfx` object. (Note that `betamfx` objects receive their own set of tidiers.)
data	A base::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 base::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	Passed to stats::predict.glm() type argument. Defaults to "link".
type.residuals	Passed to stats::residuals.glm() and to stats::rstandard.glm() type arguments. Defaults to "deviance".
se_fit	Logical indicating whether or not a .se.fit column should be added to the augmented output. For some models, this calculation can be somewhat time-consuming. 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

This generic augment method wraps augment.glm() for applicable objects from the mfx package.

Value

A tibble::tibble() with columns:

.cooksd	Cooks distance.
.fitted	Fitted or predicted value.
.hat	Diagonal of the hat matrix.
.resid	The difference between observed and fitted values.
.se.fit	Standard errors of fitted values.
.sigma	Estimated residual standard deviation when corresponding observation is dropped from model.
.std.resid	Standardised residuals.

See Also

augment.glm(), mfx::logitmfx(), mfx::negbinmfx(), mfx::poissonmfx(), mfx::probitmfx()

Other mfx tidiers: augment.betamfx(), glance.betamfx(), glance.mfx(), tidy.betamfx(), tidy.mfx()

Examples

```
# load libraries for models and data
library(mfx)

# get the marginal effects from a logit regression
mod_logmfx <- logitmfx(am ~ cyl + hp + wt, atmean = TRUE, data = mtcars)

tidy(mod_logmfx, conf.int = TRUE)

# compare with the naive model coefficients of the same logit call
tidy(
  glm(am ~ cyl + hp + wt, family = binomial, data = mtcars),
  conf.int = TRUE
)

augment(mod_logmfx)
glance(mod_logmfx)

# another example, this time using probit regression
mod_probmfx <- probitmfx(am ~ cyl + hp + wt, atmean = TRUE, data = mtcars)

tidy(mod_probmfx, conf.int = TRUE)
augment(mod_probmfx)
glance(mod_probmfx)
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 [base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

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:

`.fitted_j_0`	population-level fitted values for the j-th longitudinal process
`.fitted_j_1`	individuals-level fitted values for the j-th longitudinal process
`.resid_j_0`	population-level residuals for the j-th longitudinal process
`.resid_j_1`	individual-level residuals for the j-th longitudinal process

Examples

```
# broom only skips running these examples because the example models take a
# while to generate—they should run just fine, though!
## Not run:


# load libraries for models and data
library(joineRML)

# fit a joint model with bivariate longitudinal outcomes
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)
```

---

augment.mlogit   *Augment data with information from a(n) mlogit 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'mlogit'
augment(x, data = x$model, ...)
```

Arguments

x	an object returned from [mlogit::mlogit()]().
data	Not currently used
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

At the moment this only works on the estimation dataset. Need to set it up to predict on another dataset.

Value

A [tibble::tibble()]() with columns:

.fitted	Fitted or predicted value.
.probability	Class probability of modal class.
.resid	The difference between observed and fitted values.

See Also

[augment()]()

Other mlogit tidiers: [glance.mlogit](), [tidy.mlogit]()

Examples

```
# load libraries for models and data
library(mlogit)

data("Fishing", package = "mlogit")
Fish <- dfidx(Fishing, varying = 2:9, shape = "wide", choice = "mode")

# fit model
m <- mlogit(mode ~ price + catch | income, data = Fish)

# summarize model fit with tidiers
tidy(m)
augment(m)
glance(m)
```

augment.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 across 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, data = NULL, newdata = NULL, ...)
```

Arguments

x	A nlrq object returned from quantreg::nlrq().
data	A base::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 base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

See Also

augment(), quantreg::nlrq()

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

Examples

```
# fit model
n <- nls(mpg ~ k * e^wt, data = mtcars, start = list(k = 1, e = 2))

# summarize model fit with tidiers + visualization
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)
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses splines::ns(), stats::poly(), or survival::Surv(), it is represented as a matrix column.

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

x	An nls object returned from stats::nls().
data	A base::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 base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

augment.nls does not currently support confidence intervals due to a lack of support in stats::predict.nls().

Value

A tibble::tibble() with columns:

.fitted	Fitted or predicted value.
.resid	The difference between observed and fitted values.

See Also

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

Other nls tidiers: glance.nls(), tidy.nls()

Examples

```
# fit model
n <- nls(mpg ~ k * e^wt, data = mtcars, start = list(k = 1, e = 2))

# summarize model fit with tidiers + visualization
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)
```

---

augment.pam   *Augment data with information from a(n) pam 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'pam'
augment(x, data = NULL, ...)
```

Arguments

x	An pam object returned from cluster::pam()
data	A base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

.cluster	Cluster assignment.
.fitted	Fitted or predicted value.
.resid	The difference between observed and fitted values.

See Also

augment(), cluster::pam()

Other pam tidiers: glance.pam(), tidy.pam()

Examples

```
# load libraries for models and data
library(dplyr)
library(ggplot2)
library(cluster)
library(modeldata)
```

```
data(hpc_data)

x <- hpc_data[, 2:5]
p <- pam(x, k = 4)

# summarize model fit with tidiers + visualization
tidy(p)
glance(p)
augment(p, x)

augment(p, x) %>%
  ggplot(aes(compounds, input_fields)) +
  geom_point(aes(color = .cluster)) +
  geom_text(aes(label = cluster), data = tidy(p), size = 10)
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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

x   A `plm` objected returned by [`plm::plm()`](#).

data   A [base::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. **Cau-**
                    tionary 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.lvel = 0.9, all computation will proceed
                    using conf.level = 0.95. Two exceptions here are:

                    • tidy() methods will warn when supplied an exponentiate argument if it
                      will be ignored.
                    • augment() methods will warn when supplied a newdata argument if it will
                      be ignored.

Value

A [`tibble::tibble()`](#) with columns:

.fitted   Fitted or predicted value.
.resid   The difference between observed and fitted values.

See Also

[augment()](#), [plm::plm()](#)

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

Examples

```
# load libraries for models and data
library(plm)

# load data
data("Produc", package = "plm")

# fit model
zz <- plm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp,
  data = Produc, index = c("state", "year")
)

# summarize model fit with tidiers
summary(zz)

tidy(zz)
tidy(zz, conf.int = TRUE)
```

```
tidy(zz, conf.int = TRUE, conf.level = 0.9)

augment(zz)
glance(zz)
```

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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	A [base::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. **Cau-
                                   tionary 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.lvel = 0.9, all computation will proceed
                                   using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it
  will be ignored.
- augment() methods will warn when supplied a newdata argument if it will
  be ignored.

Details

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.

Value

A [tibble::tibble()](#) with columns:

.class   Predicted class.
.probability   Class probability of modal class.

See Also

[augment()](#), [poLCA::poLCA()](#)

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

Examples

```
# load libraries for models and data
library(poLCA)
library(dplyr)

# generate data
data(values)

f <- cbind(A, B, C, D) ~ 1

# fit model
M1 <- poLCA(f, values, nclass = 2, verbose = FALSE)

M1
```

```
# summarize model fit with tidiers + visualization
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)

# 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

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

count(au, .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)
```

---

augment.polr   *Augment data with information from a(n) polr 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses splines::ns(), stats::poly(), or survival::Surv(), it is represented as a matrix column.

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 'polr'
augment(
  x,
  data = model.frame(x),
  newdata = NULL,
  type.predict = c("class"),
  ...
)
```

Arguments

x	A polr object returned from MASS::polr().
data	A base::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 base::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	Which type of prediction to compute, passed to MASS:::predict.polr(). Only supports "class" at the moment.

`...`	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

See Also

`tidy()`, `MASS::polr()`

Other ordinal tidiers: `augment.clm()`, `glance.clm()`, `glance.clmm()`, `glance.polr()`, `glance.svyolr()`, `tidy.clm()`, `tidy.clmm()`, `tidy.polr()`, `tidy.svyolr()`

Examples

```
# load libraries for models and data
library(MASS)

# fit model
fit <- polr(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)

# summarize model fit with tidiers
tidy(fit, exponentiate = TRUE, conf.int = TRUE)

glance(fit)
augment(fit, type.predict = "class")

fit2 <- polr(factor(gear) ~ am + mpg + qsec, data = mtcars)

tidy(fit, p.values = TRUE)
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'prcomp'
augment(x, data = NULL, newdata, ...)
```

Arguments

x	A prcomp object returned by [stats::prcomp()](#).
data	A [base::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 [base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

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 data with information from a(n) rlm 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'rlm'
augment(x, data = model.frame(x), newdata = NULL, se_fit = FALSE, ...)
```

Arguments

x	An rlm object returned by MASS::rlm().
data	A base::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 base::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.
se_fit	Logical indicating whether or not a .se.fit column should be added to the augmented output. For some models, this calculation can be somewhat time-consuming. 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

.fitted	Fitted or predicted value.
.hat	Diagonal of the hat matrix.
.resid	The difference between observed and fitted values.
.se.fit	Standard errors of fitted values.
.sigma	Estimated residual standard deviation when corresponding observation is dropped from model.

See Also

MASS::rlm()

Other rlm tidiers: glance.rlm(), tidy.rlm()

Examples

```
# load libraries for models and data
library(MASS)
```

```
# fit model
r <- rlm(stack.loss ~ ., stackloss)

# summarize model fit with tidiers
tidy(r)
augment(r)
glance(r)
```

---

augment.rma *Augment data with information from a(n) rma 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in newdata, then no .resid column will be included in the output.

Augment will often behave differently depending on whether data or newdata is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses splines::ns(), stats::poly(), or survival::Surv(), it is represented as a matrix column.

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 'rma'
augment(x, interval = c("prediction", "confidence"), ...)
```

Arguments

x	An rma object such as those created by [metafor::rma()](), [metafor::rma.uni()](), [metafor::rma.glmm()](), [metafor::rma.mh()](), [metafor::rma.mv()](), or [metafor::rma.peto()]().
interval	For rma.mv models, should prediction intervals ("prediction", default) or confidence intervals ("confidence") intervals be returned? For rma.uni models, prediction intervals are always returned. For rma.mh and rma.peto models, confidence intervals are always returned.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()]() with columns:

.fitted	Fitted or predicted value.
.lower	Lower bound on interval for fitted values.
.moderator	In meta-analysis, the moderators used to calculate the predicted values.
.moderator.level	
	In meta-analysis, the level of the moderators used to calculate the predicted values.
.resid	The difference between observed and fitted values.
.se.fit	Standard errors of fitted values.
.upper	Upper bound on interval for fitted values.
.observed	The observed values for the individual studies

Examples

```
# load modeling library
library(metafor)

# generate data and fit
df <-
  escalc(
    measure = "RR",
    ai = tpos,
    bi = tneg,
    ci = cpos,
    di = cneg,
    data = dat.bcg
```

```
  )

  meta_analysis <- rma(yi, vi, data = df, method = "EB")

  # summarize model fit with tidiers
  augment(meta_analysis)
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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

x   An rq object returned from [quantreg::rq()](#).

data   A [base::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 [base::data.frame()](#) or [tibble::tibble()](#) containing all the original pre-
                dictors 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 [quantreg::predict.rq](#)

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

                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 converage probability for the 'confidence' intervals.

                type For predict.rq, the method for 'confidence' intervals, if desired. If 'per-
                    centile' 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 ma-
                    trix 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 Sil-
                    verman'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'.

Details

Depending on the arguments passed on to predict.rq via ..., a confidence interval is also cal-
culated on the fitted values resulting in columns .lower and .upper. Does not provide confidence
intervals when data is specified via the newdata argument.

Value

A [tibble::tibble()](#) with columns:

.fitted   Fitted or predicted value.

.resid   The difference between observed and fitted values.

.tau   Quantile.

See Also

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

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

Examples

```
# load modeling library and data
library(quantreg)

data(stackloss)

# median (l1) regression fit for the stackloss data.
mod1 <- rq(stack.loss ~ stack.x, .5)

# weighted sample median
mod2 <- rq(rnorm(50) ~ 1, weights = runif(50))

# summarize model fit with tidiers
tidy(mod1)
glance(mod1)
augment(mod1)

tidy(mod2)
glance(mod2)
augment(mod2)

# varying tau to generate an rqs object
mod3 <- rq(stack.loss ~ stack.x, tau = c(.25, .5))

tidy(mod3)
augment(mod3)

# glance cannot handle rqs objects like `mod3`--use a purrr
# `map`-based workflow instead
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses splines::ns(), stats::poly(), or survival::Surv(), it is represented as a matrix column.

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

x	An `rqs` object returned from quantreg::rq().
data	A base::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 base::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.
...	Arguments passed on to quantreg::predict.rq
	object object of class rq or rqs or rq.process produced by rq
	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 converage 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'.

Details

Depending on the arguments passed on to predict.rq via . . ., a confidence interval is also calculated on the fitted values resulting in columns .lower and .upper. Does not provide confidence intervals when data is specified via the newdata argument.

See Also

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

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

Examples

```
# load modeling library and data
library(quantreg)

data(stackloss)

# median (l1) regression fit for the stackloss data.
mod1 <- rq(stack.loss ~ stack.x, .5)

# weighted sample median
mod2 <- rq(rnorm(50) ~ 1, weights = runif(50))

# summarize model fit with tidiers
tidy(mod1)
glance(mod1)
augment(mod1)

tidy(mod2)
glance(mod2)
augment(mod2)

# varying tau to generate an rqs object
mod3 <- rq(stack.loss ~ stack.x, tau = c(.25, .5))

tidy(mod3)
augment(mod3)
```

```
# glance cannot handle rqs objects like `mod3`--use a purrr
# `map`-based workflow instead
```

---

augment.sarlm   *Augment data with information from a(n) spatialreg 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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 'sarlm'
augment(x, data = x$X, ...)
```

Arguments

x	An object returned from [spatialreg::lagsarlm()](#) or [spatialreg::errorsarlm()](#).
data	Ignored, but included for internal consistency. See the details below.
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

The predict method for sarlm objects assumes that the response is known. See ?predict.sarlm for more discussion. As a result, since the original data can be recovered from the fit object, this method currently does not take in `data` or `newdata` arguments.

Value

A [`tibble::tibble()`](#) with columns:

`.fitted`	Fitted or predicted value.
`.resid`	The difference between observed and fitted values.

See Also

[`augment()`](#)

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

Examples

```
# load libraries for models and data
library(spatialreg)
library(spdep)

# load data
data(oldcol, package = "spdep")

listw <- nb2listw(COL.nb, style = "W")

# fit model
crime_sar <-
  lagsarlm(CRIME ~ INC + HOVAL,
    data = COL.OLD,
    listw = listw,
    method = "eigen"
  )

# summarize model fit with tidiers
tidy(crime_sar)
tidy(crime_sar, conf.int = TRUE)
glance(crime_sar)
augment(crime_sar)

# fit another model
```

```
crime_sem <- errorsarlm(CRIME ~ INC + HOVAL, data = COL.OLD, listw)

# summarize model fit with tidiers
tidy(crime_sem)
tidy(crime_sem, conf.int = TRUE)
glance(crime_sem)
augment(crime_sem)

# fit another model
crime_sac <- sacsarlm(CRIME ~ INC + HOVAL, data = COL.OLD, listw)

# summarize model fit with tidiers
tidy(crime_sac)
tidy(crime_sac, conf.int = TRUE)
glance(crime_sac)
augment(crime_sac)
```

---

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 across 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 smooth.spline object returned from stats::smooth.spline().

data   A base::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. **Cau-
            tionary 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.lvel = 0.9, all computation will proceed
            using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

.fitted	Fitted or predicted value.
.resid	The difference between observed and fitted values.

See Also

[augment()](#), [stats::smooth.spline()](#), [stats::predict.smooth.spline()](#)

Other smoothing spline tidiers: [glance.smooth.spline](#)()

Examples

```
# fit model
spl <- smooth.spline(mtcars$wt, mtcars$mpg, df = 4)

# summarize model fit with tidiers
augment(spl, mtcars)

# calls original columns x and y
augment(spl)

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 at least all predictor variable columns used to fit the model are present. If the original outcome

variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 = NULL, ...)
```

Arguments

x	A speedlm object returned from [speedglm::speedlm()](#).
data	A [base::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 [base::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

.fitted	Fitted or predicted value.
.resid	The difference between observed and fitted values.

See Also

`speedglm::speedlm()`

Other speedlm tidiers: `glance.speedglm()`, `glance.speedlm()`, `tidy.speedglm()`, `tidy.speedlm()`

Examples

```
# load modeling library
library(speedglm)

# fit model
mod <- speedlm(mpg ~ wt + qsec, data = mtcars, fitted = TRUE)

# summarize model fit with tidiers
tidy(mod)
glance(mod)
augment(mod)
```

---

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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses `splines::ns()`, `stats::poly()`, or `survival::Surv()`, it is represented as a matrix column.

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, data = NULL, weights = TRUE, ...)
```

Arguments

x	An stl object returned from stats::stl().
data	Ignored, included for consistency with the augment generic signature only.
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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

.seasonal	The seasonal component of the decomposition.
.trend	The trend component of the decomposition.
.remainder	The remainder, or "random" component of the decomposition.
.weight	The final robust weights, if requested.
.seasadj	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 at least all predictor variable columns used to fit the model are present. If the original outcome variable used to fit the model is not included in `newdata`, then no `.resid` column will be included in the output.

Augment will often behave differently depending on whether `data` or `newdata` is given. 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 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. If a predictor enters the model as part of a matrix of covariates, such as when the model formula uses [splines::ns()](#), [stats::poly()](#), or [survival::Surv()](#), it is represented as a matrix column.

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 = model.frame(x),
  newdata = NULL,
  type.predict = "response",
  type.residuals = "response",
  ...
)
```

Arguments

x	An survreg object returned from [survival::survreg()](#).
data	A [base::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 [base::data.frame()](#) or [tibble::tibble()](#) containing all the original pre-
                      dictors 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 [stats::predict()](#) generic. Allowed arguments vary with model class, so
                      be sure to read the predict.my_class documentation.

type.residuals   Character indicating type of residuals to use. Passed to the type argument of
                      [stats::residuals()](#) generic. Allowed arguments vary with model class, so
                      be sure to read the residuals.my_class documentation.

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                      tionary 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.lvel = 0.9, all computation will proceed
                      using conf.level = 0.95. Two exceptions here are:

                      • tidy() methods will warn when supplied an exponentiate argument if it
                        will be ignored.
                      • augment() methods will warn when supplied a newdata argument if it will
                        be ignored.

Value

A [tibble::tibble()](#) with columns:

.fitted   Fitted or predicted value.

.resid   The difference between observed and fitted values.

.se.fit   Standard errors of fitted values.

See Also

[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()](#)

Examples

```
# load libraries for models and data
library(survival)

# fit model
sr <- survreg(
  Surv(futime, fustat) ~ ecog.ps + rx,
  ovarian,
  dist = "exponential"
)
```

```
# summarize model fit with tidiers + visualization
tidy(sr)
augment(sr, ovarian)
glance(sr)

# coefficient plot
td <- tidy(sr, conf.int = TRUE)

library(ggplot2)

ggplot(td, aes(estimate, term)) +
  geom_point() +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high), height = 0) +
  geom_vline(xintercept = 0)
```

---

augment_columns   *Add fitted values, residuals, and other common outputs to an augment*
                       call

Description

augment_columns is intended for use in the internals of augment methods only and is exported for developers extending the broom package. Please instead use augment() to appropriately make use of the functionality in augment_columns().

Usage

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

Arguments

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

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. Ignored for model types that do not accept an `se.fit` argument
...	extra arguments (not used)

Details

Note that, in the case that a `residuals()` or `influence()` generic is not implemented for the supplied model x, the function will 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. Functionality is no longer supported for this method.

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 tibble.

Details

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

See Also

Other deprecated: confint_tidy(), data.frame_tidiers, finish_glance(), fix_data_frame(), summary_tidiers, tidy.density(), tidy.dist(), tidy.ftable(), tidy.numeric()

confint_tidy   *(Deprecated) Calculate confidence interval as a tidy data frame*

Description

This function is now deprecated and will be removed from a future release of broom.

Usage

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

Arguments

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

Details

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.

confint_tidy

Value

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

See Also

Other deprecated: bootstrap(), data.frame_tidiers, finish_glance(), fix_data_frame(), summary_tidiers, tidy.density(), tidy.dist(), tidy.ftable(), tidy.numeric()

---

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'
augment(x, data, ...)

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

Arguments

x	A data.frame
...	Additional arguments for other methods.
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.
trim	the fraction (0 to 0.5) of observations to be trimmed from each end of x before the mean is computed. Passed to the trim argument of [mean](#)
data	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:

column	name of original column
n	Number of valid (non-NA) values
mean	mean
sd	standard deviation
median	median
trimmed	trimmed mean, with trim defaulting to .1

mad	median absolute deviation (from the median)
min	minimum value
max	maximum value
range	range
skew	skew
kurtosis	kurtosis
se	standard error

glance returns a one-row data.frame with

nrow	number of rows
ncol	number of columns
complete.obs	number of rows that have no missing values
na.fraction	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

See Also

Other deprecated: bootstrap(), confint_tidy(), finish_glance(), fix_data_frame(), summary_tidiers, tidy.density(), tidy.dist(), tidy.ftable(), tidy.numeric()

Other deprecated: bootstrap(), confint_tidy(), finish_glance(), fix_data_frame(), summary_tidiers, tidy.density(), tidy.dist(), tidy.ftable(), tidy.numeric()

Other deprecated: bootstrap(), confint_tidy(), finish_glance(), fix_data_frame(), summary_tidiers, tidy.density(), tidy.dist(), tidy.ftable(), tidy.numeric()

Examples

```
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()
```

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

x   An object of class durbinWatsonTest created by a call to car::durbinWatsonTest().

...   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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

alternative	Alternative hypothesis (character).
autocorrelation	
	Autocorrelation.
p.value	The two-sided p-value associated with the observed statistic.
statistic	Test statistic for Durbin-Watson test.
method	Always 'Durbin-Watson Test'.

See Also

tidy(), glance(), car::durbinWatsonTest()

Other car tidiers: leveneTest_tidiers

Examples

```
# load modeling library
library(car)

# fit model
dw <- durbinWatsonTest(lm(mpg ~ wt, data = mtcars))

# summarize model fit with tidiers
tidy(dw)

# same output for all durbinWatsonTests
glance(dw)
```

---

finish_glance	*(Deprecated) Add logLik, AIC, BIC, and other common measurements to a glance of a prediction*

Description

This function is now deprecated in favor of using custom logic and the appropriate `nobs()` method.

Usage

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

Arguments

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

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

See Also

Other deprecated: `bootstrap()`, `confint_tidy()`, `data.frame_tidiers`, `fix_data_frame()`, `summary_tidiers`, `tidy.density()`, `tidy.dist()`, `tidy.ftable()`, `tidy.numeric()`

---

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

Description

This function is deprecated as of broom 0.7.0 and will be removed from a future release. Please see tibble::as_tibble.

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

See Also

Other deprecated: bootstrap(), confint_tidy(), data.frame_tidiers, finish_glance(), summary_tidiers, tidy.density(), tidy.dist(), tidy.ftable(), tidy.numeric()

---

glance.aareg   *Glance at a(n) aareg 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

df	Degrees of freedom used by the model.
nobs	Number of observations used.
p.value	P-value corresponding to the test statistic.
statistic	Test statistic.

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()

Examples

```
# load libraries for models and data
library(survival)

# fit model
afit <- aareg(
  Surv(time, status) ~ age + sex + ph.ecog,
  data = lung,
  dfbeta = TRUE
)
```

```
# summarize model fit with tidiers
tidy(afit)
```

---

glance.anova   *Glance at a(n) anova 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   An anova object, such as those created by [stats::anova()](#), [car::Anova()](#), [car::leveneTest()](#), or [car::linearHypothesis()](#).

...   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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

deviance   Deviance of the model.

df.residual   Residual degrees of freedom.

Note

Note that the output of `glance.anova()` will vary depending on the initializing anova call. In some cases, it will just return an empty data frame. In other cases, `glance.anova()` may return columns that are also common to `tidy.anova()`. This is partly to preserve backwards compatibility with early versions of `broom`, but also because the underlying anova model yields components that could reasonably be interpreted as goodness-of-fit summaries too.

See Also

`glance()`

Other anova tidiers: `glance.aov()`, `tidy.TukeyHSD()`, `tidy.anova()`, `tidy.aov()`, `tidy.aovlist()`, `tidy.manova()`

Examples

```
# fit models
a <- lm(mpg ~ wt + qsec + disp, mtcars)
b <- lm(mpg ~ wt + qsec, mtcars)

mod <- anova(a, b)

# summarize model fit with tidiers
tidy(mod)
glance(mod)

# car::linearHypothesis() example
library(car)
mod_lht <- linearHypothesis(a, "wt - disp")
tidy(mod_lht)
glance(mod_lht)
```

---

glance.aov   *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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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`.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   An aov object, such as those created by [stats::aov()](#).

...   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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

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

AIC   Akaike's Information Criterion for the model.

BIC   Bayesian Information Criterion for the model.

deviance   Deviance of the model.

logLik   The log-likelihood of the model. [stats::logLik()] may be a useful reference.

nobs   Number of observations used.

Note

Note that tidy.aov() now contains the numerator and denominator degrees of freedom, which were included in the output of glance.aov() in some previous versions of the package.

See Also

[glance()](#)

Other anova tidiers: [glance.anova()](#), [tidy.TukeyHSD()](#), [tidy.anova()](#), [tidy.aov()](#), [tidy.aovlist()](#), [tidy.manova()](#)

Examples

```
a <- aov(mpg ~ wt + qsec + disp, mtcars)
tidy(a)
```

---

glance.Arima | *Glance at a(n) Arima object*

Description

Glance accepts a model object and returns a [`tibble::tibble()`](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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	An object of class Arima created by [`stats::arima()`](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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [`tibble::tibble()`](tibble::tibble()) with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
sigma	Estimated standard error of the residuals.

See Also

stats::arima()

Other Arima tidiers: tidy.Arima()

Examples

```
# fit model
fit <- arima(lh, order = c(1, 0, 0))

# summarize model fit with tidiers
tidy(fit)
glance(fit)
```

---

glance.betamfx   *Glance at a(n) betamfx 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A betamfx 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.

- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

This glance method wraps `glance.betareg()` for `mfx::betamfx()` objects.

Value

A `tibble::tibble()` with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
df.null	Degrees of freedom used by the null model.
df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
pseudo.r.squared	
	Like the R squared statistic, but for situations when the R squared statistic isn't defined.

See Also

`glance.betareg()`, `mfx::betamfx()`

Other mfx tidiers: `augment.betamfx()`, `augment.mfx()`, `glance.mfx()`, `tidy.betamfx()`, `tidy.mfx()`

Examples

```
library(mfx)

# Simulate some data
set.seed(12345)
n <- 1000
x <- rnorm(n)

# Beta outcome
y <- rbeta(n, shape1 = plogis(1 + 0.5 * x), shape2 = (abs(0.2 * x)))
# Use Smithson and Verkuilen correction
y <- (y * (n - 1) + 0.5) / n

d <- data.frame(y, x)
mod_betamfx <- betamfx(y ~ x | x, data = d)

tidy(mod_betamfx, conf.int = TRUE)

# Compare with the naive model coefficients of the equivalent betareg call (not run)
# tidy(betamfx(y ~ x | x, data = d), conf.int = TRUE)

augment(mod_betamfx)
```

```
glance(mod_betamfx)
```

---

glance.betareg   *Glance at a(n) betareg 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

AIC   Akaike's Information Criterion for the model.

BIC   Bayesian Information Criterion for the model.

df.null   Degrees of freedom used by the null model.

df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
pseudo.r.squared	

> Like the R squared statistic, but for situations when the R squared statistic isn't defined.

See Also

[glance()](), [betareg::betareg()]()

Examples

```
# load libraries for models and data
library(betareg)

# load dats
data("GasolineYield", package = "betareg")

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

mod

# summarize model fit with tidiers
tidy(mod)
tidy(mod, conf.int = TRUE)
tidy(mod, conf.int = TRUE, conf.level = .99)

augment(mod)

glance(mod)
```

---

glance.biglm   *Glance at a(n) biglm 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A biglm object created by a call to `biglm::biglm()` or `biglm::bigglm()`.

...   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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

AIC   Akaike's Information Criterion for the model.

deviance   Deviance of the model.

df.residual   Residual degrees of freedom.

nobs   Number of observations used.

r.squared   R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.

See Also

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

Other biglm tidiers: `tidy.biglm()`

Examples

```
# load modeling library
library(biglm)

# fit model -- linear regression
bfit <- biglm(mpg ~ wt + disp, mtcars)

# summarize model fit with tidiers
```

```
tidy(bfit)
tidy(bfit, conf.int = TRUE)
tidy(bfit, conf.int = TRUE, conf.level = .9)

glance(bfit)

# fit model -- logistic regression
bgfit <- bigglm(am ~ mpg, mtcars, family = binomial())

# summarize model fit with tidiers
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)
```

---

glance.binDesign   *Glance at a(n) binDesign 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A binGroup::binDesign 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it
  will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will
  be ignored.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

power	Power achieved by the analysis.
n	Sample size used to achieve this power.
power.reached	Whether the desired power was reached.
maxit	Number of iterations performed.

See Also

[`glance()`](#), [`binGroup::binDesign()`](#)

Other bingroup tidiers: [`tidy.binDesign()`](#), [`tidy.binWidth()`](#)

Examples

```
# load libraries for models and data
library(binGroup)

des <- binDesign(
  nmax = 300, delta = 0.06,
  p.hyp = 0.1, power = .8
)

glance(des)
tidy(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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   An cch object returned from [`survival::cch()`](#).

...   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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- tidy() methods will warn when supplied an `exponentiate` argument if it will be ignored.
- augment() methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

iter   Iterations of algorithm/fitting procedure completed.

p.value   P-value corresponding to the test statistic.

rscore   Robust log-rank statistic

score   Score.

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.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()

Examples

```
# load libraries for models and data
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 model
fit.ccP <- cch(Surv(edrel, rel) ~ stage + histol + age,
  data = ccoh.data,
  subcoh = ~subcohort, id = ~seqno, cohort.size = 4028
)

# summarize model fit with tidiers + visualization
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)
```

glance.clm	*Glance at a(n) clm 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	A `clm` object returned from `ordinal::clm()`.
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
df.residual	Residual degrees of freedom.
edf	The effective degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.

See Also

`tidy`, `ordinal::clm()`

Other ordinal tidiers: `augment.clm()`, `augment.polr()`, `glance.clmm()`, `glance.polr()`, `glance.svyolr()`, `tidy.clm()`, `tidy.clmm()`, `tidy.polr()`, `tidy.svyolr()`

Examples

```
# load libraries for models and data
library(ordinal)

# fit model
fit <- clm(rating ~ temp * contact, data = wine)

# summarize model fit with tidiers
tidy(fit)
tidy(fit, conf.int = TRUE, conf.level = 0.9)
tidy(fit, conf.int = TRUE, conf.type = "Wald", exponentiate = TRUE)

glance(fit)
augment(fit, type.predict = "prob")
augment(fit, type.predict = "class")

# ...and again with another model specification
fit2 <- clm(rating ~ temp, nominal = ~contact, data = wine)

tidy(fit2)
glance(fit2)
```

---

glance.clmm   *Glance at a(n) clmm 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	A `clmm` object returned from [ordinal::clmm()]().
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [tibble::tibble()]() with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
edf	The effective degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.

See Also

[tidy](), [ordinal::clmm()]()

Other ordinal tidiers: [augment.clm](), [augment.polr](), [glance.clm](), [glance.polr](), [glance.svyolr](), [tidy.clm](), [tidy.clmm](), [tidy.polr](), [tidy.svyolr]()

Examples

```
# load libraries for models and data
library(ordinal)

# fit model
fit <- clmm(rating ~ temp + contact + (1 | judge), data = wine)

# summarize model fit with tidiers
tidy(fit)
tidy(fit, conf.int = TRUE, conf.level = 0.9)
tidy(fit, conf.int = TRUE, exponentiate = TRUE)

glance(fit)

# ...and again with another model specification
fit2 <- clmm(rating ~ temp + (1 | judge), nominal = ~contact, data = wine)

tidy(fit2)
```

```
glance(fit2)
```

---

glance.coeftest   *Glance at a(n) coeftest 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A coeftest object returned from [`lmtest::coeftest()`](#).

...   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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

adj.r.squared   Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.

AIC   Akaike's Information Criterion for the model.

BIC	Bayesian Information Criterion for the model.
deviance	Deviance of the model.
df	Degrees of freedom used by the model.
df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
p.value	P-value corresponding to the test statistic.
r.squared	R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.
sigma	Estimated standard error of the residuals.
statistic	Test statistic.

Note

Because of the way that lmtest::coeftest() retains information about the underlying model object, the returned columns for glance.coeftest() will vary depending on the arguments. Specifically, four columns are returned regardless: "Loglik", "AIC", "BIC", and "nobs". Users can obtain additional columns (e.g. "r.squared", "df") by invoking the "save = TRUE" argument as part of lmtest::coeftest(). See examples.

As an aside, goodness-of-fit measures such as R-squared are unaffected by the presence of heteroskedasticity. For further discussion see, e.g. chapter 8.1 of Wooldridge (2016).

References

Wooldridge, Jeffrey M. (2016) *Introductory econometrics: A modern approach.* (6th edition). Nelson Education.

See Also

glance(), lmtest::coeftest()

Examples

```
# load libraries for models and data
library(lmtest)

m <- lm(dist ~ speed, data = cars)

coeftest(m)
tidy(coeftest(m))
tidy(coeftest(m, conf.int = TRUE))

# a very common workflow is to combine lmtest::coeftest with alternate
# variance-covariance matrices via the sandwich package. The lmtest
# tidiers support this workflow too, enabling you to adjust the standard
# errors of your tidied models on the fly.
```

```
library(sandwich)

# "HC3" (default) robust SEs
tidy(coeftest(m, vcov = vcovHC))

# "HC2" robust SEs
tidy(coeftest(m, vcov = vcovHC, type = "HC2"))

# N-W HAC robust SEs
tidy(coeftest(m, vcov = NeweyWest))

# the columns of the returned tibble for glance.coeftest() will vary
# depending on whether the coeftest object retains the underlying model.
# Users can control this with the "save = TRUE" argument of coeftest().
glance(coeftest(m))
glance(coeftest(m, save = TRUE))
```

---

glance.coxph   *Glance at a(n) coxph 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A coxph object returned from [survival::coxph()](#).

...   For tidy(), additional arguments passed to summary(x, ...). Otherwise ignored.

Value

A [tibble::tibble()] with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
n	The total number of observations.
nevent	Number of events.
nobs	Number of observations used.

See survival::coxph.object for additional column descriptions.

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]()

Examples

```
# load libraries for models and data
library(survival)

# fit model
cfit <- coxph(Surv(time, status) ~ age + sex, lung)

# summarize model fit with tidiers
tidy(cfit)
tidy(cfit, exponentiate = TRUE)

lp <- augment(cfit, lung)
risks <- augment(cfit, 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)

cl <- clogit(case ~ tocc + tocc:education + strata(id), logan2)

tidy(cl)
glance(cl)

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()
```

---

glance.crr   *Glance at a(n) crr 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A crr object returned from [cmprsk::crr()](#).

... 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

converged	Logical indicating if the model fitting procedure was succesful and converged.
df	Degrees of freedom used by the model.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
statistic	Test statistic.

See Also

[glance()](#), [cmprsk::crr()](#)

Other cmprsk tidiers: [tidy.crr](#)()

Examples

```
library(cmprsk)

# time to loco-regional failure (lrf)
lrf_time <- rexp(100)
lrf_event <- sample(0:2, 100, replace = TRUE)
trt <- sample(0:1, 100, replace = TRUE)
strt <- sample(1:2, 100, replace = TRUE)

# fit model
x <- crr(lrf_time, lrf_event, cbind(trt, strt))

# summarize model fit with tidiers
tidy(x, conf.int = TRUE)
glance(x)
```

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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`.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an `NA` of the appropriate type.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

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.
lambda.min	The value of the penalization parameter lambda that achieved minimum loss as estimated by cross validation.
nobs	Number of observations used.

See Also

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

Other glmnet tidiers: glance.glmnet(), tidy.cv.glmnet(), tidy.glmnet()

Examples

```
# load libraries for models and data
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)
```

---

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

Description

Glance accepts a model object and returns a [`tibble::tibble()`](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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A drc object produced by a call to [`drc::drm()`](drc::drm()).

...   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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
AICc	AIC corrected for small samples

See Also

[glance()](#), [drc::drm()](#)

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

Examples

```
# load libraries for models and data
library(drc)

# fit model
mod <- drm(dead / total ~ conc, type,
  weights = total, data = selenium, fct = LL.2(), type = "binomial"
)

# summarize model fit with tidiers
tidy(mod)
tidy(mod, conf.int = TRUE)

glance(mod)

augment(mod, selenium)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

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

Value

glance.ergm returns a one-row tibble with the columns

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

If deviance = TRUE, and if the model supports it, the tibble will also contain the columns

null.deviance	The null deviance of the model
df.null	The degrees of freedom of the null deviance
residual.deviance	
	The residual deviance of the model
df.residual	The degrees of freedom of the residual deviance

See Also

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

Other ergm tidiers: `tidy.ergm()`

glance.factanal   *Glance at a(n) factanal 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

```
## S3 method for class 'factanal'
glance(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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

converged	Logical indicating if the model fitting procedure was succesful and converged.
df	Degrees of freedom used by the model.
method	Which method was used.
n	The total number of observations.
n.factors	The number of fitted factors.

nobs	Number of observations used.
p.value	P-value corresponding to the test statistic.
statistic	Test statistic.
total.variance	Total cumulative proportion of variance accounted for by all factors.

See Also

glance(), stats::factanal()

Other factanal tidiers: augment.factanal(), tidy.factanal()

Examples

```
set.seed(123)

# generate data
library(dplyr)
library(purrr)

m1 <- tibble(
  v1 = c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 3, 3, 3, 3, 3, 4, 5, 6),
  v2 = c(1, 2, 1, 1, 1, 1, 2, 1, 2, 1, 3, 4, 3, 3, 3, 4, 6, 5),
  v3 = c(3, 3, 3, 3, 3, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 5, 4, 6),
  v4 = c(3, 3, 4, 3, 3, 1, 1, 2, 1, 1, 1, 1, 2, 1, 1, 5, 6, 4),
  v5 = c(1, 1, 1, 1, 1, 3, 3, 3, 3, 3, 1, 1, 1, 1, 1, 6, 4, 5),
  v6 = c(1, 1, 1, 2, 1, 3, 3, 3, 4, 3, 1, 1, 1, 2, 1, 6, 5, 4)
)

# new data
m2 <- map_dfr(m1, rev)

# factor analysis objects
fit1 <- factanal(m1, factors = 3, scores = "Bartlett")
fit2 <- factanal(m1, factors = 3, scores = "regression")

# tidying the object
tidy(fit1)
tidy(fit2)

# augmented dataframe
augment(fit1)
augment(fit2)

# augmented dataframe (with new data)
augment(fit1, data = m2)
augment(fit2, data = m2)
```

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

adj.r.squared	Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.
df	Degrees of freedom used by the model.
df.residual	Residual degrees of freedom.
nobs	Number of observations used.
p.value	P-value corresponding to the test statistic.

r.squared   R squared statistic, or the percent of variation explained by the model. Also
                known as the coefficient of determination.

sigma   Estimated standard error of the residuals.

statistic   Test statistic.

Examples

```
# load libraries for models and data
library(lfe)

# use built-in `airquality` dataset
head(airquality)

# no FEs; same as lm()
est0 <- felm(Ozone ~ Temp + Wind + Solar.R, airquality)

# summarize model fit with tidiers
tidy(est0)
augment(est0)

# add month fixed effects
est1 <- felm(Ozone ~ Temp + Wind + Solar.R | Month, airquality)

# summarize model fit with tidiers
tidy(est1)
tidy(est1, fe = TRUE)
augment(est1)
glance(est1)

# the "se.type" argument can be used to switch out different standard errors
# types on the fly. In turn, this can be useful exploring the effect of
# different error structures on model inference.
tidy(est1, se.type = "iid")
tidy(est1, se.type = "robust")

# add clustered SEs (also by month)
est2 <- felm(Ozone ~ Temp + Wind + Solar.R | Month | 0 | Month, airquality)

# summarize model fit with tidiers
tidy(est2, conf.int = TRUE)
tidy(est2, conf.int = TRUE, se.type = "cluster")
tidy(est2, conf.int = TRUE, se.type = "robust")
tidy(est2, conf.int = TRUE, se.type = "iid")
```

---

glance.fitdistr   *Glance at a(n) fitdistr 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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`.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an `NA` of the appropriate type.

Usage

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

Arguments

x	A `fitdistr` object returned by `MASS::fitdistr()`.
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.

See Also

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

Other fitdistr tidiers: `tidy.fitdistr()`

Examples

```
# load libraries for models and data
library(MASS)

# generate data
set.seed(2015)
x <- rnorm(100, 5, 2)

#  fit models
fit <- fitdistr(x, dnorm, list(mean = 3, sd = 1))

# summarize model fit with tidiers
tidy(fit)
glance(fit)
```

---

glance.fixest   *Glance at a(n) fixest 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A fixest object returned from any of the fixest estimators

...   Additional arguments passed to summary and confint. Important arguments
                are se and cluster. Other arguments are dof, exact_dof, forceCovariance,
                and keepBounded. See summary.fixest.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

adj.r.squared	Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.
AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
pseudo.r.squared	
	Like the R squared statistic, but for situations when the R squared statistic isn't defined.
r.squared	R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.
sigma	Estimated standard error of the residuals.
within.r.squared	
	R squared within fixed-effect groups.

Note

All columns listed below will be returned, but some will be NA, depending on the type of model estimated. `sigma`, `r.squared`, `adj.r.squared`, and `within.r.squared` will be NA for any model other than `feols`. `pseudo.r.squared` will be NA for `feols`.

Examples

```
# load libraries for models and data
library(fixest)

gravity <-
  feols(
    log(Euros) ~ log(dist_km) | Origin + Destination + Product + Year, trade
  )

tidy(gravity)
glance(gravity)
augment(gravity, trade)

# to get robust or clustered SEs, users can either:

# 1) specify the arguments directly in the `tidy()` call

tidy(gravity, conf.int = TRUE, cluster = c("Product", "Year"))

tidy(gravity, conf.int = TRUE, se = "threeway")

# 2) or, feed tidy() a summary.fixest object that has already accepted
# these arguments
```

```
gravity_summ <- summary(gravity, cluster = c("Product", "Year"))

tidy(gravity_summ, conf.int = TRUE)

# approach (1) is preferred.
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

Glance at gam objects created by calls to [mgcv::gam()](#) with [glance.gam()](#).

Value

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

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
deviance	Deviance of the model.
df	Degrees of freedom used by the model.
df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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. **Cau-
                tionary 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.lvel = 0.9`, all computation will proceed
                using `conf.level = 0.95`. Two exceptions here are:

                - `tidy()` methods will warn when supplied an `exponentiate` argument if it
                  will be ignored.
                - `augment()` methods will warn when supplied a `newdata` argument if it will
                  be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

adj.r.squared   Adjusted R squared statistic, which is like the R squared statistic except taking
                degrees of freedom into account.

AIC   Akaike's Information Criterion for the model.

BIC   Bayesian Information Criterion for the model.

deviance   Deviance of the model.

df   Degrees of freedom used by the model.

df.residual   Residual degrees of freedom.

logLik   The log-likelihood of the model. [stats::logLik()] may be a useful reference.

nobs   Number of observations used.

npar   Number of parameters in the model.

See Also

`glance()`, `mgcv::gam()`

Other mgcv tidiers: `tidy.gam()`

Examples

```
# load libraries for models and data
library(mgcv)

# fit model
g <- gam(mpg ~ s(hp) + am + qsec, data = mtcars)

# summarize model fit with tidiers
tidy(g)
tidy(g, parametric = TRUE)
glance(g)
augment(g)
```

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 across 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 conf.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

AIC   Akaike's Information Criterion for the model.

BIC   Bayesian Information Criterion for the model.

logLik   The log-likelihood of the model. [stats::logLik()] may be a useful reference.

method   Which method was used.

nobs   Number of observations used.

p.value   P-value corresponding to the test statistic.

statistic   Test statistic.

parameter   Parameter field in the htest, typically degrees of freedom.

See Also

glance(), tseries::garch(), []

Other garch tidiers: tidy.garch()

---

glance.geeglm   *Glance at a(n) geeglm 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A geeglm object returned from a call to geepack::geeglm().

...   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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

alpha   Estimated correlation parameter for geepack::geeglm.

df.residual   Residual degrees of freedom.

gamma	Estimated scale parameter for geepack::geeglm.
max.cluster.size	
	Max number of elements in clusters.
n.clusters	Number of clusters.

See Also

[glance()](), [geepack::geeglm()]()

Examples

```
# load modeling library
library(geepack)

# load data
data(state)


ds <- data.frame(state.region, state.x77)

# fit model
geefit <- geeglm(Income ~ Frost + Murder,
  id = state.region,
  data = ds,
  corstr = "exchangeable"
)

# summarize model fit with tidiers
tidy(geefit)
tidy(geefit, conf.int = TRUE)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
deviance	Deviance of the model.
df.null	Degrees of freedom used by the null model.
df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
null.deviance	Deviance of the null model.

See Also

stats::glm()

Other lm tidiers: augment.glm(), augment.lm(), glance.lm(), glance.summary.lm(), glance.svyglm(), tidy.glm(), tidy.lm(), tidy.lm.beta(), tidy.mlm(), tidy.summary.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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

nobs   Number of observations used.

npasses   Total passes over the data across all lambda values.

nulldev   Null deviance.

See Also

glance(), glmnet::glmnet()

Other glmnet tidiers: glance.cv.glmnet(), tidy.cv.glmnet(), tidy.glmnet()

Examples

```
# load libraries for models and data
library(glmnet)

set.seed(2014)
x <- matrix(rnorm(100 * 20), 100, 20)
y <- rnorm(100)
fit1 <- glmnet(x, y)

# summarize model fit with tidiers + visualization
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)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- tidy() methods will warn when supplied an `exponentiate` argument if it will be ignored.
- augment() methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

deviance   Deviance of the model.

df.residual   Residual degrees of freedom.

nobs   Number of observations used.

null.deviance   Deviance of the null model.

sigma   Estimated standard error of the residuals.

See Also

robust::glmRob()

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

Examples

```
# load libraries for models and data
library(robust)

# fit model
gm <- glmRob(am ~ wt, data = mtcars, family = "binomial")

# summarize model fit with tidiers
tidy(gm)
glance(gm)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

df	Degrees of freedom used by the model.
df.residual	Residual degrees of freedom.
nobs	Number of observations used.
p.value	P-value corresponding to the test statistic.
statistic	Test statistic.

See Also

[glance()](#), [gmm::gmm()](#)

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

Examples

```
# load libraries for models and data
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(term, estimate)) %>%
  ggplot(aes(estimate, variable)) +
  geom_point() +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high)) +
  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(term, estimate)) %>%
  ggplot(aes(estimate, variable)) +
  geom_point() +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high)) +
  geom_vline(xintercept = 0, color = "red", lty = 2)
```

---

glance.ivreg   *Glance at a(n) ivreg 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	An ivreg object created by a call to [AER::ivreg()]().
diagnostics	Logical indicating whether or not to return the Wu-Hausman and Sargan diagnostic information.
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

This tidier currently only supports ivreg-classed objects outputted by the AER package. The ivreg package also outputs objects of class ivreg, and will be supported in a later release.

Value

A [tibble::tibble()]() with exactly one row and columns:

adj.r.squared	Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.
df	Degrees of freedom used by the model.
df.residual	Residual degrees of freedom.
nobs	Number of observations used.
r.squared	R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.
sigma	Estimated standard error of the residuals.
statistic	Wald test statistic.
p.value	P-value for the Wald test.

Note

Beginning 0.7.0, glance.ivreg returns statistics for the Wu-Hausman test for endogeneity and the Sargan test of overidentifying restrictions. Sargan test values are returned as NA if the number of instruments is not greater than the number of endogenous regressors.

See Also

glance(), AER::ivreg()

Other ivreg tidiers: augment.ivreg(), tidy.ivreg()

Examples

```
# load libraries for models and data
library(AER)

# load data
data("CigarettesSW", package = "AER")

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

# summarize model fit with tidiers
tidy(ivr)
tidy(ivr, conf.int = TRUE)
tidy(ivr, conf.int = TRUE, instruments = TRUE)

augment(ivr)
augment(ivr, data = CigarettesSW)
augment(ivr, newdata = CigarettesSW)

glance(ivr)
```

---

glance.kmeans   *Glance at a(n) kmeans 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A kmeans object created by `stats::kmeans()`.

...   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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

betweenss   The total between-cluster sum of squares.

iter   Iterations of algorithm/fitting procedure completed.

tot.withinss   The total within-cluster sum of squares.

totss   The total sum of squares.

See Also

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

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

Examples

```
library(cluster)
library(modeldata)
library(dplyr)

data(hpc_data)

x <- hpc_data[, 2:5]

fit <- pam(x, k = 4)

tidy(fit)
glance(fit)
augment(fit, x)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A lavaan object, such as those returned 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A one-row tibble::tibble with columns:

chisq   Model chi squared

npar   Number of parameters in the model

rmsea   Root mean square error of approximation

rmsea.conf.high

                95 percent upper bound on RMSEA

srmr	Standardised root mean residual
agfi	Adjusted goodness of fit
cfi	Comparative fit index
tli	Tucker Lewis index
AIC	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

```
library(lavaan)

# fit model
cfa.fit <- cfa(
  "F =~ x1 + x2 + x3 + x4 + x5",
  data = HolzingerSwineford1939, group = "school"
)

# summarize model fit with tidiers
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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

```
## S3 method for class '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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

adj.r.squared	Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.
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.

`logLik`	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
`nobs`	Number of observations used.
`p.value`	P-value corresponding to the test statistic.
`r.squared`	R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.
`sigma`	Estimated standard error of the residuals.
`statistic`	Test statistic.
`df`	The degrees for freedom from the numerator of the overall F-statistic. This is new in broom 0.7.0. Previously, this reported the rank of the design matrix, which is one more than the numerator degrees of freedom of the overall F-statistic.

See Also

glance(), glance.summary.lm()

Other lm tidiers: augment.glm(), augment.lm(), glance.glm(), glance.summary.lm(), glance.svyglm(), tidy.glm(), tidy.lm(), tidy.lm.beta(), tidy.mlm(), tidy.summary.lm()

Examples

```
library(ggplot2)
library(dplyr)

mod <- lm(mpg ~ wt + qsec, data = mtcars)

tidy(mod)
glance(mod)

# coefficient plot
d <- tidy(mod, conf.int = TRUE)

ggplot(d, aes(estimate, term, xmin = conf.low, xmax = conf.high, height = 0)) +
  geom_point() +
  geom_vline(xintercept = 0, lty = 4) +
  geom_errorbarh()

# aside: There are tidy() and glance() methods for lm.summary objects too.
# this can be useful when you want to conserve memory by converting large lm
# objects into their leaner summary.lm equivalents.
s <- summary(mod)
tidy(s, conf.int = TRUE)
glance(s)

augment(mod)
augment(mod, mtcars, interval = "confidence")

# predict on new data
newdata <- mtcars %>%
```

```
  head(6) %>%
  mutate(wt = wt + 1)
augment(mod, newdata = newdata)

# ggplot2 example where we also construct 95% prediction interval

# simpler bivariate model since we're plotting in 2D
mod2 <- lm(mpg ~ wt, data = mtcars)

au <- augment(mod2, newdata = newdata, interval = "prediction")

ggplot(au, aes(wt, mpg)) +
  geom_point() +
  geom_line(aes(y = .fitted)) +
  geom_ribbon(aes(ymin = .lower, ymax = .upper), col = NA, alpha = 0.3)

# predict on new data without outcome variable. Output does not include .resid
newdata <- newdata %>%
  select(-mpg)

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, .cooksd)) +
  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)
```

---

glance.lmodel2   *Glance at a(n) lmodel2 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

```
## S3 method for class 'lmodel2'
glance(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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

nobs	Number of observations used.
p.value	P-value corresponding to the test statistic.
r.squared	R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.
theta	Angle between OLS lines 'lm(y ~ x)' and 'lm(x ~ y)'
H	H statistic for computing confidence interval of major axis slope

See Also

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

Other lmodel2 tidiers: `tidy.lmodel2()`

Examples

```
# load libraries for models and data
library(lmodel2)

data(mod2ex2)
Ex2.res <- lmodel2(Prey ~ Predators, data = mod2ex2, "relative", "relative", 99)
Ex2.res

# summarize model fit with tidiers + visualization
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))
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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. **Cau-
           tionary 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.lvel = 0.9`, all computation will proceed
           using `conf.level = 0.95`. Two exceptions here are:

           - `tidy()` methods will warn when supplied an `exponentiate` argument if it
             will be ignored.
           - `augment()` methods will warn when supplied a `newdata` argument if it will
             be ignored.

Value

A tibble::tibble() with exactly one row and columns:

deviance   Deviance of the model.

df.residual   Residual degrees of freedom.

nobs   Number of observations used.

r.squared   R squared statistic, or the percent of variation explained by the model. Also
                known as the coefficient of determination.

sigma   Estimated standard error of the residuals.

See Also

robust::lmRob()

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

Examples

```
# load modeling library
library(robust)

# fit model
m <- lmRob(mpg ~ wt, data = mtcars)

# summarize model fit with tidiers
tidy(m)
augment(m)
glance(m)
```

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	A lmrob object returned from [`robustbase::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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

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

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

df.residual	Residual degrees of freedom.
r.squared	R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.
sigma	Estimated standard error of the residuals.

See Also

robustbase::lmrob()

Other robustbase tidiers: augment.glmrob(), augment.lmrob(), tidy.glmrob(), tidy.lmrob()

Examples

```
if (requireNamespace("robustbase", quietly = TRUE)) {
  # load libraries for models and data
  library(robustbase)

  data(coleman)
  set.seed(0)

  m <- lmrob(Y ~ ., data = coleman)
  tidy(m)
  augment(m)
  glance(m)

  data(carrots)

  Rfit <- glmrob(cbind(success, total - success) ~ logdose + block,
    family = binomial, data = carrots, method = "Mqle",
    control = glmrobMqle.control(tcc = 1.2)
  )

  tidy(Rfit)
  augment(Rfit)
}
```

glance.margins	*Glance at a(n) margins 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	A margins object returned from margins::margins().
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

adj.r.squared	Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.
df	Degrees of freedom used by the model.
df.residual	Residual degrees of freedom.
nobs	Number of observations used.
p.value	P-value corresponding to the test statistic.
r.squared	R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.
sigma	Estimated standard error of the residuals.
statistic	Test statistic.

Examples

```
# load libraries for models and data
library(margins)

# example 1: logit model
mod_log <- glm(am ~ cyl + hp + wt, data = mtcars, family = binomial)

# get tidied "naive" model coefficients
tidy(mod_log)

# convert to marginal effects with margins()
marg_log <- margins(mod_log)
```

```
# get tidied marginal effects
tidy(marg_log)
tidy(marg_log, conf.int = TRUE)

# requires running the underlying model again. quick for this example
glance(marg_log)

# augmenting `margins` outputs isn't supported, but
# you can get the same info by running on the underlying model
augment(mod_log)

# example 2: threeway interaction terms
mod_ie <- lm(mpg ~ wt * cyl * disp, data = mtcars)

# get tidied "naive" model coefficients
tidy(mod_ie)

# convert to marginal effects with margins()
marg_ie0 <- margins(mod_ie)
# get tidied marginal effects
tidy(marg_ie0)
glance(marg_ie0)

# marginal effects evaluated at specific values of a variable (here: cyl)
marg_ie1 <- margins(mod_ie, at = list(cyl = c(4,6,8)))

# summarize model fit with tidiers
tidy(marg_ie1)

# marginal effects of one interaction variable (here: wt), modulated at
# specific values of the two other interaction variables (here: cyl and drat)
marg_ie2 <- margins(mod_ie,
                    variables = "wt",
                    at = list(cyl = c(4,6,8), drat = c(3, 3.5, 4)))

# summarize model fit with tidiers
tidy(marg_ie2)
```

---

glance.Mclust   *Glance at a(n) Mclust 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   An Mclust object return from mclust::Mclust().

...   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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

BIC   Bayesian Information Criterion for the model.

df   Degrees of freedom used by the model.

logLik   The log-likelihood of the model. [stats::logLik()] may be a useful reference.

nobs   Number of observations used.

model   A string denoting the model type with optimal BIC

G   Number mixture components in optimal model

hypvol   If the other model contains a noise component, the value of the hypervolume parameter. Otherwise 'NA'.

Examples

```
# load library for models and data
library(mclust)

# load data manipulation libraries
library(dplyr)
library(tibble)
```

```
library(purrr)
library(tidyr)

set.seed(27)

centers <- tibble(
  cluster = factor(1:3),
  # number points in each cluster
  num_points = c(100, 150, 50),
  # x1 coordinate of cluster center
  x1 = c(5, 0, -3),
  # x2 coordinate of cluster center
  x2 = c(-1, 1, -2)
)

points <- centers %>%
  mutate(
    x1 = map2(num_points, x1, rnorm),
    x2 = map2(num_points, x2, rnorm)
  ) %>%
  select(-num_points, -cluster) %>%
  unnest(c(x1, x2))

# fit model
m <- Mclust(points)

# summarize model fit with tidiers
tidy(m)
augment(m, points)
glance(m)
```

---

glance.mfx   *Glance at a(n) mfx 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

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

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

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

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

Arguments

x	A logitmfx, negbinmfx, poissonmfx, or probitmfx object. (Note that betamfx objects receive their own set of tidiers.)
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

This generic glance method wraps [glance.glm()](#) for applicable objects from the mfx package.

Value

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

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
deviance	Deviance of the model.
df.null	Degrees of freedom used by the null model.
df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
null.deviance	Deviance of the null model.

See Also

glance.glm(), mfx::logitmfx(), mfx::negbinmfx(), mfx::poissonmfx(), mfx::probitmfx()

Other mfx tidiers: augment.betamfx(), augment.mfx(), glance.betamfx(), tidy.betamfx(), tidy.mfx()

Examples

```
# load libraries for models and data
library(mfx)

# get the marginal effects from a logit regression
mod_logmfx <- logitmfx(am ~ cyl + hp + wt, atmean = TRUE, data = mtcars)

tidy(mod_logmfx, conf.int = TRUE)

# compare with the naive model coefficients of the same logit call
tidy(
  glm(am ~ cyl + hp + wt, family = binomial, data = mtcars),
  conf.int = TRUE
)

augment(mod_logmfx)
glance(mod_logmfx)

# another example, this time using probit regression
mod_probmfx <- probitmfx(am ~ cyl + hp + wt, atmean = TRUE, data = mtcars)

tidy(mod_probmfx, conf.int = TRUE)
augment(mod_probmfx)
glance(mod_probmfx)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

AIC   Akaike's Information Criterion for the model.

BIC   Bayesian Information Criterion for the model.

logLik   The log-likelihood of the model. [stats::logLik()] may be a useful reference.

sigma2_j   The square root of the estimated residual variance for the j-th longitudinal process

See Also

glance(), joineRML::mjoint()

Other mjoint tidiers: tidy.mjoint()

Examples

```
# broom only skips running these examples because the example models take a
# while to generate—they should run just fine, though!
## Not run:


# load libraries for models and data
library(joineRML)

# fit a joint model with bivariate longitudinal outcomes
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)
```

glance.mlogit *Glance at a(n) mlogit 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   an object returned from `mlogit::mlogit()`.

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-tionary 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
rho2	McFadden's rho squared with respect to a market shares (constants-only) model.
rho20	McFadden's rho squared with respect to an equal shares (no information) model.

See Also

`glance()`, `mlogit::mlogit()`

Other mlogit tidiers: `augment.mlogit()`, `tidy.mlogit()`

Examples

```
# load libraries for models and data
library(mlogit)
```

```
data("Fishing", package = "mlogit")
Fish <- dfidx(Fishing, varying = 2:9, shape = "wide", choice = "mode")

# fit model
m <- mlogit(mode ~ price + catch | income, data = Fish)

# summarize model fit with tidiers
tidy(m)
augment(m)
glance(m)
```

---

glance.muhaz   *Glance at a(n) muhaz 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

```
## S3 method for class 'muhaz'
glance(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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

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

See Also

[glance()](#), [muhaz::muhaz()](#)

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

Examples

```
# load libraries for models and data
library(muhaz)
library(survival)

# fit model
x <- muhaz(ovarian$futime, ovarian$fustat)

# summarize model fit with tidiers
tidy(x)
glance(x)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A multinom object returned from `nnet::multinom()`.

...   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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

AIC   Akaike's Information Criterion for the model.

deviance   Deviance of the model.

edf   The effective degrees of freedom.

nobs   Number of observations used.

See Also

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

Other multinom tidiers: `tidy.multinom()`

Examples

```
# load libraries for models and data
library(nnet)
library(MASS)

example(birthwt)

bwt.mu <- multinom(low ~ ., bwt)

tidy(bwt.mu)
glance(bwt.mu)

# or, for output from a multinomial logistic regression
fit.gear <- multinom(gear ~ mpg + factor(am), data = mtcars)
tidy(fit.gear)
```

```
glance(fit.gear)
```

---

glance.negbin   *Glance at a(n) negbin 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A negbin object returned by MASS::glm.nb().

...   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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- tidy() methods will warn when supplied an `exponentiate` argument if it will be ignored.
- augment() methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

AIC   Akaike's Information Criterion for the model.

BIC   Bayesian Information Criterion for the model.

deviance   Deviance of the model.

df.null	Degrees of freedom used by the null model.
df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
null.deviance	Deviance of the null model.

See Also

[glance()](), [MASS::glm.nb()]()

Other glm.nb tidiers: [tidy.negbin]()

Examples

```
# load libraries for models and data
library(MASS)

# fit model
r <- glm.nb(Days ~ Sex / (Age + Eth * Lrn), data = quine)

# summarize model fit with tidiers
tidy(r)
glance(r)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	A nlrq object returned from quantreg::nlrq().
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
tau	Quantile.

See Also

glance(), quantreg::nlrq()

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

Examples

```
# load modeling library
library(quantreg)

# build artificial data with multiplicative error
set.seed(1)
dat <- NULL
dat$x <- rep(1:25, 20)
dat$y <- SSlogis(dat$x, 10, 12, 2) * rnorm(500, 1, 0.1)

# fit the median using nlrq
mod <- nlrq(y ~ SSlogis(x, Asym, mid, scal),
  data = dat, tau = 0.5, trace = TRUE
)

# summarize model fit with tidiers
tidy(mod)
glance(mod)
```

```
augment(mod)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

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.
finTol	The achieved convergence tolerance.
isConv	Whether the fit successfully converged.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
sigma	Estimated standard error of the residuals.

See Also

tidy, stats::nls()

Other nls tidiers: augment.nls(), tidy.nls()

Examples

```
# fit model
n <- nls(mpg ~ k * e^wt, data = mtcars, start = list(k = 1, e = 2))

# summarize model fit with tidiers + visualization
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)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

adj.r.squared   Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.

dw.original   Durbin-Watson statistic of original fit.

dw.transformed Durbin-Watson statistic of transformed fit.

nobs   Number of observations used.
number.interaction
                Number of interactions.
p.value.original
                P-value of original Durbin-Watson statistic.
p.value.transformed
                P-value of autocorrelation after transformation.

r.squared   R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.

rho   Spearman's rho autocorrelation

See Also

`glance()`, `orcutt::cochrane.orcutt()`

Other orcutt tidiers: `tidy.orcutt()`

Examples

```
# load libraries for models and data
library(orcutt)

# fit model and summarize results
reg <- lm(mpg ~ wt + qsec + disp, mtcars)
tidy(reg)


co <- cochrane.orcutt(reg)
tidy(co)
glance(co)
```

---

glance.pam   *Glance at a(n) pam 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	An pam object returned from cluster::pam()
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

avg.silhouette.width

The average silhouette width for the dataset.

See Also

[glance()](#), [cluster::pam()](#)

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

Examples

```
# load libraries for models and data
library(dplyr)
library(ggplot2)
library(cluster)
library(modeldata)
data(hpc_data)

x <- hpc_data[, 2:5]
p <- pam(x, k = 4)

# summarize model fit with tidiers + visualization
tidy(p)
glance(p)
augment(p, x)

augment(p, x) %>%
  ggplot(aes(compounds, input_fields)) +
  geom_point(aes(color = .cluster)) +
  geom_text(aes(label = cluster), data = tidy(p), size = 10)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	A `plm` objected 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

adj.r.squared	Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.
deviance	Deviance of the model.
df.residual	Residual degrees of freedom.
nobs	Number of observations used.
p.value	P-value corresponding to the test statistic.
r.squared	R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.
statistic	F-statistic

See Also

glance(), plm::plm()

Other plm tidiers: augment.plm(), tidy.plm()

Examples

```
# load libraries for models and data
library(plm)

# load data
data("Produc", package = "plm")

# fit model
zz <- plm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp,
  data = Produc, index = c("state", "year")
)

# summarize model fit with tidiers
summary(zz)

tidy(zz)
tidy(zz, conf.int = TRUE)
tidy(zz, conf.int = TRUE, conf.level = 0.9)

augment(zz)
glance(zz)
```

---

glance.poLCA   *Glance at a(n) poLCA 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [tibble::tibble()]() with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
chi.squared	The Pearson Chi-Square goodness of fit statistic for multiway tables.
df	Degrees of freedom used by the model.
df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
g.squared	The likelihood ratio/deviance statistic

See Also

[glance()](), [poLCA::poLCA()]()

Other poLCA tidiers: [augment.poLCA()](), [tidy.poLCA()]()

Examples

```
# load libraries for models and data
library(poLCA)
library(dplyr)

# generate data
data(values)

f <- cbind(A, B, C, D) ~ 1
```

```
# fit model
M1 <- poLCA(f, values, nclass = 2, verbose = FALSE)

M1

# summarize model fit with tidiers + visualization
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)

# 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

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

count(au, .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)
```

---

glance.polr   *Glance at a(n) polr 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	A polr object returned from [MASS::polr()](#).
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

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.
edf	The effective degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.

See Also

tidy, MASS::polr()

Other ordinal tidiers: augment.clm(), augment.polr(), glance.clm(), glance.clmm(), glance.svyolr(), tidy.clm(), tidy.clmm(), tidy.polr(), tidy.svyolr()

Examples

```
# load libraries for models and data
library(MASS)

# fit model
fit <- polr(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)

# summarize model fit with tidiers
tidy(fit, exponentiate = TRUE, conf.int = TRUE)

glance(fit)
augment(fit, type.predict = "class")

fit2 <- polr(factor(gear) ~ am + mpg + qsec, data = mtcars)

tidy(fit, p.values = TRUE)
```

---

glance.pyears   *Glance at a(n) pyears 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

nobs	Number of observations used.
total	total number of person-years tabulated
offtable	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()`

Examples

```
# load libraries for models and data
library(survival)

# generate and format data
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
)

# summarize model fit with tidiers
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)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

This is similar to the output of select.ridgelm, but it is returned rather than printed.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

kHKB	modified HKB estimate of the ridge constant
kLW	modified L-W estimate of the ridge constant
lambdaGCV	choice of lambda that minimizes GCV

See Also

[`glance()`](#), [`MASS::select.ridgelm()`](#), [`MASS::lm.ridge()`](#)

Other ridgelm tidiers: [`tidy.ridgelm`](#)()

Examples

```
# load libraries for models and data
library(MASS)

names(longley)[1] <- "y"

# fit model and summarizd results
fit1 <- lm.ridge(y ~ ., longley)
tidy(fit1)

fit2 <- 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)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

AIC   Akaike's Information Criterion for the model.
BIC   Bayesian Information Criterion for the model.
converged   Logical indicating if the model fitting procedure was succesful and converged.
deviance   Deviance of the model.
logLik   The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs   Number of observations used.
sigma   Estimated standard error of the residuals.

See Also

[glance()](#), [MASS::rlm()](#)

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

Examples

```
# load libraries for models and data
library(MASS)

# fit model
r <- rlm(stack.loss ~ ., stackloss)

# summarize model fit with tidiers
tidy(r)
augment(r)
glance(r)
```

---

glance.rma   *Glance at a(n) rma 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 modeling function. This includes the
name of the modeling function or any arguments passed to the modeling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropri-
ate 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient
or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of
the appropriate type.

Usage

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

Arguments

x   An rma object such as those created by [metafor::rma()](#), [metafor::rma.uni()](#),
             [metafor::rma.glmm()](#), [metafor::rma.mh()](#), [metafor::rma.mv()](#), or [metafor::rma.peto()](#).

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
             tionary 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.lvel = 0.9, all computation will proceed
             using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`](tibble::tibble()) with exactly one row and columns:

`cochran.qe`	In meta-analysis, test statistic for the Cochran's Q_e test of residual heterogeneity.
`cochran.qm`	In meta-analysis, test statistic for the Cochran's Q_m omnibus test of coefficients.
`df.residual`	Residual degrees of freedom.
`h.squared`	Value of the H-Squared statistic.
`i.squared`	Value of the I-Squared statistic.
`measure`	The measure used in the meta-analysis.
`method`	Which method was used.
`nobs`	Number of observations used.
`p.value.cochran.qe`	
	In meta-analysis, p-value for the Cochran's Q_e test of residual heterogeneity.
`p.value.cochran.qm`	
	In meta-analysis, p-value for the Cochran's Q_m omnibus test of coefficients.
`tau.squared`	In meta-analysis, estimated amount of residual heterogeneity.
`tau.squared.se`	In meta-analysis, standard error of residual heterogeneity.

Examples

```
library(metafor)

df <-
  escalc(
    measure = "RR",
    ai = tpos,
    bi = tneg,
    ci = cpos,
    di = cneg,
    data = dat.bcg
  )

meta_analysis <- rma(yi, vi, data = df, method = "EB")

glance(meta_analysis)
```

---

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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`.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an `NA` of the appropriate type.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

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 [tibble::tibble()](#) with exactly one row and columns:

`AIC`	Akaike's Information Criterion for the model.
`BIC`	Bayesian Information Criterion for the model.
`df.residual`	Residual degrees of freedom.
`logLik`	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
`tau`	Quantile.

See Also

[glance()](#), [quantreg::rq()](#)

Other quantreg tidiers: [augment.nlrq()](#), [augment.rq()](#), [augment.rqs()](#), [glance.nlrq()](#), [tidy.nlrq()](#), [tidy.rq()](#), [tidy.rqs()](#)

Examples

```
# load modeling library and data
library(quantreg)

data(stackloss)

# median (l1) regression fit for the stackloss data.
mod1 <- rq(stack.loss ~ stack.x, .5)

# weighted sample median
mod2 <- rq(rnorm(50) ~ 1, weights = runif(50))

# summarize model fit with tidiers
tidy(mod1)
glance(mod1)
augment(mod1)

tidy(mod2)
glance(mod2)
augment(mod2)

# varying tau to generate an rqs object
mod3 <- rq(stack.loss ~ stack.x, tau = c(.25, .5))

tidy(mod3)
augment(mod3)

# glance cannot handle rqs objects like `mod3`--use a purrr
# `map`-based workflow instead
```

---

glance.sarlm   *Glance at a(n) spatialreg 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x	An object returned from [spatialreg::lagsarlm()](#) or [spatialreg::errorsarlm()](#).
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
deviance	Deviance of the model.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.

See Also

glance(), spatialreg::lagsarlm(), spatialreg::errorsarlm(), spatialreg::sacsarlm()

Other spatialreg tidiers: augment.sarlm(), tidy.sarlm()

Examples

```
# load libraries for models and data
library(spatialreg)
library(spdep)

# load data
data(oldcol, package = "spdep")

listw <- nb2listw(COL.nb, style = "W")

# fit model
crime_sar <-
  lagsarlm(CRIME ~ INC + HOVAL,
    data = COL.OLD,
    listw = listw,
    method = "eigen"
  )

# summarize model fit with tidiers
tidy(crime_sar)
tidy(crime_sar, conf.int = TRUE)
glance(crime_sar)
augment(crime_sar)

# fit another model
crime_sem <- errorsarlm(CRIME ~ INC + HOVAL, data = COL.OLD, listw)

# summarize model fit with tidiers
tidy(crime_sem)
tidy(crime_sem, conf.int = TRUE)
glance(crime_sem)
augment(crime_sem)

# fit another model
crime_sac <- sacsarlm(CRIME ~ INC + HOVAL, data = COL.OLD, listw)

# summarize model fit with tidiers
tidy(crime_sac)
tidy(crime_sac, conf.int = TRUE)
glance(crime_sac)
augment(crime_sac)
```

---

glance.smooth.spline   *Tidy a(n) smooth.spine 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 across 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

x   A smooth.spline object returned from `stats::smooth.spline()`.

...   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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

crit   Minimized criterion

cv.crit   Cross-validation score

df   Degrees of freedom used by the model.

lambda   Choice of lambda corresponding to 'spar'.

nobs   Number of observations used.

pen.crit   Penalized criterion.

spar   Smoothing parameter.

See Also

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

Other smoothing spline tidiers: `augment.smooth.spline()`

Examples

```
# fit model
spl <- smooth.spline(mtcars$wt, mtcars$mpg, df = 4)

# summarize model fit with tidiers
augment(spl, mtcars)

# calls original columns x and y
augment(spl)

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

---

glance.speedglm   *Glance at a(n) speedglm 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A speedglm object returned from [speedglm::speedglm()](#).

...   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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
deviance	Deviance of the model.
df.null	Degrees of freedom used by the null model.
df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
null.deviance	Deviance of the null model.

See Also

speedglm::speedlm()

Other speedlm tidiers: augment.speedlm(), glance.speedlm(), tidy.speedglm(), tidy.speedlm()

Examples

```
# load libraries for models and data
library(speedglm)

# generate data
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)
)

# fit model
fit <- speedglm(lot1 ~ log(u), data = clotting, family = Gamma(log))

# summarize model fit with tidiers
tidy(fit)
glance(fit)
```

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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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 conf.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

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

adj.r.squared	Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.
AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
deviance	Deviance of the model.
df	Degrees of freedom used by the model.

df.residual	Residual degrees of freedom.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
p.value	P-value corresponding to the test statistic.
r.squared	R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.
statistic	F-statistic.

See Also

speedglm::speedlm()

Other speedlm tidiers: augment.speedlm(), glance.speedglm(), tidy.speedglm(), tidy.speedlm()

Examples

```
# load modeling library
library(speedglm)

# fit model
mod <- speedlm(mpg ~ wt + qsec, data = mtcars, fitted = TRUE)

# summarize model fit with tidiers
tidy(mod)
glance(mod)
augment(mod)
```

---

glance.summary.lm   *Glance at a(n) summary.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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

```
## 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

The glance.summary.lm() method is a potentially useful alternative to `glance.lm()`. For instance, if users have already converted large lm objects into their leaner summary.lm equivalents to conserve memory. Note, however, that this method does not return all of the columns of the non-summary method (e.g. AIC and BIC will be missing.)

Value

A `tibble::tibble()` with exactly one row and columns:

adj.r.squared   Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.

df.residual   Residual degrees of freedom.

nobs   Number of observations used.

p.value   P-value corresponding to the test statistic.

r.squared   R squared statistic, or the percent of variation explained by the model. Also known as the coefficient of determination.

sigma   Estimated standard error of the residuals.

statistic   Test statistic.

df   The degrees for freedom from the numerator of the overall F-statistic. This is new in broom 0.7.0. Previously, this reported the rank of the design matrix, which is one more than the numerator degrees of freedom of the overall F-statistic.

See Also

`glance()`, `glance.summary.lm()`

Other lm tidiers: `augment.glm()`, `augment.lm()`, `glance.glm()`, `glance.lm()`, `glance.svyglm()`, `tidy.glm()`, `tidy.lm()`, `tidy.lm.beta()`, `tidy.mlm()`, `tidy.summary.lm()`

Examples

```
library(ggplot2)
library(dplyr)

mod <- lm(mpg ~ wt + qsec, data = mtcars)

tidy(mod)
glance(mod)

# coefficient plot
d <- tidy(mod, conf.int = TRUE)

ggplot(d, aes(estimate, term, xmin = conf.low, xmax = conf.high, height = 0)) +
  geom_point() +
  geom_vline(xintercept = 0, lty = 4) +
  geom_errorbarh()

# aside: There are tidy() and glance() methods for lm.summary objects too.
# this can be useful when you want to conserve memory by converting large lm
# objects into their leaner summary.lm equivalents.
s <- summary(mod)
tidy(s, conf.int = TRUE)
glance(s)

augment(mod)
augment(mod, mtcars, interval = "confidence")

# predict on new data
newdata <- mtcars %>%
  head(6) %>%
  mutate(wt = wt + 1)
augment(mod, newdata = newdata)

# ggplot2 example where we also construct 95% prediction interval

# simpler bivariate model since we're plotting in 2D
mod2 <- lm(mpg ~ wt, data = mtcars)

au <- augment(mod2, newdata = newdata, interval = "prediction")

ggplot(au, aes(wt, mpg)) +
  geom_point() +
  geom_line(aes(y = .fitted)) +
  geom_ribbon(aes(ymin = .lower, ymax = .upper), col = NA, alpha = 0.3)

# predict on new data without outcome variable. Output does not include .resid
newdata <- newdata %>%
  select(-mpg)

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, .cooksd)) +
  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)
```

| glance.survdiff | *Glance at a(n) survdiff 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

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. **Cau-
                tionary 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.lvel = 0.9, all computation will proceed
                using conf.level = 0.95. Two exceptions here are:

                • tidy() methods will warn when supplied an exponentiate argument if it
                  will be ignored.
                • augment() methods will warn when supplied a newdata argument if it will
                  be ignored.

Value

A tibble::tibble() with exactly one row and columns:

df   Degrees of freedom used by the model.

p.value   P-value corresponding to the test statistic.

statistic   Test statistic.

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()

Examples

```
# load libraries for models and data
library(survival)

# fit model
s <- survdiff(
  Surv(time, status) ~ pat.karno + strata(inst),
  data = lung
)

# summarize model fit with tidiers
tidy(s)
glance(s)
```

---

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

Description

Glance accepts a model object and returns a [`tibble::tibble()`](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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   An survexp object returned from [`survival::survexp()`](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 `conf.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`](tibble::tibble()) with exactly one row and columns:

n.max   Maximum number of subjects at risk.

n.start   Initial 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()

Examples

```
# load libraries for models and data
library(survival)

# fit model
sexpfit <- survexp(
  futime ~ 1,
  rmap = list(
    sex = "male",
    year = accept.dt,
    age = (accept.dt - birth.dt)
  ),
  method = "conditional",
  data = jasa
)

# summarize model fit with tidiers
tidy(sexpfit)
glance(sexpfit)
```

---

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 modeling function. This includes the
name of the modeling function or any arguments passed to the modeling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropri-
ate 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient
or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of
the appropriate type.

Usage

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

Arguments

x	An survfit object returned from survival::survfit().
...	Additional arguments passed to survival::summary.survfit(). Important arguments include rmean.

Value

A tibble::tibble() with exactly one row and columns:

events	Number of events.
n.max	Maximum number of subjects at risk.
n.start	Initial number of subjects at risk.
nobs	Number of observations used.
records	Number of observations
rmean	Restricted mean (see [survival::print.survfit()]).
rmean.std.error	
	Restricted mean standard error.
conf.low	lower end of confidence interval on median
conf.high	upper end of confidence interval on median
median	median survival

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()

Examples

```
# load libraries for models and data
library(survival)

# fit model
cfit <- coxph(Surv(time, status) ~ age + sex, lung)
sfit <- survfit(cfit)

# summarize model fit with tidiers + visualization
```

```
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)
```

---

glance.survreg   *Glance at a(n) survreg 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 modeling function. This includes the
name of the modeling function or any arguments passed to the modeling function.

Glance does not calculate summary measures. Rather, it farms out these computations to appropri-
ate 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient
or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of
the appropriate type.

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 `conf.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

AIC	Akaike's Information Criterion for the model.
BIC	Bayesian Information Criterion for the model.
df	Degrees of freedom used by the model.
df.residual	Residual degrees of freedom.
iter	Iterations of algorithm/fitting procedure completed.
logLik	The log-likelihood of the model. [stats::logLik()] may be a useful reference.
nobs	Number of observations used.
p.value	P-value corresponding to the test statistic.
statistic	Chi-squared statistic.

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()`

Examples

```
# load libraries for models and data
library(survival)

# fit model
sr <- survreg(
  Surv(futime, fustat) ~ ecog.ps + rx,
  ovarian,
  dist = "exponential"
```

```
)

# summarize model fit with tidiers + visualization
tidy(sr)
augment(sr, ovarian)
glance(sr)

# coefficient plot
td <- tidy(sr, conf.int = TRUE)

library(ggplot2)

ggplot(td, aes(estimate, term)) +
  geom_point() +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high), height = 0) +
  geom_vline(xintercept = 0)
```

---

glance.svyglm   *Glance at a(n) svyglm 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

```
## S3 method for class 'svyglm'
glance(x, maximal = x, ...)
```

Arguments

x   A svyglm object returned from survey::svyglm().

maximal   A svyglm object corresponding to the maximal model against which to compute the BIC. See Lumley and Scott (2015) for details. Defaults to x, which is equivalent to not using a maximal model.

...   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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

`AIC`	Akaike's Information Criterion for the model.
`BIC`	Bayesian Information Criterion for the model.
`deviance`	Deviance of the model.
`df.null`	Degrees of freedom used by the null model.
`df.residual`	Residual degrees of freedom.
`null.deviance`	Deviance of the null model.

References

Lumley T, Scott A (2015). AIC and BIC for modelling with complex survey data. *Journal of Survey Statistics and Methodology*, 3(1).

See Also

[`survey::svyglm()`](#), [`stats::glm()`](#), survey::anova.svyglm

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

Examples

```
# load libraries for models and data
library(survey)

set.seed(123)
data(api)

# survey design
dstrat <-
  svydesign(
    id = ~1,
    strata = ~stype,
    weights = ~pw,
    data = apistrat,
    fpc = ~fpc
```

```
  )

  # model
  m <- svyglm(
    formula = sch.wide ~ ell + meals + mobility,
    design = dstrat,
    family = quasibinomial()
  )

  glance(m)
```

---

glance.svyolr   *Glance at a(n) svyolr 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A svyolr object returned from survey::svyolr().

...   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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with exactly one row and columns:

df.residual	Residual degrees of freedom.
edf	The effective degrees of freedom.
nobs	Number of observations used.

See Also

[tidy](#), [survey::svyolr()](#)

Other ordinal tidiers: [augment.clm()](#), [augment.polr()](#), [glance.clm()](#), [glance.clmm()](#), [glance.polr()](#), [tidy.clm()](#), [tidy.clmm()](#), [tidy.polr()](#), [tidy.svyolr()](#)

Examples

```
library(broom)
library(survey)

data(api)
dclus1 <- svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc)
dclus1 <- update(dclus1, mealcat = cut(meals, c(0, 25, 50, 75, 100)))

m <- svyolr(mealcat ~ avg.ed + mobility + stype, design = dclus1)

m

tidy(m, conf.int = TRUE)
```

---

glance.varest   *Glance at a(n) varest 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 modeling function. This includes the name of the modeling function or any arguments passed to the modeling 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.

Glance returns the same number of columns regardless of whether the model matrix is rank-deficient or not. If so, entries in columns that no longer have a well-defined value are filled in with an NA of the appropriate type.

Usage

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

Arguments

x   A varest object produced by a call to [vars::VAR()].

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                  tionary 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.lvel = 0.9`, all computation will proceed
                  using `conf.level = 0.95`. Two exceptions here are:

                  - `tidy()` methods will warn when supplied an `exponentiate` argument if it
                    will be ignored.
                  - `augment()` methods will warn when supplied a `newdata` argument if it will
                    be ignored.

Value

A [tibble::tibble()] with exactly one row and columns:

lag.order   Lag order.

logLik   The log-likelihood of the model. [stats::logLik()] may be a useful reference.

n   The total number of observations.

nobs   Number of observations used.

See Also

[glance()], [vars::VAR()]

Examples

```
# load libraries for models and data
library(vars)

# load data
data("Canada", package = "vars")

# fit models
mod <- VAR(Canada, p = 1, type = "both")

# summarize model fit with tidiers
tidy(mod)
glance(mod)
```

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 `interp::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 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, they throw 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with exactly one row and columns:

convergence	Convergence code.
function.count	Number of calls to 'fn'.
gradient.count	Number of calls to 'gr'.
value	Minimized or maximized output value.

See Also

`glance()`, `stats::optim()`

Other list tidiers: `list_tidiers`, `tidy_irlba()`, `tidy_optim()`, `tidy_svd()`, `tidy_xyz()`

Examples

```
f <- function(x) (x[1] - 2)^2 + (x[2] - 3)^2 + (x[3] - 8)^2
o <- optim(c(1, 1, 1), f)
```

---

leveneTest_tidiers   *Tidy/glance a(n) leveneTest 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 'leveneTest'
tidy(x, ...)
```

Arguments

x   An object of class anova created by a call to [car::leveneTest()](#).

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                 tionary 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.lvel = 0.9, all computation will proceed
                 using conf.level = 0.95. Two exceptions here are:

                 • tidy() methods will warn when supplied an exponentiate argument if it
                   will be ignored.
                 • augment() methods will warn when supplied a newdata argument if it will
                   be ignored.

Value

A [tibble::tibble()](#) with columns:

df   Degrees of freedom used by this term in the model.

p.value   The two-sided p-value associated with the observed statistic.

statistic   The value of a T-statistic to use in a hypothesis that the regression term is non-
                 zero.

df.residual   Residual degrees of freedom.

See Also

[tidy()](#), [glance()](#), [car::leveneTest()](#)

Other car tidiers: [durbinWatsonTest_tidiers](#)

Examples

```
# load libraries for models and data
library(car)

data(Moore)

lt <- with(Moore, leveneTest(conformity, fcategory))

tidy(lt)
glance(lt)
```

---

list_tidiers   *Tidying methods for lists / returned values that are not S3 objects*

Description

Broom tidies a number of lists that are effectively S3 objects without a class attribute. For example, stats::optim(), base::svd() and interp::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 are 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()

---

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

---

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 across 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 recommended approach to
spatial data. sp tidiers are now deprecated in favor of sf::st_as_sf() and coercion methods found
in other packages. See https://r-spatial.org/r/2023/05/15/evolution4.html for more on
migration from retiring spatial packages.

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

x	A `SpatialPolygonsDataFrame`, `SpatialPolygons`, `Polygons`, `Polygon`, `SpatialLinesDataFrame`, `Lines` or `Line` object.
region	name of variable used to split up regions
...	not used by this method

---

summary_tidiers   *(Deprecated) Tidy summaryDefault objects*

Description

Tidiers for summaryDefault objects have been deprecated as of broom 0.7.0 in favor of `skimr::skim()`.

Usage

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

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

Arguments

x   A summaryDefault object, created by calling [summary()](#) on a vector.

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                     tionary 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.lvel = 0.9, all computation will proceed
                     using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it
  will be ignored.
- augment() methods will warn when supplied a newdata argument if it will
  be ignored.

Value

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

minimum   Minimum value in original vector.

q1   First quartile of original vector.

median   Median of original vector.

mean   Mean of original vector.

q3   Third quartile of original vector.

maximum   Maximum value in original vector.

na   Number of NA values in original vector. Column present only when original
                     vector had at least one NA entry.

See Also

Other deprecated: [bootstrap()](#), [confint_tidy()](#), [data.frame_tidiers](#), [finish_glance()](#), [fix_data_frame()](#),
[tidy.density()](#), [tidy.dist()](#), [tidy.ftable()](#), [tidy.numeric()](#)

Other deprecated: [bootstrap()](#), [confint_tidy()](#), [data.frame_tidiers](#), [finish_glance()](#), [fix_data_frame()](#),
[tidy.density()](#), [tidy.dist()](#), [tidy.ftable()](#), [tidy.numeric()](#)

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 across 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 `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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

`robust.se` is only present when x was created with `dfbeta = TRUE`.

Value

A `tibble::tibble()` with columns:

estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
robust.se	robust version of standard error estimate.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.
z	z score.

See Also

tidy(), survival::aareg()

Other aareg tidiers: glance.aareg()

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

Examples

```
# load libraries for models and data
library(survival)

# fit model
afit <- aareg(
  Surv(time, status) ~ age + sex + ph.ecog,
  data = lung,
  dfbeta = TRUE
)

# summarize model fit with tidiers
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 across 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

acf	Autocorrelation.
lag	Lag values.

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 across 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 object, such as those created by [stats::anova()](#), [car::Anova()](#), [car::leveneTest()](#), or [car::linearHypothesis()](#).
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

The `term` column of an ANOVA table can come with leading or trailing whitespace, which this tidying method trims.

For documentation on the tidier for car::leveneTest() output, see tidy.leveneTest()

Value

A tibble::tibble() with columns:

df	Degrees of freedom used by this term in the model.
meansq	Mean sum of squares. Equal to total sum of squares divided by degrees of freedom.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
sumsq	Sum of squares explained by this term.
term	The name of the regression term.

See Also

tidy(), stats::anova(), car::Anova(), car::leveneTest()

Other anova tidiers: glance.anova(), glance.aov(), tidy.TukeyHSD(), tidy.aov(), tidy.aovlist(), tidy.manova()

Examples

```
# fit models
a <- lm(mpg ~ wt + qsec + disp, mtcars)
b <- lm(mpg ~ wt + qsec, mtcars)

mod <- anova(a, b)

# summarize model fit with tidiers
tidy(mod)
glance(mod)

# car::linearHypothesis() example
library(car)
mod_lht <- linearHypothesis(a, "wt - disp")
tidy(mod_lht)
glance(mod_lht)
```

---

tidy.aov   *Tidy a(n) aov 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 across 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, intercept = FALSE, ...)
```

Arguments

x   An aov object, such as those created by `stats::aov()`.

intercept   A logical indicating whether information on the intercept ought to be included.
            Passed to `stats::summary.aov()`.

...   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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

  - tidy() methods will warn when supplied an `exponentiate` argument if it will be ignored.
  - augment() methods will warn when supplied a `newdata` argument if it will be ignored.

Details

The `term` column of an ANOVA table can come with leading or trailing whitespace, which this tidying method trims.

For documentation on the tidier for `car::leveneTest()` output, see `tidy.leveneTest()`

See Also

`tidy()`, `stats::aov()`

Other anova tidiers: `glance.anova()`, `glance.aov()`, `tidy.TukeyHSD()`, `tidy.anova()`, `tidy.aovlist()`, `tidy.manova()`

Examples

```
a <- aov(mpg ~ wt + qsec + disp, mtcars)
tidy(a)
```

| tidy.aovlist | *Tidy a(n) aovlist 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 across 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 stats::aov().
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

The term column of an ANOVA table can come with leading or trailing whitespace, which this tidying method trims.

For documentation on the tidier for car::leveneTest() output, see tidy.leveneTest()

Value

A tibble::tibble() with columns:

df	Degrees of freedom used by this term in the model.
meansq	Mean sum of squares. Equal to total sum of squares divided by degrees of freedom.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
stratum	The error stratum.
sumsq	Sum of squares explained by this term.
term	The name of the regression term.

See Also

tidy(), stats::aov()

Other anova tidiers: glance.anova(), glance.aov(), tidy.TukeyHSD(), tidy.anova(), tidy.aov(), tidy.manova()

Examples

```
a <- aov(mpg ~ wt + qsec + Error(disp / 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 across 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

x	An object of class Arima created by stats::arima().
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[stats::arima()](#)

Other Arima tidiers: [glance.Arima](#)()

Examples

```
# fit model
fit <- arima(lh, order = c(1, 0, 0))

# summarize model fit with tidiers
tidy(fit)
glance(fit)
```

---

tidy.betamfx   *Tidy a(n) betamfx 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 across 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 'betamfx'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A betamfx 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 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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

The mfx package provides methods for calculating marginal effects for various generalized linear models (GLMs). Unlike standard linear models, estimated model coefficients in a GLM cannot be directly interpreted as marginal effects (i.e., the change in the response variable predicted after a one unit change in one of the regressors). This is because the estimated coefficients are multiplicative, dependent on both the link function that was used for the estimation and any other variables that were included in the model. When calculating marginal effects, users must typically choose whether they want to use i) the average observation in the data, or ii) the average of the sample marginal effects. See vignette("mfxarticle") from the mfx package for more details.

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.
atmean	TRUE if the marginal effects were originally calculated as the partial effects for the average observation. If FALSE, then these were instead calculated as average partial effects.

See Also

[tidy.betareg()](#), [mfx::betamfx()](#)

Other mfx tidiers: [augment.betamfx()](#), [augment.mfx()](#), [glance.betamfx()](#), [glance.mfx()](#), [tidy.mfx()](#)

Examples

```
library(mfx)

# Simulate some data
set.seed(12345)
n <- 1000
x <- rnorm(n)

# Beta outcome
y <- rbeta(n, shape1 = plogis(1 + 0.5 * x), shape2 = (abs(0.2 * x)))
# Use Smithson and Verkuilen correction
y <- (y * (n - 1) + 0.5) / n

d <- data.frame(y, x)
mod_betamfx <- betamfx(y ~ x | x, data = d)

tidy(mod_betamfx, conf.int = TRUE)

# Compare with the naive model coefficients of the equivalent betareg call (not run)
# tidy(betamfx(y ~ x | x, data = d), conf.int = TRUE)

augment(mod_betamfx)
glance(mod_betamfx)
```

`tidy.betareg`	*Tidy a(n) betareg 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 across 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

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

...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

The tibble has one row for each term in the regression. The `component` column 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 `phi`. At least one term will have been used to model the precision `phi`.

Value

A [`tibble::tibble()`](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.
component	Whether a particular term was used to model the mean or the precision in the regression. See details.

See Also

[`tidy()`](#), [`betareg::betareg()`](#)

Examples

```
# load libraries for models and data
library(betareg)

# load dats
data("GasolineYield", package = "betareg")

# fit model
mod <- betareg(yield ~ batch + temp, data = GasolineYield)
```

```
mod

# summarize model fit with tidiers
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 across 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, ...)
```

Arguments

x	A biglm object created by a call to `biglm::biglm()` or `biglm::bigglm()`.
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.
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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

  • tidy() methods will warn when supplied an `exponentiate` argument if it will be ignored.
  • augment() methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[tidy()](#), [biglm::biglm()](#), [biglm::bigglm()](#)

Other biglm tidiers: [glance.biglm](#)()

Examples

```
# load modeling library
library(biglm)

# fit model -- linear regression
bfit <- biglm(mpg ~ wt + disp, mtcars)

# summarize model fit with tidiers
tidy(bfit)
tidy(bfit, conf.int = TRUE)
tidy(bfit, conf.int = TRUE, conf.level = .9)

glance(bfit)

# fit model -- logistic regression
bgfit <- bigglm(am ~ mpg, mtcars, family = binomial())

# summarize model fit with tidiers
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   *Tidy a(n) binDesign 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 across 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 `binGroup::binDesign()` 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

  - `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
  - `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `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

```
library(binGroup)
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 across 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 `binGroup::binWidth()` 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

alternative	Alternative hypothesis (character).
ci.width	Expected width of confidence interval.
p	True proportion.
n	Total sample size

See Also

tidy(), binGroup::binWidth()

Other bingroup tidiers: glance.binDesign(), tidy.binDesign()

Examples

```
# load libraries
library(binGroup)

# fit model
bw <- binWidth(100, .1)

bw

# summarize model fit with tidiers
tidy(bw)
```

---

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 across 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 = c("perc", "bca", "basic", "norm"),
  exponentiate = FALSE,
  ...
)
```

Arguments

x   A boot::boot() 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 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.
conf.method	Passed to the type argument of [boot::boot.ci()](). Defaults to "perc". The allowed types are "perc", "basic", "bca", and "norm". Does not support "stud" or "all".
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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

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.

Value

A [tibble::tibble()]() with columns:

bias	Bias of the statistic.
std.error	The standard error of the regression term.
term	The name of the regression term.
statistic	Original value of the statistic.

See Also

[tidy()](), [boot::boot()](), [boot::tsboot()](), [boot::boot.ci()](), [rsample::bootstraps()]()

Examples

```
# load modeling library
library(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)
)

# fit models
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)

# summarize model fits with tidiers
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 across 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, ...)
```

Arguments

x	A [btergm::btergm()](#) 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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
term	The name of the regression term.

See Also

tidy(), btergm::btergm()

Examples

```
library(btergm)
library(network)

set.seed(5)

# 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(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 the model
mod <- btergm(networks ~ edges + istar(2) + edgecov(covariates), R = 100)

# summarize model fit with tidiers
tidy(mod)
```

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 across 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 survival::cch().
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 conf.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

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

```
# load libraries for models and data
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 model
fit.ccP <- cch(Surv(edrel, rel) ~ stage + histol + age,
  data = ccoh.data,
  subcoh = ~subcohort, id = ~seqno, cohort.size = 4028
)

# summarize model fit with tidiers + visualization
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 across 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

contrast   Levels being compared.
letters   Compact letter display denoting all pair-wise comparisons.

See Also

`tidy()`, `multcomp::cld()`, `multcomp::summary.glht()`, `multcomp::confint.glht()`, `multcomp::glht()`

Other multcomp tidiers: `tidy.confint.glht()`, `tidy.glht()`, `tidy.summary.glht()`

Examples

```
# load libraries for models and data
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.clm   *Tidy a(n) clm 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 across 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 'clm'
tidy(
  x,
  conf.int = FALSE,
  conf.level = 0.95,
  conf.type = c("profile", "Wald"),
  exponentiate = FALSE,
  ...
)
```

Arguments

x   A clm object returned from ordinal::clm().

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.
conf.type	Whether to use "profile" or "Wald" confidence intervals, passed to the type argument of ordinal::confint.clm(). Defaults to "profile".
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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

In broom 0.7.0 the coefficient_type column was renamed to coef.type, and the contents were changed as well.

Note that intercept type coefficients correspond to alpha parameters, location type coefficients correspond to beta parameters, and scale type coefficients correspond to zeta parameters.

Value

A tibble::tibble() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

tidy, ordinal::clm(), ordinal::confint.clm()

Other ordinal tidiers: augment.clm(), augment.polr(), glance.clm(), glance.clmm(), glance.polr(), glance.svyolr(), tidy.clmm(), tidy.polr(), tidy.svyolr()

Examples

```
# load libraries for models and data
library(ordinal)

# fit model
fit <- clm(rating ~ temp * contact, data = wine)

# summarize model fit with tidiers
tidy(fit)
tidy(fit, conf.int = TRUE, conf.level = 0.9)
tidy(fit, conf.int = TRUE, conf.type = "Wald", exponentiate = TRUE)

glance(fit)
augment(fit, type.predict = "prob")
augment(fit, type.predict = "class")

# ...and again with another model specification
fit2 <- clm(rating ~ temp, nominal = ~contact, data = wine)

tidy(fit2)
glance(fit2)
```

---

tidy.clmm   *Tidy a(n) clmm 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 across 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 'clmm'
tidy(x, conf.int = FALSE, conf.level = 0.95, exponentiate = FALSE, ...)
```

Arguments

x	A clmm object returned from [ordinal::clmm()]().
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.

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. **Cau-
               tionary 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.lvel = 0.9, all computation will proceed
               using conf.level = 0.95. Two exceptions here are:

               • tidy() methods will warn when supplied an exponentiate argument if it
                 will be ignored.
               • augment() methods will warn when supplied a newdata argument if it will
                 be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high   Upper bound on the confidence interval for the estimate.

conf.low   Lower bound on the confidence interval for the estimate.

estimate   The estimated value of the regression term.

p.value   The two-sided p-value associated with the observed statistic.

statistic   The value of a T-statistic to use in a hypothesis that the regression term is non-
               zero.

std.error   The standard error of the regression term.

term   The name of the regression term.

Note

In broom 0.7.0 the coefficient_type column was renamed to coef.type, and the contents were
changed as well.

Note that intercept type coefficients correspond to alpha parameters, location type coefficients
correspond to beta parameters, and scale type coefficients correspond to zeta parameters.

See Also

[tidy](#), [ordinal::clmm()](#), [ordinal::confint.clm()](#)

Other ordinal tidiers: [augment.clm()](#), [augment.polr()](#), [glance.clm()](#), [glance.clmm()](#), [glance.polr()](#),
[glance.svyolr()](#), [tidy.clm()](#), [tidy.polr()](#), [tidy.svyolr()](#)

Examples

```
# load libraries for models and data
library(ordinal)

# fit model
fit <- clmm(rating ~ temp + contact + (1 | judge), data = wine)
```

```
# summarize model fit with tidiers
tidy(fit)
tidy(fit, conf.int = TRUE, conf.level = 0.9)
tidy(fit, conf.int = TRUE, exponentiate = TRUE)

glance(fit)

# ...and again with another model specification
fit2 <- clmm(rating ~ temp + (1 | judge), nominal = ~contact, data = wine)

tidy(fit2)
glance(fit2)
```

tidy.coeftest	*Tidy a(n) coeftest 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 across 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 'coeftest'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A coeftest object returned from lmtest::coeftest().
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:
	• tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
	• augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[tidy()](#), [lmtest::coeftest()](#)

Examples

```
# load libraries for models and data
library(lmtest)

m <- lm(dist ~ speed, data = cars)

coeftest(m)
tidy(coeftest(m))
tidy(coeftest(m, conf.int = TRUE))

# a very common workflow is to combine lmtest::coeftest with alternate
# variance-covariance matrices via the sandwich package. The lmtest
# tidiers support this workflow too, enabling you to adjust the standard
# errors of your tidied models on the fly.
library(sandwich)

# "HC3" (default) robust SEs
tidy(coeftest(m, vcov = vcovHC))

# "HC2" robust SEs
tidy(coeftest(m, vcov = vcovHC, type = "HC2"))

# N-W HAC robust SEs
tidy(coeftest(m, vcov = NeweyWest))

# the columns of the returned tibble for glance.coeftest() will vary
# depending on whether the coeftest object retains the underlying model.
# Users can control this with the "save = TRUE" argument of coeftest().
glance(coeftest(m))
glance(coeftest(m, save = TRUE))
```

---

tidy.confint.glht   *Tidy a(n) confint.glht 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 across 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.glht'
tidy(x, ...)
```

Arguments

x   A confint.glht object created by calling [multcomp::confint.glht()](#) on a
                glht object created with [multcomp::glht()](#).

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                tionary 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.lvel = 0.9, all computation will proceed
                using conf.level = 0.95. Two exceptions here are:

                • tidy() methods will warn when supplied an exponentiate argument if it
                  will be ignored.
                • augment() methods will warn when supplied a newdata argument if it will
                  be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high   Upper bound on the confidence interval for the estimate.

conf.low   Lower bound on the confidence interval for the estimate.

contrast   Levels being compared.

estimate   The estimated value of the regression term.

See Also

[tidy()](#), [multcomp::confint.glht()](#), [multcomp::glht()](#)

Other multcomp tidiers: [tidy.cld()](#), [tidy.glht()](#), [tidy.summary.glht()](#)

Examples

```
# load libraries for models and data
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.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 across 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 caret::confusionMatrix().
by_class	Logical indicating whether or not to show performance measures broken down by class. Defaults to TRUE. When by_class = FALSE only returns a tibble with accuracy, kappa, and McNemar 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 conf.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

class	The class under consideration.
conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
term	The name of the regression term.
p.value	P-value for accuracy and kappa statistics.

See Also

tidy(), caret::confusionMatrix()

Examples

```
# load libraries for models and data
library(caret)

set.seed(27)

# generate data
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 <- confusionMatrix(
  two_class_sample1,
  two_class_sample2
)

# summarize model fit with tidiers
```

```
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 <- confusionMatrix(
  six_class_sample1,
  six_class_sample2
)

# summarize model fit with tidiers
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 across 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 = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A coxph object returned from survival::coxph().
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.
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.
...	For tidy(), additional arguments passed to summary(x, ...). Otherwise ignored.

Value

A [tibble::tibble()](#) with columns:

estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.

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

```
# load libraries for models and data
library(survival)

# fit model
cfit <- coxph(Surv(time, status) ~ age + sex, lung)

# summarize model fit with tidiers
tidy(cfit)
tidy(cfit, exponentiate = TRUE)

lp <- augment(cfit, lung)
risks <- augment(cfit, 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)

cl <- clogit(case ~ tocc + tocc:education + strata(id), logan2)
```

```
tidy(cl)
glance(cl)

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.crr   *Tidy a(n) cmprsk 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 across 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 'crr'
tidy(x, exponentiate = FALSE, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A crr object returned from [cmprsk::crr()]().
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.
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`statistic`	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
`std.error`	The standard error of the regression term.

See Also

[`tidy()`](#), [`cmprsk::crr()`](#)

Other cmprsk tidiers: [`glance.crr()`](#)

Examples

```
library(cmprsk)

# time to loco-regional failure (lrf)
lrf_time <- rexp(100)
lrf_event <- sample(0:2, 100, replace = TRUE)
trt <- sample(0:1, 100, replace = TRUE)
strt <- sample(1:2, 100, replace = TRUE)

# fit model
x <- crr(lrf_time, lrf_event, cbind(trt, strt))

# summarize model fit with tidiers
tidy(x, conf.int = TRUE)
glance(x)
```

| 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 across 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

lambda	Value of penalty parameter lambda.
nzero	Number of non-zero coefficients for the given lambda.
std.error	The standard error of the regression term.
conf.low	lower bound on confidence interval for cross-validation estimated loss.
conf.high	upper bound on confidence interval for cross-validation estimated loss.
estimate	Median loss across all cross-validation folds for a given lamdba

See Also

tidy(), glmnet::cv.glmnet()

Other glmnet tidiers: glance.cv.glmnet(), glance.glmnet(), tidy.glmnet()

Examples

```
# load libraries for models and data
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   *(Deprecated) Tidy density objects*

Description

(Deprecated) Tidy density objects

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. **Cau-tionary 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble with two columns: points x where the density is estimated, and estimated density y.

See Also

Other deprecated: bootstrap(), confint_tidy(), data.frame_tidiers, finish_glance(), fix_data_frame(), summary_tidiers, tidy.dist(), tidy.ftable(), tidy.numeric()

---

tidy.dist   *(Deprecated) Tidy dist objects*

Description

(Deprecated) Tidy dist objects

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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

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:

item1	First item
item2	Second item
distance	Distance between items

See Also

Other deprecated: bootstrap(), confint_tidy(), data.frame_tidiers, finish_glance(), fix_data_frame(), summary_tidiers, tidy.density(), tidy.ftable(), tidy.numeric()

Examples

```
cars_dist <- dist(t(mtcars[, 1:4]))
cars_dist

tidy(cars_dist)
tidy(cars_dist, upper = TRUE)
tidy(cars_dist, diagonal = TRUE)
```

---

tidy.drc   *Tidy a(n) drc 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 across 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 'drc'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A drc object produced by a call to [drc::drm()]().
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

The tibble has one row for each curve and term in the regression. The curveid column indicates the curve.

Value

A [`tibble::tibble()`](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.
curve	Index identifying the curve.

See Also

[`tidy()`](#), [`drc::drm()`](#)

Other drc tidiers: [`augment.drc()`](#), [`glance.drc()`](#)

Examples

```
# load libraries for models and data
library(drc)

# fit model
mod <- drm(dead / total ~ conc, type,
  weights = total, data = selenium, fct = LL.2(), type = "binomial"
)

# summarize model fit with tidiers
tidy(mod)
tidy(mod, conf.int = TRUE)

glance(mod)

augment(mod, selenium)
```

`tidy.emmGrid`	*Tidy a(n) emmGrid 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 across 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 'emmGrid'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	An emmGrid 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 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.
...	Additional arguments passed to emmeans::summary.emmGrid() or lsmeans::summary.ref.grid(). **Cautionary note**: misspecified arguments may be silently ignored!

Details

Returns a data frame with one observation for each estimated marginal mean, and one column for each combination of factors. When the input is a contrast, each row will contain one estimated contrast.

There are a large number of arguments that can be passed on to emmeans::summary.emmGrid() or lsmeans::summary.ref.grid().

Value

A tibble::tibble() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
df	Degrees of freedom used by this term in the model.
p.value	The two-sided p-value associated with the observed statistic.
std.error	The standard error of the regression term.
estimate	Expected marginal mean
statistic	T-ratio statistic

See Also

tidy(), emmeans::ref_grid(), emmeans::emmeans(), emmeans::contrast()

Other emmeans tidiers: tidy.lsmobj(), tidy.ref.grid(), tidy.summary_emm()

Examples

```
# load libraries for models and data
library(emmeans)

# linear model for sales of oranges per day
oranges_lm1 <- lm(sales1 ~ price1 + price2 + day + store, data = oranges)

# reference grid; see vignette("basics", package = "emmeans")
oranges_rg1 <- ref_grid(oranges_lm1)
td <- tidy(oranges_rg1)
td

# marginal averages
marginal <- emmeans(oranges_rg1, "day")
tidy(marginal)

# contrasts
tidy(contrast(marginal))
tidy(contrast(marginal, method = "pairwise"))

# plot confidence intervals
library(ggplot2)

ggplot(tidy(marginal, conf.int = TRUE), aes(day, estimate)) +
  geom_point() +
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high))

# by multiple prices
by_price <- emmeans(oranges_lm1, "day",
  by = "price2",
  at = list(
    price1 = 50, price2 = c(40, 60, 80),
    day = c("2", "3", "4")
  )
)

by_price

tidy(by_price)

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

# joint_tests
tidy(joint_tests(oranges_lm1))
```

---

tidy.epi.2by2   *Tidy a(n) epi.2by2 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 across 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 'epi.2by2'
tidy(x, parameters = c("moa", "stat"), ...)
```

Arguments

x	A epi.2by2 object produced by a call to epiR::epi.2by2()
parameters	Return measures of association (moa) or test statistics (stat), default is moa (measures of association)
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

The tibble has a column for each of the measures of association or tests contained in massoc or massoc.detail when epiR::epi.2by2() is called.

Value

A tibble::tibble() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
df	Degrees of freedom used by this term in the model.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
term	The name of the regression term.
estimate	Estimated measure of association

See Also

tidy(), epiR::epi.2by2()

Examples

```
# load libraries for models and data
library(epiR)

# generate data
dat <- matrix(c(13, 2163, 5, 3349), nrow = 2, byrow = TRUE)

rownames(dat) <- c("DF+", "DF-")
colnames(dat) <- c("FUS+", "FUS-")

# fit model
fit <- epi.2by2(
  dat = as.table(dat), method = "cross.sectional",
  conf.level = 0.95, units = 100, outcome = "as.columns"
)

# summarize model fit with tidiers
tidy(fit, parameters = "moa")
tidy(fit, parameters = "stat")
```

---

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 across 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, ...)
```

Arguments

x	An ergm object returned from a call to `ergm::ergm()`.
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.

| 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 to pass to ergm::summary(). **Cautionary note**: Misspecified 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

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). https://www.jstatsoft.org/v24/i03/.

See Also

tidy(), ergm::ergm(), ergm::control.ergm(), ergm::summary()

Other ergm tidiers: glance.ergm()

Examples

```
# load libraries for models and data
library(ergm)

# 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)
```

---

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 across 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

variable   Variable under consideration.

uniqueness   Proportion of residual, or unexplained variance

flX   Factor loading for level X.

See Also

`tidy()`, `stats::factanal()`

Other factanal tidiers: `augment.factanal()`, `glance.factanal()`

Examples

```
set.seed(123)

# generate data
library(dplyr)
library(purrr)

m1 <- tibble(
  v1 = c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 3, 3, 3, 3, 3, 4, 5, 6),
  v2 = c(1, 2, 1, 1, 1, 1, 2, 1, 2, 1, 3, 4, 3, 3, 3, 4, 6, 5),
  v3 = c(3, 3, 3, 3, 3, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 5, 4, 6),
  v4 = c(3, 3, 4, 3, 3, 1, 1, 2, 1, 1, 1, 1, 2, 1, 1, 5, 6, 4),
  v5 = c(1, 1, 1, 1, 1, 3, 3, 3, 3, 3, 1, 1, 1, 1, 1, 6, 4, 5),
  v6 = c(1, 1, 1, 2, 1, 3, 3, 3, 4, 3, 1, 1, 1, 2, 1, 6, 5, 4)
)

# new data
m2 <- map_dfr(m1, rev)

# factor analysis objects
fit1 <- factanal(m1, factors = 3, scores = "Bartlett")
fit2 <- factanal(m1, factors = 3, scores = "regression")

# tidying the object
tidy(fit1)
tidy(fit2)

# augmented dataframe
augment(fit1)
augment(fit2)

# augmented dataframe (with new data)
augment(fit1, data = m2)
augment(fit2, data = m2)
```

---

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 across 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,
  se.type = c("default", "iid", "robust", "cluster"),
  ...
)
```

Arguments

x	A `felm` object returned from [`lfe::felm()`]().
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.
fe	Logical indicating whether or not to include estimates of fixed effects. Defaults to `FALSE`.
se.type	Character indicating the type of standard errors. Defaults to using those of the underlying felm() model object, e.g. clustered errors for models that were provided a cluster specification. Users can override these defaults by specifying an appropriate alternative: "iid" (for homoskedastic errors), "robust" (for Eicker-Huber-White robust errors), or "cluster" (for clustered standard errors; if the model object supports it).
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are: - tidy() methods will warn when supplied an `exponentiate` argument if it will be ignored. - augment() methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`]() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

tidy(), lfe::felm()

Other felm tidiers: augment.felm()

Examples

```
# load libraries for models and data
library(lfe)

# use built-in `airquality` dataset
head(airquality)

# no FEs; same as lm()
est0 <- felm(Ozone ~ Temp + Wind + Solar.R, airquality)

# summarize model fit with tidiers
tidy(est0)
augment(est0)

# add month fixed effects
est1 <- felm(Ozone ~ Temp + Wind + Solar.R | Month, airquality)

# summarize model fit with tidiers
tidy(est1)
tidy(est1, fe = TRUE)
augment(est1)
glance(est1)

# the "se.type" argument can be used to switch out different standard errors
# types on the fly. In turn, this can be useful exploring the effect of
# different error structures on model inference.
tidy(est1, se.type = "iid")
tidy(est1, se.type = "robust")

# add clustered SEs (also by month)
est2 <- felm(Ozone ~ Temp + Wind + Solar.R | Month | 0 | Month, airquality)

# summarize model fit with tidiers
tidy(est2, conf.int = TRUE)
tidy(est2, conf.int = TRUE, se.type = "cluster")
tidy(est2, conf.int = TRUE, se.type = "robust")
tidy(est2, conf.int = TRUE, se.type = "iid")
```

---

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 across 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 MASS::fitdistr().

...   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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

estimate   The estimated value of the regression term.

std.error   The standard error of the regression term.

term   The name of the regression term.

See Also

tidy(), MASS::fitdistr()

Other fitdistr tidiers: glance.fitdistr()

Examples

```
# load libraries for models and data
library(MASS)

# generate data
set.seed(2015)
x <- rnorm(100, 5, 2)

#  fit models
```

```
fit <- fitdistr(x, dnorm, list(mean = 3, sd = 1))

# summarize model fit with tidiers
tidy(fit)
glance(fit)
```

---

tidy.fixest   *Tidy a(n) fixest 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 across 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 'fixest'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A fixest object returned from any of the fixest estimators
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.
...	Additional arguments passed to summary and confint. Important arguments are se and cluster. Other arguments are dof, exact_dof, forceCovariance, and keepBounded. See summary.fixest.

Details

The fixest package provides a family of functions for estimating models with arbitrary numbers of fixed-effects, in both an OLS and a GLM context. The package also supports robust (i.e. White) and clustered standard error reporting via the generic summary.fixest() command. In a similar vein, the tidy() method for these models allows users to specify a desired standard error correction either 1) implicitly via the supplied fixest object, or 2) explicitly as part of the tidy call. See examples below.

Note that fixest confidence intervals are calculated assuming a normal distribution – this assumes infinite degrees of freedom for the CI. (This assumption is distinct from the degrees of freedom used to calculate the standard errors. For more on degrees of freedom with clusters and fixed effects, see https://github.com/lrberge/fixest/issues/6 and https://github.com/sgaure/lfe/issues/1#issuecomment-530646990)

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[tidy()](#), [fixest::feglm()](#), [fixest::fenegbin()](#), [fixest::feNmlm()](#), [fixest::femlm()](#), [fixest::feols()](#), [fixest::fepois()](#)

Other fixest tidiers: [augment.fixest()](#)

Examples

```
# load libraries for models and data
library(fixest)

gravity <-
  feols(
    log(Euros) ~ log(dist_km) | Origin + Destination + Product + Year, trade
  )

tidy(gravity)
glance(gravity)
augment(gravity, trade)

# to get robust or clustered SEs, users can either:

# 1) specify the arguments directly in the `tidy()` call

tidy(gravity, conf.int = TRUE, cluster = c("Product", "Year"))

tidy(gravity, conf.int = TRUE, se = "threeway")

# 2) or, feed tidy() a summary.fixest object that has already accepted
# these arguments

gravity_summ <- summary(gravity, cluster = c("Product", "Year"))

tidy(gravity_summ, conf.int = TRUE)

# approach (1) is preferred.
```

---

tidy.ftable   *(Deprecated) Tidy ftable objects*

Description

This function is deprecated. Please use `tibble::as_tibble()` instead.

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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

An ftable contains a "flat" contingency table. This melts it into a tibble::tibble with one column for each variable, then a `Freq` column.

See Also

Other deprecated: `bootstrap()`, `confint_tidy()`, `data.frame_tidiers`, `finish_glance()`, `fix_data_frame()`, `summary_tidiers`, `tidy.density()`, `tidy.dist()`, `tidy.numeric()`

---

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 across 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

Tidy gam objects created by calls to `mgcv::gam()` with `tidy.gam()`.

Value

A `tibble::tibble()` with columns:

df	Degrees of freedom used by this term in the model.
meansq	Mean sum of squares. Equal to total sum of squares divided by degrees of freedom.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
sumsq	Sum of squares explained by this term.
term	The name of the regression term.

See Also

`tidy()`, `gam::gam()`, `tidy.anova()`, `tidy.gam()`

Other gam tidiers: `glance.Gam()`

Examples

```
# load libraries for models and data
library(gam)

# fit model
g <- gam(mpg ~ s(hp, 4) + am + qsec, data = mtcars)
```

```
# summarize model fit with tidiers
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 across 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,
  conf.int = FALSE,
  conf.level = 0.95,
  exponentiate = 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.
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.
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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

When parametric = FALSE return columns edf and ref.df rather than estimate and std.error.

Value

A [tibble::tibble()](#) with columns:

estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.
edf	The effective degrees of freedom. Only reported when 'parametric = FALSE'
ref.df	The reference degrees of freedom. Only reported when 'parametric = FALSE'

See Also

[tidy()](#), [mgcv::gam()](#)

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

Examples

```
# load libraries for models and data
library(mgcv)

# fit model
g <- gam(mpg ~ s(hp) + am + qsec, data = mtcars)

# summarize model fit with tidiers
tidy(g)
tidy(g, parametric = TRUE)
glance(g)
augment(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 across 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, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A garch object returned by `tseries::garch()`.
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:
• tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
• augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

tidy(), tseries::garch()

Other garch tidiers: glance.garch()

Examples

```
# load libraries for models and data
library(tseries)

# load data
data(EuStockMarkets)

# fit model
dax <- diff(log(EuStockMarkets))[, "DAX"]
dax.garch <- garch(dax)
dax.garch

# summarize model fit with tidiers
tidy(dax.garch)
glance(dax.garch)
```

---

tidy.geeglm   *Tidy a(n) geeglm 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 across 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, ...)
```

Arguments

x	A geeglm object returned from a call to geepack::geeglm().
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.

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. **Cau-**
                 tionary 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.lvel = 0.9, all computation will proceed
                 using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it
  will be ignored.
- augment() methods will warn when supplied a newdata argument if it will
  be ignored.

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 columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

tidy(), geepack::geeglm()

Examples

```
# load modeling library
library(geepack)

# load data
data(state)
```

```
ds <- data.frame(state.region, state.x77)

# fit model
geefit <- geeglm(Income ~ Frost + Murder,
  id = state.region,
  data = ds,
  corstr = "exchangeable"
)

# summarize model fit with tidiers
tidy(geefit)
tidy(geefit, conf.int = TRUE)
```

---

tidy.glht   *Tidy a(n) glht 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 across 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, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A glht object returned by [multcomp::glht()]().
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.
...	Additional arguments passed to [summary()]() and [tidy.summary.glht()]().

Value

A [tibble::tibble()]() with columns:

contrast	Levels being compared.
estimate	The estimated value of the regression term.
null.value	Value to which the estimate is compared.

See Also

tidy(), multcomp::glht()

Other multcomp tidiers: tidy.cld(), tidy.confint.glht(), tidy.summary.glht()

Examples

```
# load libraries for models and data
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

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 across 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 'glm'
tidy(x, conf.int = FALSE, conf.level = 0.95, exponentiate = FALSE, ...)
```

Arguments

x	A glm object returned from [stats::glm()]().
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.
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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

See Also

[stats::glm()]()

Other lm tidiers: [augment.glm()](), [augment.lm()](), [glance.glm()](), [glance.lm()](), [glance.summary.lm()](), [glance.svyglm()](), [tidy.lm()](), [tidy.lm.beta()](), [tidy.mlm()](), [tidy.summary.lm()]()

---

tidy.glmnet	*Tidy a(n) 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 across 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 glmnet object returned from `glmnet::glmnet()`.
return_zeros	Logical indicating whether coefficients with value zero zero should be included in the results. 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

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:

dev.ratio	Fraction of null deviance explained at each value of lambda.
estimate	The estimated value of the regression term.
lambda	Value of penalty parameter lambda.
step	Which step of lambda choices was used.
term	The name of the regression term.

See Also

`tidy()`, `glmnet::glmnet()`

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

Examples

```
# load libraries for models and data
library(glmnet)

set.seed(2014)
x <- matrix(rnorm(100 * 20), 100, 20)
y <- rnorm(100)
fit1 <- glmnet(x, y)
```

```
# summarize model fit with tidiers + visualization
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

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 across 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 'glmRob'
tidy(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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

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

See Also

`robust::glmRob()`

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

Examples

```
# load libraries for models and data
library(robust)

# fit model
gm <- glmRob(am ~ wt, data = mtcars, family = "binomial")

# summarize model fit with tidiers
tidy(gm)
glance(gm)
```

---

tidy.glmrob   *Tidy a(n) glmrob 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 across 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 'glmrob'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A glmrob object returned from [robustbase::glmrob()]().
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

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

Value

A [tibble::tibble()]() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[robustbase::glmrob()]()

Other robustbase tidiers: [augment.glmrob()](), [augment.lmrob()](), [glance.lmrob()](), [tidy.lmrob]()

Examples

```
if (requireNamespace("robustbase", quietly = TRUE)) {
  # load libraries for models and data
  library(robustbase)

  data(coleman)
```

```
  set.seed(0)

  m <- lmrob(Y ~ ., data = coleman)
  tidy(m)
  augment(m)
  glance(m)

  data(carrots)

  Rfit <- glmrob(cbind(success, total - success) ~ logdose + block,
    family = binomial, data = carrots, method = "Mqle",
    control = glmrobMqle.control(tcc = 1.2)
  )

  tidy(Rfit)
  augment(Rfit)
}
```

---

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 across 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, ...)
```

Arguments

x	A gmm object returned from gmm::gmm().
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.
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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[tidy()](#), [gmm::gmm()](#)

Other gmm tidiers: [glance.gmm()](#)

Examples

```
# load libraries for models and data
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(term, estimate)) %>%
  ggplot(aes(estimate, variable)) +
  geom_point() +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high)) +
  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(term, estimate)) %>%
  ggplot(aes(estimate, variable)) +
  geom_point() +
  geom_errorbarh(aes(xmin = conf.low, xmax = conf.high)) +
  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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

alternative	Alternative hypothesis (character).
conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
estimate1	Sometimes two estimates are computed, such as in a two-sample t-test.
estimate2	Sometimes two estimates are computed, such as in a two-sample t-test.
method	Method used.
p.value	The two-sided p-value associated with the observed statistic.
parameter	The parameter being modeled.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.

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)

# the glance output will be the same for each of the below tests
glance(tt)

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   *Tidy a(n) ivreg 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 across 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, instruments = FALSE, ...)
```

Arguments

x	An ivreg object created by a call to AER::ivreg().
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.

instruments	Logical indicating whether to return coefficients from the second-stage or diagnostics tests for each endogenous regressor (F-statistics). 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

This tidier currently only supports `ivreg`-classed objects outputted by the `AER` package. The `ivreg` package also outputs objects of class `ivreg`, and will be supported in a later release.

Value

A [`tibble::tibble()`](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
p.value.Sargan	p-value for Sargan test of overidentifying restrictions.
p.value.weakinst	p-value for weak instruments test.
p.value.Wu.Hausman	p-value for Wu-Hausman weak instruments test for endogeneity.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
statistic.Sargan	Statistic for Sargan test of overidentifying restrictions.
statistic.weakinst	Statistic for Wu-Hausman test.
statistic.Wu.Hausman	Statistic for Wu-Hausman weak instruments test for endogeneity.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[`tidy()`](#), [`AER::ivreg()`](#)

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

Examples

```
# load libraries for models and data
library(AER)

# load data
data("CigarettesSW", package = "AER")

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

# summarize model fit with tidiers
tidy(ivr)
tidy(ivr, conf.int = TRUE)
tidy(ivr, conf.int = TRUE, instruments = TRUE)

augment(ivr)
augment(ivr, data = CigarettesSW)
augment(ivr, newdata = CigarettesSW)

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 across 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. **Cau-
                  tionary 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

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:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
type	Either 'weighted' or 'unweighted'.

See Also

tidy(), psych::cohen.kappa()

Examples

```
# load libraries for models and data
library(psych)

# generate example data
rater1 <- 1:9
rater2 <- c(1, 3, 1, 6, 1, 5, 5, 6, 7)

# fit model
ck <- cohen.kappa(cbind(rater1, rater2))

# summarize model fit with tidiers + visualization
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 across 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

Returns a data frame in long format with four columns. Use `tidyr::pivot_wider(..., names_from = variable, values_from = value)` on the output to return to a wide format.

Value

A `tibble::tibble()` with columns:

estimate   The estimated value of the regression term.
obs   weighted observed number of events in each group.
value   The value/estimate of the component. Results from data reshaping.
variable   Variable under consideration.

See Also

`tidy()`, `ks::kde()`

Examples

```
# load libraries for models and data
library(ks)

# generate data
dat <- replicate(2, rnorm(100))
k <- kde(dat)

# summarize model fit with tidiers + visualization
td <- tidy(k)
td

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

td %>%
  pivot_wider(c(obs, estimate),
    names_from = variable,
    values_from = value
  ) %>%
  ggplot(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 across 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

kendall_score   Kendall score.

p.value   The two-sided p-value associated with the observed statistic.

var_kendall_score

                      Variance of the kendall_score.

statistic   Kendall's tau statistic

denominator   The denominator, which is tau=kendall_score/denominator.

See Also

`tidy()`, `Kendall::Kendall()`, `Kendall::MannKendall()`, `Kendall::SeasonalMannKendall()`

Examples

```
# load libraries for models and data
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, 2, 2, 2)

# fit models and summarize results
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   *Tidy a(n) kmeans 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 across 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 = colnames(x$centers), ...)
```

Arguments

x	A kmeans object created by `stats::kmeans()`.
col.names	Dimension names. Defaults to the names of the variables in x. Set to NULL to get names 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

cluster	A factor describing the cluster from 1:k.
size	Number of points assigned to cluster.
withinss	The within-cluster sum of squares.

See Also

`tidy()`, `stats::kmeans()`

Other kmeans tidiers: `augment.kmeans()`, `glance.kmeans()`

Examples

```
library(cluster)
library(modeldata)
library(dplyr)

data(hpc_data)

x <- hpc_data[, 2:5]

fit <- pam(x, k = 4)

tidy(fit)
glance(fit)
augment(fit, x)
```

---

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 across 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 = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A lavaan object, such as those returned from `lavaan::cfa()`, and `lavaan::sem()`.
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.
...	Additional arguments passed to `lavaan::parameterEstimates()`. **Cautionary note**: Misspecified arguments may be silently ignored.

Value

A [`tibble::tibble()`](#) with one row for each estimated parameter and columns:

term	The result of paste(lhs, op, rhs)
op	The operator in the model syntax (e.g. ~~ for covariances, or ~ for regression parameters)
group	The group (if specified) in the lavaan model
estimate	The parameter estimate (may be standardized)
std.error	
statistic	The z value returned by [`lavaan::parameterEstimates()`](#)
p.value	
conf.low	
conf.high	
std.lv	Standardized estimates based on the variances of the (continuous) latent variables only
std.all	Standardized estimates based on both the variances of both (continuous) observed and latent variables.
std.nox	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

```
# load libraries for models and data
library(lavaan)

cfa.fit <- cfa("F =~ x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8 + x9",
  data = HolzingerSwineford1939, group = "school"
)

tidy(cfa.fit)
```

---

tidy.lm   *Tidy a(n) lm 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 across 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, ...)
```

Arguments

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.
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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

> • tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
> • augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

If the linear model is an mlm object (multiple linear model), there is an additional column response. See `tidy.mlm()`.

Value

A `tibble::tibble()` with columns:

conf.high	Upper bound on the confidence interval for the estimate.

conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

tidy(), stats::summary.lm()

Other lm tidiers: augment.glm(), augment.lm(), glance.glm(), glance.lm(), glance.summary.lm(), glance.svyglm(), tidy.glm(), tidy.lm.beta(), tidy.mlm(), tidy.summary.lm()

Examples

```
library(ggplot2)
library(dplyr)

mod <- lm(mpg ~ wt + qsec, data = mtcars)

tidy(mod)
glance(mod)

# coefficient plot
d <- tidy(mod, conf.int = TRUE)

ggplot(d, aes(estimate, term, xmin = conf.low, xmax = conf.high, height = 0)) +
  geom_point() +
  geom_vline(xintercept = 0, lty = 4) +
  geom_errorbarh()

# aside: There are tidy() and glance() methods for lm.summary objects too.
# this can be useful when you want to conserve memory by converting large lm
# objects into their leaner summary.lm equivalents.
s <- summary(mod)
tidy(s, conf.int = TRUE)
glance(s)

augment(mod)
augment(mod, mtcars, interval = "confidence")

# predict on new data
newdata <- mtcars %>%
  head(6) %>%
  mutate(wt = wt + 1)
augment(mod, newdata = newdata)

# ggplot2 example where we also construct 95% prediction interval
```

```
# simpler bivariate model since we're plotting in 2D
mod2 <- lm(mpg ~ wt, data = mtcars)

au <- augment(mod2, newdata = newdata, interval = "prediction")

ggplot(au, aes(wt, mpg)) +
  geom_point() +
  geom_line(aes(y = .fitted)) +
  geom_ribbon(aes(ymin = .lower, ymax = .upper), col = NA, alpha = 0.3)

# predict on new data without outcome variable. Output does not include .resid
newdata <- newdata %>%
  select(-mpg)

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, .cooksd)) +
  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.lm.beta   *Tidy a(n) lm.beta 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 across 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.beta'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	An `lm.beta` object created by [lm.beta::lm.beta]().
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.
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

If the linear model is an `mlm` object (multiple linear model), there is an additional column `response`.

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 columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

Other lm tidiers: [augment.glm]()(), [augment.lm]()(), [glance.glm]()(), [glance.lm]()(), [glance.summary.lm]()(), [glance.svyglm]()(), [tidy.glm]()(), [tidy.lm]()(), [tidy.mlm]()(), [tidy.summary.lm]()()

Examples

```
# load libraries for models and data
library(lm.beta)

# fit models
mod <- stats::lm(speed ~ ., data = cars)
std <- lm.beta(mod)

# summarize model fit with tidiers
tidy(std, conf.int = TRUE)

# generate data
ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)

# fit models
mod2 <- lm(weight ~ group)
std2 <- lm.beta(mod2)

# summarize model fit with tidiers
tidy(std2, conf.int = TRUE)
```

---

 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 across 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. **Cau-
                 tionary 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.lvel = 0.9, all computation will proceed
                 using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

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).

The returned p-value is one-tailed and calculated via a permutation test. A permutational test is used because distributional assumptions may not be valid. More information can be found in `vignette("mod2user", package = "lmodel2")`.

Value

A [`tibble::tibble()`](#) with columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`term`	The name of the regression term.
`method`	Either OLS/MA/SMA/RMA

See Also

[`tidy()`](#), [`lmodel2::lmodel2()`](#)

Other lmodel2 tidiers: [`glance.lmodel2()`](#)

Examples

```
# load libraries for models and data
library(lmodel2)

data(mod2ex2)
Ex2.res <- lmodel2(Prey ~ Predators, data = mod2ex2, "relative", "relative", 99)
Ex2.res

# summarize model fit with tidiers + visualization
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   *Tidy a(n) lmRob 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 across 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 'lmRob'
tidy(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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

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

See Also

robust::lmRob()

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

Examples

```
# load modeling library
library(robust)

# fit model
m <- lmRob(mpg ~ wt, data = mtcars)

# summarize model fit with tidiers
tidy(m)
augment(m)
glance(m)
```

---

tidy.lmrob   *Tidy a(n) lmrob 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 across 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 'lmrob'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A lmrob object returned from [robustbase::lmrob()]().
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

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

See Also

`robustbase::lmrob()`

Other robustbase tidiers: `augment.glmrob()`, `augment.lmrob()`, `glance.lmrob()`, `tidy.glmrob()`

Examples

```
if (requireNamespace("robustbase", quietly = TRUE)) {
  # load libraries for models and data
  library(robustbase)

  data(coleman)
  set.seed(0)

  m <- lmrob(Y ~ ., data = coleman)
  tidy(m)
  augment(m)
  glance(m)

  data(carrots)

  Rfit <- glmrob(cbind(success, total - success) ~ logdose + block,
    family = binomial, data = carrots, method = "Mqle",
    control = glmrobMqle.control(tcc = 1.2)
  )

  tidy(Rfit)
  augment(Rfit)
}
```

---

tidy.lsmobj   *Tidy a(n) lsmobj 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 across 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 'lsmobj'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	An lsmobj 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 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.
...	Additional arguments passed to emmeans::summary.emmGrid() or lsmeans::summary.ref.grid(). **Cautionary note**: misspecified arguments may be silently ignored!

Details

Returns a data frame with one observation for each estimated marginal mean, and one column for each combination of factors. When the input is a contrast, each row will contain one estimated contrast.

There are a large number of arguments that can be passed on to emmeans::summary.emmGrid() or lsmeans::summary.ref.grid().

Value

A tibble::tibble() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
contrast	Levels being compared.
df	Degrees of freedom used by this term in the model.
null.value	Value to which the estimate is compared.
p.value	The two-sided p-value associated with the observed statistic.
std.error	The standard error of the regression term.
estimate	Expected marginal mean
statistic	T-ratio statistic

See Also

tidy(), emmeans::ref_grid(), emmeans::emmeans(), emmeans::contrast()

Other emmeans tidiers: tidy.emmGrid(), tidy.ref.grid(), tidy.summary_emm()

Examples

```
# load libraries for models and data
library(emmeans)

# linear model for sales of oranges per day
oranges_lm1 <- lm(sales1 ~ price1 + price2 + day + store, data = oranges)
```

```
# reference grid; see vignette("basics", package = "emmeans")
oranges_rg1 <- ref_grid(oranges_lm1)
td <- tidy(oranges_rg1)
td

# marginal averages
marginal <- emmeans(oranges_rg1, "day")
tidy(marginal)

# contrasts
tidy(contrast(marginal))
tidy(contrast(marginal, method = "pairwise"))

# plot confidence intervals
library(ggplot2)

ggplot(tidy(marginal, conf.int = TRUE), aes(day, estimate)) +
  geom_point() +
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high))

# by multiple prices
by_price <- emmeans(oranges_lm1, "day",
  by = "price2",
  at = list(
    price1 = 50, price2 = c(40, 60, 80),
    day = c("2", "3", "4")
  )
)

by_price

tidy(by_price)

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

# joint_tests
tidy(joint_tests(oranges_lm1))
```

---

tidy.manova	*Tidy a(n) manova 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 across 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

x	A manova object return from `stats::manova()`.
test	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".
...	Arguments passed on to `stats::summary.manova`
	`object` An object of class "manova" or an aov object with multiple responses.
	`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`.

Details

Depending on which test statistic is specified only one of `pillai`, `wilks`, `hl` or `roy` is included.

Value

A `tibble::tibble()` with columns:

den.df	Degrees of freedom of the denominator.
num.df	Degrees of freedom.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
term	The name of the regression term.
pillai	Pillai's trace.
wilks	Wilk's lambda.
hl	Hotelling-Lawley trace.
roy	Roy's greatest root.

See Also

`tidy()`, `stats::summary.manova()`

Other anova tidiers: `glance.anova()`, `glance.aov()`, `tidy.TukeyHSD()`, `tidy.anova()`, `tidy.aov()`, `tidy.aovlist()`

Examples

```
npk2 <- within(npk, foo <- rnorm(24))
m <- manova(cbind(yield, foo) ~ block + N * P * K, npk2)
tidy(m)
```

---

tidy.map   *Tidy a(n) map 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 across 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 `maps::map()`.

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                  tionary 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.lvel = 0.9`, all computation will proceed
                  using `conf.level = 0.95`. Two exceptions here are:

                  • `tidy()` methods will warn when supplied an `exponentiate` argument if it
                    will be ignored.
                  • `augment()` methods will warn when supplied a `newdata` argument if it will
                    be ignored.

Value

A `tibble::tibble()` with columns:

term   The name of the regression term.

long   Longitude.

lat   Latitude.

Remaining columns give information on geographic attributes and depend on the inputted map
object. See ?maps::map for more information.

See Also

`tidy()`, `maps::map()`

Examples

```
# load libraries for models and data
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.margins   *Tidy a(n) margins 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 across 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 'margins'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A margins object returned from margins::margins().
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

The `margins` package provides a way to obtain coefficient marginal effects for a variety of (non-linear) models, such as logit or models with multiway interaction terms. Note that the `glance.margins()` method requires rerunning the underlying model again, which can take some time. Similarly, an `augment.margins()` method is not currently supported, but users can simply run the underlying model to obtain the same information.

Value

A [`tibble::tibble()`](#) with columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`statistic`	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
`std.error`	The standard error of the regression term.
`term`	The name of the regression term.

See Also

[`tidy()`](#), [`margins::margins()`](#)

Examples

```
# load libraries for models and data
library(margins)

# example 1: logit model
mod_log <- glm(am ~ cyl + hp + wt, data = mtcars, family = binomial)

# get tidied "naive" model coefficients
tidy(mod_log)

# convert to marginal effects with margins()
marg_log <- margins(mod_log)

# get tidied marginal effects
tidy(marg_log)
tidy(marg_log, conf.int = TRUE)
```

```
# requires running the underlying model again. quick for this example
glance(marg_log)

# augmenting `margins` outputs isn't supported, but
# you can get the same info by running on the underlying model
augment(mod_log)

# example 2: threeway interaction terms
mod_ie <- lm(mpg ~ wt * cyl * disp, data = mtcars)

# get tidied "naive" model coefficients
tidy(mod_ie)

# convert to marginal effects with margins()
marg_ie0 <- margins(mod_ie)
# get tidied marginal effects
tidy(marg_ie0)
glance(marg_ie0)

# marginal effects evaluated at specific values of a variable (here: cyl)
marg_ie1 <- margins(mod_ie, at = list(cyl = c(4,6,8)))

# summarize model fit with tidiers
tidy(marg_ie1)

# marginal effects of one interaction variable (here: wt), modulated at
# specific values of the two other interaction variables (here: cyl and drat)
marg_ie2 <- margins(mod_ie,
                    variables = "wt",
                    at = list(cyl = c(4,6,8), drat = c(3, 3.5, 4)))

# summarize model fit with tidiers
tidy(marg_ie2)
```

---

tidy.Mclust   *Tidy a(n) Mclust 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 across 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 mclust::Mclust().

...   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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

proportion   The mixing proportion of each component

size   Number of points assigned to cluster.

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

variance   In case of one-dimensional and spherical models, the variance for each component, omitted otherwise. NA for noise component

component   Cluster id as a factor.

See Also

tidy(), mclust::Mclust()

Other mclust tidiers: augment.Mclust()

Examples

```
# load library for models and data
library(mclust)

# load data manipulation libraries
library(dplyr)
library(tibble)
library(purrr)
library(tidyr)

set.seed(27)

centers <- tibble(
  cluster = factor(1:3),
  # number points in each cluster
  num_points = c(100, 150, 50),
  # x1 coordinate of cluster center
```

```
  x1 = c(5, 0, -3),
  # x2 coordinate of cluster center
  x2 = c(-1, 1, -2)
)

points <- centers %>%
  mutate(
    x1 = map2(num_points, x1, rnorm),
    x2 = map2(num_points, x2, rnorm)
  ) %>%
  select(-num_points, -cluster) %>%
  unnest(c(x1, x2))

# fit model
m <- Mclust(points)

# summarize model fit with tidiers
tidy(m)
augment(m, points)
glance(m)
```

---

tidy.mediate   *Tidy a(n) mediate 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 across 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 'mediate'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A mediate object produced by a call to [mediation::mediate()]().
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.
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

The tibble has four rows. The first two indicate the mediated effect in the control and treatment groups, respectively. And the last two the direct effect in each group.

Value

A [tibble::tibble()](#) with columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`statistic`	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
`std.error`	The standard error of the regression term.
`term`	The name of the regression term.

See Also

[tidy()](#), [mediation::mediate()](#)

Examples

```
# load libraries for models and data
library(mediation)

data(jobs)

# fit models
b <- lm(job_seek ~ treat + econ_hard + sex + age, data = jobs)
c <- lm(depress2 ~ treat + job_seek + econ_hard + sex + age, data = jobs)
mod <- mediate(b, c, sims = 50, treat = "treat", mediator = "job_seek")

# summarize model fit with tidiers
tidy(mod)
tidy(mod, conf.int = TRUE)
tidy(mod, conf.int = TRUE, conf.level = .99)
```

---

tidy.mfx   *Tidy a(n) mfx 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 across 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 particular functions below provide generic tidy methods for objects returned by the `mfx` package, preserving the calculated marginal effects instead of the naive model coefficients. The returned tidy tibble will also include an additional "atmean" column indicating how the marginal effects were originally calculated (see Details below).

Usage

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

## S3 method for class 'logitmfx'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)

## S3 method for class 'negbinmfx'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)

## S3 method for class 'poissonmfx'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)

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

Arguments

x	A `logitmfx`, `negbinmfx`, `poissonmfx`, or `probitmfx` object. (Note that `betamfx` objects receive their own set of tidiers.)
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.
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

The `mfx` package provides methods for calculating marginal effects for various generalized linear models (GLMs). Unlike standard linear models, estimated model coefficients in a GLM cannot be directly interpreted as marginal effects (i.e., the change in the response variable predicted after a one unit change in one of the regressors). This is because the estimated coefficients are multiplicative, dependent on both the link function that was used for the estimation and any other variables that were included in the model. When calculating marginal effects, users must typically choose whether they want to use i) the average observation in the data, or ii) the average of the sample marginal effects. See `vignette("mfxarticle")` from the `mfx` package for more details.

Value

A [`tibble::tibble()`](#) with columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`statistic`	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
`std.error`	The standard error of the regression term.
`term`	The name of the regression term.
`atmean`	TRUE if the marginal effects were originally calculated as the partial effects for the average observation. If FALSE, then these were instead calculated as average partial effects.

See Also

[`tidy()`](#), [`mfx::logitmfx()`](#), [`mfx::negbinmfx()`](#), [`mfx::poissonmfx()`](#), [`mfx::probitmfx()`](#)

Other mfx tidiers: [`augment.betamfx()`](#), [`augment.mfx()`](#), [`glance.betamfx()`](#), [`glance.mfx()`](#), [`tidy.betamfx()`](#)

Examples

```
# load libraries for models and data
library(mfx)

# get the marginal effects from a logit regression
mod_logmfx <- logitmfx(am ~ cyl + hp + wt, atmean = TRUE, data = mtcars)

tidy(mod_logmfx, conf.int = TRUE)
```

```
# compare with the naive model coefficients of the same logit call
tidy(
  glm(am ~ cyl + hp + wt, family = binomial, data = mtcars),
  conf.int = TRUE
)

augment(mod_logmfx)
glance(mod_logmfx)

# another example, this time using probit regression
mod_probmfx <- probitmfx(am ~ cyl + hp + wt, atmean = TRUE, data = mtcars)

tidy(mod_probmfx, conf.int = TRUE)
augment(mod_probmfx)
glance(mod_probmfx)
```

---

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 across 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 [joineRML::bootSE()](). 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 conf.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()]() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[tidy()](), [joineRML::mjoint()](), [joineRML::bootSE()]()

Other mjoint tidiers: [glance.mjoint]()()

Examples

```
# broom only skips running these examples because the example models take a
# while to generate—they should run just fine, though!
## Not run:


# load libraries for models and data
library(joineRML)

# fit a joint model with bivariate longitudinal outcomes
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 across 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

x	An mle2 object created by a call to `bbmle::mle2()`.
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is nonzero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[tidy()](#), [bbmle::mle2()](#), [tidy_optim()](#)

Examples

```
# load libraries for models and data
library(bbmle)

# generate data
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
d <- data.frame(x, y)

# fit model
fit <- mle2(y ~ dpois(lambda = ymean),
  start = list(ymean = mean(y)), data = d
)

# summarize model fit with tidiers
tidy(fit)
```

---

tidy.mlm   *Tidy a(n) mlm 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 across 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 'mlm'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	An mlm object created by stats::lm() with a matrix as the response.
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

In contrast to `lm` object (simple linear model), tidy output for `mlm` (multiple linear model) objects contain an additional column `response`.

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 columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`statistic`	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
`std.error`	The standard error of the regression term.
`term`	The name of the regression term.

See Also

tidy()

Other lm tidiers: augment.glm(), augment.lm(), glance.glm(), glance.lm(), glance.summary.lm(), glance.svyglm(), tidy.glm(), tidy.lm(), tidy.lm.beta(), tidy.summary.lm()

Examples

```
# fit model
mod <- lm(cbind(mpg, disp) ~ wt, mtcars)

# summarize model fit with tidiers
tidy(mod, conf.int = TRUE)
```

---

tidy.mlogit	*Tidying methods for logit models*

Description

These methods tidy the coefficients of mnl and nl models generated by the functions of the `mlogit` package.

Usage

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

Arguments

x	an object returned from [mlogit::mlogit()]().
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.
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

  - tidy() methods will warn when supplied an `exponentiate` argument if it will be ignored.
  - augment() methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [tibble::tibble()]() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

tidy(), mlogit::mlogit()

Other mlogit tidiers: augment.mlogit(), glance.mlogit()

Examples

```
# load libraries for models and data
library(mlogit)

data("Fishing", package = "mlogit")
Fish <- dfidx(Fishing, varying = 2:9, shape = "wide", choice = "mode")

# fit model
m <- mlogit(mode ~ price + catch | income, data = Fish)

# summarize model fit with tidiers
tidy(m)
augment(m)
glance(m)
```

---

tidy.muhaz   *Tidy a(n) muhaz 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 across 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

time	Point in time.
estimate	Estimated hazard rate.

See Also

[tidy()](#), [muhaz::muhaz()](#)

Other muhaz tidiers: [glance.muhaz](#)()

Examples

```
# load libraries for models and data
library(muhaz)
library(survival)

# fit model
x <- muhaz(ovarian$futime, ovarian$fustat)

# summarize model fit with tidiers
tidy(x)
glance(x)
```

---

tidy.multinom   *Tidying methods for multinomial logistic regression models*

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 = FALSE, ...)
```

Arguments

x	A multinom object returned from [nnet::multinom()](#).
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.

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. **Cau-
                tionary 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.lvel = 0.9, all computation will proceed
                using conf.level = 0.95. Two exceptions here are:

                • tidy() methods will warn when supplied an exponentiate argument if it
                  will be ignored.
                • augment() methods will warn when supplied a newdata argument if it will
                  be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.
y.value	The response level.

See Also

[tidy()](#), [nnet::multinom()](#)

Other multinom tidiers: [glance.multinom](#)()

Examples

```
# load libraries for models and data
library(nnet)
library(MASS)

example(birthwt)

bwt.mu <- multinom(low ~ ., bwt)

tidy(bwt.mu)
glance(bwt.mu)

# or, for output from a multinomial logistic regression
```

```
fit.gear <- multinom(gear ~ mpg + factor(am), data = mtcars)
tidy(fit.gear)
glance(fit.gear)
```

---

tidy.negbin   *Tidy a(n) negbin 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 across 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 'negbin'
tidy(x, conf.int = FALSE, conf.level = 0.95, exponentiate = FALSE, ...)
```

Arguments

x	A glm.nb object returned by MASS::glm.nb().
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.
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.
...	For tidy(), additional arguments passed to summary(). Otherwise ignored.

See Also

MASS::glm.nb()

Other glm.nb tidiers: glance.negbin()

Examples

```
# load libraries for models and data
library(MASS)

# fit model
r <- glm.nb(Days ~ Sex / (Age + Eth * Lrn), data = quine)
```

```
# summarize model fit with tidiers
tidy(r)
glance(r)
```

---

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 across 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 [quantreg::nlrq()]().
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:
	• tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
	• augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()]() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.

statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

tidy(), quantreg::nlrq()

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

Examples

```
# load modeling library
library(quantreg)

# build artificial data with multiplicative error
set.seed(1)
dat <- NULL
dat$x <- rep(1:25, 20)
dat$y <- SSlogis(dat$x, 10, 12, 2) * rnorm(500, 1, 0.1)

# fit the median using nlrq
mod <- nlrq(y ~ SSlogis(x, Asym, mid, scal),
  data = dat, tau = 0.5, trace = TRUE
)

# summarize model fit with tidiers
tidy(mod)
glance(mod)
augment(mod)
```

---

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 across 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, ...)
```

Arguments

x	An nls object returned from `stats::nls()`.
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[tidy](#), [stats::nls()](#), [stats::summary.nls()](#)

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

Examples

```
# fit model
n <- nls(mpg ~ k * e^wt, data = mtcars, start = list(k = 1, e = 2))

# summarize model fit with tidiers + visualization
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.

See Also

Other deprecated: bootstrap(), confint_tidy(), data.frame_tidiers, finish_glance(), fix_data_frame(),
summary_tidiers, tidy.density(), tidy.dist(), tidy.ftable()

Other deprecated: bootstrap(), confint_tidy(), data.frame_tidiers, finish_glance(), fix_data_frame(),
summary_tidiers, tidy.density(), tidy.dist(), tidy.ftable()

Other deprecated: bootstrap(), confint_tidy(), data.frame_tidiers, finish_glance(), fix_data_frame(),
summary_tidiers, tidy.density(), tidy.dist(), tidy.ftable()

Examples

```
## Not run:
x <- 1:5
names(x) <- letters[1:5]
tidy(x)

## End(Not run)
```

---

tidy.orcutt   *Tidy a(n) orcutt 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 across 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 'orcutt'
tidy(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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

orcutt::cochrane.orcutt()

Other orcutt tidiers: glance.orcutt()

Examples

```
# load libraries for models and data
library(orcutt)

# fit model and summarize results
reg <- lm(mpg ~ wt + qsec + disp, mtcars)
tidy(reg)


co <- cochrane.orcutt(reg)
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 across 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 stats::pairwise.t.test()
                  or stats::pairwise.wilcox.test().

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                  tionary 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.lvel = 0.9, all computation will proceed
                  using conf.level = 0.95. Two exceptions here are:

                  • tidy() methods will warn when supplied an exponentiate argument if it
                    will be ignored.
                  • augment() methods will warn when supplied a newdata argument if it will
                    be ignored.

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 columns:

group1	First group being compared.
group2	Second group being compared.
p.value	The two-sided p-value associated with the observed statistic.

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)

library(modeldata)
data(hpc_data)
attach(hpc_data)
ptt2 <- pairwise.t.test(compounds, class)
tidy(ptt2)

tidy(pairwise.t.test(compounds, class, alternative = "greater"))
tidy(pairwise.t.test(compounds, class, alternative = "less"))

tidy(pairwise.wilcox.test(compounds, class))
```

---

tidy.pam   *Tidy a(n) pam 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 across 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 'pam'
tidy(x, col.names = paste0("x", 1:ncol(x$medoids)), ...)
```

Arguments

`x`	An pam object returned from `cluster::pam()`
`col.names`	Column names in the input data frame. Defaults to the names of the variables in 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

For examples, see the pam vignette.

Value

A `tibble::tibble()` with columns:

`size`	Size of each cluster.
`max.diss`	Maximal dissimilarity between the observations in the cluster and that cluster's medoid.
`avg.diss`	Average dissimilarity between the observations in the cluster and that cluster's medoid.
`diameter`	Diameter of the cluster.
`separation`	Separation of the cluster.
`avg.width`	Average silhouette width of the cluster.
`cluster`	A factor describing the cluster from 1:k.

See Also

`tidy()`, `cluster::pam()`

Other pam tidiers: `augment.pam()`, `glance.pam()`

Examples

```
# load libraries for models and data
library(dplyr)
library(ggplot2)
library(cluster)
library(modeldata)
data(hpc_data)

x <- hpc_data[, 2:5]
p <- pam(x, k = 4)

# summarize model fit with tidiers + visualization
tidy(p)
glance(p)
augment(p, x)

augment(p, x) %>%
  ggplot(aes(compounds, input_fields)) +
  geom_point(aes(color = .cluster)) +
  geom_text(aes(label = cluster), data = tidy(p), size = 10)
```

---

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 across 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, ...)
```

Arguments

x	A plm objected returned by plm::plm().
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.

...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [`tibble::tibble()`](#) with columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`statistic`	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
`std.error`	The standard error of the regression term.
`term`	The name of the regression term.

See Also

[`tidy()`](#), [`plm::plm()`](#), [`tidy.lm()`](#)

Other plm tidiers: [`augment.plm()`](#), [`glance.plm()`](#)

Examples

```
# load libraries for models and data
library(plm)

# load data
data("Produc", package = "plm")

# fit model
zz <- plm(log(gsp) ~ log(pcap) + log(pc) + log(emp) + unemp,
  data = Produc, index = c("state", "year")
)

# summarize model fit with tidiers
summary(zz)

tidy(zz)
tidy(zz, conf.int = TRUE)
tidy(zz, conf.int = TRUE, conf.level = 0.9)
```

```
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 across 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it
  will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will
  be ignored.

Value

A `tibble::tibble()` with columns:

class	The class under consideration.
outcome	Outcome of manifest variable.
std.error	The standard error of the regression term.
variable	Manifest variable
estimate	Estimated class-conditional response probability

See Also

`tidy()`, `poLCA::poLCA()`

Other poLCA tidiers: `augment.poLCA()`, `glance.poLCA()`

Examples

```
# load libraries for models and data
library(poLCA)
library(dplyr)

# generate data
data(values)

f <- cbind(A, B, C, D) ~ 1

# fit model
M1 <- poLCA(f, values, nclass = 2, verbose = FALSE)

M1

# summarize model fit with tidiers + visualization
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)

# 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

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

count(au, .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   *Tidy a(n) polr 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 across 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 'polr'
tidy(
  x,
  conf.int = FALSE,
  conf.level = 0.95,
  exponentiate = FALSE,
  p.values = FALSE,
  ...
)
```

Arguments

x	A polr object returned from MASS::polr().
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.
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.
p.values	Logical. Should p-values be returned, based on chi-squared tests from MASS::dropterm(). 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

In `broom 0.7.0` the `coefficient_type` column was renamed to `coef.type`, and the contents were changed as well. Now the contents are `coefficient` and `scale`, rather than `coefficient` and `zeta`.

Calculating p.values with the `dropterm()` function is the approach suggested by the MASS package author. This approach is computationally intensive so that p.values are only returned if requested explicitly. Additionally, it only works for models containing no variables with more than two categories. If this condition is not met, a message is shown and NA is returned instead of p-values.

Value

A [`tibble::tibble()`](#) with columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`statistic`	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
`std.error`	The standard error of the regression term.
`term`	The name of the regression term.

See Also

[tidy](#), [`MASS::polr()`](#)

Other ordinal tidiers: [augment.clm()](#), [augment.polr()](#), [glance.clm()](#), [glance.clmm()](#), [glance.polr()](#), [glance.svyolr()](#), [tidy.clm()](#), [tidy.clmm()](#), [tidy.svyolr()](#)

Examples

```
# load libraries for models and data
library(MASS)

# fit model
fit <- polr(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)

# summarize model fit with tidiers
tidy(fit, exponentiate = TRUE, conf.int = TRUE)

glance(fit)
augment(fit, type.predict = "class")
```

```
fit2 <- polr(factor(gear) ~ am + mpg + qsec, data = mtcars)

tidy(fit, p.values = TRUE)
```

---

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 across 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

  • tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
  • augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

delta   True difference in means.

n   Number of observations by component.

power   Power achieved for given value of n.

sd   Standard deviation.

sig.level   Significance level (Type I error probability).

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 across 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 stats::prcomp().
matrix	Character specifying which component of the PCA should be tidied.

- "u", "samples", "scores", or "x": returns information about the map from the original space into principle components space.
- "v", "rotation", "loadings" or "variables": returns information about the map from principle components space back into the original space.
- "d", "eigenvalues" or "pcs": returns information about the eigenvalues.

...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

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"`, `"scores"`, 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 principal component.
value	The score of the observation for that particular principal component. That is, the location of the observation in PCA space.

If `matrix` is `"v"`, `"rotation"`, `"loadings"` 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"`, `"eigenvalues"` or `"pcs"`, the columns are:

PC	An integer vector indicating the principal component.
std.dev	Standard deviation explained by this PC.
percent	Fraction of variation explained by this component (a numeric value between 0 and 1).
cumulative	Cumulative fraction of variation explained by principle components up to this component (a numeric value between 0 and 1).

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)
library(maps)

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.pyears	*Tidy a(n) pyears 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 across 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 'pyears'
tidy(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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

expected is only present in the output when if a ratetable term is present.

If the data.frame = TRUE argument is supplied to pyears, this is simply the contents of x$data.

Value

A [tibble::tibble()]() with columns:

expected	Expected number of events.
pyears	Person-years of exposure.
n	number of subjects contributing time
event	observed number of events

See Also

[tidy()](), [survival::pyears()]()

Other pyears tidiers: [glance.pyears]()()

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.survdiff](), [tidy.survexp](), [tidy.survfit](), [tidy.survreg]()()

Examples

```
# load libraries for models and data
library(survival)

# generate and format data
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
)

# summarize model fit with tidiers
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 across 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 Hmisc::rcorr().

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. **Cau-
             tionary 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.lvel = 0.9, all computation will proceed
             using conf.level = 0.95. Two exceptions here are:

             • tidy() methods will warn when supplied an exponentiate argument if it
               will be ignored.
             • augment() methods will warn when supplied a newdata argument if it will
               be ignored.

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 columns:

column1	Name or index of the first column being described.
column2	Name or index of the second column being described.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
n	Number of observations used to compute the correlation

See Also

[tidy()](#), [Hmisc::rcorr()](#)

Examples

```
# load libraries for models and data
library(Hmisc)

mat <- replicate(52, rnorm(100))

# add some NAs
mat[sample(length(mat), 2000)] <- NA

# also, column names
colnames(mat) <- c(LETTERS, letters)

# fit model
rc <- rcorr(mat)

# summarize model fit with tidiers  + visualization
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.ref.grid *Tidy a(n) ref.grid 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 across 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 'ref.grid'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A ref.grid object created by emmeans::ref_grid().
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.
...	Additional arguments passed to emmeans::summary.emmGrid() or lsmeans::summary.ref.grid(). **Cautionary note**: misspecified arguments may be silently ignored!

Details

Returns a data frame with one observation for each estimated marginal mean, and one column for each combination of factors. When the input is a contrast, each row will contain one estimated contrast.

There are a large number of arguments that can be passed on to emmeans::summary.emmGrid() or lsmeans::summary.ref.grid().

Value

A tibble::tibble() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
df	Degrees of freedom used by this term in the model.
p.value	The two-sided p-value associated with the observed statistic.
std.error	The standard error of the regression term.
estimate	Expected marginal mean
statistic	T-ratio statistic

See Also

tidy(), emmeans::ref_grid(), emmeans::emmeans(), emmeans::contrast()

Other emmeans tidiers: tidy.emmGrid(), tidy.lsmobj(), tidy.summary_emm()

Examples

```
# load libraries for models and data
library(emmeans)

# linear model for sales of oranges per day
oranges_lm1 <- lm(sales1 ~ price1 + price2 + day + store, data = oranges)

# reference grid; see vignette("basics", package = "emmeans")
oranges_rg1 <- ref_grid(oranges_lm1)
td <- tidy(oranges_rg1)
td

# marginal averages
marginal <- emmeans(oranges_rg1, "day")
tidy(marginal)

# contrasts
tidy(contrast(marginal))
tidy(contrast(marginal, method = "pairwise"))

# plot confidence intervals
library(ggplot2)

ggplot(tidy(marginal, conf.int = TRUE), aes(day, estimate)) +
  geom_point() +
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high))

# by multiple prices
by_price <- emmeans(oranges_lm1, "day",
  by = "price2",
  at = list(
    price1 = 50, price2 = c(40, 60, 80),
    day = c("2", "3", "4")
  )
)

by_price

tidy(by_price)

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

# joint_tests
tidy(joint_tests(oranges_lm1))
```

---

tidy.regsubsets *Tidy a(n) regsubsets 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 across 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 'regsubsets'
tidy(x, ...)
```

Arguments

x	A regsubsets object created by `leaps::regsubsets()`.
...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

r.squared	R squared statistic, or the percent of variation explained by the model.
adj.r.squared	Adjusted R squared statistic
BIC	Bayesian information criterion for the component.
mallows_cp	Mallow's Cp statistic.

See Also

`tidy()`, `leaps::regsubsets()`

Examples

```
# load libraries for models and data
library(leaps)

# fit model
all_fits <- regsubsets(hp ~ ., mtcars)

# summarize model fit with tidiers
tidy(all_fits)
```

---

tidy.ridgelm   *Tidy a(n) ridgelm 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 across 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 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

GCV	Generalized cross validation error estimate.
lambda	Value of penalty parameter lambda.
term	The name of the regression term.

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

```
# load libraries for models and data
library(MASS)

names(longley)[1] <- "y"

# fit model and summarizd results
fit1 <- lm.ridge(y ~ ., longley)
tidy(fit1)

fit2 <- 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

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 across 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 'rlm'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	An rlm object returned by MASS::rlm().
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

See Also

MASS::rlm()

Other rlm tidiers: augment.rlm(), glance.rlm()

---

tidy.rma	*Tidy a(n) rma 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 across 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 'rma'
tidy(
  x,
  conf.int = FALSE,
  conf.level = 0.95,
  exponentiate = FALSE,
```

```
    include_studies = FALSE,
    measure = "GEN",
    ...
)
```

Arguments

x	An rma object such as those created by [metafor::rma()](), [metafor::rma.uni()](), [metafor::rma.glmm()](), [metafor::rma.mh()](), [metafor::rma.mv()](), or [metafor::rma.peto()]().
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.
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.
include_studies	
	Logical. Should individual studies be included in the output? Defaults to FALSE.
measure	Measure type. See [metafor::escalc()]()
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()]() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the individual study
type	The estimate type (summary vs individual study)

Examples

```
# load libraries for models and data
library(metafor)

df <-
  escalc(
    measure = "RR",
    ai = tpos,
    bi = tneg,
    ci = cpos,
    di = cneg,
    data = dat.bcg
  )

meta_analysis <- rma(yi, vi, data = df, method = "EB")

tidy(meta_analysis)
```

---

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 across 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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

cutoff	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.
fpr	False positive rate.
tpr	The true positive rate at the given cutoff.

See Also

[tidy()](#), [AUC::roc()](#)

Examples

```
# load libraries for models and data
library(AUC)

# load data
data(churn)

# fit model
r <- roc(churn$predictions, churn$labels)

# summarize with tidiers + visualization
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 %>%
  pivot_longer(contains("predictions"),
    names_to = "algorithm",
    values_to = "value"
  ) %>%
  nest(data = -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 across 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 = NULL, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	An rq object returned from [quantreg::rq()]().
se.type	Character specifying the method to use to calculate standard errors. Passed to [quantreg::summary.rq()]() se argument. Defaults to "rank" if the sample size is less than 1000, otherwise defaults to "nid".
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.
...	Additional arguments passed to [quantreg::summary.rq()]().

Details

If se.type = "rank" confidence intervals are calculated by summary.rq and statistic and p.value values are not returned. 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 columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

tidy(), quantreg::rq()

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

Examples

```
# load modeling library and data
library(quantreg)

data(stackloss)

# median (l1) regression fit for the stackloss data.
mod1 <- rq(stack.loss ~ stack.x, .5)

# weighted sample median
mod2 <- rq(rnorm(50) ~ 1, weights = runif(50))

# summarize model fit with tidiers
tidy(mod1)
glance(mod1)
augment(mod1)

tidy(mod2)
glance(mod2)
augment(mod2)

# varying tau to generate an rqs object
mod3 <- rq(stack.loss ~ stack.x, tau = c(.25, .5))

tidy(mod3)
augment(mod3)

# glance cannot handle rqs objects like `mod3`--use a purrr
# `map`-based workflow instead
```

---

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 across 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 = FALSE, conf.level = 0.95, ...)
```

Arguments

x	An rqs object returned from `quantreg::rq()`.
se.type	Character specifying the method to use to calculate standard errors. Passed to `quantreg::summary.rq()` 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 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.
...	Additional arguments passed to `quantreg::summary.rqs()`

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 columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.
quantile	Linear conditional quantile.

See Also

`tidy()`, `quantreg::rq()`

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

Examples

```
# load modeling library and data
library(quantreg)

data(stackloss)

# median (l1) regression fit for the stackloss data.
mod1 <- rq(stack.loss ~ stack.x, .5)

# weighted sample median
mod2 <- rq(rnorm(50) ~ 1, weights = runif(50))

# summarize model fit with tidiers
tidy(mod1)
glance(mod1)
augment(mod1)

tidy(mod2)
glance(mod2)
augment(mod2)

# varying tau to generate an rqs object
mod3 <- rq(stack.loss ~ stack.x, tau = c(.25, .5))

tidy(mod3)
augment(mod3)

# glance cannot handle rqs objects like `mod3`--use a purrr
# `map`-based workflow instead
```

---

tidy.sarlm   *Tidying methods for spatially autoregressive models*

Description

These methods tidy the coefficients of spatial autoregression models generated by functions in the
spatialreg package.

Usage

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

Arguments

x   An object returned from spatialreg::lagsarlm() or spatialreg::errorsarlm().

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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

[tidy()](#), [spatialreg::lagsarlm()](#), [spatialreg::errorsarlm()](#), [spatialreg::sacsarlm()](#)

Other spatialreg tidiers: [augment.sarlm()](#), [glance.sarlm()](#)

Examples

```
# load libraries for models and data
library(spatialreg)
library(spdep)

# load data
data(oldcol, package = "spdep")

listw <- nb2listw(COL.nb, style = "W")

# fit model
```

```
crime_sar <-
  lagsarlm(CRIME ~ INC + HOVAL,
    data = COL.OLD,
    listw = listw,
    method = "eigen"
  )

# summarize model fit with tidiers
tidy(crime_sar)
tidy(crime_sar, conf.int = TRUE)
glance(crime_sar)
augment(crime_sar)

# fit another model
crime_sem <- errorsarlm(CRIME ~ INC + HOVAL, data = COL.OLD, listw)

# summarize model fit with tidiers
tidy(crime_sem)
tidy(crime_sem, conf.int = TRUE)
glance(crime_sem)
augment(crime_sem)

# fit another model
crime_sac <- sacsarlm(CRIME ~ INC + HOVAL, data = COL.OLD, listw)

# summarize model fit with tidiers
tidy(crime_sac)
tidy(crime_sac, conf.int = TRUE)
glance(crime_sac)
augment(crime_sac)
```

---

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 across 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

freq	Vector of frequencies at which the spectral density is estimated.
spec	Vector (for univariate series) or matrix (for multivariate series) of estimates of the spectral density at frequencies corresponding to freq.

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.speedglm   *Tidy a(n) speedglm 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 across 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 'speedglm'
tidy(x, conf.int = FALSE, conf.level = 0.95, exponentiate = FALSE, ...)
```

Arguments

x	A speedglm object returned from `speedglm::speedglm()`.
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.
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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

`speedglm::speedglm()`

Other speedlm tidiers: `augment.speedlm()`, `glance.speedglm()`, `glance.speedlm()`, `tidy.speedlm()`

Examples

```
# load libraries for models and data
library(speedglm)

# generate data
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)
)

# fit model
fit <- speedglm(lot1 ~ log(u), data = clotting, family = Gamma(log))

# summarize model fit with tidiers
tidy(fit)
glance(fit)
```

---

tidy.speedlm   *Tidy a(n) speedlm 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 across 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 'speedlm'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A speedlm object returned from speedglm::speedlm().
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`statistic`	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
`std.error`	The standard error of the regression term.
`term`	The name of the regression term.

See Also

[speedglm::speedlm()](#), [tidy.lm()](#)

Other speedlm tidiers: [augment.speedlm()](#), [glance.speedglm()](#), [glance.speedlm()](#), [tidy.speedglm()](#)

Examples

```
# load modeling library
library(speedglm)

# fit model
mod <- speedlm(mpg ~ wt + qsec, data = mtcars, fitted = TRUE)

# summarize model fit with tidiers
tidy(mod)
glance(mod)
augment(mod)
```

---

tidy.summary.glht   *Tidy a(n) summary.glht 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 across 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.glht'
tidy(x, ...)
```

Arguments

x	A summary.glht object created by calling multcomp::summary.glht() on a glht object created with multcomp::glht().
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble() with columns:

contrast	Levels being compared.
estimate	The estimated value of the regression term.
null.value	Value to which the estimate is compared.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.

See Also

tidy(), multcomp::summary.glht(), multcomp::glht()

Other multcomp tidiers: tidy.cld(), tidy.confint.glht(), tidy.glht()

Examples

```
# load libraries for models and data
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.summary.lm   *Tidy a(n) summary.lm 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 across 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.lm'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A summary.lm object created by stats::summary.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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it
  will be ignored.
- augment() methods will warn when supplied a newdata argument if it will
  be ignored.

Details

The tidy.summary.lm() method is a potentially useful alternative to tidy.lm(). For instance, if
users have already converted large lm objects into their leaner summary.lm equivalents to conserve
memory.

Value

A tibble::tibble() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

tidy(), stats::summary.lm()

Other lm tidiers: augment.glm(), augment.lm(), glance.glm(), glance.lm(), glance.summary.lm(),
glance.svyglm(), tidy.glm(), tidy.lm(), tidy.lm.beta(), tidy.mlm()

Examples

```
# fit model
mod <- lm(mpg ~ wt + qsec, data = mtcars)
modsumm <- summary(mod)

# summarize model fit with tidiers
tidy(mod, conf.int = TRUE)

# equivalent to the above
tidy(modsumm, conf.int = TRUE)

glance(mod)

# mostly the same, except for a few missing columns
glance(modsumm)
```

---

tidy.summary_emm   *Tidy a(n) summary_emm 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 across 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_emm'
tidy(x, null.value = NULL, ...)
```

Arguments

x	A `summary_emm` object.
null.value	Value to which estimate is compared.
...	Additional arguments passed to `emmeans::summary.emmGrid()` or `lsmeans::summary.ref.grid()`. **Cautionary note**: misspecified arguments may be silently ignored!

Details

Returns a data frame with one observation for each estimated marginal mean, and one column for each combination of factors. When the input is a contrast, each row will contain one estimated contrast.

There are a large number of arguments that can be passed on to `emmeans::summary.emmGrid()` or `lsmeans::summary.ref.grid()`.

Value

A `tibble::tibble()` with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
contrast	Levels being compared.
den.df	Degrees of freedom of the denominator.
df	Degrees of freedom used by this term in the model.
null.value	Value to which the estimate is compared.
num.df	Degrees of freedom.
p.value	The two-sided p-value associated with the observed statistic.
std.error	The standard error of the regression term.
level1	One level of the factor being contrasted

level2	The other level of the factor being contrasted
term	Model term in joint tests
estimate	Expected marginal mean
statistic	T-ratio statistic or F-ratio statistic

See Also

tidy(), emmeans::ref_grid(), emmeans::emmeans(), emmeans::contrast()

Other emmeans tidiers: tidy.emmGrid(), tidy.lsmobj(), tidy.ref.grid()

Examples

```
# load libraries for models and data
library(emmeans)

# linear model for sales of oranges per day
oranges_lm1 <- lm(sales1 ~ price1 + price2 + day + store, data = oranges)

# reference grid; see vignette("basics", package = "emmeans")
oranges_rg1 <- ref_grid(oranges_lm1)
td <- tidy(oranges_rg1)
td

# marginal averages
marginal <- emmeans(oranges_rg1, "day")
tidy(marginal)

# contrasts
tidy(contrast(marginal))
tidy(contrast(marginal, method = "pairwise"))

# plot confidence intervals
library(ggplot2)

ggplot(tidy(marginal, conf.int = TRUE), aes(day, estimate)) +
  geom_point() +
  geom_errorbar(aes(ymin = conf.low, ymax = conf.high))

# by multiple prices
by_price <- emmeans(oranges_lm1, "day",
  by = "price2",
  at = list(
    price1 = 50, price2 = c(40, 60, 80),
    day = c("2", "3", "4")
  )
)

by_price

tidy(by_price)
```

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

# joint_tests
tidy(joint_tests(oranges_lm1))
```

---

tidy.survdiff   *Tidy a(n) survdiff 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 across 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 `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 `conf.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

exp   Weighted expected number of events in each group.

N   Number of subjects in each group.

obs   weighted observed number of events 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.pyears(), glance.survdiff(), glance.survexp(), glance.survfit(), glance.survreg(), tidy.aareg(), tidy.cch(), tidy.coxph(), tidy.pyears(), tidy.survexp(), tidy.survfit(), tidy.survreg()

Examples

```
# load libraries for models and data
library(survival)

# fit model
s <- survdiff(
  Surv(time, status) ~ pat.karno + strata(inst),
  data = lung
)

# summarize model fit with tidiers
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 across 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 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 conf.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

`n.risk`	Number of individuals at risk at time zero.
`time`	Point in time.
`estimate`	Estimate survival

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

```
# load libraries for models and data
library(survival)

# fit model
sexpfit <- survexp(
  futime ~ 1,
  rmap = list(
    sex = "male",
    year = accept.dt,
    age = (accept.dt - birth.dt)
  ),
  method = "conditional",
  data = jasa
)

# summarize model fit with tidiers
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 across 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()`.
...	For glance.survfit(), additional arguments passed to `summary()`. Otherwise ignored.

Value

A `tibble::tibble()` with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
n.censor	Number of censored events.
n.event	Number of events at time t.
n.risk	Number of individuals at risk at time zero.
std.error	The standard error of the regression term.
time	Point in time.
estimate	estimate of survival or cumulative incidence rate when multistate
state	state if multistate survfit object input
strata	strata if stratified survfit object input

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

```
# load libraries for models and data
library(survival)

# fit model
cfit <- coxph(Surv(time, status) ~ age + sex, lung)
sfit <- survfit(cfit)

# summarize model fit with tidiers + visualization
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 across 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, conf.int = FALSE, ...)
```

Arguments

x	An survreg object returned from `survival::survreg()`.
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.
conf.int	Logical indicating whether or not to include a confidence interval in the tidied output. 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A [tibble::tibble()](#) with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.
p.value	The two-sided p-value associated with the observed statistic.
statistic	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
std.error	The standard error of the regression term.
term	The name of the regression term.

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

```
# load libraries for models and data
library(survival)
```

```
# fit model
sr <- survreg(
  Surv(futime, fustat) ~ ecog.ps + rx,
  ovarian,
  dist = "exponential"
)

# summarize model fit with tidiers + visualization
tidy(sr)
augment(sr, ovarian)
glance(sr)

# coefficient plot
td <- tidy(sr, conf.int = TRUE)

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.svyglm   *Tidy a(n) svyglm 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 across 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 'svyglm'
tidy(x, conf.int = FALSE, conf.level = 0.95, exponentiate = FALSE, ...)
```

Arguments

x	A svyglm object returned from `survey::svyglm()`.
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.
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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

See Also

`survey::svyglm()`, `stats::glm()`

---

tidy.svyolr   *Tidy a(n) svyolr 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 across 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 'svyolr'
tidy(x, conf.int = FALSE, conf.level = 0.95, exponentiate = FALSE, ...)
```

Arguments

x	A svyolr object returned from `survey::svyolr()`.
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.
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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

The `tidy.svyolr()` tidier is a light wrapper around [`tidy.polr()`](). However, the implementation for p-value calculation in [`tidy.polr()`]() is both computationally intensive and specific to that model, so the `p.values` argument to `tidy.svyolr()` is currently ignored, and will raise a warning when passed.

Value

A [`tibble::tibble()`]() with columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`statistic`	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
`std.error`	The standard error of the regression term.
`term`	The name of the regression term.

See Also

[tidy](), [survey::svyolr()]()

Other ordinal tidiers: [augment.clm](), [augment.polr](), [glance.clm](), [glance.clmm](), [glance.polr](), [glance.svyolr](), [tidy.clm](), [tidy.clmm](), [tidy.polr]()

Examples

```
library(broom)
library(survey)

data(api)
dclus1 <- svydesign(id = ~dnum, weights = ~pw, data = apiclus1, fpc = ~fpc)
dclus1 <- update(dclus1, mealcat = cut(meals, c(0, 25, 50, 75, 100)))

m <- svyolr(mealcat ~ avg.ed + mobility + stype, design = dclus1)

m

tidy(m, conf.int = TRUE)
```

---

tidy.systemfit   *Tidy a(n) systemfit 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 across 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 'systemfit'
tidy(x, conf.int = TRUE, conf.level = 0.95, ...)
```

Arguments

x	A systemfit object produced by a call to [systemfit::systemfit()]().
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.
...	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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Details

This tidy method works with any model objects of class systemfit. Default returns a tibble of six columns.

Value

A [tibble::tibble()]() with columns:

conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
estimate	The estimated value of the regression term.

p.value	The two-sided p-value associated with the observed statistic.
std.error	The standard error of the regression term.
term	The name of the regression term.

See Also

tidy(), systemfit::systemfit()

Examples

```
set.seed(27)

# load libraries for models and data
library(systemfit)

# generate data
df <- data.frame(
  X = rnorm(100),
  Y = rnorm(100),
  Z = rnorm(100),
  W = rnorm(100)
)

# fit model
fit <- systemfit(formula = list(Y ~ Z, W ~ X), data = df, method = "SUR")

# summarize model fit with tidiers
tidy(fit)
tidy(fit, conf.int = TRUE)
```

---

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 across models but is usually self-evident. If a model has several distinct types of components, you will need to specify which components to return.

Deprecated. Please use tibble::as_tibble() instead.

Usage

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

Arguments

x   A base::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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

Directly calls [`tibble::as_tibble()`](tibble::as_tibble()) on a base::table object.

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::pivot_longer()`](tidyr::pivot_longer()).

See Also

[`tibble::as_tibble.table()`](tibble::as_tibble.table())

---

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 across 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Details

`series` column is only present for multivariate `ts` objects.

Value

A [`tibble::tibble()`](#) with columns:

index	Index (i.e. date or time) for a 'ts' or 'zoo' object.
series	Name of the series (present only for multivariate time series).
value	The value/estimate of the component. Results from data reshaping.

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 across 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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

adj.p.value	P-value adjusted for multiple comparisons.
conf.high	Upper bound on the confidence interval for the estimate.
conf.low	Lower bound on the confidence interval for the estimate.
contrast	Levels being compared.
estimate	The estimated value of the regression term.
null.value	Value to which the estimate is compared.
term	The name of the regression term.

See Also

`tidy()`, `stats::TukeyHSD()`

Other anova tidiers: `glance.anova()`, `glance.aov()`, `tidy.anova()`, `tidy.aov()`, `tidy.aovlist()`, `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.varest   *Tidy a(n) varest 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 across 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 'varest'
tidy(x, conf.int = FALSE, conf.level = 0.95, ...)
```

Arguments

x	A varest object produced by a call to vars::VAR().
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.
...	For glance(), additional arguments passed to summary(). Otherwise ignored.

Details

The tibble has one row for each term in the regression. The component column 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 phi. At least one term will have been used to model the precision phi.

The vars package does not include a confint method and does not report confidence intervals for varest objects. Setting the tidy argument conf.int = TRUE will return a warning.

Value

A [tibble::tibble()](#) with columns:

`conf.high`	Upper bound on the confidence interval for the estimate.
`conf.low`	Lower bound on the confidence interval for the estimate.
`estimate`	The estimated value of the regression term.
`p.value`	The two-sided p-value associated with the observed statistic.
`statistic`	The value of a T-statistic to use in a hypothesis that the regression term is non-zero.
`std.error`	The standard error of the regression term.
`term`	The name of the regression term.
`component`	Whether a particular term was used to model the mean or the precision in the regression. See details.

See Also

[tidy()](#), [vars::VAR()](#)

Examples

```
# load libraries for models and data
library(vars)

# load data
data("Canada", package = "vars")

# fit models
mod <- VAR(Canada, p = 1, type = "both")

# summarize model fit with tidiers
tidy(mod)
glance(mod)
```

---

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 across 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 `zoo::zoo()`.

...   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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

Value

A `tibble::tibble()` with columns:

index   Index (i.e. date or time) for a 'ts' or 'zoo' object.

series   Name of the series (present only for multivariate time series).

value   The value/estimate of the component. Results from data reshaping.

See Also

`tidy()`, `zoo::zoo()`

Other time series tidiers: `tidy.acf()`, `tidy.spec()`, `tidy.ts()`

Examples

```
# load libraries for models and data
library(zoo)
library(ggplot2)

set.seed(1071)

# generate data
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)

# summarize model fit with tidiers + visualization
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 [interp::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 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, they throw an error.

Usage

```
tidy_irlba(x, ...)
```

Arguments

x   A list returned from [irlba::irlba()]().

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                    tionary 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.lvel = 0.9, all computation will proceed
                    using conf.level = 0.95. Two exceptions here are:

                      • tidy() methods will warn when supplied an exponentiate argument if it
                        will be ignored.
                      • augment() methods will warn when supplied a newdata argument if it will
                        be ignored.

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"`, `"scores"`, 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 principal component.
value	The score of the observation for that particular principal component. That is, the location of the observation in PCA space.

If `matrix` is `"v"`, `"rotation"`, `"loadings"` 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"`, `"eigenvalues"` or `"pcs"`, the columns are:

PC	An integer vector indicating the principal component.
std.dev	Standard deviation explained by this PC.
percent	Fraction of variation explained by this component (a numeric value between 0 and 1).
cumulative	Cumulative fraction of variation explained by principle components up to this component (a numeric value between 0 and 1).

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()](#)

Examples

```
library(modeldata)
data(hpc_data)

mat <- scale(as.matrix(hpc_data[, 2:5]))
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(class = hpc_data$class[row]) %>%
  ggplot(aes(class, value)) +
  geom_boxplot() +
  facet_wrap(~PC, scale = "free_y")
```

---

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 interp::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 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, they throw an error.

Usage

```
tidy_optim(x, ...)
```

Arguments

x   A list returned from stats::optim().

...   Additional arguments. Not used. Needed to match generic signature only. **Cau-
                  tionary 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.lvel = 0.9, all computation will proceed
                  using conf.level = 0.95. Two exceptions here are:

                  • tidy() methods will warn when supplied an exponentiate argument if it
                    will be ignored.
                  • augment() methods will warn when supplied a newdata argument if it will
                    be ignored.

Value

A tibble::tibble() with columns:

`parameter`	The parameter being modeled.
`std.error`	The standard error of the regression term.
`value`	The value/estimate of the component. Results from data reshaping.

`std.error` is only provided as a column if the Hessian is calculated.

Note

This function assumes that the provided objective function is a negative log-likelihood function. Results will be invalid if an incorrect function is supplied.

tidy(o) glance(o)

See Also

tidy(), stats::optim()

Other list tidiers: glance_optim(), list_tidiers, tidy_irlba(), tidy_svd(), tidy_xyz()

Examples

```
f <- function(x) (x[1] - 2)^2 + (x[2] - 3)^2 + (x[3] - 8)^2
o <- optim(c(1, 1, 1), f)
```

---

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()](svd()) and interp::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 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, they throw an error.

Usage

```
tidy_svd(x, matrix = "u", ...)
```

Arguments

x	A list with components u, d, v returned by [base::svd()]().
matrix	Character specifying which component of the PCA should be tidied.

- `"u"`, `"samples"`, `"scores"`, or `"x"`: returns information about the map from the original space into principle components space.
- `"v"`, `"rotation"`, `"loadings"` or `"variables"`: returns information about the map from principle components space back into the original space.
- `"d"`, `"eigenvalues"` or `"pcs"`: returns information about the eigenvalues.

...	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.lvel = 0.9`, all computation will proceed using `conf.level = 0.95`. Two exceptions here are:

- `tidy()` methods will warn when supplied an `exponentiate` argument if it will be ignored.
- `augment()` methods will warn when supplied a `newdata` argument if it will be ignored.

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"`, `"scores"`, 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 principal component.
value	The score of the observation for that particular principal component. That is, the location of the observation in PCA space.

If matrix is `"v"`, `"rotation"`, `"loadings"` 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"`, `"eigenvalues"` or `"pcs"`, the columns are:

PC	An integer vector indicating the principal component.
std.dev	Standard deviation explained by this PC.

percent	Fraction of variation explained by this component (a numeric value between 0 and 1).
cumulative	Cumulative fraction of variation explained by principle components up to this component (a numeric value between 0 and 1).

See Also

[base::svd()](#)

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

Other list tidiers: [glance_optim()](#), [list_tidiers](#), [tidy_irlba()](#), [tidy_optim()](#), [tidy_xyz()](#)

Examples

```
library(modeldata)
data(hpc_data)

mat <- scale(as.matrix(hpc_data[, 2:5]))
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(class = hpc_data$class[row]) %>%
  ggplot(aes(class, 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 interp::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 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, they throw an error.

xyz lists (lists where x and y are vectors 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 interp::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.lvel = 0.9, all computation will proceed using conf.level = 0.95. Two exceptions here are:

- tidy() methods will warn when supplied an exponentiate argument if it will be ignored.
- augment() methods will warn when supplied a newdata argument if it will be ignored.

Value

A tibble::tibble with vector columns x, y and z.

See Also

tidy(), graphics::persp(), graphics::image(), interp::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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