Package 'GGally'

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Title Extension to 'ggplot2'

Type Package

LazyLoad yes

LazyData true

URL https://ggobi.github.io/ggally, https://github.com/ggobi/ggally

BugReports https://github.com/ggobi/ggally/issues

Description The R package 'ggplot2' is a plotting system based on the grammar of graphics. 'GGally' extends 'ggplot2' by adding several functions to reduce the complexity of combining geometric objects with transformed data. Some of these functions include a pairwise plot matrix, a two group pairwise plot matrix, a parallel coordinates plot, a survival plot, and several functions to plot networks.

Depends R (>= 3.1)

Imports ggplot2 (>= 2.2.0), grid, gtable (>= 0.2.0), plyr (>= 1.8.3), progress, RColorBrewer, reshape (>= 0.8.5), utils

Suggests broom (>= 0.4.0), chemometrics, geosphere (>= 1.5-1), igraph (>= 1.0.1), intergraph (>= 2.0-2), maps (>= 3.1.0), mapproj, network (>= 1.12.0), scagnostics, scales (>= 0.4.0), sna (>= 2.3-2), survival, packagedocs (>= 0.4.0), rmarkdown, roxygen2, testthat

RoxygenNote 6.0.1

VignetteBuilder packagedocs

NeedsCompilation no

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R topics documented:

+.gg *Modify a ggmatrix object by adding an ggplot2 object to all plots*

Description

This operator allows you to add ggplot2 objects to a ggmatrix object.

Usage

```
## S3 method for class 'gg'
e1 + e2
```

Arguments

e1	An object of class ggplot or theme
e2	A component to add to e1

Details

If the first object is an object of class ggmatrix, you can add the following types of objects, and it will return a modified ggplot object.

- theme: update plot theme

The + operator completely replaces elements with elements from e2.

See Also

+.gg and theme

Examples

```
data(tips, package = "reshape")
pm <- ggpairs(tips[, 2:3])
## change to black and white theme
pm + ggplot2::theme_bw()
## change to linedraw theme
# pm + ggplot2::theme_linedraw()
## change to custom theme
# pm + ggplot2::theme(panel.background = ggplot2::element_rect(fill = "lightblue"))
## add a list of information
extra <- list(ggplot2::theme_bw(), ggplot2::labs(caption = "My caption!"))
pm + extra
```

add_ref_boxes *Add reference boxes around each cell of the glyphmap.*

Description

Add reference boxes around each cell of the glyphmap.

Usage

```
add_ref_boxes(data, var_fill = NULL, color = "white", size = 0.5,
  fill = NA, ...)
```

Arguments

data	A glyphmap structure.
var_fill	Variable name to use to set the fill color
color	Set the color to draw in, default is "white"
size	Set the line size, default is 0.5
fill	fill value used if var_fill is NULL
...	other arguments passed onto geom_rect

add_ref_lines *Add reference lines for each cell of the glyphmap.*

Description

Add reference lines for each cell of the glyphmap.

Usage

```
add_ref_lines(data, color = "white", size = 1.5, ...)
```

Arguments

data	A glyphmap structure.
color	Set the color to draw in, default is "white"
size	Set the line size, default is 1.5
...	other arguments passed onto geom_line

`australia_PISA2012` *Programme for International Student Assesment (PISA) 2012 Data for Australia*

Description

About PISA

Usage

```
data(australia_PISA2012)
```

Format

A data frame with 8247 rows and 32 variables

Details

The Programme for International Student Assessment (PISA) is a triennial international survey which aims to evaluate education systems worldwide by testing the skills and knowledge of 15-year-old students. To date, students representing more than 70 economies have participated in the assessment.

While 65 economies took part in the 2012 study, this data set only contains information from the country of Australia.

- gender : Factor w/ 2 levels "female","male": 1 1 2 2 2 1 1 1 2 1 ...
- age : Factor w/ 4 levels "4","5","6","7": 2 2 2 4 3 1 2 2 2 2 ...
- homework : num 5 5 9 3 2 3 4 3 5 1 ...
- desk : num 1 0 1 1 1 1 1 1 1 1 ...
- room : num 1 1 1 1 1 1 1 1 1 1 ...
- study : num 1 1 1 1 1 1 1 1 1 1 ...
- computer : num 1 1 1 1 1 1 1 1 1 1 ...
- software : num 1 1 1 1 1 1 1 1 1 1 ...
- internet : num 1 1 1 1 1 1 1 1 1 1 ...
- literature : num 0 0 1 0 1 1 1 1 1 0 ...
- poetry : num 0 0 1 0 1 1 0 1 1 1 ...
- art : num 1 0 1 0 1 1 0 1 1 1 ...
- textbook : num 1 1 1 1 1 0 1 1 1 1 ...
- dictionary : num 1 1 1 1 1 1 1 1 1 1 ...
- dishwasher : num 1 1 1 1 0 1 1 1 1 1 ...
- PV1MATH : num 562 565 602 520 613 ...
- PV2MATH : num 569 557 594 507 567 ...

- PV3MATH : num 555 553 552 501 585 ...
- PV4MATH : num 579 538 526 521 596 ...
- PV5MATH : num 548 573 619 547 603 ...
- PV1READ : num 582 617 650 554 605 ...
- PV2READ : num 571 572 608 560 557 ...
- PV3READ : num 602 560 594 517 627 ...
- PV4READ : num 572 564 575 564 597 ...
- PV5READ : num 585 565 620 572 598 ...
- PV1SCIE : num 583 627 668 574 639 ...
- PV2SCIE : num 579 600 665 612 635 ...
- PV3SCIE : num 593 574 620 571 666 ...
- PV4SCIE : num 567 582 592 598 700 ...
- PV5SCIE : num 587 625 656 662 670 ...
- SENWGT_STU : num 0.133 0.133 0.141 0.141 0.141 ...
- possessions: num 10 8 12 9 11 11 10 12 12 11 ...

Source

http://www.oecd.org/pisa/pisaproducts/database-cbapisa2012.htm

---

`brew_colors` *RColorBrewer Set1 colors*

Description

RColorBrewer Set1 colors

Usage

```
brew_colors(col)
```

Arguments

`col`	standard color name used to retrieve hex color value

broomify *Broomify a model*

Description

broom::augment a model and add broom::glance and broom::tidy output as attributes. X and Y variables are also added.

Usage

```
broomify(model, lmStars = TRUE)
```

Arguments

model	model to be sent to broom::augment, broom::glance, and broom::tidy
lmStars	boolean that determines if stars are added to labels

Value

broom::augmented data frame with the broom::glance data.frame and broom::tidy data.frame as 'broom_glance' and 'broom_tidy' attributes respectively. var_x and var_y variables are also added as attributes

Examples

```
data(mtcars)
model <- stats::lm(mpg ~ wt + qsec + am, data = mtcars)
broomified_model <- broomify(model)
str(broomified_model)
```

find_plot_type *Find Plot Types*

Description

Retrieves the type of plot for the specific columns

Usage

```
find_plot_type(col1Name, col2Name, type1, type2, isAllNa, allowDiag)
```

Arguments

col1Name	x column name
col2Name	y column name
type1	x column type
type2	y column type
isAllNa	is.na(data)
allowDiag	allow for diag values to be returned

Author(s)

Barret Schloerke <schloerke@gmail.com>

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flea *Historical data used for classification examples.*

Description

This data contains physical measurements on three species of flea beetles.

Usage

```
data(flea)
```

Format

A data frame with 74 rows and 7 variables

Details

- species Ch. concinna, Ch. heptapotamica, Ch. heikertingeri
- tars1 width of the first joint of the first tarsus in microns
- tars2 width of the second joint of the first tarsus in microns
- head the maximal width of the head between the external edges of the eyes in 0.01 mm
- aede1 the maximal width of the aedeagus in the fore-part in microns
- aede2 the front angle of the aedeagus (1 unit = 7.5 degrees)
- aede3 the aedeagus width from the side in microns

References

Lubischew, A. A. (1962), On the Use of Discriminant Functions in Taxonomy, Biometrics 18:455-477.

fn_switch *Function switch*

Description

Function that allows you to call different functions based upon an aesthetic variable value.

Usage

```
fn_switch(types, mapping_val = "y")
```

Arguments

types	list of functions that follow the ggmatrix function standard: `function(data, mapping, ...){ #make gg` One key should be a 'default' key for a default switch case.
mapping_val	mapping value to switch on. Defaults to the 'y' variable of the aesthetics list.

Examples

```
ggnostic_continuous_fn <- fn_switch(list(
  default = ggally_points,
  .fitted = ggally_points,
  .se.fit = ggally_nostic_se_fit,
  .resid = ggally_nostic_resid,
  .hat = ggally_nostic_hat,
  .sigma = ggally_nostic_sigma,
  .cooksd = ggally_nostic_cooksd,
  .std.resid = ggally_nostic_std_resid
))

ggnostic_combo_fn <- fn_switch(list(
  default = ggally_box_no_facet,
  fitted = ggally_box_no_facet,
  .se.fit = ggally_nostic_se_fit,
  .resid = ggally_nostic_resid,
  .hat = ggally_nostic_hat,
  .sigma = ggally_nostic_sigma,
  .cooksd = ggally_nostic_cooksd,
  .std.resid = ggally_nostic_std_resid
))
```

getPlot *getPlot*

Description

Retrieves the ggplot object at the desired location.

Usage

```
getPlot(pm, i, j)

## S3 method for class 'ggmatrix'
pm[i, j, ...]
```

Arguments

pm	ggmatrix object to select from
i	row from the top
j	column from the left
...	ignored

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
plotMatrix2 <- ggpairs(tips[, 3:2], upper = list(combo = "denstrip"))
plotMatrix2[1, 2]
```

ggally_barDiag *Plots the Bar Plots by Using Diagonal*

Description

Plots the bar plots by using Diagonal.

Usage

```
ggally_barDiag(data, mapping, ..., rescale = FALSE)
```

Arguments

data	data set using
mapping	aesthetics being used
...	other arguments are sent to geom_bar
rescale	boolean to decide whether or not to rescale the count output. Only applies to numeric data

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_barDiag(tips, mapping = ggplot2::aes(x = day))
ggally_barDiag(tips, mapping = ggplot2::aes(x = tip), binwidth = 0.25)
```

---

ggally_blank *Blank*

Description

Draws nothing.

Usage

```
ggally_blank(...)

ggally_blankDiag(...)
```

Arguments

...	other arguments ignored

Details

Makes a "blank" ggplot object that will only draw white space

Author(s)

Barret Schloerke <schloerke@gmail.com>

ggally_box *Plots the Box Plot*

Description

Make a box plot with a given data set. `ggally_box_no_facet` will be a single panel plot, while `ggally_box` will be a faceted plot

Usage

```
ggally_box(data, mapping, ...)

ggally_box_no_facet(data, mapping, ...)
```

Arguments

`data`	data set using
`mapping`	aesthetics being used
`...`	other arguments being supplied to geom_boxplot

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_box(tips, mapping = ggplot2::aes(x = total_bill, y = sex))
ggally_box(tips, mapping = ggplot2::aes_string(x = "total_bill", y = "sex"))
ggally_box(
  tips,
  mapping        = ggplot2::aes_string(y = "total_bill", x = "sex", color = "sex"),
  outlier.colour = "red",
  outlier.shape  = 13,
  outlier.size   = 8
)
```

ggally_cor *Correlation from the Scatter Plot*

Description

Estimate correlation from the given data.

Usage

```
ggally_cor(data, mapping, alignPercent = 0.6, method = "pearson",
  use = "complete.obs", corAlignPercent = NULL, corMethod = NULL,
  corUse = NULL, ...)
```

Arguments

data	data set using
mapping	aesthetics being used
alignPercent	right align position of numbers. Default is 60 percent across the horizontal
method	method supplied to cor function
use	use supplied to cor function
corAlignPercent	deprecated. Use parameter alignPercent
corMethod	deprecated. Use parameter method
corUse	deprecated. Use parameter use
...	other arguments being supplied to geom_text

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_cor(tips, mapping = ggplot2::aes_string(x = "total_bill", y = "tip"))
ggally_cor(
  tips,
  mapping = ggplot2::aes(x = total_bill, y = tip),
  size = 15,
  colour = I("red")
)
ggally_cor(
  tips,
  mapping = ggplot2::aes_string(x = "total_bill", y = "tip", color = "sex"),
  size = 5
)
```

---

ggally_density *Plots the Scatter Density Plot*

Description

Make a scatter density plot from a given data.

Usage

```
ggally_density(data, mapping, ...)
```

Arguments

data	data set using
mapping	aesthetics being used
...	parameters sent to either stat_density2d or geom_density2d

Details

The aesthetic "fill" determines whether or not stat_density2d (filled) or geom_density2d (lines) is used.

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_density(tips, mapping = ggplot2::aes(x = total_bill, y = tip))
ggally_density(tips, mapping = ggplot2::aes_string(x = "total_bill", y = "tip"))
ggally_density(
  tips,
  mapping = ggplot2::aes_string(x = "total_bill", y = "tip", fill = "..level..")
)
ggally_density(
  tips,
  mapping = ggplot2::aes_string(x = "total_bill", y = "tip", fill = "..level..")
) + ggplot2::scale_fill_gradient(breaks = c(0.05, 0.1, 0.15, 0.2))
```

---

ggally_densityDiag *Plots the Density Plots by Using Diagonal*

Description

Plots the density plots by using Diagonal.

Usage

```
ggally_densityDiag(data, mapping, ..., rescale = FALSE)
```

Arguments

data	data set using
mapping	aesthetics being used.
...	other arguments sent to stat_density
rescale	boolean to decide whether or not to rescale the count output

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_densityDiag(tips, mapping = ggplot2::aes(x = total_bill))
ggally_densityDiag(tips, mapping = ggplot2::aes(x = total_bill, color = day))
```

---

ggally_denstrip *Plots a tile plot with facets*

Description

Make Tile Plot as densely as possible.

Usage

```
ggally_denstrip(data, mapping, ...)
```

Arguments

data	data set using
mapping	aesthetics being used
...	other arguments being sent to stat_bin

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_denstrip(tips, mapping = ggplot2::aes(x = total_bill, y = sex))
ggally_denstrip(tips, mapping = ggplot2::aes_string(x = "total_bill", y = "sex"))
ggally_denstrip(
  tips,
  mapping = ggplot2::aes_string(x = "sex", y = "tip", binwidth = "0.2")
) + ggplot2::scale_fill_gradient(low = "grey80", high = "black")
```

ggally_diagAxis *Internal Axis Labeling Plot for ggpairs*

Description

This function is used when `axisLabels == "internal"`.

Usage

```
ggally_diagAxis(data, mapping, label = mapping$x, labelSize = 5,
  labelXPercent = 0.5, labelYPercent = 0.55, labelHJust = 0.5,
  labelVJust = 0.5, gridLabelSize = 4, ...)
```

Arguments

`data`	dataset being plotted
`mapping`	aesthetics being used (x is the variable the plot will be made for)
`label`	title to be displayed in the middle. Defaults to `mapping$x`
`labelSize`	size of variable label
`labelXPercent`	percent of horizontal range
`labelYPercent`	percent of vertical range
`labelHJust`	hjust supplied to label
`labelVJust`	vjust supplied to label
`gridLabelSize`	size of grid labels
`...`	other arguments for geom_text

Author(s)

Jason Crowley <crowley.jason.s@gmail.com> and Barret Schloerke

Examples

```
data(tips, package = "reshape")
ggally_diagAxis(tips, ggplot2::aes(x=tip))
ggally_diagAxis(tips, ggplot2::aes(x=sex))
```

ggally_dot *Plots the Box Plot with Dot*

Description

Add jittering with the box plot. `ggally_dot_no_facet` will be a single panel plot, while `ggally_dot` will be a faceted plot

Usage

```
ggally_dot(data, mapping, ...)

ggally_dot_no_facet(data, mapping, ...)
```

Arguments

`data`	data set using
`mapping`	aesthetics being used
`...`	other arguments being supplied to geom_jitter

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_dot(tips, mapping = ggplot2::aes(x = total_bill, y = sex))
ggally_dot(tips, mapping = ggplot2::aes_string(x = "total_bill", y = "sex"))
ggally_dot(
  tips,
  mapping = ggplot2::aes_string(y = "total_bill", x = "sex", color = "sex")
)
ggally_dot(
  tips,
 mapping = ggplot2::aes_string(y = "total_bill", x = "sex", color = "sex", shape = "sex")
) + ggplot2::scale_shape(solid=FALSE)
```

ggally_dot_and_box *Plots either Box Plot or Dot Plots*

Description

Place box plots or dot plots on the graph

Usage

```
ggally_dot_and_box(data, mapping, ..., boxPlot = TRUE)
```

Arguments

data	data set using
mapping	aesthetics being used
...	parameters passed to either geom_jitter or geom_boxplot
boxPlot	boolean to decide to plot either box plots (TRUE) or dot plots (FALSE)

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_dot_and_box(
  tips,
  mapping = ggplot2::aes(x = total_bill, y = sex, color = sex),
  boxPlot = TRUE
)
ggally_dot_and_box(
  tips,
  mapping = ggplot2::aes(x = total_bill, y = sex, color = sex),
  boxPlot = FALSE
)
```

ggally_facetbar *Plots the Bar Plots Faceted by Conditional Variable*

Description

X variables are plotted using geom_bar and faceted by the Y variable.

Usage

```
ggally_facetbar(data, mapping, ...)
```

Arguments

data	data set using
mapping	aesthetics being used
...	other arguments are sent to geom_bar

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_facetbar(tips, ggplot2::aes(x = sex, y = smoker, fill = time))
ggally_facetbar(tips, ggplot2::aes(x = smoker, y = sex, fill = time))
```

---

ggally_facetdensity *Plots the density plots by faceting*

Description

Make density plots by displaying subsets of the data in different panels.

Usage

```
ggally_facetdensity(data, mapping, ...)
```

Arguments

data	data set using
mapping	aesthetics being used
...	other arguments being sent to stat_density

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_facetdensity(tips, mapping = ggplot2::aes(x = total_bill, y = sex))
ggally_facetdensity(
  tips,
  mapping = ggplot2::aes_string(y = "total_bill", x = "sex", color = "sex")
)
```

ggally_facetdensitystrip *Plots a density plot with facets or a tile plot with facets*

Description

Make Tile Plot as densely as possible.

Usage

```
ggally_facetdensitystrip(data, mapping, ..., den_strip = FALSE)
```

Arguments

data	data set using
mapping	aesthetics being used
...	other arguments being sent to either geom_histogram or stat_density
den_strip	boolean to decide whether or not to plot a density strip(TRUE) or a facet density(FALSE) plot.

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
example(ggally_facetdensity)
example(ggally_denstrip)
```

ggally_facethist *Plots the Histograms by Faceting*

Description

Make histograms by displaying subsets of the data in different panels.

Usage

```
ggally_facethist(data, mapping, ...)
```

Arguments

data	data set using
mapping	aesthetics being used
...	parameters sent to stat_bin()

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_facethist(tips, mapping = ggplot2::aes(x = tip, y = sex))
ggally_facethist(tips, mapping = ggplot2::aes_string(x = "tip", y = "sex"), binwidth = 0.1)
```

---

ggally_na *NA plot*

Description

Draws a large NA in the middle of the plotting area. This plot is useful when all X or Y data is NA

Usage

```
ggally_na(data = NULL, mapping = NULL, size = 10, color = "grey20", ...)

ggally_naDiag(...)
```

Arguments

data	ignored
mapping	ignored
size	size of the geom_text 'NA'
color	color of the geom_text 'NA'
...	other arguments sent to geom_text

Author(s)

Barret Schloerke <schloerke@gmail.com>

`ggally_nostic_cooksd` *ggnostic - Cook's distance*

Description

A function to display `stats::cooks.distance`.

Usage

```
ggally_nostic_cooksd(data, mapping, ..., linePosition = 4/nrow(data),
  lineColor = brew_colors("grey"), lineType = 2)
```

Arguments

`data, mapping, ..., lineColor, lineType`	parameters supplied to `ggally_nostic_line`
`linePosition`	4 / n is the general cutoff point for Cook's Distance

Details

A line is added at 4 / n to display the general cutoff point for Cook's Distance.

Reference: Cook, R. Dennis; Weisberg, Sanford (1982). Residuals and Influence in Regression. New York, NY: Chapman & Hall. ISBN 0-412-24280-X

Value

ggplot2 plot object

See Also

`stats::cooks.distance`

Examples

```
dt <- broomify(stats::lm(mpg ~ wt + qsec + am, data = mtcars))
ggally_nostic_cooksd(dt, ggplot2::aes(wt, .cooksd))
```

`ggally_nostic_hat` *ggnostic - leverage points*

Description

A function to display stats::influence's hat information against a given explanatory variable.

Usage

```
ggally_nostic_hat(data, mapping, ..., linePosition = 2 *
  sum(data[[deparse(mapping$y)]])/nrow(data), lineColor = brew_colors("grey"),
  lineSize = 0.5, lineAlpha = 1, lineType = 2,
  avgLinePosition = sum(data[[deparse(mapping$y)]])/nrow(data),
  avgLineColor = brew_colors("grey"), avgLineSize = lineSize,
  avgLineAlpha = lineAlpha, avgLineType = 1)
```

Arguments

`data, mapping, ...`
: supplied directly to `ggally_nostic_line`

`linePosition, lineColor, lineSize, lineAlpha, lineType`
: parameters supplied to ggplot2::`geom_line` for the cutoff line

`avgLinePosition, avgLineColor, avgLineSize, avgLineAlpha, avgLineType`
: parameters supplied to ggplot2::`geom_line` for the average line

Details

As stated in `stats::influence` documentation:

hat: a vector containing the diagonal of the 'hat' matrix.

The diagonal elements of the 'hat' matrix describe the influence each response value has on the fitted value for that same observation.

A suggested "cutoff" line is added to the plot at a height of 2 * p / n and an expected line at a height of p / n. If either `linePosition` or `avgLinePosition` is `NULL`, the respective line will not be drawn.

Value

ggplot2 plot object

See Also

`stats::influence`

Examples

```
dt <- broomify(stats::lm(mpg ~ wt + qsec + am, data = mtcars))
ggally_nostic_hat(dt, ggplot2::aes(wt, .hat))
```

`ggally_nostic_line` *ggnostic -background line with geom*

Description

If a non-null `linePosition` value is given, a line will be drawn before the given `continuous_geom` or `combo_geom` is added to the plot.

Usage

```
ggally_nostic_line(data, mapping, ..., linePosition = NULL,
  lineColor = "red", lineSize = 0.5, lineAlpha = 1, lineType = 1,
  continuous_geom = ggplot2::geom_point, combo_geom = ggplot2::geom_boxplot,
  mapColorToFill = TRUE)
```

Arguments

`data, mapping`	supplied directly to `ggplot2::ggplot(data, mapping)`
`...`	parameters supplied to `continuous_geom` or `combo_geom`
`linePosition, lineColor, lineSize, lineAlpha, lineType`	parameters supplied to `ggplot2::geom_line`
`continuous_geom`	ggplot2 geom that is executed after the line is (possibly) added and if the x data is continuous
`combo_geom`	ggplot2 geom that is executed after the line is (possibly) added and if the x data is discrete
`mapColorToFill`	boolean to determine if combo plots should cut the color mapping to the fill mapping

Details

Functions with a color in their name have different default color behavior.

Value

ggplot2 plot object

ggally_nostic_resid *ggnostic - residuals*

Description

If non-null pVal and sigma values are given, confidence interval lines will be added to the plot at the specified pVal percentiles of a N(0, sigma) distribution.

Usage

```
ggally_nostic_resid(data, mapping, ..., linePosition = 0,
  lineColor = brew_colors("grey"), lineSize = 0.5, lineAlpha = 1,
  lineType = 1, lineConfColor = brew_colors("grey"),
  lineConfSize = lineSize, lineConfAlpha = lineAlpha, lineConfType = 2,
  pVal = c(0.025, 0.975), sigma = attr(data, "broom_glance")$sigma,
  se = TRUE, method = "auto")
```

Arguments

data, mapping, ...	parameters supplied to ggally_nostic_line
linePosition, lineColor, lineSize, lineAlpha, lineType	parameters supplied to ggplot2::geom_line
lineConfColor, lineConfSize, lineConfAlpha, lineConfType	parameters supplied to the confidence interval lines
pVal	percentiles of a N(0, sigma) distribution to be drawn
sigma	sigma value for the pVal percentiles
se	boolean to determine if the confidence intervals should be displayed
method	parameter supplied to ggplot2::geom_smooth. Defaults to "auto"

Value

ggplot2 plot object

See Also

stats::residuals

Examples

```
dt <- broomify(stats::lm(mpg ~ wt + qsec + am, data = mtcars))
ggally_nostic_resid(dt, ggplot2::aes(wt, .resid))
```

ggally_nostic_se_fit *ggnostic - fitted value standard error*

Description

A function to display stats::predict's standard errors

Usage

```
ggally_nostic_se_fit(data, mapping, ..., lineColor = brew_colors("grey"),
  linePosition = NULL)
```

Arguments

data, mapping, ..., lineColor	parameters supplied to ggally_nostic_line
linePosition	base comparison for a perfect fit

Details

As stated in stats::predict documentation:

If the logical 'se.fit' is 'TRUE', standard errors of the predictions are calculated. If the numeric argument 'scale' is set (with optional "df"), it is used as the residual standard deviation in the computation of the standard errors, otherwise this is extracted from the model fit.

Since the se.fit is TRUE and scale is unset by default, the standard errors are extracted from the model fit.

A base line of 0 is added to give reference to a perfect fit.

Value

ggplot2 plot object

See Also

stats::influence

Examples

```
dt <- broomify(stats::lm(mpg ~ wt + qsec + am, data = mtcars))
ggally_nostic_se_fit(dt, ggplot2::aes(wt, .se.fit))
```

`ggally_nostic_sigma` *ggnostic - leave one out model sigma*

Description

A function to display `stats::influence`'s sigma value.

Usage

```
ggally_nostic_sigma(data, mapping, ..., lineColor = brew_colors("grey"),
  linePosition = attr(data, "broom_glance")$sigma)
```

Arguments

`data, mapping, ..., lineColor`	parameters supplied to `ggally_nostic_line`
`linePosition`	line that is drawn in the background of the plot. Defaults to the overall model's sigma value.

Details

As stated in `stats::influence` documentation:

sigma: a vector whose i-th element contains the estimate of the residual standard deviation obtained when the i-th case is dropped from the regression. (The approximations needed for GLMs can result in this being 'NaN'.)

A line is added to display the overall model's sigma value. This gives a baseline for comparison

Value

ggplot2 plot object

See Also

`stats::influence`

Examples

```
dt <- broomify(stats::lm(mpg ~ wt + qsec + am, data = mtcars))
ggally_nostic_sigma(dt, ggplot2::aes(wt, .sigma))
```

ggally_nostic_std_resid *ggnostic - standardized residuals*

Description

If non-null `pVal` and `sigma` values are given, confidence interval lines will be added to the plot at the specified `pVal` locations of a N(0, 1) distribution.

Usage

```
ggally_nostic_std_resid(data, mapping, ..., sigma = 1)
```

Arguments

`data, mapping, ...`	parameters supplied to `ggally_nostic_resid`
`sigma`	sigma value for the `pVal` percentiles. Set to 1 for standardized residuals

Value

ggplot2 plot object

See Also

`stats::rstandard`

Examples

```
dt <- broomify(stats::lm(mpg ~ wt + qsec + am, data = mtcars))
ggally_nostic_std_resid(dt, ggplot2::aes(wt, .std.resid))
```

ggally_points *Plots the Scatter Plot*

Description

Make a scatter plot with a given data set.

Usage

```
ggally_points(data, mapping, ...)
```

Arguments

data	data set using
mapping	aesthetics being used
...	other arguments are sent to geom_point

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(mtcars)
ggally_points(mtcars, mapping = ggplot2::aes(x = disp, y = hp))
ggally_points(mtcars, mapping = ggplot2::aes_string(x = "disp", y = "hp"))
ggally_points(
  mtcars,
  mapping = ggplot2::aes_string(
    x     = "disp",
    y     = "hp",
    color = "as.factor(cyl)",
    size  = "gear"
  )
)
```

---

ggally_ratio *Plots a mosaic plot*

Description

Plots the mosaic plot by using fluctuation.

Usage

```
ggally_ratio(data, mapping = do.call(ggplot2::aes_string,
  as.list(colnames(data)[1:2])), ..., floor = 0, ceiling = NULL)
```

Arguments

data	data set using
mapping	aesthetics being used. Only x and y will used and both are required
...	passed to geom_tile(...)
floor	don't display cells smaller than this value
ceiling	max value to scale frequencies. If any frequency is larger than the ceiling, the fill color is displayed darker than other rectangles

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_ratio(tips, ggplot2::aes(sex, day))
ggally_ratio(tips, ggplot2::aes(sex, day)) + ggplot2::coord_equal()
# only plot tiles greater or equal to 20 and scale to a max of 50
ggally_ratio(
  tips, ggplot2::aes(sex, day),
  floor = 20, ceiling = 50
) + ggplot2::theme(aspect.ratio = 4/2)
```

---

ggally_smooth *Plots the Scatter Plot with Smoothing*

Description

Add a smoothed condition mean with a given scatter plot.

Usage

```
ggally_smooth(data, mapping, ..., method = "lm")

ggally_smooth_loess(data, mapping, ...)

ggally_smooth_lm(data, mapping, ...)
```

Arguments

data	data set using
mapping	aesthetics being used
...	other arguments to add to geom_point
method	method parameter supplied to geom_smooth

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
ggally_smooth(tips, mapping = ggplot2::aes(x = total_bill, y = tip))
ggally_smooth(tips, mapping = ggplot2::aes_string(x = "total_bill", y = "tip"))
ggally_smooth(tips, mapping = ggplot2::aes_string(x = "total_bill", y = "tip", color = "sex"))
```

ggally_text *GGplot Text*

Description

Plot text for a plot.

Usage

```
ggally_text(label, mapping = ggplot2::aes(color = "black"), xP = 0.5,
  yP = 0.5, xrange = c(0, 1), yrange = c(0, 1), ...)
```

Arguments

label	text that you want to appear
mapping	aesthetics that don't relate to position (such as color)
xP	horizontal position percentage
yP	vertical position percentage
xrange	range of the data around it. Only nice to have if plotting in a matrix
yrange	range of the data around it. Only nice to have if plotting in a matrix
...	other arguments for geom_text

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
ggally_text("Example 1")
ggally_text("Example\nTwo", mapping = ggplot2::aes(size = 15), color = I("red"))
```

ggcoef *ggcoef - Plot Model Coefficients with broom and ggplot2*

Description

Plot the coefficients of a model with **broom** and **ggplot2**.

Usage

```
ggcoef(x, mapping = aes_string(y = "term", x = "estimate"), conf.int = TRUE,
  conf.level = 0.95, exponentiate = FALSE, exclude_intercept = FALSE,
  vline = TRUE, vline_intercept = "auto", vline_color = "gray50",
  vline_linetype = "dotted", vline_size = 1, errorbar_color = "gray25",
  errorbar_height = 0, errorbar_linetype = "solid", errorbar_size = 0.5,
  ...)
```

Arguments

x	a model object to be tidied with tidy or a data frame (see Details)
mapping	default aesthetic mapping
conf.int	display confidence intervals as error bars?
conf.level	level of confidence intervals (passed to tidy if x is not a data frame)
exponentiate	if TRUE, x-axis will be logarithmic (also passed to tidy if x is not a data frame)
exclude_intercept	should the intercept be excluded from the plot?
vline	print a vertical line?
vline_intercept	xintercept for the vertical line. "auto" for x = 0 (or x = 1 if exponentiate is TRUE)
vline_color	color of the vertical line
vline_linetype	line type of the vertical line
vline_size	size of the vertical line
errorbar_color	color of the error bars
errorbar_height	height of the error bars
errorbar_linetype	line type of the error bars
errorbar_size	size of the error bars
...	additional arguments sent to geom_point

Examples

```
library(broom)
reg <- lm(Sepal.Length ~ Sepal.Width + Petal.Length + Petal.Width, data = iris)
ggcoef(reg)

d <- as.data.frame(Titanic)
reg2 <- glm(Survived ~ Sex + Age + Class, family = binomial, data = d, weights = d$Freq)
ggcoef(reg2, exponentiate = TRUE)
ggcoef(reg2, exponentiate = TRUE, exclude_intercept = TRUE, errorbar_height = .2, color = "blue")
```

---

ggcorr *ggcorr - Plot a correlation matrix with ggplot2*

Description

Function for making a correlation matrix plot, using ggplot2. The function is directly inspired by Tian Zheng and Yu-Sung Su's corrplot function in the 'arm' package. Please visit http://github.com/briatte/ggcorr for the latest version of ggcorr, and see the vignette at https://briatte.github.io/ggcorr/ for many examples of how to use it.

Usage

```
ggcorr(data, method = c("pairwise", "pearson"), cor_matrix = NULL,
  nbreaks = NULL, digits = 2, name = "", low = "#3B9AB2",
  mid = "#EEEEEE", high = "#F21A00", midpoint = 0, palette = NULL,
  geom = "tile", min_size = 2, max_size = 6, label = FALSE,
  label_alpha = FALSE, label_color = "black", label_round = 1,
  label_size = 4, limits = c(-1, 1), drop = is.null(limits) ||
  identical(limits, FALSE), layout.exp = 0, legend.position = "right",
  legend.size = 9, ...)
```

Arguments

data	a data frame or matrix containing numeric (continuous) data. If any of the columns contain non-numeric data, they will be dropped with a warning.
method	a vector of two character strings. The first value gives the method for computing covariances in the presence of missing values, and must be (an abbreviation of) one of "everything", "all.obs", "complete.obs", "na.or.complete" or "pairwise.complete.obs". The second value gives the type of correlation coefficient to compute, and must be one of "pearson", "kendall" or "spearman". See cor for details. Defaults to c("pairwise", "pearson").
cor_matrix	the named correlation matrix to use for calculations. Defaults to the correlation matrix of data when data is supplied.
nbreaks	the number of breaks to apply to the correlation coefficients, which results in a categorical color scale. See 'Note'. Defaults to NULL (no breaks, continuous scaling).
digits	the number of digits to show in the breaks of the correlation coefficients: see cut for details. Defaults to 2.
name	a character string for the legend that shows the colors of the correlation coefficients. Defaults to "" (no legend name).
low	the lower color of the gradient for continuous scaling of the correlation coefficients. Defaults to "#3B9AB2" (blue).
mid	the midpoint color of the gradient for continuous scaling of the correlation coefficients. Defaults to "#EEEEEE" (very light grey).
high	the upper color of the gradient for continuous scaling of the correlation coefficients. Defaults to "#F21A00" (red).
midpoint	the midpoint value for continuous scaling of the correlation coefficients. Defaults to 0.
palette	if nbreaks is used, a ColorBrewer palette to use instead of the colors specified by low, mid and high. Defaults to NULL.
geom	the geom object to use. Accepts either "tile", "circle", "text" or "blank".
min_size	when geom has been set to "circle", the minimum size of the circles. Defaults to 2.
max_size	when geom has been set to "circle", the maximum size of the circles. Defaults to 6.

label	whether to add correlation coefficients to the plot. Defaults to FALSE.
label_alpha	whether to make the correlation coefficients increasingly transparent as they come close to 0. Also accepts any numeric value between 0 and 1, in which case the level of transparency is set to that fixed value. Defaults to FALSE (no transparency).
label_color	the color of the correlation coefficients. Defaults to "grey75".
label_round	the decimal rounding of the correlation coefficients. Defaults to 1.
label_size	the size of the correlation coefficients. Defaults to 4.
limits	bounding of color scaling for correlations, set limits = NULL or FALSE to remove
drop	if using nbreaks, whether to drop unused breaks from the color scale. Defaults to FALSE (recommended).
layout.exp	a multiplier to expand the horizontal axis to the left if variable names get clipped. Defaults to 0 (no expansion).
legend.position	where to put the legend of the correlation coefficients: see theme for details. Defaults to "bottom".
legend.size	the size of the legend title and labels, in points: see theme for details. Defaults to 9.
...	other arguments supplied to geom_text for the diagonal labels.

Note

Recommended values for the nbreaks argument are 3 to 11, as values above 11 are visually difficult to separate and are not supported by diverging ColorBrewer palettes.

Author(s)

Francois Briatte, with contributions from Amos B. Elberg and Barret Schloerke

See Also

cor and corrplot in the arm package.

Examples

```
# Basketball statistics provided by Nathan Yau at Flowing Data.
dt <- read.csv("http://datasets.flowingdata.com/ppg2008.csv")

# Default output.
ggcorr(dt[, -1])

# Labelled output, with coefficient transparency.
ggcorr(dt[, -1],
       label = TRUE,
       label_alpha = TRUE)
```

```
# Custom options.
ggcorr(
  dt[, -1],
  name = expression(rho),
  geom = "circle",
  max_size = 10,
  min_size = 2,
  size = 3,
  hjust = 0.75,
  nbreaks = 6,
  angle = -45,
  palette = "PuOr" # colorblind safe, photocopy-able
)

# Supply your own correlation matrix
ggcorr(
  data = NULL,
  cor_matrix = cor(dt[, -1], use = "pairwise")
)
```

---

ggduo *ggduo - A ggplot2 generalized pairs plot for two columns sets of a data.frame*

Description

Make a matrix of plots with a given data set with two different column sets

Usage

```
ggduo(data, mapping = NULL, columnsX = 1:ncol(data),
  columnsY = 1:ncol(data), title = NULL, types = list(continuous =
  "smooth_loess", comboVertical = "box_no_facet", comboHorizontal = "facethist",
  discrete = "ratio"), axisLabels = c("show", "none"),
  columnLabelsX = colnames(data[columnsX]),
  columnLabelsY = colnames(data[columnsY]), labeller = "label_value",
  switch = NULL, xlab = NULL, ylab = NULL, showStrips = NULL,
  legend = NULL, cardinality_threshold = 15, legends = stop("deprecated"))
```

Arguments

`data`	data set using. Can have both numerical and categorical data.
`mapping`	aesthetic mapping (besides x and y). See `aes()`. If `mapping` is numeric, `columns` will be set to the `mapping` value and `mapping` will be set to `NULL`.
`columnsX, columnsY`	which columns are used to make plots. Defaults to all columns.
`title, xlab, ylab`	title, x label, and y label for the graph

types see Details

axisLabels either "show" to display axisLabels or "none" for no axis labels

columnLabelsX, columnLabelsY
label names to be displayed. Defaults to names of columns being used.

labeller labeller for facets. See labellers. Common values are "label_value" (default) and "label_parsed".

switch switch parameter for facet_grid. See ggplot2::facet_grid. By default, the labels are displayed on the top and right of the plot. If "x", the top labels will be displayed to the bottom. If "y", the right-hand side labels will be displayed to the left. Can also be set to "both"

showStrips boolean to determine if each plot's strips should be displayed. NULL will default to the top and right side plots only. TRUE or FALSE will turn all strips on or off respectively.

legend May be the two objects described below or the default NULL value. The legend position can be moved by using ggplot2's theme element pm + theme(legend.position = "bottom")

a numeric vector of length 2 provides the location of the plot to use the legend for the plot matrix's legend. Such as legend = c(3,5) which will use the legend from the plot in the third row and fifth column

a single numeric value provides the location of a plot according to the display order. Such as legend = 3 in a plot matrix with 2 rows and 5 columns displayed by column will return the plot in position c(1,2)

a object from grab_legend() a predetermined plot legend that will be displayed directly

cardinality_threshold
maximum number of levels allowed in a character / factor column. Set this value to NULL to not check factor columns. Defaults to 15

legends deprecated

Details

types is a list that may contain the variables 'continuous', 'combo', 'discrete', and 'na'. Each element of the list may be a function or a string. If a string is supplied, it must implement one of the following options:

continuous exactly one of ('points', 'smooth', 'smooth_loess', 'density', 'cor', 'blank'). This option is used for continuous X and Y data.

comboHorizontal exactly one of ('box', 'box_no_facet', 'dot', 'dot_no_facet', 'facethist', 'facetdensity', 'denstrip', 'blank'). This option is used for either continuous X and categorical Y data or categorical X and continuous Y data.

comboVertical exactly one of ('box', 'box_no_facet', 'dot', 'dot_no_facet', 'facethist', 'facetdensity', 'denstrip', 'blank'). This option is used for either continuous X and categorical Y data or categorical X and continuous Y data.

discrete exactly one of ('facetbar', 'ratio', 'blank'). This option is used for categorical X and Y data.

na exactly one of ('na', 'blank'). This option is used when all X data is NA, all Y data is NA, or either all X or Y data is NA.

If 'blank' is ever chosen as an option, then ggduo will produce an empty plot.

If a function is supplied as an option, it should implement the function api of `function(data, mapping, ...){#make ggplo`
If a specific function needs its parameters set, `wrap(fn, param1 = val1, param2 = val2)` the function with its parameters.

Examples

```
# small function to display plots only if it's interactive
p_ <- GGally::print_if_interactive

data(baseball, package = "plyr")

# Keep players from 1990-1995 with at least one at bat
# Add how many singles a player hit
# (must do in two steps as X1b is used in calculations)
dt <- transform(
  subset(baseball, year >= 1990 & year <= 1995 & ab > 0),
  X1b = h - X2b - X3b - hr
)
# Add
#  the player's batting average,
#  the player's slugging percentage,
#  and the player's on base percentage
# Make factor a year, as each season is discrete
dt <- transform(
  dt,
  batting_avg = h / ab,
  slug = (X1b + 2*X2b + 3*X3b + 4*hr) / ab,
  on_base = (h + bb + hbp) / (ab + bb + hbp),
  year = as.factor(year)
)


pm <- ggduo(
  dt,
  c("year", "g", "ab", "lg"),
  c("batting_avg", "slug", "on_base"),
  mapping = ggplot2::aes(color = lg)
)
# Prints, but
#   there is severe over plotting in the continuous plots
#   the labels could be better
#   want to add more hitting information
p_(pm)

# address overplotting issues and add a title
pm <- ggduo(
  dt,
  c("year", "g", "ab", "lg"),
  c("batting_avg", "slug", "on_base"),
  columnLabelsX = c("year", "player game count", "player at bat count", "league"),
  columnLabelsY = c("batting avg", "slug %", "on base %"),
```

```
  title = "Baseball Hitting Stats from 1990-1995",
  mapping = ggplot2::aes(color = lg),
  types = list(
    # change the shape and add some transparency to the points
    continuous = wrap("smooth_loess", alpha = 0.50, shape = "+")
  ),
  showStrips = FALSE
);

p_(pm)



# Example derived from:
## R Data Analysis Examples | Canonical Correlation Analysis.  UCLA: Institute for Digital
##   Research and Education.
##   from http://www.stats.idre.ucla.edu/r/dae/canonical-correlation-analysis
##   (accessed May 22, 2017).
# "Example 1. A researcher has collected data on three psychological variables, four
#  academic variables (standardized test scores) and gender for 600 college freshman.
#  She is interested in how the set of psychological variables relates to the academic
#  variables and gender. In particular, the researcher is interested in how many
#  dimensions (canonical variables) are necessary to understand the association between
#  the two sets of variables."
data(psychademic)
summary(psychademic)

(psych_variables <- attr(psychademic, "psychology"))
(academic_variables <- attr(psychademic, "academic"))

## Within correlation
p_(ggpairs(psychademic, columns = psych_variables))
p_(ggpairs(psychademic, columns = academic_variables))

## Between correlation
loess_with_cor <- function(data, mapping, ..., method = "pearson") {
  x <- eval(mapping$x, data)
  y <- eval(mapping$y, data)
  cor <- cor(x, y, method = method)
  ggally_smooth_loess(data, mapping, ...) +
    ggplot2::geom_label(
      data = data.frame(
        x = min(x, na.rm = TRUE),
        y = max(y, na.rm = TRUE),
        lab = round(cor, digits = 3)
      ),
      mapping = ggplot2::aes(x = x, y = y, label = lab),
      hjust = 0, vjust = 1,
      size = 5, fontface = "bold",
      inherit.aes = FALSE # do not inherit anything from the ...
    )
}
pm <- ggduo(
```

```
  psychademic,
  rev(psych_variables), academic_variables,
  types = list(continuous = loess_with_cor),
  showStrips = FALSE
)
suppressWarnings(p_(pm)) # ignore warnings from loess

# add color according to sex
pm <- ggduo(
  psychademic,
  mapping = ggplot2::aes(color = sex),
  rev(psych_variables), academic_variables,
  types = list(continuous = loess_with_cor),
  showStrips = FALSE,
  legend = c(5,2)
)
suppressWarnings(p_(pm))


# add color according to sex
pm <- ggduo(
  psychademic,
  mapping = ggplot2::aes(color = motivation),
  rev(psych_variables), academic_variables,
  types = list(continuous = loess_with_cor),
  showStrips = FALSE,
  legend = c(5,2)
) +
  ggplot2::theme(legend.position = "bottom")
suppressWarnings(p_(pm))
```

---

ggfacet *ggfacet - single ggplot2 plot matrix with facet_grid*

Description

ggfacet - single ggplot2 plot matrix with facet_grid

Usage

```
ggfacet(data, mapping = NULL, columnsX = 1:ncol(data),
  columnsY = 1:ncol(data), fn = ggally_points, ...,
  columnLabelsX = names(data[columnsX]),
  columnLabelsY = names(data[columnsY]), xlab = NULL, ylab = NULL,
  title = NULL, scales = "free")
```

Arguments

data	data.frame that contains all columns to be displayed. This data will be melted before being passed into the function fn

mapping	aesthetic mapping (besides x and y). See aes()
columnsX	columns to be displayed in the plot matrix
columnsY	rows to be displayed in the plot matrix
fn	function to be executed. Similar to ggpairs and ggduo, the function may either be a string identifier or a real function that wrap understands.
...	extra arguments passed directly to fn
columnLabelsX, columnLabelsY	column and row labels to display in the plot matrix
xlab, ylab, title	plot matrix labels
scales	parameter supplied to ggplot2::facet_grid. Default behavior is "free"

Examples

```
# Small function to display plots only if it's interactive
p_ <- GGally::print_if_interactive
library(chemometrics)
data(NIR)
NIR_sub <- data.frame(NIR$yGlcEtOH, NIR$xNIR[,1:3])
str(NIR_sub)
x_cols <- c("X1115.0", "X1120.0", "X1125.0")
y_cols <- c("Glucose", "Ethanol")

# using ggduo directly
p <- ggduo(NIR_sub, x_cols, y_cols, types = list(continuous = "points"))
p_(p)

# using ggfacet
p <- ggfacet(NIR_sub, x_cols, y_cols)
p_(p)

# add a smoother
p <- ggfacet(NIR_sub, x_cols, y_cols, fn = 'smooth_loess')
p_(p)
# same output
p <- ggfacet(NIR_sub, x_cols, y_cols, fn = ggally_smooth_loess)
p_(p)

# Change scales to be the same in for every row and for every column
p <- ggfacet(NIR_sub, x_cols, y_cols, scales = "fixed")
p_(p)
```

---

gglegend *Plot only legend of plot function*

Description

Plot only legend of plot function

Usage

```
gglegend(fn)
```

Arguments

fn	this value is passed directly to an empty wrap call. Please see ?wrap for more details.

Value

a function that when called with arguments will produce the legend of the plotting function supplied.

Examples

```
# display regular plot
ggally_points(iris, ggplot2::aes(Sepal.Length, Sepal.Width, color = Species))

# Make a function that will only print the legend
points_legend <- gglegend(ggally_points)
points_legend(iris, ggplot2::aes(Sepal.Length, Sepal.Width, color = Species))

# produce the sample legend plot, but supply a string that 'wrap' understands
same_points_legend <- gglegend("points")
identical(
  attr(attr(points_legend, "fn"), "original_fn"),
  attr(attr(same_points_legend, "fn"), "original_fn")
)

# Complicated examples
custom_legend <- wrap(gglegend("points"), size = 6)
custom_legend(iris, ggplot2::aes(Sepal.Length, Sepal.Width, color = Species))

# Use within ggpairs
pm <- ggpairs(
  iris, 1:2,
  mapping = ggplot2::aes(color = Species),
  upper = list(continuous = gglegend("points"))
)
# pm

# Place a legend in a specific location
pm <- ggpairs(iris, 1:2, mapping = ggplot2::aes(color = Species))
# Make the legend
pm[1,2] <- points_legend(iris, ggplot2::aes(Sepal.Width, Sepal.Length, color = Species))
pm
```

ggmatrix *ggmatrix - A ggplot2 Matrix*

Description

Make a generic matrix of ggplot2 plots.

Usage

```
ggmatrix(plots, nrow, ncol, xAxisLabels = NULL, yAxisLabels = NULL,
  title = NULL, xlab = NULL, ylab = NULL, byrow = TRUE,
  showStrips = NULL, showAxisPlotLabels = TRUE,
  showXAxisPlotLabels = TRUE, showYAxisPlotLabels = TRUE, labeller = NULL,
  switch = NULL, xProportions = NULL, yProportions = NULL, data = NULL,
  gg = NULL, legend = NULL)
```

Arguments

plots	list of plots to be put into matrix
nrow, ncol	number of rows and columns
xAxisLabels, yAxisLabels	strip titles for the x and y axis respectively. Set to NULL to not be displayed
title, xlab, ylab	title, x label, and y label for the graph. Set to NULL to not be displayed
byrow	boolean that determines whether the plots should be ordered by row or by column
showStrips	boolean to determine if each plot's strips should be displayed. NULL will default to the top and right side plots only. TRUE or FALSE will turn all strips on or off respectively.
showAxisPlotLabels, showXAxisPlotLabels, showYAxisPlotLabels	booleans that determine if the plots axis labels are printed on the X (bottom) or Y (left) part of the plot matrix. If showAxisPlotLabels is set, both showXAxisPlotLabels and showYAxisPlotLabels will be set to the given value.
labeller	labeller for facets. See labellers. Common values are "label_value" (default) and "label_parsed".
switch	switch parameter for facet_grid. See ggplot2::facet_grid. By default, the labels are displayed on the top and right of the plot. If "x", the top labels will be displayed to the bottom. If "y", the right-hand side labels will be displayed to the left. Can also be set to "both"
xProportions, yProportions	Value to change how much area is given for each plot. Either NULL (default), numeric value matching respective length, or grid::unit object with matching respective length
data	data set using. This is the data to be used in place of 'ggally_data' if the plot is a string to be evaluated at print time

gg ggplot2 theme objects to be applied to every plot

legend May be the two objects described below or the default NULL value. The legend position can be moved by using ggplot2's theme element `pm + theme(legend.position = "bottom")`

a numeric vector of length 2 provides the location of the plot to use the legend for the plot matrix's legend. Such as `legend = c(3,5)` which will use the legend from the plot in the third row and fifth column

a single numeric value provides the location of a plot according to the display order. Such as `legend = 3` in a plot matrix with 2 rows and 5 columns displayed by column will return the plot in position `c(1,2)`

a object from `grab_legend()` a predetermined plot legend that will be displayed directly

Memory usage

Now that the print.ggmatrix method uses a large gtable object, rather than print each plot independently, memory usage may be of concern. From small tests, memory usage flutters around `object.size(data) * 0.3 * length(plots)`. So, for a 80Mb random noise dataset with 100 plots, about 2.4 Gb of memory needed to print. For the 3.46 Mb diamonds dataset with 100 plots, about 100 Mb of memory was needed to print. The benefits of using the ggplot2 format greatly outweigh the price of about 20

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
# small function to display plots only if it's interactive
p_ <- GGally::print_if_interactive

plotList <- list()
for (i in 1:6) {
  plotList[[i]] <- ggally_text(paste("Plot #", i, sep = ""))
}
pm <- ggmatrix(
  plotList,
  2, 3,
  c("A", "B", "C"),
  c("D", "E"),
  byrow = TRUE
)
p_(pm)

pm <- ggmatrix(
  plotList,
  2, 3,
  xAxisLabels = c("A", "B", "C"),
  yAxisLabels = NULL,
  byrow = FALSE,
  showXAxisPlotLabels = FALSE
```

```
)
p_(pm)
```

---

ggmatrix_gtable *Print ggmatrix object*

Description

Specialized method to print the ggmatrix object-

Usage

```
ggmatrix_gtable(pm, ..., progress = interactive() && (pm$ncol * pm$nrow) > 15,
  progress_format = " plot: [:plot_i,:plot_j] [:bar]:percent est::eta ")
```

Arguments

pm	ggmatrix object to be plotted
...	ignored
progress	boolean to determine if a progress bar should be displayed. This defaults to interactive sessions only
progress_format	string supplied directly to progress::progress_bar(format = progress_format). Defaults to display the plot number, progress bar, percent complete, and estimated time to finish.

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
data(tips, package = "reshape")
pm <- ggpairs(tips, c(1,3,2), mapping = ggplot2::aes_string(color = "sex"))
ggmatrix_gtable(pm)
```

ggnet *ggnet - Plot a network with ggplot2*

Description

Function for plotting network objects using ggplot2, now replaced by the ggnet2 function, which provides additional control over plotting parameters. Please visit http://github.com/briatte/ggnet for the latest version of ggnet2, and https://briatte.github.io/ggnet for a vignette that contains many examples and explanations.

Usage

```
ggnet(net, mode = "fruchtermanreingold", layout.par = NULL,
  layout.exp = 0, size = 9, alpha = 1, weight = "none",
  weight.legend = NA, weight.method = weight, weight.min = NA,
  weight.max = NA, weight.cut = FALSE, group = NULL, group.legend = NA,
  node.group = group, node.color = NULL, node.alpha = alpha,
  segment.alpha = alpha, segment.color = "grey50", segment.label = NULL,
  segment.size = 0.25, arrow.size = 0, arrow.gap = 0,
  arrow.type = "closed", label = FALSE, label.nodes = label,
  label.size = size/2, label.trim = FALSE, legend.size = 9,
  legend.position = "right", names = c("", ""), quantize.weights = FALSE,
  subset.threshold = 0, top8.nodes = FALSE, trim.labels = FALSE, ...)
```

Arguments

net	an object of class network, or any object that can be coerced to this class, such as an adjacency or incidence matrix, or an edge list: see edgeset.constructors and network for details. If the object is of class igraph and the intergraph package is installed, it will be used to convert the object: see asNetwork for details.
mode	a placement method from those provided in the sna package: see gplot.layout for details. Also accepts the names of two numeric vertex attributes of net, or a matrix of numeric coordinates, in which case the first two columns of the matrix are used. Defaults to the Fruchterman-Reingold force-directed algorithm.
layout.par	options to be passed to the placement method, as listed in gplot.layout. Defaults to NULL.
layout.exp	a multiplier to expand the horizontal axis if node labels get clipped: see expand_range for details. Defaults to 0 (no expansion).
size	size of the network nodes. If the nodes are weighted, their area is proportionally scaled up to the size set by size. Defaults to 9.
alpha	a level of transparency for nodes, vertices and arrows. Defaults to 1.
weight	the weighting method for the nodes, which might be a vertex attribute or a vector of size values. Also accepts "indegree", "outdegree", "degree" or "freeman" to size the nodes by their unweighted degree centrality ("degree"

	and "freeman" are equivalent): see degree for details. All node weights must be positive. Defaults to "none" (no weighting).
weight.legend	the name to assign to the legend created by weight. Defaults to NA (no name).
weight.method	see weight
weight.min	whether to subset the network to nodes with a minimum size, based on the values of weight. Defaults to NA (preserves all nodes).
weight.max	whether to subset the network to nodes with a maximum size, based on the values of weight. Defaults to NA (preserves all nodes).
weight.cut	whether to cut the size of the nodes into a certain number of quantiles. Accepts TRUE, which tries to cut the sizes into quartiles, or any positive numeric value, which tries to cut the sizes into that many quantiles. If the size of the nodes do not contain the specified number of distinct quantiles, the largest possible number is used. See quantile and cut for details. Defaults to FALSE (does nothing).
group	the groups of the nodes, either as a vector of values or as a vertex attribute. If set to mode on a bipartite network, the nodes will be grouped as "actor" if they belong to the primary mode and "event" if they belong to the secondary mode.
group.legend	the name to assign to the legend created by group.
node.group	see group
node.color	a vector of character strings to color the nodes with, holding as many colors as there are levels in node.group. Defaults to NULL, which will assign grayscale colors to each group.
node.alpha	transparency of the nodes. Inherits from alpha.
segment.alpha	the level of transparency of the edges. Defaults to alpha, which defaults to 1.
segment.color	the color of the edges, as a color value, a vector of color values, or as an edge attribute containing color values. Defaults to "grey50".
segment.label	the labels to plot at the middle of the edges, as a single value, a vector of values, or as an edge attribute. Defaults to NULL (no edge labels).
segment.size	the size of the edges, in points, as a single numeric value, a vector of values, or as an edge attribute. Defaults to 0.25.
arrow.size	the size of the arrows for directed network edges, in points. See arrow for details. Defaults to 0 (no arrows).
arrow.gap	a setting aimed at improving the display of edge arrows by plotting slightly shorter edges. Accepts any value between 0 and 1, where a value of 0.05 will generally achieve good results when the size of the nodes is reasonably small. Defaults to 0 (no shortening).
arrow.type	the type of the arrows for directed network edges. See arrow for details. Defaults to "closed".
label	whether to label the nodes. If set to TRUE, nodes are labeled with their vertex names. If set to a vector that contains as many elements as there are nodes in net, nodes are labeled with these. If set to any other vector of values, the nodes are labeled only when their vertex name matches one of these values. Defaults to FALSE (no labels).

label.nodes	see label
label.size	the size of the node labels, in points, as a numeric value, a vector of numeric values, or as a vertex attribute containing numeric values. Defaults to size / 2 (half the maximum node size), which defaults to 6.
label.trim	whether to apply some trimming to the node labels. Accepts any function that can process a character vector, or a strictly positive numeric value, in which case the labels are trimmed to a fixed-length substring of that length: see substr for details. Defaults to FALSE (does nothing).
legend.size	the size of the legend symbols and text, in points. Defaults to 9.
legend.position	the location of the plot legend(s). Accepts all legend.position values supported by theme. Defaults to "right".
names	deprecated: see group.legend and size.legend
quantize.weights	deprecated: see weight.cut
subset.threshold	deprecated: see weight.min
top8.nodes	deprecated: this functionality was experimental and has been removed entirely from ggnet
trim.labels	deprecated: see label.trim
...	other arguments passed to the geom_text object that sets the node labels: see geom_text for details.

Details

The degree centrality measures that can be produced through the weight argument will take the directedness of the network into account, but will be unweighted. To compute weighted network measures, see the tnet package by Tore Opsahl (help("tnet", package = "tnet")).

Author(s)

Moritz Marbach and Francois Briatte, with help from Heike Hoffmann, Pedro Jordano and Ming-Yu Liu

See Also

ggnet2 in this package, gplot in the sna package, and plot.network in the network package

Examples

```
library(network)

# random adjacency matrix
x           <- 10
ndyads      <- x * (x - 1)
density     <- x / ndyads
m           <- matrix(0, nrow = x, ncol = x)
```

```
dimnames(m) <- list(letters[ 1:x ], letters[ 1:x ])
m[ row(m) != col(m) ] <- runif(ndyads) < density
m

# random undirected network
n <- network::network(m, directed = FALSE)
n

ggnet(n, label = TRUE, alpha = 1, color = "white", segment.color = "black")

# random groups
g <- sample(letters[ 1:3 ], 10, replace = TRUE)

# color palette
p <- c("a" = "steelblue", "b" = "forestgreen", "c" = "tomato")

ggnet(n, node.group = g, node.color = p, label = TRUE, color = "white")

# edge arrows on a directed network
ggnet(network(m, directed = TRUE), arrow.gap = 0.05, arrow.size = 10)
```

---

ggnet2 *ggnet2 - Plot a network with ggplot2*

Description

Function for plotting network objects using ggplot2, with additional control over graphical parameters that are not supported by the ggnet function. Please visit http://github.com/briatte/ggnet for the latest version of ggnet2, and https://briatte.github.io/ggnet for a vignette that contains many examples and explanations.

Usage

```
ggnet2(net, mode = "fruchtermanreingold", layout.par = NULL,
  layout.exp = 0, alpha = 1, color = "grey75", shape = 19, size = 9,
  max_size = 9, na.rm = NA, palette = NULL, alpha.palette = NULL,
  alpha.legend = NA, color.palette = palette, color.legend = NA,
  shape.palette = NULL, shape.legend = NA, size.palette = NULL,
  size.legend = NA, size.zero = FALSE, size.cut = FALSE, size.min = NA,
  size.max = NA, label = FALSE, label.alpha = 1, label.color = "black",
  label.size = max_size/2, label.trim = FALSE, node.alpha = alpha,
  node.color = color, node.label = label, node.shape = shape,
  node.size = size, edge.alpha = 1, edge.color = "grey50",
  edge.lty = "solid", edge.size = 0.25, edge.label = NULL,
  edge.label.alpha = 1, edge.label.color = label.color,
  edge.label.fill = "white", edge.label.size = max_size/2, arrow.size = 0,
  arrow.gap = 0, arrow.type = "closed", legend.size = 9,
  legend.position = "right", ...)
```

Arguments

net	an object of class network, or any object that can be coerced to this class, such as an adjacency or incidence matrix, or an edge list: see edgeset.constructors and network for details. If the object is of class igraph and the intergraph package is installed, it will be used to convert the object: see asNetwork for details.
mode	a placement method from those provided in the sna package: see gplot.layout for details. Also accepts the names of two numeric vertex attributes of net, or a matrix of numeric coordinates, in which case the first two columns of the matrix are used. Defaults to the Fruchterman-Reingold force-directed algorithm.
layout.par	options to be passed to the placement method, as listed in gplot.layout. Defaults to NULL.
layout.exp	a multiplier to expand the horizontal axis if node labels get clipped: see expand_range for details. Defaults to 0 (no expansion).
alpha	the level of transparency of the edges and nodes, which might be a single value, a vertex attribute, or a vector of values. Also accepts "mode" on bipartite networks (see 'Details'). Defaults to 1 (no transparency).
color	the color of the nodes, which might be a single value, a vertex attribute, or a vector of values. Also accepts "mode" on bipartite networks (see 'Details'). Defaults to grey75.
shape	the shape of the nodes, which might be a single value, a vertex attribute, or a vector of values. Also accepts "mode" on bipartite networks (see 'Details'). Defaults to 19 (solid circle).
size	the size of the nodes, in points, which might be a single value, a vertex attribute, or a vector of values. Also accepts "indegree", "outdegree", "degree" or "freeman" to size the nodes by their unweighted degree centrality ("degree" and "freeman" are equivalent): see degree for details. All node sizes must be strictly positive. Also accepts "mode" on bipartite networks (see 'Details'). Defaults to 9.
max_size	the *maximum* size of the node when size produces nodes of different sizes, in points. Defaults to 9.
na.rm	whether to subset the network to nodes that are *not* missing a given vertex attribute. If set to any vertex attribute of net, the nodes for which this attribute is NA will be removed. Defaults to NA (does nothing).
palette	the palette to color the nodes, when color is not a color value or a vector of color values. Accepts named vectors of color values, or if RColorBrewer is installed, any ColorBrewer palette name: see brewer.pal and http://colorbrewer2.org/ for details. Defaults to NULL, which will create an array of grayscale color values if color is not a color value or a vector of color values.
alpha.palette	the palette to control the transparency levels of the nodes set by alpha when the levels are not numeric values. Defaults to NULL, which will create an array of alpha transparency values if alpha is not a numeric value or a vector of numeric values.
alpha.legend	the name to assign to the legend created by alpha when its levels are not numeric values. Defaults to NA (no name).

color.palette	see palette
color.legend	the name to assign to the legend created by palette. Defaults to NA (no name).
shape.palette	the palette to control the shapes of the nodes set by shape when the shapes are not numeric values. Defaults to NULL, which will create an array of shape values if shape is not a numeric value or a vector of numeric values.
shape.legend	the name to assign to the legend created by shape when its levels are not numeric values. Defaults to NA (no name).
size.palette	the palette to control the sizes of the nodes set by size when the sizes are not numeric values.
size.legend	the name to assign to the legend created by size. Defaults to NA (no name).
size.zero	whether to accept zero-sized nodes based on the value(s) of size. Defaults to FALSE, which ensures that zero-sized nodes are still shown in the plot and its size legend.
size.cut	whether to cut the size of the nodes into a certain number of quantiles. Accepts TRUE, which tries to cut the sizes into quartiles, or any positive numeric value, which tries to cut the sizes into that many quantiles. If the size of the nodes do not contain the specified number of distinct quantiles, the largest possible number is used. See quantile and cut for details. Defaults to FALSE (does nothing).
size.min	whether to subset the network to nodes with a minimum size, based on the values of size. Defaults to NA (preserves all nodes).
size.max	whether to subset the network to nodes with a maximum size, based on the values of size. Defaults to NA (preserves all nodes).
label	whether to label the nodes. If set to TRUE, nodes are labeled with their vertex names. If set to a vector that contains as many elements as there are nodes in net, nodes are labeled with these. If set to any other vector of values, the nodes are labeled only when their vertex name matches one of these values. Defaults to FALSE (no labels).
label.alpha	the level of transparency of the node labels, as a numeric value, a vector of numeric values, or as a vertex attribute containing numeric values. Defaults to 1 (no transparency).
label.color	the color of the node labels, as a color value, a vector of color values, or as a vertex attribute containing color values. Defaults to "black".
label.size	the size of the node labels, in points, as a numeric value, a vector of numeric values, or as a vertex attribute containing numeric values. Defaults to max_size / 2 (half the maximum node size), which defaults to 4.5.
label.trim	whether to apply some trimming to the node labels. Accepts any function that can process a character vector, or a strictly positive numeric value, in which case the labels are trimmed to a fixed-length substring of that length: see substr for details. Defaults to FALSE (does nothing).
node.alpha	see alpha
node.color	see color
node.label	see label

node.shape see shape

node.size see size

edge.alpha the level of transparency of the edges. Defaults to the value of alpha, which defaults to 1.

edge.color the color of the edges, as a color value, a vector of color values, or as an edge attribute containing color values. Defaults to "grey50".

edge.lty the linetype of the edges, as a linetype value, a vector of linetype values, or as an edge attribute containing linetype values. Defaults to "solid".

edge.size the size of the edges, in points, as a numeric value, a vector of numeric values, or as an edge attribute containing numeric values. All edge sizes must be strictly positive. Defaults to 0.25.

edge.label the labels to plot at the middle of the edges, as a single value, a vector of values, or as an edge attribute. Defaults to NULL (no edge labels).

edge.label.alpha
the level of transparency of the edge labels, as a numeric value, a vector of numeric values, or as an edge attribute containing numeric values. Defaults to 1 (no transparency).

edge.label.color
the color of the edge labels, as a color value, a vector of color values, or as an edge attribute containing color values. Defaults to label.color, which defaults to "black".

edge.label.fill
the background color of the edge labels. Defaults to "white".

edge.label.size
the size of the edge labels, in points, as a numeric value, a vector of numeric values, or as an edge attribute containing numeric values. All edge label sizes must be strictly positive. Defaults to max_size / 2 (half the maximum node size), which defaults to 4.5.

arrow.size the size of the arrows for directed network edges, in points. See arrow for details. Defaults to 0 (no arrows).

arrow.gap a setting aimed at improving the display of edge arrows by plotting slightly shorter edges. Accepts any value between 0 and 1, where a value of 0.05 will generally achieve good results when the size of the nodes is reasonably small. Defaults to 0 (no shortening).

arrow.type the type of the arrows for directed network edges. See arrow for details. Defaults to "closed".

legend.size the size of the legend symbols and text, in points. Defaults to 9.

legend.position
the location of the plot legend(s). Accepts all legend.position values supported by theme. Defaults to "right".

... other arguments passed to the geom_text object that sets the node labels: see geom_text for details.

Details

The degree centrality measures that can be produced through the `size` argument will take the directedness of the network into account, but will be unweighted. To compute weighted network measures, see the `tnet` package by Tore Opsahl (`help("tnet", package = "tnet")`).

The nodes of bipartite networks can be mapped to their mode by passing the `"mode"` argument to any of `alpha`, `color`, `shape` and `size`, in which case the nodes of the primary mode will be mapped as `"actor"`, and the nodes of the secondary mode will be mapped as `"event"`.

Author(s)

Moritz Marbach and Francois Briatte, with help from Heike Hoffmann, Pedro Jordano and Ming-Yu Liu

See Also

`ggnet` in this package, `gplot` in the `sna` package, and `plot.network` in the `network` package

Examples

```
library(network)

# random adjacency matrix
x           <- 10
ndyads      <- x * (x - 1)
density     <- x / ndyads
m           <- matrix(0, nrow = x, ncol = x)
dimnames(m) <- list(letters[ 1:x ], letters[ 1:x ])
m[ row(m) != col(m) ] <- runif(ndyads) < density
m

# random undirected network
n <- network::network(m, directed = FALSE)
n

ggnet2(n, label = TRUE)
ggnet2(n, label = TRUE, shape = 15)
ggnet2(n, label = TRUE, shape = 15, color = "black", label.color = "white")

# add vertex attribute
x = network.vertex.names(n)
x = ifelse(x %in% c("a", "e", "i"), "vowel", "consonant")
n %v% "phono" = x

ggnet2(n, color = "phono")
ggnet2(n, color = "phono", palette = c("vowel" = "gold", "consonant" = "grey"))
ggnet2(n, shape = "phono", color = "phono")

if (require(RColorBrewer)) {

  # random groups
  n %v% "group" <- sample(LETTERS[1:3], 10, replace = TRUE)
```

```
  ggnet2(n, color = "group", palette = "Set2")

}

# random weights
n %e% "weight" <- sample(1:3, network.edgecount(n), replace = TRUE)
ggnet2(n, edge.size = "weight", edge.label = "weight")

# edge arrows on a directed network
ggnet2(network(m, directed = TRUE), arrow.gap = 0.05, arrow.size = 10)

# Padgett's Florentine wedding data
data(flo, package = "network")
flo

ggnet2(flo, label = TRUE)
ggnet2(flo, label = TRUE, label.trim = 4, vjust = -1, size = 3, color = 1)
ggnet2(flo, label = TRUE, size = 12, color = "white")
```

---

ggnetworkmap *ggnetworkmap - Plot a network with ggplot2 suitable for overlay on a ggmap:: map ggplot, or other ggplot*

Description

This is a descendent of the original ggnet function. ggnet added the innovation of plotting the network geographically. However, ggnet needed to be the first object in the ggplot chain. ggnetworkmap does not. If passed a ggplot object as its first argument, such as output from ggmap, ggnetworkmap will plot on top of that chart, looking for vertex attributes lon and lat as coordinates. Otherwise, ggnetworkmap will generate coordinates using the Fruchterman-Reingold algorithm.

Usage

```
ggnetworkmap(gg, net, size = 3, alpha = 0.75, weight, node.group,
  node.color = NULL, node.alpha = NULL, ring.group, segment.alpha = NULL,
  segment.color = "grey", great.circles = FALSE, segment.size = 0.25,
  arrow.size = 0, label.nodes = FALSE, label.size = size/2, ...)
```

Arguments

gg	an object of class ggplot.
net	an object of class network, or any object that can be coerced to this class, such as an adjacency or incidence matrix, or an edge list: see edgeset.constructors and network for details. If the object is of class igraph and the intergraph package is installed, it will be used to convert the object: see asNetwork for details.

size	size of the network nodes. Defaults to 3. If the nodes are weighted, their area is proportionally scaled up to the size set by size.
alpha	a level of transparency for nodes, vertices and arrows. Defaults to 0.75.
weight	if present, the unquoted name of a vertex attribute in data. Otherwise nodes are unweighted.
node.group	NULL, the default, or the unquoted name of a vertex attribute that will be used to determine the color of each node.
node.color	If node.group is null, a character string specifying a color.
node.alpha	transparency of the nodes. Inherits from alpha.
ring.group	if not NULL, the default, the unquoted name of a vertex attribute that will be used to determine the color of each node border.
segment.alpha	transparency of the vertex links. Inherits from alpha
segment.color	color of the vertex links. Defaults to "grey".
great.circles	whether to draw edges as great circles using the geosphere package. Defaults to FALSE
segment.size	size of the vertex links, as a vector of values or as a single value. Defaults to 0.25.
arrow.size	size of the vertex arrows for directed network plotting, in centimeters. Defaults to 0.
label.nodes	label nodes with their vertex names attribute. If set to TRUE, all nodes are labelled. Also accepts a vector of character strings to match with vertex names.
label.size	size of the labels. Defaults to size / 2.
...	other arguments supplied to geom_text for the node labels. Arguments pertaining to the title or other items can be achieved through ggplot2 methods.

Details

This is a function for plotting graphs generated by network or igraph in a more flexible and elegant manner than permitted by ggnet. The function does not need to be the first plot in the ggplot chain, so the graph can be plotted on top of a map or other chart. Segments can be straight lines, or plotted as great circles. Note that the great circles feature can produce odd results with arrows and with vertices beyond the plot edges; this is a gglot2 limitation and cannot yet be fixed. Nodes can have two color schemes, which are then plotted as the center and ring around the node. The color schemes are selected by adding scale_fill_ or scale_color_ just like any other ggplot2 plot. If there are no rings, scale_color sets the color of the nodes. If there are rings, scale_color sets the color of the rings, and scale_fill sets the color of the centers. Note that additional arguments in the ... are passed to geom_text for plotting labels.

Author(s)

Amos Elberg <amos.elberg@gmail.com>. Original by Moritz Marbach <mmarbach@mail.uni-mannheim.de>, Francois Briatte <f.briatte@gmail.com>

Examples

```
# small function to display plots only if it's interactive
p_ <- GGally::print_if_interactive

invisible(lapply(c("ggplot2", "maps", "network", "sna"), base::library, character.only = TRUE))

## Example showing great circles on a simple map of the USA
## http://flowingdata.com/2011/05/11/how-to-map-connections-with-great-circles/

airports <- read.csv("http://datasets.flowingdata.com/tuts/maparcs/airports.csv", header = TRUE)
rownames(airports) <- airports$iata

# select some random flights
set.seed(1234)
flights <- data.frame(
  origin = sample(airports[200:400, ]$iata, 200, replace = TRUE),
  destination = sample(airports[200:400, ]$iata, 200, replace = TRUE)
)

# convert to network
flights <- network(flights, directed = TRUE)

# add geographic coordinates
flights %v% "lat" <- airports[ network.vertex.names(flights), "lat" ]
flights %v% "lon" <- airports[ network.vertex.names(flights), "long" ]

# drop isolated airports
delete.vertices(flights, which(degree(flights) < 2))

# compute degree centrality
flights %v% "degree" <- degree(flights, gmode = "digraph")

# add random groups
flights %v% "mygroup" <- sample(letters[1:4], network.size(flights), replace = TRUE)

# create a map of the USA
usa <- ggplot(map_data("usa"), aes(x = long, y = lat)) +
  geom_polygon(aes(group = group), color = "grey65",
               fill = "#f9f9f9", size = 0.2)

# overlay network data to map
p <- ggnetworkmap(
  usa, flights, size = 4, great.circles = TRUE,
  node.group = mygroup, segment.color = "steelblue",
  ring.group = degree, weight = degree
)
p_(p)

## Exploring a community of spambots found on Twitter
## Data by Amos Elberg: see ?twitter_spambots for details

data(twitter_spambots)
```

```
# create a world map
world <- fortify(map("world", plot = FALSE, fill = TRUE))
world <- ggplot(world, aes(x = long, y = lat)) +
  geom_polygon(aes(group = group), color = "grey65",
               fill = "#f9f9f9", size = 0.2)

# view global structure
p <- ggnetworkmap(world, twitter_spambots)
p_(p)

# domestic distribution
p <- ggnetworkmap(net = twitter_spambots)
p_(p)

# topology
p <- ggnetworkmap(net = twitter_spambots, arrow.size = 0.5)
p_(p)

# compute indegree and outdegree centrality
twitter_spambots %v% "indegree" <- degree(twitter_spambots, cmode = "indegree")
twitter_spambots %v% "outdegree" <- degree(twitter_spambots, cmode = "outdegree")

p <- ggnetworkmap(
  net = twitter_spambots,
  arrow.size = 0.5,
  node.group = indegree,
  ring.group = outdegree, size = 4
) +
  scale_fill_continuous("Indegree", high = "red", low = "yellow") +
  labs(color = "Outdegree")
p_(p)

# show some vertex attributes associated with each account
p <- ggnetworkmap(
  net = twitter_spambots,
  arrow.size = 0.5,
  node.group = followers,
  ring.group = friends,
  size = 4,
  weight = indegree,
  label.nodes = TRUE, vjust = -1.5
) +
  scale_fill_continuous("Followers", high = "red", low = "yellow") +
  labs(color = "Friends") +
  scale_color_continuous(low = "lightgreen", high = "darkgreen")
p_(p)
```

---

ggnostic *ggnostic - Plot matrix of statistical model diagnostics*

Description

ggnostic - Plot matrix of statistical model diagnostics

Usage

```
ggnostic(model, ..., columnsX = attr(data, "var_x"), columnsY = c(".resid",
  ".sigma", ".hat", ".cooksd"), columnLabelsX = attr(data, "var_x_label"),
  columnLabelsY = gsub("\\.", " ", gsub("^\\.", "", columnsY)),
  xlab = "explanatory variables", ylab = "diagnostics",
  title = paste(deparse(model$call, width.cutoff = 500L), collapse = "\n"),
  continuous = list(default = ggally_points, .fitted = ggally_points, .se.fit
  = ggally_nostic_se_fit, .resid = ggally_nostic_resid, .hat =
  ggally_nostic_hat, .sigma = ggally_nostic_sigma, .cooksd =
  ggally_nostic_cooksd, .std.resid = ggally_nostic_std_resid),
  combo = list(default = ggally_box_no_facet, fitted = ggally_box_no_facet,
  .se.fit = ggally_nostic_se_fit, .resid = ggally_nostic_resid, .hat =
  ggally_nostic_hat, .sigma = ggally_nostic_sigma, .cooksd =
  ggally_nostic_cooksd, .std.resid = ggally_nostic_std_resid),
  discrete = list(default = ggally_ratio, .fitted = ggally_ratio, .se.fit =
  ggally_ratio, .resid = ggally_ratio, .hat = ggally_ratio, .sigma =
  ggally_ratio, .cooksd = ggally_ratio, .std.resid = ggally_ratio),
  data = broomify(model))
```

Arguments

`model`	statistical model object such as output from `stats::lm` or `stats::glm`
`...`	arguments passed directly to `ggduo`
`columnsX`	columns to be displayed in the plot matrix. Defaults to the predictor columns of the `model`
`columnsY`	rows to be displayed in the plot matrix. Defaults to residuals, leave one out sigma value, diagonal of the hat matrix, and Cook's Distance. The possible values are the response variables in the model and the added columns provided by `broom::augment(model)`. See details for more information.
`columnLabelsX, columnLabelsY`	column and row labels to display in the plot matrix
`xlab, ylab, title`	plot matrix labels passed directly to `ggmatrix`
`continuous, combo, discrete`	list of functions for each y variable. See details for more information.
`data`	data defaults to a 'broomify'ed model object. This object will contain information about the X variables, Y variables, and multiple broom outputs. See `broomify(model)` for more information

'columnsY'

`broom::augment()` collects data from the supplied model and returns a data.frame with the following columns (taken directly from broom documentation). These columns are the only allowed values in the `columnsY` parameter to `ggnostic`.

.resid Residuals

.hat Diagonal of the hat matrix

.sigma Estimate of residual standard deviation when corresponding observation is dropped from model

.cooksd Cooks distance, `cooks.distance`

.fitted Fitted values of model

.se.fit Standard errors of fitted values

.std.resid Standardized residuals

response variable name The response variable in the model may be added. Such as `"mpg"` in the model `lm(mpg ~ ., data = mtcars)`

'continuous', 'combo', 'discrete' types

Similar to `ggduo` and `ggpairs`, functions may be supplied to display the different column types. However, since the Y rows are fixed, each row has it's own corresponding function in each of the plot types: continuous, combo, and discrete. Each plot type list can have keys that correspond to the `broom::augment()` output: `".fitted"`, `".resid"`, `".std.resid"`, `".sigma"`, `".se.fit"`, `".hat"`, `".cooksd"`. An extra key, `"default"`, is used to plot the response variables of the model if they are included. Having a function for each diagnostic allows for very fine control over the diagnostics plot matrix. The functions for each type list are wrapped into a switch function that calls the function corresponding to the y variable being plotted. These switch functions are then passed directly to the `types` parameter in `ggduo`.

Examples

```
# small function to display plots only if it's interactive
p_ <- GGally::print_if_interactive
data(mtcars)

# use mtcars dataset and alter the 'am' column to display actual name values
mtc <- mtcars
mtc$am <- c("0" = "automatic", "1" = "manual")[as.character(mtc$am)]

# step the complete model down to a smaller model
mod <- stats::step(stats::lm(mpg ~ ., data = mtc), trace = FALSE)

# display using defaults
pm <- ggnostic(mod)
p_(pm)

# color by am value
pm <- ggnostic(mod, mapping = ggplot2::aes(color = am))
p_(pm)

# turn resid smooth error ribbon off
pm <- ggnostic(mod, continuous = list(.resid = wrap("nostic_resid", se = FALSE)))
p_(pm)
```

```
## plot residuals vs fitted in a ggpairs plot matrix
dt <- broomify(mod)
pm <- ggpairs(
  dt, c(".fitted", ".resid"),
  columnLabels = c("fitted", "residuals"),
  lower = list(continuous = ggally_nostic_resid)
)
p_(pm)
```

---

ggpairs *ggpairs - A ggplot2 generalized pairs plot*

Description

Make a matrix of plots with a given data set

Usage

```
ggpairs(data, mapping = NULL, columns = 1:ncol(data), title = NULL,
  upper = list(continuous = "cor", combo = "box_no_facet", discrete =
  "facetbar", na = "na"), lower = list(continuous = "points", combo =
  "facethist", discrete = "facetbar", na = "na"), diag = list(continuous =
  "densityDiag", discrete = "barDiag", na = "naDiag"), params = NULL, ...,
  xlab = NULL, ylab = NULL, axisLabels = c("show", "internal", "none"),
  columnLabels = colnames(data[columns]), labeller = "label_value",
  switch = NULL, showStrips = NULL, legend = NULL,
  cardinality_threshold = 15, legends = stop("deprecated"))
```

Arguments

`data`	data set using. Can have both numerical and categorical data.
`mapping`	aesthetic mapping (besides x and y). See `aes()`. If `mapping` is numeric, `columns` will be set to the `mapping` value and `mapping` will be set to `NULL`.
`columns`	which columns are used to make plots. Defaults to all columns.
`title, xlab, ylab`	title, x label, and y label for the graph
`upper`	see Details
`lower`	see Details
`diag`	see Details
`params`	deprecated. Please see `wrap_fn_with_param_arg`
`...`	deprecated. Please use `mapping`
`axisLabels`	either "show" to display axisLabels, "internal" for labels in the diagonal plots, or "none" for no axis labels
`columnLabels`	label names to be displayed. Defaults to names of columns being used.

`labeller` labeller for facets. See `labellers`. Common values are `"label_value"` (default) and `"label_parsed"`.

`switch` switch parameter for facet_grid. See `ggplot2::facet_grid`. By default, the labels are displayed on the top and right of the plot. If `"x"`, the top labels will be displayed to the bottom. If `"y"`, the right-hand side labels will be displayed to the left. Can also be set to `"both"`

`showStrips` boolean to determine if each plot's strips should be displayed. `NULL` will default to the top and right side plots only. `TRUE` or `FALSE` will turn all strips on or off respectively.

`legend` May be the two objects described below or the default `NULL` value. The legend position can be moved by using ggplot2's theme element `pm + theme(legend.position = "bottom")`

a numeric vector of length 2 provides the location of the plot to use the legend for the plot matrix's legend. Such as `legend = c(3,5)` which will use the legend from the plot in the third row and fifth column

a single numeric value provides the location of a plot according to the display order. Such as `legend = 3` in a plot matrix with 2 rows and 5 columns displayed by column will return the plot in position `c(1,2)`

a object from `grab_legend()` a predetermined plot legend that will be displayed directly

`cardinality_threshold`
maximum number of levels allowed in a character / factor column. Set this value to NULL to not check factor columns. Defaults to 15

`legends` deprecated

Details

`upper` and `lower` are lists that may contain the variables 'continuous', 'combo', 'discrete', and 'na'. Each element of the list may be a function or a string. If a string is supplied, it must implement one of the following options:

continuous exactly one of ('points', 'smooth', 'smooth_loess', 'density', 'cor', 'blank'). This option is used for continuous X and Y data.

combo exactly one of ('box', 'box_no_facet', 'dot', 'dot_no_facet', 'facethist', 'facetdensity', 'denstrip', 'blank'). This option is used for either continuous X and categorical Y data or categorical X and continuous Y data.

discrete exactly one of ('facetbar', 'ratio', 'blank'). This option is used for categorical X and Y data.

na exactly one of ('na', 'blank'). This option is used when all X data is `NA`, all Y data is `NA`, or either all X or Y data is `NA`.

`diag` is a list that may only contain the variables 'continuous', 'discrete', and 'na'. Each element of the diag list is a string implementing the following options:

continuous exactly one of ('densityDiag', 'barDiag', 'blankDiag'). This option is used for continuous X data.

discrete exactly one of ('barDiag', 'blankDiag'). This option is used for categorical X and Y data.

na exactly one of ('naDiag', 'blankDiag'). This option is used when all X data is NA.

If 'blank' is ever chosen as an option, then ggpairs will produce an empty plot.

If a function is supplied as an option to upper, lower, or diag, it should implement the function api of function(data, mapping, ...){#make ggplot2 plot}. If a specific function needs its parameters set, wrap(fn, param1 = val1, param2 = val2) the function with its parameters.

Value

ggmatrix object that if called, will print

Author(s)

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References

John W Emerson, Walton A Green, Barret Schloerke, Jason Crowley, Dianne Cook, Heike Hofmann, Hadley Wickham. The Generalized Pairs Plot. Journal of Computational and Graphical Statistics, vol. 22, no. 1, pp. 79-91, 2012.

See Also

wrap v1_ggmatrix_theme

Examples

```
 # small function to display plots only if it's interactive
 p_ <- GGally::print_if_interactive


## Quick example, with and without colour
data(flea)
ggpairs(flea, columns = 2:4)
pm <- ggpairs(flea, columns = 2:4, ggplot2::aes(colour=species))
p_(pm)
# Note: colour should be categorical, else you will need to reset
# the upper triangle to use points instead of trying to compute corr

data(tips, package = "reshape")
pm <- ggpairs(tips[, 1:3])
p_(pm)
pm <- ggpairs(tips, 1:3, columnLabels = c("Total Bill", "Tip", "Sex"))
p_(pm)
pm <- ggpairs(tips, upper = "blank")
p_(pm)

## Plot Types
# Change default plot behavior
pm <- ggpairs(
  tips[, c(1, 3, 4, 2)],
```

```
  upper = list(continuous = "density", combo = "box_no_facet"),
  lower = list(continuous = "points", combo = "dot_no_facet")
)
p_(pm)
# Supply Raw Functions (may be user defined functions!)
pm <- ggpairs(
  tips[, c(1, 3, 4, 2)],
  upper = list(continuous = ggally_density, combo = ggally_box_no_facet),
  lower = list(continuous = ggally_points, combo = ggally_dot_no_facet)
)
p_(pm)

# Use sample of the diamonds data
data(diamonds, package="ggplot2")
diamonds.samp <- diamonds[sample(1:dim(diamonds)[1], 1000), ]

# Different aesthetics for different plot sections and plot types
pm <- ggpairs(
 diamonds.samp[, 1:5],
 mapping = ggplot2::aes(color = cut),
 upper = list(continuous = wrap("density", alpha = 0.5), combo = "box_no_facet"),
 lower = list(continuous = wrap("points", alpha = 0.3), combo = wrap("dot_no_facet", alpha = 0.4)),
 title = "Diamonds"
)
p_(pm)

## Axis Label Variations
# Only Variable Labels on the diagonal (no axis labels)
pm <- ggpairs(tips[, 1:3], axisLabels="internal")
p_(pm)
# Only Variable Labels on the outside (no axis labels)
pm <- ggpairs(tips[, 1:3], axisLabels="none")
p_(pm)

## Facet Label Variations
#  Default:
df_x <- rnorm(100)
df_y <- df_x + rnorm(100, 0, 0.1)
df <- data.frame(x = df_x, y = df_y, c = sqrt(df_x^2 + df_y^2))
pm <- ggpairs(
  df,
  columnLabels = c("alpha[foo]", "alpha[bar]", "sqrt(alpha[foo]^2 + alpha[bar]^2)")
)
p_(pm)
#  Parsed labels:
pm <- ggpairs(
  df,
  columnLabels = c("alpha[foo]", "alpha[bar]", "sqrt(alpha[foo]^2 + alpha[bar]^2)"),
  labeller = "label_parsed"
)
p_(pm)

## Plot Insertion Example
```

```
custom_car <- ggpairs(mtcars[, c("mpg", "wt", "cyl")], upper = "blank", title = "Custom Example")
# ggplot example taken from example(geom_text)
  plot <- ggplot2::ggplot(mtcars, ggplot2::aes(x=wt, y=mpg, label=rownames(mtcars)))
  plot <- plot +
    ggplot2::geom_text(ggplot2::aes(colour=factor(cyl)), size = 3) +
    ggplot2::scale_colour_discrete(l=40)
custom_car[1, 2] <- plot
personal_plot <- ggally_text(
  "ggpairs allows you\nto put in your\nown plot.\nLike that one.\n <---"
)
custom_car[1, 3] <- personal_plot
p_(custom_car)

## Remove binwidth warning from ggplot2
# displays warning about picking a better binwidth
pm <- ggpairs(tips, 2:3)
p_(pm)
# no warning displayed
pm <- ggpairs(tips, 2:3, lower = list(combo = wrap("facethist", binwidth = 0.5)))
p_(pm)
# no warning displayed with user supplied function
pm <- ggpairs(tips, 2:3, lower = list(combo = wrap(ggally_facethist, binwidth = 0.5)))
p_(pm)
```

---

ggparcoord *ggparcoord - A ggplot2 Parallel Coordinate Plot*

Description

A function for plotting static parallel coordinate plots, utilizing the ggplot2 graphics package.

Usage

```
ggparcoord(data, columns = 1:ncol(data), groupColumn = NULL,
  scale = "std", scaleSummary = "mean", centerObsID = 1,
  missing = "exclude", order = columns, showPoints = FALSE,
  splineFactor = FALSE, alphaLines = 1, boxplot = FALSE,
  shadeBox = NULL, mapping = NULL, title = "")
```

Arguments

data	the dataset to plot
columns	a vector of variables (either names or indices) to be axes in the plot
groupColumn	a single variable to group (color) by
scale	method used to scale the variables (see Details)
scaleSummary	if scale=="center", summary statistic to univariately center each variable by
centerObsID	if scale=="centerObs", row number of case plot should univariately be centered on

missing	method used to handle missing values (see Details)
order	method used to order the axes (see Details)
showPoints	logical operator indicating whether points should be plotted or not
splineFactor	logical or numeric operator indicating whether spline interpolation should be used. Numeric values will multiplied by the number of columns, TRUE will default to cubic interpolation, AsIs to set the knot count directly and 0, FALSE, or non-numeric values will not use spline interpolation.
alphaLines	value of alpha scaler for the lines of the parcoord plot or a column name of the data
boxplot	logical operator indicating whether or not boxplots should underlay the distribution of each variable
shadeBox	color of underlaying box which extends from the min to the max for each variable (no box is plotted if shadeBox == NULL)
mapping	aes string to pass to ggplot object
title	character string denoting the title of the plot

Details

scale is a character string that denotes how to scale the variables in the parallel coordinate plot. Options:

- std: univariately, subtract mean and divide by standard deviation
- robust: univariately, subtract median and divide by median absolute deviation
- uniminmax: univariately, scale so the minimum of the variable is zero, and the maximum is one
- globalminmax: no scaling is done; the range of the graphs is defined by the global minimum and the global maximum
- center: use uniminmax to standardize vertical height, then center each variable at a value specified by the scaleSummary param
- centerObs: use uniminmax to standardize vertical height, then center each variable at the value of the observation specified by the centerObsID param

missing is a character string that denotes how to handle missing missing values. Options:

- exclude: remove all cases with missing values
- mean: set missing values to the mean of the variable
- median: set missing values to the median of the variable
- min10: set missing values to 10% below the minimum of the variable
- random: set missing values to value of randomly chosen observation on that variable

order is either a vector of indices or a character string that denotes how to order the axes (variables) of the parallel coordinate plot. Options:

- (default): order by the vector denoted by columns
- (given vector): order by the vector specified

- anyClass: order variables by their separation between any one class and the rest (as opposed to their overall variation between classes). This is accomplished by calculating the F-statistic for each class vs. the rest, for each axis variable. The axis variables are then ordered (decreasing) by their maximum of k F-statistics, where k is the number of classes.
- allClass: order variables by their overall F statistic (decreasing) from an ANOVA with groupColumn as the explanatory variable (note: it is required to specify a groupColumn with this ordering method). Basically, this method orders the variables by their variation between classes (most to least).
- skewness: order variables by their sample skewness (most skewed to least skewed)
- Outlying: order by the scagnostic measure, Outlying, as calculated by the package scagnostics. Other scagnostic measures available to order by are Skewed, Clumpy, Sparse, Striated, Convex, Skinny, Stringy, and Monotonic. Note: To use these methods of ordering, you must have the scagnostics package loaded.

Value

ggplot object that if called, will print

Author(s)

Jason Crowley <crowley.jason.s@gmail.com>, Barret Schloerke <schloerke@gmail.com>, Di Cook <dicook@iastate.edu>, Heike Hofmann <hofmann@iastate.edu>, Hadley Wickham <h.wickham@gmail.com>

Examples

```
# small function to display plots only if it's interactive
p_ <- GGally::print_if_interactive

# use sample of the diamonds data for illustrative purposes
data(diamonds, package="ggplot2")
diamonds.samp <- diamonds[sample(1:dim(diamonds)[1], 100), ]

# basic parallel coordinate plot, using default settings
p <- ggparcoord(data = diamonds.samp, columns = c(1, 5:10))
p_(p)

# this time, color by diamond cut
p <- ggparcoord(data = diamonds.samp, columns = c(1, 5:10), groupColumn = 2)
p_(p)

# underlay univariate boxplots, add title, use uniminmax scaling
p <- ggparcoord(data = diamonds.samp, columns = c(1, 5:10), groupColumn = 2,
  scale = "uniminmax", boxplot = TRUE, title = "Parallel Coord. Plot of Diamonds Data")
p_(p)

# utilize ggplot2 aes to switch to thicker lines
p <- ggparcoord(data = diamonds.samp, columns = c(1, 5:10), groupColumn = 2,
  title ="Parallel Coord. Plot of Diamonds Data", mapping = ggplot2::aes(size = 1)) +
  ggplot2::scale_size_identity()
p_(p)
```

```
# basic parallel coord plot of the msleep data, using 'random' imputation and
# coloring by diet (can also use variable names in the columns and groupColumn
# arguments)
data(msleep, package="ggplot2")
p <- ggparcoord(data = msleep, columns = 6:11, groupColumn = "vore", missing =
  "random", scale = "uniminmax")
p_(p)

# center each variable by its median, using the default missing value handler,
# 'exclude'
p <- ggparcoord(data = msleep, columns = 6:11, groupColumn = "vore", scale =
  "center", scaleSummary = "median")
p_(p)

# with the iris data, order the axes by overall class (Species) separation using
# the anyClass option
p <- ggparcoord(data = iris, columns = 1:4, groupColumn = 5, order = "anyClass")
p_(p)

# add points to the plot, add a title, and use an alpha scalar to make the lines
# transparent
p <- ggparcoord(data = iris, columns = 1:4, groupColumn = 5, order = "anyClass",
  showPoints = TRUE, title = "Parallel Coordinate Plot for the Iris Data",
  alphaLines = 0.3)
p_(p)

# color according to a column
iris2 <- iris
iris2$alphaLevel <- c("setosa" = 0.2, "versicolor" = 0.3, "virginica" = 0)[iris2$Species]
p <- ggparcoord(data = iris2, columns = 1:4, groupColumn = 5, order = "anyClass",
  showPoints = TRUE, title = "Parallel Coordinate Plot for the Iris Data",
  alphaLines = "alphaLevel")
p_(p)

## Use splines on values, rather than lines (all produce the same result)
columns <- c(1, 5:10)
p <- ggparcoord(diamonds.samp, columns, groupColumn = 2, splineFactor = TRUE)
p_(p)
p <- ggparcoord(diamonds.samp, columns, groupColumn = 2, splineFactor = 3)
p_(p)
splineFactor <- length(columns) * 3
p <- ggparcoord(diamonds.samp, columns, groupColumn = 2, splineFactor = I(splineFactor))
p_(p)
```

---

ggscatmat *ggscatmat - a traditional scatterplot matrix for purely quantitative variables*

Description

This function makes a scatterplot matrix for quantitative variables with density plots on the diagonal and correlation printed in the upper triangle.

Usage

```
ggscatmat(data, columns = 1:ncol(data), color = NULL, alpha = 1,
  corMethod = "pearson")
```

Arguments

data	a data matrix. Should contain numerical (continuous) data.
columns	an option to choose the column to be used in the raw dataset. Defaults to 1:ncol(data).
color	an option to group the dataset by the factor variable and color them by different colors. Defaults to NULL.
alpha	an option to set the transparency in scatterplots for large data. Defaults to 1.
corMethod	method argument supplied to cor

Author(s)

Mengjia Ni, Di Cook <dicook@monash.edu>

Examples

```
data(flea)
ggscatmat(flea, columns = 2:4)
ggscatmat(flea, columns = 2:4, color = "species")
```

---

ggsurv *Survival curves with ggplot2*

Description

This function produces Kaplan-Meier plots using ggplot2. As a first argument it needs a survfit object, created by the survival package. Default settings differ for single stratum and multiple strata objects.

Usage

```
ggsurv(s, CI = "def", plot.cens = TRUE, surv.col = "gg.def",
  cens.col = "gg.def", lty.est = 1, lty.ci = 2, size.est = 0.5,
  size.ci = size.est, cens.size = 2, cens.shape = 3, back.white = FALSE,
  xlab = "Time", ylab = "Survival", main = "", order.legend = TRUE)
```

Arguments

s	an object of class survfit
CI	should a confidence interval be plotted? Defaults to TRUE for single stratum objects and FALSE for multiple strata objects.
plot.cens	mark the censored observations?
surv.col	colour of the survival estimate. Defaults to black for one stratum, and to the default ggplot2 colours for multiple strata. Length of vector with colour names should be either 1 or equal to the number of strata.
cens.col	colour of the points that mark censored observations.
lty.est	linetype of the survival curve(s). Vector length should be either 1 or equal to the number of strata.
lty.ci	linetype of the bounds that mark the 95% CI.
size.est	line width of the survival curve
size.ci	line width of the 95% CI
cens.size	point size of the censoring points
cens.shape	shape of the points that mark censored observations.
back.white	if TRUE the background will not be the default grey of ggplot2 but will be white with borders around the plot.
xlab	the label of the x-axis.
ylab	the label of the y-axis.
main	the plot label.
order.legend	boolean to determine if the legend display should be ordered by final survival time

Value

An object of class ggplot

Author(s)

Edwin Thoen <edwinthoen@gmail.com>

Examples

```
if (require(survival) && require(scales)) {
  data(lung, package = "survival")
  sf.lung <- survival::survfit(Surv(time, status) ~ 1, data = lung)
  ggsurv(sf.lung)

  # Multiple strata examples
  sf.sex <- survival::survfit(Surv(time, status) ~ sex, data = lung)
  pl.sex <- ggsurv(sf.sex)
  pl.sex
```

```
# Adjusting the legend of the ggsurv fit
pl.sex +
  ggplot2::guides(linetype = FALSE) +
  ggplot2::scale_colour_discrete(
    name   = 'Sex',
    breaks = c(1,2),
    labels = c('Male', 'Female')
  )

# We can still adjust the plot after fitting
data(kidney, package = "survival")
sf.kid <- survival::survfit(Surv(time, status) ~ disease, data = kidney)
pl.kid <- ggsurv(sf.kid, plot.cens = FALSE)
pl.kid

# Zoom in to first 80 days
pl.kid + ggplot2::coord_cartesian(xlim = c(0, 80), ylim = c(0.45, 1))

# Add the diseases names to the plot and remove legend
pl.kid +
  ggplot2::annotate(
    "text",
    label  = c("PKD", "Other", "GN", "AN"),
    x      = c(90, 125, 5, 60),
    y      = c(0.8, 0.65, 0.55, 0.30),
    size   = 5,
    colour = scales::hue_pal(
      h         = c(0, 360) + 15,
      c         = 100,
      l         = 65,
      h.start   = 0,
      direction = 1
    )(4)
  ) +
  ggplot2::guides(color = FALSE, linetype = FALSE)
}
```

---

ggts *Multiple Time Series*

Description

GGally implementation of ts.plot. Wraps around the ggduo function and removes the column strips

Usage

```
ggts(..., columnLabelsX = NULL, xlab = "time")
```

Arguments

...	supplied directly to ggduo
columnLabelsX	remove top strips for the X axis by default
xlab	defaults to "time"

Value

ggmatrix object

Examples

```
ggts(pigs, "time", c("gilts", "profit", "s_per_herdsz", "production", "herdsz"))
```

---

glyphplot *Glyph plot class*

Description

Glyph plot class

Usage

```
glyphplot(data, width, height, polar, x_major, y_major)

is.glyphplot(x)

## S3 method for class 'glyphplot'
x[...]

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

Arguments

data	A data frame containing variables named in x_major, x_minor, y_major and y_minor.
height, width	The height and width of each glyph. Defaults to 95% of the resolution of the data. Specify the width absolutely by supplying a numeric vector of length 1, or relative to the
polar	A logical of length 1, specifying whether the glyphs should be drawn in polar coordinates. Defaults to FALSE.
x_major, y_major	The name of the variable (as a string) for the major x and y axes. Together, the
x	glyphplot to be printed
...	ignored

Author(s)

Di Cook <dicook@monash.edu>, Heike Hofmann, Hadley Wickham

`glyphs` *Create the data needed to generate a glyph plot.*

Description

Create the data needed to generate a glyph plot.

Usage

```
glyphs(data, x_major, x_minor, y_major, y_minor, polar = FALSE,
  height = ggplot2::rel(0.95), width = ggplot2::rel(0.95),
  y_scale = identity, x_scale = identity)
```

Arguments

`data`	A data frame containing variables named in `x_major`, `x_minor`, `y_major` and `y_minor`.
`x_major, x_minor, y_major, y_minor`	The name of the variable (as a string) for the major and minor x and y axes. Together, each unique
`polar`	A logical of length 1, specifying whether the glyphs should be drawn in polar coordinates. Defaults to `FALSE`.
`height, width`	The height and width of each glyph. Defaults to 95% of the `resolution` of the data. Specify the width absolutely by supplying a numeric vector of length 1, or relative to the
`y_scale, x_scale`	The scaling function to be applied to each set of minor values within a grid cell. Defaults to `identity` so that no scaling is performed.

Author(s)

Di Cook <dicook@monash.edu>, Heike Hofmann, Hadley Wickham

Examples

```
data(nasa)
nasaLate <- nasa[
  nasa$date >= as.POSIXct("1998-01-01") &
  nasa$lat >= 20 &
  nasa$lat <= 40 &
  nasa$long >= -80 &
  nasa$long <= -60
, ]
temp.gly <- glyphs(nasaLate, "long", "day", "lat", "surftemp", height=2.5)
```

```
 ggplot2::ggplot(temp.gly, ggplot2::aes(gx, gy, group = gid)) +
   add_ref_lines(temp.gly, color = "grey90") +
   add_ref_boxes(temp.gly, color = "grey90") +
   ggplot2::geom_path() +
   ggplot2::theme_bw() +
   ggplot2::labs(x = "", y = "")
```

---

grab_legend *Grab the legend and print it as a plot*

Description

Grab the legend and print it as a plot

Usage

```
grab_legend(p)

## S3 method for class 'legend_guide_box'
print(x, ..., plotNew = FALSE)
```

Arguments

p	ggplot2 plot object
x	legend object that has been grabbed from a ggplot2 object
...	ignored
plotNew	boolean to determine if the ‘grid.newpage()‘ command and a new blank rectangle should be printed

Examples

```
library(ggplot2)
histPlot <- qplot(
  x = Sepal.Length,
  data = iris,
  fill = Species,
  geom = "histogram",
  binwidth = 1/4
)
(right <- histPlot)
(bottom <- histPlot + theme(legend.position = "bottom"))
(top <- histPlot + theme(legend.position = "top"))
(left <- histPlot + theme(legend.position = "left"))

grab_legend(right)
grab_legend(bottom)
grab_legend(top)
grab_legend(left)
```

happy *Data related to happiness from the General Social Survey, 1972-2006.*

Description

This data extract is taken from Hadley Wickham's `productplots` package. The original description follows, with minor edits.

Usage

```
data(happy)
```

Format

A data frame with 51020 rows and 10 variables

Details

The data is a small sample of variables related to happiness from the General Social Survey (GSS). The GSS is a yearly cross-sectional survey of Americans, run from 1972. We combine data for 25 years to yield 51,020 observations, and of the over 5,000 variables, we select nine related to happiness:

- age. age in years: 18–89.
- degree. highest education: lt high school, high school, junior college, bachelor, graduate.
- finrela. relative financial status: far above, above average, average, below average, far below.
- happy. happiness: very happy, pretty happy, not too happy.
- health. health: excellent, good, fair, poor.
- marital. marital status: married, never married, divorced, widowed, separated.
- sex. sex: female, male.
- wtsall. probability weight. 0.43–6.43.

References

Smith, Tom W., Peter V. Marsden, Michael Hout, Jibum Kim. *General Social Surveys, 1972-2006*. [machine-readable data file]. Principal Investigator, Tom W. Smith; Co-Principal Investigators, Peter V. Marsden and Michael Hout, NORC ed. Chicago: National Opinion Research Center, producer, 2005; Storrs, CT: The Roper Center for Public Opinion Research, University of Connecticut, distributor. 1 data file (57,061 logical records) and 1 codebook (3,422 pp).

lowertriangle *lowertriangle - rearrange dataset as the preparation of ggscatmat function*

Description

function for making the melted dataset used to plot the lowertriangle scatterplots.

Usage

```
lowertriangle(data, columns = 1:ncol(data), color = NULL)
```

Arguments

data	a data matrix. Should contain numerical (continuous) data.
columns	an option to choose the column to be used in the raw dataset. Defaults to 1:ncol(data)
color	an option to choose a factor variable to be grouped with. Defaults to (NULL)

Author(s)

Mengjia Ni, Di Cook <dicook@monash.edu>

Examples

```
data(flea)
head(lowertriangle(flea, columns= 2:4))
head(lowertriangle(flea))
head(lowertriangle(flea, color="species"))
```

model_response_variables *Model term names*

Description

Retrieve either the response variable names, the beta variable names, or beta variable names. If the model is an object of class 'lm', by default, the beta variable names will include anova significance stars.

Usage

```
model_response_variables(model, data = broom::augment(model))

model_beta_variables(model, data = broom::augment(model))

model_beta_label(model, data = broom::augment(model), lmStars = TRUE)
```

Arguments

`model`	model in question
`data`	equivalent to `broom::augment(model)`
`lmStars`	boolean that determines if stars are added to labels

Value

character vector of names

`nasa` *Data from the Data Expo JSM 2006.*

Description

This data was provided by NASA for the competition.

Usage

```
data(nasa)
```

Format

A data frame with 41472 rows and 17 variables

Details

The data shows 6 years of monthly measurements of a 24x24 spatial grid from Central America:

- time integer specifying temporal order of measurements
- x, y, lat, long spatial location of measurements.
- cloudhigh, cloudlow, cloudmid, ozone, pressure, surftemp, temperature are the various satellite measurements.
- date, day, month, year specifying the time of measurements.
- id unique ide for each spatial position.

References

Murrell, P. (2010) The 2006 Data Expo of the American Statistical Association. Computational Statistics, 25:551-554.

`pigs` *United Kingdom Pig Production*

Description

This data contains about the United Kingdom Pig Production from the book 'Data' by Andrews and Herzberg. The original data can be on Statlib: http://lib.stat.cmu.edu/datasets/Andrews/T62.1

Usage

```
data(pigs)
```

Format

A data frame with 48 rows and 8 variables

Details

The time variable has been added from a combination of year and quarter

- time year + (quarter - 1) / 4
- year year of production
- quarter quarter of the year of production
- gilts number of sows giving birth for the first time
- profit ratio of price to an index of feed price
- s_per_herdsz ratio of the number of breeding pigs slaughtered to the total breeding herd size
- production number of pigs slaughtered that were reared for meat
- herdsz breeding herd size

References

Andrews, David F., and Agnes M. Herzberg. Data: a collection of problems from many fields for the student and research worker. Springer Science & Business Media, 2012.

print.ggmatrix *Print ggmatrix object*

Description

Print method taken from `ggplot2:::print.ggplot` and altered for a ggmatrix object

Usage

```
## S3 method for class 'ggmatrix'
print(x, newpage = is.null(vp), vp = NULL, ...)
```

Arguments

x	plot to display
newpage	draw new (empty) page first?
vp	viewport to draw plot in
...	arguments passed onto ggmatrix_gtable

Author(s)

Barret Schloerke

Examples

```
data(tips, package = "reshape")
pMat <- ggpairs(tips, c(1,3,2), mapping = ggplot2::aes_string(color = "sex"))
pMat # calls print(pMat), which calls print.ggmatrix(pMat)
```

print_if_interactive *Print if not CRAN*

Description

Small function to print a plot if the R session is interactive or in a travis build

Usage

```
print_if_interactive(p)
```

Arguments

p	plot to be displayed

psychademic *UCLA canonical correlation analysis data*

Description

This data contains 600 observations on eight variables

Usage

```
data(psychademic)
```

Format

A data frame with 600 rows and 8 variables

Details

- locus_of_control - psychological
- self_concept - psychological
- motivation - psychological. Converted to four character groups
- read - academic
- write - academic
- math - academic
- science - academic
- female - academic. Dropped from original source
- sex - academic. Added as a character version of female column

References

R Data Analysis Examples | Canonical Correlation Analysis. UCLA: Institute for Digital Research and Education. from http://www.stats.idre.ucla.edu/r/dae/canonical-correlation-analysis (accessed May 22, 2017).

putPlot *Put Plot*

Description

Function to place your own plot in the layout.

Usage

```
putPlot(pm, value, i, j)

## S3 replacement method for class 'ggmatrix'
pm[i, j, ...] <- value
```

Arguments

pm	ggally object to be altered
value	ggplot object to be placed
i	row from the top
j	column from the left
...	ignored

Author(s)

Barret Schloerke <schloerke@gmail.com>

Examples

```
custom_car <- ggpairs(mtcars[, c("mpg", "wt", "cyl")], upper = "blank", title = "Custom Example")
# ggplot example taken from example(geom_text)
  plot <- ggplot2::ggplot(mtcars, ggplot2::aes(x=wt, y=mpg, label=rownames(mtcars)))
  plot <- plot +
    ggplot2::geom_text(ggplot2::aes(colour=factor(cyl)), size = 3) +
    ggplot2::scale_colour_discrete(l=40)
custom_car[1, 2] <- plot
personal_plot <- ggally_text(
  "ggpairs allows you\nto put in your\nown plot.\nLike that one.\n <---"
)
custom_car[1, 3] <- personal_plot
# custom_car

# remove plots after creating a plot matrix
custom_car[2,1] <- NULL
custom_car[3,1] <- "blank" # the same as storing null
custom_car[3,2] <- NULL
custom_car
```

rescale01 *Rescaling functions*

Description

Rescaling functions

Usage

```
range01(x)

max1(x)

mean0(x)

min0(x)

rescale01(x, xlim = NULL)

rescale11(x, xlim = NULL)
```

Arguments

x	numeric vector
xlim	value used in range

scag_order *Find order of variables*

Description

Find order of variables based on a specified scagnostic measure by maximizing the index values of that measure along the path.

Usage

```
scag_order(scag, vars, measure)
```

Arguments

scag	scagnostics object
vars	character vector of the variables to be ordered
measure	scagnostics measure to order according to

Value

character vector of variable ordered according to the given scagnostic measure

Author(s)

Barret Schloerke

`scatmat` *scatmat - plot the lowertriangle plots and density plots of the scatter plot matrix.*

Description

function for making scatterplots in the lower triangle and diagonal density plots.

Usage

```
scatmat(data, columns = 1:ncol(data), color = NULL, alpha = 1)
```

Arguments

`data`	a data matrix. Should contain numerical (continuous) data.
`columns`	an option to choose the column to be used in the raw dataset. Defaults to `1:ncol(data)`
`color`	an option to group the dataset by the factor variable and color them by different colors. Defaults to `NULL`
`alpha`	an option to set the transparency in scatterplots for large data. Defaults to `1`.

Author(s)

Mengjia Ni, Di Cook <dicook@monash.edu>

Examples

```
data(flea)
scatmat(flea, columns=2:4)
scatmat(flea, columns= 2:4, color="species")
```

singleClassOrder *Order axis variables*

Description

Order axis variables by separation between one class and the rest (most separation to least).

Usage

```
singleClassOrder(classVar, axisVars, specClass = NULL)
```

Arguments

classVar	class variable (vector from original dataset)
axisVars	variables to be plotted as axes (data frame)
specClass	character string matching to level of classVar; instead of looking for separation between any class and the rest, will only look for separation between this class and the rest

Value

character vector of names of axisVars ordered such that the first variable has the most separation between one of the classes and the rest, and the last variable has the least (as measured by F-statistics from an ANOVA)

Author(s)

Jason Crowley <crowley.jason.s@gmail.com>

skewness *Sample skewness*

Description

Calculate the sample skewness of a vector while ignoring missing values.

Usage

```
skewness(x)
```

Arguments

x	numeric vector

Value

sample skewness of x

Author(s)

Jason Crowley <crowley.jason.s@gmail.com>

---

str.ggmatrix *ggmatrix structure*

Description

View the condensed version of the ggmatrix object. The attribute "class" is ALWAYS altered to "_class" to avoid recursion.

Usage

```
## S3 method for class 'ggmatrix'
str(object, ..., raw = FALSE)
```

Arguments

object	ggmatrix object to be viewed
...	passed on to the default str method
raw	boolean to determine if the plots should be converted to text or kept as original objects

---

twitter_spambots *Twitter spambots*

Description

A network of spambots found on Twitter as part of a data mining project.

Usage

```
data(twitter_spambots)
```

Format

An object of class network with 120 edges and 94 vertices.

Details

Each node of the network is identified by the Twitter screen name of the account and further carries five vertex attributes:

- location user's location, as provided by the user
- lat latitude, based on the user's location
- lon longitude, based on the user's location
- followers number of Twitter accounts that follow this account
- friends number of Twitter accounts followed by the account

Author(s)

Amos Elberg

`uppertriangle` *uppertriangle - rearrange dataset as the preparation of ggscatmat function*

Description

function for making the dataset used to plot the uppertriangle plots.

Usage

```
uppertriangle(data, columns = 1:ncol(data), color = NULL,
  corMethod = "pearson")
```

Arguments

`data`	a data matrix. Should contain numerical (continuous) data.
`columns`	an option to choose the column to be used in the raw dataset. Defaults to `1:ncol(data)`
`color`	an option to choose a factor variable to be grouped with. Defaults to `(NULL)`
`corMethod`	method argument supplied to `cor`

Author(s)

Mengjia Ni, Di Cook <dicook@monash.edu>

Examples

```
data(flea)
head(uppertriangle(flea, columns=2:4))
head(uppertriangle(flea))
head(uppertriangle(flea, color="species"))
```

v1_ggmatrix_theme *Modify a ggmatrix object by adding an ggplot2 object to all plots*

Description

Modify a ggmatrix object by adding an ggplot2 object to all plots

Usage

```
v1_ggmatrix_theme()
```

Examples

```
ggpairs(iris, 1:2) + v1_ggmatrix_theme()
# move the column names to the left and bottom
ggpairs(iris, 1:2, switch = "both") + v1_ggmatrix_theme()
```

wrap_fn_with_param_arg *Wrap a function with different parameter values*

Description

Wraps a function with the supplied parameters to force different default behavior. This is useful for functions that are supplied to ggpairs. It allows you to change the behavior of one function, rather than creating multiple functions with different parameter settings.

Usage

```
wrap_fn_with_param_arg(funcVal, params = NULL,
  funcArgName = deparse(substitute(funcVal)))

wrapp(funcVal, params = NULL, funcArgName = deparse(substitute(funcVal)))

wrap(funcVal, ..., funcArgName = deparse(substitute(funcVal)))

wrap_fn_with_params(funcVal, ..., funcArgName = deparse(substitute(funcVal)))
```

Arguments

funcVal	function that the params will be applied to. The function should follow the api of function(data, mapping, ...){}. funcVal is allowed to be a string of one of the ggally_NAME functions, such as "points" for ggally_points or "facetdensity" for ggally_facetdensity.

params	named vector or list of parameters to be applied to the funcVal
funcArgName	name of function to be displayed
...	named parameters to be supplied to wrap_fn_with_param_arg

Details

wrap is identical to wrap_fn_with_params. These function take the new parameters as arguments.

wrapp is identical to wrap_fn_with_param_arg. These functions take the new parameters as a single list.

The params and fn attributes are there for debugging purposes. If either attribute is altered, the function must be re-wrapped to have the changes take effect.

Value

a function(data, mapping, ...){} that will wrap the original function with the parameters applied as arguments

Examples

```
 # small function to display plots only if it's interactive
 p_ <- GGally::print_if_interactive

# example function that prints 'val'
fn <- function(data, mapping, val = 2) {
  print(val)
}
fn(data = NULL, mapping = NULL) # 2

# wrap function to change default value 'val' to 5 instead of 2
wrapped_fn1 <- wrap(fn, val = 5)
wrapped_fn1(data = NULL, mapping = NULL) # 5
# you may still supply regular values
wrapped_fn1(data = NULL, mapping = NULL, val = 3) # 3

# wrap function to change 'val' to 5 using the arg list
wrapped_fn2 <- wrap_fn_with_param_arg(fn, params = list(val = 5))
wrapped_fn2(data = NULL, mapping = NULL) # 5

# change parameter settings in ggpairs for a particular function
## Goal output:
regularPlot <- ggally_points(
  iris,
  ggplot2::aes(Sepal.Length, Sepal.Width),
  size = 5, color = "red"
)
p_(regularPlot)

# Wrap ggally_points to have parameter values size = 5 and color = 'red'
w_ggally_points <- wrap(ggally_points, size = 5, color = "red")
wrappedPlot <- w_ggally_points(
  iris,
```

```
  ggplot2::aes(Sepal.Length, Sepal.Width)
)
p_(wrappedPlot)

# Double check the aes parameters are the same for the geom_point layer
identical(regularPlot$layers[[1]]$aes_params, wrappedPlot$layers[[1]]$aes_params)

# Use a wrapped function in ggpairs
pm <- ggpairs(iris, 1:3, lower = list(continuous = wrap(ggally_points, size = 5, color = "red")))
p_(pm)
pm <- ggpairs(iris, 1:3, lower = list(continuous = w_ggally_points))
p_(pm)
```

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