Package ‘ggplot2’

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Title Create Elegant Data Visualisations Using the Grammar of Graphics
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    'utilities-checks.R' 'legend-draw.R' 'geom-.R'

1
R topics documented:

coord_flip .......................................................... 39
coord_map ............................................................ 40
coord_polar .......................................................... 43
coord_trans .......................................................... 45
cut_interval ......................................................... 47
diamonds ............................................................. 49
draw_key ............................................................. 49
economics ............................................................ 51
element ................................................................. 52
expand_limits ....................................................... 54
expansion ............................................................. 55
facet_grid ............................................................ 56
facet_wrap ........................................................... 58
faithful ............................................................... 59
fortify ................................................................. 61
geom_abline .......................................................... 62
geom_bar ............................................................. 65
geom_bin_2d .......................................................... 69
geom_blank .......................................................... 72
geom_boxplot ....................................................... 73
geom_contour ........................................................ 78
geom_density ........................................................ 89
geom_density_2d ..................................................... 92
geom_dotplot ......................................................... 97
geom_errorbarh ...................................................... 101
geom_freqpoly ...................................................... 103
geom_function ....................................................... 108
geom_hex ............................................................ 111
geom_jitter .......................................................... 114
geom_label ............................................................ 116
geom_map ............................................................ 121
geom_path ........................................................... 124
geom_point .......................................................... 128
geom_polygon ....................................................... 131
geom_qq_line ......................................................... 134
geom_quantile ....................................................... 137
geom_raster .......................................................... 140
geomribbon .......................................................... 143
geom_rug ............................................................. 147
geom_segment ......................................................... 150
geom_smooth ........................................................ 153
geom_spline ........................................................ 158
geom_spike .......................................................... 160
geom_violin .......................................................... 164
getalt_text ........................................................... 165
ggplot ................................................................. 167
ggproto ............................................................... 167
R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>ggsave</td>
<td>169</td>
</tr>
<tr>
<td>ggh.theme</td>
<td>171</td>
</tr>
<tr>
<td>guides</td>
<td>174</td>
</tr>
<tr>
<td>guide_axis</td>
<td>175</td>
</tr>
<tr>
<td>guide_axis_logticks</td>
<td>177</td>
</tr>
<tr>
<td>guide_axis_stack</td>
<td>179</td>
</tr>
<tr>
<td>guide_axis_theta</td>
<td>180</td>
</tr>
<tr>
<td>guide_bins</td>
<td>182</td>
</tr>
<tr>
<td>guide_colourbar</td>
<td>184</td>
</tr>
<tr>
<td>guide_coloursteps</td>
<td>187</td>
</tr>
<tr>
<td>guide_custom</td>
<td>189</td>
</tr>
<tr>
<td>guide_legend</td>
<td>191</td>
</tr>
<tr>
<td>guide_none</td>
<td>193</td>
</tr>
<tr>
<td>hmisc</td>
<td>194</td>
</tr>
<tr>
<td>labeller</td>
<td>195</td>
</tr>
<tr>
<td>labellers</td>
<td>197</td>
</tr>
<tr>
<td>label_bquote</td>
<td>199</td>
</tr>
<tr>
<td>labs</td>
<td>200</td>
</tr>
<tr>
<td>lims</td>
<td>201</td>
</tr>
<tr>
<td>luv_colours</td>
<td>203</td>
</tr>
<tr>
<td>mean_se</td>
<td>204</td>
</tr>
<tr>
<td>midwest</td>
<td>204</td>
</tr>
<tr>
<td>mpg</td>
<td>206</td>
</tr>
<tr>
<td>msleep</td>
<td>206</td>
</tr>
<tr>
<td>position_dodge</td>
<td>207</td>
</tr>
<tr>
<td>position_identity</td>
<td>209</td>
</tr>
<tr>
<td>position_jitter</td>
<td>210</td>
</tr>
<tr>
<td>position_jitterdodge</td>
<td>211</td>
</tr>
<tr>
<td>position_nudge</td>
<td>212</td>
</tr>
<tr>
<td>position_stack</td>
<td>213</td>
</tr>
<tr>
<td>presidential</td>
<td>215</td>
</tr>
<tr>
<td>print.ggplot</td>
<td>216</td>
</tr>
<tr>
<td>print.ggproto</td>
<td>217</td>
</tr>
<tr>
<td>qplot</td>
<td>218</td>
</tr>
<tr>
<td>resolution</td>
<td>220</td>
</tr>
<tr>
<td>scale_alpha</td>
<td>220</td>
</tr>
<tr>
<td>scale_binned</td>
<td>221</td>
</tr>
<tr>
<td>scale_colour_brewer</td>
<td>224</td>
</tr>
<tr>
<td>scale_colour_continuous</td>
<td>228</td>
</tr>
<tr>
<td>scale_colour_discrete</td>
<td>230</td>
</tr>
<tr>
<td>scale_colour_gradient</td>
<td>231</td>
</tr>
<tr>
<td>scale_colour_grey</td>
<td>236</td>
</tr>
<tr>
<td>scale_colour_hue</td>
<td>239</td>
</tr>
<tr>
<td>scale_colour_steps</td>
<td>242</td>
</tr>
<tr>
<td>scale_colour_viridis_d</td>
<td>246</td>
</tr>
<tr>
<td>scale_continuous</td>
<td>250</td>
</tr>
<tr>
<td>scale_date</td>
<td>254</td>
</tr>
<tr>
<td>scale_identity</td>
<td>258</td>
</tr>
</tbody>
</table>
*.gg

Add components to a plot

Description

* is the key to constructing sophisticated ggplot2 graphics. It allows you to start simple, then get more and more complex, checking your work at each step.

Usage

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

Arguments

- **e1**: An object of class `ggplot()` or a `theme()`.
- **e2**: A plot component, as described below.
What can you add?

You can add any of the following types of objects:

- An `aes()` object replaces the default aesthetics.
- A layer created by a `geom_` or `stat_` function adds a new layer.
- A scale overrides the existing scale.
- A `theme()` modifies the current theme.
- A `coord` overrides the current coordinate system.
- A facet specification overrides the current faceting.

To replace the current default data frame, you must use `%+%`, due to S3 method precedence issues.

You can also supply a list, in which case each element of the list will be added in turn.

See Also

`theme()`

Examples

```r
data(base)

base <- ggplot(mpg, aes(displ, hwy)) + geom_point()
base + geom_smooth()

# To override the data, you must use %++%
base %+% subset(mpg, fl == "p")

# Alternatively, you can add multiple components with a list.
# This can be useful to return from a function.
base + list(subset(mpg, fl == "p"), geom_smooth())
```

---

```r
aes

Construct aesthetic mappings
```

Description

Aesthetic mappings describe how variables in the data are mapped to visual properties (aesthetics) of geoms. Aesthetic mappings can be set in `ggplot()` and in individual layers.

Usage

```r
aes(x, y, ...)
```
Arguments

x, y, ...  
<data-masking> List of name-value pairs in the form aesthetic = variable describing which variables in the layer data should be mapped to which aesthetics used by the paired geom/stat. The expression variable is evaluated within the layer data, so there is no need to refer to the original dataset (i.e., use ggplot(df, aes(variable)) instead of ggplot(df, aes(df$variable))). The names for x and y aesthetics are typically omitted because they are so common; all other aesthetics must be named.

Details

This function also standardises aesthetic names by converting color to colour (also in substrings, e.g., point_color to point_colour) and translating old style R names to ggplot names (e.g., pch to shape and cex to size).

Value

A list with class uneval. Components of the list are either quosures or constants.

Quasiquotation

aes() is a quoting function. This means that its inputs are quoted to be evaluated in the context of the data. This makes it easy to work with variables from the data frame because you can name those directly. The flip side is that you have to use quasiquotation to program with aes(). See a tidy evaluation tutorial such as the dplyr programming vignette to learn more about these techniques.

See Also

vars() for another quoting function designed for faceting specifications.
Run vignette(“ggplot2-specs”) to see an overview of other aesthetics that can be modified.
Delayed evaluation for working with computed variables.
Other aesthetics documentation: aes_colour_fill_alpha, aes_group_order, aes_linetype_size_shape, aes_position

Examples

aes(x = mpg, y = wt)
aes(mpg, wt)

# You can also map aesthetics to functions of variables
aes(x = mpg ^ 2, y = wt / cyl)

# Or to constants
aes(x = 1, colour = "smooth")

# Aesthetic names are automatically standardised
aes(col = x)
aes(fg = x)
aes(color = x)
aes_colour_fill_alpha

aes(colour = x)

# aes() is passed to either ggplot() or specific layer. Aesthetics supplied
# to ggplot() are used as defaults for every layer.
ggplot(mpg, aes(displ, hwy)) + geom_point()
ggplot(mpg) + geom_point(aes(displ, hwy))

# Tidy evaluation ----------------------------------------------------
# aes() automatically quotes all its arguments, so you need to use tidy
# evaluation to create wrappers around ggplot2 pipelines. The
# simplest case occurs when your wrapper takes dots:
scatter_by <- function(data, ...) {
  ggplot(data) + geom_point(aes(...))
}
scatter_by(mtcars, disp, drat)

# If your wrapper has a more specific interface with named arguments,
# you need the "embrace operator":
scatter_by <- function(data, x, y) {
  ggplot(data) + geom_point(aes({{ x }}, {{ y }}))
}
scatter_by(mtcars, disp, drat)

# Note that users of your wrapper can use their own functions in the
# quoted expressions and all will resolve as it should!
cut3 <- function(x) cut_number(x, 3)
scatter_by(mtcars, cut3(disp), drat)

---

aes_colour_fill_alpha  Colour related aesthetics: colour, fill, and alpha

Description

These aesthetics parameters change the colour (colour and fill) and the opacity (alpha) of geom
elements on a plot. Almost every geom has either colour or fill (or both), as well as can have their
alpha modified. Modifying colour on a plot is a useful way to enhance the presentation of data,
often especially when a plot graphs more than two variables.

Colour and fill

The colour aesthetic is used to draw lines and strokes, such as in geom_point() and geom_line(),
but also the line contours of geom_rect() and geom_polygon(). The fill aesthetic is used to
colour the inside areas of geoms, such as geom_rect() and geom_polygon(), but also the insides
of shapes 21-25 of geom_point().

Colours and fills can be specified in the following ways:

- A name, e.g., "red". R has 657 built-in named colours, which can be listed with grDevices::colors().
- An rgb specification, with a string of the form "#RRGGBB" where each of the pairs RR, GG, BB
  consists of two hexadecimal digits giving a value in the range 00 to FF. You can optionally
  make the colour transparent by using the form "#RRGGBBAA".
• An NA, for a completely transparent colour.

**Alpha**

Alpha refers to the opacity of a geom. Values of alpha range from 0 to 1, with lower values corresponding to more transparent colors.  

Alpha can additionally be modified through the `colour` or `fill` aesthetic if either aesthetic provides color values using an rgb specification ("#RRGGBBAA"), where AA refers to transparency values.

**See Also**

• Other options for modifying colour: `scale_colour_brewer()`, `scale_colour_gradient()`, `scale_colour_grey()`, `scale_colour_hue()`, `scale_colour_identity()`, `scale_colour_manual()`, `scale_colour_viridis_d()`

• Other options for modifying fill: `scale_fill_brewer()`, `scale_fill_gradient()`, `scale_fill_grey()`, `scale_fill_hue()`, `scale_fill_identity()`, `scale_fill_manual()`, `scale_fill_viridis_d()`

• Other options for modifying alpha: `scale_alpha()`, `scale_alpha_manual()`, `scale_alpha_identity()`

• Run vignette("ggplot2-specs") to see an overview of other aesthetics that can be modified.

Other aesthetics documentation: `aes_group_order`, `aes_linetype_size_shape`, `aes_position`, `aes()`

**Examples**

```r
# Bar chart example
p <- ggplot(mtcars, aes(factor(cyl)))
# Default plotting
p + geom_bar()
# To change the interior colouring use fill aesthetic
p + geom_bar(fill = "red")
# Compare with the colour aesthetic which changes just the bar outline
p + geom_bar(colour = "red")
# Combining both, you can see the changes more clearly
p + geom_bar(fill = "white", colour = "red")
# Both colour and fill can take an rgb specification.
p + geom_bar(fill = "#00abff")
# Use NA for a completely transparent colour.
p + geom_bar(fill = NA, colour = "#00abff")

# Colouring scales differ depending on whether a discrete or
# continuous variable is being mapped. For example, when mapping
# fill to a factor variable, a discrete colour scale is used.
ggplot(mtcars, aes(factor(cyl), fill = factor(vs))) + geom_bar()

# When mapping fill to continuous variable a continuous colour
# scale is used.
ggplot(faithfuld, aes(waiting, eruptions)) +
  geom_raster(aes(fill = density))
```
# Some geoms only use the colour aesthetic but not the fill
# aesthetic (e.g. geom_point() or geom_line()).
p <- ggplot(economics, aes(x = date, y = unemploy))
p + geom_line()
p + geom_line(colour = "green")
p + geom_point()
p + geom_point(colour = "red")

# For large datasets with overplotting the alpha
# aesthetic will make the points more transparent.
set.seed(1)
df <- data.frame(x = rnorm(5000), y = rnorm(5000))
p <- ggplot(df, aes(x,y))
p + geom_point()
p + geom_point(alpha = 0.5)
p + geom_point(alpha = 1/10)

# Alpha can also be used to add shading.
p <- ggplot(economics, aes(x = date, y = unemploy)) + geom_line()
yrng <- range(economics$unemploy)
p <- p + geom_rect(
  aes(NULL, NULL, xmin = start, xmax = end, fill = party),
  y = yrng[1], ymax = yrng[2], data = presidential
)
p + scale_fill_manual(values = alpha(c("blue", "red"), .3))

---

**aes_eval**  
*Control aesthetic evaluation*

**Description**

Most aesthetics are mapped from variables found in the data. Sometimes, however, you want to delay the mapping until later in the rendering process. ggplot2 has three stages of the data that you can map aesthetics from, and three functions to control at which stage aesthetics should be evaluated.

after_stat() replaces the old approaches of using either stat(), e.g. stat(density), or surrounding the variable names with ...e.g. ...density...

**Usage**

# These functions can be used inside the `aes()` function
# used as the `mapping` argument in layers, for example:
# geom_density(mapping = aes(y = after_stat(scaled)))
after_stat(x)

after_scale(x)

stage(start = NULL, after_stat = NULL, after_scale = NULL)

Arguments

x <data-masking> An aesthetic expression using variables calculated by the stat (after_stat()) or layer aesthetics (after_scale()).

start <data-masking> An aesthetic expression using variables from the layer data.

after_stat <data-masking> An aesthetic expression using variables calculated by the stat.

after_scale <data-masking> An aesthetic expression using layer aesthetics.

Staging

Below follows an overview of the three stages of evaluation and how aesthetic evaluation can be controlled.

Stage 1: direct input:
The default is to map at the beginning, using the layer data provided by the user. If you want to map directly from the layer data you should not do anything special. This is the only stage where the original layer data can be accessed.

# 'x' and 'y' are mapped directly
ggplot(mtcars) + geom_point(aes(x = mpg, y = disp))

Stage 2: after stat transformation:
The second stage is after the data has been transformed by the layer stat. The most common example of mapping from stat transformed data is the height of bars in geom_histogram(): the height does not come from a variable in the underlying data, but is instead mapped to the count computed by stat_bin(). In order to map from stat transformed data you should use the after_stat() function to flag that evaluation of the aesthetic mapping should be postponed until after stat transformation. Evaluation after stat transformation will have access to the variables calculated by the stat, not the original mapped values. The 'computed variables' section in each stat lists which variables are available to access.

# The 'y' values for the histogram are computed by the stat
ggplot(faithful, aes(x = waiting)) + geom_histogram()

# Choosing a different computed variable to display, matching up the histogram with the density plot
ggplot(faithful, aes(x = waiting)) + geom_histogram(aes(y = after_stat(density))) + geom_density()

Stage 3: after scale transformation:
The third and last stage is after the data has been transformed and mapped by the plot scales. An example of mapping from scaled data could be to use a desaturated version of the stroke colour for fill. You should use `after_scale()` to flag evaluation of mapping for after data has been scaled. Evaluation after scaling will only have access to the final aesthetics of the layer (including non-mapped, default aesthetics).

```r
# The exact colour is known after scale transformation
ggplot(mpg, aes(cty, colour = factor(cyl))) +
  geom_density()

# We re-use colour properties for the fill without a separate fill scale
ggplot(mpg, aes(cty, colour = factor(cyl))) +
  geom_density(aes(fill = after_scale(alpha(colour, 0.3))))
```

**Complex staging:**
If you want to map the same aesthetic multiple times, e.g. map `x` to a data column for the stat, but remap it for the geom, you can use the `stage()` function to collect multiple mappings.

```r
# Use stage to modify the scaled fill
ggplot(mpg, aes(class, hwy)) +
  geom_boxplot(aes(fill = stage(class, after_scale = alpha(fill, 0.4))))

# Using data for computing summary, but placing label elsewhere.
# Also, we're making our own computed variable to use for the label.
ggplot(mpg, aes(class, displ)) +
  geom_violin() +
  stat_summary(
    aes(
      y = stage(displ, after_stat = 8),
      label = after_stat(paste(mean, "±", sd))
    ),
    geom = "text",
    fun.data = ~ round(data.frame(mean = mean(.x), sd = sd(.x)), 2)
  )
```

**Examples**

```r
# Default histogram display
ggplot(mpg, aes(displ)) +
  geom_histogram(aes(y = after_stat(count)))

# Scale tallest bin to 1
ggplot(mpg, aes(displ)) +
  geom_histogram(aes(y = after_stat(count / max(count))))

# Use a transparent version of colour for fill
ggplot(mpg, aes(class, hwy)) +
  geom_boxplot(aes(colour = class, fill = after_scale(alpha(colour, 0.4))))

# Use stage to modify the scaled fill
ggplot(mpg, aes(class, hwy)) +
```
# Making a proportional stacked density plot
```r
ggplot(mpg, aes(cty)) +
  geom_density(
    aes(
      colour = factor(cyl),
      fill = after_scale(alpha(colour, 0.3)),
      y = after_stat(count / sum(n[!duplicated(group)]))
    ),
    position = "stack", bw = 1
  ) +
  geom_density(bw = 1)
```

# Imitating a ridgeline plot
```r
ggplot(mpg, aes(cty, colour = factor(cyl))) +
  geom_ribbon(
    stat = "density", outline.type = "upper",
    aes(
      fill = after_scale(alpha(colour, 0.3)),
      ymin = after_stat(group),
      ymax = after_stat(group + ndensity)
    )
  )
```

# Labelling a bar plot
```r
ggplot(mpg, aes(class)) +
  geom_bar() +
  geom_text(
    aes(
      y = after_stat(count + 2),
      label = after_stat(count)
    ),
    stat = "count"
  )
```

# Labelling the upper hinge of a boxplot,
# inspired by June Choe
```r
ggplot(mpg, aes(displ, class)) +
  geom_boxplot(outlier.shape = NA) +
  geom_text(
    aes(
      label = after_stat(xmax),
      x = stage(displ, after_stat = xmax)
    ),
    stat = "boxplot",
    hjust = -0.5
  )
```

---

**aes_group_order**

- **Aesthetics:** grouping
Description

The group aesthetic is by default set to the interaction of all discrete variables in the plot. This choice often partitions the data correctly, but when it does not, or when no discrete variable is used in the plot, you will need to explicitly define the grouping structure by mapping group to a variable that has a different value for each group.

Details

For most applications the grouping is set implicitly by mapping one or more discrete variables to x, y, colour, fill, alpha, shape, size, and/or linetype. This is demonstrated in the examples below.

There are three common cases where the default does not display the data correctly.

1. `geom_line()` where there are multiple individuals and the plot tries to connect every observation, even across individuals, with a line.
2. `geom_line()` where a discrete x-position implies groups, whereas observations span the discrete x-positions.
3. When the grouping needs to be different over different layers, for example when computing a statistic on all observations when another layer shows individuals.

The examples below use a longitudinal dataset, Oxboys, from the nlme package to demonstrate these cases. Oxboys records the heights (height) and centered ages (age) of 26 boys (Subject), measured on nine occasions (Occasion).

See Also

- Geoms commonly used with groups: `geom_bar()`, `geom_histogram()`, `geom_line()`
- Run vignette("ggplot2-specs") to see an overview of other aesthetics that can be modified.

Other aesthetics documentation: `aes_colour_fill_alpha`, `aes_linetype_size_shape`, `aes_position`, `aes()`

Examples

```r
p <- ggplot(mtcars, aes(wt, mpg))
# A basic scatter plot
p + geom_point(size = 4)
# Using the colour aesthetic
p + geom_point(aes(colour = factor(cyl)), size = 4)
# Using the shape aesthetic
p + geom_point(aes(shape = factor(cyl)), size = 4)

# Using fill
p <- ggplot(mtcars, aes(factor(cyl)))
p + geom_bar()
p + geom_bar(aes(fill = factor(cyl)))
p + geom_bar(aes(fill = factor(vs)))
```
Differentiation related aesthetics: linetype, size, shape

Description

The linetype, linewidth, size, and shape aesthetics modify the appearance of lines and/or points. They also apply to the outlines of polygons (linetype and linewidth) or to text (size).

Linetype

The linetype aesthetic can be specified with either an integer (0-6), a name (0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash), a mapping to a discrete variable, or a
string of an even number (up to eight) of hexadecimal digits which give the lengths in consecutive positions in the string. See examples for a hex string demonstration.

Linewidth and stroke

The linewidth aesthetic sets the widths of lines, and can be specified with a numeric value (for historical reasons, these units are about 0.75 millimetres). Alternatively, they can also be set via mapping to a continuous variable. The stroke aesthetic serves the same role for points, but is distinct for discriminating points from lines in geoms such as `geom_pointrange()`.

Size

The size aesthetic control the size of points and text, and can be specified with a numerical value (in millimetres) or via a mapping to a continuous variable.

Shape

The shape aesthetic controls the symbols of points, and can be specified with an integer (between 0 and 25), a single character (which uses that character as the plotting symbol), a . to draw the smallest rectangle that is visible (i.e., about one pixel), an NA to draw nothing, or a mapping to a discrete variable. Symbols and filled shapes are described in the examples below.

See Also

- `geom_line()` and `geom_point()` for geoms commonly used with these aesthetics.
- `aes_group_order()` for using linetype, size, or shape for grouping.
- Scales that can be used to modify these aesthetics: `scale_linetype()`, `scale_linewidth()`, `scale_size()`, and `scale_shape()`.
- Run vignette("ggplot2-specs") to see an overview of other aesthetics that can be modified.

Other aesthetics documentation: `aes_colour_fill_alpha`, `aes_group_order`, `aes_position`, `aes()`

Examples

def <- data.frame(x = 1:10, y = 1:10)
p <- ggplot(def, aes(x, y))
p + geom_line(linetype = 2)
p + geom_line(linetype = "dotdash")

# An example with hex strings; the string "33" specifies three units on followed # by three off and "3313" specifies three units on followed by three off followed # by one on and finally three off.
p + geom_line(linetype = "3313")

# Mapping line type from a grouping variable
ggplot(economics_long, aes(date, value01)) +
    geom_line(aes(linetype = variable))
# Linewidth examples
ggplot(economics, aes(date, unemploy)) +
  geom_line(linewidth = 2, lineend = "round")
ggplot(economics, aes(date, unemploy)) +
  geom_line(aes(linewidth = uempmed), lineend = "round")

# Size examples
p <- ggplot(mtcars, aes(wt, mpg))
p + geom_point(size = 4)
p + geom_point(aes(size = qsec))
p + geom_point(size = 2.5) +
  geom_hline(yintercept = 25, size = 3.5)

# Shape examples
p + geom_point()
p + geom_point(shape = 5)
p + geom_point(shape = "k", size = 3)
p + geom_point(shape = ".")
p + geom_point(shape = NA)
p + geom_point(aes(shape = factor(cyl)))

# A look at all 25 symbols
df2 <- data.frame(x = 1:5 , y = 1:25, z = 1:25)
p <- ggplot(df2, aes(x, y))
p + geom_point(aes(shape = z), size = 4) +
  scale_shape_identity()

# While all symbols have a foreground colour, symbols 19-25 also take a
# background colour (fill)
p + geom_point(aes(shape = z), size = 4, colour = "Red") +
  scale_shape_identity()
p + geom_point(aes(shape = z), size = 4, colour = "Red", fill = "Black") +
  scale_shape_identity()

---

**aes_position**

*Position related aesthetics: x, y, xmin, xmax, ymin, ymax, xend, yend*

**Description**

The following aesthetics can be used to specify the position of elements: x, y, xmin, xmax, ymin, ymax, xend, yend.

**Details**

- x and y define the locations of points or of positions along a line or path.
- x, y and xend, yend define the starting and ending points of segment and curve geometries.
- xmin, xmax, ymin and ymax can be used to specify the position of annotations and to represent rectangular areas.
- In addition, there are position aesthetics that are contextual to the geometry that they’re used in. These are xintercept, yintercept, xmin_final, ymin_final, xmax_final, ymax_final,
xlower, lower, xmiddle, middle, xupper, upper, x0 and y0. Many of these are used and automatically computed in `geom_boxplot()`.

See Also

- Geoms that commonly use these aesthetics: `geom_crossbar()`, `geom_curve()`, `geom_errorbar()`, `geom_line()`, `geom_linerange()`, `geom_path()`, `geom_point()`, `geom_pointrange()`, `geom_rect()`, `geom_segment()`
- Scales that can be used to modify positions: `scale_continuous()`, `scale_discrete()`, `scale_binned()`, `scale_date()`.
- See also `annotate()` for placing annotations.

Other aesthetics documentation: `aes_colour_fill_alpha`, `aes_group_order`, `aes_linetype_size_shape`, `aes()`

Examples

```r
# Generate data: means and standard errors of means for prices
# for each type of cut
dmod <- lm(price ~ cut, data = diamonds)
cut <- unique(diamonds$cut)
cuts_df <- data.frame(
  cut,
  predict(dmod, data.frame(cut), se = TRUE)[c("fit", "se.fit")]
)ggplot(cuts_df) +
aes(
  x = cut,
  y = fit,
  ymin = fit - se.fit,
  ymax = fit + se.fit,
  colour = cut
) +
  geom_pointrange()

# Using annotate
p <- ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point()
p + annotate(
  "rect", xmin = 2, xmax = 3.5, ymin = 2, ymax = 25,
  fill = "dark grey", alpha = .5
)

# Geom_segment examples
p + geom_segment(
  aes(x = 2, y = 15, xend = 2, yend = 25),
  arrow = arrow(length = unit(0.5, "cm"))
)
p + geom_segment(
  aes(x = 2, y = 15, xend = 3, yend = 15),
  arrow = arrow(length = unit(0.5, "cm"))
)
```
```r
p + geom_segment(
  aes(x = 5, y = 30, xend = 3.5, yend = 25),
  arrow = arrow(length = unit(0.5, "cm"))
)

# You can also use geom_segment() to recreate plot(type = "h")
# from base R:
set.seed(1)
counts <- as.data.frame(table(x = rpois(100, 5)))
counts$x <- as.numeric(as.character(counts$x))
with(counts, plot(x, Freq, type = "h", lwd = 10))
ggplot(counts, aes(x = x, y = Freq)) +
  geom_segment(aes(yend = 0, xend = x), size = 10)
```

---

**annotate**  
*Create an annotation layer*

**Description**

This function adds geoms to a plot, but unlike a typical geom function, the properties of the geoms are not mapped from variables of a data frame, but are instead passed in as vectors. This is useful for adding small annotations (such as text labels) or if you have your data in vectors, and for some reason don’t want to put them in a data frame.

**Usage**

```r
annotate(
  geom,
  x = NULL,
  y = NULL,
  xmin = NULL,
  xmax = NULL,
  ymin = NULL,
  ymax = NULL,
  xend = NULL,
  yend = NULL,
  ..., 
  na.rm = FALSE
)
```

**Arguments**

- `geom` name of geom to use for annotation
- `x, y, xmin, ymin, xmax, ymax, xend, yend` positioning aesthetics - you must specify at least one of these.
Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

`na.rm` If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.

**Details**

Note that all position aesthetics are scaled (i.e. they will expand the limits of the plot so they are visible), but all other aesthetics are set. This means that layers created with this function will never affect the legend.

**Unsupported geoms**

Due to their special nature, reference line geoms `geom_abline()`, `geom_hline()`, and `geom_vline()` can’t be used with `annotate()`. You can use these geoms directly for annotations.

**Examples**

```r
p <- ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point()
p + annotate("text", x = 4, y = 25, label = "Some text")
p + annotate("text", x = 2:5, y = 25, label = "Some text")
p + annotate("rect", xmin = 3, xmax = 4.2, ymin = 12, ymax = 21, alpha = .2)
p + annotate("segment", x = 2.5, xend = 4, y = 15, yend = 25, colour = "blue")
p + annotate("pointrange", x = 3.5, y = 20, ymin = 12, ymax = 28, colour = "red", size = 2.5, linewidth = 1.5)
p + annotate("text", x = 4, y = 25, label = "italic(R) ^ 2 == 0.75", parse = TRUE)
p + annotate("text", x = 4, y = 25, label = "paste(italic(R) ^ 2, \" = .75\")", parse = TRUE)
```

**Description**

This is a special geom intended for use as static annotations that are the same in every panel. These annotations will not affect scales (i.e. the x and y axes will not grow to cover the range of the grob, and the grob will not be modified by any ggplot settings or mappings).

**Usage**

```r
annotation_custom(grob, xmin = -Inf, xmax = Inf, ymin = -Inf, ymax = Inf)
```
Arguments

- **grob**: grob to display
- **xmin, xmax**: x location (in data coordinates) giving horizontal location of raster
- **ymin, ymax**: y location (in data coordinates) giving vertical location of raster

Details

Most useful for adding tables, inset plots, and other grid-based decorations.

Note

`annotation_custom()` expects the grob to fill the entire viewport defined by xmin, xmax, ymin, ymax. Grobs with a different (absolute) size will be center-justified in that region. Inf values can be used to fill the full plot panel (see examples).

Examples

```r
# Dummy plot
df <- data.frame(x = 1:10, y = 1:10)
base <- ggplot(df, aes(x, y)) +
  geom_blank() +
  theme_bw()

# Full panel annotation
base + annotation_custom(
  grob = grid::roundrectGrob(),
  xmin = -Inf, xmax = Inf, ymin = -Inf, ymax = Inf
)

# Inset plot
df2 <- data.frame(x = 1, y = 1)
g <- ggplotGrob(ggplot(df2, aes(x, y)) +
  geom_point() +
  theme(plot.background = element_rect(colour = "black")))
base +
  annotation_custom(grob = g, xmin = 1, xmax = 10, ymin = 8, ymax = 10)
```

Description

[Superseded]

This function is superseded by using `guide_axis_logticks()`.

This annotation adds log tick marks with diminishing spacing. These tick marks probably make sense only for base 10.
Usage

```r
annotation_logticks(
  base = 10,
  sides = "bl",
  outside = FALSE,
  scaled = TRUE,
  short = unit(0.1, "cm"),
  mid = unit(0.2, "cm"),
  long = unit(0.3, "cm"),
  colour = "black",
  linewidth = 0.5,
  linetype = 1,
  alpha = 1,
  color = NULL,
  ...,  
  size = deprecated()
)
```

Arguments

- **base**
  - the base of the log (default 10)
- **sides**
  - a string that controls which sides of the plot the log ticks appear on. It can be set to a string containing any of "trbl", for top, right, bottom, and left.
- **outside**
  - logical that controls whether to move the log ticks outside of the plot area. Default is off (FALSE). You will also need to use `coord_cartesian(clip = "off")`. See examples.
- **scaled**
  - is the data already log-scaled? This should be TRUE (default) when the data is already transformed with log10() or when using `scale_y_log10()`. It should be FALSE when using `coord_trans(y = "log10")`.
- **short**
  - a `grid::unit()` object specifying the length of the short tick marks
- **mid**
  - a `grid::unit()` object specifying the length of the middle tick marks. In base 10, these are the "5" ticks.
- **long**
  - a `grid::unit()` object specifying the length of the long tick marks. In base 10, these are the "1" (or "10") ticks.
- **colour**
  - Colour of the tick marks.
- **linewidth**
  - Thickness of tick marks, in mm.
- **linetype**
  - Linetype of tick marks (solid, dashed, etc.)
- **alpha**
  - The transparency of the tick marks.
- **color**
  - An alias for `colour`.
- **...**
  - Other parameters passed on to the layer
- **size**
  - [Deprecated]

See Also

- `scale_y_continuous()`, `scale_y_log10()` for log scale transformations.
- `coord_trans()` for log coordinate transformations.
Examples

# Make a log-log plot (without log ticks)
a <- ggplot(msleep, aes(bodywt, brainwt)) +
  geom_point(na.rm = TRUE) +
  scale_x_log10(
    breaks = scales::trans_breaks("log10", function(x) 10^x),
    labels = scales::trans_format("log10", scales::math_format(10^.x))
  ) +
  scale_y_log10(
    breaks = scales::trans_breaks("log10", function(x) 10^x),
    labels = scales::trans_format("log10", scales::math_format(10^.x))
  ) +
  theme_bw()

a + annotation_logticks() # Default: log ticks on bottom and left
a + annotation_logticks(sides = "lr") # Log ticks for y, on left and right
a + annotation_logticks(sides = "trbl") # All four sides

a + annotation_logticks(sides = "lr", outside = TRUE) +
  coord_cartesian(clip = "off") # Ticks outside plot

# Hide the minor grid lines because they don't align with the ticks
a + annotation_logticks(sides = "trbl") + theme(panel.grid.minor = element_blank())

# Another way to get the same results as 'a' above: log-transform the data before
# plotting it. Also hide the minor grid lines.
b <- ggplot(msleep, aes(log10(bodywt), log10(brainwt))) +
  geom_point(na.rm = TRUE) +
  scale_x_continuous(name = "body", labels = scales::label_math(10^.x)) +
  scale_y_continuous(name = "brain", labels = scales::label_math(10^.x)) +
  theme_bw() + theme(panel.grid.minor = element_blank())

b + annotation_logticks()

# Using a coordinate transform requires scaled = FALSE
t <- ggplot(msleep, aes(bodywt, brainwt)) +
  geom_point() +
  coord_trans(x = "log10", y = "log10") +
  theme_bw()

t + annotation_logticks(scaled = FALSE)

# Change the length of the ticks
a + annotation_logticks(
  short = unit(.5,"mm"),
  mid = unit(3,"mm"),
  long = unit(4,"mm")
)
annotation_map

Description
Display a fixed map on a plot. This function predates the `geom_sf()` framework and does not work with sf geometry columns as input. However, it can be used in conjunction with `geom_sf()` layers and/or `coord_sf()` (see examples).

Usage
`annotation_map(map, ...)`

Arguments
map Data frame representing a map. See `geom_map()` for details.
...
Other arguments used to modify visual parameters, such as `colour` or `fill`.

Examples
```
## Not run:
if (requireNamespace("maps", quietly = TRUE)) {
  # location of cities in North Carolina
  df <- data.frame(
      name = c("Charlotte", "Raleigh", "Greensboro"),
      lat = c(35.227, 35.772, 36.073),
      long = c(-80.843, -78.639, -79.792)
  )

  p <- ggplot(df, aes(x = long, y = lat)) +
  annotation_map(
      map_data("state"),
      fill = "antiquewhite", colour = "darkgrey"
  ) +
  geom_point(color = "blue") +
  geom_text(
      aes(label = name),
      hjust = 1.105, vjust = 1.05, color = "blue"
  )

  # use without coord_sf() is possible but not recommended
  p + xlim(-84, -76) + ylim(34, 37.2)
}

if (requireNamespace("sf", quietly = TRUE)) {
  # use with coord_sf() for appropriate projection
  p +
  coord_sf(
      crs = sf::st_crs(3347),
      default_crs = sf::st_crs(4326), # data is provided as long-lat
      xlim = c(-84, -76),
      ylim = c(34, 37.2)
  )
}

# you can mix annotation_map() and geom_sf()
nc <- sf::st_read(system.file("shape/nc.shp", package = "sf"), quiet = TRUE)
```
annotation_raster

Annotation: high-performance rectangular tiling

Description

This is a special version of `geom_raster()` optimised for static annotations that are the same in every panel. These annotations will not affect scales (i.e. the x and y axes will not grow to cover the range of the raster, and the raster must already have its own colours). This is useful for adding bitmap images.

Usage

```r
annotation_raster(raster, xmin, xmax, ymin, ymax, interpolate = FALSE)
```

Arguments

- `raster` raster object to display, may be an array or a nativeRaster
- `xmin, xmax` x location (in data coordinates) giving horizontal location of raster
- `ymin, ymax` y location (in data coordinates) giving vertical location of raster
- `interpolate` If TRUE interpolate linearly, if FALSE (the default) don’t interpolate.

Examples

```r
# Generate data
rainbow <- matrix(hcl(seq(0, 360, length.out = 50 * 50), 80, 70), nrow = 50)
ggplot(mtcars, aes(mpg, wt)) +
  geom_point() +
  annotation_raster(rainbow, 15, 20, 3, 4)
# To fill up whole plot
ggplot(mtcars, aes(mpg, wt)) +
  annotation_raster(rainbow, -Inf, Inf, -Inf, Inf) +
  geom_point()
```

```r
rainbow2 <- matrix(hcl(seq(0, 360, length.out = 10), 80, 70), nrow = 1)
ggplot(mtcars, aes(mpg, wt)) +
  annotation_raster(rainbow2, -Inf, Inf, -Inf, Inf) +
  geom_point()
```
autolayer

Create a ggplot layer appropriate to a particular data type

Description
autolayer() uses ggplot2 to draw a particular layer for an object of a particular class in a single command. This defines the S3 generic that other classes and packages can extend.

Usage
autolayer(object, ...)

Arguments
object an object, whose class will determine the behaviour of autolayer
... other arguments passed to specific methods

Value
a ggplot layer

See Also
autoplot(), ggplot() and fortify()

autoplot

Create a complete ggplot appropriate to a particular data type

Description
autoplot() uses ggplot2 to draw a particular plot for an object of a particular class in a single command. This defines the S3 generic that other classes and packages can extend.

Usage
autoplot(object, ...)

Arguments
object an object, whose class will determine the behaviour of autoplot
... other arguments passed to specific methods

Value
a ggplot object
See Also

`autolayer()`, `ggplot()` and `fortify()`

---

**borders**

*Create a layer of map borders*

---

**Description**

This is a quick and dirty way to get map data (from the `maps` package) onto your plot. This is a good place to start if you need some crude reference lines, but you’ll typically want something more sophisticated for communication graphics.

**Usage**

```r
borders(
  database = "world",
  regions = ".",
  fill = NA,
  colour = "grey50",
  xlim = NULL,
  ylim = NULL,
  ...
)
```

**Arguments**

- `database` (map data, see `maps::map()` for details)
- `regions` (map region)
- `fill` (fill colour)
- `colour` (border colour)
- `xlim, ylim` (latitudinal and longitudinal ranges for extracting map polygons, see `maps::map()` for details).
- `...` (Arguments passed on to `geom_polygon`

**Rule** Either "evenodd" or "winding". If polygons with holes are being drawn (using the subgroup aesthetic) this argument defines how the hole coordinates are interpreted. See the examples in `grid::pathGrob()` for an explanation.

**Mapping** Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

**Data** The data to be displayed in this layer. There are three options:
- If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.

A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

**stat** The statistical transformation to use on the data for this layer, either as a `ggproto Geom` subclass or as a string naming the stat stripped of the `stat_` prefix (e.g. "count" rather than "stat_count")

**position** Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

**show.legend** logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display.

**inherit.aes** If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

**na.rm** If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.

**Examples**

```r
if (require("maps")) {

    ia <- map_data("county", "iowa")
    mid_range <- function(x) mean(range(x))
    seats <- do.call(rbind, lapply(split(ia, ia$subregion), function(d) {
        data.frame(lat = mid_range(d$lat), long = mid_range(d$long), subregion = unique(d$subregion))
    })))

    ggplot(ia, aes(long, lat)) +
    geom_polygon(aes(group = group), fill = NA, colour = "grey60") +
    geom_text(aes(label = subregion), data = seats, size = 2, angle = 45)
}

if (require("maps")) {
    data(us.cities)
    capitals <- subset(us.cities, capital == 2)
    ggplot(capitals, aes(long, lat)) +
    borders("state") +
    geom_point(aes(size = pop)) +
    scale_size_area() +
    coord_quickmap()
}

if (require("maps")) {

```
# Same map, with some world context

ggplot(capitals, aes(long, lat)) +
  borders("world", xlim = c(-130, -60), ylim = c(20, 50)) +
  geom_point(aes(size = pop)) +
  scale_size_area() +
  coord_quickmap()
}

---

CoordSf | Visualise sf objects

### Description

This set of geom, stat, and coord are used to visualise simple feature (sf) objects. For simple plots, you will only need `geom_sf()` as it uses `stat_sf()` and adds `coord_sf()` for you. `geom_sf()` is an unusual geom because it will draw different geometric objects depending on what simple features are present in the data: you can get points, lines, or polygons. For text and labels, you can use `geom_sf_text()` and `geom_sf_label()`.

### Usage

```
coord_sf(
  xlim = NULL,
  ylim = NULL,
  expand = TRUE,
  crs = NULL,
  default_crs = NULL,
  datum = sf::st_crs(4326),
  label_graticule = waiver(),
  label_axes = waiver(),
  lims_method = "cross",
  ndiscr = 100,
  default = FALSE,
  clip = "on"
)
```

```
geom_sf(
  mapping = aes(),
  data = NULL,
  stat = "sf",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```
geom_sf_label(
  mapping = aes(),
  data = NULL,
  stat = "sf_coordinates",
  position = "identity",
  ...,
  parse = FALSE,
  nudge_x = 0,
  nudge_y = 0,
  label.padding = unit(0.25, "lines"),
  label.r = unit(0.15, "lines"),
  label.size = 0.25,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  fun.geometry = NULL
)

gem_sf_text(
  mapping = aes(),
  data = NULL,
  stat = "sf_coordinates",
  position = "identity",
  ...,
  parse = FALSE,
  nudge_x = 0,
  nudge_y = 0,
  check_overlap = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  fun.geometry = NULL
)

stat_sf(
  mapping = NULL,
  data = NULL,
  geom = "rect",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)

Arguments

xlim, ylim Limits for the x and y axes. These limits are specified in the units of the default CRS. By default, this means projected coordinates (default_crs = NULL).
How limit specifications translate into the exact region shown on the plot can be confusing when non-linear or rotated coordinate systems are used as the default crs. First, different methods can be preferable under different conditions. See parameter lims_method for details. Second, specifying limits along only one direction can affect the automatically generated limits along the other direction. Therefore, it is best to always specify limits for both x and y. Third, specifying limits via position scales or xlim()/ylim() is strongly discouraged, as it can result in data points being dropped from the plot even though they would be visible in the final plot region.

expand
If TRUE, the default, adds a small expansion factor to the limits to ensure that data and axes don’t overlap. If FALSE, limits are taken exactly from the data or xlim/ylim.

crs
The coordinate reference system (CRS) into which all data should be projected before plotting. If not specified, will use the CRS defined in the first sf layer of the plot.

default_crs
The default CRS to be used for non-sf layers (which don’t carry any CRS information) and scale limits. The default value of NULL means that the setting for crs is used. This implies that all non-sf layers and scale limits are assumed to be specified in projected coordinates. A useful alternative setting is default_crs = sf::st_crs(4326), which means x and y positions are interpreted as longitude and latitude, respectively, in the World Geodetic System 1984 (WGS84).
datum
CRS that provides datum to use when generating graticules.

label_graticule
Character vector indicating which graticule lines should be labeled where. Meridians run north-south, and the letters "N" and "S" indicate that they should be labeled on their north or south end points, respectively. Parallels run east-west, and the letters "E" and "W" indicate that they should be labeled on their east or west end points, respectively. Thus, label_graticule = "SW" would label meridians at their south end and parallels at their west end, whereas label_graticule = "EW" would label parallels at both ends and meridians not at all. Because meridians and parallels can in general intersect with any side of the plot panel, for any choice of label_graticule labels are not guaranteed to reside on only one particular side of the plot panel. Also, label_graticule can cause labeling artifacts, in particular if a graticule line coincides with the edge of the plot panel. In such circumstances, label_axes will generally yield better results and should be used instead.

This parameter can be used alone or in combination with label_axes.

label_axes
Character vector or named list of character values specifying which graticule lines (meridians or parallels) should be labeled on which side of the plot. Meridians are indicated by "E" (for East) and parallels by "N" (for North). Default is "--EN", which specifies (clockwise from the top) no labels on the top, none on the right, meridians on the bottom, and parallels on the left. Alternatively, this setting could have been specified with list(bottom = "E", left = "N").

This parameter can be used alone or in combination with label_graticule.

lims_method
Method specifying how scale limits are converted into limits on the plot region. Has no effect when default_crs = NULL. For a very non-linear CRS
(e.g., a perspective centered around the North pole), the available methods yield widely differing results, and you may want to try various options. Methods currently implemented include "cross" (the default), "box", "orthogonal", and "geometry_bbox". For method "cross", limits along one direction (e.g., longitude) are applied at the midpoint of the other direction (e.g., latitude). This method avoids excessively large limits for rotated coordinate systems but means that sometimes limits need to be expanded a little further if extreme data points are to be included in the final plot region. By contrast, for method "box", a box is generated out of the limits along both directions, and then limits in projected coordinates are chosen such that the entire box is visible. This method can yield plot regions that are too large. Finally, method "orthogonal" applies limits separately along each axis, and method "geometry_bbox" ignores all limit information except the bounding boxes of any objects in the geometry aesthetic.

ndiscr
Number of segments to use for discretising graticule lines; try increasing this number when graticules look incorrect.

default
Is this the default coordinate system? If FALSE (the default), then replacing this coordinate system with another one creates a message alerting the user that the coordinate system is being replaced. If TRUE, that warning is suppressed.

clip
Should drawing be clipped to the extent of the plot panel? A setting of "on" (the default) means yes, and a setting of "off" means no. In most cases, the default of "on" should not be changed, as setting clip = "off" can cause unexpected results. It allows drawing of data points anywhere on the plot, including in the plot margins. If limits are set via xlim and ylim and some data points fall outside those limits, then those data points may show up in places such as the axes, the legend, the plot title, or the plot margins.

mapping
Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data
The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

stat
The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")

position
Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

na.rm
If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend  logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. You can also set this to one of "polygon", "line", and "point" to override the default legend.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

parse If TRUE, the labels will be parsed into expressions and displayed as described in ?plotmath.

nudge_x, nudge_y Horizontal and vertical adjustment to nudge labels by. Useful for offsetting text from points, particularly on discrete scales. Cannot be jointly specified with position.

label.padding Amount of padding around label. Defaults to 0.25 lines.

label.r Radius of rounded corners. Defaults to 0.15 lines.

label.size Size of label border, in mm.

fun.geometry A function that takes a sf object and returns a sf POINT with the same length as the input. If NULL, function(x) sf::st_point_on_surface(sf::st_zm(x)) will be used. Note that the function may warn about the incorrectness of the result if the data is not projected, but you can ignore this except when you really care about the exact locations.

check.overlap If TRUE, text that overlaps previous text in the same layer will not be plotted. check.overlap happens at draw time and in the order of the data. Therefore data should be arranged by the label column before calling geom_text(). Note that this argument is not supported by geom_label().

geom The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")

Geometry aesthetic

gemm_sf() uses a unique aesthetic: geometry, giving an column of class sfc containing simple features data. There are three ways to supply the geometry aesthetic:

- Do nothing: by default geom_sf() assumes it is stored in the geometry column.
- Explicitly pass an sf object to the data argument. This will use the primary geometry column, no matter what it’s called.
- Supply your own using aes(geometry = my_column)

Unlike other aesthetics, geometry will never be inherited from the plot.

CRS

cord_sf() ensures that all layers use a common CRS. You can either specify it using the crs param, or coord_sf() will take it from the first layer that defines a CRS.
Combining sf layers and regular geoms

Most regular geoms, such as `geom_point()`, `geom_path()`, `geom_text()`, `geom_polygon()` etc. will work fine with `coord_sf()`. However when using these geoms, two problems arise. First, what CRS should be used for the x and y coordinates used by these non-sf geoms? The CRS applied to non-sf geoms is set by the `default_crs` parameter, and it defaults to `NULL`, which means positions for non-sf geoms are interpreted as projected coordinates in the coordinate system set by the `crs` parameter. This setting allows you complete control over where exactly items are placed on the plot canvas, but it may require some understanding of how projections work and how to generate data in projected coordinates. As an alternative, you can set `default_crs = sf::st_crs(4326)`, the World Geodetic System 1984 (WGS84). This means that x and y positions are interpreted as longitude and latitude, respectively. You can also specify any other valid CRS as the default CRS for non-sf geoms.

The second problem that arises for non-sf geoms is how straight lines should be interpreted in projected space when `default_crs` is not set to `NULL`. The approach `coord_sf()` takes is to break straight lines into small pieces (i.e., segmentize them) and then transform the pieces into projected coordinates. For the default setting where x and y are interpreted as longitude and latitude, this approach means that horizontal lines follow the parallels and vertical lines follow the meridians. If you need a different approach to handling straight lines, then you should manually segmentize and project coordinates and generate the plot in projected coordinates.

See Also

`stat_sf_coordinates()`

Examples

```r
if (requireNamespace("sf", quietly = TRUE)) {
  nc <- sf::st_read(system.file("shape/nc.shp", package = "sf"), quiet = TRUE)
  ggplot(nc) +
    geom_sf(aes(fill = AREA))

  # If not supplied, coord_sf() will take the CRS from the first layer
  # and automatically transform all other layers to use that CRS. This
  # ensures that all data will correctly line up
  nc_3857 <- sf::st_transform(nc, 3857)
  ggplot() +
    geom_sf(data = nc) +
    geom_sf(data = nc_3857, colour = "red", fill = NA)

  # Unfortunately if you plot other types of feature you'll need to use
  # show.legend to tell ggplot2 what type of legend to use
  nc_3857$mid <- sf::st_centroid(nc_3857$geometry)
  ggplot(nc_3857) +
    geom_sf(colour = "white") +
    geom_sf(aes(geometry = mid, size = AREA), show.legend = "point")

  # You can also use layers with x and y aesthetics. To have these interpreted
  # as longitude/latitude you need to set the default CRS in coord_sf()
  ggplot(nc_3857) +
    geom_sf() +
```
annotate("point", x = -80, y = 35, colour = "red", size = 4) +
coord_sf(default_crs = sf::st_crs(4326))

# To add labels, use geom_sf_label().
ggplot(nc_3857[1:3, ]) +
  geom_sf(aes(fill = AREA)) +
  geom_sf_label(aes(label = NAME))
}

# Thanks to the power of sf, a geom_sf nicely handles varying projections
# setting the aspect ratio correctly.
if (requireNamespace("maps", quietly = TRUE)) {
  library(maps)
  world1 <- sf::st_as_sf(map("world", plot = FALSE, fill = TRUE))
  ggplot() + geom_sf(data = world1)

  world2 <- sf::st_transform(
    world1,
    "+proj=laea +y_0=0 +lon_0=155 +lat_0=-90 +ellps=WGS84 +no_defs"
  )
  ggplot() + geom_sf(data = world2)
}

---

coord_cartesian  

**Cartesian coordinates**

**Description**

The Cartesian coordinate system is the most familiar, and common, type of coordinate system. Setting limits on the coordinate system will zoom the plot (like you’re looking at it with a magnifying glass), and will not change the underlying data like setting limits on a scale will.

**Usage**

```r
coord_cartesian(
  xlim = NULL,
  ylim = NULL,
  expand = TRUE,
  default = FALSE,
  clip = "on"
)
```

**Arguments**

- `xlim`, `ylim` Limits for the x and y axes.
- `expand` If TRUE, the default, adds a small expansion factor to the limits to ensure that data and axes don’t overlap. If FALSE, limits are taken exactly from the data or `xlim/ylim`. 
default Is this the default coordinate system? If FALSE (the default), then replacing this coordinate system with another one creates a message alerting the user that the coordinate system is being replaced. If TRUE, that warning is suppressed.

clip Should drawing be clipped to the extent of the plot panel? A setting of "on" (the default) means yes, and a setting of "off" means no. In most cases, the default of "on" should not be changed. However, setting clip = "off" can cause unexpected results. It allows drawing of data points anywhere on the plot, including in the plot margins. If limits are set via xlim and ylim and some data points fall outside those limits, then those data points may show up in places such as the axes, the legend, the plot title, or the plot margins.

Examples

# There are two ways of zooming the plot display: with scales or
# with coordinate systems. They work in two rather different ways.

p <- ggplot(mtcars, aes(disp, wt)) +
  geom_point() +
  geom_smooth()

p

# Setting the limits on a scale converts all values outside the range to NA.
p + scale_x_continuous(limits = c(325, 500))

# Setting the limits on the coordinate system performs a visual zoom.
# The data is unchanged, and we just view a small portion of the original
# plot. Note how smooth continues past the points visible on this plot.
p + coord_cartesian(xlim = c(325, 500))

# By default, the same expansion factor is applied as when setting scale
# limits. You can set the limits precisely by setting expand = FALSE
p + coord_cartesian(xlim = c(325, 500), expand = FALSE)

# Similarly, we can use expand = FALSE to turn off expansion with the
# default limits
p + coord_cartesian(expand = FALSE)

# You can see the same thing with this 2d histogram
d <- ggplot(diamonds, aes(carat, price)) +
  stat_bin_2d(bins = 25, colour = "white")
d

# When zooming the scale, the we get 25 new bins that are the same
# size on the plot, but represent smaller regions of the data space
d + scale_x_continuous(limits = c(0, 1))

# When zooming the coordinate system, we see a subset of original 50 bins,
# displayed bigger
d + coord_cartesian(xlim = c(0, 1))
Description

A fixed scale coordinate system forces a specified ratio between the physical representation of data units on the axes. The ratio represents the number of units on the y-axis equivalent to one unit on the x-axis. The default, \texttt{ratio = 1}, ensures that one unit on the x-axis is the same length as one unit on the y-axis. Ratios higher than one make units on the y axis longer than units on the x-axis, and vice versa. This is similar to \texttt{MASS::eqscplot()}, but it works for all types of graphics.

Usage

\begin{verbatim}
coord_fixed(ratio = 1, xlim = NULL, ylim = NULL, expand = TRUE, clip = "on")
\end{verbatim}

Arguments

- \texttt{ratio}: aspect ratio, expressed as \( y / x \)
- \texttt{xlim, ylim}: Limits for the x and y axes.
- \texttt{expand}: If \texttt{TRUE}, the default, adds a small expansion factor to the limits to ensure that data and axes don’t overlap. If \texttt{FALSE}, limits are taken exactly from the data or \texttt{xlim/ylim}.
- \texttt{clip}: Should drawing be clipped to the extent of the plot panel? A setting of "on" (the default) means yes, and a setting of "off" means no. In most cases, the default of "on" should not be changed, as setting \texttt{clip = "off"} can cause unexpected results. It allows drawing of data points anywhere on the plot, including in the plot margins. If limits are set via \texttt{xlim} and \texttt{ylim} and some data points fall outside those limits, then those data points may show up in places such as the axes, the legend, the plot title, or the plot margins.

Examples

\begin{verbatim}
# ensures that the ranges of axes are equal to the specified ratio by
# adjusting the plot aspect ratio

p <- ggplot(mtcars, aes(mpg, wt)) + geom_point()
p + coord_fixed(ratio = 1)
p + coord_fixed(ratio = 5)
p + coord_fixed(ratio = 1/5)
p + coord_fixed(xlim = c(15, 30))

# Resize the plot to see that the specified aspect ratio is maintained
\end{verbatim}
**Description**

**[Superseded]**

This function is superseded because in many cases, `coord_flip()` can easily be replaced by swapping the x and y aesthetics, or optionally setting the orientation argument in geom and stat layers. `coord_flip()` is useful for geoms and statistics that do not support the orientation setting, and converting the display of y conditional on x, to x conditional on y.

**Usage**

```r
coord_flip(xlim = NULL, ylim = NULL, expand = TRUE, clip = "on")
```

**Arguments**

- `xlim`, `ylim` Limits for the x and y axes.
- `expand` If TRUE, the default, adds a small expansion factor to the limits to ensure that data and axes don’t overlap. If FALSE, limits are taken exactly from the data or `xlim`/`ylim`.
- `clip` Should drawing be clipped to the extent of the plot panel? A setting of "on" (the default) means yes, and a setting of "off" means no. In most cases, the default of "on" should not be changed, as setting clip = "off" can cause unexpected results. It allows drawing of data points anywhere on the plot, including in the plot margins. If limits are set via `xlim` and `ylim` and some data points fall outside those limits, then those data points may show up in places such as the axes, the legend, the plot title, or the plot margins.

**Examples**

```r
# The preferred method of creating horizontal instead of vertical boxplots
ggplot(diamonds, aes(price, cut)) +
  geom_boxplot()

# Using `coord_flip()` to make the same plot
ggplot(diamonds, aes(cut, price)) +
  geom_boxplot() +
  coord_flip()

# With swapped aesthetics, the y-scale controls the left axis
ggplot(diamonds, aes(y = carat)) +
  geom_histogram() +
  scale_y_reverse()

# In `coord_flip()`, the x-scale controls the left axis
ggplot(diamonds, aes(carat)) +
  geom_histogram() +
  scale_x_reverse()
```
coord_map() projects a portion of the earth, which is approximately spherical, onto a flat 2D plane using any projection defined by the mapproj package. Map projections do not, in general, preserve straight lines, so this requires considerable computation. coord_quickmap() is a quick approximation that does preserve straight lines. It works best for smaller areas closer to the equator.

Both coord_map() and coord_quickmap() are superseded by coord_sf(), and should no longer be used in new code. All regular (non-sf) geoms can be used with coord_sf() by setting the default coordinate system via the default_crs argument. See also the examples for annotation_map() and geom_map().

Usage

coord_map(
  projection = "mercator",
  ..., 
  parameters = NULL, 
  orientation = NULL, 
  xlim = NULL, 
  ylim = NULL, 
  clip = "on"
)

coord_quickmap(xlim = NULL, ylim = NULL, expand = TRUE, clip = "on")

Arguments

projection projection to use, see mapproj::mapproject() for list
... parameters
Other arguments passed on to `mapproj::mapproject()`. Use ... for named parameters to the projection, and parameters for unnamed parameters. ... is ignored if the parameters argument is present.

orientation projection orientation, which defaults to `c(90, 0, mean(range(x)))`. This is not optimal for many projections, so you will have to supply your own. See `mapproj::mapproject()` for more information.

xlim, ylim Manually specific x/y limits (in degrees of longitude/latitude)

clip Should drawing be clipped to the extent of the plot panel? A setting of "on" (the default) means yes, and a setting of "off" means no. For details, please see `coord_cartesian()`.

expand If TRUE, the default, adds a small expansion factor to the limits to ensure that data and axes don’t overlap. If FALSE, limits are taken exactly from the data or xlim/ylim.

Details
Map projections must account for the fact that the actual length (in km) of one degree of longitude varies between the equator and the pole. Near the equator, the ratio between the lengths of one degree of latitude and one degree of longitude is approximately 1. Near the pole, it tends towards infinity because the length of one degree of longitude tends towards 0. For regions that span only a few degrees and are not too close to the poles, setting the aspect ratio of the plot to the appropriate lat/lon ratio approximates the usual mercator projection. This is what `coord_quickmap()` does, and is much faster (particularly for complex plots like `geom_tile()`) at the expense of correctness.

Examples
```r
if (require("maps")) {
  nz <- map_data("nz")
  # Prepare a map of NZ
  nzmap <- ggplot(nz, aes(x = long, y = lat, group = group)) +
    geom_polygon(fill = "white", colour = "black")
    # Plot it in cartesian coordinates
    nzmap
}

if (require("maps")) {
  # With correct mercator projection
  nzmap + coord_map()
}

if (require("maps")) {
  # With the aspect ratio approximation
  nzmap + coord_quickmap()
}

if (require("maps")) {
  # Other projections
  nzmap + coord_map("azequalarea", orientation = c(-36.92, 174.6, 0))
```
if (require("maps")) {
    states <- map_data("state")
    usamap <- ggplot(states, aes(long, lat, group = group)) +
        geom_polygon(fill = "white", colour = "black")

    # Use cartesian coordinates
    usamap
}

if (require("maps")) {
    # With mercator projection
    usamap + coord_map()
}

if (require("maps")) {
    # See ?mapproject for coordinate systems and their parameters
    usamap + coord_map("gilbert")
}

if (require("maps")) {
    # For most projections, you'll need to set the orientation yourself
    # as the automatic selection done by mapproject is not available to
    # ggplot
    usamap + coord_map("orthographic")
}

if (require("maps")) {
    usamap + coord_map("conic", lat0 = 30)
}

if (require("maps")) {
    usamap + coord_map("bonne", lat0 = 50)
}

## Not run:
if (require("maps")) {
    # World map, using geom_path instead of geom_polygon
    world <- map_data("world")
    worldmap <- ggplot(world, aes(x = long, y = lat, group = group)) +
        geom_path() +
        scale_y_continuous(breaks = (-2:2) * 30) +
        scale_x_continuous(breaks = (-4:4) * 45)

    # Orthographic projection with default orientation (looking down at North pole)
    worldmap + coord_map("ortho")
}

if (require("maps")) {
    # Looking up up at South Pole
    worldmap + coord_map("ortho", orientation = c(-90, 0, 0))
}
if (require("maps")) {
  # Centered on New York (currently has issues with closing polygons)
  worldmap + coord_map("ortho", orientation = c(41, -74, 0))
}

## End(Not run)

---

**coord_polar**

**Polar coordinates**

**Description**

The polar coordinate system is most commonly used for pie charts, which are a stacked bar chart in polar coordinates. `coord_radial()` has extended options.

**Usage**

```
coord_polar(theta = "x", start = 0, direction = 1, clip = "on")
```

```
coord_radial(
  theta = "x",
  start = 0,
  end = NULL,
  expand = TRUE,
  direction = 1,
  clip = "off",
  r_axis_inside = NULL,
  rotate_angle = FALSE,
  inner.radius = 0
)
```

**Arguments**

- **theta**: variable to map angle to (x or y)
- **start**: Offset of starting point from 12 o’clock in radians. Offset is applied clockwise or anticlockwise depending on value of direction.
- **direction**: 1, clockwise; -1, anticlockwise
- **clip**: Should drawing be clipped to the extent of the plot panel? A setting of "on" (the default) means yes, and a setting of "off" means no. For details, please see `coord_cartesian()`.
- **end**: Position from 12 o’clock in radians where plot ends, to allow for partial polar coordinates. The default, NULL, is set to start + 2 * pi.
- **expand**: If TRUE, the default, adds a small expansion factor the the limits to prevent overlap between data and axes. If FALSE, limits are taken directly from the scale.
r_axis_inside
If TRUE, places the radius axis inside the panel. If FALSE, places the radius axis next to the panel. The default, NULL, places the radius axis outside if the start and end arguments form a full circle.

rotate_angle
If TRUE, transforms the angle aesthetic in data in accordance with the computed theta position. If FALSE (default), no such transformation is performed. Can be useful to rotate text geoms in alignment with the coordinates.

inner.radius
A numeric between 0 and 1 setting the size of a inner.radius hole.

Note
In coord_radial(), position guides are can be defined by using guides(r = ..., theta = ..., r.sec = ..., theta.sec = ...). Note that these guides require r and theta as available aesthetics. The classic guide_axis() can be used for the r positions and guide_axis_theta() can be used for the theta positions. Using the theta.sec position is only sensible when inner.radius > 0.

Examples

# NOTE: Use these plots with caution - polar coordinates has
# major perceptual problems. The main point of these examples is
# to demonstrate how these common plots can be described in the
# grammar. Use with EXTREME caution.

#' # A pie chart = stacked bar chart + polar coordinates
pie <- ggplot(mtcars, aes(x = factor(1), fill = factor(cyl))) +
  geom_bar(width = 1)
pie + coord_polar(theta = "y")

# A coxcomb plot = bar chart + polar coordinates
cxc <- ggplot(mtcars, aes(x = factor(cyl))) +
  geom_bar(width = 1, colour = "black")
cxc + coord_polar()
# A new type of plot?
cxc + coord_polar(theta = "y")

# The bullseye chart
pie + coord_polar()

# Hadley's favourite pie chart
df <- data.frame(
  variable = c("does not resemble", "resembles"),
  value = c(20, 80)
)
ggplot(df, aes(x = ",", y = value, fill = variable)) +
  geom_col(width = 1) +
  scale_fill_manual(values = c("red", "yellow")) +
  coord_polar("y", start = pi / 3) +
  labs(title = "Pac man")
# Windrose + doughnut plot
if (require("ggplot2movies")) {
movies$rating <- cut_interval(movies$rating, length = 1)
movies$budgetq <- cut_number(movies$budget, 4)

doh <- ggplot(movies, aes(x = rrating, fill = budgetq))

# Wind rose
doh + geom_bar(width = 1) + coord_polar()
# Race track plot

doh + geom_bar(width = 0.9, position = "fill") + coord_polar(theta = "y")
}

# A partial polar plot
ggplot(mtcars, aes(disp, mpg)) +
  geom_point() +
  coord_radial(start = -0.4 * pi, end = 0.4 * pi, inner.radius = 0.3)

---

### coord_trans

**Transformed Cartesian coordinate system**

**Description**

`coord_trans()` is different to scale transformations in that it occurs after statistical transformation and will affect the visual appearance of geoms - there is no guarantee that straight lines will continue to be straight.

**Usage**

```r
coord_trans(
  x = "identity",
  y = "identity",
  xlim = NULL,
  ylim = NULL,
  limx = deprecated(),
  limy = deprecated(),
  clip = "on",
  expand = TRUE
)
```

**Arguments**

- **x, y** Transformers for x and y axes or their names.
- **xlim, ylim** Limits for the x and y axes.
- **limx, limy** [Deprecated] use xlim and ylim instead.
clip

Should drawing be clipped to the extent of the plot panel? A setting of "on" (the default) means yes, and a setting of "off" means no. In most cases, the default of "on" should not be changed, as setting clip = "off" can cause unexpected results. It allows drawing of data points anywhere on the plot, including in the plot margins. If limits are set via xlim and ylim and some data points fall outside those limits, then those data points may show up in places such as the axes, the legend, the plot title, or the plot margins.

expand

If TRUE, the default, adds a small expansion factor to the limits to ensure that data and axes don’t overlap. If FALSE, limits are taken exactly from the data or xlim/ylim.

Details

Transformations only work with continuous values: see scales::new_transform() for list of transformations, and instructions on how to create your own.

Examples

```r
# See ?geom_boxplot for other examples

# Three ways of doing transformation in ggplot:
# * by transforming the data
ggplot(diamonds, aes(log10(carat), log10(price))) +
  geom_point()
# * by transforming the scales
ggplot(diamonds, aes(carat, price)) +
  geom_point() +
  scale_x_log10() +
  scale_y_log10()
# * by transforming the coordinate system:
ggplot(diamonds, aes(carat, price)) +
  geom_point() +
  coord_trans(x = "log10", y = "log10")

# The difference between transforming the scales and
# transforming the coordinate system is that scale
# transformation occurs BEFORE statistics, and coordinate
# transformation afterwards. Coordinate transformation also
# changes the shape of geoms:

d <- subset(diamonds, carat > 0.5)

ggplot(d, aes(carat, price)) +
  geom_point() +
  geom_smooth(method = "lm") +
  scale_x_log10() +
  scale_y_log10()

```

cut_interval

Discretise numeric data into categorical

description

cut_interval() makes n groups with equal range, cut_number() makes n groups with (approximately) equal numbers of observations; cut_width() makes groups of width width.

usage

cut_interval(x, n = NULL, length = NULL, ...) 
cut_number(x, n = NULL, ...) 
cut_width(x, width, center = NULL, boundary = NULL, closed = "right", ...) 

arguments

x numeric vector
number of intervals to create, OR
length

Arguments passed on to base::cut.default

either a numeric vector of two or more unique cut points or a single
number (greater than or equal to 2) giving the number of intervals into
which x is to be cut.

labels labels for the levels of the resulting category. By default, labels are
constructed using "(a,b]" interval notation. If labels = FALSE, simple
integer codes are returned instead of a factor.

right logical, indicating if the intervals should be closed on the right (and open
on the left) or vice versa.

dig.lab integer which is used when labels are not given. It determines the
number of digits used in formatting the break numbers.

ordered_result logical: should the result be an ordered factor?

The bin width.

Specify either the position of edge or the center of a bin. Since all bins are
aligned, specifying the position of a single bin (which doesn’t need to be in the
range of the data) affects the location of all bins. If not specified, uses the "tile
layers algorithm", and sets the boundary to half of the binwidth.

To center on integers, width = 1 and center = 0. boundary = 0.5.

One of "right" or "left" indicating whether right or left edges of bins are
included in the bin.

Randall Prium contributed most of the implementation of cut_width().

Examples

table(cut_interval(1:100, 10))
table(cut_interval(1:100, 11))

set.seed(1)
table(cut_number(runif(1000), 10))
table(cut_width(runif(1000), 0.1))
table(cut_width(runif(1000), 0.1, boundary = 0))
table(cut_width(runif(1000), 0.1, center = 0))
table(cut_width(runif(1000), 0.1, labels = FALSE))
Description

A dataset containing the prices and other attributes of almost 54,000 diamonds. The variables are as follows:

Usage

diamonds

Format

A data frame with 53940 rows and 10 variables:

price  price in US dollars ($326–$18,823)
carat  weight of the diamond (0.2–5.01)
cut    quality of the cut (Fair, Good, Very Good, Premium, Ideal)
color  diamond colour, from D (best) to J (worst)
clarity a measurement of how clear the diamond is (I1 (worst), SI2, SI1, VS2, VS1, VVS2, VVS1, IF (best))
x      length in mm (0–10.74)
y      width in mm (0–58.9)
z      depth in mm (0–31.8)
depth  total depth percentage = z / mean(x, y) = 2 * z / (x + y) (43–79)
table  width of top of diamond relative to widest point (43–95)

draw_key  KEY GYPS FOR LEGENDS

Description

Each geom has an associated function that draws the key when the geom needs to be displayed in a legend. These functions are called draw_key_*(), where * stands for the name of the respective key glyph. The key glyphs can be customized for individual geoms by providing a geom with the key_glyph argument (see layer() or examples below.)
Usage

draw_key_point(data, params, size)
draw_key_abline(data, params, size)
draw_key_rect(data, params, size)
draw_key_polygon(data, params, size)
draw_key_blank(data, params, size)
draw_key_boxplot(data, params, size)
draw_key_crossbar(data, params, size)
draw_key_path(data, params, size)
draw_key_vpath(data, params, size)
draw_key_dotplot(data, params, size)
draw_key_linerange(data, params, size)
draw_key_pointrange(data, params, size)
draw_key_smooth(data, params, size)
draw_key_text(data, params, size)
draw_key_label(data, params, size)
draw_key_vline(data, params, size)
draw_key_timeseries(data, params, size)

Arguments

data A single row data frame containing the scaled aesthetics to display in this key
params A list of additional parameters supplied to the geom.
size Width and height of key in mm.

Value
A grid grob.

Examples
p <- ggplot(economics, aes(date, psavert, color = "savings rate"))
# key glyphs can be specified by their name
p + geom_line(key_glyph = "timeseries")

# key glyphs can be specified via their drawing function
p + geom_line(key_glyph = draw_key_rect)

economics

US economic time series

Description

This dataset was produced from US economic time series data available from https://fred.stlouisfed.org/. economics is in "wide" format, economics_long is in "long" format.

Usage

economics
economics_long

Format

A data frame with 574 rows and 6 variables:

date  Month of data collection
pce  personal consumption expenditures, in billions of dollars, https://fred.stlouisfed.org/series/PCE
pop  total population, in thousands, https://fred.stlouisfed.org/series/POP
psavert  personal savings rate, https://fred.stlouisfed.org/series/PSAVERT/
unemplmed  median duration of unemployment, in weeks, https://fred.stlouisfed.org/series/UEMMPMED
unemploy  number of unemployed in thousands, https://fred.stlouisfed.org/series/UNEMPLOY

An object of class tbl_df (inherits from tbl.data.frame) with 2870 rows and 4 columns.
Description

In conjunction with the theme system, the element_ functions specify the display of how non-data components of the plot are drawn.

- element_blank(): draws nothing, and assigns no space.
- element_rect(): borders and backgrounds.
- element_line(): lines.
- element_text(): text.

rel() is used to specify sizes relative to the parent, margin() is used to specify the margins of elements.

Usage

element_blank()

element_rect(
    fill = NULL,
    colour = NULL,
    linewidth = NULL,
    linetype = NULL,
    color = NULL,
    inherit.blank = FALSE,
    size = deprecated()
)

element_line(
    colour = NULL,
    linewidth = NULL,
    linetype = NULL,
    lineend = NULL,
    color = NULL,
    arrow = NULL,
    inherit.blank = FALSE,
    size = deprecated()
)

element_text(
    family = NULL,
    face = NULL,
    colour = NULL,
    size = NULL,
    hjust = NULL,
vjust = NULL,
angle = NULL,
lineheight = NULL,
color = NULL,
margin = NULL,
debug = NULL,
inherit.blank = FALSE
)

rel(x)

margin(t = 0, r = 0, b = 0, l = 0, unit = "pt")

Arguments

fill Fill colour.
colour, color Line/border colour. Color is an alias for colour.
linewidth Line/border size in mm.
linetype Line type. An integer (0:8), a name (blank, solid, dashed, dotted, dotdash, long-dash, twodash), or a string with an even number (up to eight) of hexadecimal digits which give the lengths in consecutive positions in the string.
inherit.blank Should this element inherit the existence of an `element_blank` among its parents? If TRUE the existence of a blank element among its parents will cause this element to be blank as well. If FALSE any blank parent element will be ignored when calculating final element state.

size text size in pts.
lineend Line end style (round, butt, square)
arrow Arrow specification, as created by `grid::arrow()`
family Font family
face Font face ("plain", "italic", "bold", "bold.italic")
hjust Horizontal justification (in \([0, 1]\))
vjust Vertical justification (in \([0, 1]\))
angle Angle (in \([0, 360]\))
lineheight Line height
margin Margins around the text. See `margin()` for more details. When creating a theme, the margins should be placed on the side of the text facing towards the center of the plot.
debug If TRUE, aids visual debugging by drawing a solid rectangle behind the complete text area, and a point where each label is anchored.
x A single number specifying size relative to parent element.
t, r, b, l Dimensions of each margin. (To remember order, think trouble).
unit Default units of dimensions. Defaults to "pt" so it can be most easily scaled with the text.
Value

An S3 object of class `element`, `rel`, or `margin`.

Examples

```r
plot <- ggplot(mpg, aes(displ, hwy)) + geom_point()

plot + theme(
  panel.background = element_blank(),
  axis.text = element_blank()
)

plot + theme(
  axis.text = element_text(colour = "red", size = rel(1.5))
)

plot + theme(
  axis.line = element_line(arrow = arrow())
)

plot + theme(
  panel.background = element_rect(fill = "white"),
  plot.margin = margin(2, 2, 2, 2, "cm"),
  plot.background = element_rect(
    fill = "grey90",
    colour = "black",
    linewidth = 1
  )
)
```

---

expand_limits

**Expand the plot limits, using data**

Description

Sometimes you may want to ensure limits include a single value, for all panels or all plots. This function is a thin wrapper around `geom_blank()` that makes it easy to add such values.

Usage

```r
expand_limits(...)  
```

Arguments

```r

... named list of aesthetics specifying the value (or values) that should be included in each scale.
```
Examples

p <- ggplot(mtcars, aes(mpg, wt)) + geom_point()
p + expand_limits(x = 0)
p + expand_limits(y = c(1, 9))
p + expand_limits(x = 0, y = 0)

ggplot(mtcars, aes(mpg, wt)) +
  geom_point(aes(colour = cyl)) +
  expand_limits(colour = seq(2, 10, by = 2))

ggplot(mtcars, aes(mpg, wt)) +
  geom_point(aes(colour = factor(cyl))) +
  expand_limits(colour = factor(seq(2, 10, by = 2)))

expansion

Generate expansion vector for scales

Description

This is a convenience function for generating scale expansion vectors for the expand argument of scale_(x|y)_continuous and scale_(x|y)_discrete. The expansion vectors are used to add some space between the data and the axes.

Usage

expansion(mult = 0, add = 0)

expand_scale(mult = 0, add = 0)

Arguments

mult  vector of multiplicative range expansion factors. If length 1, both the lower and upper limits of the scale are expanded outwards by mult. If length 2, the lower limit is expanded by mult[1] and the upper limit by mult[2].

add   vector of additive range expansion constants. If length 1, both the lower and upper limits of the scale are expanded outwards by add units. If length 2, the lower limit is expanded by add[1] and the upper limit by add[2].

Examples

# No space below the bars but 10% above them
ggplot(mtcars) +
  geom_bar(aes(x = factor(cyl))) +
  scale_y_continuous(expand = expansion(mult = c(0, .1)))

# Add 2 units of space on the left and right of the data
ggplot(subset(diamonds, carat > 2), aes(cut, clarity)) +
  geom_jitter() +
  scale_x_discrete(expand = expansion(add = 2))
# Reproduce the default range expansion used when the 'expand' argument is not specified

```r
ggplot(subset(diamonds, carat > 2), aes(cut, price)) +
  geom_jitter() +
  scale_x_discrete(expand = expansion(add = .6)) +
  scale_y_continuous(expand = expansion(mult = .05))
```

---

**facet_grid**

*Lay out panels in a grid*

**Description**

`facet_grid()` forms a matrix of panels defined by row and column faceting variables. It is most useful when you have two discrete variables, and all combinations of the variables exist in the data. If you have only one variable with many levels, try `facet_wrap()`.

**Usage**

```r
facet_grid(
  rows = NULL,
  cols = NULL,
  scales = "fixed",
  space = "fixed",
  shrink = TRUE,
  labeller = "label_value",
  as.table = TRUE,
  switch = NULL,
  drop = TRUE,
  margins = FALSE,
  axes = "margins",
  axis.labels = "all",
  facets = deprecated()
)
```

**Arguments**

- **rows, cols**  
  A set of variables or expressions quoted by `vars()` and defining faceting groups on the rows or columns dimension. The variables can be named (the names are passed to `labeller`).
  For compatibility with the classic interface, `rows` can also be a formula with the rows (of the tabular display) on the LHS and the columns (of the tabular display) on the RHS; the dot in the formula is used to indicate there should be no faceting on this dimension (either row or column).

- **scales**  
  Are scales shared across all facets (the default, "fixed"), or do they vary across rows ("free_x"), columns ("free_y"), or both rows and columns ("free")?
facet_grid

space
If "fixed", the default, all panels have the same size. If "free_y" their height will be proportional to the length of the y scale; if "free_x" their width will be proportional to the length of the x scale; or if "free" both height and width will vary. This setting has no effect unless the appropriate scales also vary.

shrink
If TRUE, will shrink scales to fit output of statistics, not raw data. If FALSE, will be range of raw data before statistical summary.

labeller
A function that takes one data frame of labels and returns a list or data frame of character vectors. Each input column corresponds to one factor. Thus there will be more than one with vars(cyl, am). Each output column gets displayed as one separate line in the strip label. This function should inherit from the "labeller" S3 class for compatibility with labeller(). You can use different labeling functions for different kind of labels, for example use label_parsed() for formatting facet labels. label_value() is used by default, check it for more details and pointers to other options.

as.table
If TRUE, the default, the facets are laid out like a table with highest values at the bottom-right. If FALSE, the facets are laid out like a plot with the highest value at the top-right.

switch
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".

drop
If TRUE, the default, all factor levels not used in the data will automatically be dropped. If FALSE, all factor levels will be shown, regardless of whether or not they appear in the data.

margins
Either a logical value or a character vector. Margins are additional facets which contain all the data for each of the possible values of the faceting variables. If FALSE, no additional facets are included (the default). If TRUE, margins are included for all faceting variables. If specified as a character vector, it is the names of variables for which margins are to be created.

axes
Determines which axes will be drawn. When "margins" (default), axes will be drawn at the exterior margins. "all_x" and "all_y" will draw the respective axes at the interior panels too, whereas "all" will draw all axes at all panels.

axis.labels
Determines whether to draw labels for interior axes when the axes argument is not "margins". When "all" (default), all interior axes get labels. When "margins", only the exterior axes get labels and the interior axes get none. When "all_x" or "all_y", only draws the labels at the interior axes in the x- or y-direction respectively.

facets
[Deprecated] Please use rows and cols instead.

Examples

p <- ggplot(mpg, aes(displ, cty)) + geom_point()

# Use vars() to supply variables from the dataset:
p + facet_grid(rows = vars(drv))
p + facet_grid(cols = vars(cyl))
p + facet_grid(vars(drv), vars(cyl))
# To change plot order of facet grid,
# change the order of variable levels with factor()

# If you combine a faceted dataset with a dataset that lacks those
# faceting variables, the data will be repeated across the missing
# combinations:
df <- data.frame(displ = mean(mpg$displ), cty = mean(mpg$cty))
p +
  facet_grid(cols = vars(cyl)) +
  geom_point(data = df, colour = "red", size = 2)

# When scales are constant, duplicated axes can be shown with
# or without labels
ggplot(mpg, aes(cty, hwy)) +
  geom_point() +
  facet_grid(year ~ drv, axes = "all", axis.labels = "all_x")

# Free scales -------------------------------------------------------
# You can also choose whether the scales should be constant
# across all panels (the default), or whether they should be allowed
# to vary
mt <- ggplot(mtcars, aes(mpg, wt, colour = factor(cyl))) +
  geom_point()
mt + facet_grid(vars(cyl), scales = "free")

# If scales and space are free, then the mapping between position
# and values in the data will be the same across all panels. This
# is particularly useful for categorical axes
ggplot(mpg, aes(driv, model)) +
  geom_point() +
  facet_grid(manufacturer ~ ., scales = "free", space = "free") +
  theme(strip.text.y = element_text(angle = 0))

# Margins ----------------------------------------------------------
# Margins can be specified logically (all yes or all no) or for specific
# variables as (character) variable names
mg <- ggplot(mtcars, aes(x = mpg, y = wt)) + geom_point()
mg + facet_grid(vs + am ~ gear, margins = TRUE)
mg + facet_grid(vs + am ~ gear, margins = "am")
# when margins are made over "vs", since the facets for "am" vary
# within the values of "vs", the marginal facet for "vs" is also
# a margin over "am".
mg + facet_grid(vs + am ~ gear, margins = "vs")

---

facet_wrap

Wrap a 1d ribbon of panels into 2d
Description

facet_wrap() wraps a 1d sequence of panels into 2d. This is generally a better use of screen space than facet_grid() because most displays are roughly rectangular.

Usage

```r
facet_wrap(
  facets,
  nrow = NULL,
  ncol = NULL,
  scales = "fixed",
  shrink = TRUE,
  labeller = "label_value",
  as.table = TRUE,
  switch = deprecated(),
  drop = TRUE,
  dir = "h",
  strip.position = "top",
  axes = "margins",
  axis.labels = "all"
)
```

Arguments

- **facets**: A set of variables or expressions quoted by `vars()` and defining faceting groups on the rows or columns dimension. The variables can be named (the names are passed to `labeller`). For compatibility with the classic interface, can also be a formula or character vector. Use either a one sided formula, `~a + b`, or a character vector, `c("a", "b")`.

- **nrow, ncol**: Number of rows and columns.

- **scales**: Should scales be fixed ("fixed", the default), free ("free"), or free in one dimension ("free_x", "free_y")?

- **shrink**: If TRUE, will shrink scales to fit output of statistics, not raw data. If FALSE, will be range of raw data before statistical summary.

- **labeller**: A function that takes one data frame of labels and returns a list or data frame of character vectors. Each input column corresponds to one factor. Thus there will be more than one with `vars(cyl, am)`. Each output column gets displayed as one separate line in the strip label. This function should inherit from the "labeller" S3 class for compatibility with `labeller()`. You can use different labeling functions for different kind of labels, for example use `label_parsed()` for formatting facet labels. `label_value()` is used by default, check it for more details and pointers to other options.

- **as.table**: If TRUE, the default, the facets are laid out like a table with highest values at the bottom-right. If FALSE, the facets are laid out like a plot with the highest value at the top-right.
facet_wrap

switch
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".

drop
If TRUE, the default, all factor levels not used in the data will automatically be dropped. If FALSE, all factor levels will be shown, regardless of whether or not they appear in the data.

dir
Direction: either "h" for horizontal, the default, or "v", for vertical.

strip.position
By default, the labels are displayed on the top of the plot. Using strip.position it is possible to place the labels on either of the four sides by setting strip.position = c("top", "bottom", "left", "right")

axes
Determines which axes will be drawn in case of fixed scales. When "margins" (default), axes will be drawn at the exterior margins. "all_x" and "all_y" will draw the respective axes at the interior panels too, whereas "all" will draw all axes at all panels.

axis.labels
Determines whether to draw labels for interior axes when the scale is fixed and the axis argument is not "margins". When "all" (default), all interior axes get labels. When "margins", only the exterior axes get labels, and the interior axes get none. When "all_x" or "all_y", only draws the labels at the interior axes in the x- or y-direction respectively.

Examples

```r
p <- ggplot(mpg, aes(displ, hwy)) + geom_point()

# Use vars() to supply faceting variables:
p + facet_wrap(vars(class))

# Control the number of rows and columns with nrow and ncol
p + facet_wrap(vars(class), nrow = 4)

# You can facet by multiple variables
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  facet_wrap(vars(cyl, drv))

# Use the 'labeller' option to control how labels are printed:
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  facet_wrap(vars(cyl, drv), labeller = "label_both")

# To change the order in which the panels appear, change the levels
# of the underlying factor.
mpg$class2 <- reorder(mpg$class, mpg$displ)
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  facet_wrap(vars(class2))

# By default, the same scales are used for all panels. You can allow
# scales to vary across the panels with the 'scales' argument.
```
# Free scales make it easier to see patterns within each panel, but
# harder to compare across panels.
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  facet_wrap(vars(class), scales = "free")

# When scales are constant, duplicated axes can be shown with
# or without labels
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  facet_wrap(vars(class), axes = "all", axis.labels = "all_y")

# To repeat the same data in every panel, simply construct a data frame
# that does not contain the faceting variable.
ggplot(mpg, aes(displ, hwy)) +
  geom_point(data = transform(mpg, class = NULL), colour = "grey85") +
  geom_point() +
  facet_wrap(vars(class))

# Use `strip.position` to display the facet labels at the side of your
# choice. Setting it to `bottom` makes it act as a subtitle for the axis.
# This is typically used with free scales and a theme without boxes around
# strip labels.
ggplot(economics_long, aes(date, value)) +
  geom_line() +
  facet_wrap(vars(variable), scales = "free_y", nrow = 2, strip.position = "top") +
  theme(strip.background = element_blank(), strip.placement = "outside")

faithfuld  # 2d density estimate of Old Faithful data

**Description**

A 2d density estimate of the waiting and eruptions variables data faithful.

**Usage**

faithfuld

**Format**

A data frame with 5,625 observations and 3 variables:

- **eruptions** Eruption time in mins
- **waiting** Waiting time to next eruption in mins
- **density** 2d density estimate
fortify

Fortify a model with data.

Description

Rather than using this function, I now recommend using the broom package, which implements a much wider range of methods. fortify() may be deprecated in the future.

Usage

fortify(model, data, ...)

Arguments

- model: model or other R object to convert to data frame
- data: original dataset, if needed
- ...: other arguments passed to methods

See Also

fortify.lm

geom_abline

Reference lines: horizontal, vertical, and diagonal

Description

These geoms add reference lines (sometimes called rules) to a plot, either horizontal, vertical, or diagonal (specified by slope and intercept). These are useful for annotating plots.

Usage

```r
geom_abline(
  mapping = NULL,
  data = NULL,
  ..., slope, intercept, na.rm = FALSE,
  show.legend = NA
)
```

```r
gem_hline(
  mapping = NULL,
  data = NULL,
```
geom_abline

..., 
yintercept, 
na.rm = FALSE, 
show.legend = NA 
)

geom_vline(
    mapping = NULL, 
data = NULL, 
..., 
xintercept, 
na.rm = FALSE, 
show.legend = NA 
)

Arguments

mapping Set of aesthetic mappings created by aes().
data The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot(). 
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created. 
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)). 
...
Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.
na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
xintercept, yintercept, slope, intercept 
Parameters that control the position of the line. If these are set, data, mapping and show.legend are overridden.

Details

These geoms act slightly differently from other geoms. You can supply the parameters in two ways: either as arguments to the layer function, or via aesthetics. If you use arguments, e.g. geom_abline(intercept = 0, slope = 1), then behind the scenes the geom makes a new data frame containing just the data you’ve supplied. That means that the lines will be the same in all facets; if you want them to vary across facets, construct the data frame yourself and use aesthetics.
Unlike most other geoms, these geoms do not inherit aesthetics from the plot default, because they
do not understand x and y aesthetics which are commonly set in the plot. They also do not affect
the x and y scales.

Aesthetics

These geoms are drawn using `geom_line()` so they support the same aesthetics: alpha, colour,
linetype and linewidth. They also each have aesthetics that control the position of the line:

- `geom_vline()`: xintercept
- `geom_hline()`: yintercept
- `geom_abline()`: slope and intercept

See Also

See `geom_segment()` for a more general approach to adding straight line segments to a plot.

Examples

```r
p <- ggplot(mtcars, aes(wt, mpg)) + geom_point()

# Fixed values
p + geom_vline(xintercept = 5)
p + geom_vline(xintercept = 1:5)
p + geom_hline(yintercept = 20)

p + geom_abline() # Can't see it - outside the range of the data
p + geom_abline(intercept = 20)

# Calculate slope and intercept of line of best fit
coeff(lm(mpg ~ wt, data = mtcars))
p + geom_abline(intercept = 37, slope = -5)
# But this is easier to do with geom_smooth:
p + geom_smooth(method = "lm", se = FALSE)

# To show different lines in different facets, use aesthetics
p <- ggplot(mtcars, aes(mpg, wt)) +
  geom_point() +
  facet_wrap(~ cyl)

mean_wt <- data.frame(cyl = c(4, 6, 8), wt = c(2.28, 3.11, 4.00))
p + geom_hline(aes(yintercept = wt), mean_wt)

# You can also control other aesthetics
ggplot(mtcars, aes(mpg, wt, colour = wt)) +
  geom_point() +
  geom_hline(aes(yintercept = wt, colour = wt), mean_wt) +
  facet_wrap(~ cyl)
```
Description

There are two types of bar charts: `geom_bar()` and `geom_col()`. `geom_bar()` makes the height of the bar proportional to the number of cases in each group (or if the weight aesthetic is supplied, the sum of the weights). If you want the heights of the bars to represent values in the data, use `geom_col()` instead. `geom_bar()` uses `stat_count()` by default: it counts the number of cases at each x position. `geom_col()` uses `stat_identity()`: it leaves the data as is.

Usage

```r
geom_bar(
  mapping = NULL,
  data = NULL,
  stat = "count",
  position = "stack",
  ...,
  just = 0.5,
  width = NULL,
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_col(
  mapping = NULL,
  data = NULL,
  position = "stack",
  ...,
  just = 0.5,
  width = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_count(
  mapping = NULL,
  data = NULL,
  geom = "bar",
  position = "stack",
  ...,
  width = NULL,
  na.rm = FALSE,
```
orientation = NA,
show.legend = NA,
inherit.aes = TRUE
)

Arguments

mapping
Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

data
The data to be displayed in this layer. There are three options:

- If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
- A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
- A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

position
Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

...
Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

just
Adjustment for column placement. Set to 0.5 by default, meaning that columns will be centered about axis breaks. Set to 0 or 1 to place columns to the left/right of axis breaks. Note that this argument may have unintended behaviour when used with alternative positions, e.g. `position_dodge()`.

width
Bar width. By default, set to 90% of the `resolution()` of the data.

na.rm
If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.

orientation
The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting `orientation` to either "x" or "y". See the Orientation section for more detail.

show.legend
logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes
If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

geom, stat
Override the default connection between `geom_bar()` and `stat_count()`.
Details

A bar chart uses height to represent a value, and so the base of the bar must always be shown to produce a valid visual comparison. Proceed with caution when using transformed scales with a bar chart. It’s important to always use a meaningful reference point for the base of the bar. For example, for log transformations the reference point is 1. In fact, when using a log scale, `geom_bar()` automatically places the base of the bar at 1. Furthermore, never use stacked bars with a transformed scale, because scaling happens before stacking. As a consequence, the height of bars will be wrong when stacking occurs with a transformed scale.

By default, multiple bars occupying the same x position will be stacked atop one another by `position_stack()`. If you want them to be dodged side-to-side, use `position_dodge()` or `position_dodge2()`. Finally, `position_fill()` shows relative proportions at each x by stacking the bars and then standardising each bar to have the same height.

Orientation

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the `orientation` parameter, which can be either "x" or "y". The value gives the axis that the geom should run along, "x" being the default orientation you would expect for the geom.

Aesthetics

`geom_bar()` understands the following aesthetics (required aesthetics are in bold):

- x
- y
- alpha
- colour
- fill
- group
- linetype
- linewidth

Learn more about setting these aesthetics in vignette("ggplot2-specs").

`geom_col()` understands the following aesthetics (required aesthetics are in bold):

- x
- y
- alpha
- colour
- fill
- group
• linetype
• linewidth

Learn more about setting these aesthetics in vignette("ggplot2-specs").

stat_count() understands the following aesthetics (required aesthetics are in bold):

• x or y
• group
• weight

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Computed variables

These are calculated by the ‘stat’ part of layers and can be accessed with delayed evaluation.

• after_stat(count)
  number of points in bin.
• after_stat(prop)
  groupwise proportion

See Also

ggeom_histogram() for continuous data, position_dodge() and position_dodge2() for creating side-by-side bar charts.

stat_bin(), which bins data in ranges and counts the cases in each range. It differs from stat_count(), which counts the number of cases at each x position (without binning into ranges). stat_bin() requires continuous x data, whereas stat_count() can be used for both discrete and continuous x data.

Examples

# geom_bar is designed to make it easy to create bar charts that show
# counts (or sums of weights)
g <- ggplot(mpg, aes(class))
# Number of cars in each class:
g + geom_bar()
# Total engine displacement of each class
g + geom_bar(aes(weight = displ))
# Map class to y instead to flip the orientation
ggplot(mpg) + geom_bar(aes(y = class))

# Bar charts are automatically stacked when multiple bars are placed
# at the same location. The order of the fill is designed to match
# the legend
g + geom_bar(aes(fill = drv))

# If you need to flip the order (because you've flipped the orientation)
# call position_stack() explicitly:
ggplot(mpg, aes(y = class)) +
### geom_bin_2d

**Heatmap of 2d bin counts**

#### Description

Divides the plane into rectangles, counts the number of cases in each rectangle, and then (by default) maps the number of cases to the rectangle’s fill. This is a useful alternative to `geom_point()` in the presence of overplotting.

#### Usage

```r
geom_bin_2d(
  mapping = NULL,
  data = NULL,
  stat = "bin2d",
  position = "identity",
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```r
stat_bin_2d(
```
geom_bin_2d

mapping = NULL,
data = NULL,
geom = "tile",
position = "identity",
...
bins = 30,
binwidth = NULL,
drop = TRUE,
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE
)

Arguments

mapping  Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data  The data to be displayed in this layer. There are three options:

- If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
- A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
- A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

position  Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function.

...  Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

na.rm  If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend  logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes  If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

gem, stat  Use to override the default connection between geom_bin_2d() and stat_bin_2d().

bins  numeric vector giving number of bins in both vertical and horizontal directions. Set to 30 by default.

binwidth  Numeric vector giving bin width in both vertical and horizontal directions. Overrides bins if both set.

drop  if TRUE removes all cells with 0 counts.
Aesthetics

`stat_bin_2d()` understands the following aesthetics (required aesthetics are in bold):

- x
- y
- fill
- group
- weight

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Computed variables

These are calculated by the ‘stat’ part of layers and can be accessed with delayed evaluation.

- `after_stat(count)`
  number of points in bin.
- `after_stat(density)`
  density of points in bin, scaled to integrate to 1.
- `after_stat(ncount)`
  count, scaled to maximum of 1.
- `after_stat(ndensity)`
  density, scaled to a maximum of 1.

See Also

- `stat_bin_hex()` for hexagonal binning

Examples

```r
library(ggplot2)

d <- ggplot(diamonds, aes(x, y)) + xlim(4, 10) + ylim(4, 10)
d + geom_bin_2d()

# You can control the size of the bins by specifying the number of
# bins in each direction:
d + geom_bin_2d(bins = 10)
d + geom_bin_2d(bins = 30)

# Or by specifying the width of the bins
# You can control the size of the bins by specifying the number of
d + geom_bin_2d(binwidth = c(0.1, 0.1))
```
Description

The blank geom draws nothing, but can be a useful way of ensuring common scales between different plots. See `expand_limits()` for more details.

Usage

```r
gem_blank(
mapping = NULL,
data = NULL,
stat = "identity",
position = "identity",
...,
show.legend = NA,
inherit.aes = TRUE
)
```

Arguments

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g., `~ head(.x, 10)`).

- **stat**: The statistical transformation to use on the data for this layer, either as a `ggproto` Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g., "count" rather than "stat_count")

- **position**: Position adjustment, either as a string naming the adjustment (e.g., "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

- **...**: Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

- **show.legend**: logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display.
If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

Examples

```r
ggplot(mtcars, aes(wt, mpg))
# Nothing to see here!
```

**geom_boxplot**

*A box and whiskers plot (in the style of Tukey)*

**Description**

The boxplot compactly displays the distribution of a continuous variable. It visualises five summary statistics (the median, two hinges and two whiskers), and all "outlying" points individually.

**Usage**

```r
geom_boxplot(
  mapping = NULL,
  data = NULL,
  stat = "boxplot",
  position = "dodge2",
  ...,
  outliers = TRUE,
  outlier.colour = NULL,
  outlier.color = NULL,
  outlier.fill = NULL,
  outlier.shape = 19,
  outlier.size = 1.5,
  outlier.stroke = 0.5,
  outlier.alpha = NULL,
  notch = FALSE,
  notchwidth = 0.5,
  staplewidth = 0,
  varwidth = FALSE,
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```r
stat_boxplot(
  mapping = NULL,
  data = NULL,
  geom = "boxplot",
)```
 Arguments

 mapping  Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

data  The data to be displayed in this layer. There are three options:
If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

 position  Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

 ...  Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

 outliers  Whether to display (TRUE) or discard (FALSE) outliers from the plot. Hiding or discarding outliers can be useful when, for example, raw data points need to be displayed on top of the boxplot. By discarding outliers, the axis limits will adapt to the box and whiskers only, not the full data range. If outliers need to be hidden and the axes needs to show the full data range, please use `outlier.shape = NA` instead.

 outlier.colour, outlier.color, outlier.fill, outlier.shape, outlier.size, outlier.stroke, outlier.alpha  Default aesthetics for outliers. Set to `NULL` to inherit from the aesthetics used for the box.
In the unlikely event you specify both US and UK spellings of colour, the US spelling will take precedence.

 notch  If FALSE (default) make a standard box plot. If TRUE, make a notched box plot. Notches are used to compare groups; if the notches of two boxes do not overlap, this suggests that the medians are significantly different.

 notchwidth  For a notched box plot, width of the notch relative to the body (defaults to `notchwidth = 0.5`).

 staplewidth  The relative width of staples to the width of the box. Staples mark the ends of the whiskers with a line.
If FALSE (default) make a standard box plot. If TRUE, boxes are drawn with widths proportional to the square-roots of the number of observations in the groups (possibly weighted, using the weight aesthetic).

If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the Orientation section for more detail.

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

Use to override the default connection between geom_boxplot() and stat_boxplot().

Length of the whiskers as multiple of IQR. Defaults to 1.5.

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the orientation parameter, which can be either "x" or "y". The value gives the axis that the geom should run along, "x" being the default orientation you would expect for the geom.

The lower and upper hinges correspond to the first and third quartiles (the 25th and 75th percentiles). This differs slightly from the method used by the boxplot() function, and may be apparent with small samples. See boxplot.stats() for more information on how hinge positions are calculated for boxplot().

The upper whisker extends from the hinge to the largest value no further than 1.5 * IQR from the hinge (where IQR is the inter-quartile range, or distance between the first and third quartiles). The lower whisker extends from the hinge to the smallest value at most 1.5 * IQR of the hinge. Data beyond the end of the whiskers are called "outlying" points and are plotted individually.

In a notched box plot, the notches extend 1.58 * IQR / sqrt(n). This gives a roughly 95% confidence interval for comparing medians. See McGill et al. (1978) for more details.

geom_boxplot() understands the following aesthetics (required aesthetics are in bold):

- x or y
- lower or xlower
• upper or xupper
• middle or xmmiddle
• ymin or xmin
• ymax or xmax
• alpha
• colour
• fill
• group
• linetype
• linewidth
• shape
• size
• weight

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Computed variables

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation. 
`stat_boxplot()` provides the following variables, some of which depend on the orientation:

• after_stat(width)
  width of boxplot.
• after_stat(ymin) or after_stat(xmin)
  lower whisker = smallest observation greater than or equal to lower hinger - 1.5 * IQR.
• after_stat(lower) or after_stat(xlower)
  lower hinge, 25% quantile.
• after_stat(notchlower)
  lower edge of notch = median - 1.58 * IQR / sqrt(n).
• after_stat(middle) or after_stat(xmiddle)
  median, 50% quantile.
• after_stat(notchupper)
  upper edge of notch = median + 1.58 * IQR / sqrt(n).
• after_stat(upper) or after_stat(xupper)
  upper hinge, 75% quantile.
• after_stat(ymax) or after_stat(xmax)
  upper whisker = largest observation less than or equal to upper hinger + 1.5 * IQR.

References

See Also

geom_quantile() for continuous x, geom_violin() for a richer display of the distribution, and geom_jitter() for a useful technique for small data.

Examples

```r
p <- ggplot(mpg, aes(class, hwy))
p + geom_boxplot()
# Orientation follows the discrete axis
ggplot(mpg, aes(hwy, class)) + geom_boxplot()

p + geom_boxplot(notch = TRUE)
p + geom_boxplot(varwidth = TRUE)
p + geom_boxplot(fill = "white", colour = "#3366FF")
# By default, outlier points match the colour of the box. Use
# outlier.colour to override
p + geom_boxplot(outlier.colour = "red", outlier.shape = 1)
# Remove outliers when overlaying boxplot with original data points
p + geom_boxplot(outlier.shape = NA) + geom_jitter(width = 0.2)

# Boxplots are automatically dodged when any aesthetic is a factor
p + geom_boxplot(aes(colour = drv))

# You can also use boxplots with continuous x, as long as you supply
# a grouping variable. cut_width is particularly useful
ggplot(diamonds, aes(carat, price)) + geom_boxplot()

# Adjust the transparency of outliers using outlier.alpha
ggplot(diamonds, aes(carat, price)) + geom_boxplot(aes(group = cut_width(carat, 0.25)), outlier.alpha = 0.1)

# It's possible to draw a boxplot with your own computations if you
# use stat = "identity":
set.seed(1)
y <- rnorm(100)
df <- data.frame(
x = 1,
y0 = min(y),
y25 = quantile(y, 0.25),
y50 = median(y),
y75 = quantile(y, 0.75),
y100 = max(y)
)
ggplot(df, aes(x)) + geom_boxplot(
aes(ymin = y0, lower = y25, middle = y50, upper = y75, ymax = y100),
   stat = "identity"
)
ggplot2 can not draw true 3D surfaces, but you can use `geom_contour()`, `geom_contour_filled()`, and `geom_tile()` to visualise 3D surfaces in 2D.

These functions require regular data, where the x and y coordinates form an equally spaced grid, and each combination of x and y appears once. Missing values of z are allowed, but contouring will only work for grid points where all four corners are non-missing. If you have irregular data, you’ll need to first interpolate on to a grid before visualising, using `interp::interp()`, `akima::bilinear()`, or similar.

**Usage**

```r
gem_contour(
  mapping = NULL,
  data = NULL,
  stat = "contour",
  position = "identity",
  ...,
  bins = NULL,
  binwidth = NULL,
  breaks = NULL,
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```r
gem_contour_filled(
  mapping = NULL,
  data = NULL,
  stat = "contour_filled",
  position = "identity",
  ...,
  bins = NULL,
  binwidth = NULL,
  breaks = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```
stat_contour(
  mapping = NULL,
  data = NULL,
  geom = "contour",
  position = "identity",
  ...,  
  bins = NULL,
  binwidth = NULL,
  breaks = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_contour_filled(
  mapping = NULL,
  data = NULL,
  geom = "contour_filled",
  position = "identity",
  ...,  
  bins = NULL,
  binwidth = NULL,
  breaks = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

Arguments

mapping Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

data The data to be displayed in this layer. There are three options:

If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.

A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.

A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

stat The statistical transformation to use on the data for this layer, either as a `ggproto` Geom subclass or as a string naming the stat stripped of the `stat_` prefix (e.g. "count" rather than "stat_count")

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
... Other arguments passed on to \code{layer()}. These are often aesthetics, used to set
an aesthetic to a fixed value, like \code{colour = "red"} or \code{size = 3}. They may also
be parameters to the paired geom/stat.

\code{bins} Number of contour bins. Overridden by \code{breaks}.
\code{binwidth} The width of the contour bins. Overridden by \code{bins}.
\code{breaks} One of:
  \begin{itemize}
  \item Numeric vector to set the contour breaks
  \item A function that takes the range of the data and \code{binwidth} as input and re-
    turns breaks as output. A function can be created from a formula (e.g. \code{~
      fullseq(x, y)}).
  \end{itemize}
Overrides \code{binwidth} and \code{bins}. By default, this is a vector of length ten with
\code{pretty()} breaks.
\code{lineend} Line end style (round, butt, square).
\code{linejoin} Line join style (round, mitre, bevel).
\code{linemitre} Line mitre limit (number greater than 1).
\code{na.rm} If \code{FALSE}, the default, missing values are removed with a warning. If \code{TRUE},
missing values are silently removed.
\code{show.legend} logical. Should this layer be included in the legends? \code{NA}, the default, includes if
any aesthetics are mapped. \code{FALSE} never includes, and \code{TRUE} always includes. It
can also be a named logical vector to finely select the aesthetics to display.
\code{inherit.aes} If \code{FALSE}, overrides the default aesthetics, rather than combining with them.
This is most useful for helper functions that define both data and aesthetics and
shouldn’t inherit behaviour from the default plot specification, e.g. \code{borders()}.  
\code{geom} The geometric object to use to display the data, either as a \code{ggproto} Geom
sub-class or as a string naming the geom stripped of the \code{geom_} prefix (e.g. "point"
rather than "geom_point")

\section*{Aesthetics}
\code{geom_contour()} understands the following aesthetics (required aesthetics are in bold):
\begin{itemize}
  \item \code{x}
  \item \code{y}
  \item \code{alpha}
  \item \code{colour}
  \item \code{group}
  \item \code{linetype}
  \item \code{linewidth}
  \item \code{weight}
\end{itemize}
Learn more about setting these aesthetics in \code{vignette("ggplot2-specs")}.
\code{geom_contour_filled()} understands the following aesthetics (required aesthetics are in bold):
\begin{itemize}
  \item \code{x}
\end{itemize}
Learn more about setting these aesthetics in vignette("ggplot2-specs").

stat_contour() understands the following aesthetics (required aesthetics are in bold):

- x
- y
- z
- group
- order

Learn more about setting these aesthetics in vignette("ggplot2-specs").

stat_contour_filled() understands the following aesthetics (required aesthetics are in bold):

- x
- y
- z
- fill
- group
- order

Learn more about setting these aesthetics in vignette("ggplot2-specs").

**Computed variables**

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation. The computed variables differ somewhat for contour lines (computed by stat_contour()) and contour bands (filled contours, computed by stat_contour_filled()). The variables `nlevel` and `piece` are available for both, whereas `level_low`, `level_high`, and `level_mid` are only available for bands. The variable `level` is a numeric or a factor depending on whether lines or bands are calculated.

- `after_stat(level)`
  Height of contour. For contour lines, this is a numeric vector that represents bin boundaries. For contour bands, this is an ordered factor that represents bin ranges.
- `after_stat(level_low), after_stat(level_high), after_stat(level_mid)`
  (contour bands only) Lower and upper bin boundaries for each band, as well as the mid point between boundaries.
• after_stat(nlevel)
  Height of contour, scaled to a maximum of 1.
• after_stat(piece)
  Contour piece (an integer).

Dropped variables

z  After contouring, the z values of individual data points are no longer available.

See Also

geom_density_2d(): 2d density contours

Examples

# Basic plot
v <- ggplot(faithful, aes(waiting, eruptions, z = density))
v + geom_contour()

# Or compute from raw data
ggplot(faithful, aes(waiting, eruptions)) +
  geom_density_2d()

# use geom_contour_filled() for filled contours
v + geom_contour_filled()

# Setting bins creates evenly spaced contours in the range of the data
v + geom_contour(bins = 3)
v + geom_contour(bins = 5)

# Setting binwidth does the same thing, parameterised by the distance
# between contours
v + geom_contour(binwidth = 0.01)
v + geom_contour(binwidth = 0.001)

# Other parameters
v + geom_contour(aes(colour = after_stat(level)))
v + geom_contour(colour = "red")
v + geom_raster(aes(fill = density)) +
  geom_contour(colour = "white")

---

geom_count  Count overlapping points

Description

This is a variant geom_point() that counts the number of observations at each location, then maps the count to point area. It useful when you have discrete data and overplotting.
geom_count

Usage

geom_count(
  mapping = NULL,
  data = NULL,
  stat = "sum",
  position = "identity",
  ...
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_sum(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  ...
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data The data to be displayed in this layer. There are three options:
  If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
  A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
  A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).
position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
...
  Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.
na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

geom, stat

Use to override the default connection between geom_count() and stat_sum().

Aesthetics

geom_point() understands the following aesthetics (required aesthetics are in bold):

• x
• y
• alpha
• colour
• fill
• group
• shape
• size
• stroke

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Computed variables

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation.

• after_stat(n)
  Number of observations at position.
• after_stat(prop)
  Percent of points in that panel at that position.

See Also

For continuous x and y, use geom_bin_2d().

Examples

```r
ggplot(mpg, aes(cty, hwy)) +
  geom_point()

ggplot(mpg, aes(cty, hwy)) +
  geom_count()
```

# Best used in conjunction with scale_size_area which ensures that
# counts of zero would be given size 0. Doesn't make much different
# here because the smallest count is already close to 0.
ggplot(mpg, aes(cty, hwy)) +
  geom_count() +
  scale_size_area()

# Display proportions instead of counts -------------------------------------
# By default, all categorical variables in the plot form the groups.
# Specifying geom_count without a group identifier leads to a plot which is
# not useful:
# d <- ggplot(diamonds, aes(x = cut, y = clarity))
# d + geom_count(aes(size = after_stat(prop)))
# To correct this problem and achieve a more desirable plot, we need
# to specify which group the proportion is to be calculated over.
# d + geom_count(aes(size = after_stat(prop), group = 1)) +
#   scale_size_area(max_size = 10)
#
# Or group by x/y variables to have rows/columns sum to 1.
# d + geom_count(aes(size = after_stat(prop), group = cut)) +
#   scale_size_area(max_size = 10)
# d + geom_count(aes(size = after_stat(prop), group = clarity)) +
#   scale_size_area(max_size = 10)

---

**geom_crossbar**

**Vertical intervals: lines, crossbars & errorbars**

**Description**

Various ways of representing a vertical interval defined by x, ymin and ymax. Each case draws a single graphical object.

**Usage**

```r
geom_crossbar(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ..., 
  fatten = 2.5,
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```r
gem_errorbar(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
```
geom_crossbar

```r
...
na.rm = FALSE,
orientation = NA,
show.legend = NA,
inherit.aes = TRUE
)
```

```r
gem_linerange(
  mapping = NULL,
data = NULL,
stat = "identity",
position = "identity",
...
na.rm = FALSE,
orientation = NA,
show.legend = NA,
inherit.aes = TRUE
)
```

```r
gem_pointrange(
  mapping = NULL,
data = NULL,
stat = "identity",
position = "identity",
...
fatten = 4,
na.rm = FALSE,
orientation = NA,
show.legend = NA,
inherit.aes = TRUE
)
```

**Arguments**

- **mapping**
  Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

- **data**
  The data to be displayed in this layer. There are three options:
  If NULL, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- **stat**
  The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g.
"count" rather than "stat_count")

position
Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

fatten
A multiplicative factor used to increase the size of the middle bar in geom_crossbar() and the middle point in geom_pointrange().

na.rm
If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

orientation
The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the Orientation section for more detail.

show.legend
logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes
If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

Orientation

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the orientation parameter, which can be either "x" or "y". The value gives the axis that the geom should run along, "x" being the default orientation you would expect for the geom.

Aesthetics

geom_linerange() understands the following aesthetics (required aesthetics are in bold):

- x or y
- ymin or xmin
- ymax or xmax
- alpha
- colour
- group
- linetype
- linewidth

Note that geom_pointrange() also understands size for the size of the points.

Learn more about setting these aesthetics in vignette("ggplot2-specs").
See Also

`stat_summary()` for examples of these guys in use, `geom_smooth()` for continuous analogue, `geom_errorbarh()` for a horizontal error bar.

Examples

```r
# Create a simple example dataset
df <- data.frame(
  trt = factor(c(1, 1, 2, 2)),
  resp = c(1, 5, 3, 4),
  group = factor(c(1, 2, 1, 2)),
  upper = c(1.1, 5.3, 3.3, 4.2),
  lower = c(0.8, 4.6, 2.4, 3.6)
)

p <- ggplot(df, aes(trt, resp, colour = group)) +
  geom_linerange(aes(ymin = lower, ymax = upper)) +
  geom_pointrange(aes(ymin = lower, ymax = upper)) +
  geom_crossbar(aes(ymin = lower, ymax = upper), width = 0.2) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2)

# Flip the orientation by changing mapping
ggplot(df, aes(resp, trt, colour = group)) +
  geom_linerange(aes(xmin = lower, xmax = upper))

# Draw lines connecting group means
p +
  geom_line(aes(group = group)) +
  geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2)

# If you want to dodge bars and errorbars, you need to manually
# specify the dodge width
p <- ggplot(df, aes(trt, resp, fill = group))
  geom_col(position = "dodge") +
  geom_errorbar(aes(ymin = lower, ymax = upper), position = "dodge", width = 0.25)

# Because the bars and errorbars have different widths
# we need to specify how wide the objects we are dodging are
dodge <- position_dodge(width=0.9)
p +
  geom_col(position = dodge) +
  geom_errorbar(aes(ymin = lower, ymax = upper), position = dodge, width = 0.25)

# When using geom_errorbar() with position_dodge2(), extra padding will be
# needed between the error bars to keep them aligned with the bars.
p +
  geom_col(position = "dodge2") +
  geom_errorbar(
    aes(ymin = lower, ymax = upper),
    position = position_dodge2(width = 0.5, padding = 0.5)
  )
```

```
Description

Computes and draws kernel density estimate, which is a smoothed version of the histogram. This is a useful alternative to the histogram for continuous data that comes from an underlying smooth distribution.

Usage

geom_density(
  mapping = NULL,
  data = NULL,
  stat = "density",
  position = "identity",
  ...,
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE,
  outline.type = "upper"
)

stat_density(
  mapping = NULL,
  data = NULL,
  geom = "area",
  position = "stack",
  ...,
  bw = "nrd0",
  adjust = 1,
  kernel = "gaussian",
  n = 512,
  trim = FALSE,
  na.rm = FALSE,
  bounds = c(-Inf, Inf),
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE
)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data  The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

position  Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

...  Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

na.rm  If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

orientation  The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the Orientation section for more detail.

show.legend  logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes  If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

outline.type  Type of the outline of the area; "both" draws both the upper and lower lines, "upper"/"lower" draws the respective lines only. "full" draws a closed polygon around the area.

geom, stat  Use to override the default connection between geom_density() and stat_density().

bw  The smoothing bandwidth to be used. If numeric, the standard deviation of the smoothing kernel. If character, a rule to choose the bandwidth, as listed in stats::bw.nrd(). Note that automatic calculation of the bandwidth does not take weights into account.

adjust  A multiplicate bandwidth adjustment. This makes it possible to adjust the bandwidth while still using the a bandwidth estimator. For example, adjust = 1/2 means use half of the default bandwidth.

kernel  Kernel. See list of available kernels in density().

n  number of equally spaced points at which the density is to be estimated, should be a power of two, see density() for details

trim  If FALSE, the default, each density is computed on the full range of the data. If TRUE, each density is computed over the range of that group: this typically means the estimated x values will not line-up, and hence you won’t be able to
stack density values. This parameter only matters if you are displaying multiple densities in one plot or if you are manually adjusting the scale limits.

**bounds**

Known lower and upper bounds for estimated data. Default \((-\infty, \infty)\) means that there are no (finite) bounds. If any bound is finite, boundary effect of default density estimation will be corrected by reflecting tails outside bounds around their closest edge. Data points outside of bounds are removed with a warning.

**Orientation**

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the orientation parameter, which can be either "x" or "y". The value gives the axis that the geom should run along, "x" being the default orientation you would expect for the geom.

**Aesthetics**

`geom_density()` understands the following aesthetics (required aesthetics are in bold):

- x
- y
- alpha
- colour
- fill
- group
- linetype
- linewidth
- weight

Learn more about setting these aesthetics in vignette("ggplot2-specs").

**Computed variables**

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation.

- after_stat(density) density estimate.
- after_stat(count) density * number of points - useful for stacked density plots.
- after_stat(scaled) density estimate, scaled to maximum of 1.
- after_stat(n) number of points.
- after_stat(ndensity) alias for scaled, to mirror the syntax of `stat_bin()`.
See Also

See `geom_histogram()`, `geom_freqpoly()` for other methods of displaying continuous distribution. See `geom_violin()` for a compact density display.

Examples

```r
ggplot(diamonds, aes(carat)) + geom_density()
# Map the values to y to flip the orientation
ggplot(diamonds, aes(y = carat)) + geom_density()

ggplot(diamonds, aes(carat)) + geom_density(adjust = 1/5)

ggplot(diamonds, aes(carat)) + geom_density(adjust = 5)

ggplot(diamonds, aes(depth, colour = cut)) + geom_density() + xlim(55, 70)

ggplot(diamonds, aes(depth, fill = cut, colour = cut)) + geom_density(alpha = 0.1) + xlim(55, 70)

# Use `bounds` to adjust computation for known data limits
big_diamonds <- diamonds[diamonds$carat >= 1, ]
ggplot(big_diamonds, aes(carat)) + geom_density(color = 'red') + geom_density(bounds = c(1, Inf), color = 'blue')

# Stacked density plots: if you want to create a stacked density plot, you probably want to 'count' (density * n) variable instead of the default density

# Loses marginal densities

# Preserves marginal densities

ggplot(diamonds, aes(carat, after_stat(count), fill = cut)) + geom_density(position = "stack")

# You can use position="fill" to produce a conditional density estimate

```
Description

Perform a 2D kernel density estimation using MASS::kde2d() and display the results with contours. This can be useful for dealing with overplotting. This is a 2D version of geom_density(). geom_density_2d() draws contour lines, and geom_density_2d_filled() draws filled contour bands.

Usage

geom_density_2d(
  mapping = NULL,
  data = NULL,
  stat = "density_2d",
  position = "identity",
  ...,
  contour_var = "density",
  lineend = "butt",
  linejoin = "round",
  linemitre = 10,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_density_2d_filled(
  mapping = NULL,
  data = NULL,
  stat = "density_2d_filled",
  position = "identity",
  ...,
  contour_var = "density",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_density_2d(
  mapping = NULL,
  data = NULL,
  geom = "density_2d",
  position = "identity",
  ...,
  contour = TRUE,
  contour_var = "density",
  n = 100,
  h = NULL,
  adjust = c(1, 1),
  na.rm = FALSE,
  show.legend = NA,
geom_density_2d

stat_density_2d_filled(
  mapping = NULL,
  data = NULL,
  geom = "density_2d_filled",
  position = "identity",
  ...
)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data The data to be displayed in this layer. There are three options: If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot(). A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.Arguments passed on to geom_contour

binwidth The width of the contour bins. Overridden by bins.
bins Number of contour bins. Overridden by breaks.
breaks One of:
  • Numeric vector to set the contour breaks
  • A function that takes the range of the data and binwidth as input and returns breaks as output. A function can be created from a formula (e.g. ~ fullseq(x, y)).
  
Overrides binwidth and bins. By default, this is a vector of length ten with pretty() breaks.
contour_var  Character string identifying the variable to contour by. Can be one of "density", "ndensity", or "count". See the section on computed variables for details.

lineend  Line end style (round, butt, square).

linejoin  Line join style (round, mitre, bevel).

linemitre  Line mitre limit (number greater than 1).

na.rm  If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend  logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes  If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

geom, stat  Use to override the default connection between geom_density_2d() and stat_density_2d().

contour  If TRUE, contour the results of the 2d density estimation.

n  Number of grid points in each direction.

h  Bandwidth (vector of length two). If NULL, estimated using MASS::bandwidth.nrd().

adjust  A multiplicative bandwidth adjustment to be used if 'h' is 'NULL'. This makes it possible to adjust the bandwidth while still using the a bandwidth estimator. For example, adjust = 1/2 means use half of the default bandwidth.

Aesthetics

geom_density_2d() understands the following aesthetics (required aesthetics are in bold):

• x
• y
• alpha
• colour
• group
• linetype
• linewidth

Learn more about setting these aesthetics in vignette("ggplot2-specs").

geom_density_2d_filled() understands the following aesthetics (required aesthetics are in bold):

• x
• y
• alpha
• colour
• fill
• group
Learn more about setting these aesthetics in vignette("ggplot2-specs").

Computed variables

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation. stat_density_2d() and stat_density_2d_filled() compute different variables depending on whether contouring is turned on or off. With contouring off (contour = FALSE), both stats behave the same, and the following variables are provided:

- after_stat(density)
  The density estimate.
- after_stat(ndensity)
  Density estimate, scaled to a maximum of 1.
- after_stat(count)
  Density estimate * number of observations in group.
- after_stat(n)
  Number of observations in each group.

With contouring on (contour = TRUE), either stat_contour() or stat_contour_filled() (for contour lines or contour bands, respectively) is run after the density estimate has been obtained, and the computed variables are determined by these stats. Contours are calculated for one of the three types of density estimates obtained before contouring, density, ndensity, and count. Which of those should be used is determined by the contour_var parameter.

Dropped variables

z  After density estimation, the z values of individual data points are no longer available.

If contouring is enabled, then similarly density, ndensity, and count are no longer available after the contouring pass.

See Also

geom_contour(), geom_contour_filled() for information about how contours are drawn; geom_bin_2d() for another way of dealing with overplotting.

Examples

m <- ggplot(faithful, aes(x = eruptions, y = waiting)) +
  geom_point() +
  xlim(0.5, 6) +
  ylim(40, 110)

# contour lines
m + geom_density_2d()
# contour bands
m + geom_density_2d_filled(alpha = 0.5)

# contour bands and contour lines
m + geom_density_2d_filled(alpha = 0.5) + geom_density_2d(linewidth = 0.25, colour = "black")

set.seed(4393)
dsmall <- diamonds[sample(nrow(diamonds), 1000), ]
d <- ggplot(dsmall, aes(x, y))
# If you map an aesthetic to a categorical variable, you will get a set of contours for each value of that variable
d + geom_density_2d(aes(colour = cut))

# If you draw filled contours across multiple facets, the same bins are used across all facets
d + geom_density_2d_filled() + facet_wrap(vars(cut))
# If you want to make sure the peak intensity is the same in each facet, use `contour_var = "ndensity"`.
d + geom_density_2d_filled(contour_var = "ndensity") + facet_wrap(vars(cut))
# If you want to scale intensity by the number of observations in each group, use `contour_var = "count"`.
d + geom_density_2d_filled(contour_var = "count") + facet_wrap(vars(cut))

# If we turn contouring off, we can use other geoms, such as tiles:
d + stat_density_2d(
  geom = "raster",
  aes(fill = after_stat(density)),
  contour = FALSE
) + scale_fill_viridis_c()
# Or points:
d + stat_density_2d(geom = "point", aes(size = after_stat(density)), n = 20, contour = FALSE)

---

**geom_dotplot**

**Dot plot**

**Description**

In a dot plot, the width of a dot corresponds to the bin width (or maximum width, depending on the binning algorithm), and dots are stacked, with each dot representing one observation.

**Usage**

```r
gem_dotplot(
  mapping = NULL,
  data = NULL,
  position = "identity",
  ...
)```

geom_dotplot

```r
binwidth = NULL,
binaxis = "x",
method = "dotdensity",
binpositions = "bygroup",
stackdir = "up",
stackratio = 1,
dotsize = 1,
stackgroups = FALSE,
origin = NULL,
right = TRUE,
width = 0.9,
drop = FALSE,
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE
)
```

### Arguments

- **mapping**
  - Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- **data**
  - The data to be displayed in this layer. There are three options:
    - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
    - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
    - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a `formula` (e.g. `~ head(.x, 10)`).

- **position**
  - Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

- **...**
  - Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

- **binwidth**
  - When method is "dotdensity", this specifies maximum bin width. When method is "histodot", this specifies bin width. Defaults to 1/30 of the range of the data

- **binaxis**
  - The axis to bin along, "x" (default) or "y"

- **method**
  - "dotdensity" (default) for dot-density binning, or "histodot" for fixed bin widths (like `stat_bin`)

- **binpositions**
  - When method is "dotdensity", "bygroup" (default) determines positions of the bins for each group separately. "all" determines positions of the bins with all the data taken together; this is used for aligning dot stacks across multiple groups.
geom_dotplot

stackdir which direction to stack the dots. "up" (default), "down", "center", "centerwhole" (centered, but with dots aligned)

stackratio how close to stack the dots. Default is 1, where dots just touch. Use smaller values for closer, overlapping dots.

dotsize The diameter of the dots relative to binwidth, default 1.

stackgroups should dots be stacked across groups? This has the effect that position = "stack" should have, but can't (because this geom has some odd properties).

origin When method is "histodot", origin of first bin

right When method is "histodot", should intervals be closed on the right (a, b], or not [a, b)

width When binaxis is "y", the spacing of the dot stacks for dodging.

drop If TRUE, remove all bins with zero counts

na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders().

Details

There are two basic approaches: dot-density and histodot. With dot-density binning, the bin positions are determined by the data and binwidth, which is the maximum width of each bin. See Wilkinson (1999) for details on the dot-density binning algorithm. With histodot binning, the bins have fixed positions and fixed widths, much like a histogram.

When binning along the x axis and stacking along the y axis, the numbers on y axis are not meaningful, due to technical limitations of ggplot2. You can hide the y axis, as in one of the examples, or manually scale it to match the number of dots.

Aesthetics

gem_dotplot() understands the following aesthetics (required aesthetics are in bold):

- x
- y
- alpha
- colour
- fill
- group
- linetype
- stroke
- weight

Learn more about setting these aesthetics in vignette("ggplot2-specs").
Computed variables

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation.

- `after_stat(x)`
  center of each bin, if binaxis is "x".
- `after_stat(y)`
  center of each bin, if binaxis is "x".
- `after_stat(binwidth)`
  maximum width of each bin if method is "dotdensity"; width of each bin if method is "histodot".
- `after_stat(count)`
  number of points in bin.
- `after_stat(ncount)`
  count, scaled to a maximum of 1.
- `after_stat(density)`
  density of points in bin, scaled to integrate to 1, if method is "histodot".
- `after_stat(ndensity)`
  density, scaled to maximum of 1, if method is "histodot".

References


Examples

```r
ggplot(mtcars, aes(x = mpg)) +
  geom_dotplot()

ggplot(mtcars, aes(x = mpg)) +
  geom_dotplot(binwidth = 1.5)

# Use fixed-width bins
ggplot(mtcars, aes(x = mpg)) +
  geom_dotplot(binwidth = 1.5, stackdir = "center")

# Some other stacking methods
ggplot(mtcars, aes(x = mpg)) +
  geom_dotplot(binwidth = 1.5, stackdir = "centerwhole")

# y axis isn't really meaningful, so hide it
qqplot(mtcars, aes(x = mpg)) + geom_dotplot(binwidth = 1.5) +
  scale_y_continuous(NULL, breaks = NULL)

# Overlap dots vertically
qqplot(mtcars, aes(x = mpg)) +
  geom_dotplot(binwidth = 1.5, stackratio = .7)
```
# Expand dot diameter
ggplot(mtcars, aes(x = mpg)) +
  geom_dotplot(binwidth = 1.5, dotsize = 1.25)

# Change dot fill colour, stroke width
ggplot(mtcars, aes(x = mpg)) +
  geom_dotplot(binwidth = 1.5, fill = "white", stroke = 2)

# Examples with stacking along y axis instead of x
ggplot(mtcars, aes(x = 1, y = mpg)) +
  geom_dotplot(binaxis = "y", stackdir = "center")

ggplot(mtcars, aes(x = factor(cyl), y = mpg)) +
  geom_dotplot(binaxis = "y", stackdir = "center")

ggplot(mtcars, aes(x = factor(cyl), y = mpg)) +
  geom_dotplot(binaxis = "y", stackdir = "centerwhole")

ggplot(mtcars, aes(x = factor(vs), fill = factor(cyl), y = mpg)) +
  geom_dotplot(binaxis = "y", stackdir = "center", position = "dodge")

# binpositions="all" ensures that the bins are aligned between groups
ggplot(mtcars, aes(x = factor(am), y = mpg)) +
  geom_dotplot(binaxis = "y", stackdir = "center", binpositions = "all")

# Stacking multiple groups, with different fill
ggplot(mtcars, aes(x = mpg, fill = factor(cyl))) +
  geom_dotplot(stackgroups = TRUE, binwidth = 1, binpositions = "all")

ggplot(mtcars, aes(x = mpg, fill = factor(cyl))) +
  geom_dotplot(stackgroups = TRUE, binwidth = 1, method = "histodot")

ggplot(mtcars, aes(x = 1, y = mpg, fill = factor(cyl))) +
  geom_dotplot(binaxis = "y", stackgroups = TRUE, binwidth = 1, method = "histodot")

---

### geom_errorbarh

*Horizontal error bars*

**Description**

A rotated version of `geom_errorbar()`. 

**Usage**

```r
geom_errorbarh(
  mapping = NULL,
  data = NULL,
```
stat = "identity",
position = "identity",
...,
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE)

Arguments

mapping Set of aesthetic mappings created by \texttt{aes()}. If specified and \texttt{inherit.aes = TRUE} (the default), it is combined with the default mapping at the top level of the plot. You must supply \texttt{mapping} if there is no plot mapping.

data The data to be displayed in this layer. There are three options:
If \texttt{NULL}, the default, the data is inherited from the plot data as specified in the call to \texttt{ggplot()}.
A \texttt{data.frame}, or other object, will override the plot data. All objects will be fortified to produce a data frame. See \texttt{fortify()} for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a \texttt{data.frame}, and will be used as the layer data. A function can be created from a formula (e.g. \texttt{~ head(.x, 10)}).

stat The statistical transformation to use on the data for this layer, either as a \texttt{ggproto} Geom subclass or as a string naming the stat stripped of the \texttt{stat_} prefix (e.g. "count" rather than "stat_count")

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use \texttt{position_jitter}), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

... Other arguments passed on to \texttt{layer()}. These are often aesthetics, used to set an aesthetic to a fixed value, like \texttt{colour = "red"} or \texttt{size = 3}. They may also be parameters to the paired geom/stat.

na.rm If \texttt{FALSE}, the default, missing values are removed with a warning. If \texttt{TRUE}, missing values are silently removed.

show.legend logical. Should this layer be included in the legends? \texttt{NA}, the default, includes if any aesthetics are mapped. \texttt{FALSE} never includes, and \texttt{TRUE} always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If \texttt{FALSE}, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. \texttt{borders()}. 

Aesthetics

gem\_errorbarh() understands the following aesthetics (required aesthetics are in bold):

\begin{itemize}
\item \texttt{xmin}
\item \texttt{xmax}
\end{itemize}
Learn more about setting these aesthetics in vignette("ggplot2-specs").

Examples

df <- data.frame(
  trt = factor(c(1, 1, 2, 2)),
  resp = c(1, 5, 3, 4),
  group = factor(c(1, 2, 1, 2)),
  se = c(0.1, 0.3, 0.3, 0.2)
)

# Define the top and bottom of the errorbars
p <- ggplot(df, aes(resp, trt, colour = group))
p +
  geom_point() +
  geom_errorbarh(aes(xmax = resp + se, xmin = resp - se))

p +
  geom_point() +
  geom_errorbarh(aes(xmax = resp + se, xmin = resp - se, height = .2))

---

**geom_freqpoly**

**Histograms and frequency polygons**

**Description**

Visualise the distribution of a single continuous variable by dividing the x axis into bins and counting the number of observations in each bin. Histograms (geom_histogram()) display the counts with bars; frequency polygons (geom_freqpoly()) display the counts with lines. Frequency polygons are more suitable when you want to compare the distribution across the levels of a categorical variable.

**Usage**

`geom_freqpoly(
  mapping = NULL,
  data = NULL,
  stat = "bin",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...)
`
geom_freqpoly(  
  position = "identity",  
  ...,  
  na.rm = FALSE,  
  show.legend = NA,  
  inherit.aes = TRUE
)

geom_histogram(  
  mapping = NULL,  
  data = NULL,  
  stat = "bin",  
  position = "stack",  
  ...,  
  binwidth = NULL,  
  bins = NULL,  
  na.rm = FALSE,  
  orientation = NA,  
  show.legend = NA,  
  inherit.aes = TRUE
)

stat_bin(  
  mapping = NULL,  
  data = NULL,  
  geom = "bar",  
  position = "stack",  
  ...,  
  binwidth = NULL,  
  bins = NULL,  
  center = NULL,  
  boundary = NULL,  
  breaks = NULL,  
  closed = c("right", "left"),  
  pad = FALSE,  
  na.rm = FALSE,  
  orientation = NA,  
  show.legend = NA,  
  inherit.aes = TRUE
)

Arguments

mapping  
Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data  
The data to be displayed in this layer. There are three options:  
If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.

A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

**position**  
Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

**...**  
Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

**na.rm**  
If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.

**show.legend**  
Logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display.

**inherit.aes**  
If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

**binwidth**  
The width of the bins. Can be specified as a numeric value or as a function that calculates width from unscaled x. Here, "unscaled x" refers to the original x values in the data, before application of any scale transformation. When specifying a function along with a grouping structure, the function will be called once per group. The default is to use the number of bins in `bins`, covering the range of the data. You should always override this value, exploring multiple widths to find the best to illustrate the stories in your data.

The bin width of a date variable is the number of days in each time; the bin width of a time variable is the number of seconds.

**bins**  
Number of bins. Overridden by `binwidth`. Defaults to 30.

**orientation**  
The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting `orientation` to either "x" or "y". See the Orientation section for more detail.

**geom, stat**  
Use to override the default connection between `geom_histogram()`/`geom_freqpoly()` and `stat_bin()`.

**center, boundary**  
Bin position specifiers. Only one, center or boundary, may be specified for a single plot. `center` specifies the center of one of the bins. `boundary` specifies the boundary between two bins. Note that if either is above or below the range of the data, things will be shifted by the appropriate integer multiple of `binwidth`. For example, to center on integers use `binwidth = 1` and `center = 0`, even if 0 is outside the range of the data. Alternatively, this same alignment can be specified with `binwidth = 1` and `boundary = 0.5`, even if 0.5 is outside the range of the data.
breaks
Alternatively, you can supply a numeric vector giving the bin boundaries. Overrides binwidth, bins, center, and boundary.

closed
One of "right" or "left" indicating whether right or left edges of bins are included in the bin.

pad
If TRUE, adds empty bins at either end of x. This ensures frequency polygons touch 0. Defaults to FALSE.

Details

`stat_bin()` is suitable only for continuous x data. If your x data is discrete, you probably want to use `stat_count()`.

By default, the underlying computation (`stat_bin()`) uses 30 bins; this is not a good default, but the idea is to get you experimenting with different number of bins. You can also experiment modifying the binwidth with center or boundary arguments. binwidth overrides bins so you should do one change at a time. You may need to look at a few options to uncover the full story behind your data.

In addition to `geom_histogram()`, you can create a histogram plot by using `scale_x_binned()` with `geom_bar()`. This method by default plots tick marks in between each bar.

Orientation

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the orientation parameter, which can be either "x" or "y". The value gives the axis that the geom should run along, "x" being the default orientation you would expect for the geom.

Aesthetics

`geom_histogram()` uses the same aesthetics as `geom_bar()`: `geom_freqpoly()` uses the same aesthetics as `geom_line()`.

Computed variables

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation.

- `after_stat(count)`
  number of points in bin.
- `after_stat(density)`
  density of points in bin, scaled to integrate to 1.
- `after_stat(ncount)`
  count, scaled to a maximum of 1.
- `after_stat(ndensity)`
  density, scaled to a maximum of 1.
- `after_stat(width)`
  widths of bins.
Dropped variables

weight  After binning, weights of individual data points (if supplied) are no longer available.

See Also

stat_count(), which counts the number of cases at each x position, without binning. It is suitable for both discrete and continuous x data, whereas stat_bin() is suitable only for continuous x data.

Examples

ggplot(diamonds, aes(carat)) +
  geom_histogram()
ggplot(diamonds, aes(carat)) +
  geom_histogram(binwidth = 0.01)
ggplot(diamonds, aes(carat)) +
  geom_histogram(bins = 200)
# Map values to y to flip the orientation
ggplot(diamonds, aes(y = carat)) +
  geom_histogram()

# For histograms with tick marks between each bin, use `geom_bar()` with # `scale_x_binned()`.
ggplot(diamonds, aes(carat)) +
  geom_bar() +
  scale_x_binned()

# Rather than stacking histograms, it's easier to compare frequency polygons
# ggplot(diamonds, aes(price, fill = cut)) +
#  geom_histogram(binwidth = 500)
# ggplot(diamonds, aes(price, colour = cut)) +
#  geom_freqpoly(binwidth = 500)

# To make it easier to compare distributions with very different counts, # put density on the y axis instead of the default count

if (require("ggplot2movies")) {
  if (require("ggplot2movies")) {
    m <- ggplot(movies, aes(rating))
    m + geom_histogram(binwidth = 0.1)

    m +
    geom_histogram(aes(weight = votes), binwidth = 0.1) +
    ylab("votes")
}
# For transformed scales, binwidth applies to the transformed data.  
# The bins have constant width on the transformed scale.
m +  
  geom_histogram() +  
scale_x_log10()  
m +  
  geom_histogram(binwidth = 0.05) +  
scale_x_log10()  

# For transformed coordinate systems, the binwidth applies to the  
# raw data. The bins have constant width on the original scale.

# Using log scales does not work here, because the first  
# bar is anchored at zero, and so when transformed becomes negative  
# infinity. This is not a problem when transforming the scales, because  
# no observations have 0 ratings.
m +  
  geom_histogram(boundary = 0) +  
  coord_trans(x = "log10")  
# Use boundary = 0, to make sure we don't take sqrt of negative values  
m +  
  geom_histogram(boundary = 0) +  
  coord_trans(x = "sqrt")  

# You can also transform the y axis. Remember that the base of the bars  
# has value 0, so log transformations are not appropriate  
m <- ggplot(movies, aes(x = rating))  
m +  
  geom_histogram(binwidth = 0.5) +  
  scale_y_sqrt()  
}

# You can specify a function for calculating binwidth, which is  
# particularly useful when faceting along variables with  
# different ranges because the function will be called once per facet  

ggplot(economics_long, aes(value)) +  
  facet_wrap(~variable, scales = 'free_x') +  
  geom_histogram(binwidth = function(x) 2 * IQR(x) / (length(x)^((1/3))))

---

**geom_function**

*Draw a function as a continuous curve*

---

**Description**

Computes and draws a function as a continuous curve. This makes it easy to superimpose a function on top of an existing plot. The function is called with a grid of evenly spaced values along the x axis, and the results are drawn (by default) with a line.
Usage

geom_function(
    mapping = NULL,
    data = NULL,
    stat = "function",
    position = "identity",
    ..., 
    na.rm = FALSE, 
    show.legend = NA, 
    inherit.aes = TRUE 
)

stat_function(
    mapping = NULL,
    data = NULL,
    geom = "function",
    position = "identity",
    ..., 
    fun, 
    xlim = NULL, 
    n = 101,
    args = list(), 
    na.rm = FALSE, 
    show.legend = NA, 
    inherit.aes = TRUE 
)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data Ignored by stat_function(), do not use.
stat The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")
position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.
na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
**geom_function**

**inherit.aes**
If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

**geom**
The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the `geom_` prefix (e.g. “point” rather than “geom_point”).

**fun**
Function to use. Either 1) an anonymous function in the base or rlang formula syntax (see `rlang::as_function()`) or 2) a quoted or character name referencing a function; see examples. Must be vectorised.

**xlim**
Optionally, specify the range of the function.

**n**
Number of points to interpolate along the x axis.

**args**
List of additional arguments passed on to the function defined by `fun`.

**Aesthetics**

`geom_function()` understands the following aesthetics (required aesthetics are in bold):

- **x**
- **y**
- **alpha**
- **colour**
- **group**
- **linetype**
- **linewidth**

Learn more about setting these aesthetics in vignette("ggplot2-specs").

**Computed variables**

These are calculated by the `stat` part of layers and can be accessed with delayed evaluation.

- **after_stat(x)**
  - x values along a grid.
- **after_stat(y)**
  - values of the function evaluated at corresponding x.

**See Also**

`rlang::as_function()`

**Examples**

```r
# geom_function() is useful for overlaying functions
set.seed(1492)
ggplot(data.frame(x = rnorm(100)), aes(x)) +
  geom_density() +
```
geom_function(fun = dnorm, colour = "red")

# To plot functions without data, specify range of x-axis
base <-
ggplot() +
  xlim(-5, 5)

base + geom_function(fun = dnorm)

base + geom_function(fun = dnorm, args = list(mean = 2, sd = .5))

# The underlying mechanics evaluate the function at discrete points
# and connect the points with lines
base + stat_function(fun = dnorm, geom = "point")

base + stat_function(fun = dnorm, geom = "point", n = 20)

base + stat_function(fun = dnorm, geom = "polygon", color = "blue", fill = "blue", alpha = 0.5)

base + geom_function(fun = dnorm, n = 20)

# Two functions on the same plot
base +
  geom_function(aes(colour = "normal"), fun = dnorm) +
  geom_function(aes(colour = "t, df = 1"), fun = dt, args = list(df = 1))

# Using a custom anonymous function
base + geom_function(fun = function(x) 0.5*exp(-abs(x)))

base + geom_function(fun = ~ 0.5*exp(-abs(.x)))

# Using a custom named function
f <- function(x) 0.5*exp(-abs(x))

base + geom_function(fun = f)

# Using xlim to restrict the range of function
ggplot(data.frame(x = rnorm(100)), aes(x)) +
  geom_density() +
  geom_function(fun = dnorm, colour = "red", xlim=c(-1, 1))

# Using xlim to widen the range of function
ggplot(data.frame(x = rnorm(100)), aes(x)) +
  geom_density() +
  geom_function(fun = dnorm, colour = "red", xlim=c(-7, 7))
Description

Divides the plane into regular hexagons, counts the number of cases in each hexagon, and then (by default) maps the number of cases to the hexagon fill. Hexagon bins avoid the visual artefacts sometimes generated by the very regular alignment of `geom_bin_2d()`.

Usage

```r
geom_hex(
  mapping = NULL,
  data = NULL,
  stat = "binhex",
  position = "identity",
  ...,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```r
stat_bin_hex(
  mapping = NULL,
  data = NULL,
  geom = "hex",
  position = "identity",
  ...,
  bins = 30,
  binwidth = NULL,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

- `mapping`: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- `data`: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- `position`: Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

gem, stat Override the default connection between geom_hex() and stat_bin_hex().

bins numeric vector giving number of bins in both vertical and horizontal directions. Set to 30 by default.

binwidth Numeric vector giving bin width in both vertical and horizontal directions. Over-rides bins if both set.

Aesthetics

gem_hex() understands the following aesthetics (required aesthetics are in bold):

• x
• y
• alpha
• colour
• fill
• group
• linetype
• linewidth

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Computed variables

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation.

• after_stat(count) number of points in bin.
• after_stat(density) density of points in bin, scaled to integrate to 1.
• after_stat(ncount) count, scaled to maximum of 1.
• after_stat(ndensity) density, scaled to maximum of 1.
See Also

stat_bin_2d() for rectangular binning

Examples

\[
\begin{align*}
d & \leftarrow \text{ggplot(diamonds, aes(carat, price))} \\
d & + \text{geom_hex()}
\end{align*}
\]

# You can control the size of the bins by specifying the number of
# bins in each direction:
\[
\begin{align*}
d & + \text{geom_hex(bins = 10)} \\
d & + \text{geom_hex(bins = 30)}
\end{align*}
\]

# Or by specifying the width of the bins
\[
\begin{align*}
d & + \text{geom_hex(binwidth = c(1, 1000))} \\
d & + \text{geom_hex(binwidth = c(.1, 500))}
\end{align*}
\]

**Description**

The jitter geom is a convenient shortcut for \texttt{geom_point(position = “jitter”).} It adds a small amount of random variation to the location of each point, and is a useful way of handling overplotting caused by discreteness in smaller datasets.

**Usage**

\[
\text{geom_jitter(}
\begin{align*}
\text{mapping = NULL,} \\
\text{data = NULL,} \\
\text{stat = “identity”,} \\
\text{position = “jitter”,} \\
\text{...}, \\
\text{width = NULL,} \\
\text{height = NULL,} \\
\text{na.rm = FALSE,} \\
\text{show.legend = NA,} \\
\text{inherit.aes = TRUE}
\end{align*}
\)

**Arguments**

- \textbf{mapping}
  
  Set of aesthetic mappings created by \texttt{aes()}. If specified and \texttt{inherit.aes = TRUE} (the default), it is combined with the default mapping at the top level of the plot. You must supply \texttt{mapping} if there is no plot mapping.
**geom_jitter**

The data to be displayed in this layer. There are three options:

- If **NULL**, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
- A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
- A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

**stat**

The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")

**position**

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

... Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

**width, height**

Amount of vertical and horizontal jitter. The jitter is added in both positive and negative directions, so the total spread is twice the value specified here.

If omitted, defaults to 40% of the resolution of the data: this means the jitter values will occupy 80% of the implied bins. Categorical data is aligned on the integers, so a width or height of 0.5 will spread the data so it’s not possible to see the distinction between the categories.

**na.rm**

If **FALSE**, the default, missing values are removed with a warning. If **TRUE**, missing values are silently removed.

**show.legend**

logical. Should this layer be included in the legends? **NA**, the default, includes if any aesthetics are mapped. **FALSE** never includes, and **TRUE** always includes. It can also be a named logical vector to finely select the aesthetics to display.

**inherit.aes**

If **FALSE**, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

### Aesthetics

`geom_point()` understands the following aesthetics (required aesthetics are in bold):

- **x**
- **y**
- **alpha**
- **colour**
- **fill**
- **group**
- **shape**
Learn more about setting these aesthetics in vignette("ggplot2-specs").

See Also

geom_point() for regular, unjittered points. geom_boxplot() for another way of looking at the conditional distribution of a variable

Examples

p <- ggplot(mpg, aes(cyl, hwy))
p + geom_point()
p + geom_jitter()

# Add aesthetic mappings
p + geom_jitter(aes(colour = class))

# Use smaller width/height to emphasise categories
ggplot(mpg, aes(cyl, hwy)) +
  geom_jitter()
ggplot(mpg, aes(cyl, hwy)) +
  geom_jitter(width = 0.25)

# Use larger width/height to completely smooth away discreteness
ggplot(mpg, aes(cty, hwy)) +
  geom_jitter()
ggplot(mpg, aes(cty, hwy)) +
  geom_jitter(width = 0.5, height = 0.5)

Description

Text geoms are useful for labeling plots. They can be used by themselves as scatterplots or in combination with other geoms, for example, for labeling points or for annotating the height of bars. geom_text() adds only text to the plot. geom_label() draws a rectangle behind the text, making it easier to read.

Usage

geom_label(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
geom_label
grow = FALSE,
nudge_x = 0,
nudge_y = 0,
label.padding = unit(0.25, "lines"),
label.r = unit(0.15, "lines"),
label.size = 0.25,
size.unit = "mm",
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE
)

geom_text(
  mapping = NULL,
data = NULL,
  stat = "identity",
  position = "identity",
  ...
  parse = FALSE,
nudge_x = 0,
nudge_y = 0,
  check_overlap = FALSE,
  size.unit = "mm",
  na.rm = FALSE,
  show.legend = NA,
inherit.aes = TRUE
)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).
stat The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")
position Position adjustment, either as a string, or the result of a call to a position adjustment function. Cannot be jointly specified with nudge_x or nudge_y.
Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired `geom/stat`.

- `parse` If TRUE, the labels will be parsed into expressions and displayed as described in `?plotmath`.

- `nudge_x`, `nudge_y` Horizontal and vertical adjustment to nudge labels by. Useful for offsetting text from points, particularly on discrete scales. Cannot be jointly specified with `position`.

- `label.padding` Amount of padding around label. Defaults to 0.25 lines.

- `label.r` Radius of rounded corners. Defaults to 0.15 lines.

- `label.size` Size of label border, in mm.

- `size.unit` How the `size` aesthetic is interpreted: as millimetres ("mm", default), points ("pt"), centimetres ("cm"), inches ("in"), or picas ("pc").

- `na.rm` If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

- `show.legend` logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

- `inherit.aes` If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

- `check_overlap` If TRUE, text that overlaps previous text in the same layer will not be plotted. `check_overlap` happens at draw time and in the order of the data. Therefore data should be arranged by the label column before calling `geom_text()`. Note that this argument is not supported by `geom_label()`.

### Details

Note that when you resize a plot, text labels stay the same size, even though the size of the plot area changes. This happens because the "width" and "height" of a text element are 0. Obviously, text labels do have height and width, but they are physical units, not data units. For the same reason, stacking and dodging text will not work by default, and axis limits are not automatically expanded to include all text.

`geom_text()` and `geom_label()` add labels for each row in the data, even if coordinates `x`, `y` are set to single values in the call to `geom_label()` or `geom_text()`. To add labels at specified points use `annotate()` with `annotate(geom = "text", ...)` or `annotate(geom = "label", ...)`. To automatically position non-overlapping text labels see the `ggrepel` package.

### Aesthetics

`geom_text()` understands the following aesthetics (required aesthetics are in bold):

- `x`
- `y`
geom_label

- label
- alpha
- angle
- colour
- family
- fontface
- group
- hjust
- lineheight
- size
- vjust

Learn more about setting these aesthetics in vignette("ggplot2-specs").

gem_label()

Currently geom_label() does not support the check_overlap argument. Also, it is considerably slower than geom_text(). The fill aesthetic controls the background colour of the label.

Alignment

You can modify text alignment with the vjust and hjust aesthetics. These can either be a number between 0 (right/bottom) and 1 (top/left) or a character ("left", "middle", "right", "bottom", "center", "top"). There are two special alignments: "inward" and "outward". Inward always aligns text towards the center, and outward aligns it away from the center.

Examples

p <- ggplot(mtcars, aes(wt, mpg, label = rownames(mtcars)))

p + geom_text()
# Avoid overlaps
p + geom_text(check_overlap = TRUE)
# Labels with background
p + geom_label()
# Change size of the label
p + geom_text(size = 10)

# Set aesthetics to fixed value
p +
  geom_point() +
  geom_text(hjust = 0, nudge_x = 0.05)
p +
  geom_point() +
  geom_text(vjust = 0, nudge_y = 0.5)
p +
  geom_point() +
  geom_text(angle = 45)
## Not run:
# Doesn't work on all systems
p +
  geom_text(family = "Times New Roman")

## End(Not run)

# Add aesthetic mappings
p + geom_text(aes(colour = factor(cyl)))
p + geom_text(aes(colour = factor(cyl))) +
  scale_colour_discrete(l = 40)
p + geom_label(aes(fill = factor(cyl)), colour = "white", fontface = "bold")

p + geom_text(aes(size = wt))
# Scale height of text, rather than sqrt(height)
p +
  geom_text(aes(size = wt)) +
  scale_radius(range = c(3, 6))

# You can display expressions by setting parse = TRUE. The
details of the display are described in \texttt{?plotmath}, but note that
# \texttt{geom_text} uses strings, not expressions.
p +
  geom_text(
    aes(label = paste(wt, "+(", cyl, ")", sep = "")),
    parse = TRUE
  )

# Add a text annotation
p +
  geom_text() +
  annotate(
    "text", label = "plot mpg vs. wt",
    x = 2, y = 15, size = 8, colour = "red"
  )

# Aligning labels and bars -------------------------------

df <- data.frame(
  x = factor(c(1, 1, 2, 2)),
  y = c(1, 3, 2, 1),
  grp = c("a", "b", "a", "b")
)

# ggplot2 doesn't know you want to give the labels the same virtual width
# as the bars:

```r
ggplot(data = df, aes(x, y, group = grp)) +
  geom_col(aes(fill = grp), position = "dodge") +
  geom_text(aes(label = y), position = "dodge")
```

# So tell it:

```r
ggplot(data = df, aes(x, y, group = grp)) +
  geom_col(aes(fill = grp), position = "dodge") +
  geom_text(aes(label = y), position = position_dodge(0.9))
```
# You can't nudge and dodge text, so instead adjust the y position
ggplot(data = df, aes(x, y, group = grp)) +
  geom_col(aes(fill = grp), position = "dodge") +
  geom_text(
    aes(label = y, y = y + 0.05),
    position = position_dodge(0.9),
    vjust = 0
  )

# To place text in the middle of each bar in a stacked barplot, you
# need to set the vjust parameter of position_stack()

ggplot(data = df, aes(x, y, group = grp)) +
  geom_col(aes(fill = grp)) +
  geom_text(aes(label = y), position = position_stack(vjust = 0.5))

# Justification -------------------------------------------------------------

df <- data.frame(
  x = c(1, 1, 2, 2, 1.5),
  y = c(1, 2, 1, 2, 1.5),
  text = c("bottom-left", "top-left", "bottom-right", "top-right", "center")
)

ggplot(df, aes(x, y)) +
  geom_text(aes(label = text))
ggplot(df, aes(x, y)) +
  geom_text(aes(label = text), vjust = "inward", hjust = "inward")

---

**geom_map**  
**Polygons from a reference map**

**Description**

Display polygons as a map. This is meant as annotation, so it does not affect position scales. Note that this function predates the `geom_sf()` framework and does not work with sf geometry columns as input. However, it can be used in conjunction with `geom_sf()` layers and/or `coord_sf()` (see examples).

**Usage**

```r
geom_map(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  ...,
  map,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```
Arguments

mapping  Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

data  The data to be displayed in this layer. There are three options:
If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

stat  The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")

...  Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

map  Data frame that contains the map coordinates. This will typically be created using `fortify()` on a spatial object. It must contain columns `x` or `long`, `y` or `lat`, and `region` or `id`.

na.rm  If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.

show.legend  logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes  If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

Aesthetics

`geom_map()` understands the following aesthetics (required aesthetics are in bold):

- `map_id`
- `alpha`
- `colour`
- `fill`
- `group`
- `linetype`
- `linewidth`
- `subgroup`

Learn more about setting these aesthetics in `vignette("ggplot2-specs")`. 
Examples

# First, a made-up example containing a few polygons, to explain # how `geom_map()` works. It requires two data frames: # One contains the coordinates of each polygon (`positions`), and is # provided via the `map` argument. The other contains the # other the values associated with each polygon (`values`). An id # variable links the two together.

ids <- factor(c("1.1", "2.1", "1.2", "2.2", "1.3", "2.3"))

values <- data.frame(  
id = ids,  
value = c(3, 3.1, 3.1, 3.2, 3.15, 3.5)
)

positions <- data.frame(  
id = rep(ids, each = 4),  
x = c(2, 1, 1.1, 2.2, 1, 0, 0.3, 1.1, 2.2, 1.1, 1.2, 2.5, 1.1, 0.3, 0.5, 1.2, 2.5, 1.2, 1.3, 2.7, 1.2, 0.5, 0.6, 1.3),  
y = c(-0.5, 0, 1, 0.5, 0, 0.5, 1.5, 0.5, 1, 2.1, 1.7, 1, 1.5, 2.2, 2.1, 1.7, 2.1, 3.2, 2.8, 2.1, 2.2, 3, 3.2)
)

ggplot(values) +  
  geom_map(aes(map_id = id), map = positions) +  
  expand_limits(positions)

ggplot(values, aes(fill = value)) +  
  geom_map(aes(map_id = id), map = positions) +  
  expand_limits(positions)

ggplot(values, aes(fill = value)) +  
  geom_map(aes(map_id = id), map = positions) +  
  expand_limits(positions) + ylim(0, 3)

# Now some examples with real maps
if (require(maps)) {

  crimes <- data.frame(state = tolower(rownames(USArrests)), USArrests)  
  # Equivalent to crimes %>% tidyr::pivot_longer(Murder:Rape)  
  vars <- lapply(names(crimes)[-1], function(j) {  
    data.frame(state = crimes$state, variable = j, value = crimes[[j]])  
  })
  crimes_long <- do.call("rbind", vars)

  states_map <- map_data("state")
  # without geospatial coordinate system, the resulting plot
  # looks weird
  ggplot(crimes, aes(map_id = state)) +  
    geom_map(aes(fill = Murder), map = states_map) +  
    expand_limits(x = states_map$long, y = states_map$lat)
}
# in combination with 'coord_sf()' we get an appropriate result
```r
ggplot(crimes, aes(map_id = state)) +
  geom_map(aes(fill = Murder), map = states_map) +
  coord_sf(crs = 5070, default_crs = 4326, xlim = c(-125, -70), ylim = c(25, 52))
```

```r
ggplot(crimes_long, aes(map_id = state)) +
  geom_map(aes(fill = value), map = states_map) +
  coord_sf(crs = 5070, default_crs = 4326, xlim = c(-125, -70), ylim = c(25, 52)) +
  facet_wrap(~variable)
```

---

### geom_path

**Connect observations**

**Description**

`geom_path()` connects the observations in the order in which they appear in the data. `geom_line()` connects them in order of the variable on the x axis. `geom_step()` creates a stairstep plot, highlighting exactly when changes occur. The `group` aesthetic determines which cases are connected together.

**Usage**

```r
geom_path(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...
)
```

```r
geom_line(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...
)
```
geom_path

```r
data = NULL,
stat = "identity",
position = "identity",
na.rm = FALSE,
orientation = NA,
show.legend = NA,
inherit.aes = TRUE,
...)
```

Arguments

- **mapping**
  Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- **data**
  The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- **stat**
  The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the `stat_` prefix (e.g. "count" rather than "stat_count")

- **position**
  Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

- **...**
  Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

- **lineend**
  Line end style (round, butt, square).
geom_path

**linejoin**
Line join style (round, mitre, bevel).

**linemitre**
Line mitre limit (number greater than 1).

**arrow**
Arrow specification, as created by `grid::arrow()`.

**na.rm**
If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

**show.legend**
Logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

**inherit.aes**
If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

**orientation**
The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the Orientation section for more detail.

**direction**
direction of stairs: 'vh' for vertical then horizontal, 'hv' for horizontal then vertical, or 'mid' for step half-way between adjacent x-values.

**Details**

An alternative parameterisation is `geom_segment()`, where each line corresponds to a single case which provides the start and end coordinates.

**Orientation**

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the orientation parameter, which can be either "x" or "y". The value gives the axis that the geom should run along, "x" being the default orientation you would expect for the geom.

**Aesthetics**

`geom_path()` understands the following aesthetics (required aesthetics are in bold):

- x
- y
- alpha
- colour
- group
- linetype
- linewidth

Learn more about setting these aesthetics in vignette("ggplot2-specs").
Missing value handling

geom_path(), geom_line(), and geom_step() handle NA as follows:

- If an NA occurs in the middle of a line, it breaks the line. No warning is shown, regardless of whether na.rm is TRUE or FALSE.
- If an NA occurs at the start or the end of the line and na.rm is FALSE (default), the NA is removed with a warning.
- If an NA occurs at the start or the end of the line and na.rm is TRUE, the NA is removed silently, without warning.

See Also

gem_polygon(): Filled paths (polygons); geom_segment(): Line segments

Examples

# geom_line() is suitable for time series
ggplot(economics, aes(date, unemploy)) + geom_line()

# You can get a timeseries that run vertically by setting the orientation
# the y value changes
recent <- economics[economics$date > as.Date("2013-01-01"), ]
ggplot(recent, aes(date, unemploy)) + geom_line()

# geom_step() is useful when you want to highlight exactly when
# the y value changes
recent <- economics[economics$date > as.Date("2013-01-01"), ]
ggplot(recent, aes(date, unemploy)) + geom_line()

# geom_path lets you explore how two variables are related over time,
# e.g. unemployment and personal savings rate
m <- ggplot(economics, aes(unemploy/pop, psavert))
m + geom_path()

# Changing parameters
# Use the arrow parameter to add an arrow to the line
# See ?arrow for more details
c <- ggplot(economics, aes(x = date, y = pop))
c + geom_line(arrow = arrow())

df <- data.frame(x = 1:3, y = c(4, 1, 9))
base <- ggplot(df, aes(x, y))
### Points

**Description**

The point geom is used to create scatterplots. The scatterplot is most useful for displaying the relationship between two continuous variables. It can be used to compare one continuous and one categorical variable, or two categorical variables, but a variation like `geom_jitter()`, `geom_count()`, or `geom_bin_2d()` is usually more appropriate. A bubble chart is a scatterplot with a third variable mapped to the size of points.

**Usage**

```r
geom_point(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...
)
```
Arguments

mapping Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

stat The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

... Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

Overplotting

The biggest potential problem with a scatterplot is overplotting: whenever you have more than a few points, points may be plotted on top of one another. This can severely distort the visual appearance of the plot. There is no one solution to this problem, but there are some techniques that can help. You can add additional information with `geom_smooth()`, `geom_quantile()` or `geom_density_2d()`. If you have few unique x values, `geom_boxplot()` may also be useful.

Alternatively, you can summarise the number of points at each location and display that in some way, using `geom_count()`, `geom_hex()`, or `geom_density2d()`.

Another technique is to make the points transparent (e.g. `geom_point(alpha = 0.05)`) or very small (e.g. `geom_point(shape = ".")`).
Aesthetics

geom_point() understands the following aesthetics (required aesthetics are in bold):

- x
- y
- alpha
- colour
- fill
- group
- shape
- size
- stroke

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Examples

```r
p <- ggplot(mtcars, aes(wt, mpg))
p + geom_point()

# Add aesthetic mappings
p + geom_point(aes(colour = factor(cyl)))
p + geom_point(aes(shape = factor(cyl)))
# A "bubblechart":
p + geom_point(aes(size = qsec))

# Set aesthetics to fixed value
ggplot(mtcars, aes(wt, mpg)) + geom_point(colour = "red", size = 3)

# Varying alpha is useful for large datasets
d <- ggplot(diamonds, aes(carat, price))
d + geom_point(alpha = 1/10)
d + geom_point(alpha = 1/20)
d + geom_point(alpha = 1/100)

# For shapes that have a border (like 21), you can colour the inside and
# outside separately. Use the stroke aesthetic to modify the width of the
# border
ggplot(mtcars, aes(wt, mpg)) +
  geom_point(shape = 21, colour = "black", fill = "white", size = 5, stroke = 5)

# You can create interesting shapes by layering multiple points of
# different sizes
p <- ggplot(mtcars, aes(mpg, wt, shape = factor(cyl)))
p +
  geom_point(aes(colour = factor(cyl)), size = 4) +
```
```r
geom_point(colour = "grey90", size = 1.5)
p +
geom_point(colour = "black", size = 4.5) +
geom_point(colour = "pink", size = 4) +
geom_point(aes(shape = factor(cyl)))

# geom_point warns when missing values have been dropped from the data set
# and not plotted, you can turn this off by setting na.rm = TRUE
set.seed(1)
mtcars2 <- transform(mtcars, mpg = ifelse(runif(32) < 0.2, NA, mpg))
ggplot(mtcars2, aes(wt, mpg)) +
geom_point()
ggplot(mtcars2, aes(wt, mpg)) +
geom_point(na.rm = TRUE)
```

**geom_polygon**

### Polygons

Polygons are very similar to paths (as drawn by `geom_path()` except that the start and end points are connected and the inside is coloured by `fill`. The group aesthetic determines which cases are connected together into a polygon. From R 3.6 and onwards it is possible to draw polygons with holes by providing a subgroup aesthetic that differentiates the outer ring points from those describing holes in the polygon.

#### Usage

```r
gem_polygon(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  rule = "evenodd",
  ...
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

#### Arguments

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
data  The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the
call to ggplot().
A data.frame, or other object, will override the plot data. All objects will be
fortified to produce a data frame. See fortify() for which variables will be
created.
A function will be called with a single argument, the plot data. The return
value must be a data.frame, and will be used as the layer data. A function
can be created from a formula (e.g. ~ head(.x, 10)).
stat  The statistical transformation to use on the data for this layer, either as a ggproto
Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g.
"count" rather than "stat_count")
position  Position adjustment, either as a string naming the adjustment (e.g. "jitter" to
use position_jitter), or the result of a call to a position adjustment function.
Use the latter if you need to change the settings of the adjustment.
rule  Either "evenodd" or "winding". If polygons with holes are being drawn (us-
ing the subgroup aesthetic) this argument defines how the hole coordinates are
interpreted. See the examples in grid::pathGrob() for an explanation.
...  Other arguments passed on to layer(). These are often aesthetics, used to set
an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be
parameters to the paired geom/stat.
na.rm  If FALSE, the default, missing values are removed with a warning. If TRUE,
missing values are silently removed.
show.legend  logical. Should this layer be included in the legends? NA, the default, includes if
any aesthetics are mapped. FALSE never includes, and TRUE always includes. It
can also be a named logical vector to finely select the aesthetics to display.
inherit.aes  If FALSE, overrides the default aesthetics, rather than combining with them.
This is most useful for helper functions that define both data and aesthetics and
shouldn’t inherit behaviour from the default plot specification, e.g. borders().

Aesthetics

geom_polygon() understands the following aesthetics (required aesthetics are in bold):

- x
- y
- alpha
- colour
- fill
- group
- linetype
- linewidth
- subgroup

Learn more about setting these aesthetics in vignette("ggplot2-specs").
See Also

`geom_path()` for an unfilled polygon, `geom_ribbon()` for a polygon anchored on the x-axis

Examples

# When using geom_polygon, you will typically need two data frames:
# one contains the coordinates of each polygon (positions), and the
# other the values associated with each polygon (values). An id
# variable links the two together

ids <- factor(c("1.1", "2.1", "1.2", "2.2", "1.3", "2.3"))

values <- data.frame(
    id = ids,
    value = c(3, 3.1, 3.1, 3.2, 3.15, 3.5)
)

positions <- data.frame(
    id = rep(ids, each = 4),
    x = c(2, 1, 1.1, 2.2, 1, 0, 0.3, 1.1, 2.2, 1.1, 1.2, 2.5, 1.1, 0.3,
          0.5, 1.2, 2.5, 1.2, 1.3, 2.7, 1.2, 0.5, 0.6, 1.3),
    y = c(-0.5, 0, 1, 0.5, 0, 0.5, 1.5, 0.5, 1, 0.5, 1, 2.1, 1.7, 1, 1.5,
          2.2, 2.1, 1.7, 2.1, 3.2, 2.8, 2.1, 2.2, 3.3, 3.2)
)

# Currently we need to manually merge the two together
datapoly <- merge(values, positions, by = c("id"))

p <- ggplot(datapoly, aes(x = x, y = y)) +
    geom_polygon(aes(fill = value, group = id))

p

# Which seems like a lot of work, but then it's easy to add on
# other features in this coordinate system, e.g.:

set.seed(1)
stream <- data.frame(
    x = cumsum(runif(50, max = 0.1)),
    y = cumsum(runif(50, max = 0.1))
)

p + geom_line(data = stream, colour = "grey30", linewidth = 5)

# And if the positions are in longitude and latitude, you can use
# coord_map to produce different map projections.

if (packageVersion("grid") >= "3.6") {
    # As of R version 3.6 geom_polygon() supports polygons with holes
    # Use the subgroup aesthetic to differentiate holes from the main polygon

    holes <- do.call(rbind, lapply(split(datapoly, datapoly$id), function(df) {
        df$x <- df$x + 0.5 * (mean(df$x) - df$x)
    }))

    p + geom_polygon(aes(fill = value, subgroup = id),
                     data = datapoly, group = id,
                )
}

df$y <- df$y + 0.5 * (mean(df$y) - df$y)
}
datapoly$subid <- 1L
holes$subid <- 2L
datapoly <- rbind(datapoly, holes)

p <- ggplot(datapoly, aes(x = x, y = y)) +
  geom_polygon(aes(fill = value, group = id, subgroup = subid))
p

---

**geom_qq_line**

*A quantile-quantile plot*

**Description**

`geom_qq()` and `stat_qq()` produce quantile-quantile plots. `geom_qq_line()` and `stat_qq_line()` compute the slope and intercept of the line connecting the points at specified quartiles of the theoretical and sample distributions.

**Usage**

```r
gem_qq_line(
  mapping = NULL,
  data = NULL,
  geom = "path",
  position = "identity",
  ...
  distribution = stats::qnorm,
  dparams = list(),
  line.p = c(0.25, 0.75),
  fullrange = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```r
stat_qq_line(
  mapping = NULL,
  data = NULL,
  geom = "path",
  position = "identity",
  ...
  distribution = stats::qnorm,
  dparams = list(),
  line.p = c(0.25, 0.75),
  fullrange = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)```
Arguments

mapping Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

data The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

gem The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point")
rather than "geom_point")

position  Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

...  Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

distribution  Distribution function to use, if x not specified
dparams  Additional parameters passed on to distribution function.
line.p  Vector of quantiles to use when fitting the Q-Q line, defaults defaults to (.25,

fullrange  Should the q-q line span the full range of the plot, or just the data
na.rm  If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend  logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes  If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

Aesthetics

stat_qq() understands the following aesthetics (required aesthetics are in bold):

• sample
• group
• x
• y

Learn more about setting these aesthetics in vignette("ggplot2-specs").

stat_qq_line() understands the following aesthetics (required aesthetics are in bold):

• sample
• group
• x
• y

Learn more about setting these aesthetics in vignette("ggplot2-specs").
Computed variables

These are calculated by the ’stat’ part of layers and can be accessed with delayed evaluation. Variables computed by `stat_qq()`:

- `after_stat(sample)`
  Sample quantiles.
- `after_stat(theoretical)`
  Theoretical quantiles.

Variables computed by `stat_qq_line()`:

- `after_stat(x)`
  x-coordinates of the endpoints of the line segment connecting the points at the chosen quantiles of the theoretical and the sample distributions.
- `after_stat(y)`
  y-coordinates of the endpoints.

Examples

```r
df <- data.frame(y = rt(200, df = 5))
p <- ggplot(df, aes(sample = y))
p + stat_qq() + stat_qq_line()

# Use fitdistr from MASS to estimate distribution params
params <- as.list(MASS::fitdistr(df$y, "t")$estimate)
ggplot(df, aes(sample = y)) +
  stat_qq(distribution = qt, dparams = params["df"]) +
  stat_qq_line(distribution = qt, dparams = params["df"]) +

# Using to explore the distribution of a variable
ggplot(mtcars, aes(sample = mpg)) +
  stat_qq() +
  stat_qq_line()
ggplot(mtcars, aes(sample = mpg, colour = factor(cyl))) +
  stat_qq() +
  stat_qq_line()
```

geom_quantile Quantile regression

Description

This fits a quantile regression to the data and draws the fitted quantiles with lines. This is as a continuous analogue to `geom_boxplot()`.
Usage

```r
gem_quantile(
    mapping = NULL,
    data = NULL,
    stat = "quantile",
    position = "identity",
    ...
    lineend = "butt",
    linejoin = "round",
    linemitre = 10,
    na.rm = FALSE,
    show.legend = NA,
    inherit.aes = TRUE
)
```

```r
stat_quantile(
    mapping = NULL,
    data = NULL,
    geom = "quantile",
    position = "identity",
    ...
    quantiles = c(0.25, 0.5, 0.75),
    formula = NULL,
    method = "rq",
    method.args = list(),
    na.rm = FALSE,
    show.legend = NA,
    inherit.aes = TRUE
)
```

Arguments

- **mapping** Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- **data** The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- **position** Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
... Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired `geom/stat`.

- `lineend` Line end style (round, butt, square).
- `linejoin` Line join style (round, mitre, bevel).
- `linemitre` Line mitre limit (number greater than 1).
- `na.rm` If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.
- `show.legend` logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display.
- `inherit.aes` If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.
- `geom, stat` Use to override the default connection between `geom_quantile()` and `stat_quantile()`.
- `quantiles` conditional quantiles of y to calculate and display
- `formula` formula relating y variables to x variables
- `method` Quantile regression method to use. Available options are "rq" (for `quantreg::rq()`) and "rqss" (for `quantreg::rqss()`).
- `method.args` List of additional arguments passed on to the modelling function defined by `method`.

Aesthetics

tabular summary:

```
geom_quantile() understands the following aesthetics (required aesthetics are in bold):

  • x
  • y
  • alpha
  • colour
  • group
  • linetype
  • linewidth
  • weight
```

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Computed variables

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation.

- `after_stat(quantile)`
  Quantile of distribution.
Examples

```r
m <-
   ggplot(mpg, aes(displ, 1 / hwy)) +
   geom_point()

m + geom_quantile()
m + geom_quantile(quantiles = 0.5)
q10 <- seq(0.05, 0.95, by = 0.05)
m + geom_quantile(quantiles = q10)

# You can also use rqss to fit smooth quantiles
m + geom_quantile(method = "rqss")
# Note that rqss doesn't pick a smoothing constant automatically, so
# you'll need to tweak lambda yourself
m + geom_quantile(method = "rqss", lambda = 0.1)

# Set aesthetics to fixed value
m + geom_quantile(colour = "red", linewidth = 2, alpha = 0.5)
```

---

**geom_raster**

_Rectangles_

Description

`geom_rect()` and `geom_tile()` do the same thing, but are parameterised differently: `geom_rect()` uses the locations of the four corners (`xmin`, `xmax`, `ymin` and `ymax`), while `geom_tile()` uses the center of the tile and its size (`x`, `y`, `width`, `height`). `geom_raster()` is a high performance special case for when all the tiles are the same size, and no pattern fills are applied.

Usage

```r
geom_raster(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...
)
```

```r
geom_rect(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...
)
```
geom_raster

```r
position = "identity",
...,
linejoin = "mitre",
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE
)
```

```r
geom_tile(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...
  linejoin = "mitre",
  na.rm = FALSE,
  show.legend = NA,
inherit.aes = TRUE
)
```

### Arguments

- **mapping**
  Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- **data**
  The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- **stat**
  The statistical transformation to use on the data for this layer, either as a `ggproto` Geom subclass or as a string naming the stat stripped of the `stat_` prefix (e.g. "count" rather than "stat_count")

- **position**
  Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

- **hjust, vjust**
  Horizontal and vertical justification of the grob. Each justification value should be a number between 0 and 1. Defaults to 0.5 for both, centering each pixel over its data location.

- **interpolate**
  If TRUE interpolate linearly, if FALSE (the default) don’t interpolate.
na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

linejoin Line join style (round, mitre, bevel).

Details

geom_rect() and geom_tile()'s respond differently to scale transformations due to their parameterisation. In geom_rect(), the scale transformation is applied to the corners of the rectangles. In geom_tile(), the transformation is applied only to the centres and its size is determined after transformation.

Aesthetics

geom_tile() understands the following aesthetics (required aesthetics are in bold):

- x
- y
- alpha
- colour
- fill
- group
- height
- linetype
- linewidth
- width

Note that geom_raster() ignores colour.

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Examples

# The most common use for rectangles is to draw a surface. You always want # to use geom_raster here because it's so much faster, and produces # smaller output when saving to PDF
ggplot(faithfuld, aes(waiting, eruptions)) + geom_raster(aes(fill = density))

# Interpolation smooths the surface & is most helpful when rendering images. ggplot(faithfuld, aes(waiting, eruptions)) + geom_raster(aes(fill = density), interpolate = TRUE)
If you want to draw arbitrary rectangles, use `geom_tile()` or `geom_rect()`

```r
df <- data.frame(
  x = rep(c(2, 5, 7, 9, 12), 2),
  y = rep(c(1, 2), each = 5),
  z = factor(rep(1:5, each = 2)),
  w = rep(diff(c(0, 4, 6, 8, 10, 14)), 2)
)
ggplot(df, aes(x, y)) +
  geom_tile(aes(fill = z), colour = "grey50")
ggplot(df, aes(x, y, width = w)) +
  geom_tile(aes(fill = z), colour = "grey50")
ggplot(df, aes(xmin = x - w / 2, xmax = x + w / 2, ymin = y, ymax = y + 1)) +
  geom_rect(aes(fill = z), colour = "grey50")
```

Justification controls where the cells are anchored

```r
df <- expand.grid(x = 0:5, y = 0:5)
set.seed(1)
df$z <- runif(nrow(df))
# default is compatible with geom_tile()
ggplot(df, aes(x, y, fill = z)) +
  geom_raster()
# zero padding
ggplot(df, aes(x, y, fill = z)) +
  geom_raster(hjust = 0, vjust = 0)
```

Inspired by the image-density plots of Ken Knoblauch

```r
cars <- ggplot(mtcars, aes(mpg, factor(cyl)))
cars + geom_point()
cars + stat_bin_2d(aes(fill = after_stat(count)), binwidth = c(3,1))
cars + stat_bin_2d(aes(fill = after_stat(density)), binwidth = c(3,1))
cars +
  stat_density(
    aes(fill = after_stat(density)),
    geom = "raster",
    position = "identity"
  )
cars +
  stat_density(
    aes(fill = after_stat(count)),
    geom = "raster",
    position = "identity"
  )
```
**Description**

For each x value, `geom_ribbon()` displays a y interval defined by `ymin` and `ymax`. `geom_area()` is a special case of `geom_ribbon()`, where the `ymin` is fixed to 0 and y is used instead of `ymax`.

**Usage**

```r
geom_ribbon(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE,
  outline.type = "both"
)
```

```r
geom_area(
  mapping = NULL,
  data = NULL,
  stat = "align",
  position = "stack",
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

```r
stat_align(
  mapping = NULL,
  data = NULL,
  geom = "area",
  position = "identity",
  ...
)
```

**Arguments**

- `mapping` Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
The data to be displayed in this layer. There are three options:

If NULL, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.

A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.

A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the Orientation section for more detail.

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

Type of the outline of the area; "both" draws both the upper and lower lines, "upper"/"lower" draws the respective lines only. "full" draws a closed polygon around the area.

The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")

An area plot is the continuous analogue of a stacked bar chart (see `geom_bar()`), and can be used to show how composition of the whole varies over the range of x. Choosing the order in which different components is stacked is very important, as it becomes increasing hard to see the individual pattern as you move up the stack. See `position_stack()` for the details of stacking algorithm. To facilitate stacking, the default `stat = "align"` interpolates groups to a common set of x-coordinates. To turn off this interpolation, `stat = "identity"` can be used instead.
Orientation

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the `orientation` parameter, which can be either "x" or "y". The value gives the axis that the geom should run along, "x" being the default orientation you would expect for the geom.

Aesthetics

gem_ribbon() understands the following aesthetics (required aesthetics are in bold):

- `x` or `y`
- `ymin` or `xmin`
- `ymax` or `xmax`
- `alpha`
- `colour`
- `fill`
- `group`
- `linetype`
- `linewidth`

Learn more about setting these aesthetics in vignette("ggplot2-specs").

See Also

- `geom_bar()` for discrete intervals (bars), `geom_linerange()` for discrete intervals (lines), `geom_polygon()` for general polygons

Examples

# Generate data
huron <- data.frame(year = 1875:1972, level = as.vector(LakeHuron))
h <- ggplot(huron, aes(year))

h + geom_ribbon(aes(ymin=0, ymax=level))
h + geom_area(aes(y = level))

# Orientation cannot be deduced by mapping, so must be given explicitly for
# flipped orientation
h + geom_area(aes(x = level, y = year), orientation = "y")

# Add aesthetic mappings
h +
  geom_ribbon(aes(ymin = level - 1, ymax = level + 1), fill = "grey70") +
  geom_line(aes(y = level))
# The underlying stat_align() takes care of unaligned data points
{r}

```r
df <- data.frame(
    g = c("a", "a", "a", "b", "b", "b"),
    x = c(1, 3, 5, 2, 4, 6),
    y = c(2, 5, 1, 3, 6, 7)
)
a <- ggplot(df, aes(x, y, fill = g)) +
    geom_area()

# Two groups have points on different X values.
a + geom_point(size = 8) + facet_grid(g ~ .)

# stat_align() interpolates and aligns the value so that the areas can stack
# properly.
a + geom_point(stat = "align", position = "stack", size = 8)

# To turn off the alignment, the stat can be set to "identity"

```

---

table

<table>
<thead>
<tr>
<th>geom_rug</th>
<th>Rug plots in the margins</th>
</tr>
</thead>
</table>

**Description**

A rug plot is a compact visualisation designed to supplement a 2d display with the two 1d marginal distributions. Rug plots display individual cases so are best used with smaller datasets.

**Usage**

```r
geom_rug(
    mapping = NULL,
    data = NULL,
    stat = "identity",
    position = "identity",
    ...
)
```

**Arguments**

- `mapping`: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
The data to be displayed in this layer. There are three options:

If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().

A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.

A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

logical that controls whether to move the rug tassels outside of the plot area. Default is off (FALSE). You will also need to use coord_cartesian(clip = "off"). When set to TRUE, also consider changing the sides argument to "tr". See examples.

A string that controls which sides of the plot the rugs appear on. It can be set to a string containing any of "trbl", for top, right, bottom, and left.

A grid::unit() object that sets the length of the rug lines. Use scale expansion to avoid overplotting of data.

If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

By default, the rug lines are drawn with a length that corresponds to 3% of the total plot size. Since the default scale expansion of for continuous variables is 5% at both ends of the scale, the rug will not overlap with any data points under the default settings.

geom_rug() understands the following aesthetics (required aesthetics are in bold):

- alpha
• `colour`
• `group`
• `linetype`
• `linewidth`
• `x`
• `y`

Learn more about setting these aesthetics in vignette("ggplot2-specs").

**Examples**

```r
p <- ggplot(mtcars, aes(wt, mpg)) +
  geom_point()
p
p + geom_rug()
p + geom_rug(sides="b")  # Rug on bottom only
p + geom_rug(sides="trbl")  # All four sides

# Use jittering to avoid overplotting for smaller datasets
ggplot(mpg, aes(displ, cty)) +
  geom_point() +
  geom_rug()

ggplot(mpg, aes(displ, cty)) +
  geom_jitter() +
  geom_rug(alpha = 1/2, position = "jitter")

# move the rug tassels to outside the plot
# remember to set clip = "off".
p +
  geom_rug(outside = TRUE) +
  coord_cartesian(clip = "off")

# set sides to top right, and then move the margins
p +
  geom_rug(outside = TRUE, sides = "tr") +
  coord_cartesian(clip = "off") +
  theme(plot.margin = margin(1, 1, 1, 1, "cm"))

# increase the line length and
# expand axis to avoid overplotting
p +
  geom_rug(length = unit(0.05, "npc")) +
  scale_y_continuous(expand = c(0.1, 0.1))
```
geom_segment() draws a straight line between points (x, y) and (xend, yend). geom_curve() draws a curved line. See the underlying drawing function grid::curveGrob() for the parameters that control the curve.

Usage

```r
geom_segment(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  arrow = NULL,
  arrow.fill = NULL,
  lineend = "butt",
  linejoin = "round",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```r
geom_curve(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  curvature = 0.5,
  angle = 90,
  ncp = 5,
  arrow = NULL,
  arrow.fill = NULL,
  lineend = "butt",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

- **mapping** Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the
call to ggplot().
A data.frame, or other object, will override the plot data. All objects will be
fortified to produce a data frame. See fortify() for which variables will be
created.
A function will be called with a single argument, the plot data. The return
value must be a data.frame, and will be used as the layer data. A function
can be created from a formula (e.g. ~ head(.x, 10)).

stat The statistical transformation to use on the data for this layer, either as a ggproto
Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g.
"count" rather than "stat_count")

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to
use position_jitter), or the result of a call to a position adjustment function.
Use the latter if you need to change the settings of the adjustment.

... Other arguments passed on to layer(). These are often aesthetics, used to set
an aesthetic to a fixed value, like colour = "red" or size = 3. They may also
be parameters to the paired geom/stat.

arrow specification for arrow heads, as created by grid::arrow().
arrow.fill fill colour to use for the arrow head (if closed). NULL means use colour aes-
thetic.
lineend Line end style (round, butt, square).
linejoin Line join style (round, mitre, bevel).
na.rm If FALSE, the default, missing values are removed with a warning. If TRUE,
missing values are silently removed.
show.legend logical. Should this layer be included in the legends? NA, the default, includes if
any aesthetics are mapped. FALSE never includes, and TRUE always includes. It
can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them.
This is most useful for helper functions that define both data and aesthetics and
shouldn’t inherit behaviour from the default plot specification, e.g. borders().

curvature A numeric value giving the amount of curvature. Negative values produce left-
hand curves, positive values produce right-hand curves, and zero produces a
straight line.

angle A numeric value between 0 and 180, giving an amount to skew the control points
of the curve. Values less than 90 skew the curve towards the start point and
values greater than 90 skew the curve towards the end point.

ncp The number of control points used to draw the curve. More control points creates
a smoother curve.

Details
Both geoms draw a single segment/curve per case. See geom_path() if you need to connect points
across multiple cases.
Aesthetics

`geom_segment()` understands the following aesthetics (required aesthetics are in bold):

- x
- y
- xend or yend
- alpha
- colour
- group
- linetype
- linewidth

Learn more about setting these aesthetics in vignette("ggplot2-specs").

See Also

`geom_path()` and `geom_line()` for multi-segment lines and paths.

`geom_spoke()` for a segment parameterised by a location (x, y), and an angle and radius.

Examples

```r
b <- ggplot(mtcars, aes(wt, mpg)) +
  geom_point()

df <- data.frame(x1 = 2.62, x2 = 3.57, y1 = 21.0, y2 = 15.0)
b +
  geom_curve(aes(x = x1, y = y1, xend = x2, yend = y2, colour = "curve"), data = df) +
  geom_segment(aes(x = x1, y = y1, xend = x2, yend = y2, colour = "segment"), data = df)

b + geom_curve(aes(x = x1, y = y1, xend = x2, yend = y2), data = df, curvature = -0.2)
b + geom_curve(aes(x = x1, y = y1, xend = x2, yend = y2), data = df, curvature = 1)

b + geom_curve(aes(x = x1, y = y1, xend = x2, yend = y2),
  data = df,
  arrow = arrow(length = unit(0.03, "npc")))

if (requireNamespace('maps', quietly = TRUE)) {
  ggplot(seals, aes(long, lat)) +
    geom_segment(aes(xend = long + delta_long, yend = lat + delta_lat),
                 arrow = arrow(length = unit(0.1,"cm"))) +
    borders("state")
}

# Use lineend and linejoin to change the style of the segments
df2 <- expand.grid(
  lineend = c('round', 'butt', 'square'),
  linejoin = c('round', 'mitre', 'bevel'),
  stringsAsFactors = FALSE)
df2 <- data.frame(df2, y = 1:9)
ggplot(df2, aes(x = 1, y = y, xend = 2, yend = y, label = paste(lineend, linejoin))) +
  geom_segment(
    lineend = df2$lineend, linejoin = df2$linejoin,
    size = 3, arrow = arrow(length = unit(0.3, "inches"))
  ) +
  geom_text(hjust = 'outside', nudge_x = -0.2) +
  xlim(0.5, 2)

# You can also use geom_segment to recreate plot(type = "h") :
set.seed(1)
counts <- as.data.frame(table(x = rpois(100,5)))
counts$x <- as.numeric(as.character(counts$x))
with(counts, plot(x, Freq, type = "h", lwd = 10))
ggplot(counts, aes(x, Freq)) +
  geom_segment(aes(xend = x, yend = 0), linewidth = 10, lineend = "butt")

---

**geom_smooth**

*Smoothed conditional means*

**Description**

Aids the eye in seeing patterns in the presence of overplotting. `geom_smooth()` and `stat_smooth()` are effectively aliases: they both use the same arguments. Use `stat_smooth()` if you want to display the results with a non-standard geom.

**Usage**

```r
geom_smooth(
  mapping = NULL,
  data = NULL,
  stat = "smooth",
  position = "identity",
  ...,
  method = NULL,
  formula = NULL,
  se = TRUE,
  na.rm = FALSE,
  orientation = NA,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```r
stat_smooth(
  mapping = NULL,
  data = NULL,
```
geom = "smooth",
position = "identity",
...
method = NULL,
formula = NULL,
se = TRUE,
n = 80,
span = 0.75,
fullrange = FALSE,
level = 0.95,
method.args = list(),
na.rm = FALSE,
orientation = NA,
show.legend = NA,
inherit.aes = TRUE)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

method Smoothing method (function) to use, accepts either NULL or a character vector, e.g. "lm", "glm", "gam", "loess" or a function, e.g. MASS::rlm or mgcv::gam, stats::lm, or stats::loess. "auto" is also accepted for backwards compatibility. It is equivalent to NULL.
For method = NULL the smoothing method is chosen based on the size of the largest group (across all panels). stats::loess() is used for less than 1,000 observations; otherwise mgcv::gam() is used with formula = y ~ s(x, bs = "cs") with method = "REML". Somewhat anecdotally, loess gives a better appearance, but is $O(N^2)$ in memory, so does not work for larger datasets.
geom_smooth

If you have fewer than 1,000 observations but want to use the same `gam()` model that `method = NULL` would use, then set `method = "gam"`, `formula = y ~ s(x, bs = "cs")`.

**formula**
Formula to use in smoothing function, eg. `y ~ x, y ~ poly(x, 2), y ~ log(x)`. NULL by default, in which case `method = NULL` implies `formula = y ~ x` when there are fewer than 1,000 observations and `formula = y ~ s(x, bs = "cs")` otherwise.

**se**
Display confidence interval around smooth? (TRUE by default, see level to control.)

**na.rm**
If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

**orientation**
The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting `orientation` to either "x" or "y". See the Orientation section for more detail.

**show.legend**
logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

**inherit.aes**
If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

**geom, stat**
Use to override the default connection between `geom_smooth()` and `stat_smooth()`.

**n**
Number of points at which to evaluate smoother.

**span**
Controls the amount of smoothing for the default loess smoother. Smaller numbers produce wigglier lines, larger numbers produce smoother lines. Only used with loess, i.e. when `method = "loess"`, or when `method = NULL` (the default) and there are fewer than 1,000 observations.

**fullrange**
If TRUE, the smoothing line gets expanded to the range of the plot, potentially beyond the data. This does not extend the line into any additional padding created by expansion.

**level**
Level of confidence interval to use (0.95 by default).

**method.args**
List of additional arguments passed on to the modelling function defined by method.

### Details
Calculation is performed by the (currently undocumented) predictdf() generic and its methods. For most methods the standard error bounds are computed using the predict() method – the exceptions are loess(), which uses a t-based approximation, and glm(), where the normal confidence interval is constructed on the link scale and then back-transformed to the response scale.

### Orientation
This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under
rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation
can be specified directly using the orientation parameter, which can be either "x" or "y". The
value gives the axis that the geom should run along, "x" being the default orientation you would
expect for the geom.

Aesthetics

`geom_smooth()` understands the following aesthetics (required aesthetics are in bold):

- `x`
- `y`
- `alpha`
- `colour`
- `fill`
- `group`
- `linetype`
- `linewidth`
- `weight`
- `ymax`
- `ymin`

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Computed variables

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation. `stat_smooth()` provides the following variables, some of which depend on the orientation:

- `after_stat(y)` or `after_stat(x)`
  Predicted value.
- `after_stat(ymin)` or `after_stat(xmin)`
  Lower pointwise confidence interval around the mean.
- `after_stat(ymax)` or `after_stat(xmax)`
  Upper pointwise confidence interval around the mean.
- `after_stat(se)`
  Standard error.

See Also

See individual modelling functions for more details: `lm()` for linear smooths, `glm()` for generalised
linear smooths, and `loess()` for local smooths.
Examples

```r
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  geom_smooth()

# If you need the fitting to be done along the y-axis set the orientation
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  geom_smooth(orientation = "y")

# Use span to control the "wiggliness" of the default loess smoother.
# The span is the fraction of points used to fit each local regression:
# small numbers make a wigglier curve, larger numbers make a smoother curve.

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  geom_smooth(span = 0.3)

# Instead of a loess smooth, you can use any other modelling function:

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  geom_smooth(method = lm, se = FALSE)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  geom_smooth(method = lm, formula = y ~ splines::bs(x, 3), se = FALSE)

# Smooths are automatically fit to each group (defined by categorical
# aesthetics or the group aesthetic) and for each facet.

ggplot(mpg, aes(displ, hwy, colour = class)) +
  geom_point() +
  geom_smooth(se = FALSE, method = lm)

ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  geom_smooth(span = 0.8) +
  facet_wrap(~drv)

binomial_smooth <- function(...) {
  geom_smooth(method = "glm", method.args = list(family = "binomial"), ...)
}

# To fit a logistic regression, you need to coerce the values to
# a numeric vector lying between 0 and 1.

ggplot(rpart::kyphosis, aes(Age, Kyphosis)) +
  geom_jitter(height = 0.05) +
  binomial_smooth()

ggplot(rpart::kyphosis, aes(Age, as.numeric(Kyphosis) - 1)) +
  geom_jitter(height = 0.05) +
  binomial_smooth()

ggplot(rpart::kyphosis, aes(Age, as.numeric(Kyphosis) - 1)) +
```
geom_jitter(height = 0.05) +
  binomial_smooth(formula = y ~ splines::ns(x, 2))

# But in this case, it's probably better to fit the model yourself
# so you can exercise more control and see whether or not it's a good model.

---

**geom_spoke**  
*Line segments parameterised by location, direction and distance*

### Description

This is a polar parameterisation of `geom_segment()`. It is useful when you have variables that describe direction and distance. The angles start from east and increase counterclockwise.

### Usage

```r
geom_spoke(
mapping = NULL,
data = NULL,
stat = "identity",
position = "identity",
..., 
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE
)
```

### Arguments

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).
- **stat**: The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")
Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

Aesthetics

geom_spoke() understands the following aesthetics (required aesthetics are in bold):

• x
• y
• angle
• radius
• alpha
• colour
• group
• linetype
• linewidth

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Examples

df <- expand.grid(x = 1:10, y=1:10)

set.seed(1)
df$angle <- runif(100, 0, 2*pi)
df$speed <- runif(100, 0, sqrt(0.1 * df$x))

ggplot(df, aes(x, y)) +
  geom_point() +
  geom_spoke(aes(angle = angle), radius = 0.5)

ggplot(df, aes(x, y)) +
  geom_point() +
  geom_spoke(aes(angle = angle, radius = speed))
 Viola plot

Description

A violin plot is a compact display of a continuous distribution. It is a blend of `geom_boxplot()` and `geom_density()`: a violin plot is a mirrored density plot displayed in the same way as a boxplot.

Usage

```r
geom_violin(
mapping = NULL,
data = NULL,
stat = "ydensity",
position = "dodge",
..., 
draw_quantiles = NULL,
trim = TRUE,
bounds = c(-Inf, Inf),
scale = "area",
na.rm = FALSE,
orientation = NA,
show.legend = NA,
inherit.aes = TRUE
)
```

```r
stat_ydensity(
mapping = NULL,
data = NULL,
geom = "violin",
position = "dodge",
..., 
bw = "nrd0",
adjust = 1,
kernel = "gaussian",
trim = TRUE,
scale = "area",
drop = TRUE,
na.rm = FALSE,
orientation = NA,
show.legend = NA,
inherit.aes = TRUE,
bounds = c(-Inf, Inf)
)
```
Arguments

mapping Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data The data to be displayed in this layer. There are three options:

If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.

A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.

A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

... Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

draw_quantiles If not(NULL) (default), draw horizontal lines at the given quantiles of the density estimate.

trim If TRUE (default), trim the tails of the violins to the range of the data. If FALSE, don’t trim the tails.

bounds Known lower and upper bounds for estimated data. Default `c(-Inf, Inf)` means that there are no (finite) bounds. If any bound is finite, boundary effect of default density estimation will be corrected by reflecting tails outside bounds around their closest edge. Data points outside of bounds are removed with a warning.

scale if "area" (default), all violins have the same area (before trimming the tails). If "count", areas are scaled proportionally to the number of observations. If "width", all violins have the same maximum width.

na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

orientation The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the Orientation section for more detail.

show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

geom, stat Use to override the default connection between `geom_violin()` and `stat_ydensity()`.
**bw**  The smoothing bandwidth to be used. If numeric, the standard deviation of the smoothing kernel. If character, a rule to choose the bandwidth, as listed in `stats::bw.nrd()`. Note that automatic calculation of the bandwidth does not take weights into account.

**adjust**  A multiplicative bandwidth adjustment. This makes it possible to adjust the bandwidth while still using the a bandwidth estimator. For example, `adjust = 1/2` means use half of the default bandwidth.

**kernel**  Kernel. See list of available kernels in `density()`.

**drop**  Whether to discard groups with less than 2 observations (TRUE, default) or keep such groups for position adjustment purposes (FALSE).

**Orientation**

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the `orientation` parameter, which can be either "x" or "y". The value gives the axis that the geom should run along, "x" being the default orientation you would expect for the geom.

**Aesthetics**

`geom_violin()` understands the following aesthetics (required aesthetics are in bold):

- **x**  
- **y**  
- **alpha**  
- **colour**  
- **fill**  
- **group**  
- **linetype**  
- **linewidth**  
- **weight**

Learn more about setting these aesthetics in `vignette("ggplot2-specs")`.

**Computed variables**

These are calculated by the 'stat' part of layers and can be accessed with delayed evaluation.

- **after_stat(density)**  
  Density estimate.
- **after_stat(scaled)**  
  Density estimate, scaled to a maximum of 1.
- **after_stat(count)**  
  Density * number of points - probably useless for violin plots.
• `after_stat(violinwidth)`
  Density scaled for the violin plot, according to area, counts or to a constant maximum width.
• `after_stat(n)`
  Number of points.
• `after_stat(width)`
  Width of violin bounding box.

References


See Also

`geom_violin()` for examples, and `stat_density()` for examples with data along the x axis.

Examples

```r
p <- ggplot(mtcars, aes(factor(cyl), mpg))
p + geom_violin()

# Orientation follows the discrete axis
ggplot(mtcars, aes(mpg, factor(cyl))) +
  geom_violin()

p + geom_violin() + geom_jitter(height = 0, width = 0.1)

# Scale maximum width proportional to sample size:
p + geom_violin(scale = "count")

# Scale maximum width to 1 for all violins:
p + geom_violin(scale = "width")

# Default is to trim violins to the range of the data. To disable:
p + geom_violin(trim = FALSE)

# Use a smaller bandwidth for closer density fit (default is 1).
p + geom_violin(adjust = .5)

# Add aesthetic mappings
# Note that violins are automatically dodged when any aesthetic is
# a factor
p + geom_violin(aes(fill = cyl))
p + geom_violin(aes(fill = factor(cyl)))
p + geom_violin(aes(fill = factor(vs)))
p + geom_violin(aes(fill = factor(am)))

# Set aesthetics to fixed value
p + geom_violin(fill = "grey80", colour = "#3366FF")
```
# Show quartiles
p + geom_violin(draw_quantiles = c(0.25, 0.5, 0.75))

# Scales vs. coordinate transforms -------
if (require("ggplot2movies")) {
  m <- ggplot(movies, aes(y = votes, x = rating, group = cut_width(rating, 0.5)))
  m + geom_violin()
  m + geom_violin() + scale_y_log10()
  m + geom_violin() + coord_trans(y = "log10")
  m + geom_violin() + scale_y_log10() + coord_trans(y = "log10")
}

get_alt_text(p, ...)

get_alt_text

Description

This function returns a text that can be used as alt-text in webpages etc. Currently it will use the alt label, added with + labs(alt = <...>), or a return an empty string, but in the future it might try to generate an alt text from the information stored in the plot.

Usage

get_alt_text(p, ...)

Arguments

p a ggplot object
...

Currently ignored

Value

A text string
ggplot

**Examples**

```r
p <- ggplot(mpg, aes(displ, hwy)) + geom_point()

# Returns an empty string
get_alt_text(p)

# A user provided alt text
p <- p + labs(  
  alt = paste("A scatterplot showing the negative correlation between engine",
              "displacement as a function of highway miles per gallon")
)

get_alt_text(p)
```

---

**Description**

`ggplot()` initializes a ggplot object. It can be used to declare the input data frame for a graphic and to specify the set of plot aesthetics intended to be common throughout all subsequent layers unless specifically overridden.

**Usage**

```r
ggplot(data = NULL, mapping = aes(), ..., environment = parent.frame())
```

**Arguments**

- **data**: Default dataset to use for plot. If not already a data.frame, will be converted to one by `fortify()`. If not specified, must be supplied in each layer added to the plot.
- **mapping**: Default list of aesthetic mappings to use for plot. If not specified, must be supplied in each layer added to the plot.
- **...**: Other arguments passed on to methods. Not currently used.
- **environment**: [Deprecated] Used prior to tidy evaluation.

**Details**

`ggplot()` is used to construct the initial plot object, and is almost always followed by a plus sign (+) to add components to the plot.

There are three common patterns used to invoke `ggplot()`:

- `ggplot(data = df, mapping = aes(x, y, other aesthetics))`
- `ggplot(data = df)`
• ggplot()

The first pattern is recommended if all layers use the same data and the same set of aesthetics, although this method can also be used when adding a layer using data from another data frame.

The second pattern specifies the default data frame to use for the plot, but no aesthetics are defined up front. This is useful when one data frame is used predominantly for the plot, but the aesthetics vary from one layer to another.

The third pattern initializes a skeleton ggplot object, which is fleshed out as layers are added. This is useful when multiple data frames are used to produce different layers, as is often the case in complex graphics.

The `data =` and `mapping =` specifications in the arguments are optional (and are often omitted in practice), so long as the data and the mapping values are passed into the function in the right order. In the examples below, however, they are left in place for clarity.

Examples

```r
# Create a data frame with some sample data, then create a data frame
# containing the mean value for each group in the sample data.
set.seed(1)

sample_df <- data.frame(
  group = factor(rep(letters[1:3], each = 10)),
  value = rnorm(30)
)

group_means_df <- setNames(
  aggregate(value ~ group, sample_df, mean),
  c("group", "group_mean")
)

# The following three code blocks create the same graphic, each using one
# of the three patterns specified above. In each graphic, the sample data
# are plotted in the first layer and the group means data frame is used to
# plot larger red points on top of the sample data in the second layer.

# Pattern 1
# Both the `data` and `mapping` arguments are passed into the `ggplot()`
# call. Those arguments are omitted in the first `geom_point()` layer
# because they get passed along from the `ggplot()` call. Note that the
# second `geom_point()` layer re-uses the `x = group` aesthetic through
# that mechanism but overrides the y-position aesthetic.

ggplot(data = sample_df, mapping = aes(x = group, y = value)) +
  geom_point() +
  geom_point(
    mapping = aes(y = group_mean), data = group_means_df,
    colour = 'red', size = 3
  )

# Pattern 2
# Same plot as above, passing only the `data` argument into the `ggplot()`
# call. The `mapping` arguments are now required in each `geom_point()`
```
# layer because there is no `mapping` argument passed along from the
# `ggplot()` call.
ggplot(data = sample_df) +
  geom_point(mapping = aes(x = group, y = value)) +
  geom_point(
    mapping = aes(x = group, y = group_mean), data = group_means_df,
    colour = 'red', size = 3
  )

# Pattern 3
# Same plot as above, passing neither the `data` or `mapping` arguments
# into the `ggplot()` call. Both those arguments are now required in
# each `geom_point()` layer. This pattern can be particularly useful when
# creating more complex graphics with many layers using data from multiple
# data frames.
ggplot() +
  geom_point(mapping = aes(x = group, y = value), data = sample_df) +
  geom_point(
    mapping = aes(x = group, y = group_mean), data = group_means_df,
    colour = 'red', size = 3
  )

---

**ggproto**

Create a new `ggproto` object

**Description**

Construct a new object with `ggproto()`, test with `is.ggproto()`, and access parent methods/fields with `ggproto_parent()`.

**Usage**

```r
ggproto(`_class` = NULL, `_inherit` = NULL, ...)

ggproto_parent(parent, self)

is.ggproto(x)
```

**Arguments**

- `_class` (Class name to assign to the object. This is stored as the class attribute of the object. This is optional: if NULL (the default), no class name will be added to the object.
- `_inherit` (ggproto object to inherit from. If NULL, don’t inherit from any object.
- `...` (A list of members in the ggproto object.
- `parent, self` (Access parent class parent of object self.
- `x` (An object to test.)
Details

ggproto implements a prototype based OO system which blurs the lines between classes and instances. It is inspired by the proto package, but it has some important differences. Notably, it cleanly supports cross-package inheritance, and has faster performance.

In most cases, creating a new OO system to be used by a single package is not a good idea. However, it was the least-bad solution for ggplot2 because it required the fewest changes to an already complex code base.

Calling methods

ggproto methods can take an optional self argument: if it is present, it is a regular method; if it’s absent, it’s a "static" method (i.e. it doesn’t use any fields).

Imagine you have a ggproto object Adder, which has a method addx = function(self, n) n + self$x. Then, to call this function, you would use Adder$addx(10) – the self is passed in automatically by the wrapper function. self be located anywhere in the function signature, although customarily it comes first.

Calling methods in a parent

To explicitly call a methods in a parent, use ggproto_parent(Parent, self).

Examples

Adder <- ggproto("Adder",
               x = 0,
               add = function(self, n) {
                 self$x <- self$x + n
                 self$x
               })
is.ggproto(Adder)

Adder$add(10)
Adder$add(10)

Doubler <- ggproto("Doubler", Adder,
                   add = function(self, n) {
                     ggproto_parent(Adder, self)$add(n * 2)
                   })
Doubler$x
Doubler$add(10)
Description

`ggsave()` is a convenient function for saving a plot. It defaults to saving the last plot that you displayed, using the size of the current graphics device. It also guesses the type of graphics device from the extension.

Usage

```r
ggsave(
  filename,
  plot = last_plot(),
  device = NULL,
  path = NULL,
  scale = 1,
  width = NA,
  height = NA,
  units = c("in", "cm", "mm", "px"),
  dpi = 300,
  limitsize = TRUE,
  bg = NULL,
  create.dir = FALSE,
  ...
)
```

Arguments

- `filename`: File name to create on disk.
- `plot`: Plot to save, defaults to last plot displayed.
- `device`: Device to use. Can either be a device function (e.g. `png`), or one of "eps", "ps", "tex" (pictex), "pdf", "jpeg", "tiff", "png", "bmp", "svg" or "wmf" (windows only). If `NULL` (default), the device is guessed based on the `filename` extension.
- `path`: Path of the directory to save plot to: `path` and `filename` are combined to create the fully qualified file name. Defaults to the working directory.
- `scale`: Multiplicative scaling factor.
- `width`, `height`: Plot size in units expressed by the `units` argument. If not supplied, uses the size of the current graphics device.
- `units`: One of the following units in which the `width` and `height` arguments are expressed: "in", "cm", "mm" or "px".
- `dpi`: Plot resolution. Also accepts a string input: "retina" (320), "print" (300), or "screen" (72). Applies only to raster output types.
- `limitsize`: When `TRUE` (the default), `ggsave()` will not save images larger than 50x50 inches, to prevent the common error of specifying dimensions in pixels.
bg  Background colour. If NULL, uses the plot.background fill value from the plot theme.

create.dir  Whether to create new directories if a non-existing directory is specified in the filename or path (TRUE) or return an error (FALSE, default). If FALSE and run in an interactive session, a prompt will appear asking to create a new directory when necessary.

...  Other arguments passed on to the graphics device function, as specified by device.

Details

Note: Filenames with page numbers can be generated by including a C integer format expression, such as %03d (as in the default file name for most R graphics devices, see e.g. png()). Thus, filename = "figure%03d.png" will produce successive filenames figure001.png, figure002.png, figure003.png, etc. To write a filename containing the % sign, use %%%. For example, filename = "figure-100%%.png" will produce the filename figure-100%.png.

Saving images without ggsave()

In most cases ggsave() is the simplest way to save your plot, but sometimes you may wish to save the plot by writing directly to a graphics device. To do this, you can open a regular R graphics device such as png() or pdf(), print the plot, and then close the device using dev.off(). This technique is illustrated in the examples section.

Examples

```r
## Not run:
ggplot(mtcars, aes(mpg, wt)) +
  geom_point()

# here, the device is inferred from the filename extension
ggsave("mtcars.pdf")
ggsave("mtcars.png")

# setting dimensions of the plot
ggsave("mtcars.pdf", width = 4, height = 4)
ggsave("mtcars.pdf", width = 20, height = 20, units = "cm")

# passing device-specific arguments to '...
ggsave("mtcars.pdf", colormodel = "cmyk")

# delete files with base::unlink()
unlink("mtcars.pdf")
unlink("mtcars.png")

# specify device when saving to a file with unknown extension
# (for example a server supplied temporary file)
file <- tempfile()
ggsave(file, device = "pdf")
unlink(file)
```
# save plot to file without using ggsave
p <-
  ggplot(mtcars, aes(mpg, wt)) +
  geom_point()
png("mtcars.png")
print(p)
dev.off()

## End(Not run)

ggtheme

**Complete themes**

**Description**

These are complete themes which control all non-data display. Use `theme()` if you just need to tweak the display of an existing theme.

**Usage**

```r
theme_grey(
  base_size = 11,
  base_family = "",
  base_line_size = base_size/22,
  base_rect_size = base_size/22
)

theme_gray(
  base_size = 11,
  base_family = "",
  base_line_size = base_size/22,
  base_rect_size = base_size/22
)

theme_bw(
  base_size = 11,
  base_family = "",
  base_line_size = base_size/22,
  base_rect_size = base_size/22
)

theme_linedraw(
  base_size = 11,
  base_family = "",
  base_line_size = base_size/22,
  base_rect_size = base_size/22
)
```
theme_light(
  base_size = 11,
  base_family = "",
  base_line_size = base_size/22,
  base_rect_size = base_size/22
)

theme_dark(
  base_size = 11,
  base_family = "",
  base_line_size = base_size/22,
  base_rect_size = base_size/22
)

theme_minimal(
  base_size = 11,
  base_family = "",
  base_line_size = base_size/22,
  base_rect_size = base_size/22
)

theme_classic(
  base_size = 11,
  base_family = "",
  base_line_size = base_size/22,
  base_rect_size = base_size/22
)

theme_void(
  base_size = 11,
  base_family = "",
  base_line_size = base_size/22,
  base_rect_size = base_size/22
)

theme_test(
  base_size = 11,
  base_family = "",
  base_line_size = base_size/22,
  base_rect_size = base_size/22
)

Arguments

base_size base font size, given in pts.
base_family base font family
base_line_size base size for line elements
base_rect_size  base size for rect elements

Details

theme_gray() The signature ggplot2 theme with a grey background and white gridlines, designed to put the data forward yet make comparisons easy.

theme_bw() The classic dark-on-light ggplot2 theme. May work better for presentations displayed with a projector.

theme_linedraw() A theme with only black lines of various widths on white backgrounds, reminiscent of a line drawing. Serves a purpose similar to theme_bw(). Note that this theme has some very thin lines (< 1 pt) which some journals may refuse.

theme_light() A theme similar to theme_linedraw() but with light grey lines and axes, to direct more attention towards the data.

theme_dark() The dark cousin of theme_light(), with similar line sizes but a dark background. Useful to make thin coloured lines pop out.

theme_minimal() A minimalistic theme with no background annotations.

theme_classic() A classic-looking theme, with x and y axis lines and no gridlines.

theme_void() A completely empty theme.

theme_test() A theme for visual unit tests. It should ideally never change except for new features.

Examples

cmpcars2 <- within(mtcars, {
    vs <- factor(vs, labels = c("V-shaped", "Straight"))
    am <- factor(am, labels = c("Automatic", "Manual"))
    cyl <- factor(cyl)
    gear <- factor(gear)
})

p1 <- ggplot(mtcars2) +
    geom_point(aes(x = wt, y = mpg, colour = gear)) +
    labs(
        title = "Fuel economy declines as weight increases",
        subtitle = "(1973-74)",
        caption = "Data from the 1974 Motor Trend US magazine."
    )

p1 + theme_gray() # the default
p1 + theme_bw()
p1 + theme_linedraw()
p1 + theme_light()

p1 + theme_dark()

p1 + theme_minimal()

p1 + theme_classic()

p1 + theme_void()
# Theme examples with panels

p2 <- p1 + facet_grid(vs ~ am)

p2 + theme_gray() # the default
p2 + theme_bw()
p2 + theme_linedraw()
p2 + theme_light()
p2 + theme_dark()
p2 + theme_minimal()
p2 + theme_classic()
p2 + theme_void()

---

## guides

### Set guides for each scale

**Description**

Guides for each scale can be set scale-by-scale with the `guide` argument, or en masse with `guides()`.

**Usage**

```
guides(...)```

**Arguments**

```
... List of scale name-guide pairs. The guide can either be a string (i.e. "color-
bar" or "legend"), or a call to a guide function (i.e. `guide_colourbar()` or
`guide_legend()`) specifying additional arguments.
```

**Value**

A list containing the mapping between scale and guide.

**See Also**

Other guides: `guide_bins()`, `guide_colourbar()`, `guide_coloursteps()`, `guide_legend()`

**Examples**

```
# ggplot object

dat <- data.frame(x = 1:5, y = 1:5, p = 1:5, q = factor(1:5),
r = factor(1:5))
p <-
  ggplot(dat, aes(x, y, colour = p, size = q, shape = r)) +
  geom_point()
```
# without guide specification
p

# Show colorbar guide for colour.
# All these examples below have a same effect.
p + guides(colour = "colorbar", size = "legend", shape = "legend")
p + guides(colour = guide_colorbar(), size = guide_legend(),
  shape = guide_legend())
p +
scale_colour_continuous(guide = "colorbar") +
scale_size_discrete(guide = "legend") +
scale_shape(guide = "legend")

# Remove some guides
p + guides(colour = "none")
p + guides(colour = "colorbar", size = "none")

# Guides are integrated where possible
p +
guides(
  colour = guide_legend("title"),
  size = guide_legend("title"),
  shape = guide_legend("title")
)
# same as
g <- guide_legend("title")
p + guides(colour = g, size = g, shape = g)

p + theme(legend.position = "bottom")

# position of guides

# Set order for multiple guides
ggplot(mpg, aes(displ, cty)) +
  geom_point(aes(size = hwy, colour = cyl, shape = drv)) +
guides(
  colour = guide_colourbar(order = 1),
  shape = guide_legend(order = 2),
  size = guide_legend(order = 3)
)
Description

Axis guides are the visual representation of position scales like those created with `scale_(x|y)_continuous()` and `scale_(x|y)_discrete()`.

Usage

```r
guide_axis(
  title = waiver(),
  theme = NULL,
  check.overlap = FALSE,
  angle = waiver(),
  n.dodge = 1,
  minor.ticks = FALSE,
  cap = "none",
  order = 0,
  position = waiver()
)
```

Arguments

- **title**: A character string or expression indicating a title of guide. If NULL, the title is not shown. By default (`waiver()`), the name of the scale object or the name specified in `labs()` is used for the title.
- **theme**: A `theme` object to style the guide individually or differently from the plot’s theme settings. The theme argument in the guide overrides, and is combined with, the plot’s theme.
- **check.overlap**: Silently remove overlapping labels, (recursively) prioritizing the first, last, and middle labels.
- **angle**: Compared to setting the angle in `theme() / element_text()`, this also uses some heuristics to automatically pick the `hjust` and `vjust` that you probably want. Can be one of the following:
  - NULL to take the angles and `hjust/vjust` directly from the theme.
  - waiver() to allow reasonable defaults in special cases.
  - A number representing the text angle in degrees.
- **n.dodge**: The number of rows (for vertical axes) or columns (for horizontal axes) that should be used to render the labels. This is useful for displaying labels that would otherwise overlap.
- **minor.ticks**: Whether to draw the minor ticks (TRUE) or not draw minor ticks (FALSE, default).
- **cap**: A character to cut the axis line back to the last breaks. Can be "none" (default) to draw the axis line along the whole panel, or "upper" and "lower" to draw the axis to the upper or lower break, or "both" to only draw the line in between the most extreme breaks. TRUE and FALSE are shorthand for "both" and "none" respectively.
- **order**: A positive integer of length 1 that specifies the order of this guide among multiple guides. This controls in which order guides are merged if there are multiple guides for the same position. If 0 (default), the order is determined by a secret algorithm.
position Where this guide should be drawn: one of top, bottom, left, or right.

Examples

# plot with overlapping text
p <- ggplot(mpg, aes(cty * 100, hwy * 100)) +
  geom_point() +
  facet_wrap(vars(class))

# axis guides can be customized in the scale_* functions or
# using guides()
# can also be used to add a duplicate guide
p + guides(x = guide_axis(n.dodge = 2), y.sec = guide_axis())


guide_axis_logticks Axis with logarithmic tick marks

Description

This axis guide replaces the placement of ticks marks at intervals in log10 space.

Usage

guide_axis_logticks(
  long = 2.25,
  mid = 1.5,
  short = 0.75,
  prescale_base = NULL,
  negative_small = 0.1,
  short_theme = element_line(),
  expanded = TRUE,
  cap = "none",
  theme = NULL,
  ...
)

Arguments

long, mid, short

A grid::unit() object or rel() object setting the (relative) length of the long, middle and short ticks. Numeric values are interpreted as rel() objects. The rel() values are used to multiply values of the axis.ticks.length theme setting.
prescale_base  Base of logarithm used to transform data manually. The default, NULL, will use the scale transformation to calculate positions. Only set prescale_base if the data has already been log-transformed. When using a log-transform in the position scale or in coord_trans(), keep the default NULL argument.

negative_small  When the scale limits include 0 or negative numbers, what should be the smallest absolute value that is marked with a tick?

short_theme  A theme element for customising the display of the shortest ticks. Must be a line or blank element, and it inherits from the axis.minor.ticks setting for the relevant position.

expanded  Whether the ticks should cover the range after scale expansion (TRUE, default), or be restricted to the scale limits (FALSE).

cap  A character to cut the axis line back to the last breaks. Can be "none" (default) to draw the axis line along the whole panel, or "upper" and "lower" to draw the axis to the upper or lower break, or "both" to only draw the line in between the most extreme breaks. TRUE and FALSE are shorthand for "both" and "none" respectively.

theme  A theme object to style the guide individually or differently from the plot’s theme settings. The theme argument in the guide overrides, and is combined with, the plot’s theme.

...  Arguments passed on to guide_axis

check.overlap silently remove overlapping labels, (recursively) prioritizing the first, last, and middle labels.

angle  Compared to setting the angle in theme()/element_text(), this also uses some heuristics to automatically pick the hjust and vjust that you probably want. Can be one of the following:
  • NULL to take the angles and hjust/vjust directly from the theme.
  • waiver() to allow reasonable defaults in special cases.
  • A number representing the text angle in degrees.

n.dodge  The number of rows (for vertical axes) or columns (for horizontal axes) that should be used to render the labels. This is useful for displaying labels that would otherwise overlap.

order  A positive integer of length 1 that specifies the order of this guide among multiple guides. This controls in which order guides are merged if there are multiple guides for the same position. If 0 (default), the order is determined by a secret algorithm.

position  Where this guide should be drawn: one of top, bottom, left, or right.

title  A character string or expression indicating a title of guide. If NULL, the title is not shown. By default (waiver()), the name of the scale object or the name specified in labs() is used for the title.

Examples

# A standard plot
p <- ggplot(msleep, aes(bodywt, brainwt)) + geom_point(na.rm = TRUE)
# The logticks axis works well with log scales
p + scale_x_log10(guide = "axis_logticks") +
    scale_y_log10(guide = "axis_logticks")

# Or with log-transformed coordinates
p + coord_trans(x = "log10", y = "log10") +
    guides(x = "axis_logticks", y = "axis_logticks")

# When data is transformed manually, one should provide `prescale_base`
# Keep in mind that this axis uses log10 space for placement, not log2
p + aes(x = log2(bodywt), y = log10(brainwt)) +
    guides(
        x = guide_axis_logticks(prescale_base = 2),
        y = guide_axis_logticks(prescale_base = 10)
    )

# A plot with both positive and negative extremes, pseudo-log transformed
set.seed(42)
p2 <- ggplot(data.frame(x = rcauchy(1000)), aes(x = x)) +
    geom_density() +
    scale_x_continuous(
        breaks = c(-10^(4:0), 0, 10^(0:4)),
        transform = "pseudo_log"
    )

# The log ticks are mirrored when 0 is included
p2 + guides(x = "axis_logticks")

# To control the tick density around 0, one can set `negative_small`
p2 + guides(x = guide_axis_logticks(negative_small = 1))

guide_axis_stack  Stacked axis guides

Description
This guide can stack other position guides that represent position scales, like those created with scale_(x|y)_continuous() and scale_(x|y)_discrete().

Usage

```r
guide_axis_stack(
    first = "axis",
    ...,  # Additional arguments
    title = waiver(),
    theme = NULL,
    spacing = NULL,
    order = 0,
    position = waiver()
)
```
**Arguments**

- **first**: A position guide given as one of the following:
  - A string, for example "axis".
  - A call to a guide function, for example `guide_axis()`.
- **title**: A character string or expression indicating a title of guide. If NULL, the title is not shown. By default (`waiver()`), the name of the scale object or the name specified in `labs()` is used for the title.
- **theme**: A `theme` object to style the guide individually or differently from the plot’s theme settings. The theme argument in the guide overrides, and is combined with, the plot’s theme.
- **spacing**: A `unit()` objects that determines how far separate guides are spaced apart.
- **order**: A positive integer of length 1 that specifies the order of this guide among multiple guides. This controls in which order guides are merged if there are multiple guides for the same position. If 0 (default), the order is determined by a secret algorithm.
- **position**: Where this guide should be drawn: one of top, bottom, left, or right.

**Details**

The first guide will be placed closest to the panel and any subsequent guides provided through ... will follow in the given order.

**Examples**

```r
# A standard plot
p <- ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  theme(axis.line = element_line())

# A normal axis first, then a capped axis
p + guides(x = guide_axis_stack("axis", guide_axis(cap = "both")))
```

---

**guide_axis_theta**

*Angle axis guide*

**Description**

This is a specialised guide used in `coord_radial()` to represent the theta position scale.
Usage

guide_axis_theta(
  title = waiver(),
  theme = NULL,
  angle = waiver(),
  minor.ticks = FALSE,
  cap = "none",
  order = 0,
  position = waiver()
)

Arguments

title A character string or expression indicating a title of guide. If NULL, the title is not shown. By default (waiver()), the name of the scale object or the name specified in labs() is used for the title.

theme A theme object to style the guide individually or differently from the plot’s theme settings. The theme argument in the guide overrides, and is combined with, the plot’s theme.

angle Compared to setting the angle in theme() / element_text(), this also uses some heuristics to automatically pick the hjust and vjust that you probably want. Can be one of the following:

  • NULL to take the angles and hjust/vjust directly from the theme.
  • waiver() to allow reasonable defaults in special cases.
  • A number representing the text angle in degrees.

minor.ticks Whether to draw the minor ticks (TRUE) or not draw minor ticks (FALSE, default).

cap A character to cut the axis line back to the last breaks. Can be "none" (default) to draw the axis line along the whole panel, or "upper" and "lower" to draw the axis to the upper or lower break, or "both" to only draw the line in between the most extreme breaks. TRUE and FALSE are shorthand for "both" and "none" respectively.

order A positive integer of length 1 that specifies the order of this guide among multiple guides. This controls in which order guides are merged if there are multiple guides for the same position. If 0 (default), the order is determined by a secret algorithm.

position Where this guide should be drawn: one of top, bottom, left, or right.

Note

The axis labels in this guide are insensitive to hjust and vjust settings. The distance from the tick marks to the labels is determined by the largest margin size set in the theme.

Examples

# A plot using coord_radial
p <- ggplot(mtcars, aes(disp, mpg)) +


```
geom_point() +
coord_radial()

# The `angle` argument can be used to set relative angles
p + guides(theta = guide_axis_theta(angle = 0))
```

---

**guide_bins**  
*A binned version of guide_legend*

---

**Description**

This guide is a version of the `guide_legend()` guide for binned scales. It differs in that it places ticks correctly between the keys, and sports a small axis to better show the binning. Like `guide_legend()` it can be used for all non-position aesthetics though colour and fill defaults to `guide_coloursteps()`, and it will merge aesthetics together into the same guide if they are mapped in the same way.

**Usage**

```
guide_bins(
  title = waiver(),
  theme = NULL,
  position = NULL,
  direction = NULL,
  override.aes = list(),
  reverse = FALSE,
  order = 0,
  show.limits = NULL,
  ...
)
```

**Arguments**

- **title**: A character string or expression indicating a title of guide. If NULL, the title is not shown. By default (`waiver()`), the name of the scale object or the name specified in `labs()` is used for the title.

- **theme**: A `theme` object to style the guide individually or differently from the plot’s theme settings. The theme argument in the guide overrides, and is combined with, the plot’s theme.

- **position**: A character string indicating where the legend should be placed relative to the plot panels.

- **direction**: A character string indicating the direction of the guide. One of "horizontal" or "vertical."

- **override.aes**: A list specifying aesthetic parameters of legend key. See details and examples.

- **reverse**: logical. If TRUE the order of legends is reversed.
order positive integer less than 99 that specifies the order of this guide among multiple guides. This controls the order in which multiple guides are displayed, not the contents of the guide itself. If 0 (default), the order is determined by a secret algorithm.

show.limits Logical. Should the limits of the scale be shown with labels and ticks. Default is NULL meaning it will take the value from the scale. This argument is ignored if labels is given as a vector of values. If one or both of the limits is also given in breaks it will be shown irrespective of the value of show.limits.

Value

A guide object

Use with discrete scale

This guide is intended to show binned data and work together with ggplot2's binning scales. However, it is sometimes desirable to perform the binning in a separate step, either as part of a stat (e.g. `stat_contour_filled()`) or prior to the visualisation. If you want to use this guide for discrete data the levels must follow the naming scheme implemented by `base::cut()`. This means that a bin must be encoded as "(<lower>, <upper>]" with <lower> giving the lower bound of the bin and <upper> giving the upper bound ("[<lower>, <upper>)" is also accepted). If you use `base::cut()` to perform the binning everything should work as expected, if not, some recoding may be needed.

See Also

Other guides: `guide_colourbar()`, `guide_coloursteps()`, `guide_legend()`, `guides()`

Examples

```r
p <- ggplot(mtcars) +
  geom_point(aes(disp, mpg, size = hp)) +
  scale_size_binned()

# Standard look
p

# Remove the axis or style it
p + guides(size = guide_bins(
  theme = theme(legend.axis.line = element_blank())
))

p + guides(size = guide_bins(show.limits = TRUE))

my_arrow <- arrow(length = unit(1.5, "mm"), ends = "both")
p + guides(size = guide_bins(
  theme = theme(legend.axis.line = element_line(arrow = my_arrow))
))
```
# Guides are merged together if possible

```r
ggplot(mtcars) +
  geom_point(aes(disp, mpg, size = hp, colour = hp)) +
  scale_size_binned() +
  scale_colour_binned(guide = "bins")
```

---

**guide_colourbar**  
**Continuous colour bar guide**

**Description**

Colour bar guide shows continuous colour scales mapped onto values. Colour bar is available with `scale_fill` and `scale_colour`. For more information, see the inspiration for this function: Matlab’s `colorbar` function.

**Usage**

```r
guide_colourbar(
  title = waiver(),
  theme = NULL,
  nbin = NULL,
  display = "raster",
  raster = deprecated(),
  alpha = NA,
  draw.ulim = TRUE,
  draw.llim = TRUE,
  position = NULL,
  direction = NULL,
  reverse = FALSE,
  order = 0,
  available_aes = c("colour", "color", "fill"),
  ...
)
```

```r
guide_colorbar(
  title = waiver(),
  theme = NULL,
  nbin = NULL,
  display = "raster",
  raster = deprecated(),
  alpha = NA,
  draw.ulim = TRUE,
  draw.llim = TRUE,
  position = NULL,
  direction = NULL,
  reverse = FALSE,
  order = 0,
  available_aes = c("colour", "color", "fill"),
  ...
)
```
Arguments

**title**  
A character string or expression indicating a title of guide. If NULL, the title is not shown. By default (\texttt{waiver()}), the name of the scale object or the name specified in \texttt{labs()} is used for the title.

**theme**  
A \texttt{theme} object to style the guide individually or differently from the plot's theme settings. The theme argument in the guide overrides, and is combined with, the plot's theme.

**nbin**  
A numeric specifying the number of bins for drawing the colourbar. A smoother colourbar results from a larger value.

**display**  
A string indicating a method to display the colourbar. Can be one of the following:

- "raster" to display as a bitmap image.
- "rectangles" to display as a series of rectangles.
- "gradient" to display as a linear gradient.

Note that not all devices are able to render rasters and gradients.

**raster**  
[\texttt{Deprecated}] A logical. If TRUE then the colourbar is rendered as a raster object. If FALSE then the colourbar is rendered as a set of rectangles. Note that not all graphics devices are capable of rendering raster image.

**alpha**  
A numeric between 0 and 1 setting the colour transparency of the bar. Use \texttt{NA} to preserve the alpha encoded in the colour itself (default).

**draw.ulim**  
A logical specifying if the upper limit tick marks should be visible.

**draw.llim**  
A logical specifying if the lower limit tick marks should be visible.

**position**  
A character string indicating where the legend should be placed relative to the plot panels.

**direction**  
A character string indicating the direction of the guide. One of "horizontal" or "vertical."

**reverse**  
logical. If TRUE the colourbar is reversed. By default, the highest value is on the top and the lowest value is on the bottom

**order**  
positive integer less than 99 that specifies the order of this guide among multiple guides. This controls the order in which multiple guides are displayed, not the contents of the guide itself. If 0 (default), the order is determined by a secret algorithm.

**available_aes**  
A vector of character strings listing the aesthetics for which a colourbar can be drawn.

...  
ignored.
Details
Guides can be specified in each scale_* or in guides(). guide="legend" in scale_* is syntactic sugar for guide=guide_legend() (e.g. scale_colour_manual(guide = "legend")). As for how to specify the guide for each scale in more detail, see guides().

Value
A guide object

See Also
Other guides: guide_bins(), guide_coloursteps(), guide_legend(), guides()

Examples
```r
df <- expand.grid(X1 = 1:10, X2 = 1:10)
df$value <- df$X1 * df$X2

p1 <- ggplot(df, aes(X1, X2)) + geom_tile(aes(fill = value))
p2 <- p1 + geom_point(aes(size = value))

# Basic form
p1 + scale_fill_continuous(guide = "colourbar")
p1 + scale_fill_continuous(guide = guide_colourbar())
p1 + guides(fill = guide_colourbar())

# Control styles
# bar size
p1 + guides(fill = guide_colourbar(theme = theme(
  legend.key.width = unit(0.5, "lines"),
  legend.key.height = unit(10, "lines")
)))

# no label
p1 + guides(fill = guide_colourbar(theme = theme(
  legend.text = element_blank())
)))

# no tick marks
p1 + guides(fill = guide_colourbar(theme = theme(
  legend.ticks = element_blank())
)))

# label position
p1 + guides(fill = guide_colourbar(theme = theme(
  legend.text.position = "left"
)))

# label theme
p1 + guides(fill = guide_colourbar(theme = theme(
```

guide_coloursteps

Discretized colourbar guide

Description

This guide is version of `guide_colourbar()` for binned colour and fill scales. It shows areas between breaks as a single constant colour instead of the gradient known from the colourbar counterpart.

Usage

guide_coloursteps(
  title = waiver(),
  theme = NULL,
  alpha = NA,
  even.steps = TRUE,
  show.limits = NULL,
  direction = NULL,
  reverse = FALSE,
order = 0,
available_aes = c("colour", "color", "fill"),
...
)

guide_colorsteps(
  title = waiver(),
  theme = NULL,
  alpha = NA,
  even.steps = TRUE,
  show.limits = NULL,
  direction = NULL,
  reverse = FALSE,
  order = 0,
  available_aes = c("colour", "color", "fill"),
  ...
)

Arguments

title A character string or expression indicating a title of guide. If NULL, the title is not shown. By default (waiver()), the name of the scale object or the name specified in labs() is used for the title.
theme A theme object to style the guide individually or differently from the plot’s theme settings. The theme argument in the guide overrides, and is combined with, the plot’s theme.
alpha A numeric between 0 and 1 setting the colour transparency of the bar. Use NA to preserve the alpha encoded in the colour itself (default).
even.steps Should the rendered size of the bins be equal, or should they be proportional to their length in the data space? Defaults to TRUE.
show.limits Logical. Should the limits of the scale be shown with labels and ticks. Default is NULL meaning it will take the value from the scale. This argument is ignored if labels is given as a vector of values. If one or both of the limits is also given in breaks it will be shown irrespective of the value of show.limits.
direction A character string indicating the direction of the guide. One of "horizontal" or "vertical."
reverse logical. If TRUE the colourbar is reversed. By default, the highest value is on the top and the lowest value is on the bottom.
order positive integer less than 99 that specifies the order of this guide among multiple guides. This controls the order in which multiple guides are displayed, not the contents of the guide itself. If 0 (default), the order is determined by a secret algorithm.
available_aes A vector of character strings listing the aesthetics for which a colourbar can be drawn.
... ignored.
Value

A guide object

Use with discrete scale

This guide is intended to show binned data and work together with ggplot2’s binning scales. However, it is sometimes desirable to perform the binning in a separate step, either as part of a stat (e.g. `stat_contour_filled()`) or prior to the visualisation. If you want to use this guide for discrete data the levels must follow the naming scheme implemented by `base::cut()`. This means that a bin must be encoded as "(<lower>, <upper>]" with <lower> giving the lower bound of the bin and <upper> giving the upper bound ("[<lower>, <upper>)" is also accepted). If you use `base::cut()` to perform the binning everything should work as expected, if not, some recoding may be needed.

See Also

Other guides: `guide_bins()`, `guide_colourbar()`, `guide_legend()`, `guides()`

Examples

df <- expand.grid(X1 = 1:10, X2 = 1:10)
df$value <- df$X1 * df$X2

p <- ggplot(df, aes(X1, X2)) + geom_tile(aes(fill = value))
# Coloursteps guide is the default for binned colour scales
p + scale_fill_binned()

# By default each bin in the guide is the same size irrespectively of how
# their sizes relate in data space
p + scale_fill_binned(breaks = c(10, 25, 50))

# This can be changed with the `even.steps` argument
p + scale_fill_binned(
    breaks = c(10, 25, 50),
    guide = guide_coloursteps(even.steps = FALSE)
)

# By default the limits is not shown, but this can be changed
p + scale_fill_binned(guide = guide_coloursteps(show.limits = TRUE))

# (can also be set in the scale)
p + scale_fill_binned(show.limits = TRUE)
**Description**

This is a special guide that can be used to display any graphical object (grob) along with the regular guides. This guide has no associated scale.

**Usage**

```r
guide_custom(
  grob,  
  width = grobWidth(grob),  
  height = grobHeight(grob),  
  title = NULL,  
  theme = NULL,  
  position = NULL,  
  order = 0
)
```

**Arguments**

- **grob**: A grob to display.
- **width, height**: The allocated width and height to display the grob, given in `grid::unit()`s.
- **title**: A character string or expression indicating the title of guide. If `NULL` (default), no title is shown.
- **theme**: A `theme` object to style the guide individually or differently from the plot’s theme settings. The `theme` argument in the guide overrides, and is combined with, the plot’s theme.
- **position**: A character string indicating where the legend should be placed relative to the plot panels.
- **order**: Positive integer less than 99 that specifies the order of this guide among multiple guides. This controls the order in which multiple guides are displayed, not the contents of the guide itself. If 0 (default), the order is determined by a secret algorithm.

**Examples**

```r
# A standard plot
p <- ggplot(mpg, aes(displ, hwy)) + geom_point()

# Define a graphical object
circle <- grid::circleGrob()

# Rendering a grob as a guide
p + guides(custom = guide_custom(circle, title = "My circle"))

# Controlling the size of the grob defined in relative units
p + guides(custom = guide_custom(
  circle, title = "My circle",
  width = unit(2, "cm"), height = unit(2, "cm")))
```
# Size of grobs in absolute units is taken directly without the need to
# set these manually
p + guides(custom = guide_custom(
  title = "My circle",
  grob = grid::circleGrob(r = unit(1, "cm")))
)

guide_legend

Legend guide

Description

Legend type guide shows key (i.e., geoms) mapped onto values. Legend guides for various scales
are integrated if possible.

Usage

guide_legend(
  title = waiver(),
  theme = NULL,
  position = NULL,
  direction = NULL,
  override.aes = list(),
  nrow = NULL,
  ncol = NULL,
  reverse = FALSE,
  order = 0,
  ...
)

Arguments

title A character string or expression indicating a title of guide. If NULL, the title is
not shown. By default (waiver()), the name of the scale object or the name
specified in labs() is used for the title.

theme A theme object to style the guide individually or differently from the plot's
theme settings. The theme argument in the guide overrides, and is combined
with, the plot's theme.

position A character string indicating where the legend should be placed relative to the
plot panels.

direction A character string indicating the direction of the guide. One of "horizontal" or
"vertical."

override.aes A list specifying aesthetic parameters of legend key. See details and examples.
nrow, ncol The desired number of rows and column of legends respectively.
reverse logical. If TRUE the order of legends is reversed.
order positive integer less than 99 that specifies the order of this guide among multiple guides. This controls the order in which multiple guides are displayed, not the contents of the guide itself. If 0 (default), the order is determined by a secret algorithm.

Details
Guides can be specified in each scale_* or in guides(). guide = "legend" in scale_* is syntactic sugar for guide = guide_legend() (e.g. scale_color_manual(guide = "legend")). As for how to specify the guide for each scale in more detail, see guides().

See Also
Other guides: guide_bins(), guide_colourbar(), guide_coloursteps(), guides()

Examples

```r
df <- expand.grid(X1 = 1:10, X2 = 1:10)
df$value <- df$X1 * df$X2

p1 <- ggplot(df, aes(X1, X2)) + geom_tile(aes(fill = value))
p2 <- p1 + geom_point(aes(size = value))

# Basic form
p1 + scale_fill_continuous(guide = guide_legend())

# Control styles
# title position
p1 + guides(fill = guide_legend(
  title = "LEFT", theme(legend.title.position = "left")
))

# title text styles via element_text
p1 + guides(fill = guide_legend(theme = theme(  
  legend.title = element_text(size = 15, face = "italic", colour = "red")
)))

# label position
p1 + guides(fill = guide_legend(theme = theme(  
  legend.text.position = "left",  
  legend.text = element_text(hjust = 1)
)))

# label styles
p1 +
  scale_fill_continuous(    
    breaks = c(5, 10, 15),
)```
guide_none

```
guide = guide_legend(theme = theme(
  legend.direction = "horizontal",
  legend.title.position = "top",
  legend.text.position = "bottom",
  legend.text = element_text(hjust = 0.5, vjust = 1, angle = 90)
))
```

# Set aesthetic of legend key
# very low alpha value make it difficult to see legend key
p3 <- ggplot(mtcars, aes(vs, am, colour = factor(cyl))) +
  geom_jitter(alpha = 1/5, width = 0.01, height = 0.01)
p3
# override.aes overwrites the alpha
p3 + guides(colour = guide_legend(override.aes = list(alpha = 1)))

# multiple row/col legends
df <- data.frame(x = 1:20, y = 1:20, color = letters[1:20])
p <- ggplot(df, aes(x, y)) +
  geom_point(aes(colour = color))
p + guides(col = guide_legend(nrow = 8))
p + guides(col = guide_legend(ncol = 8))
p + guides(col = guide_legend(nrow = 8, theme = theme(legend.byrow = TRUE)))

# reversed order legend
p + guides(col = guide_legend(reverse = TRUE))
```

guide_none

Empty guide

Description

This guide draws nothing.

Usage

guide_none(title = waiver(), position = waiver())

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>title</td>
<td>A character string or expression indicating a title of guide. If NULL, the title is not shown. By default (waiver()), the name of the scale object or the name specified in labs() is used for the title.</td>
</tr>
<tr>
<td>position</td>
<td>Where this guide should be drawn: one of top, bottom, left, or right.</td>
</tr>
</tbody>
</table>
Description

These are wrappers around functions from Hmisc designed to make them easier to use with `stat_summary()`. See the Hmisc documentation for more details:

- `Hmisc::smean.cl.boot()`
- `Hmisc::smean.cl.normal()`
- `Hmisc::smean.sdl()`
- `Hmisc::smedian.hilow()`

Usage

```r
mean_cl_boot(x, ...)
mean_cl_normal(x, ...)
mean_sdl(x, ...)
median_hilow(x, ...)
```

Arguments

- `x` a numeric vector
- `...` other arguments passed on to the respective Hmisc function.

Value

A data frame with columns `y`, `ymin`, and `ymax`.

Examples

```r
if (requireNamespace("Hmisc", quietly = TRUE)) {
  set.seed(1)
  x <- rnorm(100)
  mean_cl_boot(x)
  mean_cl_normal(x)
  mean_sdl(x)
  median_hilow(x)
}
```
Description

This function makes it easy to assign different labellers to different factors. The labeller can be a function or it can be a named character vectors that will serve as a lookup table.

Usage

```r
labeller(
  ..., 
  .rows = NULL,
  .cols = NULL,
  keep.as.numeric = deprecated(),
  .multi_line = TRUE,
  .default = label_value
)
```

Arguments

... Named arguments of the form `variable = labeller`. Each labeller is passed to `as_labeller()` and can be a lookup table, a function taking and returning character vectors, or simply a labeller function.

.rows, .cols Labeller for a whole margin (either the rows or the columns). It is passed to `as_labeller()`. When a margin-wide labeller is set, make sure you don’t mention in ... any variable belonging to the margin.

keep.as.numeric [Deprecated] All supplied labellers and on-labeller functions should be able to work with character labels.

.multi_line Whether to display the labels of multiple factors on separate lines. This is passed to the labeller function.

.default Default labeller for variables not specified. Also used with lookup tables or non-labeller functions.

Details

In case of functions, if the labeller has class `labeller`, it is directly applied on the data frame of labels. Otherwise, it is applied to the columns of the data frame of labels. The data frame is then processed with the function specified in the .default argument. This is intended to be used with functions taking a character vector such as `Hmisc::capitalize()`.

Value

A labeller function to supply to `facet_grid()` or `facet_wrap()` for the argument labeller.
See Also

as_labeller(), labellers

Examples

```r
p1 <- ggplot(mtcars, aes(x = mpg, y = wt)) + geom_point()

# You can assign different labellers to variables:
p1 + facet_grid(
  vs + am ~ gear,
  labeller = labeller(vs = label_both, am = label_value)
)

# Or whole margins:
p1 + facet_grid(
  vs + am ~ gear,
  labeller = labeller(.rows = label_both, .cols = label_value)
)

# You can supply functions operating on strings:
capitalize <- function(string) {
  substr(string, 1, 1) <- toupper(substr(string, 1, 1))
  string
}
p2 <- ggplot(msleep, aes(x = sleep_total, y = awake)) + geom_point()
p2 + facet_grid(vore ~ conservation, labeller = labeller(vore = capitalize))

# Or use character vectors as lookup tables:
conservation_status <- c(
  cd = "Conservation Dependent",
  en = "Endangered",
  lc = "Least concern",
  nt = "Near Threatened",
  vu = "Vulnerable",
  domesticated = "Domesticated"
)

p2 + facet_grid(vore ~ conservation, labeller = labeller(
  .default = capitalize,
  conservation = conservation_status
))

# In the following example, we rename the levels to the long form,
# then apply a wrap labeller to the columns to prevent cropped text
idx <- match(msleep$conservation, names(conservation_status))
msleep$conservation2 <- conservation_status[idx]

p3 <- ggplot(msleep, aes(x = sleep_total, y = awake)) + geom_point()
p3 +
  facet_grid(vore ~ conservation2,
```
labeller = labeller(conservation2 = label_wrap_gen(10))

# labeller() is especially useful to act as a global labeller. You
# can set it up once and use it on a range of different plots with
# different facet specifications.

global_labeller <- labeller(
  vore = capitalize,
  conservation = conservation_status,
  conservation2 = label_wrap_gen(10),
  .default = label_both
)

p2 + facet_grid(vore ~ conservation, labeller = global_labeller)
p3 + facet_wrap(~conservation2, labeller = global_labeller)

labellers

Useful labeller functions

Description

Labeller functions are in charge of formatting the strip labels of facet grids and wraps. Most of
them accept a multi_line argument to control whether multiple factors (defined in formulae such
as ~first + second) should be displayed on a single line separated with commas, or each on their
own line.

Usage

label_value(labels, multi_line = TRUE)

label_both(labels, multi_line = TRUE, sep = "::")

label_context(labels, multi_line = TRUE, sep = "::")

label_parsed(labels, multi_line = TRUE)

label_wrap_gen(width = 25, multi_line = TRUE)

Arguments

labels Data frame of labels. Usually contains only one element, but faceting over mul-
tiple factors entails multiple label variables.

multi_line Whether to display the labels of multiple factors on separate lines.

sep String separating variables and values.

width Maximum number of characters before wrapping the strip.
Details

label_value() only displays the value of a factor while label_both() displays both the variable name and the factor value. label_context() is context-dependent and uses label_value() for single factor faceting and label_both() when multiple factors are involved. label_wrap_gen() uses base::strwrap() for line wrapping.

label_parsed() interprets the labels as plotmath expressions. label_bquote() offers a more flexible way of constructing plotmath expressions. See examples and bquote() for details on the syntax of the argument.

Writing New Labeller Functions

Note that an easy way to write a labeller function is to transform a function operating on character vectors with as_labeller().

A labeller function accepts a data frame of labels (character vectors) containing one column for each factor. Multiple factors occur with formula of the type ~first + second.

The return value must be a rectangular list where each 'row' characterises a single facet. The list elements can be either character vectors or lists of plotmath expressions. When multiple elements are returned, they get displayed on their own new lines (i.e., each facet gets a multi-line strip of labels).

To illustrate, let’s say your labeller returns a list of two character vectors of length 3. This is a rectangular list because all elements have the same length. The first facet will get the first elements of each vector and display each of them on their own line. Then the second facet gets the second elements of each vector, and so on.

If it’s useful to your labeller, you can retrieve the type attribute of the incoming data frame of labels. The value of this attribute reflects the kind of strips your labeller is dealing with: "cols" for columns and "rows" for rows. Note that facet_wrap() has columns by default and rows when the strips are switched with the switch option. The facet attribute also provides metadata on the labels. It takes the values "grid" or "wrap".

For compatibility with labeller(), each labeller function must have the labeller S3 class.

See Also

labeller(), as_labeller(), label_bquote()

Examples

mtcars$cyl2 <- factor(mtcars$cyl, labels = c("alpha", "beta", "gamma"))
p <- ggplot(mtcars, aes(wt, mpg)) + geom_point()

# The default is label_value
p + facet_grid(~ cyl, labeller = label_value)

# Displaying both the values and the variables
p + facet_grid(~ cyl, labeller = label_both)

# Displaying only the values or both the values and variables
# depending on whether multiple factors are faceted over
p + facet_grid(am ~ vs+cyl, labeller = label_context)

# Interpreting the labels as plotmath expressions
p + facet_grid(. ~ cyl2)
p + facet_grid(. ~ cyl2, labeller = label_parsed)

---

**label_bquote**

*Label with mathematical expressions*

**Description**

`label_bquote()` offers a flexible way of labelling facet rows or columns with plotmath expressions. Backquoted variables will be replaced with their value in the facet.

**Usage**

```r
label_bquote(rows = NULL, cols = NULL, default)
```

**Arguments**

- **rows**
  - Backquoted labelling expression for rows.
- **cols**
  - Backquoted labelling expression for columns.
- **default**
  - Unused, kept for compatibility.

**See Also**

`labellers`, `labeller()`.

**Examples**

# The variables mentioned in the plotmath expression must be
# backquoted and referred to by their names.
p <- ggplot(mtcars, aes(wt, mpg)) + geom_point()
p + facet_grid(vs ~ ., labeller = label_bquote(alpha ^ .(vs)))
p + facet_grid(. ~ vs, labeller = label_bquote(cols = .(vs) ^ .(vs)))
p + facet_grid(. ~ vs + am, labeller = label_bquote(cols = .(am) ^ .(vs)))
labs Modify axis, legend, and plot labels

Description
Good labels are critical for making your plots accessible to a wider audience. Always ensure the axis and legend labels display the full variable name. Use the plot title and subtitle to explain the main findings. It’s common to use the caption to provide information about the data source. tag can be used for adding identification tags to differentiate between multiple plots.

Usage
labs(
  ...,
  title = waiver(),
  subtitle = waiver(),
  caption = waiver(),
  tag = waiver(),
  alt = waiver(),
  alt_insight = waiver()
)

  xlab(label)

  ylab(label)

  ggtitle(label, subtitle = waiver())

Arguments
... A list of new name-value pairs. The name should be an aesthetic.
title The text for the title.
subtitle The text for the subtitle for the plot which will be displayed below the title.
caption The text for the caption which will be displayed in the bottom-right of the plot by default.
tag The text for the tag label which will be displayed at the top-left of the plot by default.
alt, alt_insight Text used for the generation of alt-text for the plot. See get_alt_text for examples.
label The title of the respective axis (for xlab() or ylab()) or of the plot (for ggtitle()).
**Details**

You can also set axis and legend labels in the individual scales (using the first argument, the name). If you’re changing other scale options, this is recommended.

If a plot already has a title, subtitle, caption, etc., and you want to remove it, you can do so by setting the respective argument to `NULL`. For example, if plot `p` has a subtitle, then `p + labs(subtitle = NULL)` will remove the subtitle from the plot.

**Examples**

```r
p <- ggplot(mtcars, aes(mpg, wt, colour = cyl)) + geom_point()
p + labs(colour = "Cylinders")
p + labs(x = "New x label")

# The plot title appears at the top-left, with the subtitle displayed in smaller text underneath it
p + labs(title = "New plot title")
p + labs(title = "New plot title", subtitle = "A subtitle")

# The caption appears in the bottom-right, and is often used for sources, notes or copyright
p + labs(caption = "(based on data from \ldots")

# The plot tag appears at the top-left, and is typically used for labelling a subplot with a letter.
p + labs(title = "title", tag = "A")

# If you want to remove a label, set it to NULL.
p + labs(title = "title") + labs(title = NULL)
```

---

**lims**

**Set scale limits**

**Description**

This is a shortcut for supplying the `limits` argument to the individual scales. By default, any values outside the limits specified are replaced with `NA`. Be warned that this will remove data outside the limits and this can produce unintended results. For changing x or y axis limits without dropping data observations, see `coord_cartesian()`.

**Usage**

```r
lims(...)  
xlim(...)  
ylim(...)
```
Arguments

For `xlim()` and `ylim()`: Two numeric values, specifying the left/lower limit and the right/upper limit of the scale. If the larger value is given first, the scale will be reversed. You can leave one value as `NA` if you want to compute the corresponding limit from the range of the data.

For `lims()`: A name–value pair. The name must be an aesthetic, and the value must be either a length-2 numeric, a character, a factor, or a date/time. A numeric value will create a continuous scale. If the larger value comes first, the scale will be reversed. You can leave one value as `NA` if you want to compute the corresponding limit from the range of the data. A character or factor value will create a discrete scale. A date-time value will create a continuous date/time scale.

See Also

To expand the range of a plot to always include certain values, see `expand_limits()`. For other types of data, see `scale_x_discrete()`, `scale_x_continuous()`, `scale_x_date()`.

Examples

```r
# Zoom into a specified area
ggplot(mtcars, aes(mpg, wt)) +
  geom_point() +
  xlim(15, 20)

# reverse scale
ggplot(mtcars, aes(mpg, wt)) +
  geom_point() +
  xlim(20, 15)

# with automatic lower limit
ggplot(mtcars, aes(mpg, wt)) +
  geom_point() +
  xlim(NA, 20)

# You can also supply limits that are larger than the data.
# This is useful if you want to match scales across different plots
small <- subset(mtcars, cyl == 4)
big <- subset(mtcars, cyl > 4)

ggplot(small, aes(mpg, wt, colour = factor(cyl))) +
  geom_point() +
  lims(colour = c("4", "6", "8"))

ggplot(big, aes(mpg, wt, colour = factor(cyl))) +
  geom_point() +
  lims(colour = c("4", "6", "8"))

# There are two ways of setting the axis limits: with limits or
# with coordinate systems. They work in two rather different ways.
```
set.seed(1)
last_month <- Sys.Date() - 0:59
df <- data.frame(
  date = last_month,
  price = c(rnorm(30, mean = 15), runif(30) + 0.2 * (1:30))
)

p <- ggplot(df, aes(date, price)) +
  geom_line() +
  stat_smooth()

p

# Setting the limits with the scale discards all data outside the range.
p + lims(x= c(Sys.Date() - 30, NA), y = c(10, 20))

# For changing x or y axis limits **without** dropping data
# observations use [coord_cartesian()]. Setting the limits on the
# coordinate system performs a visual zoom.
p + coord_cartesian(xlim =c(Sys.Date() - 30, NA), ylim = c(10, 20))

---

luv_colours colors() in Luv space

Description

All built-in colors() translated into Luv colour space.

Usage

luv_colours

Format

A data frame with 657 observations and 4 variables:

L,u,v  Position in Luv colour space

col  Colour name
**mean_se**

*Calculate mean and standard error of the mean*

**Description**

For use with `stat_summary()`

**Usage**

```r
mean_se(x, mult = 1)
```

**Arguments**

- `x` numeric vector.
- `mult` number of multiples of standard error.

**Value**

A data frame with three columns:

- `y` The mean.
- `ymin` The mean minus the multiples of the standard error.
- `ymax` The mean plus the multiples of the standard error.

**Examples**

```r
set.seed(1)
x <- rnorm(100)
mean_se(x)
```

---

**midwest**

*Midwest demographics*

**Description**

Demographic information of midwest counties from 2000 US census

**Usage**

```r
midwest
```
Format

A data frame with 437 rows and 28 variables:

- **PID** Unique county identifier.
- **county** County name.
- **state** State to which county belongs to.
- **area** Area of county (units unknown).
- **poptotal** Total population.
- **popdensity** Population density (person/unit area).
- **popwhite** Number of whites.
- **popblack** Number of blacks.
- **popamerindian** Number of American Indians.
- **popasian** Number of Asians.
- **popother** Number of other races.
- **percwhite** Percent white.
- **percblack** Percent black.
- **percamerindian** Percent American Indian.
- **percasian** Percent Asian.
- **percother** Percent other races.
- **popadults** Number of adults.
- **perchsd** Percent with high school diploma.
- **percollege** Percent college educated.
- **percpprof** Percent with professional degree.
- **poppovertyknown** Population with known poverty status.
- **percpovertyknown** Percent of population with known poverty status.
- **percbelowpoverty** Percent of people below poverty line.
- **perccchildbelowpovert** Percent of children below poverty line.
- **percadultpoverty** Percent of adults below poverty line.
- **percelderlypoverty** Percent of elderly below poverty line.
- **inmetro** County considered in a metro area.
- **category** Miscellaneous.

Details

Note: this dataset is included for illustrative purposes. The original descriptions were not documented and the current descriptions here are based on speculation. For more accurate and up-to-date US census data, see the [acs package](#).
Fuel economy data from 1999 to 2008 for 38 popular models of cars

Description
This dataset contains a subset of the fuel economy data that the EPA makes available on https://fueleconomy.gov/. It contains only models which had a new release every year between 1999 and 2008 - this was used as a proxy for the popularity of the car.

Usage
mpg

Format
A data frame with 234 rows and 11 variables:

- **manufacturer**: manufacturer name
- **model**: model name
- **displ**: engine displacement, in litres
- **year**: year of manufacture
- **cyl**: number of cylinders
- **trans**: type of transmission
- **drv**: the type of drive train, where f = front-wheel drive, r = rear wheel drive, 4 = 4wd
- **cty**: city miles per gallon
- **hwy**: highway miles per gallon
- **fl**: fuel type
- **class**: "type" of car

An updated and expanded version of the mammals sleep dataset

Description
This is an updated and expanded version of the mammals sleep dataset. Updated sleep times and weights were taken from V. M. Savage and G. B. West. A quantitative, theoretical framework for understanding mammalian sleep. Proceedings of the National Academy of Sciences, 104 (3):1051-1056, 2007.

Usage
msleep
position_dodge

Format

A data frame with 83 rows and 11 variables:

- **name**: common name
- **genus**: 
- **vore**: carnivore, omnivore or herbivore?
- **order**: 
- **conservation**: the conservation status of the animal
- **sleep_total**: total amount of sleep, in hours
- **sleep_rem**: rem sleep, in hours
- **sleep_cycle**: length of sleep cycle, in hours
- **awake**: amount of time spent awake, in hours
- **brainwt**: brain weight in kilograms
- **bodywt**: body weight in kilograms

Details

Additional variables order, conservation status and vore were added from wikipedia.

position_dodge

*Dodging preserves the vertical position of an geom while adjusting the horizontal position.* position_dodge() requires the grouping variable to be be specified in the global or geom_* layer. Unlike position_dodge(), position_dodge2() works without a grouping variable in a layer. position_dodge2() works with bars and rectangles, but is particularly useful for arranging box plots, which can have variable widths.

Usage

```r
position_dodge(width = NULL, preserve = "total")

position_dodge2(  
  width = NULL,  
  preserve = "total",  
  padding = 0.1,  
  reverse = FALSE
)
```
Arguments

- **width**: Dodging width, when different to the width of the individual elements. This is useful when you want to align narrow geoms with wider geoms. See the examples.
- **preserve**: Should dodging preserve the "total" width of all elements at a position, or the width of a "single" element?
- **padding**: Padding between elements at the same position. Elements are shrunk by this proportion to allow space between them. Defaults to 0.1.
- **reverse**: If TRUE, will reverse the default stacking order. This is useful if you’re rotating both the plot and legend.

See Also
Other position adjustments: `position_identity()`, `position_jitterdodge()`, `position_jitter()`, `position_nudge()`, `position_stack()`

Examples

```r
ggplot(mtcars, aes(factor(cyl), fill = factor(vs))) + geom_bar(position = "dodge2")
# By default, dodging with `position_dodge2()` preserves the total width of
# the elements. You can choose to preserve the width of each element with:
ggplot(mtcars, aes(factor(cyl), fill = factor(vs))) + geom_bar(position = position_dodge2(preserve = "single"))

ggplot(diamonds, aes(price, fill = cut)) + geom_histogram(position="dodge2")
# see ?geom_bar for more examples

# In this case a frequency polygon is probably a better choice
ggplot(diamonds, aes(price, colour = cut)) + geom_freqpoly()

# Dodging with various widths -------------------------------------
# To dodge items with different widths, you need to be explicit
df <- data.frame(
  x = c("a","a","b","b"),
  y = 2:5,
  g = rep(1:2, 2)
)
p <- ggplot(df, aes(x, y, group = g)) + geom_col(position = "dodge", fill = "grey50", colour = "black")
p

# A line range has no width:
p + geom_linerange(aes(ymin = y - 1, ymax = y + 1), position = "dodge")
```
position_identity

# So you must explicitly specify the width
p + geom_linerange(
  aes(ymin = y - 1, ymax = y + 1),
  position = position_dodge(width = 0.9)
)

# The same principle applies to error bars, which are usually
# narrower than the bars
p + geom_errorbar(
  aes(ymin = y - 1, ymax = y + 1),
  width = 0.2,
  position = "dodge"
)
p + geom_errorbar(
  aes(ymin = y - 1, ymax = y + 1),
  width = 0.2,
  position = position_dodge(width = 0.9)
)

# Box plots use position_dodge2 by default, and bars can use it too
ggplot(mpg, aes(factor(year), displ)) +
  geom_boxplot(aes(colour = hwy < 30))

ggplot(mpg, aes(factor(year), displ)) +
  geom_boxplot(aes(colour = hwy < 30), varwidth = TRUE)

ggplot(mtcars, aes(factor(cyl), fill = factor(vs))) +
  geom_bar(position = position_dodge2(preserve = "single"))

ggplot(mtcars, aes(factor(cyl), fill = factor(vs))) +
  geom_bar(position = position_dodge2(preserve = "total"))

position_identity

Don’t adjust position

Description

Don’t adjust position

Usage

position_identity()

See Also

Other position adjustments: position_dodge(), position_jitterdodge(), position_jitter(), position_nudge(), position_stack()
position_jitter

Jitter points to avoid overplotting

Description

Counterintuitively adding random noise to a plot can sometimes make it easier to read. Jittering is particularly useful for small datasets with at least one discrete position.

Usage

position_jitter(width = NULL, height = NULL, seed = NA)

Arguments

width, height Amount of vertical and horizontal jitter. The jitter is added in both positive and negative directions, so the total spread is twice the value specified here. If omitted, defaults to 40% of the resolution of the data: this means the jitter values will occupy 80% of the implied bins. Categorical data is aligned on the integers, so a width or height of 0.5 will spread the data so it’s not possible to see the distinction between the categories.

seed A random seed to make the jitter reproducible. Useful if you need to apply the same jitter twice, e.g., for a point and a corresponding label. The random seed is reset after jittering. If NA (the default value), the seed is initialised with a random value; this makes sure that two subsequent calls start with a different seed. Use NULL to use the current random seed and also avoid resetting (the behaviour of ggplot 2.2.1 and earlier).

See Also

Other position adjustments: position_dodge(), position_identity(), position_jitterdodge(), position_nudge(), position_stack()

Examples

# Jittering is useful when you have a discrete position, and a relatively small number of points
# take up as much space as a boxplot or a bar
ggplot(mpg, aes(class, hwy)) +
  geom_boxplot(colour = "grey50") +
  geom_jitter()

# If the default jittering is too much, as in this plot:
ggplot(mtcars, aes(am, vs)) +
  geom_jitter()

# You can adjust it in two ways
ggplot(mtcars, aes(am, vs)) +
  geom_jitter(width = 0.1, height = 0.1)
position_jitterdodge

Simultaneously dodge and jitter

Description

This is primarily used for aligning points generated through `geom_point()` with dodged boxplots (e.g., a `geom_boxplot()` with a fill aesthetic supplied).

Usage

```r
position_jitterdodge(
  jitter.width = NULL,
  jitter.height = 0,
  dodge.width = 0.75,
  seed = NA
)
```

Arguments

- `jitter.width` degree of jitter in x direction. Defaults to 40% of the resolution of the data.
- `jitter.height` degree of jitter in y direction. Defaults to 0.
- `dodge.width` the amount to dodge in the x direction. Defaults to 0.75, the default `position_dodge()` width.
- `seed` A random seed to make the jitter reproducible. Useful if you need to apply the same jitter twice, e.g., for a point and a corresponding label. The random seed is reset after jittering. If `NA` (the default value), the seed is initialised with a random value; this makes sure that two subsequent calls start with a different seed. Use `NULL` to use the current random seed and also avoid resetting (the behaviour of `ggplot 2.2.1` and earlier).

See Also

Other position adjustments: `position_dodge()`, `position_identity()`, `position_jitter()`, `position_nudge()`, `position_stack()`
Examples

```r
set.seed(596)
dsub <- diamonds[sample(nrow(diamonds), 1000), ]
ggplot(dsub, aes(x = cut, y = carat, fill = clarity)) +
  geom_boxplot(outlier.size = 0) +
  geom_point(pch = 21, position = position_jitterdodge())
```

---

**position_nudge**

*Nudge points a fixed distance*

Description

`position_nudge()` is generally useful for adjusting the position of items on discrete scales by a small amount. Nudging is built in to `geom_text()` because it’s so useful for moving labels a small distance from what they’re labelling.

Usage

`position_nudge(x = 0, y = 0)`

Arguments

- `x, y` Amount of vertical and horizontal distance to move.

See Also

Other position adjustments: `position_dodge()`, `position_identity()`, `position_jitterdodge()`, `position_jitter()`, `position_stack()`

Examples

```r
df <- data.frame(
  x = c(1,3,2,5),
  y = c("a","c","d","c")
)
ggplot(df, aes(x, y)) +
  geom_point() +
  geom_text(aes(label = y))

ggplot(df, aes(x, y)) +
  geom_point() +
  geom_text(aes(label = y), position = position_nudge(y = -0.1))

# Or, in brief
ggplot(df, aes(x, y)) +
  geom_point() +
  geom_text(aes(label = y), nudge_y = -0.1)
```
position_stack

Stack overlapping objects on top of each other

Description

position_stack() stacks bars on top of each other; position_fill() stacks bars and standardises each stack to have constant height.

Usage

position_stack(vjust = 1, reverse = FALSE)

position_fill(vjust = 1, reverse = FALSE)

Arguments

vjust
Vertical adjustment for geoms that have a position (like points or lines), not a dimension (like bars or areas). Set to 0 to align with the bottom, 0.5 for the middle, and 1 (the default) for the top.

reverse
If TRUE, will reverse the default stacking order. This is useful if you’re rotating both the plot and legend.

Details

position_fill() and position_stack() automatically stack values in reverse order of the group aesthetic, which for bar charts is usually defined by the fill aesthetic (the default group aesthetic is formed by the combination of all discrete aesthetics except for x and y). This default ensures that bar colours align with the default legend.

There are three ways to override the defaults depending on what you want:

1. Change the order of the levels in the underlying factor. This will change the stacking order, and the order of keys in the legend.
2. Set the legend breaks to change the order of the keys without affecting the stacking.
3. Manually set the group aesthetic to change the stacking order without affecting the legend.

Stacking of positive and negative values are performed separately so that positive values stack upwards from the x-axis and negative values stack downward.

Because stacking is performed after scale transformations, stacking with non-linear scales gives distortions that easily lead to misinterpretations of the data. It is therefore discouraged to use these position adjustments in combination with scale transformations, such as logarithmic or square root scales.

See Also

See geom_bar() and geom_area() for more examples.

Other position adjustments: position_dodge(), position_identity(), position_jitterdodge(), position_jitter(), position_nudge()
Examples

# Stacking and filling

# Stacking is the default behaviour for most area plots.
# Fill makes it easier to compare proportions

ggplot(mtcars, aes(factor(cyl), fill = factor(vs))) +
  geom_bar()

ggplot(mtcars, aes(factor(cyl), fill = factor(vs))) +
  geom_bar(position = "fill")

ggplot(diamonds, aes(price, fill = cut)) +
  geom_histogram(binwidth = 500)

ggplot(diamonds, aes(price, fill = cut)) +
  geom_histogram(binwidth = 500, position = "fill")

# Stacking is also useful for time series

set.seed(1)

series <- data.frame(
  time = c(rep(1, 4), rep(2, 4), rep(3, 4), rep(4, 4)),
  type = rep(c("a", "b", "c", "d"), 4),
  value = rpois(16, 10)
)

ggplot(series, aes(time, value)) +
  geom_area(aes(fill = type))

# Stacking order

# The stacking order is carefully designed so that the plot matches
# the legend.

# You control the stacking order by setting the levels of the underlying
# factor. See the forcats package for convenient helpers.

series$type2 <- factor(series$type, levels = c("c", "b", "d", "a"))

ggplot(series, aes(time, value)) +
  geom_area(aes(fill = type2))

# You can change the order of the levels in the legend using the scale

ggplot(series, aes(time, value)) +
  geom_area(aes(fill = type2)) +
  scale_fill_discrete(breaks = c("a", "b", "c", "d"))

# If you've flipped the plot, use reverse = TRUE so the levels
# continue to match

ggplot(series, aes(time, value)) +
  geom_area(aes(fill = type2), position = position_stack(reverse = TRUE)) +
  coord_flip() +
  theme(legend.position = "top")

# Non-area plots

# When stacking across multiple layers it's a good idea to always set
# the 'group' aesthetic in the ggplot() call. This ensures that all layers
# are stacked in the same way.
presidential

```
presidential

```
Format

A data frame with 12 rows and 4 variables:

- **name**: Last name of president
- **start**: Presidency start date
- **end**: Presidency end date
- **party**: Party of president

---

Description

Generally, you do not need to print or plot a `ggplot2` plot explicitly: the default top-level `print` method will do it for you. You will, however, need to call `print()` explicitly if you want to draw a plot inside a function or for loop.

Usage

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

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

Arguments

- `x`: plot to display
- `newpage`: draw new (empty) page first?
- `vp`: viewport to draw plot in
- `...`: other arguments not used by this method

Value

Invisibly returns the original plot.

Examples

```r
colours <- list(~class, ~drv, ~fl)

# Doesn't seem to do anything!
for (colour in colours) {
  ggplot(mpg, aes_(~ displ, ~ hwy, colour = colour)) +
  geom_point()
}
```
# Works when we explicitly print the plots
for (colour in colours) {
    print(ggplot(mpg, aes_(~ displ, ~ hwy, colour = colour)) +
          geom_point())
}

---

## print.ggproto

### Format or print a ggproto object

#### Description

If a ggproto object has a `print` method, this will call that method. Otherwise, it will print out the members of the object, and optionally, the members of the inherited objects.

#### Usage

```r
## S3 method for class 'ggproto'
print(x, ..., flat = TRUE)

## S3 method for class 'ggproto'
format(x, ..., flat = TRUE)
```

#### Arguments

- **x**: A ggproto object to print.
- **...**: If the ggproto object has a `print` method, further arguments will be passed to it. Otherwise, these arguments are unused.
- **flat**: If TRUE (the default), show a flattened list of all local and inherited members. If FALSE, show the inheritance hierarchy.

#### Examples

```r
Dog <- ggproto(
    print = function(self, n) {
        cat("Woof!\n"
    }
)

Dog

cat(format(Dog), "\n")
```
Description

qplot() is now deprecated in order to encourage the users to learn ggplot() as it makes it easier to create complex graphics.

Usage

qplot(
  x,
  y,
  ..., 
  data,
  facets = NULL,
  margins = FALSE,
  geom = "auto",
  xlim = c(NA, NA),
  ylim = c(NA, NA),
  log = "",
  main = NULL,
  xlab = NULL,
  ylab = NULL,
  asp = NA,
  stat = deprecated(),
  position = deprecated()
)

quickplot(
  x,
  y,
  ..., 
  data,
  facets = NULL,
  margins = FALSE,
  geom = "auto",
  xlim = c(NA, NA),
  ylim = c(NA, NA),
  log = "",
  main = NULL,
  xlab = NULL,
  ylab = NULL,
  asp = NA,
  stat = deprecated(),
  position = deprecated()
)
**qplot**

**Arguments**

- **x, y, ...** Aesthetics passed into each layer
- **data** Data frame to use (optional). If not specified, will create one, extracting vectors from the current environment.
- **facets** Faceting formula to use. Picks `facet_wrap()` or `facet_grid()` depending on whether the formula is one- or two-sided
- **margins** See `facet_grid()`: display marginal facets?
- **geom** Character vector specifying geom(s) to draw. Defaults to "point" if x and y are specified, and "histogram" if only x is specified.
- **xlim, ylim** X and y axis limits
- **log** Which variables to log transform ("x", "y", or "xy")
- **main, xlab, ylab** Character vector (or expression) giving plot title, x axis label, and y axis label respectively.
- **asp** The y/x aspect ratio
- **stat, position** [Deprecated]

**Examples**

```r
# Use data from data.frame
qplot(mpg, wt, data = mtcars)
qplot(mpg, wt, data = mtcars, colour = cyl)
qplot(mpg, wt, data = mtcars, size = cyl)
qplot(mpg, wt, data = mtcars, facets = vs ~ am)

set.seed(1)
qplot(1:10, rnorm(10), colour = runif(10))
qplot(1:10, letters[1:10])
mod <- lm(mpg ~ wt, data = mtcars)
qplot(resid(mod), fitted(mod))

f <- function() {
  a <- 1:10
  b <- a ^ 2
  qplot(a, b)
}
f()

# To set aesthetics, wrap in I()
qplot(mpg, wt, data = mtcars, colour = I("red"))

# qplot will attempt to guess what geom you want depending on the input
# both x and y supplied = scatterplot
qplot(mpg, wt, data = mtcars)
# just x supplied = histogram
qplot(mpg, data = mtcars)
# just y supplied = scatterplot, with x = seq_along(y)
```
qplot(y = mpg, data = mtcars)

# Use different geoms
qplot(mpg, wt, data = mtcars, geom = "path")
qplot(factor(cyl), wt, data = mtcars, geom = c("boxplot", "jitter"))
qplot(mpg, data = mtcars, geom = "dotplot")

---

### resolution

*Compute the "resolution" of a numeric vector*

**Description**

The resolution is the smallest non-zero distance between adjacent values. If there is only one unique value, then the resolution is defined to be one. If `x` is an integer vector, then it is assumed to represent a discrete variable, and the resolution is 1.

**Usage**

```r
resolution(x, zero = TRUE)
```

**Arguments**

- `x` numeric vector
- `zero` should a zero value be automatically included in the computation of resolution

**Examples**

```r
resolution(1:10)
resolution((1:10) - 0.5)
resolution((1:10) - 0.5, FALSE)

# Note the difference between numeric and integer vectors
resolution(c(2, 10, 20, 50))
resolution(c(2L, 10L, 20L, 50L))
```

---

### scale_alpha

*Alpha transparency scales*

**Description**

Alpha-transparency scales are not tremendously useful, but can be a convenient way to visually down-weight less important observations. `scale_alpha()` is an alias for `scale_alpha_continuous()` since that is the most common use of alpha, and it saves a bit of typing.
Usage

```r
scale_alpha(name = waiver(), ..., range = c(0.1, 1))
scale_alpha_continuous(name = waiver(), ..., range = c(0.1, 1))
scale_alpha_binned(name = waiver(), ..., range = c(0.1, 1))
scale_alpha_discrete(...)
scale_alpha_ordinal(name = waiver(), ..., range = c(0.1, 1))
```

Arguments

- **name** (default: `waiver()`)
  - The name of the scale. Used as the axis or legend title. If `waiver()`, the default, the name of the scale is taken from the first mapping used for that aesthetic. If `NULL`, the legend title will be omitted.

- **...**
  - Other arguments passed on to `continuous_scale()`, `binned_scale()`, or `discrete_scale()` as appropriate, to control name, limits, breaks, labels and so forth.

- **range** (default: `c(0.1, 1)`)
  - Output range of alpha values. Must lie between 0 and 1.

See Also

- The documentation on colour aesthetics.
- Other alpha scales: `scale_alpha_manual()`, `scale_alpha_identity()`.
- Other colour scales: `scale_colour_brewer()`, `scale_colour_continuous()`, `scale_colour_gradient()`, `scale_colour_grey()`, `scale_colour_hue()`, `scale_colour_identity()`, `scale_colour_manual()`, `scale_colour_steps()`, `scale_colour_viridis_d()`

Examples

```r
p <- ggplot(mpg, aes(displ, hwy)) + geom_point(aes(alpha = year))

p + scale_alpha("cylinders")
p + scale_alpha(range = c(0.4, 0.8))
```

Positional scales for binning continuous data (x & y)

Description

`scale_x_binned()` and `scale_y_binned()` are scales that discretize continuous position data. You can use these scales to transform continuous inputs before using it with a geom that requires discrete positions. An example is using `scale_x_binned()` with `geom_bar()` to create a histogram.
scale_binned

Usage

scale_x_binned(  
  name = waiver(),  
  n.breaks = 10,  
  nice.breaks = TRUE,  
  breaks = waiver(),  
  labels = waiver(),  
  limits = NULL,  
  expand = waiver(),  
  oob = squish,  
  na.value = NA_real_,  
  right = TRUE,  
  show.limits = FALSE,  
  transform = "identity",  
  trans = deprecated(),  
  guide = waiver(),  
  position = "bottom"
)

scale_y_binned(  
  name = waiver(),  
  n.breaks = 10,  
  nice.breaks = TRUE,  
  breaks = waiver(),  
  labels = waiver(),  
  limits = NULL,  
  expand = waiver(),  
  oob = squish,  
  na.value = NA_real_,  
  right = TRUE,  
  show.limits = FALSE,  
  transform = "identity",  
  trans = deprecated(),  
  guide = waiver(),  
  position = "left"
)

Arguments

name

The name of the scale. Used as the axis or legend title. If waiver(), the default, the name of the scale is taken from the first mapping used for that aesthetic. If NULL, the legend title will be omitted.

n.breaks

The number of break points to create if breaks are not given directly.

nice.breaks

Logical. Should breaks be attempted placed at nice values instead of exactly evenly spaced between the limits. If TRUE (default) the scale will ask the transformation object to create breaks, and this may result in a different number of breaks than requested. Ignored if breaks are given explicitly.
scale_binned

breaks One of:
  • NULL for no breaks
  • waiver() for the default breaks computed by the transformation object
  • A numeric vector of positions
  • A function that takes the limits as input and returns breaks as output (e.g., a function returned by scales::extended_breaks()). Also accepts rlang lambda function notation.

labels One of:
  • NULL for no labels
  • waiver() for the default labels computed by the transformation object
  • A character vector giving labels (must be same length as breaks)
  • An expression vector (must be the same length as breaks). See ?plotmath for details.
  • A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

limits One of:
  • NULL to use the default scale range
  • A numeric vector of length two providing limits of the scale. Use NA to refer to the existing minimum or maximum
  • A function that accepts the existing (automatic) limits and returns new limits. Also accepts rlang lambda function notation. Note that setting limits on positional scales will remove data outside of the limits. If the purpose is to zoom, use the limit argument in the coordinate system (see coord_cartesian()).

expand For position scales, a vector of range expansion constants used to add some padding around the data to ensure that they are placed some distance away from the axes. Use the convenience function expansion() to generate the values for the expand argument. The defaults are to expand the scale by 5% on each side for continuous variables, and by 0.6 units on each side for discrete variables.

oob One of:
  • Function that handles limits outside of the scale limits (out of bounds). Also accepts rlang lambda function notation.
  • The default (scales::censor()) replaces out of bounds values with NA.
  • scales::squish() for squishing out of bounds values into range.
  • scales::squish_infinite() for squishing infinite values into range.

na.value Missing values will be replaced with this value.

right Should the intervals be closed on the right (TRUE, default) or should the intervals be closed on the left (FALSE)? ’Closed on the right’ means that values at break positions are part of the lower bin (open on the left), whereas they are part of the upper bin when intervals are closed on the left (open on the right).

show.limits should the limits of the scale appear as ticks
scale_colour_brewer

transform
For continuous scales, the name of a transformation object or the object itself. Built-in transformations include "asn", "atanh", "boxcox", "date", "exp", "hms", "identity", "log", "log10", "log1p", "log2", "logit", "modulus", "probability", "probit", "pseudo_log", "reciprocal", "reverse", "sqrt" and "time". A transformation object bundles together a transform, its inverse, and methods for generating breaks and labels. Transformation objects are defined in the scales package, and are called transform_<name>. If transformations require arguments, you can call them from the scales package, e.g. scales::transform_boxcox(p = 2). You can create your own transformation with scales::new_transform().

trans [Deprecated] Deprecated in favour of transform.

guide
A function used to create a guide or its name. See guides() for more information.

position
For position scales, The position of the axis. left or right for y axes, top or bottom for x axes.

See Also
The position documentation.
Other position scales: scale_x_continuous(), scale_x_date(), scale_x_discrete()

Examples

# Create a histogram by binning the x-axis
geom_bar(aes(mpg)) +
  scale_x_binned()

scale_colour_brewer

Sequential, diverging and qualitative colour scales from ColorBrewer

Description
The brewer scales provide sequential, diverging and qualitative colour schemes from ColorBrewer. These are particularly well suited to display discrete values on a map. See https://colorbrewer2.org for more information.

Usage

scale_colour_brewer(
  name = waiver(),
  ..., 
  type = "seq",
  palette = 1,
  direction = 1,
  aesthetics = "colour"
)
scale_fill_brewer(
    name = waiver(),
    ...,
    type = "seq",
    palette = 1,
    direction = 1,
    aesthetics = "fill"
)

scale_colour_distiller(
    name = waiver(),
    ...,
    type = "seq",
    palette = 1,
    direction = -1,
    values = NULL,
    space = "Lab",
    na.value = "grey50",
    guide = "colourbar",
    aesthetics = "colour"
)

color_fill_distiller(
    name = waiver(),
    ...,
    type = "seq",
    palette = 1,
    direction = -1,
    values = NULL,
    space = "Lab",
    na.value = "grey50",
    guide = "colourbar",
    aesthetics = "fill"
)

color_fill_fermenter(
    name = waiver(),
    ...,
    type = "seq",
    palette = 1,
    direction = -1,
    na.value = "grey50",
    guide = "coloursteps",
    aesthetics = "colour"
)

scale_fill_fermenter(
name = waiver(),
...

Arguments

name  The name of the scale. Used as the axis or legend title. If waiver(), the default, the name of the scale is taken from the first mapping used for that aesthetic. If NULL, the legend title will be omitted.

...  Other arguments passed on to discrete_scale(), continuous_scale(), or binned_scale(), for brewer, distiller, and fermenter variants respectively, to control name, limits, breaks, labels and so forth.

type  One of "seq" (sequential), "div" (diverging) or "qual" (qualitative)

palette  If a string, will use that named palette. If a number, will index into the list of palettes of appropriate type. The list of available palettes can found in the Palettes section.

direction  Sets the order of colours in the scale. If 1, the default, colours are as output by RColorBrewer::brewer.pal(). If -1, the order of colours is reversed.

aesthetics  Character string or vector of character strings listing the name(s) of the aesthetic(s) that this scale works with. This can be useful, for example, to apply colour settings to the colour and fill aesthetics at the same time, via aesthetics = c("colour", "fill").

values  if colours should not be evenly positioned along the gradient this vector gives the position (between 0 and 1) for each colour in the colours vector. See rescale() for a convenience function to map an arbitrary range to between 0 and 1.

space  colour space in which to calculate gradient. Must be "Lab" - other values are deprecated.

na.value  Colour to use for missing values

guide  Type of legend. Use "colourbar" for continuous colour bar, or "legend" for discrete colour legend.

Details

The brewer scales were carefully designed and tested on discrete data. They were not designed to be extended to continuous data, but results often look good. Your mileage may vary.

Palettes

The following palettes are available for use with these scales:
**Diverging**  BrBG, PiYG, PRGn, PuOr, RdBu, RdGy, RdYI1Bu, RdYI1Gn, Spectral

**Qualitative**  Accent, Dark2, Paired, Pastel1, Pastel2, Set1, Set2, Set3

**Sequential**  Blues, BuGn, BuPu, GnBu, Greens, Greys, Oranges, OrRd, PuBu, PuBuGn, PuRd, Purples, RdPu, Reds, YI1Gn, YI1GnBu, YI1OrBr, YI1OrRd

Modify the palette through the `palette` argument.

**Note**

The distiller scales extend brewer scales by smoothly interpolating 7 colours from any palette to a continuous scale. The distiller scales have a default direction = -1. To reverse, use direction = 1. The fermenter scales provide binned versions of the brewer scales.

**See Also**

The documentation on `colour aesthetics`.

Other colour scales: `scale_alpha()`, `scale_colour_continuous()`, `scale_colour_gradient()`, `scale_colour_grey()`, `scale_colour_hue()`, `scale_colour_identity()`, `scale_colour_manual()`, `scale_colour_steps()`, `scale_colour_viridis_d()`

**Examples**

```r
set.seed(596)
dsamp <- diamonds[sample(nrow(diamonds), 1000), ]
(d <- ggplot(dsamp, aes(carat, price)) +
  geom_point(aes(colour = clarity)))
d + scale_colour_brewer()
# Change scale label
d + scale_colour_brewer("Diamond\nclarity")
# Select brewer palette to use, see ?scales::pal_brewer for more details
d + scale_colour_brewer(palette = "Greens")
d + scale_colour_brewer(palette = "Set1")

# scale_fill_brewer works just the same as
# scale_colour_brewer but for fill colours
p <- ggplot(diamonds, aes(x = price, fill = cut)) +
  geom_histogram(position = "dodge", binwidth = 1000)
p + scale_fill_brewer()
# the order of colour can be reversed
p + scale_fill_brewer(direction = -1)
# the brewer scales look better on a darker background
p +
  scale_fill_brewer(direction = -1) +
  theme_dark()

# Use distiller variant with continuous data
v <- ggplot(faithfuld) +
```
The scales `scale_colour_continuous()` and `scale_fill_continuous()` are the default colour scales `ggplot2` uses when continuous data values are mapped onto the colour or fill aesthetics, respectively. The scales `scale_colour_binned()` and `scale_fill_binned()` are equivalent scale functions that assign discrete color bins to the continuous values instead of using a continuous color spectrum.

**Usage**

```r
ggplot(data, aes(x = x, y = y)) + geom_point(aes(color = z))
```

```r
ggplot(data, aes(x = x, y = y)) + geom_point(aes(fill = z))
```

**Arguments**

- `...` Additional parameters passed on to the scale type
- `type` One of the following:
  - "gradient" (the default)
  - "viridis"
  - A function that returns a continuous colour scale.

**Details**

All these colour scales use the `options()` mechanism to determine default settings. Continuous colour scales default to the values of the `ggplot2.continuous.colour` and `ggplot2.continuous.fill` options, and binned colour scales default to the values of the `ggplot2.binned.colour` and `ggplot2.binned.fill` options.
options. These option values default to "gradient", which means that the scale functions actually used are `scale_colour_gradient()`/`scale_fill_gradient()` for continuous scales and `scale_colour_steps()`/`scale_fill_steps()` for binned scales. Alternative option values are "viridis" or a different scale function. See description of the type argument for details.

Note that the binned colour scales will use the settings of `ggplot2.continuous.colour` and `ggplot2.continuous.fill` as fallback, respectively, if `ggplot2.binned.colour` or `ggplot2.binned.fill` are not set.

These scale functions are meant to provide simple defaults. If you want to manually set the colors of a scale, consider using `scale_colour_gradient()` or `scale_colour_steps()`.

### Color Blindness

Many color palettes derived from RGB combinations (like the "rainbow" color palette) are not suitable to support all viewers, especially those with color vision deficiencies. Using `viridis` type, which is perceptually uniform in both colour and black-and-white display is an easy option to ensure good perceptive properties of your visualizations. The `colorspace` package offers functionalities

- to generate color palettes with good perceptive properties,
- to analyse a given color palette, like emulating color blindness,
- and to modify a given color palette for better perceptivity.

For more information on color vision deficiencies and suitable color choices see the paper on the `colorspace` package and references therein.

### See Also

`scale_colour_gradient()`, `scale_colour_viridis_c()`, `scale_colour_steps()`, `scale_colour_viridis_b()`, `scale_fill_gradient()`, `scale_fill_viridis_c()`, `scale_fill_steps()`, and `scale_fill_viridis_b()`

The documentation on `colour aesthetics`.

Other colour scales: `scale_alpha()`, `scale_colour_brewer()`, `scale_colour_gradient()`, `scale_colour_grey()`, `scale_colour_hue()`, `scale_colour_identity()`, `scale_colour_manual()`, `scale_colour_steps()`, `scale_colour_viridis_d()`

### Examples

```r
v <- ggplot(faithfuld, aes(waiting, eruptions, fill = density)) + geom_tile()
v
v + scale_fill_continuous(type = "gradient")
v + scale_fill_continuous(type = "viridis")

# The above are equivalent to
v + scale_fill_gradient()
v + scale_fill_viridis_c()

# To make a binned version of this plot
v + scale_fill_binned(type = "viridis")
```
# Set a different default scale using the options
# mechanism
tmp <- getOption("ggplot2.continuous.fill") # store current setting
options(ggplot2.continuous.fill = scale_fill_distiller)
v
options(ggplot2.continuous.fill = tmp) # restore previous setting

### scale_colour_discrete  Discrete colour scales

**Description**

The default discrete colour scale. Defaults to `scale_fill_hue()`/`scale_fill_brewer()` unless type (which defaults to the `ggplot2.discrete.fill`/`ggplot2.discrete.colour` options) is specified.

**Usage**

```r
scale_colour_discrete(..., type = getOption("ggplot2.discrete.colour"))

scale_fill_discrete(..., type = getOption("ggplot2.discrete.fill"))
```

**Arguments**

- `...` Additional parameters passed on to the scale type.
- `type` One of the following:
  - A character vector of color codes. The codes are used for a 'manual' color scale as long as the number of codes exceeds the number of data levels (if there are more levels than codes, `scale_colour_hue()`/`scale_fill_hue()` are used to construct the default scale). If this is a named vector, then the color values will be matched to levels based on the names of the vectors. Data values that don’t match will be set as `na.value`.
  - A list of character vectors of color codes. The minimum length vector that exceeds the number of data levels is chosen for the color scaling. This is useful if you want to change the color palette based on the number of levels.
  - A function that returns a discrete colour/fill scale (e.g., `scale_fill_hue()`, `scale_fill_brewer()`, etc).

**Examples**

```r
# Template function for creating densities grouped by a variable
cby_by_var <- function(var) {
  ggplot(mpg, aes(cty, colour = factor({{var}}), fill = factor({{var}}))) +
  geom_density(alpha = 0.2)
}

# The default, `scale_fill_hue()`, is not colour-blind safe
cby_by_var(class)
```
# (Temporarily) set the default to Okabe-Ito (which is colour-blind safe)
okabe <- c("#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7")
withr::with_options(
  list(ggplot2.discrete.fill = okabe),
  print(cty_by_var(class))
)

# Define a collection of palettes to alter the default based on number of levels to encode
discrete_palettes <- list(
  c("skyblue", "orange"),
  RColorBrewer::brewer.pal(3, "Set2"),
  RColorBrewer::brewer.pal(6, "Accent")
)
withr::with_options(
  list(ggplot2.discrete.fill = discrete_palettes), {
    # 1st palette is used when there 1-2 levels (e.g., year)
    print(cty_by_var(year))
    # 2nd palette is used when there are 3 levels
    print(cty_by_var(drv))
    # 3rd palette is used when there are 4-6 levels
    print(cty_by_var(fl))
  })

scale_colour_gradient  Gradient colour scales

Description

scale_*_gradient creates a two colour gradient (low-high), scale_*_gradient2 creates a diverging colour gradient (low-mid-high), scale_*_gradientn creates an n-colour gradient. For binned variants of these scales, see the color steps scales.

Usage

scale_colour_gradient(
  name = waiver(),
  ..., 
  low = "#132B43",
  high = "#56B1F7",
  space = "Lab",
  na.value = "grey50",
  guide = "colourbar",
  aesthetics = "colour"
)

scale_fill_gradient(
  name = waiver(),
..., low = "#132B43",
high = "#56B1F7",
space = "Lab",
na.value = "grey50",
guide = "colourbar",
aesthetics = "fill"
)

scale_colour_gradient2(
  name = waiver(),
  ...
  low = muted("red"),
  mid = "white",
  high = muted("blue"),
  midpoint = 0,
  space = "Lab",
  na.value = "grey50",
  transform = "identity",
  guide = "colourbar",
  aesthetics = "colour"
)

scale_fill_gradient2(
  name = waiver(),
  ...
  low = muted("red"),
  mid = "white",
  high = muted("blue"),
  midpoint = 0,
  space = "Lab",
  na.value = "grey50",
  transform = "identity",
  guide = "colourbar",
  aesthetics = "fill"
)

scale_colour_gradientn( 
  name = waiver(),
  ...
  colours,
  values = NULL,
  space = "Lab",
  na.value = "grey50",
  guide = "colourbar",
  aesthetics = "colour",
  colors 
)
```r
scale_fill_gradientn(
    name = waiver(),
    ...,
    colours,
    values = NULL,
    space = "Lab",
    na.value = "grey50",
    guide = "colourbar",
    aesthetics = "fill",
    colors
)
```

Arguments

- **name**: The name of the scale. Used as the axis or legend title. If `waiver()`, the default, the name of the scale is taken from the first mapping used for that aesthetic. If `NULL`, the legend title will be omitted.
- **...**: Arguments passed on to `continuous_scale`
- **scale_name**: [Deprecated] The name of the scale that should be used for error messages associated with this scale.
- **palette**: A palette function that when called with a numeric vector with values between 0 and 1 returns the corresponding output values (e.g., `scales::pal_area()`).
- **breaks**: One of:
  - `NULL` for no breaks
  - `waiver()` for the default breaks computed by the transformation object
  - A numeric vector of positions
  - A function that takes the limits as input and returns breaks as output (e.g., a function returned by `scales::extended_breaks()`). Also accepts rlang lambda function notation.
- **minor_breaks**: One of:
  - `NULL` for no minor breaks
  - `waiver()` for the default breaks (one minor break between each major break)
  - A numeric vector of positions
  - A function that given the limits returns a vector of minor breaks. Also accepts rlang lambda function notation. When the function has two arguments, it will be given the limits and major breaks.
- **n.breaks**: An integer guiding the number of major breaks. The algorithm may choose a slightly different number to ensure nice break labels. Will only have an effect if `breaks = waiver()`. Use `NULL` to use the default number of breaks given by the transformation.
- **labels**: One of:
  - `NULL` for no labels
  - `waiver()` for the default labels computed by the transformation object
  - A character vector giving labels (must be same length as breaks)
• An expression vector (must be the same length as breaks). See ?plotmath for details.
• A function that takes the breaks as input and returns labels as output. Also accepts rlang `lambda` function notation.

`limits` One of:
• `NULL` to use the default scale range
• A numeric vector of length two providing limits of the scale. Use `NA` to refer to the existing minimum or maximum
• A function that accepts the existing (automatic) limits and returns new limits. Also accepts rlang `lambda` function notation. Note that setting limits on positional scales will remove data outside of the limits. If the purpose is to zoom, use the limit argument in the coordinate system (see `coord_cartesian()`).

`rescaler` A function used to scale the input values to the range [0, 1]. This is always `scales::rescale()` except for diverging and n colour gradients (i.e., `scale_colour_gradient2()`, `scale_colour_gradientn()`). The rescaler is ignored by position scales, which always use `scales::rescale()`. Also accepts rlang `lambda` function notation.

`oob` One of:
• Function that handles limits outside of the scale limits (out of bounds). Also accepts rlang `lambda` function notation.
• The default (`scales::censor()`) replaces out of bounds values with `NA`.
• `scales::squish()` for squishing out of bounds values into range.
• `scales::squish_infinite()` for squishing infinite values into range.

`trans` [Deprecated] Deprecated in favour of `transform`.

`expand` For position scales, a vector of range expansion constants used to add some padding around the data to ensure that they are placed some distance away from the axes. Use the convenience function `expansion()` to generate the values for the expand argument. The defaults are to expand the scale by 5% on each side for continuous variables, and by 0.6 units on each side for discrete variables.

`position` For position scales, The position of the axis. `left` or `right` for y axes, `top` or `bottom` for x axes.

`call` The call used to construct the scale for reporting messages.

`super` The super class to use for the constructed scale

`low`, `high` Colours for low and high ends of the gradient.

`space` colour space in which to calculate gradient. Must be "Lab" - other values are deprecated.

`na.value` Colour to use for missing values

`guide` Type of legend. Use "colourbar" for continuous colour bar, or "legend" for discrete colour legend.

`aesthetics` Character string or vector of character strings listing the name(s) of the aesthetic(s) that this scale works with. This can be useful, for example, to apply colour settings to the colour and fill aesthetics at the same time, via aesthetics = c("colour", "fill").
mid  colour for mid point
midpoint  The midpoint (in data value) of the diverging scale. Defaults to 0.
transform  For continuous scales, the name of a transformation object or the object itself. Built-in transformations include "asn", "atanh", "boxcox", "date", "exp", "hms", "identity", "log", "log10", "log1p", "log2", "logit", "modulo", "probability", "probit", "pseudo_log", "reciprocal", "reverse", "sqrt" and "time". A transformation object bundles together a transform, its inverse, and methods for generating breaks and labels. Transformation objects are defined in the scales package, and are called transform_<name>. If transformations require arguments, you can call them from the scales package, e.g. scales::transform_boxcox(p = 2). You can create your own transformation with scales::new_transform().
colours, colors  Vector of colours to use for n-colour gradient.
values  if colours should not be evenly positioned along the gradient this vector gives the position (between 0 and 1) for each colour in the colours vector. See rescale() for a convenience function to map an arbitrary range to between 0 and 1.

details
Default colours are generated with munsell and mns1(c("2.5PB 2/4", "2.5PB 7/10"). Generally, for continuous colour scales you want to keep hue constant, but vary chroma and luminance. The munsell package makes this easy to do using the Munsell colour system.

see also
scales::pal_seq_gradient() for details on underlying palette, scale_colour_steps() for binned variants of these scales.
The documentation on colour aesthetics.

other colour scales: scale_alpha(), scale_colour_brewer(), scale_colour_continuous(), scale_colour_grey(), scale_colour_hue(), scale_colour_identity(), scale_colour_manual(), scale_colour_steps(), scale_colour_viridis_d()

elements
set.seed(1)
df <- data.frame(
  x = runif(100),
  y = runif(100),
  z1 = rnorm(100),
  z2 = abs(rnorm(100))
)

df_na <- data.frame(
  value = seq(1, 20),
  x = runif(20),
  y = runif(20),
  z1 = c(rep(NA, 10), rnorm(10)))
# Default colour scale colours from light blue to dark blue
```r
ggplot(df, aes(x, y)) +
  geom_point(aes(colour = z2))
```

# For diverging colour scales use gradient2
```r
ggplot(df, aes(x, y)) +
  geom_point(aes(colour = z1)) +
  scale_colour_gradient2()
```

# Use your own colour scale with gradientn
```r
ggplot(df, aes(x, y)) +
  geom_point(aes(colour = z1)) +
  scale_colour_gradientn(colours = terrain.colors(10))
```

# Equivalent fill scales do the same job for the fill aesthetic
```r
ggplot(faithfuld, aes(waiting, eruptions)) +
  geom_raster(aes(fill = density)) +
  scale_fill_gradientn(colours = terrain.colors(10))
```

# Adjust colour choices with low and high
```r
ggplot(df, aes(x, y)) +
  geom_point(aes(colour = z2)) +
  scale_colour_gradient(low = "white", high = "black")
```

# Avoid red-green colour contrasts because ~10% of men have difficulty seeing them

# Use `na.value = NA` to hide missing values but keep the original axis range
```r
ggplot(df_na, aes(x = value, y)) +
  geom_bar(aes(fill = z1), stat = "identity") +
  scale_fill_gradient(low = "yellow", high = "red", na.value = NA)
```

```r
ggplot(df_na, aes(x, y)) +
  geom_point(aes(colour = z1)) +
  scale_colour_gradient(low = "yellow", high = "red", na.value = NA)
```

---

### scale_colour_grey

**Sequential grey colour scales**

#### Description

Based on `gray.colors()`. This is black and white equivalent of `scale_colour_gradient()`.  

#### Usage

```r
scale_colour_grey(
  name = waiver(),
  ...,  
)```
scale_colour_grey

    start = 0.2,
    end = 0.8,
    na.value = "red",
    aesthetics = "colour"

)

scale_fill_grey(
    name = waiver(),
    ...,
    start = 0.2,
    end = 0.8,
    na.value = "red",
    aesthetics = "fill"

)

Arguments

name

The name of the scale. Used as the axis or legend title. If waiver(), the default, the name of the scale is taken from the first mapping used for that aesthetic. If NULL, the legend title will be omitted.

... Arguments passed on to discrete_scale

palette A palette function that when called with a single integer argument (the number of levels in the scale) returns the values that they should take (e.g., scales::pal_hue()).

breaks One of:
  - NULL for no breaks
  - waiver() for the default breaks (the scale limits)
  - A character vector of breaks
  - A function that takes the limits as input and returns breaks as output. Also accepts rlang lambda function notation.

limits One of:
  - NULL to use the default scale values
  - A character vector that defines possible values of the scale and their order
  - A function that accepts the existing (automatic) values and returns new ones. Also accepts rlang lambda function notation.

don Should unused factor levels be omitted from the scale? The default, TRUE, uses the levels that appear in the data; FALSE uses all the levels in the factor.

na_translate Unlike continuous scales, discrete scales can easily show missing values, and do so by default. If you want to remove missing values from a discrete scale, specify na.translate = FALSE.

scale_name [Deprecated] The name of the scale that should be used for error messages associated with this scale.

labels One of:
  - NULL for no labels
  - waiver() for the default labels computed by the transformation object
- A character vector giving labels (must be same length as breaks)
- An expression vector (must be the same length as breaks). See \texttt{?plotmath} for details.
- A function that takes the breaks as input and returns labels as output. Also accepts \texttt{rlang \texttt{lambda}} function notation.

guide  A function used to create a guide or its name. See \texttt{guides()} for more information.

expand  For position scales, a vector of range expansion constants used to add some padding around the data to ensure that they are placed some distance away from the axes. Use the convenience function \texttt{expansion()} to generate the values for the expand argument. The defaults are to expand the scale by 5\% on each side for continuous variables, and by 0.6 units on each side for discrete variables.

position  For position scales, The position of the axis. \texttt{left} or \texttt{right} for \texttt{y} axes, \texttt{top} or \texttt{bottom} for \texttt{x} axes.

call  The call used to construct the scale for reporting messages.

super  The super class to use for the constructed scale

start  grey value at low end of palette

end  grey value at high end of palette

na.value  Colour to use for missing values

aesthetics  Character string or vector of character strings listing the name(s) of the aesthetic(s) that this scale works with. This can be useful, for example, to apply colour settings to the \texttt{colour} and \texttt{fill} aesthetics at the same time, via aesthetics = c(“colour”, “fill”).

\textbf{See Also}

The documentation on \texttt{colour aesthetics}.

Other colour scales: \texttt{scale_alpha()}, \texttt{scale_colour_brewer()}, \texttt{scale_colour_continuous()}, \texttt{scale_colour_gradient()}, \texttt{scale_colour_hue()}, \texttt{scale_colour_identity()}, \texttt{scale_colour_manual()}, \texttt{scale_colour_steps()}, \texttt{scale_colour_viridis_d()}

\textbf{Examples}

p <- \texttt{ggplot(mtcars, aes(mpg, wt)) + geom_point(aes(colour = factor(cyl)))}
p + \texttt{scale_colour_grey()}
p + \texttt{scale_colour_grey(end = 0)}

# You may want to turn off the pale grey background with this scale
p + \texttt{scale_colour_grey() + theme_bw()}

# Colour of missing values is controlled with \texttt{na.value}:
\texttt{miss <- factor(sample(c(NA, 1:5), nrow(mtcars), replace = TRUE))}
\texttt{ggplot(mtcars, aes(mpg, wt)) + geom_point(aes(colour = miss)) +}
\texttt{scale_colour_grey()}
\texttt{ggplot(mtcars, aes(mpg, wt)) +}
scale_colour_hue

\[
\text{geom_point(aes(colour = miss)) + scale_colour_grey(na.value = "green")}
\]

<table>
<thead>
<tr>
<th>scale_colour_hue</th>
<th>Evenly spaced colours for discrete data</th>
</tr>
</thead>
</table>

**Description**

Maps each level to an evenly spaced hue on the colour wheel. It does not generate colour-blind safe palettes.

**Usage**

```r
scale_colour_hue(
  name = waiver(),
  ..., 
  h = c(0, 360) + 15,
  c = 100,
  l = 65,
  h.start = 0,
  direction = 1,
  na.value = "grey50",
  aesthetics = "colour"
)

scale_fill_hue(
  name = waiver(),
  ..., 
  h = c(0, 360) + 15,
  c = 100,
  l = 65,
  h.start = 0,
  direction = 1,
  na.value = "grey50",
  aesthetics = "fill"
)
```

**Arguments**

- **name**
  The name of the scale. Used as the axis or legend title. If `waiver()`, the default, the name of the scale is taken from the first mapping used for that aesthetic. If `NULL`, the legend title will be omitted.
- **...**
  Arguments passed on to `discrete_scale`
- **palette**
  A palette function that when called with a single integer argument (the number of levels in the scale) returns the values that they should take (e.g., `scales::pal_hue()`).
- **breaks**
  One of:
• NULL for no breaks
• waiver() for the default breaks (the scale limits)
• A character vector of breaks
• A function that takes the limits as input and returns breaks as output.
  Also accepts rlang lambda function notation.

limits One of:
• NULL to use the default scale values
• A character vector that defines possible values of the scale and their order
• A function that accepts the existing (automatic) values and returns new ones. Also accepts rlang lambda function notation.

drop Should unused factor levels be omitted from the scale? The default, TRUE, uses the levels that appear in the data; FALSE uses all the levels in the factor.

na.translate Unlike continuous scales, discrete scales can easily show missing values, and do so by default. If you want to remove missing values from a discrete scale, specify na.translate = FALSE.

scale_name [Deprecated] The name of the scale that should be used for error messages associated with this scale.

labels One of:
• NULL for no labels
• waiver() for the default labels computed by the transformation object
• A character vector giving labels (must be same length as breaks)
• An expression vector (must be the same length as breaks). See ?plotmath for details.
• A function that takes the breaks as input and returns labels as output.
  Also accepts rlang lambda function notation.

guide A function used to create a guide or its name. See guides() for more information.

expand For position scales, a vector of range expansion constants used to add some padding around the data to ensure that they are placed some distance away from the axes. Use the convenience function expansion() to generate the values for the expand argument. The defaults are to expand the scale by 5% on each side for continuous variables, and by 0.6 units on each side for discrete variables.

position For position scales, The position of the axis. left or right for y axes, top or bottom for x axes.

call The call used to construct the scale for reporting messages.
super The super class to use for the constructed scale

h range of hues to use, in [0, 360]
c chroma (intensity of colour), maximum value varies depending on combination of hue and luminance.
l luminance (lightness), in [0, 100]
h.start hue to start at
direction direction to travel around the colour wheel, 1 = clockwise, -1 = counter-clockwise
na.value  Colour to use for missing values
aesthetics Character string or vector of character strings listing the name(s) of the aesthetic(s) that this scale works with. This can be useful, for example, to apply colour settings to the colour and fill aesthetics at the same time, via aesthetics = c("colour", "fill").

See Also

The documentation on colour aesthetics.

Other colour scales: scale_alpha(), scale_colour_brewer(), scale_colour_continuous(), scale_colour_gradient(), scale_colour_grey(), scale_colour_identity(), scale_colour_manual(), scale_colour_steps(), scale_colour_viridis_d()

Examples

set.seed(596)
dsamp <- diamonds[sample(nrow(diamonds), 1000), ]
(d <- ggplot(dsamp, aes(carat, price)) + geom_point(aes(colour = clarity)))

# Change scale label
d + scale_colour_hue()
d + scale_colour_hue("clarity")
d + scale_colour_hue(expression(clarity[beta]))

# Adjust luminosity and chroma
d + scale_colour_hue(l = 40, c = 30)
d + scale_colour_hue(l = 70, c = 30)
d + scale_colour_hue(l = 70, c = 150)
d + scale_colour_hue(l = 80, c = 150)

# Change range of hues used
d + scale_colour_hue(h = c(0, 90))
d + scale_colour_hue(h = c(90, 180))
d + scale_colour_hue(h = c(180, 270))
d + scale_colour_hue(h = c(270, 360))

# Vary opacity
# (only works with pdf, quartz and cairo devices)
d <- ggplot(dsamap, aes(carat, price, colour = clarity))
d + geom_point(alpha = 0.9)
d + geom_point(alpha = 0.5)
d + geom_point(alpha = 0.2)

# Colour of missing values is controlled with na.value:
miss <- factor(sample(c(NA, 1:5), nrow(mtcars), replace = TRUE))
ggplot(mtcars, aes(mpg, wt)) +
  geom_point(aes(colour = miss))
ggplot(mtcars, aes(mpg, wt)) +
  geom_point(aes(colour = miss)) +
  scale_colour_hue(na.value = "black")
scale_colour_steps  Binned gradient colour scales

Description

scale_*_steps creates a two colour binned gradient (low-high), scale_*_steps2 creates a diverging binned colour gradient (low-mid-high), and scale_*_stepsn creates a n-colour binned gradient. These scales are binned variants of the gradient scale family and works in the same way.

Usage

scale_colour_steps(
  name = waiver(),
...
  low = "#132B43",
  high = "#56B1F7",
  space = "Lab",
  na.value = "grey50",
  guide = "coloursteps",
  aesthetics = "colour"
)

scale_colour_steps2(
  name = waiver(),
...
  low = muted("red"),
  mid = "white",
  high = muted("blue"),
  midpoint = 0,
  space = "Lab",
  na.value = "grey50",
  transform = "identity",
  guide = "coloursteps",
  aesthetics = "colour"
)

scale_colour_stepsn(
  name = waiver(),
...
  colours,
  values = NULL,
  space = "Lab",
  na.value = "grey50",
  guide = "coloursteps",
  aesthetics = "colour",
  colors
)
scale_fill_steps(
  name = waiver(),
  ..., 
  low = "#132B43",
  high = "#56B1F7",
  space = "Lab",
  na.value = "grey50",
  guide = "coloursteps",
  aesthetics = "fill"
)

color_steps2(
  name = waiver(),
  ..., 
  low = muted("red"),
  mid = "white",
  high = muted("blue"),
  midpoint = 0,
  space = "Lab",
  na.value = "grey50",
  transform = "identity",
  guide = "coloursteps",
  aesthetics = "fill"
)

color_stepsn(
  name = waiver(),
  ..., 
  colours,
  values = NULL,
  space = "Lab",
  na.value = "grey50",
  guide = "coloursteps",
  aesthetics = "fill",
  colors
)

Arguments

name The name of the scale. Used as the axis or legend title. If waiver(), the default, 
the name of the scale is taken from the first mapping used for that aesthetic. If 
NULL, the legend title will be omitted.

... Arguments passed on to binned_scale

n.breaks The number of break points to create if breaks are not given directly.
nice.breaks Logical. Should breaks be attempted placed at nice values instead of exactly evenly spaced between the limits. If TRUE (default) the scale will ask the transformation object to create breaks, and this may re-
sult in a different number of breaks than requested. Ignored if breaks are
given explicitly.

right Should the intervals be closed on the right (TRUE, default) or should the
intervals be closed on the left (FALSE)? 'Closed on the right' means that
values at break positions are part of the lower bin (open on the left), whereas
they are part of the upper bin when intervals are closed on the left (open on
the right).

show.limits should the limits of the scale appear as ticks

breaks One of:
  • NULL for no breaks
  • waiver() for the default breaks computed by the transformation object
  • A numeric vector of positions
  • A function that takes the limits as input and returns breaks as output
    (e.g., a function returned by scales::extended_breaks()). Also ac-
    cepts rlang lambda function notation.

labels One of:
  • NULL for no labels
  • waiver() for the default labels computed by the transformation object
  • A character vector giving labels (must be same length as breaks)
  • An expression vector (must be the same length as breaks). See ?plot-
    math for details.
  • A function that takes the breaks as input and returns labels as output.
    Also accepts rlang lambda function notation.

limits One of:
  • NULL to use the default scale range
  • A numeric vector of length two providing limits of the scale. Use NA to
    refer to the existing minimum or maximum
  • A function that accepts the existing (automatic) limits and returns new
    limits. Also accepts rlang lambda function notation. Note that setting
    limits on positional scales will remove data outside of the limits. If
    the purpose is to zoom, use the limit argument in the coordinate system
    (see coord_cartesian()).

oob One of:
  • Function that handles limits outside of the scale limits (out of bounds).
    Also accepts rlang lambda function notation.
  • The default (scales::censor()) replaces out of bounds values with
    NA.
  • scales::squish() for squishing out of bounds values into range.
  • scales::squish_infinite() for squishing infinite values into range.

trans [Deprecated] Deprecated in favour of transform.

expand For position scales, a vector of range expansion constants used to add
some padding around the data to ensure that they are placed some distance
away from the axes. Use the convenience function expansion() to gen-
erate the values for the expand argument. The defaults are to expand the
scale by 5% on each side for continuous variables, and by 0.6 units on each
side for discrete variables.
position For position scales, the position of the axis. left or right for y axes, top or bottom for x axes.
call The call used to construct the scale for reporting messages.
super The super class to use for the constructed scale
low, high Colours for low and high ends of the gradient.
space colour space in which to calculate gradient. Must be "Lab" - other values are deprecated.
na.value Colour to use for missing values
guide Type of legend. Use "colourbar" for continuous colour bar, or "legend" for discrete colour legend.
aesthetics Character string or vector of character strings listing the name(s) of the aesthetic(s) that this scale works with. This can be useful, for example, to apply colour settings to the colour and fill aesthetics at the same time, via aesthetics = c("colour", "fill").
mid colour for mid point
midpoint The midpoint (in data value) of the diverging scale. Defaults to 0.
transform For continuous scales, the name of a transformation object or the object itself. Built-in transformations include "asn", "atanh", "boxcox", "date", "exp", "hms", "identity", "log", "log10", "log1p", "log2", "logit", "modulus", "probability", "probit", "pseudo_log", "reciprocal", "reverse", "sqrt" and "time".
A transformation object bundles together a transform, its inverse, and methods for generating breaks and labels. Transformation objects are defined in the scales package, and are called transform_<name>. If transformations require arguments, you can call them from the scales package, e.g. scales::transform_boxcox(p = 2). You can create your own transformation with scales::new_transform().
colours, colors Vector of colours to use for n-colour gradient.
values if colours should not be evenly positioned along the gradient this vector gives the position (between 0 and 1) for each colour in the colours vector. See rescale() for a convenience function to map an arbitrary range to between 0 and 1.

details Default colours are generated with munsell and mns1(c("2.5PB 2/4", "2.5PB 7/10"). Generally, for continuous colour scales you want to keep hue constant, but vary chroma and luminance. The munsell package makes this easy to do using the Munsell colour system.

see also
scales::pal_seq_gradient() for details on underlying palette, scale_colour_gradient() for continuous scales without binning.
The documentation on colour aesthetics.
Other colour scales: scale_alpha(), scale_colour_brewer(), scale_colour_continuous(), scale_colour_gradient(), scale_colour_hue(), scale_colour_identity(), scale_colour_manual(), scale_colour_viridis_d()
scale_colour_viridis_d

Viridis colour scales from viridisLite

Description

The viridis scales provide colour maps that are perceptually uniform in both colour and black-and-white. They are also designed to be perceived by viewers with common forms of colour blindness. See also https://bids.github.io/colormap/.

Usage

```r
scale_colour_viridis_d(
  name = waiver(),
  ...,  
  alpha = 1,
  begin = 0,
  end = 1,
  direction = 1,
  option = "D",
  aesthetics = "colour"
)

scale_fill_viridis_d(
  name = waiver(),
```

Examples

```r
set.seed(1)
df <- data.frame(
  x = runif(100),
  y = runif(100),
  z1 = rnorm(100)
)

# Use scale_colour_steps for a standard binned gradient
ggplot(df, aes(x, y)) +
  geom_point(aes(colour = z1)) +
  scale_colour_steps()

# Get a divergent binned scale with the *2 variant
ggplot(df, aes(x, y)) +
  geom_point(aes(colour = z1)) +
  scale_colour_steps2()

# Define your own colour ramp to extract binned colours from
ggplot(df, aes(x, y)) +
  geom_point(aes(colour = z1)) +
  scale_colour_stepsn(colours = terrain.colors(10))
```
scale_colour_viridis_d

..., 
alpha = 1, 
begin = 0, 
end = 1, 
direction = 1, 
option = "D", 
aesthetics = "fill"
}

scale_colour_viridis_c( 
    name = waiver(), 
    ..., 
alpha = 1, 
begin = 0, 
end = 1, 
direction = 1, 
option = "D", 
values = NULL, 
space = "Lab", 
na.value = "grey50", 
guide = "colourbar", 
aesthetics = "colour"
)

scale_fill_viridis_c( 
    name = waiver(), 
    ..., 
alpha = 1, 
begin = 0, 
end = 1, 
direction = 1, 
option = "D", 
values = NULL, 
space = "Lab", 
na.value = "grey50", 
guide = "colourbar", 
aesthetics = "fill"
)

scale_colour_viridis_b( 
    name = waiver(), 
    ..., 
alpha = 1, 
begin = 0, 
end = 1, 
direction = 1, 
option = "D", 
values = NULL,
scale_colour_viridis_d

```r
space = "Lab",
na.value = "grey50",
guide = "coloursteps",
aesthetics = "colour"
)

scale_fill_viridis_b(
  name = waiver(),
  ...,
  alpha = 1,
  begin = 0,
  end = 1,
  direction = 1,
  option = "D",
  values = NULL,
  space = "Lab",
  na.value = "grey50",
  guide = "coloursteps",
  aesthetics = "fill"
)
```

Arguments

name  The name of the scale. Used as the axis or legend title. If `waiver()`, the default, the name of the scale is taken from the first mapping used for that aesthetic. If `NULL`, the legend title will be omitted.

...  Other arguments passed on to `discrete_scale()`, `continuous_scale()`, or `binned_scale()` to control name, limits, breaks, labels and so forth.

alpha  The alpha transparency, a number in [0,1], see argument alpha in `hsv`.

begin, end  The (corrected) hue in [0,1] at which the color map begins and ends.

direction  Sets the order of colors in the scale. If 1, the default, colors are ordered from darkest to lightest. If -1, the order of colors is reversed.

option  A character string indicating the color map option to use. Eight options are available:

- "magma" (or "A")
- "inferno" (or "B")
- "plasma" (or "C")
- "viridis" (or "D")
- "cividis" (or "E")
- "rocket" (or "F")
- "mako" (or "G")
- "turbo" (or "H")

aesthetics  Character string or vector of character strings listing the name(s) of the aesthetic(s) that this scale works with. This can be useful, for example, to apply colour settings to the colour and fill aesthetics at the same time, via `aesthetics = c("colour", "fill")`. 
values

if colours should not be evenly positioned along the gradient this vector gives
the position (between 0 and 1) for each colour in the colours vector. See
rescale() for a convenience function to map an arbitrary range to between
0 and 1.

space
colour space in which to calculate gradient. Must be "Lab" - other values are
deprecated.

na.value
Missing values will be replaced with this value.

guide
A function used to create a guide or its name. See guides() for more informa-
tion.

See Also

The documentation on colour aesthetics.

Other colour scales: scale_alpha(), scale colour_brewer(), scale colour_continuous(),
scale colour gradient(), scale colour grey(), scale colour hue(), scale colour identity(),
scale colour manual(), scale colour steps()

Examples

# viridis is the default colour/fill scale for ordered factors
set.seed(596)
dsamp &lt;- diamonds[sample(nrow(diamonds), 1000), ]
ggplot(dsamp, aes(carat, price)) +
  geom_point(aes(colour = clarity))

# Use viridis_d with discrete data
txsamp &lt;- subset(txhousing, city %in%
  c("Houston", "Fort Worth", "San Antonio", "Dallas", "Austin"))
(d &lt;- ggplot(data = txsamp, aes(x = sales, y = median)) +
  geom.point(aes(colour = city)))
d + scale colour_viridis_d()

# Change scale label
d + scale colour_viridis_d("City\nCenter")

# Select palette to use, see ?scales::pal_viridis for more details
d + scale colour_viridis_d(option = "plasma")
d + scale colour_viridis_d(option = "inferno")

# scale fill_viridis_d works just the same as
# scale colour_viridis_d but for fill colours
p &lt;- ggplot(txsamp, aes(x = median, fill = city)) +
  geom_histogram(position = "dodge", binwidth = 15000)
p + scale fill_viridis_d()
# the order of colour can be reversed
p + scale fill_viridis_d(direction = -1)

# Use viridis_c with continuous data
(v &lt;- ggplot(faithfuld) +
  geom_tile(aes(waiting, eruptions, fill = density)))
v + scale_fill_viridis_c()

v + scale_fill_viridis_c(option = "plasma")

# Use viridis_b to bin continuous data before mapping
v + scale_fill_viridis_b()

---

**scale_continuous**  
*Position scales for continuous data (x & y)*

**Description**

`scale_x_continuous()` and `scale_y_continuous()` are the default scales for continuous x and y aesthetics. There are three variants that set the `transform` argument for commonly used transformations: `scale_*_log10()`, `scale_*_sqrt()` and `scale_*_reverse()`.

**Usage**

```r
scale_x_continuous(
  name = waiver(),
  breaks = waiver(),
  minor_breaks = waiver(),
  n.breaks = NULL,
  labels = waiver(),
  limits = NULL,
  expand = waiver(),
  oob = censor,
  na.value = NA_real_,
  transform = "identity",
  trans = deprecated(),
  guide = waiver(),
  position = "bottom",
  sec.axis = waiver()
)

scale_y_continuous(
  name = waiver(),
  breaks = waiver(),
  minor_breaks = waiver(),
  n.breaks = NULL,
  labels = waiver(),
  limits = NULL,
  expand = waiver(),
  oob = censor,
  na.value = NA_real_,
  transform = "identity",
  trans = deprecated(),
```
scale_continuous

```
guide = waiver(),
position = "left",
sec.axis = waiver()
)
scale_x_log10(...)
scale_y_log10(...)
scale_x_reverse(...)
scale_y_reverse(...)
scale_x_sqrt(...)
scale_y_sqrt(...)
```

**Arguments**

- **name**
  - The name of the scale. Used as the axis or legend title. If `waiver()`, the default, the name of the scale is taken from the first mapping used for that aesthetic. If `NULL`, the legend title will be omitted.

- **breaks**
  - One of:
    - `NULL` for no breaks
    - `waiver()` for the default breaks computed by the transformation object
    - A numeric vector of positions
    - A function that takes the limits as input and returns breaks as output (e.g., a function returned by `scales::extended_breaks()`). Also accepts rlang lambda function notation.

- **minor_breaks**
  - One of:
    - `NULL` for no minor breaks
    - `waiver()` for the default breaks (one minor break between each major break)
    - A numeric vector of positions
    - A function that given the limits returns a vector of minor breaks. Also accepts rlang lambda function notation. When the function has two arguments, it will be given the limits and major breaks.

- **n.breaks**
  - An integer guiding the number of major breaks. The algorithm may choose a slightly different number to ensure nice break labels. Will only have an effect if `breaks = waiver()`. Use `NULL` to use the default number of breaks given by the transformation.

- **labels**
  - One of:
    - `NULL` for no labels
    - `waiver()` for the default labels computed by the transformation object
    - A character vector giving labels (must be same length as breaks)
• An expression vector (must be the same length as breaks). See ?plotmath for details.
• A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

limits

One of:
• NULL to use the default scale range
• A numeric vector of length two providing limits of the scale. Use NA to refer to the existing minimum or maximum
• A function that accepts the existing (automatic) limits and returns new limits. Also accepts rlang lambda function notation. Note that setting limits on positional scales will remove data outside of the limits. If the purpose is to zoom, use the limit argument in the coordinate system (see coord_cartesian()).

expand

For position scales, a vector of range expansion constants used to add some padding around the data to ensure that they are placed some distance away from the axes. Use the convenience function expansion() to generate the values for the expand argument. The defaults are to expand the scale by 5% on each side for continuous variables, and by 0.6 units on each side for discrete variables.

oob

One of:
• Function that handles limits outside of the scale limits (out of bounds). Also accepts rlang lambda function notation.
• The default (scales::censor()) replaces out of bounds values with NA.
• scales::squish() for squishing out of bounds values into range.
• scales::squish_infinite() for squishing infinite values into range.

na.value

Missing values will be replaced with this value.

transform

For continuous scales, the name of a transformation object or the object itself. Built-in transformations include "asn", "atanh", "boxcox", "date", "exp", "hms", "identity", "log", "log10", "log1p", "log2", "logit", "modulus", "probability", "probit", "pseudo_log", "reciprocal", "reverse", "sqrt" and "time".

A transformation object bundles together a transform, its inverse, and methods for generating breaks and labels. Transformation objects are defined in the scales package, and are called transform_<name>. If transformations require arguments, you can call them from the scales package, e.g. scales::transform_boxcox(p = 2). You can create your own transformation with scales::new_transform().

trans [Deprecated] Deprecatecd in favour of transform.

guide

A function used to create a guide or its name. See guides() for more information.

position

For position scales, The position of the axis. left or right for y axes, top or bottom for x axes.

sec.axis

sec_axis() is used to specify a secondary axis.

... Other arguments passed on to scale_(x|y)_continuous()

Details

For simple manipulation of labels and limits, you may wish to use labs() and lims() instead.
scale_continuous

See Also

The position documentation.

Other position scales: scale_x_binned(), scale_x_date(), scale_x_discrete()

Examples

```r
p1 <- ggplot(mpg, aes(displ, hwy)) + geom_point()
p1

# Manipulating the default position scales lets you:
# * change the axis labels
p1 +
  scale_x_continuous("Engine displacement (L)") +
  scale_y_continuous("Highway MPG")

# You can also use the short-cut labs().
# Use NULL to suppress axis labels
p1 + labs(x = NULL, y = NULL)

# * modify the axis limits
p1 + scale_x_continuous(limits = c(2, 6))
p1 + scale_x_continuous(limits = c(0, 10))

# you can also use the short hand functions `xlim()` and `ylim()`
p1 + xlim(2, 6)

# * choose where the ticks appear
p1 + scale_x_continuous(breaks = c(2, 4, 6))

# * choose your own labels
p1 + scale_x_continuous(
  breaks = c(2, 4, 6),
  label = c("two", "four", "six")
)

# Typically you'll pass a function to the `labels` argument.
# Some common formats are built into the scales package:
set.seed(1)
df <- data.frame(
  x = rnorm(10) * 100000,
  y = seq(0, 1, length.out = 10)
)
p2 <- ggplot(df, aes(x, y)) + geom_point()
p2 + scale_y_continuous(labels = scales::label_percent())
p2 + scale_y_continuous(labels = scales::label_dollar())
p2 + scale_x_continuous(labels = scales::label_comma())

# You can also override the default linear mapping by using a
# transformation. There are three shortcuts:
p1 + scale_y_log10()
p1 + scale_y_sqrt()
```
p1 + scale_y_reverse()

# Or you can supply a transformation in the 'trans' argument:
p1 + scale_y_continuous(transform = scales::transform_reciprocal())

# You can also create your own. See ?scales::new_transform

---

**scale_date**

*Position scales for date/time data*

**Description**

These are the default scales for the three date/time class. These will usually be added automatically. To override manually, use `scale_*_date` for dates (class `Date`), `scale_*_datetime` for datetimes (class `POSIXct`), and `scale_*_time` for times (class `hms`).

**Usage**

```r
scale_x_date(
  name = waiver(),
  breaks = waiver(),
  date_breaks = waiver(),
  labels = waiver(),
  date_labels = waiver(),
  minor_breaks = waiver(),
  date_minor_breaks = waiver(),
  limits = NULL,
  expand = waiver(),
  oob = censor,
  guide = waiver(),
  position = "bottom",
  sec.axis = waiver()
)
```

```r
scale_y_date(
  name = waiver(),
  breaks = waiver(),
  date_breaks = waiver(),
  labels = waiver(),
  date_labels = waiver(),
  minor_breaks = waiver(),
  date_minor_breaks = waiver(),
  limits = NULL,
  expand = waiver(),
  oob = censor,
  guide = waiver(),
```
scale_date

    position = "left",
    sec.axis = waiver()
)

scale_x_datetime(
    name = waiver(),
    breaks = waiver(),
    date_breaks = waiver(),
    labels = waiver(),
    date_labels = waiver(),
    minor_breaks = waiver(),
    date_minor_breaks = waiver(),
    timezone = NULL,
    limits = NULL,
    expand = waiver(),
    oob = censor,
    guide = waiver(),
    position = "bottom",
    sec.axis = waiver()
)

scale_y_datetime(
    name = waiver(),
    breaks = waiver(),
    date_breaks = waiver(),
    labels = waiver(),
    date_labels = waiver(),
    minor_breaks = waiver(),
    date_minor_breaks = waiver(),
    timezone = NULL,
    limits = NULL,
    expand = waiver(),
    oob = censor,
    guide = waiver(),
    position = "left",
    sec.axis = waiver()
)

scale_x_time(
    name = waiver(),
    breaks = waiver(),
    minor_breaks = waiver(),
    labels = waiver(),
    limits = NULL,
    expand = waiver(),
    oob = censor,
    na.value = NA_real_,
    guide = waiver(),
    position = "left",
    sec.axis = waiver()
position = "bottom",
sec.axis = waiver()
)

scale_y_time(
  name = waiver(),
  breaks = waiver(),
  minor_breaks = waiver(),
  labels = waiver(),
  limits = NULL,
  expand = waiver(),
  oob = censor,
  na.value = NA_real_,
  guide = waiver(),
  position = "left",
  sec.axis = waiver()
)

Arguments

name

The name of the scale. Used as the axis or legend title. If waiver(), the default, the name of the scale is taken from the first mapping used for that aesthetic. If NULL, the legend title will be omitted.

breaks

One of:

- NULL for no breaks
- waiver() for the breaks specified by date_breaks
- A Date/POSIXct vector giving positions of breaks
- A function that takes the limits as input and returns breaks as output

date_breaks

A string giving the distance between breaks like "2 weeks", or "10 years". If both breaks and date_breaks are specified, date_breaks wins. Valid specifications are 'sec', 'min', 'hour', 'day', 'week', 'month' or 'year', optionally followed by 's'.

labels

One of:

- NULL for no labels
- waiver() for the default labels computed by the transformation object
- A character vector giving labels (must be same length as breaks)
- An expression vector (must be the same length as breaks). See ?plotmath for details.
- A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

date_labels

A string giving the formatting specification for the labels. Codes are defined instrftime(). If both labels and date_labels are specified, date_labels wins.

minor_breaks

One of:

- NULL for no breaks
• waiver() for the breaks specified by date_minor_breaks
• A Date.POSIXct vector giving positions of minor breaks
• A function that takes the limits as input and returns minor breaks as output

date_minor_breaks
A string giving the distance between minor breaks like "2 weeks", or "10 years". If both minor_breaks and date_minor_breaks are specified, date_minor_breaks wins. Valid specifications are 'sec', 'min', 'hour', 'day', 'week', 'month' or 'year', optionally followed by 's'.

limits
One of:
• NULL to use the default scale range
• A numeric vector of length two providing limits of the scale. Use NA to refer to the existing minimum or maximum
• A function that accepts the existing (automatic) limits and returns new limits. Also accepts rlang lambda function notation. Note that setting limits on positional scales will remove data outside of the limits. If the purpose is to zoom, use the limit argument in the coordinate system (see coord_cartesian()).

expand
For position scales, a vector of range expansion constants used to add some padding around the data to ensure that they are placed some distance away from the axes. Use the convenience function expansion() to generate the values for the expand argument. The defaults are to expand the scale by 5% on each side for continuous variables, and by 0.6 units on each side for discrete variables.

oob
One of:
• Function that handles limits outside of the scale limits (out of bounds). Also accepts rlang lambda function notation.
• The default (scales::censor()) replaces out of bounds values with NA.
• scales::squish() for squishing out of bounds values into range.
• scales::squish_infinite() for squishing infinite values into range.

guide
A function used to create a guide or its name. See guides() for more information.

position
For position scales, The position of the axis. left or right for y axes, top or bottom for x axes.

sec.axis
sec.axis() is used to specify a secondary axis.

timezone
The timezone to use for display on the axes. The default (NULL) uses the timezone encoded in the data.

na.value
Missing values will be replaced with this value.

See Also
sec_axis() for how to specify secondary axes
The position documentation.
Other position scales: scale_x_binned(), scale_x_continuous(), scale_x_discrete()
Examples

```r
last_month <- Sys.Date() - 0:29
set.seed(1)
df <- data.frame(
  date = last_month,
  price = runif(30)
)
base <- ggplot(df, aes(date, price)) +
  geom_line()
#
# The date scale will attempt to pick sensible defaults for
# major and minor tick marks. Override with date_breaks, date_labels
# date_minor_breaks arguments.
  base + scale_x_date(date_labels = "%b %d")
  base + scale_x_date(date_breaks = "1 week", date_labels = "%W")
  base + scale_x_date(date_minor_breaks = "1 day")
#
# Set limits
  base + scale_x_date(limits = c(Sys.Date() - 7, NA))
```

---

**scale_identity**

*Use values without scaling*

**Description**

Use this set of scales when your data has already been scaled, i.e. it already represents aesthetic values that ggplot2 can handle directly. These scales will not produce a legend unless you also supply the breaks, labels, and type of guide you want.

**Usage**

```r
scale_colour_identity(name = waiver(),
  ...,
  guide = "none",
  aesthetics = "colour"
)
scale_fill_identity(name = waiver(), ..., guide = "none", aesthetics = "fill")
scale_shape_identity(name = waiver(), ..., guide = "none")
scale_linetype_identity(name = waiver(), ..., guide = "none")
scale_linewidth_identity(name = waiver(), ..., guide = "none")
scale_alpha_identity(name = waiver(), ..., guide = "none")
```
scale_identity(name = waiver(), ..., guide = "none")

scale_discrete_identity(aesthetics, name = waiver(), ..., guide = "none")

scale_continuous_identity(aesthetics, name = waiver(), ..., guide = "none")

Arguments

name
The name of the scale. Used as the axis or legend title. If waiver(), the default, the name of the scale is taken from the first mapping used for that aesthetic. If NULL, the legend title will be omitted.

... 
Other arguments passed on to discrete_scale() or continuous_scale()

guide
Guide to use for this scale. Defaults to "none".

aesthetics
Character string or vector of character strings listing the name(s) of the aesthetic(s) that this scale works with. This can be useful, for example, to apply colour settings to the colour and fill aesthetics at the same time, via aesthetics = c("colour", "fill").

Details

The functions scale_colour_identity(), scale_fill_identity(), scale_size_identity(), etc. work on the aesthetics specified in the scale name: colour, fill, size, etc. However, the functions scale_colour_identity() and scale_fill_identity() also have an optional aesthetics argument that can be used to define both colour and fill aesthetic mappings via a single function call. The functions scale_discrete_identity() and scale_continuous_identity() are generic scales that can work with any aesthetic or set of aesthetics provided via the aesthetics argument.

See Also

Other shape scales: scale_shape(), scale_shape_manual().
Other linetype scales: scale_linetype(), scale_linetype_manual().
Other alpha scales: scale_alpha(), scale_alpha_manual().
Other size scales: scale_size(), scale_size_manual().
Other colour scales: scale_alpha(), scale_colour_brewer(), scale_colour_continuous(), scale_colour_gradient(), scale_colour_hue(), scale_colour_manual(), scale_colour_steps(), scale_colour_viridis_d()
y = 1:4,
colour = c("red", "green", "blue", "yellow")
)
ggplot(df, aes(x, y)) + geom_tile(aes(fill = colour))
ggplot(df, aes(x, y)) +
  geom_tile(aes(fill = colour)) +
  scale_fill_identity()

# To get a legend guide, specify guide = "legend"
ggplot(df, aes(x, y)) +
  geom_tile(aes(fill = colour)) +
  scale_fill_identity(guide = "legend")
# But you'll typically also need to supply breaks and labels:
ggplot(df, aes(x, y)) +
  geom_tile(aes(fill = colour)) +
  scale_fill_identity("trt", labels = letters[1:4], breaks = df$colour,
                   guide = "legend")

# cyl scaled to appropriate size
ggplot(mtcars, aes(mpg, wt)) +
  geom_point(aes(size = cyl))

# cyl used as point size
ggplot(mtcars, aes(mpg, wt)) +
  geom_point(aes(size = cyl)) +
  scale_size_identity()

scale_linetype  Scale for line patterns

Description

Default line types based on a set supplied by Richard Pearson, University of Manchester. Continuous values can not be mapped to line types unless scale_linetype_binned() is used. Still, as linetypes has no inherent order, this use is not advised.

Usage

scale_linetype(name = waiver(), ..., na.value = "blank")
scale_linetype_binned(name = waiver(), ..., na.value = "blank")
scale_linetype_continuous(...)
scale_linetype_discrete(name = waiver(), ..., na.value = "blank")
Arguments

name The name of the scale. Used as the axis or legend title. If `waiver()`, the default, the name of the scale is taken from the first mapping used for that aesthetic. If `NULL`, the legend title will be omitted.

Arguments passed on to `discrete_scale`

palette A palette function that when called with a single integer argument (the number of levels in the scale) returns the values that they should take (e.g., `scales::pal_hue()`).

breaks One of:
- `NULL` for no breaks
- `waiver()` for the default breaks (the scale limits)
- A character vector of breaks
- A function that takes the limits as input and returns breaks as output. Also accepts rlang lambda function notation.

limits One of:
- `NULL` to use the default scale values
- A character vector that defines possible values of the scale and their order
- A function that accepts the existing (automatic) values and returns new ones. Also accepts rlang lambda function notation.

drop Should unused factor levels be omitted from the scale? The default, `TRUE`, uses the levels that appear in the data; `FALSE` uses all the levels in the factor.

na.translate Unlike continuous scales, discrete scales can easily show missing values, and do so by default. If you want to remove missing values from a discrete scale, specify `na.translate = FALSE`.

aesthetics The names of the aesthetics that this scale works with.

scale_name [Deprecated] The name of the scale that should be used for error messages associated with this scale.

labels One of:
- `NULL` for no labels
- `waiver()` for the default labels computed by the transformation object
- A character vector giving labels (must be same length as breaks)
- An expression vector (must be the same length as breaks). See ?plotmath for details.
- A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

guide A function used to create a guide or its name. See `guides()` for more information.

call The call used to construct the scale for reporting messages.

super The super class to use for the constructed scale

na.value The linetype to use for NA values.
See Also

The documentation for differentiation related aesthetics.

Other linetype scales: `scale_linetype_manual()`, `scale_linetype_identity()`.

Examples

```r
base <- ggplot(economics_long, aes(date, value01))
base + geom_line(aes(group = variable))
base + geom_line(aes(linetype = variable))

# See scale_manual for more flexibility

# Common line types -----------------------------
df_lines <- data.frame(
  linetype = factor(1:4,
    labels = c("solid", "longdash", "dashed", "dotted")
  )
)
ggplot(df_lines) +
  geom_hline(aes(linetype = linetype, yintercept = 0), linewidth = 2) +
  scale_linetype_identity() +
  facet_grid(linetype ~ .) +
  theme_void(20)
```

---

### scale_linewidth

**Scales for line width**

**Description**

`scale_linewidth` scales the width of lines and polygon strokes. Due to historical reasons, it is also possible to control this with the size aesthetic, but using linewidth is encourage to clearly differentiate area aesthetics from stroke width aesthetics.

**Usage**

```r
scale_linewidth(
  name = waiver(),
  breaks = waiver(),
  labels = waiver(),
  limits = NULL,
  range = c(1, 6),
  transform = "identity",
  trans = deprecated(),
  guide = "legend"
)
```

```r
scale_linewidth_binned(
```
name = waiver(),
breaks = waiver(),
lables = waiver(),
limits = NULL,
range = c(1, 6),
n.breaks = NULL,
nice.breaks = TRUE,
trans = deprecated(),
guide = "bins"
)

Arguments

name
The name of the scale. Used as the axis or legend title. If waiver(), the default, the name of the scale is taken from the first mapping used for that aesthetic. If NULL, the legend title will be omitted.

breaks
One of:

- NULL for no breaks
- waiver() for the default breaks computed by the transformation object
- A numeric vector of positions
- A function that takes the limits as input and returns breaks as output (e.g., a function returned by scales::extended_breaks()). Also accepts rlang lambda function notation.

labels
One of:

- NULL for no labels
- waiver() for the default labels computed by the transformation object
- A character vector giving labels (must be same length as breaks)
- An expression vector (must be the same length as breaks). See ?plotmath for details.
- A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

limits
One of:

- NULL to use the default scale range
- A numeric vector of length two providing limits of the scale. Use NA to refer to the existing minimum or maximum
- A function that accepts the existing (automatic) limits and returns new limits. Also accepts rlang lambda function notation. Note that setting limits on positional scales will remove data outside of the limits. If the purpose is to zoom, use the limit argument in the coordinate system (see coord_cartesian()).

range
a numeric vector of length 2 that specifies the minimum and maximum size of the plotting symbol after transformation.

transform
For continuous scales, the name of a transformation object or the object itself. Built-in transformations include "asn", "atanh", "boxcox", "date", "exp", "hms", "identity", "inverse", "log", "log10", "log1p", "log2", "n swell", "sin", "sqrt", "trans_new".

A transformation object bundles together a transform, its inverse, and methods for generating breaks and labels. Transformation objects are defined in the scales package, and are called `transform_<name>`. If transformations require arguments, you can call them from the scales package, e.g. `scales::transform_boxcox(p = 2)`. You can create your own transformation with `scales::new_transform()`.

**trans**  
[Deprecated] Deprecated in favour of `transform`.

**guide**  
A function used to create a guide or its name. See `guides()` for more information.

**n.breaks**  
An integer guiding the number of major breaks. The algorithm may choose a slightly different number to ensure nice break labels. Will only have an effect if `breaks = waiver()`. Use `NULL` to use the default number of breaks given by the transformation.

**nice.breaks**  
Logical. Should breaks be attempted placed at nice values instead of exactly evenly spaced between the limits. If `TRUE` (default) the scale will ask the transformation object to create breaks, and this may result in a different number of breaks than requested. Ignored if breaks are given explicitly.

**See Also**

The documentation for differentiation related aesthetics.

**Examples**

```r
p <- ggplot(economics, aes(date, unemploy, linewidth = uempmed)) + geom_line(lineend = "round")
p
p + scale_linewidth("Duration of\nunemployment")
p + scale_linewidth(range = c(0, 4))

# Binning can sometimes make it easier to match the scaled data to the legend
p + scale_linewidth_binned()
```

---

**Description**

These functions allow you to specify your own set of mappings from levels in the data to aesthetic values.
scale_manual

Usage

scale_colour_manual(
  ...,
  values,
  aesthetics = "colour",
  breaks = waiver(),
  na.value = "grey50"
)

scale_fill_manual(
  ...,
  values,
  aesthetics = "fill",
  breaks = waiver(),
  na.value = "grey50"
)

scale_size_manual(..., values, breaks = waiver(), na.value = NA)

scale_shape_manual(..., values, breaks = waiver(), na.value = NA)

scale_linetype_manual(..., values, breaks = waiver(), na.value = "blank")

scale_linewidth_manual(..., values, breaks = waiver(), na.value = NA)

scale_alpha_manual(..., values, breaks = waiver(), na.value = NA)

scale_discrete_manual(aesthetics, ..., values, breaks = waiver())

Arguments

... Arguments passed on to discrete_scale

palette A palette function that when called with a single integer argument (the
  number of levels in the scale) returns the values that they should take (e.g.,
  scales::pal_hue()).

limits One of:
  • NULL to use the default scale values
  • A character vector that defines possible values of the scale and their
    order
  • A function that accepts the existing (automatic) values and returns new
    ones. Also accepts rlang lambda function notation.

drop Should unused factor levels be omitted from the scale? The default, TRUE,
  uses the levels that appear in the data; FALSE uses all the levels in the factor.

na.translate Unlike continuous scales, discrete scales can easily show missing
  values, and do so by default. If you want to remove missing values from
  a discrete scale, specify na.translate = FALSE.
scale_name  [Deprecated] The name of the scale that should be used for error messages associated with this scale.

name The name of the scale. Used as the axis or legend title. If waiver(), the default, the name of the scale is taken from the first mapping used for that aesthetic. If NULL, the legend title will be omitted.

labels One of:
- NULL for no labels
- waiver() for the default labels computed by the transformation object
- A character vector giving labels (must be same length as breaks)
- An expression vector (must be the same length as breaks). See ?plotmath for details.
- A function that takes the breaks as input and returns labels as output.
  Also accepts rlang lambda function notation.

guide A function used to create a guide or its name. See guides() for more information.
call The call used to construct the scale for reporting messages.
super The super class to use for the constructed scale

values a set of aesthetic values to map data values to. The values will be matched in order (usually alphabetical) with the limits of the scale, or with breaks if provided. If this is a named vector, then the values will be matched based on the names instead. Data values that don’t match will be given na.value.
aesthetics Character string or vector of character strings listing the name(s) of the aesthetic(s) that this scale works with. This can be useful, for example, to apply colour settings to the colour and fill aesthetics at the same time, via aesthetics = c("colour", "fill").
breaks One of:
- NULL for no breaks
- waiver() for the default breaks (the scale limits)
- A character vector of breaks
- A function that takes the limits as input and returns breaks as output

na.value The aesthetic value to use for missing (NA) values

Details

The functions scale_colour_manual(), scale_fill_manual(), scale_size_manual(), etc. work on the aesthetics specified in the scale name: colour, fill, size, etc. However, the functions scale_colour_manual() and scale_fill_manual() also have an optional aesthetics argument that can be used to define both colour and fill aesthetic mappings via a single function call (see examples). The function scale_discrete_manual() is a generic scale that can work with any aesthetic or set of aesthetics provided via the aesthetics argument.

Color Blindness

Many color palettes derived from RGB combinations (like the "rainbow" color palette) are not suitable to support all viewers, especially those with color vision deficiencies. Using viridis type, which is perceptually uniform in both colour and black-and-white display is an easy option to ensure good perceptive properties of your visualizations. The colorspace package offers functionalities
• to generate color palettes with good perceptive properties,
• to analyse a given color palette, like emulating color blindness,
• and to modify a given color palette for better perceptivity.

For more information on color vision deficiencies and suitable color choices see the paper on the colorspace package and references therein.

See Also
The documentation for differentiation related aesthetics.
The documentation on colour aesthetics.
Other size scales: scale_size(), scale_size_identity().
Other shape scales: scale_shape(), scale_shape_identity().
Other linetype scales: scale_linetype(), scale_linetype_identity().
Other alpha scales: scale_alpha(), scale_alpha_identity().
Other colour scales: scale_alpha(), scale_colour_brewer(), scale_colour_continuous(), scale_colour_gradient(), scale_colour_hue(), scale_colour_identity(), scale_colour_steps(), scale_colour_viridis_d()

Examples

```r
p <- ggplot(mtcars, aes(mpg, wt)) +
  geom_point(aes(colour = factor(cyl)))
p + scale_colour_manual(values = c("red", "blue", "green"))

# It's recommended to use a named vector
cols <- c("8" = "red", "4" = "blue", "6" = "darkgreen", "10" = "orange")
p + scale_colour_manual(values = cols)

# You can set color and fill aesthetics at the same time
ggplot(
  mtcars,
  aes(mpg, wt, colour = factor(cyl), fill = factor(cyl))
) +
  geom_point(shape = 21, alpha = 0.5, size = 2) +
  scale_colour_manual(
    values = cols,
    aesthetics = c("colour", "fill")
  )

# As with other scales you can use breaks to control the appearance
# of the legend.
p + scale_colour_manual(values = cols)
p + scale_colour_manual(
  values = cols,
  breaks = c("4", "6", "8"),
  labels = c("four", "six", "eight")
)
```
# And limits to control the possible values of the scale
p + scale_colour_manual(values = cols, limits = c("4", "8"))
p + scale_colour_manual(values = cols, limits = c("4", "6", "8", "10"))

---

### scale_shape

**Scales for shapes, aka glyphs**

#### Description

`scale_shape()` maps discrete variables to six easily discernible shapes. If you have more than six levels, you will get a warning message, and the seventh and subsequent levels will not appear on the plot. Use `scale_shape_manual()` to supply your own values. You can not map a continuous variable to shape unless `scale_shape_binned()` is used. Still, as shape has no inherent order, this use is not advised.

#### Usage

```r
scale_shape(name = waiver(), ..., solid = TRUE)
scale_shape_binned(name = waiver(), ..., solid = TRUE)
```

#### Arguments

- **name**
  - The name of the scale. Used as the axis or legend title. If `waiver()`, the default, the name of the scale is taken from the first mapping used for that aesthetic. If `NULL`, the legend title will be omitted.

- **...**
  - Arguments passed on to `discrete_scale`

- **palette**
  - A palette function that when called with a single integer argument (the number of levels in the scale) returns the values that they should take (e.g., `scales::pal_hue()`).

- **breaks**
  - One of:
    - `NULL` for no breaks
    - `waiver()` for the default breaks (the scale limits)
    - A character vector of breaks
    - A function that takes the limits as input and returns breaks as output. Also accepts rlang lambda function notation.

- **limits**
  - One of:
    - `NULL` to use the default scale values
    - A character vector that defines possible values of the scale and their order
    - A function that accepts the existing (automatic) values and returns new ones. Also accepts rlang lambda function notation.

- **drop**
  - Should unused factor levels be omitted from the scale? The default, `TRUE`, uses the levels that appear in the data; `FALSE` uses all the levels in the factor.
na.translate  Unlike continuous scales, discrete scales can easily show missing values, and do so by default. If you want to remove missing values from a discrete scale, specify `na.translate = FALSE`.

na.value  If `na.translate = TRUE`, what aesthetic value should the missing values be displayed as? Does not apply to position scales where NA is always placed at the far right.

aesthetics  The names of the aesthetics that this scale works with.

scale_name  [Deprecated]  The name of the scale that should be used for error messages associated with this scale.

labels  One of:
  • `NULL` for no labels
  • `waiver()` for the default labels computed by the transformation object
  • A character vector giving labels (must be same length as breaks)
  • An expression vector (must be the same length as breaks). See ?plotmath for details.
  • A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

guide  A function used to create a guide or its name. See `guides()` for more information.

call  The call used to construct the scale for reporting messages.

super  The super class to use for the constructed scale

solid  Should the shapes be solid, TRUE, or hollow, FALSE?

See Also

The documentation for differentiation related aesthetics.

Other shape scales: `scale_shape_manual()`, `scale_shape_identity()`.

Examples

```r
set.seed(596)
dsmall <- diamonds[sample(nrow(diamonds), 100),]

(d <- ggplot(dsmall, aes(carat, price)) + geom_point(aes(shape = cut)))
d + scale_shape(solid = TRUE)  # the default
d + scale_shape(solid = FALSE)
d + scale_shape(name = "Cut of diamond")

# To change order of levels, change order of
# underlying factor
levels(dsmall$cut) <- c("Fair", "Good", "Very Good", "Premium", "Ideal")

# Need to recreate plot to pick up new data
ggplot(dsmall, aes(price, carat)) + geom_point(aes(shape = cut))

# Show a list of available shapes
df_shapes <- data.frame(shape = 0:24)
ggplot(df Shapes, aes(0, 0, shape = shape)) +
```
scale_size

Scales for area or radius

**Description**

`scale_size()` scales area, `scale_radius()` scales radius. The size aesthetic is most commonly used for points and text, and humans perceive the area of points (not their radius), so this provides for optimal perception. `scale_size_area()` ensures that a value of 0 is mapped to a size of 0. `scale_size_binned()` is a binned version of `scale_size()` that scales by area (but does not ensure 0 equals an area of zero). For a binned equivalent of `scale_size_area()` use `scale_size_binned_area()`.

**Usage**

```r
text ex1
```
nice.breaks = TRUE,
transform = "identity",
trans = deprecated(),
guide = "bins"
)

scale_size_area(name = waiver(), ..., max_size = 6)

scale_size_binned_area(name = waiver(), ..., max_size = 6)

Arguments

name
The name of the scale. Used as the axis or legend title. If waiver(), the default, the name of the scale is taken from the first mapping used for that aesthetic. If NULL, the legend title will be omitted.

breaks One of:
• NULL for no breaks
• waiver() for the default breaks computed by the transformation object
• A numeric vector of positions
• A function that takes the limits as input and returns breaks as output (e.g., a function returned by scales::extended_breaks()). Also accepts rlang lambda function notation.

labels One of:
• NULL for no labels
• waiver() for the default labels computed by the transformation object
• A character vector giving labels (must be same length as breaks)
• An expression vector (must be the same length as breaks). See ?plotmath for details.
• A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

limits One of:
• NULL to use the default scale range
• A numeric vector of length two providing limits of the scale. Use NA to refer to the existing minimum or maximum
• A function that accepts the existing (automatic) limits and returns new limits. Also accepts rlang lambda function notation. Note that setting limits on positional scales will remove data outside of the limits. If the purpose is to zoom, use the limit argument in the coordinate system (see coord_cartesian()).

range a numeric vector of length 2 that specifies the minimum and maximum size of the plotting symbol after transformation.

transform For continuous scales, the name of a transformation object or the object itself. Built-in transformations include "asn", "atanh", "boxcox", "date", "exp", "hms", "identity", "log", "log10", "log1p", "log2", "logit", "modulus", "probability", "probit", "pseudo_log", "reciprocal", "reverse", "sqrt" and "time".
A transformation object bundles together a transform, its inverse, and methods for generating breaks and labels. Transformation objects are defined in the scales package, and are called transform_<name>. If transformations require arguments, you can call them from the scales package, e.g. scales::transform_boxcox(p = 2). You can create your own transformation with scales::new_transform().

trans

[Deprecated] Deprecated in favour of transform.

guide

A function used to create a guide or its name. See guides() for more information.

n.breaks

An integer guiding the number of major breaks. The algorithm may choose a slightly different number to ensure nice break labels. Will only have an effect if breaks = waiver(). Use NULL to use the default number of breaks given by the transformation.

nice.breaks

Logical. Should breaks be attempted placed at nice values instead of exactly evenly spaced between the limits. If TRUE (default) the scale will ask the transformation object to create breaks, and this may result in a different number of breaks than requested. Ignored if breaks are given explicitly.

... Arguments passed on to continuous_scale

minor_breaks One of:

- NULL for no minor breaks
- waiver() for the default breaks (one minor break between each major break)
  - A numeric vector of positions
  - A function that given the limits returns a vector of minor breaks. Also accepts rlang lambda function notation. When the function has two arguments, it will be given the limits and major breaks.

oob One of:

- Function that handles limits outside of the scale limits (out of bounds). Also accepts rlang lambda function notation.
  - The default (scales::censor()) replaces out of bounds values with NA.
  - scales::squish() for squishing out of bounds values into range.
  - scales::squish_infinite() for squishing infinite values into range.

na.value Missing values will be replaced with this value.

expand For position scales, a vector of range expansion constants used to add some padding around the data to ensure that they are placed some distance away from the axes. Use the convenience function expansion() to generate the values for the expand argument. The defaults are to expand the scale by 5% on each side for continuous variables, and by 0.6 units on each side for discrete variables.

position For position scales, The position of the axis. left or right for y axes, top or bottom for x axes.

call The call used to construct the scale for reporting messages.

super The super class to use for the constructed scale

max.size Size of largest points.
Note

Historically the size aesthetic was used for two different things: Scaling the size of object (like points and glyphs) and scaling the width of lines. From ggplot2 3.4.0 the latter has been moved to its own linewidth aesthetic. For backwards compatibility using size is still possible, but it is highly advised to switch to the new linewidth aesthetic for these cases.

See Also

scale_size_area() if you want 0 values to be mapped to points with size 0. scale_linewidth() if you want to scale the width of lines.

The documentation for differentiation related aesthetics.

Examples

```r
p <- ggplot(mpg, aes(displ, hwy, size = hwy)) +
  geom_point()
p + scale_size("Highway mpg")
p + scale_size(range = c(0, 10))

# If you want zero value to have zero size, use scale_size_area:
p + scale_size_area()

# Binning can sometimes make it easier to match the scaled data to the legend
p + scale_size_binned()

# This is most useful when size is a count
ggplot(mpg, aes(class, cyl)) +
  geom_count() +
  scale_size_area()

# If you want to map size to radius (usually bad idea), use scale_radius
p + scale_radius()
```

scale_x_discrete

Position scales for discrete data

Description

scale_x_discrete() and scale_y_discrete() are used to set the values for discrete x and y scale aesthetics. For simple manipulation of scale labels and limits, you may wish to use labs() and lims() instead.

Usage

```r
scale_x_discrete(
  name = waiver(),
  ...,inion
```
scale_x_discrete

    expand = waiver(),
    guide = waiver(),
    position = "bottom"
)

scale_y_discrete(
    name = waiver(),
    ..., 
    expand = waiver(),
    guide = waiver(),
    position = "left"
)

Arguments

name The name of the scale. Used as the axis or legend title. If waiver(), the default, the name of the scale is taken from the first mapping used for that aesthetic. If NULL, the legend title will be omitted.

... Arguments passed on to discrete_scale

palette A palette function that when called with a single integer argument (the number of levels in the scale) returns the values that they should take (e.g., scales::pal_hue()).

breaks One of:
- NULL for no breaks
- waiver() for the default breaks (the scale limits)
- A character vector of breaks
- A function that takes the limits as input and returns breaks as output. Also accepts rlang lambda function notation.

limits One of:
- NULL to use the default scale values
- A character vector that defines possible values of the scale and their order
- A function that accepts the existing (automatic) values and returns new ones. Also accepts rlang lambda function notation.

drop Should unused factor levels be omitted from the scale? The default, TRUE, uses the levels that appear in the data; FALSE uses all the levels in the factor.

na.translate Unlike continuous scales, discrete scales can easily show missing values, and do so by default. If you want to remove missing values from a discrete scale, specify na.translate = FALSE.

na.value If na.translate = TRUE, what aesthetic value should the missing values be displayed as? Does not apply to position scales where NA is always placed at the far right.

aesthetics The names of the aesthetics that this scale works with.

scale_name [Deprecated] The name of the scale that should be used for error messages associated with this scale.

labels One of:
scale_x_discrete

• NULL for no labels
• waiver() for the default labels computed by the transformation object
• A character vector giving labels (must be same length as breaks)
• An expression vector (must be the same length as breaks). See ?plotmath for details.
• A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.

call The call used to construct the scale for reporting messages.
super The super class to use for the constructed scale
expand For position scales, a vector of range expansion constants used to add some padding around the data to ensure that they are placed some distance away from the axes. Use the convenience function expansion() to generate the values for the expand argument. The defaults are to expand the scale by 5% on each side for continuous variables, and by 0.6 units on each side for discrete variables.
guide A function used to create a guide or its name. See guides() for more information.
position For position scales, The position of the axis. left or right for y axes, top or bottom for x axes.

Details

You can use continuous positions even with a discrete position scale - this allows you (e.g.) to place labels between bars in a bar chart. Continuous positions are numeric values starting at one for the first level, and increasing by one for each level (i.e. the labels are placed at integer positions). This is what allows jittering to work.

See Also

The position documentation.

Other position scales: scale_x_binned(), scale_x_continuous(), scale_x_date()

Examples

ggplot(diamonds, aes(cut)) + geom_bar()

# The discrete position scale is added automatically whenever you
# have a discrete position.

(d <- ggplot(subset(diamonds, carat > 1), aes(cut, clarity)) +
  geom_jitter())

d + scale_x_discrete("Cut")

d +
scale_x_discrete(
  "Cut",
  labels = c(
    "Fair" = "F",
...
"Good" = "G",
"Very Good" = "VG",
"Perfect" = "P",
"Ideal" = "I"
)
)

# Use limits to adjust the which levels (and in what order)
# are displayed
d + scale_x_discrete(limits = c("Fair","Ideal"))

# you can also use the short hand functions xlim and ylim
d + xlim("Fair","Ideal", "Good")
d + ylim("IF", "IF")

# See ?reorder to reorder based on the values of another variable
ggplot(mpg, aes(manufacturer, cty)) +
  geom_point()
ggplot(mpg, aes(reorder(manufacturer, cty), cty)) +
  geom_point()
ggplot(mpg, aes(reorder(manufacturer, displ), cty)) +
  geom_point()

# Use abbreviate as a formatter to reduce long names
fggplot(mpg, aes(reorder(manufacturer, displ), cty)) +
  geom_point() +
  scale_x_discrete(labels = abbreviate)

seals

Vector field of seal movements

Description


Usage

seals

Format

A data frame with 1155 rows and 4 variables

References

https://www.stat.berkeley.edu/~brill/Papers/jspifinal.pdf
**sec_axis**

*Specify a secondary axis*

**Description**

This function is used in conjunction with a position scale to create a secondary axis, positioned opposite of the primary axis. All secondary axes must be based on a one-to-one transformation of the primary axes.

**Usage**

```r
sec_axis(
  transform = NULL,
  name = waiver(),
  breaks = waiver(),
  labels = waiver(),
  guide = waiver(),
  trans = deprecated()
)
```

```r
dup_axis(
  transform = ~.,
  name = derive(),
  breaks = derive(),
  labels = derive(),
  guide = derive(),
  trans = deprecated()
)
```

```r
derive()
```

**Arguments**

- **transform** A formula or function of transformation
- **name** The name of the secondary axis
- **breaks** One of:
  - NULL for no breaks
  - waiver() for the default breaks computed by the transformation object
  - A numeric vector of positions
  - A function that takes the limits as input and returns breaks as output
- **labels** One of:
  - NULL for no labels
  - waiver() for the default labels computed by the transformation object
  - A character vector giving labels (must be same length as breaks)
  - A function that takes the breaks as input and returns labels as output
guide A position guide that will be used to render the axis on the plot. Usually this is `guide_axis()`.

trans [Deprecated]

Details

`sec_axis()` is used to create the specifications for a secondary axis. Except for the `trans` argument any of the arguments can be set to `derive()` which would result in the secondary axis inheriting the settings from the primary axis.

`dup_axis()` is provide as a shorthand for creating a secondary axis that is a duplication of the primary axis, effectively mirroring the primary axis.

As of v3.1, date and datetime scales have limited secondary axis capabilities.Unlike other continuous scales, secondary axis transformations for date and datetime scales must respect their primary POSIX data structure. This means they may only be transformed via addition or subtraction, e.g. `~ . + hms::hms(days = 8)`, or `~ - 8*60*60`. Nonlinear transformations will return an error. To produce a time-since-event secondary axis in this context, users may consider adapting secondary axis labels.

Examples

```r
p <- ggplot(mtcars, aes(cyl, mpg)) + geom_point()

# Create a simple secondary axis
p + scale_y_continuous(sec.axis = sec_axis(~ . + 10))

# Inherit the name from the primary axis
p + scale_y_continuous("Mile\$/gallon", sec.axis = sec_axis(~ . + 10, name = derive()))

# Duplicate the primary axis
p + scale_y_continuous(sec.axis = dup_axis())

# You can pass in a formula as a shorthand
p + scale_y_continuous(sec.axis = ~ .^2)

# Secondary axes work for date and datetime scales too:
df <- data.frame(
  dx = seq(
    as.POSIXct("2012-02-29 12:00:00", tz = "UTC"),
    length.out = 10,
    by = "4 hour"
  ),
  price = seq(20, 200000, length.out = 10)
)

# This may useful for labelling different time scales in the same plot
ggplot(df, aes(x = dx, y = price)) + geom_line() +
  scale_x_datetime("Date",
    date_labels = "%b %d",
  )
```
stat_ecdf

Compute empirical cumulative distribution

Description

The empirical cumulative distribution function (ECDF) provides an alternative visualisation of distribution. Compared to other visualisations that rely on density (like `geom_histogram()`), the ECDF doesn’t require any tuning parameters and handles both continuous and categorical variables. The downside is that it requires more training to accurately interpret, and the underlying visual tasks are somewhat more challenging.

Usage

```r
stat_ecdf(
  mapping = NULL,
  data = NULL,
  geom = "step",
  position = "identity",
  ..., 
  n = NULL,
  pad = TRUE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)```

Arguments

mapping  Set of aesthetic mappings created by \texttt{aes()}. If specified and \texttt{inherit.aes} = \texttt{TRUE} (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data  The data to be displayed in this layer. There are three options:
If \texttt{NULL}, the default, the data is inherited from the plot data as specified in the call to \texttt{ggplot()}. A \texttt{data.frame}, or other object, will override the plot data. All objects will be fortified to produce a data frame. See \texttt{fortify()} for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a \texttt{data.frame}, and will be used as the layer data. A function can be created from a formula (e.g. \texttt{~ head(.x, 10)}).

geom  The geometric object to use to display the data, either as a \texttt{ggproto} Geom subclass or as a string naming the geom stripped of the \texttt{geom_} prefix (e.g. "point" rather than "geom_point")

position  Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use \texttt{position_jitter}), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

...  Other arguments passed on to \texttt{layer()}. These are often aesthetics, used to set an aesthetic to a fixed value, like \texttt{colour = "red"} or \texttt{size = 3}. They may also be parameters to the paired geom/stat.

n  if \texttt{NULL}, do not interpolate. If not \texttt{NULL}, this is the number of points to interpolate with.

pad  If \texttt{TRUE}, pad the ecdf with additional points (-Inf, 0) and (Inf, 1)

na.rm  If \texttt{FALSE} (the default), removes missing values with a warning. If \texttt{TRUE} silently removes missing values.

show.legend  logical. Should this layer be included in the legends? \texttt{NA}, the default, includes if any aesthetics are mapped. \texttt{FALSE} never includes, and \texttt{TRUE} always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes  If \texttt{FALSE}, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. \texttt{borders()}. 

Details

The statistic relies on the aesthetics assignment to guess which variable to use as the input and which to use as the output. Either \texttt{x} or \texttt{y} must be provided and one of them must be unused. The ECDF will be calculated on the given aesthetic and will be output on the unused one.

Computed variables

These are calculated by the ‘stat’ part of layers and can be accessed with \texttt{delayed evaluation}.

- \texttt{after_stat(ecdf)}
  Cumulative density corresponding to \texttt{x}. 

\texttt{stat_ecdf}
stat_ellipse

- after_stat(y)
  [Superseded] For backward compatibility.

Examples

```r
set.seed(1)
df <- data.frame(
  x = c(rnorm(100, 0, 3), rnorm(100, 0, 10)),
  g = gl(2, 100)
)
ggplot(df, aes(x)) +
  stat_ecdf(geom = "step")

# Don't go to positive/negative infinity
ggplot(df, aes(x)) +
  stat_ecdf(geom = "step", pad = FALSE)

# Multiple ECDFs
ggplot(df, aes(x, colour = g)) +
  stat_ecdf()
```

---

stat_ellipse  

Compute normal data ellipses

Description

The method for calculating the ellipses has been modified from car::dataEllipse (Fox and Weisberg 2011, Friendly and Monette 2013)

Usage

```r
stat_ellipse(
  mapping = NULL,
  data = NULL,
  geom = "path",
  position = "identity",
  ..., 
  type = "t",
  level = 0.95,
  segments = 51,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```
Arguments

mapping Set of aesthetic mappings created by \texttt{aes()}. If specified and \texttt{inherit.aes = TRUE} (the default), it is combined with the default mapping at the top level of the plot. You must supply \texttt{mapping} if there is no plot mapping.

data The data to be displayed in this layer. There are three options:
If \texttt{NULL}, the default, the data is inherited from the plot data as specified in the call to \texttt{ggplot()}.
A \texttt{data.frame}, or other object, will override the plot data. All objects will be fortified to produce a data frame. See \texttt{fortify()} for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a \texttt{data.frame}, and will be used as the layer data. A function can be created from a \texttt{formula} (e.g. \texttt{~ head(.x, 10)}).

geom The geometric object to use to display the data, either as a \texttt{ggproto Geom} subclass or as a string naming the geom stripped of the \texttt{geom_} prefix (e.g. "point" rather than "geom_point")

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use \texttt{position_jitter}), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

... Other arguments passed on to \texttt{layer()}. These are often aesthetics, used to set an aesthetic to a fixed value, like \texttt{colour = "red"} or \texttt{size = 3}. They may also be parameters to the paired geom/stat.

type The type of ellipse. The default "t" assumes a multivariate t-distribution, and "norm" assumes a multivariate normal distribution. "euclid" draws a circle with the radius equal to \texttt{level}, representing the euclidean distance from the center. This ellipse probably won't appear circular unless \texttt{coord_fixed()} is applied.

level The level at which to draw an ellipse, or, if \texttt{type="euclid"}, the radius of the circle to be drawn.

segments The number of segments to be used in drawing the ellipse.

na.rm If \texttt{FALSE}, the default, missing values are removed with a warning. If \texttt{TRUE}, missing values are silently removed.

show.legend logical. Should this layer be included in the legends? \texttt{NA}, the default, includes if any aesthetics are mapped. \texttt{FALSE} never includes, and \texttt{TRUE} always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If \texttt{FALSE}, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. \texttt{borders()}.

References

Examples

```r
ggplot(faithful, aes(waiting, eruptions)) +
  geom_point() +
  stat_ellipse()

ggplot(faithful, aes(waiting, eruptions, color = eruptions > 3)) +
  geom_point() +
  stat_ellipse()

ggplot(faithful, aes(waiting, eruptions, color = eruptions > 3)) +
  geom_point() +
  stat_ellipse(type = "norm", linetype = 2) +
  stat_ellipse(type = "t")

ggplot(faithful, aes(waiting, eruptions, color = eruptions > 3)) +
  geom_point() +
  stat_ellipse(type = "norm", linetype = 2) +
  stat_ellipse(type = "euclid", level = 3) +
  coord_fixed()

ggplot(faithful, aes(waiting, eruptions, fill = eruptions > 3)) +
  stat_ellipse(geom = "polygon")
```

---

### Description

The identity statistic leaves the data unchanged.

### Usage

```r
stat_identity(
  mapping = NULL,
  data = NULL,
  geom = "point",
  position = "identity",
  ..., 
  show.legend = NA,
  inherit.aes = TRUE
)
```
Arguments

mapping  Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

data  The data to be displayed in this layer. There are three options:
If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a `formula` (e.g. `~ head(.x, 10)`).

geom  The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the `geom_` prefix (e.g. "point" rather than "geom_point")

position  Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

...  Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

show.legend  logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes  If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

Examples

```r
p <- ggplot(mtcars, aes(wt, mpg))
p + stat_identity()
```

stat_sf_coordinates  Extract coordinates from 'sf' objects

Description

`stat_sf_coordinates()` extracts the coordinates from 'sf' objects and summarises them to one pair of coordinates (x and y) per geometry. This is convenient when you draw an sf object as geoms like text and labels (so `geom_sf_text()` and `geom_sf_label()` relies on this).
stat_sf_coordinates

Usage

```r
stat_sf_coordinates(
  mapping = aes(),
  data = NULL,
  geom = "point",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  fun.geometry = NULL,
  ...
)
```

Arguments

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- **geom**: The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_prefix (e.g. "point" rather than "geom_point")

- **position**: Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

- **na.rm**: If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.

- **show.legend**: logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display.

- **inherit.aes**: If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

- **fun.geometry**: A function that takes a `sfc` object and returns a `sfc_POINT` with the same length as the input. If `NULL`, `function(x) sf::st_point_on_surface(sf::st_zm(x))` will be used. Note that the function may warn about the incorrectness of the result if the data is not projected, but you can ignore this except when you really care about the exact locations.
Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

Details

Coordinates of an sf object can be retrieved by `sf::st_coordinates()`. But, we cannot simply use `sf::st_coordinates()` because, whereas text and labels require exactly one coordinate per geometry, it returns multiple ones for a polygon or a line. Thus, these two steps are needed:

1. Choose one point per geometry by some function like `sf::st_centroid()` or `sf::st_point_on_surface()`.
2. Retrieve coordinates from the points by `sf::st_coordinates()`.

For the first step, you can use an arbitrary function via `fun.geometry`. By default, `function(x) sf::st_point_on_surface(sf::st_zm(x))` is used; `sf::st_point_on_surface()` seems more appropriate than `sf::st_centroid()` since labels and text usually are intended to be put within the polygon or the line. `sf::st_zm()` is needed to drop Z and M dimension beforehand, otherwise `sf::st_point_on_surface()` may fail when the geometries have M dimension.

Computed variables

These are calculated by the 'stat' part of layers and can be accessed with `delayed evaluation`.

- `after_stat(x)`
  X dimension of the simple feature.
- `after_stat(y)`
  Y dimension of the simple feature.

Examples

```r
if (requireNamespace("sf", quietly = TRUE)) {
  nc <- sf::st_read(system.file("shape/nc.shp", package="sf"))

  ggplot(nc) +
    stat_sf_coordinates()

  ggplot(nc) +
    geom_errorbarh(
      aes(geometry = geometry,
           xmin = after_stat(x) - 0.1,
           xmax = after_stat(x) + 0.1,
           y = after_stat(y),
           height = 0.04),
      stat = "sf_coordinates"
    )
}
```
stat_summary_2d

Bin and summarise in 2d (rectangle & hexagons)

Description

stat_summary_2d() is a 2d variation of stat_summary(). stat_summary_hex() is a hexagonal variation of stat_summary_2d(). The data are divided into bins defined by x and y, and then the values of z in each cell is are summarised with fun.

Usage

stat_summary_2d(
  mapping = NULL,
  data = NULL,
  geom = "tile",
  position = "identity",
  ..., 
  bins = 30,
  binwidth = NULL,
  drop = TRUE,
  fun = "mean",
  fun.args = list(),
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_summary_hex(
  mapping = NULL,
  data = NULL,
  geom = "hex",
  position = "identity",
  ..., 
  bins = 30,
  binwidth = NULL,
  drop = TRUE,
  fun = "mean",
  fun.args = list(),
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
The data to be displayed in this layer. There are three options:

- If NULL, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
- A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
- A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. “point” rather than “geom_point”)

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

Numeric vector giving number of bins in both vertical and horizontal directions. Set to 30 by default.

Numeric vector giving bin width in both vertical and horizontal directions. Overrides bins if both set.

drop

Function for summary.

A list of extra arguments to pass to `fun`.

If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

Logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

### Aesthetics

- x: horizontal position
- y: vertical position
- z: value passed to the summary function

### Computed variables

These are calculated by the ’stat’ part of layers and can be accessed with delayed evaluation.
stat_summary_bin

- `after_stat(x)`, `after_stat(y)`
  Location.
- `after_stat(value)`
  Value of summary statistic.

**Dropped variables**

- `z` After binning, the z values of individual data points are no longer available.

**See Also**

- `stat_summary_hex()` for hexagonal summarization. `stat_bin_2d()` for the binning options.

**Examples**

```r
d <- ggplot(diamonds, aes(carat, depth, z = price))
d + stat_summary_2d()

# Specifying function
if (requireNamespace("hexbin")) {
  d + stat_summary_2d(fun = function(x) sum(x^2))
  d + stat_summary_2d(fun = ~ sum(.x^2))
  d + stat_summary_2d(fun = var)
  d + stat_summary_2d(fun = "quantile", fun.args = list(probs = 0.1))
}
```

---

**stat_summary_bin**

Summarise y values at unique/binned x

**Description**

`stat_summary()` operates on unique x or y; `stat_summary_bin()` operates on binned x or y. They are more flexible versions of `stat_bin()`: instead of just counting, they can compute any aggregate.

**Usage**

```r
stat_summary_bin(
  mapping = NULL,
  data = NULL,
  geom = "pointrange",
  position = "identity",
  ...,
  fun.data = NULL,
  fun = NULL,
  fun.max = NULL,
)```

fun.min = NULL,
fun.args = list(),
bins = 30,
binwidth = NULL,
breaks = NULL,
na.rm = FALSE,
orientation = NA,
show.legend = NA,
inherit.aes = TRUE,
fun.y = deprecated(),
fun.ymin = deprecated(),
fun.ymax = deprecated()
}

stat_summary_bin(mapping = NULL,
data = NULL,
geom = "pointrange",
position = "identity",
..., 
fun.data = NULL,
fun = NULL,
fun.max = NULL,
fun.min = NULL,
fun.args = list(),
na.rm = FALSE,
orientation = NA,
show.legend = NA,
inherit.aes = TRUE,
fun.y = deprecated(),
fun.ymin = deprecated(),
fun.ymax = deprecated()
)

Arguments

mapping  Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data  The data to be displayed in this layer. There are three options:

If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().

A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.

A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).
The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

A function that is given the complete data and should return a data frame with variables ymin, y, and ymax.

Alternatively, supply three individual functions that are each passed a vector of values and should return a single number.

Optional additional arguments passed on to the functions.

Number of bins. Overridden by binwidth. Defaults to 30.

The width of the bins. Can be specified as a numeric value or as a function that calculates width from unscaled x. Here, "unscaled x" refers to the original x values in the data, before application of any scale transformation. When specifying a function along with a grouping structure, the function will be called once per group. The default is to use the number of bins in bins, covering the range of the data. You should always override this value, exploring multiple widths to find the best to illustrate the stories in your data.

The bin width of a date variable is the number of days in each time; the bin width of a time variable is the number of seconds.

Alternatively, you can supply a numeric vector giving the bin boundaries. Over-rides binwidth, bins, center, and boundary.

If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

The orientation of the layer. The default (NA) automatically determines the orientation from the aesthetic mapping. In the rare event that this fails it can be given explicitly by setting orientation to either "x" or "y". See the Orientation section for more detail.

Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

[Deprecated] Use the versions specified above instead.

This geom treats each axis differently and, thus, can thus have two orientations. Often the orientation is easy to deduce from a combination of the given mappings and the types of positional scales...
in use. Thus, ggplot2 will by default try to guess which orientation the layer should have. Under rare circumstances, the orientation is ambiguous and guessing may fail. In that case the orientation can be specified directly using the orientation parameter, which can be either "x" or "y". The value gives the axis that the geom should run along, "x" being the default orientation you would expect for the geom.

Aesthetics

stat_summary() understands the following aesthetics (required aesthetics are in bold):

- x
- y
- group

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Summary functions

You can either supply summary functions individually (fun, fun.max, fun.min), or as a single function (fun.data):

fun.data  Complete summary function. Should take numeric vector as input and return data frame as output
fun.min   min summary function (should take numeric vector and return single number)
fun       main summary function (should take numeric vector and return single number)
fun.max   max summary function (should take numeric vector and return single number)

A simple vector function is easiest to work with as you can return a single number, but is somewhat less flexible. If your summary function computes multiple values at once (e.g. min and max), use fun.data.

fun.data will receive data as if it was oriented along the x-axis and should return a data.frame that corresponds to that orientation. The layer will take care of flipping the input and output if it is oriented along the y-axis.

If no aggregation functions are supplied, will default to mean_se().

See Also

geom_errorbar(), geom_pointrange(), geom_linerange(), geom_crossbar() for geoms to display summarised data

Examples

d <- ggplot(mtcars, aes(cyl, mpg)) + geom_point()
d + stat_summary(fun.data = "mean_cl_boot", colour = "red", linewidth = 2, size = 3)

# Orientation follows the discrete axis
ggplot(mtcars, aes(mpg, factor(cyl))) + geom_point() +
    stat_summary(fun.data = "mean_cl_boot", colour = "red", linewidth = 2, size = 3)
You can supply individual functions to summarise the value at each x:

```r
d + stat_summary(fun = "median", colour = "red", size = 2, geom = "point")
d + stat_summary(fun = "mean", colour = "red", size = 2, geom = "point")
d + aes(colour = factor(vs)) + stat_summary(fun = mean, geom="line")

d + stat_summary(fun = mean, fun.min = min, fun.max = max, colour = "red")

d <- ggplot(diamonds, aes(cut))
d + geom_bar()
d + stat_summary(aes(y = price), fun = "mean", geom = "bar")

# Orientation of stat_summary_bin is ambiguous and must be specified directly
ggplot(diamonds, aes(carat, price)) +
  stat_summary_bin(fun = "mean", geom = "bar", orientation = 'y')

# Don’t use ylim to zoom into a summary plot - this throws the data away
p <- ggplot(mtcars, aes(cyl, mpg)) +
  stat_summary(fun = "mean", geom = "point")
p + ylim(15, 30)
# Instead use coord_cartesian
p + coord_cartesian(ylim = c(15, 30))

# A set of useful summary functions is provided from the Hmisc package:
stat_sum_df <- function(fun, geom="crossbar", ...) {
  stat_summary(fun.data = fun, colour = "red", geom = geom, width = 0.2, ...)
}
d <- ggplot(mtcars, aes(cyl, mpg)) + geom_point()
# The crossbar geom needs grouping to be specified when used with a continuous x axis.
d + stat_sum_df("mean_cl_boot", mapping = aes(group = cyl))
d + stat_sum_df("mean_sdl", mapping = aes(group = cyl))
d + stat_sum_df("mean_sdl", fun.args = list(mult = 1), mapping = aes(group = cyl))
d + stat_sum_df("median_hilow", mapping = aes(group = cyl))

# An example with highly skewed distributions:
if (require("ggplot2movies")) {
  set.seed(596)
mov <- movies[sample(nrow(movies), 1000),]
m2 <-
  ggplot(mov, aes(x = factor(round(rating)), y = votes)) +
  geom_point()
m2 <-
m2 +
  stat_summary(
    fun.data = "mean_cl_boot",
    geom = "crossbar",
    colour = "red", width = 0.3
  ) +
```
# Notice how the overplotting skews off visual perception of the mean
# supplementing the raw data with summary statistics is _very_ important

# Next, we'll look at votes on a log scale.

# Transforming the scale means the data are transformed
# first, after which statistics are computed:
m2 + scale_y_log10()

# Transforming the coordinate system occurs after the
# statistic has been computed. This means we're calculating the summary on the raw data
# and stretching the geoms onto the log scale. Compare the widths of the
# standard errors.
m2 + coord_trans(y="log10")
}

#### stat_unique

**Remove duplicates**

**Description**

Remove duplicates

**Usage**

```r
stat_unique(
mapping = NULL,
data = NULL,
ggeom = "point",
position = "identity",
..., 
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE
)
```

**Arguments**

- `mapping`: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- `data`: The data to be displayed in this layer. There are three options: If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`. A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

**geom**

The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_prefix (e.g. "point" rather than "geom_point")

**position**

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

... Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

**na.rm**

If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

**show.legend**

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

**inherit.aes**

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

### Aesthetics

`stat_unique()` understands the following aesthetics (required aesthetics are in bold):

- **group**

Learn more about setting these aesthetics in vignette("ggplot2-specs").

### Examples

```r
ggplot(mtcars, aes(vs, am)) +
geom_point(alpha = 0.1)

ggplot(mtcars, aes(vs, am)) +
  geom_point(alpha = 0.1, stat = "unique")
```

### Description

Themes are a powerful way to customize the non-data components of your plots: i.e. titles, labels, fonts, background, gridlines, and legends. Themes can be used to give plots a consistent customized look. Modify a single plot’s theme using `theme()`: see `theme_update()` if you want modify the active theme, to affect all subsequent plots. Use the themes available in complete themes if you would like to use a complete theme such as `theme_bw()`, `theme_minimal()`, and more. Theme elements are documented together according to inheritance, read more about theme inheritance below.
Usage

```r
theme(
  ..., 
  line, 
  rect, 
  text, 
  title, 
  aspect.ratio, 
  axis.title, 
  axis.title.x, 
  axis.title.x.top, 
  axis.title.x.bottom, 
  axis.title.y, 
  axis.title.y.left, 
  axis.title.y.right, 
  axis.text, 
  axis.text.x, 
  axis.text.x.top, 
  axis.text.x.bottom, 
  axis.text.y, 
  axis.text.y.left, 
  axis.text.y.right, 
  axis.text.theta, 
  axis.text.r, 
  axis.ticks, 
  axis.ticks.x, 
  axis.ticks.x.top, 
  axis.ticks.x.bottom, 
  axis.ticks.y, 
  axis.ticks.y.left, 
  axis.ticks.y.right, 
  axis.ticks.theta, 
  axis.ticks.r, 
  axis.minor.ticks.x.top, 
  axis.minor.ticks.x.bottom, 
  axis.minor.ticks.y.left, 
  axis.minor.ticks.y.right, 
  axis.minor.ticks.theta, 
  axis.minor.ticks.r, 
  axis.ticks.length, 
  axis.ticks.length.x, 
  axis.ticks.length.x.top, 
  axis.ticks.length.x.bottom, 
  axis.ticks.length.y, 
  axis.ticks.length.y.left, 
  axis.ticks.length.y.right, 
  axis.ticks.length.theta, 
  axis.ticks.length.r,
)```
theme

axis.minor.ticks.length,
axis.minor.ticks.length.x,
axis.minor.ticks.length.x.top,
axis.minor.ticks.length.x.bottom,
axis.minor.ticks.length.y,
axis.minor.ticks.length.y.left,
axis.minor.ticks.length.y.right,
axis.minor.ticks.length.theta,
axis.minor.ticks.length.r,
axis.line,
axis.line.x,
axis.line.x.top,
axis.line.x.bottom,
axis.line.y,
axis.line.y.left,
axis.line.y.right,
axis.line.theta,
axis.line.r,
legend.background,
legend.margin,
legend.spacing,
legend.spacing.x,
legend.spacing.y,
legend.key,
legend.key.size,
legend.key.height,
legend.key.width,
legend.key.spacing,
legend.key.spacing.x,
legend.key.spacing.y,
legend.frame,
legend.ticks,
legend.ticks.length,
legend.axis.line,
legend.text,
legend.text.position,
legend.title,
legend.title.position,
legend.position,
legend.position.inside,
legend.direction,
legend.byrow,
legend.justification,
legend.justification.top,
legend.justification.bottom,
legend.justification.left,
legend.justification.right,
legend.justification.inside,
legend.location,
legend.box,
legend.box.just,
legend.box.margin,
legend.box.background,
legend.box.spacing,
panel.background,
panel.border,
panel.spacing,
panel.spacing.x,
panel.spacing.y,
panel.grid,
panel.grid.major,
panel.grid.minor,
panel.grid.major.x,
panel.grid.major.y,
panel.grid.minor.x,
panel.grid.minor.y,
panel.ontop,
plot.background,
plot.title,
plot.title.position,
plot.subtitle,
plot.caption,
plot.caption.position,
plot.tag,
plot.tag.position,
plot.tag.location,
plot.margin,
strip.background,
strip.background.x,
strip.background.y,
strip.clip,
strip.placement,
strip.text,
strip.text.x,
strip.text.x.bottom,
strip.text.x.top,
strip.text.y,
strip.text.y.left,
strip.text.y.right,
strip.switch.pad.grid,
strip.switch.pad.wrap,
complete = FALSE,
validate = TRUE
)
Arguments

... additional element specifications not part of base ggplot2. In general, these should also be defined in the element tree argument.

line all line elements (element_line())
rect all rectangular elements (element_rect())
text all text elements (element_text())
title all title elements: plot, axes, legends (element_text(); inherits from text)
aspect.ratio aspect ratio of the panel
axis.title, axis.title.x, axis.title.y, axis.title.x.top, axis.title.x.bottom, axis.title.y.left, axis.title.y.right labels of axes (element_text()). Specify all axes’ labels (axis.title), labels by plane (using axis.title.x or axis.title.y), or individually for each axis (using axis.title.x.bottom, axis.title.x.top, axis.title.y.left, axis.title.y.right). axis.title.*.* inherits from axis.title.* which inherits from axis.title, which in turn inherits from text
axis.text, axis.text.x, axis.text.y, axis.text.x.top, axis.text.x.bottom, axis.text.y.left, axis.text.y.right tick labels along axes (element_text()). Specify all axis tick labels (axis.text), tick labels by plane (using axis.text.x or axis.text.y), or individually for each axis (using axis.text.x.bottom, axis.text.x.top, axis.text.y.left, axis.text.y.right). axis.text.*.* inherits from axis.text.* which inherits from axis.text, which in turn inherits from text
axis.ticks, axis.ticks.x, axis.ticks.x.top, axis.ticks.x.bottom, axis.ticks.y, axis.ticks.y.left, axis.ticks.y.right tick marks along axes (element_line()). Specify all tick marks (axis.ticks), ticks by plane (using axis.ticks.x or axis.ticks.y), or individually for each axis (using axis.ticks.x.bottom, axis.ticks.x.top, axis.ticks.y.left, axis.ticks.y.right). axis.ticks.*.* inherits from axis.ticks.* which inherits from axis.ticks, which in turn inherits from line
axis.minor.ticks.x.top, axis.minor.ticks.x.bottom, axis.minor.ticks.y.left, axis.minor.ticks.y.right, axis.minor.ticks.x, axis.minor.ticks.y minor tick marks along axes (element_line()). axis.minor.ticks.*.* inherit from the corresponding major ticks axis.ticks.*.*
axis.ticks.length, axis.ticks.length.x, axis.ticks.length.x.top, axis.ticks.length.x.bottom, axis.ticks.length.y, axis.ticks.length.y.top, axis.ticks.length.y.bottom length of tick marks (unit)
axis.minor.ticks.length, axis.minor.ticks.length.x, axis.minor.ticks.length.x.top, axis.minor.ticks.length.x.bottom, axis.minor.ticks.length.y, axis.minor.ticks.length.y.top, axis.minor.ticks.length.y.bottom length of minor tick marks (unit), or relative to axis.ticks.length when provided with rel()
axis.line, axis.line.x, axis.line.x.top, axis.line.x.bottom, axis.line.y, axis.line.y.left, axis.line.y.right lines along axes (element_line()). Specify lines along all axes (axis.line), lines for each plane (using axis.line.x or axis.line.y), or individually for each axis (using axis.line.x.bottom, axis.line.x.top, axis.line.y.left, axis.line.y.right). axis.line.*.* inherits from axis.line.* which inherits from axis.line, which in turn inherits from line
legend.background background of legend (element_rect(); inherits from rect)
legend.margin the margin around each legend (margin())
theme

legend.spacing, legend.spacing.x, legend.spacing.y
the spacing between legends (unit). legend.spacing.x & legend.spacing.y
inherit from legend.spacing or can be specified separately

legend.key
background underneath legend keys (element_rect(); inherits from rect)

legend.key.size, legend.key.height, legend.key.width
size of legend keys (unit); key background height & width inherit from legend.key.size
or can be specified separately

legend.key.spacing, legend.key.spacing.x, legend.key.spacing.y
spacing between legend keys given as a unit. Spacing in the horizontal (x) and vertical (y) direction inherit from legend.key.spacing or can be specified separately.

legend.frame
frame drawn around the bar (element_rect()).

legend.ticks
tick marks shown along bars or axes (element_line())

legend.ticks.length
length of tick marks in legend (unit)

legend.axis.line
lines along axes in legends (element_line())

legend.text
legend item labels (element_text(); inherits from text)

legend.text.position
placement of legend text relative to legend keys or bars ("top", "right", "bottom" or "left"). The legend text placement might be incompatible with the legend's direction for some guides.

legend.title
title of legend (element_text(); inherits from title)

legend.title.position
placement of legend title relative to the main legend ("top", "right", "bottom" or "left").

legend.position
the default position of legends ("none", "left", "right", "bottom", "top", "inside")

legend.position.inside
A numeric vector of length two setting the placement of legends that have the "inside" position.

legend.direction
layout of items in legends ("horizontal" or "vertical")

legend.byrow
whether the legend-matrix is filled by columns (FALSE, the default) or by rows (TRUE).

legend.justification
anchor point for positioning legend inside plot ("center" or two-element numeric vector) or the justification according to the plot area when positioned outside the plot

legend.justification.top, legend.justification.bottom, legend.justification.left, legend.justification.right, legend.justification.inside
Same as legend.justification but specified per legend.position option.

legend.location
Relative placement of legends outside the plot as a string. Can be "panel" (default) to align legends to the panels or "plot" to align legends to the plot as a whole.
legend.box  arrangement of multiple legends ("horizontal" or "vertical")
legend.box.just  justification of each legend within the overall bounding box, when there are multiple legends ("top", "bottom", "left", or "right")
legend.box.margin  margins around the full legend area, as specified using margin()
legend.box.background  background of legend area (element_rect(); inherits from rect)
legend.box.spacing  The spacing between the plotting area and the legend box (unit)
panel.background  background of plotting area, drawn underneath plot (element_rect(); inherits from rect)
panel.border  border around plotting area, drawn on top of plot so that it covers tick marks and grid lines. This should be used with fill = NA (element_rect(); inherits from rect)
panel.spacing, panel.spacing.x, panel.spacing.y  spacing between facet panels (unit). panel.spacing.x & panel.spacing.y inherit from panel.spacing or can be specified separately.
panel.grid, panel.grid.major, panel.grid.minor, panel.grid.major.x, panel.grid.major.y, panel.grid.minor.x, panel.grid.minor.y  grid lines (element_line()). Specify major grid lines, or minor grid lines separately (using panel.grid.major or panel.grid.minor) or individually for each axis (using panel.grid.major.x, panel.grid.minor.x, panel.grid.major.y, panel.grid.minor.y). Y axis grid lines are horizontal and x axis grid lines are vertical. panel.grid.*.* inherits from panel.grid.* which inherits from panel.grid, which in turn inherits from line
panel.ontop  option to place the panel (background, gridlines) over the data layers (logical). Usually used with a transparent or blank panel.background.
plot.background  background of the entire plot (element_rect(); inherits from rect)
plot.title  plot title (text appearance) (element_text(); inherits from title) left-aligned by default
plot.title.position, plot.caption.position  Alignment of the plot title/subtitle and caption. The setting for plot.title.position applies to both the title and the subtitle. A value of "panel" (the default) means that titles and/or caption are aligned to the plot panels. A value of "plot" means that titles and/or caption are aligned to the entire plot (minus any space for margins and plot tag).
plot.subtitle  plot subtitle (text appearance) (element_text(); inherits from title) left-aligned by default
plot.caption  caption below the plot (text appearance) (element_text(); inherits from title) right-aligned by default
plot.tag  upper-left label to identify a plot (text appearance) (element_text(); inherits from title) left-aligned by default
theme

plot.tag.position
The position of the tag as a string ("topleft", "top", "topright", "left", "right", "bottomleft", "bottom", "bottomright") or a coordinate. If a coordinate, can be a numeric vector of length 2 to set the x,y-coordinate relative to the whole plot. The coordinate option is unavailable for plot.tag.location = "margin".

plot.tag.location
The placement of the tag as a string, one of "panel", "plot" or "margin". Respectively, these will place the tag inside the panel space, anywhere in the plot as a whole, or in the margin around the panel space.

plot.margin
margin around entire plot (unit with the sizes of the top, right, bottom, and left margins)

strip.background, strip.background.x, strip.background.y
background of facet labels (element_rect(); inherits from rect). Horizontal facet background (strip.background.x) & vertical facet background (strip.background.y) inherit from strip.background or can be specified separately

strip.clip
should strip background edges and strip labels be clipped to the extend of the strip background? Options are "on" to clip, "off" to disable clipping or "inherit" (default) to take the clipping setting from the parent viewport.

strip.placement
placement of strip with respect to axes, either "inside" or "outside". Only important when axes and strips are on the same side of the plot.

strip.text, strip.text.x, strip.text.y, strip.text.x.top, strip.text.x.bottom, strip.text.y.left, strip.text.y.right
facet labels (element_text(); inherits from text). Horizontal facet labels (strip.text.x) & vertical facet labels (strip.text.y) inherit from strip.text or can be specified separately. Facet strips have dedicated position-dependent theme elements (strip.text.x.top, strip.text.x.bottom, strip.text.y.left, strip.text.y.right) that inherit from strip.text.x and strip.text.y, respectively. As a consequence, some theme stylings need to be applied to the position-dependent elements rather than to the parent elements

strip.switch.pad.grid
space between strips and axes when strips are switched (unit)

strip.switch.pad.wrap
space between strips and axes when strips are switched (unit)

complete
set this to TRUE if this is a complete theme, such as the one returned by theme_grey(). Complete themes behave differently when added to a ggplot object. Also, when setting complete = TRUE all elements will be set to inherit from blank elements.

validate
TRUE to run validate_element(), FALSE to bypass checks.

Theme inheritance
Theme elements inherit properties from other theme elements hierarchically. For example, axis.title.x.bottom inherits from axis.title.x which inherits from axis.title, which in turn inherits from text. All text elements inherit directly or indirectly from text; all lines inherit from line, and all rectangular objects inherit from rect. This means that you can modify the appearance of multiple elements by setting a single high-level component.

Learn more about setting these aesthetics in vignette("ggplot2-specs").


See Also

+.gg() and %+replace%, element_blank(), element_line(), element_rect(), and element_text() for details of the specific theme elements.

Examples

```r
p1 <- ggplot(mtcars, aes(wt, mpg)) +
  geom_point() +
  labs(title = "Fuel economy declines as weight increases")

# Plot ---------------------------------------------------------------------
p1 + theme(plot.title = element_text(size = rel(2)))
p1 + theme(plot.background = element_rect(fill = "green"))

# Panels -------------------------------------------------------------------
p1 + theme(panel.background = element_rect(fill = "white", colour = "grey50"))
p1 + theme(panel.border = element_rect(linetype = "dashed", fill = NA))
p1 + theme(panel.grid.major = element_line(colour = "black"))
p1 + theme(
  panel.grid.major.y = element_blank(),
  panel.grid.minor.y = element_blank()
)

# Put gridlines on top of data
p1 + theme(
  panel.background = element_rect(fill = NA),
  panel.grid.major = element_line(colour = "grey50"),
  panel.ontop = TRUE
)

# Axes ---------------------------------------------------------------------
# Change styles of axes texts and lines
p1 + theme(axis.line = element_line(linewidth = 3, colour = "grey80"))
p1 + theme(axis.text = element_text(colour = "blue"))
p1 + theme(axis.ticks = element_line(linewidth = 2))

# Change the appearance of the y-axis title
p1 + theme(axis.title.y = element_text(size = rel(1.5), angle = 90))

# Make ticks point outwards on y-axis and inwards on x-axis
p1 + theme(
  axis.ticks.length.y = unit(.25, "cm"),
  axis.ticks.length.x = unit(-.25, "cm"),
  axis.text.x = element_text(margin = margin(t = .3, unit = "cm"))
)

# Legend -------------------------------------------------------------------
p2 <- ggplot(mtcars, aes(wt, mpg)) +
  geom_point(aes(colour = factor(cyl), shape = factor(vs))) +
  geom_point(aes(colour = factor(cyl), shape = factor(vs))) +
```
labs(
  x = "Weight (1000 lbs)",
  y = "Fuel economy (mpg)",
  colour = "Cylinders",
  shape = "Transmission"
)
p2

# Position
p2 + theme(legend.position = "none")
p2 + theme(legend.justification = "top")
p2 + theme(legend.position = "bottom")

# Or place legends inside the plot using relative coordinates between 0 and 1
# legend.justification sets the corner that the position refers to
p2 + theme(
  legend.position = c(.95, .95),
  legend.justification = c("right", "top"),
  legend.box.just = "right",
  legend.margin = margin(6, 6, 6, 6)
)

# The legend.box properties work similarly for the space around
# all the legends
p2 + theme(
  legend.box.background = element_rect(),
  legend.box.margin = margin(6, 6, 6, 6)
)

# You can also control the display of the keys
# and the justification related to the plot area can be set
p2 + theme(legend.key = element_rect(fill = "white", colour = "black"))
p2 + theme(legend.text = element_text(size = 8, colour = "red"))
p2 + theme(legend.title = element_text(face = "bold"))

# Strips --------------------------------------------------------------------
p3 <- ggplot(mtcars, aes(wt, mpg)) +
  geom_point() +
  facet_wrap(~ cyl)
p3

p3 + theme(strip.background = element_rect(colour = "black", fill = "white"))
p3 + theme(strip.text.x = element_text(colour = "white", face = "bold"))
# More direct strip.text.x here for top
# as in the facet_wrap the default strip.position is "top"
p3 + theme(strip.text.x.top = element_text(colour = "white", face = "bold"))
p3 + theme(panel.spacing = unit(1, "lines"))
**theme_get**

**Description**

The current/active theme (see `theme()`) is automatically applied to every plot you draw. Use `theme_get()` to get the current theme, and `theme_set()` to completely override it. `theme_update()` and `theme_replace()` are shorthands for changing individual elements.

**Usage**

```r
theme_get()

theme_set(new)

theme_update(...)

theme_replace(...)

e1 %+replace% e2
```

**Arguments**

- `new` : new theme (a list of theme elements)
- `...` : named list of theme settings
- `e1, e2` : Theme and element to combine

**Value**

`theme_set()`, `theme_update()`, and `theme_replace()` invisibly return the previous theme so you can easily save it, then later restore it.

**Adding on to a theme**

`+` and `%+replace%` can be used to modify elements in themes.

`+` updates the elements of `e1` that differ from elements specified (not NULL) in `e2`. Thus this operator can be used to incrementally add or modify attributes of a ggplot theme.

In contrast, `%+replace%` replaces the entire element; any element of a theme not specified in `e2` will not be present in the resulting theme (i.e. NULL). Thus this operator can be used to overwrite an entire theme.

`theme_update()` uses the `+` operator, so that any unspecified values in the theme element will default to the values they are set in the theme. `theme_replace()` uses `%+replace%` to completely replace the element, so any unspecified values will overwrite the current value in the theme with NULL.

In summary, the main differences between `theme_set()`, `theme_update()`, and `theme_replace()` are:

- `theme_set()` completely overrides the current theme.
- `theme_update()` modifies a particular element of the current theme using the `+` operator.
- `theme_replace()` modifies a particular element of the current theme using the `%+replace%` operator.
See Also

+.gg()

Examples

```r
p <- ggplot(mtcars, aes(mpg, wt)) +
  geom_point()

# Use theme_set() to completely override the current theme.
# theme_update() and theme_replace() are similar except they
# apply directly to the current/active theme.
# theme_update() modifies a particular element of the current theme.
# Here we have the old theme so we can later restore it.
# Note that the theme is applied when the plot is drawn, not
# when it is created.
old <- theme_set(theme_bw())
p
theme_set(old)
theme_update(panel.grid.minor = element_line(colour = "red"))
p
theme_set(old)
theme_replace(panel.grid.minor = element_line(colour = "red"))
p
theme_set(old)
p

# Modifying theme objects -----------------------------------------
# You can use + and %+replace% to modify a theme object.
# They differ in how they deal with missing arguments in
# the theme elements.
add_el <- theme_grey() +
  theme(text = element_text(family = "Times"))
add_el$text
rep_el <- theme_grey() %+replace%
  theme(text = element_text(family = "Times"))
rep_el$text
```

Housing sales in TX
Description

Information about the housing market in Texas provided by the TAMU real estate center, [https://www.recenter.tamu.edu/](https://www.recenter.tamu.edu/).

Usage

txhousing

Format

A data frame with 8602 observations and 9 variables:

- **city**: Name of multiple listing service (MLS) area
- **year,month,day**: Date
- **sales**: Number of sales
- **volume**: Total value of sales
- **median**: Median sale price
- **listings**: Total active listings
- **inventory**: "Months inventory": amount of time it would take to sell all current listings at current pace of sales.

vars

<table>
<thead>
<tr>
<th>vars</th>
<th>Quote faceting variables</th>
</tr>
</thead>
</table>

Description

Just like `aes()`, `vars()` is a quoting function that takes inputs to be evaluated in the context of a dataset. These inputs can be:

- variable names
- complex expressions

In both cases, the results (the vectors that the variable represents or the results of the expressions) are used to form faceting groups.

Usage

vars(...)

Arguments

... <data-masking> Variables or expressions automatically quoted. These are evaluated in the context of the data to form faceting groups. Can be named (the names are passed to a labeller).
See Also

aes(), facet_wrap(), facet_grid()

Examples

```r
p <- ggplot(mtcars, aes(wt, disp)) + geom_point()
p + facet_wrap(vars(vs, am))

# vars() makes it easy to pass variables from wrapper functions:
wrap_by <- function(...) {
  facet_wrap(vars(...), labeller = label_both)
}
p + wrap_by(vs)
p + wrap_by(vs, am)

# You can also supply expressions to vars(). In this case it's often a
# good idea to supply a name as well:
p + wrap_by(drat = cut_number(drat, 3))

# Let's create another function for cutting and wrapping a
# variable. This time it will take a named argument instead of dots,
# so we'll have to use the "enquote and unquote" pattern:
wrap_cut <- function(var, n = 3) {
  # Let's enquote the named argument `var` to make it auto-quoting:
  var <- enquo(var)
  # `as_label()` will create a nice default name:
  nm <- as_label(var)
  # Now let's unquote everything at the right place. Note that we also
  # unquote "n" just in case the data frame has a column named
  # "n". The latter would have precedence over our local variable
  # because the data is always masking the environment.
  wrap_by(nm := cut_number(var, n))
}

# Thanks to tidy eval idioms we now have another useful wrapper:
p + wrap_cut(drat)
```
Index

* aesthetics documentation
  aes, 7
  aes_colour_fill_alpha, 9
  aes_group_order, 14
  aes_linetype_size_shape, 16
  aes_position, 18
* alpha scales
  scale_alpha, 220
* colour scales
  scale_alpha, 220
  scale_colour_brewer, 224
  scale_colour_continuous, 228
  scale_colour_gradient, 231
  scale_colour_grey, 236
  scale_colour_hue, 239
  scale_colour_steps, 242
  scale_colour_viridis_d, 246
  scale_identity, 258
  scale_manual, 264
* datasets
  CoordSf, 30
  diamonds, 49
  economics, 51
  faithful, 61
  luv_colours, 203
  midwest, 204
  mpg, 206
  msleep, 206
  presidential, 215
  seals, 276
  stat_sf_coordinates, 284
  txhousing, 306
* facet labeler
  labeller, 195
* facet
  labellers, 197
* guides
  guide_bins, 182
  guide_colourbar, 184
  guide_coloursteps, 187
  guide_legend, 191
  guides, 174
* hplot
  print.ggplot, 216
* position adjustments
  position_dodge, 207
  position_identity, 209
  position_jitter, 210
  position_jitterdodge, 211
  position_nudge, 212
  position_stack, 213
* position scales
  scale_binned, 221
  scale_continuous, 250
  scale_date, 254
  scale_x_discrete, 273
+.gg, 6
+.gg(), 303, 306
%+%(+.gg), 6
%+replace%(theme_get), 305
%+replace%, 303
aes, 7, 10, 15, 17, 19
aes(), 7, 28, 33, 63, 66, 70, 72, 74, 79, 83, 86,
  89, 94, 98, 102, 104, 109, 112, 114,
  117, 122, 125, 129, 131, 135, 138,
  141, 144, 147, 150, 154, 158, 161,
  280, 282, 284, 285, 287, 290, 294,
  307, 308
aes_colour_fill_alpha, 8, 9, 15, 17, 19
aes_eval, 11
aes_group_order, 8, 10, 14, 17, 19
aes_group_order(), 17
aes_linetype_size_shape, 8, 10, 15, 16, 19
aes_position, 8, 10, 15, 17, 18
aesthetics, 11
after_scale(aes_eval), 11
after_stat(aes_eval), 11
akima::bilinear(), 78
INDEX

alpha, 67, 76, 80, 81, 84, 87, 91, 95, 99, 103, 110, 113, 115, 119, 122, 126, 130, 132, 139, 142, 146, 148, 152, 156, 159, 162
alt_text (get_alt_text), 164
annotate, 20
annotate(), 19, 118
annotation_custom, 21
annotation_logticks, 22
annotation_map, 24
annotation_map(), 40
annotation_raster, 26
as_labeller(), 195, 196, 198
autolayer, 27
autolayer(), 28
autoplot, 27
autoplot(), 27
base::cut(), 183, 189
base::cut.default, 48
base::strwrap(), 198
binned_scale, 243
binned_scale(), 221, 226, 248
borders, 28
boxplot(), 75
boxplot.stats(), 75
bquote(), 198
color (aes_colour_fill_alpha), 9
color steps, 231
colors(), 203
colour, 67, 76, 80, 81, 84, 87, 91, 95, 99, 103, 110, 113, 115, 119, 122, 126, 130, 132, 139, 142, 146, 149, 152, 156, 159, 162
colour (aes_colour_fill_alpha), 9
colour aesthetics, 221, 227, 229, 235, 238, 241, 245, 249, 267
complete themes, 295
continuous_scale, 233, 272
continuous_scale(), 221, 226, 248, 259
coord_cartesian, 36
coord_cartesian(), 41, 43, 201, 223, 234, 244, 252, 257, 263, 271
coord_equal (coord_fixed), 38
coord_fixed, 38
coord_flip, 39
coord_map, 40
coord_polar, 43
coord_quickmap (coord_map), 40
coord_radial (coord_polar), 43
coord_sf (Coordsf), 30
coord_sf(), 25, 40, 121
coord_trans, 45
coord_trans(), 23
Coordsf, 30
cut_interval, 47
cut_number (cut_interval), 47
cut_width (cut_interval), 47
Delayed evaluation, 8
delayed evaluation, 68, 71, 76, 81, 84, 91, 96, 100, 106, 110, 113, 137, 139, 156, 162, 280, 286, 288
density(), 90, 162
derive (sec_axis), 277
diamonds, 49
differentiation related aesthetics, 262, 264, 267, 269, 273
discrete_scale, 237, 239, 261, 265, 268, 274
discrete_scale(), 221, 226, 248, 259
draw_key, 49
draw_key_abline (draw_key), 49
draw_key_blank (draw_key), 49
draw_key_boxplot (draw_key), 49
draw_key_crossbar (draw_key), 49
draw_key_dotplot (draw_key), 49
draw_key_label (draw_key), 49
draw_key_linerange (draw_key), 49
draw_key_path (draw_key), 49
draw_key_point (draw_key), 49
draw_key_pointrange (draw_key), 49
draw_key_polygon (draw_key), 49
draw_key_rect (draw_key), 49
draw_key_smooth (draw_key), 49
draw_key_text (draw_key), 49
draw_key_timeseries (draw_key), 49
draw_key_vline (draw_key), 49
draw_key_vpath (draw_key), 49
dup_axis (sec_axis), 277
economics, 51
economics_long (economics), 51
INDEX

element, 52, 178
element_blank (element), 52
element_blank(), 303
element_line (element), 52
element_line(), 299–301, 303
element_rect (element), 52
element_rect(), 299–303
element_text (element), 52
element_text(), 176, 178, 181, 299–303
expand_limits, 54
expand_limits(), 72, 202
expand_scale (expansion), 55
expansion, 55
expansion(), 223, 234, 238, 240, 244, 249, 252, 257, 272, 275

facet_grid, 56
facet_grid(), 59, 195, 219, 308
facet_wrap, 58
facet_wrap(), 56, 195, 198, 219, 308
faithful, 61
faithfulld, 61
fill, 67, 71, 76, 81, 84, 91, 95, 99, 113, 115, 122, 130, 132, 142, 146, 156, 162
fill (aes colour_fill_alpha), 9
format.ggproto (print.ggproto), 217
fortify, 62
fortify.lm(), 62

geom_abline, 62
geom_abline(), 21
geom_area (geom.ribbon), 143
geom_area(), 213
geom_bar, 65
geom_bar(), 15, 106, 145, 146, 213, 221
geom_bin2d (geom_bin2d), 69
geom_bin2d, 69
geom_bin2d(), 84, 96, 112, 128
geom_blank, 72
geom_blank(), 54
geom_boxplot, 73
geom_boxplot(), 19, 116, 129, 137, 160
geom_col (geom_bar), 65

geom_contour, 78, 94
geom_contour(), 96
geom_contour_filled (geom_contour), 78
geom_contour_filled(), 96
geom_count, 82
geom_count(), 128, 129
geom_crossbar, 85
geom_crossbar(), 19, 292
geom_curve (geom_segment), 150
geom_curve(), 19
geom_density, 89
geom_density(), 93, 160
geom_density2d (geom_density_2d), 92
geom_density2d(), 129
geom_density2d_filled
(geom_density_2d), 92
geom_density_2d, 92
geom_density_2d(), 82, 129
geom_density_2d_filled
(geom_density_2d), 92
geom_dotplot, 97
geom_errorbar (geom_crossbar), 85
geom_errorbar(), 19, 101, 292
geom_errorbarh, 101
geom_errorbarh(), 88
geom_freqpoly, 103
geom_freqpoly(), 92
geom_function, 108
geom_hex, 111
geom_hex(), 129
geom_histogram (geom_freqpoly), 103
geom_histogram(), 12, 15, 68, 92, 279
geom_hline (geom_abline), 62
geom_hline(), 21
geom_jitter, 114
geom_jitter(), 77, 128
geom_label, 116
geom_line (geom_path), 124
geom_line(), 9, 15, 17, 19, 64, 106, 152
geom_linerange (geom_crossbar), 85
geom_linerange(), 19, 146, 292
geom_map, 121
geom_map(), 25, 40
geom_path, 124
geom_path(), 19, 35, 131, 133, 152
geom_point, 128
geom_point(), 9, 17, 19, 35, 69, 82, 116
geom_pointrange (geom_crossbar), 85
geom_pointrange(), 17, 19, 292
gem_polygon, 28, 31
geom_polygon(), 9, 35, 127, 146
geom_qq (geom_qq_line), 134
geom_qq_line, 134
geom_quantile, 137
geom_quantile(), 77, 129
geom_raster, 140
geom_raster(), 26
geom_rect (geom_raster), 140
geom_rect(), 9, 19
geomribbon, 143
geomribbon(), 133
geom_segment, 150
geom_segment(), 19, 64, 126, 127, 158
geom_sf (CoordSf), 30
geom_sf(), 25, 121
geom_sf_label (CoordSf), 30
geom_sf_label(), 284
geom_sf_text (CoordSf), 30
geom_sf_text(), 284
geom_smooth, 153
geom_smooth(), 88, 129
geom_spoke, 158
geom_spoke(), 152
gem_step (geom_path), 124
geom_text (geom_label), 116
geom_text(), 25, 212
gem_tile (geom_raster), 140
gem_tile(), 41, 78
geom_violin, 160
geom_violin(), 77, 92, 163
gem_vline (geom_abline), 62
gem_vline(), 21
GeomSf (CoordSf), 30
get_alt_text, 164, 200
ggplot, 165
ggproto, 167
ggproto_parent (ggproto), 167
ggsave, 169
ggsf (CoordSf), 30
ggtheme, 171
ggtitle (labs), 200
glm(), 156
gradient scale, 242
gray.colors, 236
grDevices::colors(), 9
grid::arrow(), 53, 126, 151
grid::curveGrob(), 150
grid::pathGrob(), 28, 132
grid::unit(), 23, 148, 177, 190
group, 67, 68, 71, 76, 80, 81, 84, 87, 91, 95, 99, 103, 110, 113, 115, 119, 122, 126, 130, 132, 136, 139, 142, 146, 149, 152, 156, 159, 162, 292, 295
group (aes_group_order), 14
guide_axis, 175, 178
guide_axis(), 278
guide_axis_logticks, 177
guide_axis_logticks(), 22
guide_axis_stack, 179
guide_axis_theta, 180
guide_bins, 174, 182, 186, 189, 192
guide_colorbar (guide_colourbar), 184
guide_colorsteps (guide_coloursteps), 187
guide_colourbar, 174, 183, 184, 189, 192
guide_colourbar(), 174, 187
guide_coloursteps, 174, 183, 186, 187, 192
guide_coloursteps(), 182
guide_custom, 189
guide Legend, 174, 183, 186, 189, 191
guide_legend(), 174, 182
guide_none, 193
guides, 174, 183, 186, 189, 192
guides(), 186, 192, 224, 238, 240, 249, 252, 257, 261, 264, 266, 269, 272, 275
hmisc, 194
Hmisc::capitalize, 195
Hmisc::smean.cl.boot, 194
Hmisc::smean.cl.normal, 194
Hmisc::smean.sd, 194
Hmisc::smedian.hilow, 194
hsv, 248
interp::interp(), 78
is.ggproto (ggproto), 167
label_both (labellers), 197
INDEX

label_bquote, 199
label_bquote(), 198
label_context (labellers), 197
label_parsed (labellers), 197
label_parsed(), 57, 59
label_value (labellers), 197
label_value(), 57, 59
label_wrap_gen (labellers), 197
labeller, 195, 307
labeller(), 57, 59, 198, 199
labellers, 196, 197, 199
labs, 200
labs(), 176, 178, 180–182, 185, 188, 191, 193, 252, 273
lambda, 223, 233, 234, 237, 238, 240, 244, 251, 252, 256, 257, 261, 263, 265, 266, 268, 269, 271, 272, 274, 275
layer(), 21, 34, 49, 63, 66, 70, 72, 74, 80, 83, 87, 90, 98, 102, 105, 109, 113, 115, 118, 122, 125, 129, 132, 136, 139, 141, 145, 148, 151, 154, 159, 161, 180, 282, 284, 286, 288, 291, 295
lims, 201
lims(), 269, 273
linetype, 67, 68, 76, 80, 81, 87, 91, 95, 96, 99, 103, 110, 113, 122, 126, 132, 139, 142, 146, 149, 152, 156, 159, 162
linetype (aes_linetype_size_shape), 16
linewidth, 67, 68, 76, 80, 81, 87, 91, 95, 96, 103, 110, 113, 122, 126, 132, 139, 142, 146, 149, 152, 156, 159, 162
lm(), 156
loess(), 156
lув_colours, 203
mapproj::mapproject(), 40, 41
maps::map(), 28
margin (element), 52
margin(), 53, 299, 301
MASS::bwplot, 95
MASS::eqscplot(), 38
MASS::kde2d(), 93
mean_cl_boot (hmisc), 194
mean_cl_normal (hmisc), 194
mean_sd1 (hmisc), 194
mean_se, 204
mean_se(), 292
median_hilow (hmisc), 194
mgcv::gam(), 154
midwest, 204
mpg, 206
msleep, 206
options(), 228
plot::ggplot (print.ggplot), 216
png(), 169
png(), 170
position documentation, 224, 253, 257, 275
position_dodge, 207, 209–213
position_dodge(), 67, 68
position_dodge2 (position_dodge), 207
position_dodge2(), 67, 68
position_fill (position_stack), 213
position_fill(), 67
position_identity, 208, 209, 210–213
position_jitter, 208, 209, 210, 211–213
position_jitterdodge, 208–210, 211, 212, 213
position_nudge, 208–211, 212, 213
position_stack, 208–212, 213
position_stack(), 67, 145
predict(), 155
presidential, 215
pretty(), 80, 94
print.ggplot, 216
print.ggproto, 217
qplot, 218
quantreg::rq(), 139
quantreg::rqss(), 139
quasiquotation, 8
quickplot (qplot), 218
quoting function, 8, 307
RCColorBrewer::brewer_pal(), 226
rel (element), 52
rel(), 177
rescale(), 226, 235, 245, 249
resolution, 220
resolution(), 66
rlang::as_function(), 110
scale_alpha, 220, 227, 229, 235, 238, 241, 245, 249, 259, 267
scale_alpha(), 10, 259, 267
scale_alpha_binned (scale_alpha), 220
scale_alpha_continuous (scale_alpha), 220
scale_alpha_date (scale_alpha), 220
scale_alpha_datetime (scale_alpha), 220
scale_alpha_discrete (scale_alpha), 220
scale_alpha_identity (scale_identity), 258
scale_alpha_identity(), 10, 221, 267
scale_alpha_manual (scale_manual), 264
scale_alpha_manual(), 10, 221, 259
scale_alpha_ordinal (scale_alpha), 220
scale_binned, 221
scale_binned(), 19
scale_color_binned
(scale_colour_continuous), 228
scale_color_brewer
(scale_colour_brewer), 224
scale_color_continuous
(scale_colour_continuous), 228
scale_color_date
(scale_colour_date), 231
scale_color_datetime
(scale_colour_datetime), 231
scale_color_discrete
(scale_colour_discrete), 230
scale_color_distiller
(scale_colour_distiller), 224
scale_color_fermenter
(scale_colour_fermenter), 224
scale_color_gradient
(scale_colour_gradient), 231
scale_color_gradient2
(scale_colour_gradient), 231
scale_color_gradientn
(scale_colour_gradient), 231
scale_color_gradientn
(scale_colour_gradient), 231
scale_color_grey (scale_colour_grey), 236
scale_color_hue (scale_colour_hue), 239
scale_color_identity (scale_identity), 258
scale_color_manual (scale_manual), 264
scale_color_ordinal
(scale_colour_viridis_d), 246
scale_color_steps (scale_colour_steps), 242
scale_color_steps2
(scale_colour_steps), 242
scale_color_stepsn
(scale_colour_steps), 242
scale_color_viridis_b
(scale_colour_viridis_d), 246
scale_color_viridis_c
(scale_colour_viridis_d), 246
scale_color_viridis_d
(scale_colour_viridis_d), 246
scale_colour_binned
(scale_colour_continuous), 228
scale_colour_brewer, 221, 224, 229, 235, 238, 241, 245, 249, 259, 267
scale_colour_brewer(), 10
scale_colour_continuous, 221, 227, 228, 235, 238, 241, 245, 249, 259, 267
scale_colour_date
(scale_colour_date), 231
scale_colour_datetime
(scale_colour_date), 231
scale_colour_discrete, 230
scale_colour_distiller
(scale_colour_distiller), 224
scale_colour_fermenter
(scale_colour_fermenter), 224
scale_colour_gradient
(scale_colour_gradient), 231
scale_colour_gradient2
(scale_colour_gradient), 231
scale_colour_gradient2(), 234
scale_colour_gradientn
(scale_colour_gradient), 231
scale_colour_gradientn(), 234
scale_colour_grey, 221, 227, 229, 235, 236, 241, 245, 249, 259, 267
scale_colour_grey(), 10
scale_colour_hue, 221, 227, 229, 235, 238, 239, 245, 249, 259, 267
scale_colour_hue(), 10, 230
scale_colour_identity, 221, 227, 229, 235, 238, 241, 245, 249, 267
scale_colour_identity (scale_identity), 258
scale_colour_identity(), 10
scale_colour_manual, 221, 227, 229, 235, 238, 241, 245, 249, 259
scale_colour_manual (scale_manual), 264
scale_colour_manual()., 10
scale_colour_ordinal (scale_colour_viridis_d), 246
scale_colour_steps, 221, 227, 229, 235, 238, 241, 242, 249, 259, 267
scale_colour_steps(), 229, 235
scale_colour_steps2 (scale_colour_steps), 242
scale_colour_stepsn (scale_colour_steps), 242
scale_colour_viridis_b (scale_colour_viridis_d), 246
scale_colour_viridis_b(), 229
scale_colour_viridis_c (scale_colour_viridis_d), 246
scale_colour_viridis_c(), 229
scale_colour_viridis_d, 221, 227, 229, 235, 238, 241, 245, 246, 259, 267
scale_colour_viridis_d(), 10
scale_continuous, 250
scale_continuous(), 19
scale_continuous_identity (scale_identity), 258
scale_date, 254
scale_date(), 19
scale_discrete(), 19
scale_discrete_identity (scale_identity), 258
scale_discrete_manual (scale_manual), 264
scale_fill_binned (scale_colour_continuous), 228
scale_fill_brewer (scale_colour_brewer), 224
scale_fill_brewer(), 10, 230
scale_fill_continuous (scale_colour_continuous), 228
scale_fill_discrete (scale_colour_discrete), 228
scale_fill_date (scale_colour_gradient), 231
scale_fill_datetime (scale_colour_gradient), 231
scale_fill_distiller (scale_colour_brewer), 224
scale_fill_distiller(), 262, 267
scale_fill_fermenter (scale_colour_brewer), 224
scale_fill_gradient (scale_colour_gradient), 231
scale_fill_gradient2 (scale_colour_gradient), 231
scale_fill_gradientn (scale_colour_gradient), 231
scale_fill_grey (scale_colour_grey), 236
scale_fill_grey(), 10
scale_fill_hue (scale_colour_hue), 239
scale_fill_hue(), 10, 230
scale_fill_identity (scale_identity), 258
scale_fill_identity(), 10
scale_fill_manual (scale_manual), 264
scale_fill_manual(), 10
scale_fill_ordinal (scale_colour_viridis_d), 246
scale_fill_steps (scale_colour_steps), 242
scale_fill_steps2 (scale_colour_steps), 242
scale_fill_stepsn (scale_colour_steps), 242
scale_fill_viridis_b (scale_colour_viridis_d), 246
scale_fill_viridis_b(), 229
scale_fill_viridis_c (scale_colour_viridis_d), 246
scale_fill_viridis_c(), 229
scale_fill_viridis_d (scale_colour_viridis_d), 246
scale_fill_viridis_d(), 10
scale_identity, 258
scale_linetype, 258
scale_linetype(), 17, 259, 267
scale_linetype_binned (scale_linetype), 260
scale_linetype_continuous (scale_linetype), 260
scale_linetype_discrete (scale_linetype), 260
scale_linetype_identity (scale_identity), 258
scale_linetype_identity(), 262, 267
scale_linetype_manual (scale_manual), 264
scale_linetype_manual(), 259, 262
scale_linewidth, 262
scale_linewidth(), 17, 273
scale_linewidth_binned (scale_linewidth), 262
scale_linewidth_continuous (scale_linewidth), 262
scale_linewidth_date (scale_linewidth), 262
scale_linewidth_datetime (scale_linewidth), 262
scale_linewidth_discrete (scale_linewidth), 262
scale_linewidth_identity (scale_identity), 258
scale_linewidth_manual (scale_manual), 264
scale_linewidth_ordinal (scale_linewidth), 262
scale_manual, 264
scale_radius (scale_size), 270
scale_shape, 268
scale_shape(), 17, 259, 267
scale_shape_binned (scale_shape), 268
scale_shape_continuous (scale_shape), 268
scale_shape_discrete (scale_shape), 268
scale_shape_identity (scale_identity), 258
scale_shape_identity(), 267, 269
scale_shape_manual (scale_manual), 264
scale_shape_manual(), 259, 268, 269
scale_shape_ordinal (scale_shape), 268
scale_size, 270
scale_size(), 17, 259, 267
scale_size_area (scale_size), 270
scale_size_area(), 273
scale_size_binned (scale_size), 270
scale_size_binned_area (scale_size), 270
scale_size_continuous (scale_size), 270
scale_size_date (scale_size), 270
scale_size_datetime (scale_size), 270
scale_size_discrete (scale_size), 270
scale_size_identity (scale_identity), 258
scale_size_identity(), 267
scale_size_manual (scale_manual), 264
scale_size_manual(), 259
scale_size_ordinal (scale_size), 270
scale_x_binned (scale_binned), 221
scale_x_continuous, 224, 257, 275
scale_x_continuous (scale_continuous), 250
scale_x_continuous(), 202
scale_x_date, 224, 253, 275
scale_x_date (scale_date), 254
scale_x_date(), 202
scale_x_datetime (scale_date), 254
scale_x_discrete, 224, 253, 257, 273
scale_x_discrete(), 202
scale_x_log10 (scale_continuous), 250
scale_x_reverse (scale_continuous), 250
scale_x_sqrt (scale_continuous), 250
scale_x_time (scale_date), 254
scale_y_binned (scale_binned), 221
scale_y_continuous (scale_continuous), 250
scale_y_continuous(), 23
scale_y_date (scale_date), 254
scale_y_datetime (scale_date), 254
scale_y_discrete (scale_discrete), 273
scale_y_discrete(), 273
scale_y_log10 (scale_continuous), 250
scale_y_log10(), 23
scale_y_reverse (scale_continuous), 250
scale_y_sqrt (scale_continuous), 250
scale_y_time (scale_date), 254
scales::censor(), 223, 234, 244, 252, 257, 272
scales::extended_breaks(), 223, 233, 244, 251, 263, 271
scales::new_transform(), 46, 224, 245, 252, 264, 272
scales::pal_area(), 233
scales::pal💉(), 237, 239, 261, 265, 268, 274
scales::pal_seq_gradient(), 235, 245
scales::rescale(), 234
scales::squish(), 223, 234, 244, 252, 257, 272
scales::squish_infinite(), 223, 234, 244, 252, 257, 272
seals, 276
sec_axis, 277
sec_axis(), 252, 257
shape, 76, 84, 115, 130
shape (aes_linetype_size_shape), 16
size, 76, 84, 116, 119, 130
INDEX

size(aes_linetype_size_shape), 16
stage(aes_eval), 11
stat(aes_eval), 11
stat_align(geom_ribbon), 143
stat_bin(statgeom_frequopoly), 103
stat_bin(), 12, 68, 91, 289
stat_bin2d(stat_bin_2d), 69
stat_bin_2d(stat_bin_2d), 69
stat_bin_2d(stat_bin_2d), 114, 289
stat_bin_hex(geom_hex), 111
stat_bin_hex(), 71
stat_binhex(stat_bin_2d), 111
stat_boxplot(geom_boxplot), 73
stat_contour(geom_contour), 78
stat_contour(), 96
stat_contour_filled(geom_contour), 78
stat_contour_filled(), 96, 183, 189
stat_count(geom_bar), 65
stat_count(), 106, 107
stat_density(stat_geom_density), 89
stat_density(), 163
stat_density2d(stat_geom_density_2d), 92
stat_density2d_filled(stat_geom_density_2d), 92
stat_density2d(stat_geom_density_2d), 92
stat_density2d(stat_geom_density_2d), 92
stat_density2d_filled(stat_geom_density_2d), 92
stat_ecdf(), 279
stat_ellipse(), 281
stat_function(geom_function), 108
stat_identity(), 283
stat_qq(geom_qq_line), 134
stat_qq_line(geom_qq_line), 134
stat_quantile(geom_quantile), 137
stat_sf(CoordSf), 30
stat_sf_coordinates(), 284
stat_sf_coordinates(), 35
stat_smooth(geom_smooth), 153
stat_spoke(geom_spoke), 158
stat_sum(stat_sum), 82
stat_summary(stat_summary_bin), 289
stat_summary(), 88, 194, 204, 287
stat_summary2d(stat_summary_2d), 287
stat_summary_2d(stat_summary_2d), 287
stat_summary_2d(stat_summary_2d), 287
stat_summary_2d(stat_summary_2d), 287
stat_summary_2d(stat_summary_2d), 287
stat_summary_hex(stat_summary_2d), 287
stat_summary_hex(), 289
stat_unique, 294
stat_ydensity(geom_violin), 160
stats::bw.nrd(), 90, 162
stats::loess(), 154
StatSf(CoordSf), 30
StatSfCoordinates
(stat_sf_coordinates), 284
strftime(), 256
theme, 52, 176, 178, 180–182, 185, 188, 190, 191, 295
theme(), 6, 7, 171, 176, 178, 181, 305
theme_bw(ggtheme), 171
theme_classic(ggtheme), 171
theme_dark(ggtheme), 171
theme_get(), 304
theme_gray(ggtheme), 171
test_theme_gray(), 171
test_theme_gray(), 302
test_theme_light(ggtheme), 171
test_theme_linedraw(ggtheme), 171
test_theme_minimal(ggtheme), 171
test_theme_replace(theme_get), 305
test_theme_set(theme_get), 305
test_theme_test(ggtheme), 171
test_theme_update(theme_get), 305
test_theme_update(), 295
test_theme_update(), 171
test_theme_void(ggtheme), 171
test_transformation_object, 223, 233, 244, 251,
263, 271
txhousing, 306

unit(), 180
test_unit(), 180
vars(), 307
vars(), 8, 56, 59

waiver(), 176, 178, 180–182, 185, 188, 191, 193

x, 67, 68, 71, 75, 80, 81, 84, 87, 91, 95, 99,
110, 113, 115, 118, 126, 130, 132,
136, 139, 142, 146, 149, 152, 156,
159, 162, 292
x(aes_position), 18
xend, 152
xend(aes_position), 18
xlab(labs), 200
xlim(lims), 201
xmax, 76, 87, 102, 146
xmax(aes_position), 18
xmin, 76, 87, 102, 146
xmin(aes_position), 18
y, 67, 68, 71, 75, 80, 81, 84, 87, 91, 95, 99,
    103, 110, 113, 115, 118, 126, 130,
    132, 136, 139, 142, 146, 149, 152,
    156, 159, 162, 292
y(aes_position), 18
yend, 152
yend(aes_position), 18
ylab(labs), 200
ylim(lims), 201
ymax, 76, 87, 146, 156
ymax(aes_position), 18
ymin, 76, 87, 146, 156
ymin(aes_position), 18