

# Package ‘ggplot2’

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**Version** 2.2.1

**Title** Create Elegant Data Visualisations Using the Grammar of Graphics

**Description** A system for 'declaratively' creating graphics, based on ``The Grammar of Graphics''. You provide the data, tell 'ggplot2' how to map variables to aesthetics, what graphical primitives to use, and it takes care of the details.

**Depends** R (>= 3.1)

**Imports** digest, grid, gtable (>= 0.1.1), MASS, plyr (>= 1.7.1), reshape2, scales (>= 0.4.1), stats, tibble, lazyeval

**Suggests** covr, ggplot2movies, hexbin, Hmisc, lattice, mapproj, maps, maptools, mgcv, multcomp, nlme, testthat (>= 0.11.0), quantreg, knitr, rpart, rmarkdown, svglite

**Enhances** sp

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**URL** <http://ggplot2.tidyverse.org>, <https://github.com/tidyverse/ggplot2>

**BugReports** <https://github.com/tidyverse/ggplot2/issues>

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**Collate** 'ggproto.r' 'aaa-.r' 'aes-calculated.r'  
'aes-colour-fill-alpha.r' 'aes-group-order.r'  
'aes-linetype-size-shape.r' 'aes-position.r' 'utilities.r'  
'aes.r' 'legend-draw.r' 'geom-.r' 'annotation-custom.r'  
'annotation-logticks.r' 'geom-polygon.r' 'geom-map.r'  
'annotation-map.r' 'geom-raster.r' 'annotation-raster.r'  
'annotation.r' 'autoplot.r' 'axis-secondary.R' 'bench.r'  
'bin.R' 'coord-.r' 'coord-cartesian-.r' 'coord-fixed.r'  
'coord-flip.r' 'coord-map.r' 'coord-munch.r' 'coord-polar.r'  
'coord-quickmap.R' 'coord-transform.r' 'data.R' 'facet-.r'  
'facet-grid.r' 'facet-null.r' 'facet-wrap.r' 'fortify-lm.r'  
'fortify-map.r' 'fortify-multcomp.r' 'fortify-spatial.r'  
'fortify.r' 'stat-.r' 'geom-abline.r' 'geom-rect.r'  
'geom-bar.r' 'geom-bin2d.r' 'geom-blank.r' 'geom-boxplot.r'  
'geom-col.r' 'geom-path.r' 'geom-contour.r' 'geom-count.r'

```

'geom-crossbar.r' 'geom-segment.r' 'geom-curve.r'
'geom-defaults.r' 'geom-ribbon.r' 'geom-density.r'
'geom-density2d.r' 'geom-dotplot.r' 'geom-errorbar.r'
'geom-errorbarh.r' 'geom-freqpoly.r' 'geom-hex.r'
'geom-histogram.r' 'geom-hline.r' 'geom-jitter.r'
'geom-label.R' 'geom-linrange.r' 'geom-point.r'
'geom-pointrange.r' 'geom-quantile.r' 'geom-rug.r'
'geom-smooth.r' 'geom-spoke.r' 'geom-text.r' 'geom-tile.r'
'geom-violin.r' 'geom-vline.r' 'ggplot2.r' 'grob-absolute.r'
'grob-dotstack.r' 'grob-null.r' 'grouping.r' 'guide-colorbar.r'
'guide-legend.r' 'guides-.r' 'guides-axis.r' 'guides-grid.r'
'hexbin.R' 'labeller.r' 'labels.r' 'layer.r' 'layout.R'
'limits.r' 'margins.R' 'plot-build.r' 'plot-construction.r'
'plot-last.r' 'plot.r' 'position-.r' 'position-collide.r'
'position-dodge.r' 'position-identity.r' 'position-jitter.r'
'position-jitterdodge.R' 'position-nudge.R' 'position-stack.r'
'quick-plot.r' 'range.r' 'save.r' 'scale-.r' 'scale-alpha.r'
'scale-brewer.r' 'scale-continuous.r' 'scale-date.r'
'scale-discrete-.r' 'scale-gradient.r' 'scale-grey.r'
'scale-hue.r' 'scale-identity.r' 'scale-linetype.r'
'scale-manual.r' 'scale-shape.r' 'scale-size.r' 'scale-type.R'
'scales-.r' 'stat-bin.r' 'stat-bin2d.r' 'stat-bindot.r'
'stat-binhex.r' 'stat-boxplot.r' 'stat-contour.r'
'stat-count.r' 'stat-density-2d.r' 'stat-density.r'
'stat-ecdf.r' 'stat-ellipse.R' 'stat-function.r'
'stat-identity.r' 'stat-qq.r' 'stat-quantile.r'
'stat-smooth-methods.r' 'stat-smooth.r' 'stat-sum.r'
'stat-summary-2d.r' 'stat-summary-bin.R' 'stat-summary-hex.r'
'stat-summary.r' 'stat-unique.r' 'stat-ydensity.r' 'summary.r'
'theme-elements.r' 'theme.r' 'theme-defaults.r'
'theme-current.R' 'translate-qplot-ggplot.r'
'translate-qplot-lattice.r' 'utilities-break.r'
'utilities-grid.r' 'utilities-help.r' 'utilities-matrix.r'
'utilities-resolution.r' 'utilities-table.r' 'zxx.r' 'zzz.r'

```

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<a href="#">+.gg</a>	<a href="#">5</a>
<a href="#">aes</a>	<a href="#">6</a>
<a href="#">aes_</a>	<a href="#">7</a>
<a href="#">aes_colour_fill_alpha</a>	<a href="#">8</a>
<a href="#">aes_group_order</a>	<a href="#">9</a>
<a href="#">aes_linetype_size_shape</a>	<a href="#">11</a>
<a href="#">aes_position</a>	<a href="#">12</a>
<a href="#">annotate</a>	<a href="#">13</a>
<a href="#">annotation_custom</a>	<a href="#">14</a>
<a href="#">annotation_logticks</a>	<a href="#">15</a>
<a href="#">annotation_map</a>	<a href="#">17</a>
<a href="#">annotation_raster</a>	<a href="#">18</a>
<a href="#">autoplot</a>	<a href="#">19</a>
<a href="#">borders</a>	<a href="#">19</a>
<a href="#">coord_cartesian</a>	<a href="#">20</a>
<a href="#">coord_fixed</a>	<a href="#">21</a>
<a href="#">coord_flip</a>	<a href="#">22</a>
<a href="#">coord_map</a>	<a href="#">23</a>
<a href="#">coord_polar</a>	<a href="#">25</a>
<a href="#">coord_trans</a>	<a href="#">26</a>
<a href="#">cut_interval</a>	<a href="#">28</a>
<a href="#">diamonds</a>	<a href="#">29</a>
<a href="#">economics</a>	<a href="#">30</a>
<a href="#">expand_limits</a>	<a href="#">31</a>
<a href="#">facet_grid</a>	<a href="#">31</a>
<a href="#">facet_wrap</a>	<a href="#">34</a>
<a href="#">faithfuld</a>	<a href="#">36</a>
<a href="#">fortify</a>	<a href="#">36</a>
<a href="#">geom_abline</a>	<a href="#">37</a>
<a href="#">geom_bar</a>	<a href="#">39</a>
<a href="#">geom_bin2d</a>	<a href="#">42</a>
<a href="#">geom_blank</a>	<a href="#">43</a>
<a href="#">geom_boxplot</a>	<a href="#">44</a>
<a href="#">geom_contour</a>	<a href="#">48</a>
<a href="#">geom_count</a>	<a href="#">50</a>
<a href="#">geom_crossbar</a>	<a href="#">52</a>
<a href="#">geom_density</a>	<a href="#">55</a>
<a href="#">geom_density_2d</a>	<a href="#">57</a>
<a href="#">geom_dotplot</a>	<a href="#">59</a>
<a href="#">geom_errorbarh</a>	<a href="#">62</a>
<a href="#">geom_freqpoly</a>	<a href="#">64</a>
<a href="#">geom_hex</a>	<a href="#">67</a>
<a href="#">geom_jitter</a>	<a href="#">69</a>
<a href="#">geom_label</a>	<a href="#">71</a>
<a href="#">geom_map</a>	<a href="#">75</a>
<a href="#">geom_path</a>	<a href="#">77</a>

geom_point . . . . .	80
geom_polygon . . . . .	83
geom_qq . . . . .	85
geom_quantile . . . . .	87
geom_raster . . . . .	89
geom_ribbon . . . . .	91
geom_rug . . . . .	93
geom_segment . . . . .	95
geom_smooth . . . . .	97
geom_spoke . . . . .	100
geom_violin . . . . .	102
ggplot . . . . .	105
ggproto . . . . .	107
ggsave . . . . .	108
ggtheme . . . . .	109
guides . . . . .	111
guide_colourbar . . . . .	112
guide_legend . . . . .	115
hmisc . . . . .	118
labeller . . . . .	119
labellers . . . . .	121
label_bquote . . . . .	123
labs . . . . .	124
lims . . . . .	125
luv_colours . . . . .	126
margin . . . . .	126
mean_se . . . . .	128
midwest . . . . .	129
mpg . . . . .	130
msleep . . . . .	131
position_dodge . . . . .	132
position_identity . . . . .	133
position_jitter . . . . .	133
position_jitterdodge . . . . .	134
position_nudge . . . . .	135
position_stack . . . . .	136
presidential . . . . .	138
print.ggplot . . . . .	139
print.ggproto . . . . .	140
qplot . . . . .	141
resolution . . . . .	142
scale_alpha . . . . .	143
scale_colour_brewer . . . . .	144
scale_colour_gradient . . . . .	146
scale_colour_grey . . . . .	148
scale_colour_hue . . . . .	149
scale_continuous . . . . .	150
scale_date . . . . .	153

scale_identity . . . . .	155
scale_linetype . . . . .	156
scale_manual . . . . .	157
scale_shape . . . . .	159
scale_size . . . . .	160
scale_x_discrete . . . . .	161
seals . . . . .	163
sec_axis . . . . .	163
stat_ecdf . . . . .	165
stat_ellipse . . . . .	166
stat_function . . . . .	168
stat_identity . . . . .	170
stat_summary_2d . . . . .	171
stat_summary_bin . . . . .	173
stat_unique . . . . .	176
theme . . . . .	177
theme_get . . . . .	182
txhousing . . . . .	184

<b>Index</b>	<b>185</b>
--------------	------------

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+.gg	<i>Add components to a plot</i>
------	---------------------------------

---

## 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

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

e1 %+% e2
```

## Arguments

e1	An object of class <a href="#">ggplot</a> or a <a href="#">theme</a> .
e2	A plot component, as described below.

## What can you add?

You can add any of the following types of objects:

- A [aes\(\)](#) objects replaces the default aesthetics.
- A layer created by a `geom_` or `stat_` function adds new layer.
- A scale overrides the existing scale.

- A [theme](#) modifies the current theme.
- A [coord](#) overrides current coordinate system.
- A [facet](#) specification overrides 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

```
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())
```

---

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 [ggplot2](#) and in individual layers.

## Usage

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

## Arguments

`x, y, ...` List of name value pairs giving aesthetics to map to variables. 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 standardise aesthetic names by performing partial matching, converting `color` to `colour`, and translating old style R names to ggplot names (eg. `pch` to `shape`, `cex` to `size`)

## See Also

See [aes\\_](#) for a version of `aes` that is more suitable for programming with.

## 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)

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

# aes is almost always used with ggplot() or a layer
ggplot(mpg, aes(displ, hwy)) + geom_point()
ggplot(mpg) + geom_point(aes(displ, hwy))

# Aesthetics supplied to ggplot() are used as defaults for every layer
# you can override them, or supply different aesthetics for each layer
```

---

aes\_

*Define aesthetic mappings programmatically*

---

## Description

Aesthetic mappings describe how variables in the data are mapped to visual properties (aesthetics) of geoms. `aes` uses non-standard evaluation to capture the variable names. `aes_` and `aes_string` require you to explicitly quote the inputs either with `"` for `aes_string()`, or with `quote` or `~` for `aes_()`. (`aes_q` is an alias to `aes_`). This makes `aes_` and `aes_string` easy to program with.

## Usage

```
aes_(x, y, ...)

aes_string(x, y, ...)

aes_q(x, y, ...)
```

## Arguments

`x, y, ...` List of name value pairs. Elements must be either quoted calls, strings, one-sided formulas or constants.

## Details

`aes_string` and `aes_` are particularly useful when writing functions that create plots because you can use strings or quoted names/calls to define the aesthetic mappings, rather than having to use `substitute` to generate a call to `aes()`.

I recommend using `aes_()`, because creating the equivalents of `aes(colour = "my colour")` or `aes{x = `X$1`}` with `aes_string()` is quite clunky.

## See Also

[aes](#)

## Examples

```
# Three ways of generating the same aesthetics
aes(mpg, wt, col = cyl)
aes_(quote(mpg), quote(wt), col = quote(cyl))
aes_(~mpg, ~wt, col = ~cyl)
aes_string("mpg", "wt", col = "cyl")

# You can't easily mimic these calls with aes_string
aes(`$100`, colour = "smooth")
aes_(~ ` $100`, colour = "smooth")
# Ok, you can, but it requires a _lot_ of quotes
aes_string("` $100`", colour = "'smooth'")

# Convert strings to names with as.name
var <- "cyl"
aes(col = x)
aes_(col = as.name(var))
```

---

aes\_colour\_fill\_alpha *Colour related aesthetics: colour, fill and alpha*

---

## Description

This page demonstrates the usage of a sub-group of aesthetics; colour, fill and alpha.

## Examples

```
# Bar chart example
c <- ggplot(mtcars, aes(factor(cyl)))
# Default plotting
c + geom_bar()
# To change the interior colouring use fill aesthetic
c + geom_bar(fill = "red")
# Compare with the colour aesthetic which changes just the bar outline
c + geom_bar(colour = "red")
# Combining both, you can see the changes more clearly
c + geom_bar(fill = "white", colour = "red")

# The aesthetic fill also takes different colouring scales
# setting fill equal to a factor variable uses a discrete colour scale
```



```

k <- ggplot(mtcars, aes(factor(cyl), fill = factor(vs)))
k + geom_bar()

# Fill aesthetic can also be used with a continuous variable
m <- ggplot(faithfuld, aes(waiting, eruptions))
m + geom_raster()
m + geom_raster(aes(fill = density))

# Some geoms don't use both aesthetics (i.e. geom_point or geom_line)
b <- ggplot(economics, aes(x = date, y = unemploy))
b + geom_line()
b + geom_line(colour = "green")
b + geom_point()
b + geom_point(colour = "red")

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

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

```

---

aes\_group\_order

Aesthetics: grouping

---

## Description

Aesthetics: grouping

## Examples

```

# By default, the group is set to the interaction of all discrete variables in the
# plot. This 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.

```

```

# For most applications you can simply specify the grouping with
# various aesthetics (colour, shape, fill, linetype) or with facets.

p <- ggplot(mtcars, aes(wt, mpg))
# A basic scatter plot
p + geom_point(size = 4)
# The colour aesthetic
p + geom_point(aes(colour = factor(cyl)), size = 4)
# Or you can use shape to distinguish the data
p + geom_point(aes(shape = factor(cyl)), size = 4)

# Using fill
a <- ggplot(mtcars, aes(factor(cyl)))
a + geom_bar()
a + geom_bar(aes(fill = factor(cyl)))
a + geom_bar(aes(fill = factor(vs)))

# Using linetypes
rescale01 <- function(x) (x - min(x)) / diff(range(x))
ec_scaled <- data.frame(
  date = economics$date,
  plyr::colwise(rescale01)(economics[, -(1:2)]))
ecm <- reshape2::melt(ec_scaled, id.vars = "date")
f <- ggplot(ecm, aes(date, value))
f + geom_line(aes(linetype = variable))

# Using facets
k <- ggplot(diamonds, aes(carat, ..density..)) + geom_histogram(binwidth = 0.2)
k + facet_grid(. ~ cut)

# There are three common cases where the default is not enough, and we
# will consider each one below. In the following examples, we will use a simple
# longitudinal dataset, Oxboys, from the nlme package. It records the heights
# (height) and centered ages (age) of 26 boys (Subject), measured on nine
# occasions (Occasion).

# Multiple groups with one aesthetic
h <- ggplot(nlme::Oxboys, aes(age, height))
# A single line tries to connect all the observations
h + geom_line()
# The group aesthetic maps a different line for each subject
h + geom_line(aes(group = Subject))

# Different groups on different layers
h <- h + geom_line(aes(group = Subject))
# Using the group aesthetic with both geom_line() and geom_smooth()
# groups the data the same way for both layers
h + geom_smooth(aes(group = Subject), method = "lm", se = FALSE)
# Changing the group aesthetic for the smoother layer
# fits a single line of best fit across all boys
h + geom_smooth(aes(group = 1), size = 2, method = "lm", se = FALSE)

# Overriding the default grouping

```

```
# The plot has a discrete scale but you want to draw lines that connect across
# groups. This is the strategy used in interaction plots, profile plots, and parallel
# coordinate plots, among others. For example, we draw boxplots of height at
# each measurement occasion
boysbox <- ggplot(nlme::Oxboys, aes(Occasion, height))
boysbox + geom_boxplot()
# There is no need to specify the group aesthetic here; the default grouping
# works because occasion is a discrete variable. To overlay individual trajectories
# we again need to override the default grouping for that layer with aes(group = Subject)
boysbox <- boysbox + geom_boxplot()
boysbox + geom_line(aes(group = Subject), colour = "blue")
```

---

aes\_linetype\_size\_shape

*Differentiation related aesthetics: linetype, size, shape*

---

## Description

This page demonstrates the usage of a sub-group of aesthetics; linetype, size and shape.

## Examples

```
# Line types should be specified with either an integer, a name, or with a string of
# an even number (up to eight) of hexadecimal digits which give the lengths in
# consecutive positions in the string.
# 0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash

# Data
df <- data.frame(x = 1:10, y = 1:10)
f <- ggplot(df, aes(x, y))
f + geom_line(linetype = 2)
f + 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.
f + geom_line(linetype = "3313")

# Mapping line type from a variable
ggplot(economics_long, aes(date, value01)) +
  geom_line(aes(linetype = variable))

# Size examples
# Should be specified with a numerical value (in millimetres),
# or from a variable source
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
# Shape takes four types of values: an integer in [0, 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
p + geom_point()
p + geom_point(shape = 5)
p + geom_point(shape = "k", size = 3)
p + geom_point(shape = ".")
p + geom_point(shape = NA)

# Shape can also be mapped from a variable
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)
s <- ggplot(df2, aes(x, y))
s + 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)
s + geom_point(aes(shape = z), size = 4, colour = "Red") +
  scale_shape_identity()
s + 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

This page demonstrates the usage of a sub-group of aesthetics; x, y, xmin, xmax, ymin, ymax, xend, and yend.

## Examples

```

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

# Using annotate

```

```
p <- ggplot(mtcars, aes(wt, 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")))
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") :
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(yend = 0, xend = x), size = 10)
```

---

annotate

*Create an annotation layer*

---

## Description

This function adds geoms to a plot, but unlike typical a 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

```
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 <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like color = "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.

Examples

```
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 = 1.5)

p + annotate("text", x = 2:3, y = 20:21, label = c("my label", "label 2"))

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)
```

---

annotation_custom	<i>Annotation: Custom grob</i>
-------------------	--------------------------------

---

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

```
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**

```
# 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)
```

---

annotation\_logticks     *Annotation: log tick marks*

---

**Description**

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

**Usage**

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

**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.

scaled	is the data already log-scaled? This should be TRUE (default) when the data is already transformed with <code>log10()</code> or when using <code>scale_y_log10</code> . It should be FALSE when using <code>coord_trans(y = "log10")</code> .
short	a <a href="#">unit</a> object specifying the length of the short tick marks
mid	a <a href="#">unit</a> object specifying the length of the middle tick marks. In base 10, these are the "5" ticks.
long	a <a href="#">unit</a> 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.
size	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

### 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

# 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::math_format(10^.x)) +
  scale_y_continuous(name = "brain", labels = scales::math_format(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

*Annotation: a maps*


---

## Description

Display a fixed map on a plot.

## Usage

```
annotation_map(map, ...)
```

## Arguments

map	data frame representing a map. Most map objects can be converted into the right format by using <a href="#">fortify</a>
...	other arguments used to modify aesthetics

## Examples

```

if (require("maps")) {
  usamap <- map_data("state")

  seal.sub <- subset(seals, long > -130 & lat < 45 & lat > 40)
  ggplot(seal.sub, aes(x = long, y = lat)) +
    annotation_map(usamap, fill = "NA", colour = "grey50") +
    geom_segment(aes(xend = long + delta_long, yend = lat + delta_lat))

  seal2 <- transform(seal.sub,
    latr = cut(lat, 2),
    longr = cut(long, 2))

```

```
ggplot(seal2, aes(x = long, y = lat)) +
  annotation_map(usamap, fill = "NA", colour = "grey50") +
  geom_segment(aes(xend = long + delta_long, yend = lat + delta_lat)) +
  facet_grid(latr ~ longr, scales = "free", space = "free")
}
```

---

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

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

## Arguments

raster	raster object 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
interpolate	If TRUE interpolate linearly, if FALSE (the default) don't interpolate.

## Examples

```
# 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()

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()
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, interpolate = TRUE) +
  geom_point()
```

---

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**

[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) on to 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**

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

**Arguments**

database	map data, see <a href="#">map</a> for details
regions	map region
fill	fill colour
colour	border colour
xlim, ylim	latitudinal and longitudinal range for extracting map polygons, see <a href="#">map</a> for details.
...	other arguments passed onto <a href="#">geom_polygon</a>

**Examples**

```

if (require("maps")) {

  ia <- map_data("county", "iowa")
  mid_range <- function(x) mean(range(x))
  seats <- plyr::ddply(ia, "subregion", plyr::colwise(mid_range, c("lat", "long")))
  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)

  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()

  # 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()
}

```

---

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**

```
coord_cartesian(xlim = NULL, ylim = NULL, expand = TRUE)
```

**Arguments**

<code>xlim, ylim</code>	Limits for the x and y axes.
<code>expand</code>	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 <code>xlim/ylim</code> .

## 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(displ, 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_bin2d(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))
```

---

coord\_fixed

*Cartesian coordinates with fixed "aspect ratio"*


---

## 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, `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 [eqsplot](#), but it works for all types of graphics.

**Usage**

```
coord_fixed(ratio = 1, xlim = NULL, ylim = NULL, expand = TRUE)
```

**Arguments**

ratio	aspect ratio, expressed as y / x
xlim	Limits for the x and y axes.
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.

**Examples**

```
# 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)

# Resize the plot to see that the specified aspect ratio is maintained
```

---

coord\_flip

*Cartesian coordinates with x and y flipped*


---

**Description**

Flip cartesian coordinates so that horizontal becomes vertical, and vertical, horizontal. This is primarily useful for converting geoms and statistics which display y conditional on x, to x conditional on y.

**Usage**

```
coord_flip(xlim = NULL, ylim = NULL, expand = TRUE)
```

**Arguments**

xlim	Limits for the x and y axes.
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.

## Examples

```
# Very useful for creating boxplots, and other interval
# geoms in the horizontal instead of vertical position.
```

```
ggplot(diamonds, aes(cut, price)) +
  geom_boxplot() +
  coord_flip()
```

```
h <- ggplot(diamonds, aes(carat)) +
  geom_histogram()
h
h + coord_flip()
h + coord_flip() + scale_x_reverse()
```

```
# You can also use it to flip line and area plots:
df <- data.frame(x = 1:5, y = (1:5) ^ 2)
ggplot(df, aes(x, y)) +
  geom_area()
last_plot() + coord_flip()
```

---

coord\_map

Map projections

---

## Description

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.

## Usage

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

```
coord_quickmap(xlim = NULL, ylim = NULL, expand = TRUE)
```

## Arguments

projection	projection to use, see <a href="#">mapproject</a> for list
..., parameters	Other arguments passed on to <a href="#">mapproject</a> . 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 <code>c(90, 0, mean(range(x)))</code> . This is not optimal for many projections, so you will have to supply your own. See <a href="#">mapproject</a> for more information.

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

In general, 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

```
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
  # With correct mercator projection
  nzmap + coord_map()
  # With the aspect ratio approximation
  nzmap + coord_quickmap()

  # Other projections
  nzmap + coord_map("cylindrical")
  nzmap + coord_map("azequalarea", orientation = c(-36.92, 174.6, 0))
  nzmap + coord_map("lambert", parameters = c(-37, -44))

  states <- map_data("state")
  usamap <- ggplot(states, aes(long, lat, group = group)) +
    geom_polygon(fill = "white", colour = "black")

  # Use cartesian coordinates
  usamap
  # With mercator projection
  usamap + coord_map()
  usamap + coord_quickmap()
  # See ?mapproject for coordinate systems and their parameters
  usamap + coord_map("gilbert")
  usamap + coord_map("lagrange")

  # 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")
usamap + coord_map("stereographic")
usamap + coord_map("conic", lat0 = 30)
usamap + coord_map("bonne", lat0 = 50)

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

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.

**Usage**

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

**Arguments**

theta	variable to map angle to (x or y)
start	offset of starting point from 12 o'clock in radians
direction	1, clockwise; -1, anticlockwise

**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$rrating <- cut_interval(movies$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")
}

```

---

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**

```
coord_trans(x = "identity", y = "identity", limx = NULL, limy = NULL,
            xtrans, ytrans)
```

**Arguments**

x, y                    transformers for x and y axes  
limx, limy            limits for x and y axes. (Named so for backward compatibility)  
xtrans, ytrans    Deprecated; use x and y instead.

**Details**

Transformations only work with continuous values: see [trans\\_new](#) for list of transformations, and instructions on how to create your own.

**Examples**

```
# 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()

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

```

coord_trans(x = "log10", y = "log10")

# Here I used a subset of diamonds so that the smoothed line didn't
# drop below zero, which obviously causes problems on the log-transformed
# scale

# With a combination of scale and coordinate transformation, it's
# possible to do back-transformations:
ggplot(diamonds, aes(carat, price)) +
  geom_point() +
  geom_smooth(method = "lm") +
  scale_x_log10() +
  scale_y_log10() +
  coord_trans(x = scales::exp_trans(10), y = scales::exp_trans(10))

# cf.
ggplot(diamonds, aes(carat, price)) +
  geom_point() +
  geom_smooth(method = "lm")

# Also works with discrete scales
df <- data.frame(a = abs(rnorm(26)), letters)
plot <- ggplot(df, aes(a, letters)) + geom_point()

plot + coord_trans(x = "log10")
plot + coord_trans(x = "sqrt")

```

---

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 = c("right",
  "left"))
```

## Arguments

x	numeric vector
n	number of intervals to create, OR

length	length of each interval
...	other arguments passed on to <a href="#">cut</a>
width	The bin width.
center, boundary	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.
closed	One of "right" or "left" indicating whether right or left edges of bins are included in the bin.

**Author(s)**

Randall Prium contributed most of the implementation of cut\_width.

**See Also**

[cut\\_number](#)

**Examples**

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

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))
```

---

diamonds	<i>Prices of 50,000 round cut diamonds</i>
----------	--

---

**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 J (worst) to D (best)

**clarity** a measurement of how clear the diamond is (I1 (worst), SI1, SI2, VS1, VS2, VVS1, VVS2, 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 =  $z / \text{mean}(x, y) = 2 * z / (x + y)$  (43–79)

**table** width of top of diamond relative to widest point (43–95)

---

economics

*US economic time series*

---

**Description**

This dataset was produced from US economic time series data available from <http://research.stlouisfed.org/fred2>. economics is in "wide" format, economics\_long is in "long" format.

**Usage**

economics

economics\_long

**Format**

A data frame with 478 rows and 6 variables

**date** Month of data collection

**psavert** personal savings rate, <http://research.stlouisfed.org/fred2/series/PSAVERT/>

**pce** personal consumption expenditures, in billions of dollars, <http://research.stlouisfed.org/fred2/series/PCE>

**unemploy** number of unemployed in thousands, <http://research.stlouisfed.org/fred2/series/UNEMPLOY>

**uempmed** median duration of unemployment, in weeks, <http://research.stlouisfed.org/fred2/series/UEMPMED>

**pop** total population, in thousands, <http://research.stlouisfed.org/fred2/series/POP>

---

expand_limits	<i>Expand the plot limits, using data</i>
---------------	---

---

**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**

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

**Arguments**

...                    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)))
```

---

facet_grid	<i>Lay out panels in a grid</i>
------------	---------------------------------

---

**Description**

`facet_grid` forms a matrix of panels defined by row and column facetting variables. It is most useful when you have two discrete variables, and all combinations of the variables exist in the data.

**Usage**

```
facet_grid(facets, margins = FALSE, scales = "fixed", space = "fixed",
  shrink = TRUE, labeller = "label_value", as.table = TRUE,
  switch = NULL, drop = TRUE)
```

**Arguments**

facets	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). The formula can also be provided as a string instead of a classical formula object
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.
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")
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 formulae of the type <code>~cyl + am</code> . 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 <code>labeller()</code> . See <code>label_value</code> 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.

**Examples**

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

p + facet_grid(. ~ cyl)
p + facet_grid(drv ~ .)
p + facet_grid(drv ~ 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(. ~ cyl) +
  geom_point(data = df, colour = "red", size = 2)

# 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(. ~ 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(drv, model)) +
  geom_point() +
  facet_grid(manufacturer ~ ., scales = "free", space = "free") +
  theme(strip.text.y = element_text(angle = 0))

# Facet labels -----
p <- ggplot(mtcars, aes(wt, mpg)) + geom_point()
p

# label_both() displays both variable name and value
p + facet_grid(vs ~ cyl, labeller = label_both)

# label_parsed() parses text into mathematical expressions, see ?plotmath
mtcars$cyl2 <- factor(mtcars$cyl, labels = c("alpha", "beta", "sqrt(x, y)"))
ggplot(mtcars, aes(wt, mpg)) +
  geom_point() +
  facet_grid(. ~ cyl2, labeller = label_parsed)

# label_bquote() makes it easy to construct math expressions
p + facet_grid(. ~ vs, labeller = label_bquote(cols = alpha ^ .(vs)))

# The facet strips can be displayed near the axes with switch
data <- transform(mtcars,
  am = factor(am, levels = 0:1, c("Automatic", "Manual")),
  gear = factor(gear, levels = 3:5, labels = c("Three", "Four", "Five"))
)
p <- ggplot(data, aes(mpg, disp)) + geom_point()
p + facet_grid(am ~ gear, switch = "both")
# It looks better without boxes around the strips
p + facet_grid(am ~ gear, switch = "both") +
  theme(strip.background = element_blank())

# Margins -----
# Margins can be specified by logically (all yes or all no) or by specific

```

```
# variables as (character) variable names
mg <- ggplot(mtcars, aes(x = mpg, y = wt)) + geom_point()
mg + facet_grid(vs + am ~ gear)
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")
mg + facet_grid(vs + am ~ gear, margins = "gear")
mg + facet_grid(vs + am ~ gear, margins = c("gear", "am"))
```

---

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

```
facet_wrap(facets, nrow = NULL, ncol = NULL, scales = "fixed",
  shrink = TRUE, labeller = "label_value", as.table = TRUE,
  switch = NULL, drop = TRUE, dir = "h", strip.position = "top")
```

## Arguments

facets	Either a formula or character vector. Use either a one sided formula, <code>~a + b</code> , or a character vector, <code>c("a", "b")</code> .
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 formulae of the type <code>~cyl + am</code> . 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 <a href="#">labeller()</a> . See <a href="#">label_value</a> 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.
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").

## Examples

```
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  facet_wrap(~class)

# Control the number of rows and columns with nrow and ncol
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  facet_wrap(~class, nrow = 4)

# You can facet by multiple variables
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  facet_wrap(~ cyl + drv)
# Or use a character vector:
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  facet_wrap(c("cyl", "drv"))

# Use the `labeller` option to control how labels are printed:
ggplot(mpg, aes(displ, hwy)) +
  geom_point() +
  facet_wrap(c("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(~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(~class, scales = "free")
```

```
# To repeat the same data in every panel, simply construct a data frame
# that does not contain the facetting variable.
ggplot(mpg, aes(displ, hwy)) +
  geom_point(data = transform(mpg, class = NULL), colour = "grey85") +
  geom_point() +
  facet_wrap(~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(~variable, scales = "free_y", nrow = 2, strip.position = "bottom") +
  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.

---

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	<i>Reference lines: horizontal, vertical, and diagonal</i>
-------------	--

---

**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**

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

geom_hline(mapping = NULL, data = NULL, ..., 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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . 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.
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 different to 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 with [geom\\_line](#) so support the same aesthetics: alpha, colour, linetype and size. 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

```
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
coef(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)
```

geom\_bar

*Bars charts*

## Description

There are two types of bar charts: `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

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

geom_col(mapping = NULL, data = NULL, position = "stack", ...,
  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,
  show.legend = NA, inherit.aes = TRUE)
```

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> .

	A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.
	A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>...</code>	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
<code>width</code>	Bar width. By default, set to 90% of the resolution of the data.
<code>binwidth</code>	<code>geom_bar</code> no longer has a <code>binwidth</code> argument - if you use it you'll get an warning telling to you use <code>geom_histogram</code> instead.
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .
<code>geom, stat</code>	Override the default connection between <code>geom_bar</code> and <code>stat_count</code> .

## 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. Naomi Robbins has a nice [article on this topic](#). This is why it doesn't make sense to use a log-scaled y axis with a bar chart.

By default, multiple bar 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](#). Finally, [position\\_fill](#) shows relative proportions at each x by stacking the bars and then standardising each bar to have the same height.

## Aesthetics

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

- **x**
- **y**
- alpha
- colour
- fill
- group
- linetype
- size



**Computed variables****count** number of points in bin**prop** groupwise proportion**See Also**[geom\\_histogram](#) for continuous data, [position\\_dodge](#) for creating side-by-side barcharts.[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))

# To show (e.g.) means, you need geom_col()
# And, even more succinctly with geom_col()
df <- data.frame(trt = c("a", "b", "c"), outcome = c(2.3, 1.9, 3.2))
ggplot(df, aes(trt, outcome)) +
  geom_col()
# But geom_point() displays exactly the same information and doesn't
# require the y-axis to touch zero.
ggplot(df, aes(trt, outcome)) +
  geom_point()

# You can also use geom_bar() with continuous data, in which case
# it will show counts at unique locations
df <- data.frame(x = rep(c(2.9, 3.1, 4.5), c(5, 10, 4)))
ggplot(df, aes(x)) + geom_bar()
# cf. a histogram of the same data
ggplot(df, aes(x)) + geom_histogram(binwidth = 0.5)

# Bar charts are automatically stacked when multiple bars are placed
# at the same location
g + geom_bar(aes(fill = drv))

# You can instead dodge, or fill them
g + geom_bar(aes(fill = drv), position = "dodge")
g + geom_bar(aes(fill = drv), position = "fill")

# To change plot order of bars, change levels in underlying factor
reorder_size <- function(x) {
  factor(x, levels = names(sort(table(x))))
}
```

```
}
ggplot(mpg, aes(reorder_size(class))) + geom_bar()
```

geom\_bin2d

*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

```
geom_bin2d(mapping = NULL, data = NULL, stat = "bin2d",
  position = "identity", ..., na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE)

stat_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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.

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. <a href="#">borders</a> .
geom, stat	Use to override the default connection between geom_bin2d and stat_bin2d.
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\_bin2d understands the following aesthetics (required aesthetics are in bold):

- **x**
- **y**
- fill
- group

### See Also

[stat\\_binhex](#) for hexagonal binning

### Examples

```
d <- ggplot(diamonds, aes(x, y)) + xlim(4, 10) + ylim(4, 10)
d + geom_bin2d()

# You can control the size of the bins by specifying the number of
# bins in each direction:
d + geom_bin2d(bins = 10)
d + geom_bin2d(bins = 30)

# Or by specifying the width of the bins
d + geom_bin2d(binwidth = c(0.1, 0.1))
```

---

geom\_blank

*Draw nothing*

---

### 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**

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

**Arguments**

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> ., and will be used as the layer data.
stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

**Examples**

```
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**

```
geom_boxplot(mapping = NULL, data = NULL, stat = "boxplot",
  position = "dodge", ..., 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, varwidth = FALSE, na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE)
```

```
stat_boxplot(mapping = NULL, data = NULL, geom = "boxplot",
  position = "dodge", ..., coef = 1.5, na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE)
```

**Arguments**

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data.</p>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
outlier.colour, outlier.color, outlier.fill, outlier.shape, outlier.size, outlier.stroke, outlier.alpha	<p>Default aesthetics for outliers. Set to <code>NULL</code> to inherit from the aesthetics used for the box.</p> <p>In the unlikely event you specify both US and UK spellings of colour, the US spelling will take precedence.</p>
notch	if <code>FALSE</code> (default) make a standard box plot. If <code>TRUE</code> , 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 (default 0.5)
varwidth	if <code>FALSE</code> (default) make a standard box plot. If <code>TRUE</code> , boxes are drawn with widths proportional to the square-roots of the number of observations in the groups (possibly weighted, using the <code>weight</code> aesthetic).
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.

<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .
<code>geom, stat</code>	Use to override the default connection between <code>geom_boxplot</code> and <code>stat_boxplot</code> .
<code>coef</code>	length of the whiskers as multiple of IQR. Defaults to 1.5

### Summary statistics

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  $1.5 * \text{IQR}$  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  $1.5 * \text{IQR}$  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  $1.58 * \text{IQR} / \sqrt{n}$ . This gives a roughly 95% confidence interval for comparing medians. See McGill et al. (1978) for more details.

### Aesthetics

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

- **x**
- **lower**
- **upper**
- **middle**
- **ymin**
- **ymax**
- alpha
- colour
- fill
- group
- linetype
- shape
- size
- weight

**Computed variables**

**width** width of boxplot

**ymin** lower whisker = smallest observation greater than or equal to lower hinge - 1.5 \* IQR

**lower** lower hinge, 25% quantile

**notchlower** lower edge of notch = median - 1.58 \* IQR / sqrt(n)

**middle** median, 50% quantile

**notchupper** upper edge of notch = median + 1.58 \* IQR / sqrt(n)

**upper** upper hinge, 75% quantile

**ymax** upper whisker = largest observation less than or equal to upper hinge + 1.5 \* IQR

**References**

McGill, R., Tukey, J. W. and Larsen, W. A. (1978) Variations of box plots. The American Statistician 32, 12-16.

**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**

```
p <- ggplot(mpg, aes(class, hwy))
p + geom_boxplot()
p + geom_boxplot() + geom_jitter(width = 0.2)
p + geom_boxplot() + coord_flip()

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)

# 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()
ggplot(diamonds, aes(carat, price)) +
  geom_boxplot(aes(group = cut_width(carat, 0.25)))
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":
```

```

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"
  )

```

geom\_contour

*2d contours of a 3d surface*

## Description

ggplot2 can not draw true 3d surfaces, but you can use `geom_contour` and [geom\\_tile](#) to visualise 3d surfaces in 2d. To be a valid surface, the data must contain only a single row for each unique combination of the variables mapped to the x and y aesthetics. Contouring tends to work best when x and y form a (roughly) evenly spaced grid. If your data is not evenly spaced, you may want to interpolate to a grid before visualising.

## Usage

```

geom_contour(mapping = NULL, data = NULL, stat = "contour",
  position = "identity", ..., lineend = "butt", linejoin = "round",
  linemitre = 1, na.rm = FALSE, show.legend = NA, inherit.aes = TRUE)

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

```

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p>



	A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
<code>stat</code>	The statistical transformation to use on the data for this layer, as a string.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>...</code>	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
<code>lineend</code>	Line end style (round, butt, square)
<code>linejoin</code>	Line join style (round, mitre, bevel)
<code>linemitre</code>	Line mitre limit (number greater than 1)
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .
<code>geom</code>	The geometric object to use display the data

## Aesthetics

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

- **x**
- **y**
- alpha
- colour
- group
- linetype
- size
- weight

## Computed variables

**level** height of contour

## 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()

# Setting bins creates evenly spaced contours in the range of the data
v + geom_contour(bins = 2)
v + geom_contour(bins = 10)

# 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 = ..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.

## 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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <code>ggplot</code>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <code>fortify</code> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>., and will be used as the layer data.</p>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <code>layer</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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, stat	Use to override the default connection between <code>geom_count</code> and <code>stat_sum</code> .

## Aesthetics

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

- **x**
- **y**
- alpha
- colour
- fill
- group
- shape
- size
- stroke

## Computed variables

**n** number of observations at position  
**prop** percent of points in that panel at that position

## See Also

For continuous x and y, use `geom_bin2d`.

## Examples

```
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 = ..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 = ..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 = ..prop.., group = cut)) +
  scale_size_area(max_size = 10)
d + geom_count(aes(size = ..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

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

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

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

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

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
fatten	A multiplicative factor used to increase the size of the middle bar in <code>geom_crossbar()</code> and the middle point in <code>geom_pointrange()</code> .
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

## Aesthetics

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

- **x**
- **ymin**
- **ymax**
- alpha

- colour
- group
- linetype
- size

## See Also

[stat\\_summary](#) for examples of these guys in use, [geom\\_smooth](#) for continuous analog, [geom\\_errorbarh](#) for a horizontal error bar.

## Examples

```
#' # 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))
p + geom_linerange(aes(ymin = lower, ymax = upper))
p + geom_pointrange(aes(ymin = lower, ymax = upper))
p + geom_crossbar(aes(ymin = lower, ymax = upper), width = 0.2)
p + geom_errorbar(aes(ymin = lower, ymax = upper), width = 0.2)

# 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))
p +
  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)
```

---

geom_density	<i>Smoothed density estimates</i>
--------------	-----------------------------------

---

## Description

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

## Usage

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

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

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

<code>geom, stat</code>	Use to override the default connection between <code>geom_density</code> and <code>stat_density</code> .
<code>bw</code>	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 <a href="#">bw.nrd</a> .
<code>adjust</code>	A multiplicate bandwidth adjustment. This makes it possible to adjust the bandwidth while still using the a bandwidth estimator. For exampe, <code>adjust = 1/2</code> means use half of the default bandwidth.
<code>kernel</code>	Kernel. See list of available kernels in <a href="#">density</a> .
<code>n</code>	number of equally spaced points at which the density is to be estimated, should be a power of two, see <a href="#">density</a> for details
<code>trim</code>	This parameter only matters if you are displaying multiple densities in one plot. 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.

## Aesthetics

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

- **x**
- **y**
- alpha
- colour
- fill
- group
- linetype
- size
- weight

## Computed variables

**density** density estimate

**count** density \* number of points - useful for stacked density plots

**scaled** density estimate, scaled to maximum of 1

## See Also

See [geom\\_histogram](#), [geom\\_freqpoly](#) for other methods of displaying continuous distribution. See [geom\\_violin](#) for a compact density display.



**Examples**

```

ggplot(diamonds, aes(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)

# 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
ggplot(diamonds, aes(carat, fill = cut)) +
  geom_density(position = "stack")
# Preserves marginal densities
ggplot(diamonds, aes(carat, ..count.., fill = cut)) +
  geom_density(position = "stack")

# You can use position="fill" to produce a conditional density estimate
ggplot(diamonds, aes(carat, ..count.., fill = cut)) +
  geom_density(position = "fill")

```

geom\_density\_2d

*Contours of a 2d density estimate***Description**

Perform a 2D kernel density estimation using [kde2d](#) and display the results with contours. This can be useful for dealing with overplotting. This is a 2d version of [geom\\_density](#).

**Usage**

```

geom_density_2d(mapping = NULL, data = NULL, stat = "density2d",
  position = "identity", ..., lineend = "butt", linejoin = "round",
  linemitre = 1, na.rm = FALSE, show.legend = NA, inherit.aes = TRUE)

stat_density_2d(mapping = NULL, data = NULL, geom = "density_2d",
  position = "identity", ..., contour = TRUE, n = 100, h = NULL,
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE)

```

**Arguments**

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . 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 <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .
geom, stat	Use to override the default connection between <code>geom_density_2d</code> and <code>stat_density_2d</code> .
contour	If <code>TRUE</code> , contour the results of the 2d density estimation
n	number of grid points in each direction
h	Bandwidth (vector of length two). If <code>NULL</code> , estimated using <a href="#">bandwidth.nrd</a> .

**Aesthetics**

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

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

**Computed variables**

Same as `stat_contour`

**See Also**

`geom_contour` for information about how contours are drawn; `geom_bin2d` 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)
m + geom_density_2d()

m + stat_density_2d(aes(fill = ..level..), geom = "polygon")

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 we turn contouring off, we can use geoms like tiles:
d + stat_density_2d(geom = "raster", aes(fill = ..density..), contour = FALSE)
# Or points:
d + stat_density_2d(geom = "point", aes(size = ..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**

```
geom_dotplot(mapping = NULL, data = NULL, position = "identity", ...,
  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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data.</p>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . 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 <code>stat_bin</code> )
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.
stackdir	which direction to stack the dots. "up" (default), "down", "center", "centerw-hole" (centered, but with dots aligned)
stackratio	how close to stack the dots. Default is 1, where dots just 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 <code>position = "stack"</code> 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 <code>TRUE</code> , remove all bins with zero counts
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

## 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

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

- **x**
- **y**
- `alpha`
- `colour`
- `fill`
- `group`

## Computed variables

**x** center of each bin, if `binaxis` is "x"

**y** center of each bin, if `binaxis` is "x"

**binwidth** max width of each bin if method is "dotdensity"; width of each bin if method is "histodot"

**count** number of points in bin

**ncount** count, scaled to maximum of 1

**density** density of points in bin, scaled to integrate to 1, if method is "histodot"

**ndensity** density, scaled to maximum of 1, if method is "histodot"

## References

Wilkinson, L. (1999) Dot plots. *The American Statistician*, 53(3), 276-281.

## Examples

```
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(method="histodot", binwidth = 1.5)

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

```

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

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

# Overlap dots vertically
ggplot(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)

# 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**

```
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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

**Aesthetics**

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

- **x**
- **xmin**
- **xmax**
- **y**
- alpha
- colour
- group
- height
- linetype
- size

## 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 count 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.

`stat_bin` is suitable only for continuous x data. If your x data is discrete, you probably want to use [stat\\_count](#).

## Usage

```
geom_freqpoly(mapping = NULL, data = NULL, stat = "bin",
  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,
  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, show.legend = NA, inherit.aes = TRUE)
```



**Arguments**

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data.</p>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .
binwidth	<p>The width of the bins. The default is to use bins that cover the range of the data. <b>You should always override this value, exploring multiple widths to find the best to illustrate the stories in your data.</b></p> <p>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.</p>
bins	Number of bins. Overridden by <code>binwidth</code> . Defaults to 30
geom, stat	Use to override the default connection between <code>geom_histogram/geom_freqpoly</code> and <code>stat_bin</code> .
center	The center of one of the bins. Note that if <code>center</code> is above or below the range of the data, things will be shifted by an appropriate number of widths. To center on integers, for example, use <code>width = 1</code> and <code>center = 0</code> , even if <code>0</code> is outside the range of the data. At most one of <code>center</code> and <code>boundary</code> may be specified.
boundary	A boundary between two bins. As with <code>center</code> , things are shifted when <code>boundary</code> is outside the range of the data. For example, to center on integers, use <code>width = 1</code> and <code>boundary = 0.5</code> , even if <code>0.5</code> is outside the range of the data. At most one of <code>center</code> and <code>boundary</code> may be specified.
breaks	Alternatively, you can supply a numeric vector giving the bin boundaries. Overrides <code>binwidth</code> , <code>bins</code> , <code>center</code> , and <code>boundary</code> .
closed	One of <code>"right"</code> or <code>"left"</code> 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

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 binwidths. You may need to look at a few to uncover the full story behind your data.

## Aesthetics

`geom_histogram` uses the same aesthetics as [geom\\_bar](#); `geom_freqpoly` uses the same aesthetics as [geom\\_line](#).

## Computed variables

**count** number of points in bin  
**density** density of points in bin, scaled to integrate to 1  
**ncount** count, scaled to maximum of 1  
**ndensity** density, scaled to maximum of 1

## 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)

# 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
ggplot(diamonds, aes(price, ..density.., colour = cut)) +
  geom_freqpoly(binwidth = 500)

if (require("ggplot2movies")) {
  # Often we don't want the height of the bar to represent the
  # count of observations, but the sum of some other variable.
  # For example, the following plot shows the number of movies
```

```

# in each rating.
m <- ggplot(movies, aes(rating))
m + geom_histogram(binwidth = 0.1)

# If, however, we want to see the number of votes cast in each
# category, we need to weight by the votes variable
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()
}

```

geom\_hex

*Hexagonal heatmap of 2d bin counts***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\\_bin2d](#).

**Usage**

```

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

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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data.</p>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .
geom, stat	Override the default connection between <code>geom_hex</code> and <code>stat_binhex</code> .
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.

## Aesthetics

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

- **x**
- **y**
- alpha
- colour
- fill
- group
- size

**See Also**

[stat\\_bin2d](#) for rectangular binning

**Examples**

```
d <- ggplot(diamonds, aes(carat, price))
d + geom_hex()

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

# Or by specifying the width of the bins
d + geom_hex(binwidth = c(1, 1000))
d + geom_hex(binwidth = c(.1, 500))
```

---

geom\_jitter

*Jittered points*


---

**Description**

The jitter geom is a convenient shortcut for `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**

```
geom_jitter(mapping = NULL, data = NULL, stat = "identity",
  position = "jitter", ..., width = NULL, height = NULL, na.rm = FALSE,
  show.legend = NA, inherit.aes = TRUE)
```

**Arguments**

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>., and will be used as the layer data.</p>

<code>stat</code>	The statistical transformation to use on the data for this layer, as a string.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>...</code>	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
<code>width</code>	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.
<code>height</code>	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.
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .

## Aesthetics

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

- **x**
- **y**
- alpha
- colour
- fill
- group
- shape
- size
- stroke

## 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)
```

---

geom_label	<i>Text</i>
------------	-------------

---

## Description

geom\_text adds text directly 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", ..., 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)

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

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.

	A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
<code>stat</code>	The statistical transformation to use on the data for this layer, as a string.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>...</code>	other arguments passed on to <code>layer</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
<code>parse</code>	If TRUE, the labels will be parsed into expressions and displayed as described in <code>?plotmath</code>
<code>nudge_x</code> , <code>nudge_y</code>	Horizontal and vertical adjustment to nudge labels by. Useful for offsetting text from points, particularly on discrete scales.
<code>label.padding</code>	Amount of padding around label. Defaults to 0.25 lines.
<code>label.r</code>	Radius of rounded corners. Defaults to 0.15 lines.
<code>label.size</code>	Size of label border, in mm.
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <code>borders</code> .
<code>check_overlap</code>	If TRUE, text that overlaps previous text in the same layer will not be plotted.

## Details

Note the the "width" and "height" of a text element are 0, so stacking and dodging text will not work by default, and axis limits are not automatically expanded to include all text. Obviously, labels do have height and width, but they are physical units, not data units. The amount of space they occupy on that plot is not constant in data units: when you resize a plot, labels stay the same size, but the size of the axes changes.

## Aesthetics

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

- **x**
- **y**
- **label**
- alpha
- angle
- colour
- family



- fontface
- group
- hjust
- lineheight
- size
- vjust

## geom\_label

Currently `geom_label` does not support the `rot` parameter and 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 ?plotmath, but note that
# 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:
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:
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))
# Use 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", "bottom-right", "top-left", "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

This is pure annotation, so does not affect position scales.

## Usage

```
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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data.</p>
stat	The statistical transformation to use on the data for this layer, as a string.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
map	Data frame that contains the map coordinates. This will typically be created using <a href="#">fortify</a> on a spatial object. It must contain columns <code>x</code> or <code>long</code> , <code>y</code> or <code>lat</code> , and <code>region</code> or <code>id</code> .
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

## Aesthetics

geom\_map understands the following aesthetics (required aesthetics are in bold):

- **map\_id**
- alpha
- colour
- fill
- group
- linetype
- size

## 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, 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)
)
```

```
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)
```

```
# Better example
crimes <- data.frame(state = tolower(rownames(USArrests)), USArrests)
crimesm <- reshape2::melt(crimes, id = 1)
if (require(maps)) {
  states_map <- map_data("state")
  ggplot(crimes, aes(map_id = state)) +
    geom_map(aes(fill = Murder), map = states_map) +
```

```

    expand_limits(x = states_map$long, y = states_map$lat)

last_plot() + coord_map()
ggplot(crimesm, aes(map_id = state)) +
  geom_map(aes(fill = value), map = states_map) +
  expand_limits(x = states_map$long, y = states_map$lat) +
  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 staircase plot, highlighting exactly when changes occur. The group aesthetic determines which cases are connected together.

## Usage

```
geom_path(mapping = NULL, data = NULL, stat = "identity",
  position = "identity", ..., lineend = "butt", linejoin = "round",
  linemitre = 1, arrow = NULL, na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE)
```

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

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

## Arguments

- |         |   |
|---------|---|
| mapping | Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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    | <p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>., and will be used as the layer data.</p> |

stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . 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)
arrow	Arrow specification, as created by <a href="#">arrow</a>
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.
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. <a href="#">borders</a> .
direction	direction of stairs: 'vh' for vertical then horizontal, or 'hv' for horizontal then vertical

## Details

An alternative parameterisation is [geom\\_segment](#): each line corresponds to a single case which provides the start and end coordinates.

## Aesthetics

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

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

## See Also

[geom\\_polygon](#): Filled paths (polygons); [geom\\_segment](#): Line segments

**Examples**

```

# geom_line() is suitable for time series
ggplot(economics, aes(date, unemploy)) + geom_line()
ggplot(economics_long, aes(date, value01, colour = variable)) +
  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()
ggplot(recent, aes(date, unemploy)) + geom_step()

# 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()
m + geom_path(aes(colour = as.numeric(date)))

# Changing parameters -----
ggplot(economics, aes(date, unemploy)) +
  geom_line(colour = "red")

# 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())
c + geom_line(
  arrow = arrow(angle = 15, ends = "both", type = "closed")
)

# Control line join parameters
df <- data.frame(x = 1:3, y = c(4, 1, 9))
base <- ggplot(df, aes(x, y))
base + geom_path(size = 10)
base + geom_path(size = 10, lineend = "round")
base + geom_path(size = 10, linejoin = "mitre", lineend = "butt")

# NAs break the line. Use na.rm = T to suppress the warning message
df <- data.frame(
  x = 1:5,
  y1 = c(1, 2, 3, 4, NA),
  y2 = c(NA, 2, 3, 4, 5),
  y3 = c(1, 2, NA, 4, 5)
)
ggplot(df, aes(x, y1)) + geom_point() + geom_line()
ggplot(df, aes(x, y2)) + geom_point() + geom_line()
ggplot(df, aes(x, y3)) + geom_point() + geom_line()

# Setting line type vs colour/size
# Line type needs to be applied to a line as a whole, so it can
# not be used with colour or size that vary across a line

```

```

x <- seq(0.01, .99, length.out = 100)
df <- data.frame(
  x = rep(x, 2),
  y = c(qlogis(x), 2 * qlogis(x)),
  group = rep(c("a", "b"),
    each = 100)
)
p <- ggplot(df, aes(x=x, y=y, group=group))
# These work
p + geom_line(linetype = 2)
p + geom_line(aes(colour = group), linetype = 2)
p + geom_line(aes(colour = x))
# But this doesn't
should_stop(p + geom_line(aes(colour = x), linetype=2))

```

geom\_point

*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\\_bin2d](#) is usually more appropriate.

## Usage

```

geom_point(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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>., and will be used as the layer data.</p>
stat	The statistical transformation to use on the data for this layer, as a string.



position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . 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.
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. <a href="#">borders</a> .

### Details

The *bubblechart* is a scatterplot with a third variable mapped to the size of points. There are no special names for scatterplots where another variable is mapped to point shape or colour, however.

### 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

**Examples**

```

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)))
p + geom_point(aes(size = qsec))

# Change scales
p + geom_point(aes(colour = cyl)) + scale_colour_gradient(low = "blue")
p + geom_point(aes(shape = factor(cyl))) + scale_shape(solid = FALSE)

# 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) +
  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)))

# These extra layers don't usually appear in the legend, but we can
# force their inclusion
p + geom_point(colour = "black", size = 4.5, show.legend = TRUE) +
  geom_point(colour = "pink", size = 4, show.legend = TRUE) +
  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
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***Description**

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.

**Usage**

```
geom_polygon(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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data.</p>
stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

## Aesthetics

geom\_polygon understands the following aesthetics (required aesthetics are in bold):

- **x**
- **y**
- alpha
- colour
- fill
- group
- linetype
- size

## 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, 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.:
```

```
stream <- data.frame(
```

```

  x = cumsum(runif(50, max = 0.1)),
  y = cumsum(runif(50, max = 0.1))
)

p + geom_line(data = stream, colour = "grey30", size = 5)

# And if the positions are in longitude and latitude, you can use
# coord_map to produce different map projections.

```

geom\_qq

*A quantile-quantile plot***Description**

A quantile-quantile plot

**Usage**

```

geom_qq(mapping = NULL, data = NULL, geom = "point",
  position = "identity", ..., distribution = stats::qnorm,
  dparams = list(), na.rm = FALSE, show.legend = NA, inherit.aes = TRUE)

stat_qq(mapping = NULL, data = NULL, geom = "point",
  position = "identity", ..., distribution = stats::qnorm,
  dparams = list(), na.rm = FALSE, show.legend = NA, inherit.aes = TRUE)

```

**Arguments**

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>., and will be used as the layer data.</p>
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
distribution	Distribution function to use, if <code>x</code> not specified

<code>dparams</code>	Additional parameters passed on to distribution function.
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .

## Aesthetics

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

- **sample**
- group
- x
- y

## Computed variables

**sample** sample quantiles

**theoretical** theoretical quantiles

## Examples

```
df <- data.frame(y = rt(200, df = 5))
p <- ggplot(df, aes(sample = y))
p + stat_qq()
p + geom_point(stat = "qq")

# 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"])

# Using to explore the distribution of a variable
ggplot(mtcars) +
  stat_qq(aes(sample = mpg))
ggplot(mtcars) +
  stat_qq(aes(sample = mpg, colour = factor(cyl)))
```

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**

```
geom_quantile(mapping = NULL, data = NULL, stat = "quantile",
  position = "identity", ..., lineend = "butt", linejoin = "round",
  linemitre = 1, na.rm = FALSE, show.legend = NA, inherit.aes = TRUE)

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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . 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 <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.

<code>inherit.aes</code>	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. <a href="#">borders</a> .
<code>geom, stat</code>	Use to override the default connection between <code>geom_quantile</code> and <code>stat_quantile</code> .
<code>quantiles</code>	conditional quantiles of y to calculate and display
<code>formula</code>	formula relating y variables to x variables
<code>method</code>	Quantile regression method to use. Currently only supports <a href="#">rq</a> .
<code>method.args</code>	List of additional arguments passed on to the modelling function defined by <code>method</code> .

## Aesthetics

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

- **x**
- **y**
- alpha
- colour
- group
- linetype
- size
- weight

## Computed variables

**quantile** quantile of distribution

## Examples

```
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", size = 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.

**Usage**

```
geom_raster(mapping = NULL, data = NULL, stat = "identity",
  position = "identity", ..., hjust = 0.5, vjust = 0.5,
  interpolate = FALSE, na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE)
```

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

```
geom_tile(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 <a href="#">aes</a> or <a href="#">aes_</a> . 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 <a href="#">ggplot</a> . A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> 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.
stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like color = "red" or size = 3. They may also be parameters to the paired geom/stat.

<code>hjust</code> , <code>vjust</code>	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.
<code>interpolate</code>	If TRUE interpolate linearly, if FALSE (the default) don't interpolate.
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .

## Aesthetics

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

- **x**
- **y**
- alpha
- colour
- fill
- group
- linetype
- size

## 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()
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))
ggplot(df, aes(x, y)) +
```

```

geom_tile(aes(fill = z, width = w), colour = "grey50")
ggplot(df, aes(xmin = x - w / 2, xmax = x + w / 2, ymin = y, ymax = y + 1)) +
  geom_rect(aes(fill = z, width = w), colour = "grey50")

# Justification controls where the cells are anchored
df <- expand.grid(x = 0:5, y = 0:5)
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
cars <- ggplot(mtcars, aes(mpg, factor(cyl)))
cars + geom_point()
cars + stat_bin2d(aes(fill = ..count..), binwidth = c(3,1))
cars + stat_bin2d(aes(fill = ..density..), binwidth = c(3,1))

cars + stat_density(aes(fill = ..density..), geom = "raster", position = "identity")
cars + stat_density(aes(fill = ..count..), geom = "raster", position = "identity")

```

geom\_ribbon

*Ribbons and area plots*

## 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.

## Usage

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

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

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> .

	A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.
	A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
<code>stat</code>	The statistical transformation to use on the data for this layer, as a string.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>...</code>	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .

## Details

An area plot is the continuous analog 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 increasingly hard to see the individual pattern as you move up the stack. See [position\\_stack](#) for the details of stacking algorithm.

## Aesthetics

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

- **x**
- **ymin**
- **ymax**
- alpha
- colour
- fill
- group
- linetype
- size

## 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))

# Add aesthetic mappings
h +
  geom_ribbon(aes(ymin = level - 1, ymax = level + 1), fill = "grey70") +
  geom_line(aes(y = level))
```

---

geom_rug	<i>Rug plots in the margins</i>
----------	---------------------------------

---

## 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

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

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.

<code>sides</code>	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.
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .

## Details

The rug lines are drawn with a fixed size (3 are dependent on the overall scale expansion in order not to overplot existing data).

## Aesthetics

geom\_rug understands the following aesthetics (required aesthetics are in bold):

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

## Examples

```
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")
```

geom\_segment

*Line segments and curves***Description**

geom\_segment draws a straight line between points (x, y) and (xend, yend). geom\_curve draws a curved line. See the underlying drawing function [curveGrob](#) for the parameters that control the curve.

**Usage**

```
geom_segment(mapping = NULL, data = NULL, stat = "identity",
  position = "identity", ..., arrow = NULL, lineend = "butt",
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE)

geom_curve(mapping = NULL, data = NULL, stat = "identity",
  position = "identity", ..., curvature = 0.5, angle = 90, ncp = 5,
  arrow = NULL, lineend = "butt", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE)
```

**Arguments**

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . 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 <a href="#">ggplot</a> . A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> 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.
stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like color = "red" or size = 3. They may also be parameters to the paired geom/stat.
arrow	specification for arrow heads, as created by <a href="#">arrow()</a> .
lineend	Line end style (round, butt, square).
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .
<code>curvature</code>	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.
<code>angle</code>	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.
<code>ncp</code>	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**
- **yend**
- alpha
- colour
- group
- linetype
- size

### 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

```
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"))
)

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")

# You can also use geom_segment to recreate plot(type = "h") :
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), size = 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 `geom_smooth` unless you want to display the results with a non-standard geom.

## Usage

```

geom_smooth(mapping = NULL, data = NULL, stat = "smooth",
  position = "identity", ..., method = "auto", formula = y ~ x,
  se = TRUE, na.rm = FALSE, show.legend = NA, inherit.aes = TRUE)

stat_smooth(mapping = NULL, data = NULL, geom = "smooth",
  position = "identity", ..., method = "auto", formula = y ~ x,
  se = TRUE, n = 80, span = 0.75, fullrange = FALSE, level = 0.95,
  method.args = list(), na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE)

```

## Arguments

mapping	Set of aesthetic mappings created by <code>aes</code> or <code>aes_</code> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If NULL, the default, the data is inherited from the plot data as specified in the call to <code>ggplot</code>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <code>fortify</code> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>., and will be used as the layer data.</p>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <code>layer</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired <code>geom/stat</code> .
method	<p>smoothing method (function) to use, eg. "lm", "glm", "gam", "loess", "rlm".</p> <p>For <code>method = "auto"</code> the smoothing method is chosen based on the size of the largest group (across all panels). <code>loess</code> is used for than 1,000 observations; otherwise <code>gam</code> is used with <code>formula = y ~ s(x, bs = "cs")</code>. Somewhat anecdotally, <code>loess</code> gives a better appearance, but is <math>O(n^2)</math> in memory, so does not work for larger datasets.</p>
formula	formula to use in smoothing function, eg. <code>y ~ x</code> , <code>y ~ poly(x, 2)</code> , <code>y ~ log(x)</code>
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.
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.
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. <code>borders</code> .
geom, stat	Use to override the default connection between <code>geom_smooth</code> and <code>stat_smooth</code> .
n	number of points to evaluate smoother at
span	Controls the amount of smoothing for the default loess smoother. Smaller numbers produce wigglier lines, larger numbers produce smoother lines.
fullrange	should the fit span the full range of the plot, or just the data
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 <code>method</code> .

## 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.

## Aesthetics

geom\_smooth understands the following aesthetics (required aesthetics are in bold):

- **x**
- **y**
- alpha
- colour
- fill
- group
- linetype
- size
- weight

## Computed variables

**y** predicted value  
**ymin** lower pointwise confidence interval around the mean  
**ymax** upper pointwise confidence interval around the mean  
**se** standard error

## See Also

See individual modelling functions for more details: [lm](#) for linear smooths, [glm](#) for generalised linear smooths, [loess](#) for local smooths

## Examples

```
ggplot(mpg, aes(displ, hwy)) +  
  geom_point() +  
  geom_smooth()  
  
# Use span to control the "wiggleness" 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)
```

```

# Smoothes 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.

## Usage

```

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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data.</p>
stat	The statistical transformation to use on the data for this layer, as a string.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

**Aesthetics**

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

- **x**
- **y**
- **angle**
- **radius**
- alpha
- colour
- group
- linetype
- size

## Examples

```
df <- expand.grid(x = 1:10, y=1:10)
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))
```

---

geom\_violin

*Violin 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

```
geom_violin(mapping = NULL, data = NULL, stat = "ydensity",
  position = "dodge", ..., draw_quantiles = NULL, trim = TRUE,
  scale = "area", na.rm = FALSE, show.legend = NA, inherit.aes = TRUE)
```

```
stat_ydensity(mapping = NULL, data = NULL, geom = "violin",
  position = "dodge", ..., bw = "nrd0", adjust = 1, kernel = "gaussian",
  trim = TRUE, scale = "area", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE)
```

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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	<p>The data to be displayed in this layer. There are three options:</p> <p>If <code>NULL</code>, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A <code>data.frame</code>, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code>, and will be used as the layer data.</p>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.

...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
<code>draw_quantiles</code>	If not (NULL) (default), draw horizontal lines at the given quantiles of the density estimate.
<code>trim</code>	If TRUE (default), trim the tails of the violins to the range of the data. If FALSE, don't trim the tails.
<code>scale</code>	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.
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .
<code>geom, stat</code>	Use to override the default connection between <code>geom_violin</code> and <code>stat_ydensity</code> .
<code>bw</code>	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 <a href="#">bw.nrd</a> .
<code>adjust</code>	A multiplicative bandwidth adjustment. This makes it possible to adjust the bandwidth while still using the a bandwidth estimator. For example, <code>adjust = 1/2</code> means use half of the default bandwidth.
<code>kernel</code>	Kernel. See list of available kernels in <a href="#">density</a> .

## Aesthetics

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

- **x**
- **y**
- alpha
- colour
- fill
- group
- linetype
- size
- weight

### Computed variables

**density** density estimate

**scaled** density estimate, scaled to maximum of 1

**count** density \* number of points - probably useless for violin plots

**violinwidth** density scaled for the violin plot, according to area, counts or to a constant maximum width

**n** number of points

**width** width of violin bounding box

### References

Hintze, J. L., Nelson, R. D. (1998) Violin Plots: A Box Plot-Density Trace Synergism. The American Statistician 52, 181-184.

### See Also

[geom\\_violin](#) for examples, and [stat\\_density](#) for examples with data along the x axis.

### Examples

```
p <- ggplot(mtcars, aes(factor(cyl), mpg))
p + 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")) {
  # Scale transformations occur before the density statistics are computed.
  # Coordinate transformations occur afterwards. Observe the effect on the
  # number of outliers.
  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")

  # Violin plots with continuous x:
  # Use the group aesthetic to group observations in violins
  ggplot(movies, aes(year, budget)) + geom_violin()
  ggplot(movies, aes(year, budget)) +
    geom_violin(aes(group = cut_width(year, 10)), scale = "width")
}

```

---

ggplot

---

Create a new ggplot

---

## 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

```
ggplot(data = NULL, mapping = aes(), ..., environment = parent.frame())
```

## Arguments

<code>data</code>	Default dataset to use for plot. If not already a <code>data.frame</code> , will be converted to one by <code>fortify</code> . If not specified, must be supplied in each layer added to the plot.
<code>mapping</code>	Default list of aesthetic mappings to use for plot. If not specified, must be supplied in each layer added to the plot.
<code>...</code>	Other arguments passed on to methods. Not currently used.
<code>environment</code>	If an variable defined in the aesthetic mapping is not found in the data, <code>ggplot</code> will look for it in this environment. It defaults to using the environment in which <code>ggplot()</code> is called.

## Details

`ggplot()` is used to construct the initial plot object, and is almost always followed by `+` to add component to the plot. There are three common ways to invoke `ggplot()`:

1. `ggplot(df, aes(x, y, <other aesthetics>))`
2. `ggplot(df)`
3. `ggplot()`

The first method is recommended if all layers use the same data and the same set of aesthetics, although this method can also be used to add a layer using data from another data frame. See the first example below. The second method 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 as layers are added, but the aesthetics may vary from one layer to another. The third method initializes a skeleton `ggplot` object which is fleshed out as layers are added. This method is useful when multiple data frames are used to produce different layers, as is often the case in complex graphics.

## Examples

```
# Generate some sample data, then compute mean and standard deviation
# in each group
df <- data.frame(
  gp = factor(rep(letters[1:3], each = 10)),
  y = rnorm(30)
)
ds <- plyr::ddply(df, "gp", plyr::summarise, mean = mean(y), sd = sd(y))

# The summary data frame ds is used to plot larger red points on top
# of the raw data. Note that we don't need to supply `data` or `mapping`
# in each layer because the defaults from ggplot() are used.
ggplot(df, aes(gp, y)) +
  geom_point() +
  geom_point(data = ds, aes(y = mean), colour = 'red', size = 3)

# Same plot as above, declaring only the data frame in ggplot().
# Note how the x and y aesthetics must now be declared in
# each geom_point() layer.
ggplot(df) +
  geom_point(aes(gp, y)) +
  geom_point(data = ds, aes(gp, mean), colour = 'red', size = 3)

# Alternatively we can fully specify the plot in each layer. This
# is not useful here, but can be more clear when working with complex
# mult-dataset graphics
ggplot() +
  geom_point(data = df, aes(gp, y)) +
  geom_point(data = ds, aes(gp, mean), colour = 'red', size = 3) +
  geom_errorbar(
    data = ds,
    aes(gp, mean, ymin = mean - sd, ymax = mean + sd),
    colour = 'red',
    width = 0.4
```

)

---

ggproto

*Create a new ggproto object*

---

## Description

Construct a new object with ggproto, test with `is.proto`, and access parent methods/fields with `ggproto_parent`.

## Usage

```
ggproto(`_class` = NULL, `_inherit` = NULL, ...)
```

```
ggproto_parent(parent, self)
```

```
is.ggproto(x)
```

## Arguments

<code>_class</code>	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.
<code>_inherit</code>	ggproto object to inherit from. If NULL, don't inherit from any object.
<code>...</code>	A list of members in the ggproto object.
<code>parent, self</code>	Access parent class parent of object self.
<code>x</code>	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)
```

---

ggsave

---

*Save a ggplot (or other grid object) with sensible defaults*


---

### 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

```
ggsave(filename, plot = last_plot(), device = NULL, path = NULL,
  scale = 1, width = NA, height = NA, units = c("in", "cm", "mm"),
  dpi = 300, limitsize = TRUE, ...)
```

### Arguments

<code>filename</code>	File name to create on disk.
<code>plot</code>	Plot to save, defaults to last plot displayed.
<code>device</code>	Device to use. Can be either be a device function (e.g. <a href="#">png</a> ), or one of "eps", "ps", "tex" (pictex), "pdf", "jpeg", "tiff", "png", "bmp", "svg" or "wmf" (windows only).
<code>path</code>	Path to save plot to (combined with filename).

scale	Multiplicative scaling factor.
width, height, units	Plot size in units ("in", "cm", or "mm"). If not supplied, uses the size of current graphics device.
dpi	Plot resolution. 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.
...	Other arguments passed on to graphics device.

### Examples

```
## Not run:
ggplot(mtcars, aes(mpg, wt)) + geom_point()

ggsave("mtcars.pdf")
ggsave("mtcars.png")

ggsave("mtcars.pdf", width = 4, height = 4)
ggsave("mtcars.pdf", width = 20, height = 20, units = "cm")

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)

## 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

```
theme_grey(base_size = 11, base_family = "")

theme_gray(base_size = 11, base_family = "")

theme_bw(base_size = 11, base_family = "")

theme_linedraw(base_size = 11, base_family = "")
```

```

theme_light(base_size = 11, base_family = "")
theme_dark(base_size = 11, base_family = "")
theme_minimal(base_size = 11, base_family = "")
theme_classic(base_size = 11, base_family = "")
theme_void(base_size = 11, base_family = "")

```

### Arguments

<code>base_size</code>	base font size
<code>base_family</code>	base font family

### 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 drawings. Serves a purpose similar to `theme_bw`. Note that this theme has some very thin lines ( $\ll 1$  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.

### Examples

```

p <- ggplot(mtcars) + geom_point(aes(x = wt, y = mpg,
  colour = factor(gear))) + facet_wrap(~am)
p + theme_gray() # the default
p + theme_bw()
p + theme_linedraw()
p + theme_light()
p + theme_dark()
p + theme_minimal()
p + theme_classic()
p + theme_void()

```

---

guides	<i>Set guides for each scale</i>
--------	----------------------------------

---

## 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. "colorbar" 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\\_colourbar](#), [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_colourbar(), 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)
  )

```

---

guide\_colourbar

*Continuous colour bar guide*


---

## Description

Colour bar guide shows continuous color 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

```

guide_colourbar(title = waiver(), title.position = NULL,
  title.theme = NULL, title.hjust = NULL, title.vjust = NULL,
  label = TRUE, label.position = NULL, label.theme = NULL,
  label.hjust = NULL, label.vjust = NULL, barwidth = NULL,
  barheight = NULL, nbin = 20, raster = TRUE, ticks = TRUE,
  draw.ulim = TRUE, draw.llim = TRUE, direction = NULL,
  default.unit = "line", reverse = FALSE, order = 0, ...)

guide_colorbar(title = waiver(), title.position = NULL,
  title.theme = NULL, title.hjust = NULL, title.vjust = NULL,
  label = TRUE, label.position = NULL, label.theme = NULL,
  label.hjust = NULL, label.vjust = NULL, barwidth = NULL,
  barheight = NULL, nbin = 20, raster = TRUE, ticks = TRUE,

```



```
draw.ulim = TRUE, draw.llim = TRUE, direction = NULL,
default.unit = "line", reverse = FALSE, order = 0, ...)
```

## Arguments

<code>title</code>	A character string or expression indicating a title of guide. If <code>NULL</code> , the title is not shown. By default ( <a href="#">waiver</a> ), the name of the scale object or the name specified in <a href="#">labs</a> is used for the title.
<code>title.position</code>	A character string indicating the position of a title. One of "top" (default for a vertical guide), "bottom", "left" (default for a horizontal guide), or "right."
<code>title.theme</code>	A theme object for rendering the title text. Usually the object of <a href="#">element_text</a> is expected. By default, the theme is specified by <code>legend.title</code> in <a href="#">theme</a> or <code>theme</code> .
<code>title.hjust</code>	A number specifying horizontal justification of the title text.
<code>title.vjust</code>	A number specifying vertical justification of the title text.
<code>label</code>	logical. If <code>TRUE</code> then the labels are drawn. If <code>FALSE</code> then the labels are invisible.
<code>label.position</code>	A character string indicating the position of a label. One of "top", "bottom" (default for horizontal guide), "left", or "right" (default for vertical guide).
<code>label.theme</code>	A theme object for rendering the label text. Usually the object of <a href="#">element_text</a> is expected. By default, the theme is specified by <code>legend.text</code> in <a href="#">theme</a> or <code>theme</code> .
<code>label.hjust</code>	A numeric specifying horizontal justification of the label text.
<code>label.vjust</code>	A numeric specifying vertical justification of the label text.
<code>barwidth</code>	A numeric or a <a href="#">unit</a> object specifying the width of the colorbar. Default value is <code>legend.key.width</code> or <code>legend.key.size</code> in <a href="#">theme</a> or <code>theme</code> .
<code>barheight</code>	A numeric or a <a href="#">unit</a> object specifying the height of the colorbar. Default value is <code>legend.key.height</code> or <code>legend.key.size</code> in <a href="#">theme</a> or <code>theme</code> .
<code>nbin</code>	A numeric specifying the number of bins for drawing colorbar. A smoother colorbar for a larger value.
<code>raster</code>	A logical. If <code>TRUE</code> then the colorbar is rendered as a raster object. If <code>FALSE</code> then the colorbar is rendered as a set of rectangles. Note that not all graphics devices are capable of rendering raster image.
<code>ticks</code>	A logical specifying if tick marks on colorbar should be visible.
<code>draw.ulim</code>	A logical specifying if the upper limit tick marks should be visible.
<code>draw.llim</code>	A logical specifying if the lower limit tick marks should be visible.
<code>direction</code>	A character string indicating the direction of the guide. One of "horizontal" or "vertical."
<code>default.unit</code>	A character string indicating <a href="#">unit</a> for <code>barwidth</code> and <code>barheight</code> .
<code>reverse</code>	logical. If <code>TRUE</code> the colorbar is reversed. By default, the highest value is on the top and the lowest value is on the bottom
<code>order</code>	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.
<code>...</code>	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_color_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\\_legend](#), [guides](#)

## Examples

```
df <- reshape2::melt(outer(1:4, 1:4), varnames = c("X1", "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 = "colorbar")
p1 + scale_fill_continuous(guide = guide_colorbar())
p1 + guides(fill = guide_colorbar())

# Control styles

# bar size
p1 + guides(fill = guide_colorbar(barwidth = 0.5, barheight = 10))

# no label
p1 + guides(fill = guide_colorbar(label = FALSE))

# no tick marks
p1 + guides(fill = guide_colorbar(ticks = FALSE))

# label position
p1 + guides(fill = guide_colorbar(label.position = "left"))

# label theme
p1 + guides(fill = guide_colorbar(label.theme = element_text(colour = "blue", angle = 0)))

# small number of bins
p1 + guides(fill = guide_colorbar(nbin = 3))

# large number of bins
p1 + guides(fill = guide_colorbar(nbin = 100))

# make top- and bottom-most ticks invisible
p1 + scale_fill_continuous(limits = c(0,20), breaks = c(0, 5, 10, 15, 20),
  guide = guide_colorbar(nbin=100, draw.ulim = FALSE, draw.llim = FALSE))
```

```
# guides can be controlled independently
p2 +
  scale_fill_continuous(guide = "colorbar") +
  scale_size(guide = "legend")
p2 + guides(fill = "colorbar", size = "legend")

p2 +
  scale_fill_continuous(guide = guide_colorbar(direction = "horizontal")) +
  scale_size(guide = guide_legend(direction = "vertical"))
```

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(), title.position = NULL, title.theme = NULL,
  title.hjust = NULL, title.vjust = NULL, label = TRUE,
  label.position = NULL, label.theme = NULL, label.hjust = NULL,
  label.vjust = NULL, keywidth = NULL, keyheight = NULL,
  direction = NULL, default.unit = "line", override.aes = list(),
  nrow = NULL, ncol = NULL, byrow = FALSE, 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 ( <a href="#">waiver</a> ), the name of the scale object or the name specified in <a href="#">labs</a> is used for the title.
title.position	A character string indicating the position of a title. One of "top" (default for a vertical guide), "bottom", "left" (default for a horizontal guide), or "right."
title.theme	A theme object for rendering the title text. Usually the object of <a href="#">element_text</a> is expected. By default, the theme is specified by legend.title in <a href="#">theme</a> or theme.
title.hjust	A number specifying horizontal justification of the title text.
title.vjust	A number specifying vertical justification of the title text.
label	logical. If TRUE then the labels are drawn. If FALSE then the labels are invisible.
label.position	A character string indicating the position of a label. One of "top", "bottom" (default for horizontal guide), "left", or "right" (default for vertical guide).
label.theme	A theme object for rendering the label text. Usually the object of <a href="#">element_text</a> is expected. By default, the theme is specified by legend.text in <a href="#">theme</a> or theme.

<code>label.hjust</code>	A numeric specifying horizontal justification of the label text.
<code>label.vjust</code>	A numeric specifying vertical justification of the label text.
<code>keywidth</code>	A numeric or a <a href="#">unit</a> object specifying the width of the legend key. Default value is <code>legend.key.width</code> or <code>legend.key.size</code> in <a href="#">theme</a> or theme.
<code>keyheight</code>	A numeric or a <a href="#">unit</a> object specifying the height of the legend key. Default value is <code>legend.key.height</code> or <code>legend.key.size</code> in <a href="#">theme</a> or theme.
<code>direction</code>	A character string indicating the direction of the guide. One of "horizontal" or "vertical."
<code>default.unit</code>	A character string indicating <a href="#">unit</a> for <code>keywidth</code> and <code>keyheight</code> .
<code>override.aes</code>	A list specifying aesthetic parameters of legend key. See details and examples.
<code>nrow</code>	The desired number of rows of legends.
<code>ncol</code>	The desired number of column of legends.
<code>byrow</code>	logical. If FALSE (the default) the legend-matrix is filled by columns, otherwise the legend-matrix is filled by rows.
<code>reverse</code>	logical. If TRUE the order of legends is reversed.
<code>order</code>	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.
<code>...</code>	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_color_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\\_colourbar](#), [guides](#)

### Examples

```
df <- reshape2::melt(outer(1:4, 1:4), varnames = c("X1", "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 = "legend")
p1 + scale_fill_continuous(guide = guide_legend())
```

```

# Guide title
p1 + scale_fill_continuous(guide = guide_legend(title = "V")) # title text
p1 + scale_fill_continuous(guide = guide_legend(title = NULL)) # no title

# Control styles

# key size
p1 + guides(fill = guide_legend(keywidth = 3, keyheight = 1))

# title position
p1 + guides(fill = guide_legend(title = "LEFT", title.position = "left"))

# title text styles via element_text
p1 + guides(fill =
  guide_legend(
    title.theme = element_text(
      size = 15,
      face = "italic",
      colour = "red",
      angle = 0
    )
  )
)

# label position
p1 + guides(fill = guide_legend(label.position = "left", label.hjust = 1))

# label styles
p1 + scale_fill_continuous(breaks = c(5, 10, 15),
  labels = paste("long", c(5, 10, 15)),
  guide = guide_legend(
    direction = "horizontal",
    title.position = "top",
    label.position = "bottom",
    label.hjust = 0.5,
    label.vjust = 1,
    label.theme = element_text(angle = 90)
  )
)

# Set aesthetic of legend key

# very low alpha value make it difficult to see legend key
p3 <- ggplot(diamonds, aes(carat, price)) +
  geom_point(aes(colour = color), alpha = 1/100)
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, byrow = TRUE))
p + guides(col = guide_legend(ncol = 8, byrow = TRUE))

# reversed order legend
p + guides(col = guide_legend(reverse = TRUE))
```

---

 hmisc

*A selection of summary functions from Hmisc*


---

## 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:

- [smean.cl.boot](#)
- [smean.cl.normal](#)
- [smean.sdl](#)
- [smedian.hilow](#)

## Usage

```
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**

```
x <- rnorm(100)
mean_cl_boot(x)
mean_cl_normal(x)
mean_sdl(x)
median_hilow(x)
```

---

labeller	<i>Construct labelling specification</i>
----------	--

---

**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**

```
labeller(..., .rows = NULL, .cols = NULL, keep.as.numeric = NULL,
  .multi_line = TRUE, .default = label_value)
```

**Arguments**

...	Named arguments of the form <code>variable = labeller</code> . Each labeller is passed to <code>as_labeller()</code> 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 <code>as_labeller()</code> . 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 `capitalize`.

**Value**

A labeller function to supply to `facet_grid` for the argument `labeller`.

**See Also**

[as\\_labeller\(\)](#), [labellers](#)

**Examples**

```
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"
)
## Source: http://en.wikipedia.org/wiki/Wikipedia:Conservation\_status

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
msleep$conservation2 <- plyr::revalue(msleep$conservation,
  conservation_status)

p2 %+% msleep + facet_grid(vore ~ conservation2)
p2 %+% msleep +
  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)
p2 + facet_wrap(~vore, labeller = global_labeller)
p2 %>% msleep + 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**

<code>labels</code>	Data frame of labels. Usually contains only one element, but facetting over multiple factors entails multiple label variables.
<code>multi_line</code>	Whether to display the labels of multiple factors on separate lines.
<code>sep</code>	String separating variables and values.
<code>width</code>	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 facetting and `label_both()` when multiple factors are involved. `label_wrap_gen()` uses `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()

# Displaying only the values
p + facet_grid(. ~ cyl)
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)
p + facet_wrap(~vs + cyl2, labeller = label_parsed)
```

---

label_bquote	<i>Label with mathematical expressions</i>
--------------	--

---

## 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

```
label_bquote(rows = NULL, cols = NULL, default = label_value)
```

## Arguments

rows	Backquoted labelling expression for rows.
cols	Backquoted labelling expression for columns.
default	Default labeller function for the rows or the columns when no plotmath expression is provided.

## 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. 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.

## Usage

```
labs(...)

xlab(label)

ylab(label)

ggtitle(label, subtitle = NULL)
```

## Arguments

...	A list of new name-value pairs. The name should either be an aesthetic, or one of "title", "subtitle", or "caption".
label	The text for the axis, plot title or caption below the plot.
subtitle	the text for the subtitle for the plot which will be displayed below the title. Leave NULL for no subtitle.

## Details

You can also set axis and legend labels in the individual scales (using the first argument, the name. I recommend doing that if you're changing other scale options.

## Examples

```
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
# display 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 ...)")
```

---

lims*Set scale limits*

---

### Description

This is a shortcut for supplying the `limits` argument to the individual scales. Note that, by default, any values outside the limits will be replaced with NA.

### Usage

```
lims(...)
```

```
xlim(...)
```

```
ylim(...)
```

### Arguments

...      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 to compute 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

For changing x or y axis limits **without** dropping data observations, see [coord\\_cartesian](#). To expand the range of a plot to always include certain values, see [expand\\_limits](#).

### Examples

```
# 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"))
```

---

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

---

margin	Theme elements
--------	----------------

---

### 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, `margins()` is used to specify the margins of elements.

**Usage**

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

element_blank()

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

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

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)
```

**Arguments**

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.
fill	Fill colour.
colour, color	Line/border colour. Color is an alias for colour.
size	Line/border size in mm; text size in pts.
linetype	Line type. An integer (0:8), a name (blank, solid, dashed, dotted, dotdash, longdash, 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.
lineend	Line end Line end style (round, butt, square)
arrow	Arrow specification, as created by <a href="#">arrow</a>
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 <a href="#">margin</a> 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.

**Value**

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

**Examples**

```
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",
    size = 1
  )
)
```

---

mean_se	<i>Calculate mean and standard error</i>
---------	--

---

**Description**

For use with [stat\\_summary](#)

**Usage**

```
mean_se(x, mult = 1)
```

**Arguments**

x	numeric vector
mult	number of multiples of standard error



**Value**

A data frame with columns y, ymin, and ymax.

**Examples**

```
x <- rnorm(100)
mean_se(x)
```

---

midwest	<i>Midwest demographics</i>
---------	-----------------------------

---

**Description**

Demographic information of midwest counties

**Usage**

```
midwest
```

**Format**

A data frame with 437 rows and 28 variables

**PID**

**county**

**state**

**area**

**poptotal** Total population

**popdensity** Population density

**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**

**percollege** Percent college educated.

**percprof** Percent profession.  
**poppovertyknown**  
**percpovertyknown**  
**percbelowpoverty**  
**percchildbelowpovert**  
**percadultpoverty**  
**percelderlypoverty**  
**inmetro** In a metro area.  
**category**

---

mpg

*Fuel economy data from 1999 and 2008 for 38 popular models of car*


---

## Description

This dataset contains a subset of the fuel economy data that the EPA makes available on <http://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**  
**model** model name  
**displ** engine displacement, in litres  
**year** year of manufacture  
**cyl** number of cylinders  
**trans** type of transmission  
**drv** 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

---

msleep*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

**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

*Dodge overlapping objects side-to-side*


---

## Description

Dodging preserves the vertical position of an geom while adjusting the horizontal position.

## Usage

```
position_dodge(width = NULL)
```

## 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.

## See Also

Other position adjustments: [position\\_identity](#), [position\\_jitterdodge](#), [position\\_jitter](#), [position\\_nudge](#), [position\\_stack](#)

## Examples

```
ggplot(mtcars, aes(factor(cyl), fill = factor(vs))) +
  geom_bar(position = "dodge")

ggplot(diamonds, aes(price, fill = cut)) +
  geom_histogram(position="dodge")
# see ?geom_boxplot and ?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")

# 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)
  )

```

---

position_identity	<i>Don't adjust position</i>
-------------------	------------------------------

---

### 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	<i>Jitter points to avoid overplotting</i>
-----------------	--

---

### 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)
```

## 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.

## 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)
ggplot(mtcars, aes(am, vs)) +
  geom_jitter(position = position_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

```
position_jitterdodge(jitter.width = NULL, jitter.height = 0,
  dodge.width = 0.75)
```

**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.

**See Also**

Other position adjustments: [position\\_dodge](#), [position\\_identity](#), [position\\_jitter](#), [position\\_nudge](#), [position\\_stack](#)

**Examples**

```
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	<i>Nudge points a fixed distance</i>
----------------	--------------------------------------

---

**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**

```
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 another

---

**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.

### 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
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 -----

# 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 = type)) +
  scale_fill_discrete(breaks = c('a', 'b', 'c', 'd'))
```

```

# 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.
ggplot(series, aes(time, value, group = type)) +
  geom_line(aes(colour = type), position = "stack") +
  geom_point(aes(colour = type), position = "stack")

ggplot(series, aes(time, value, group = type)) +
  geom_area(aes(fill = type)) +
  geom_line(aes(group = type), position = "stack")

# You can also stack labels, but the default position is suboptimal.
ggplot(series, aes(time, value, group = type)) +
  geom_area(aes(fill = type)) +
  geom_text(aes(label = type), position = "stack")

# You can override this with the vjust parameter. A vjust of 0.5
# will center the labels inside the corresponding area
ggplot(series, aes(time, value, group = type)) +
  geom_area(aes(fill = type)) +
  geom_text(aes(label = type), position = position_stack(vjust = 0.5))

# Negative values -----

df <- tibble::tribble(
  ~x, ~y, ~grp,
  "a", 1,  "x",
  "a", 2,  "y",
  "b", 1,  "x",
  "b", 3,  "y",
  "b", -1, "y"
)

ggplot(data = df, aes(x, y, group = grp)) +
  geom_col(aes(fill = grp), position = position_stack(reverse = TRUE)) +
  geom_hline(yintercept = 0)

ggplot(data = df, aes(x, y, group = grp)) +
  geom_col(aes(fill = grp)) +
  geom_hline(yintercept = 0) +
  geom_text(aes(label = grp), position = position_stack(vjust = 0.5))

```

---

presidential

---

*Terms of 11 presidents from Eisenhower to Obama*


---

## Description

The names of each president, the start and end date of their term, and their party of 11 US presidents from Eisenhower to Obama.

**Usage**

```
presidential
```

**Format**

A data frame with 11 rows and 4 variables

---

print.ggplot	<i>Explicitly draw plot</i>
--------------	-----------------------------

---

**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**

```
## 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 result of `ggplot_build`, which is a list with components that contain the plot itself, the data, information about the scales, panels etc.

**Examples**

```
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	<i>Format or print a ggproto object</i>
---------------	---

---

## 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

```

## 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

```

Dog <- ggproto(
  print = function(self, n) {
    cat("Woof!\n")
  }
)
Dog
cat(format(Dog), "\n")

```

qplot

*Quick plot***Description**

qplot is a shortcut designed to be familiar if you're used to base `plot()`. It's a convenient wrapper for creating a number of different types of plots using a consistent calling scheme. It's great for allowing you to produce plots quickly, but I highly recommend learning `ggplot()` as it makes it easier to create complex graphics.

**Usage**

```
qplot(x, y = NULL, ..., data, facets = NULL, margins = FALSE,
      geom = "auto", xlim = c(NA, NA), ylim = c(NA, NA), log = "",
      main = NULL, xlab = deparse(substitute(x)),
      ylab = deparse(substitute(y)), asp = NA, stat = NULL, position = NULL)
```

```
quickplot(x, y = NULL, ..., data, facets = NULL, margins = FALSE,
          geom = "auto", xlim = c(NA, NA), ylim = c(NA, NA), log = "",
          main = NULL, xlab = deparse(substitute(x)),
          ylab = deparse(substitute(y)), asp = NA, stat = NULL, position = NULL)
```

**Arguments**

<code>x, y, ...</code>	Aesthetics passed into each layer
<code>data</code>	Data frame to use (optional). If not specified, will create one, extracting vectors from the current environment.
<code>facets</code>	faceting formula to use. Picks <code>facet_wrap</code> or <code>facet_grid</code> depending on whether the formula is one- or two-sided
<code>margins</code>	See <code>facet_grid</code> : display marginal facets?
<code>geom</code>	Character vector specifying geom(s) to draw. Defaults to "point" if x and y are specified, and "histogram" if only x is specified.
<code>xlim, ylim</code>	X and y axis limits
<code>log</code>	Which variables to log transform ("x", "y", or "xy")
<code>main, xlab, ylab</code>	Character vector (or expression) giving plot title, x axis label, and y axis label respectively.
<code>asp</code>	The y/x aspect ratio
<code>stat, position</code>	DEPRECATED.

### Examples

```
# 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)

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

```
resolution(x, zero = TRUE)
```

**Arguments**

x	numeric vector
zero	should a zero value be automatically included in the computation of resolution

**Examples**

```
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	<i>Alpha transparency scales</i>
-------------	----------------------------------

---

**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**

```
scale_alpha(..., range = c(0.1, 1))

scale_alpha_continuous(..., range = c(0.1, 1))

scale_alpha_discrete(..., range = c(0.1, 1))
```

**Arguments**

...	Other arguments passed on to <a href="#">continuous_scale</a> or <a href="#">discrete_scale</a> as appropriate, to control name, limits, breaks, labels and so forth.
range	Output range of alpha values. Must lie between 0 and 1.

**See Also**

Other colour scales: [scale\\_colour\\_brewer](#), [scale\\_colour\\_gradient](#), [scale\\_colour\\_grey](#), [scale\\_colour\\_hue](#)

**Examples**

```
p <- ggplot(mpg, aes(displ, hwy)) +
  geom_point(aes(alpha = year))

p
p + scale_alpha("cylinders")
p + scale_alpha(range = c(0.4, 0.8))
```

---

scale\_colour\_brewer     *Sequential, diverging and qualitative colour scales from color-brewer.org*

---

## Description

The brewer scales provides sequential, diverging and qualitative colour schemes from ColorBrewer. These are particularly well suited to display discrete values on a map. See <http://colorbrewer2.org> for more information.

## Usage

```
scale_colour_brewer(..., type = "seq", palette = 1, direction = 1)

scale_fill_brewer(..., type = "seq", palette = 1, direction = 1)

scale_colour_distiller(..., type = "seq", palette = 1, direction = -1,
  values = NULL, space = "Lab", na.value = "grey50",
  guide = "colourbar")

scale_fill_distiller(..., type = "seq", palette = 1, direction = -1,
  values = NULL, space = "Lab", na.value = "grey50",
  guide = "colourbar")
```

## Arguments

...	Other arguments passed on to <a href="#">discrete_scale</a> 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
direction	Sets the order of colors in the scale. If 1, the default, colors are as output by <a href="#">brewer.pal</a> . If -1, the order of colors is reversed.
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 <a href="#">rescale</a> 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, RdYlBu, RdYlGn, 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, YlGn, YlGnBu, YlOrBr, YlOrRd

## Note

The distiller scales extends brewer to continuous scales by smoothly interpolate 6 colours from any palette to a continuous scale.

## See Also

Other colour scales: [scale\\_alpha](#), [scale\\_colour\\_gradient](#), [scale\\_colour\\_grey](#), [scale\\_colour\\_hue](#)

## Examples

```
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\nclearity")

# Select brewer palette to use, see ?scales::brewer_pal 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) +
  geom_tile(aes(waiting, eruptions, fill = density))
v
v + scale_fill_distiller()
v + scale_fill_distiller(palette = "Spectral")
```

---

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 a n-colour gradient.

## Usage

```
scale_colour_gradient(..., low = "#132B43", high = "#56B1F7",
  space = "Lab", na.value = "grey50", guide = "colourbar")

scale_fill_gradient(..., low = "#132B43", high = "#56B1F7", space = "Lab",
  na.value = "grey50", guide = "colourbar")

scale_colour_gradient2(..., low = muted("red"), mid = "white",
  high = muted("blue"), midpoint = 0, space = "Lab",
  na.value = "grey50", guide = "colourbar")

scale_fill_gradient2(..., low = muted("red"), mid = "white",
  high = muted("blue"), midpoint = 0, space = "Lab",
  na.value = "grey50", guide = "colourbar")

scale_colour_gradientn(..., colours, values = NULL, space = "Lab",
  na.value = "grey50", guide = "colourbar", colors)

scale_fill_gradientn(..., colours, values = NULL, space = "Lab",
  na.value = "grey50", guide = "colourbar", colors)
```

## Arguments

...	Other arguments passed on to <a href="#">continuous_scale</a> to control name, limits, breaks, labels and so forth.
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.
mid	colour for mid point
midpoint	The midpoint (in data value) of the diverging scale. Defaults to 0.
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 `muns1(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

[seq\\_gradient\\_pal](#) for details on underlying palette

Other colour scales: [scale\\_alpha](#), [scale\\_colour\\_brewer](#), [scale\\_colour\\_grey](#), [scale\\_colour\\_hue](#)

## Examples

```
df <- data.frame(
  x = runif(100),
  y = runif(100),
  z1 = rnorm(100),
  z2 = abs(rnorm(100))
)

# Default colour scale colours from light blue to dark blue
ggplot(df, aes(x, y)) +
  geom_point(aes(colour = z2))

# For diverging colour scales use gradient2
ggplot(df, aes(x, y)) +
  geom_point(aes(colour = z1)) +
  scale_colour_gradient2()

# Use your own colour scale with gradientn
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
ggplot(faithfuld, aes(waiting, eruptions)) +
  geom_raster(aes(fill = density)) +
  scale_fill_gradientn(colours = terrain.colors(10))

# Adjust colour choices with low and high
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
```

---

scale\_colour\_grey      *Sequential grey colour scales*

---

## Description

Based on [gray.colors](#). This is black and white equivalent of [scale\\_colour\\_gradient](#).

## Usage

```
scale_colour_grey(..., start = 0.2, end = 0.8, na.value = "red")
```

```
scale_fill_grey(..., start = 0.2, end = 0.8, na.value = "red")
```

## Arguments

...	Other arguments passed on to <a href="#">discrete_scale</a> to control name, limits, breaks, labels and so forth.
start	gray value at low end of palette
end	gray value at high end of palette
na.value	Colour to use for missing values

## See Also

Other colour scales: [scale\\_alpha](#), [scale\\_colour\\_brewer](#), [scale\\_colour\\_gradient](#), [scale\\_colour\\_hue](#)

## Examples

```
p <- ggplot(mtcars, aes(mpg, wt)) + geom_point(aes(colour = factor(cyl)))
p + scale_colour_grey()
p + scale_colour_grey(end = 0)

# You may want to turn off the pale grey background with this scale
p + scale_colour_grey() + theme_bw()

# 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)) +
  scale_colour_grey()
ggplot(mtcars, aes(mpg, wt)) +
  geom_point(aes(colour = miss)) +
  scale_colour_grey(na.value = "green")
```

---

scale_colour_hue	<i>Evenly spaced colours for discrete data</i>
------------------	--

---

## Description

This is the default colour scale for categorical variables. It maps each level to an evenly spaced hue on the colour wheel. It does not generate colour-blind safe palettes.

## Usage

```
scale_colour_hue(..., h = c(0, 360) + 15, c = 100, l = 65, h.start = 0,
  direction = 1, na.value = "grey50")
```

```
scale_fill_hue(..., h = c(0, 360) + 15, c = 100, l = 65, h.start = 0,
  direction = 1, na.value = "grey50")
```

## Arguments

...	Other arguments passed on to <a href="#">discrete_scale</a> to control name, limits, breaks, labels and so forth.
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

## See Also

Other colour scales: [scale\\_alpha](#), [scale\\_colour\\_brewer](#), [scale\\_colour\\_gradient](#), [scale\\_colour\\_grey](#)

## Examples

```
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(dsamp, 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_continuous	<i>Position scales for continuous data (x &amp; y)</i>
------------------	--

---

## 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 trans argument for commonly used transformations: scale\*\_log10, scale\*\_sqrt and scale\*\_reverse.

## Usage

```

scale_x_continuous(name = waiver(), breaks = waiver(),
  minor_breaks = waiver(), labels = waiver(), limits = NULL,
  expand = waiver(), oob = censor, na.value = NA_real_,
  trans = "identity", position = "bottom", sec.axis = waiver())

scale_y_continuous(name = waiver(), breaks = waiver(),
  minor_breaks = waiver(), labels = waiver(), limits = NULL,
  expand = waiver(), oob = censor, na.value = NA_real_,
  trans = "identity", 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 axis or legend title. If NULL, the default, the name of the scale is taken from the first mapping used for that aesthetic.
breaks	One of: <ul style="list-style-type: none"> <li>• NULL for no breaks</li> <li>• <code>waiver()</code> for the default breaks computed by the transformation object</li> <li>• A numeric vector of positions</li> <li>• A function that takes the limits as input and returns breaks as output</li> </ul>
minor_breaks	One of: <ul style="list-style-type: none"> <li>• NULL for no minor breaks</li> <li>• <code>waiver()</code> for the default breaks (one minor break between each major break)</li> <li>• A numeric vector of positions</li> <li>• A function that given the limits returns a vector of minor breaks.</li> </ul>
labels	One of: <ul style="list-style-type: none"> <li>• NULL for no labels</li> <li>• <code>waiver()</code> for the default labels computed by the transformation object</li> <li>• A character vector giving labels (must be same length as breaks)</li> <li>• A function that takes the breaks as input and returns labels as output</li> </ul>
limits	A numeric vector of length two providing limits of the scale. Use NA to refer to the existing minimum or maximum.
expand	A numeric vector of length two giving multiplicative and additive expansion constants. These constants ensure that the data is placed some distance away from the axes. The defaults are <code>c(0.05, 0)</code> for continuous variables, and <code>c(0, 0.6)</code> for discrete variables.
oob	Function that handles limits outside of the scale limits (out of bounds). The default replaces out of bounds values with NA.
na.value	Missing values will be replaced with this value.
trans	Either the name of a transformation object, or the object itself. Built-in transformations include "asn", "atanh", "boxcox", "exp", "identity", "log", "log10", "log1p", "log2", "logit", "probability", "probit", "reciprocal", "reverse" and "sqrt". A transformation object bundles together a transform, it's inverse, and methods for generating breaks and labels. Transformation objects are defined in the scales package, and are called <code>name_trans</code> , e.g. <code>boxcox_trans</code> . You can create your own transformation with <code>trans_new</code> .

position	The position of the axis. "left" or "right" for vertical scales, "top" or "bottom" for horizontal scales
sec.axis	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.

### See Also

[sec.axis](#) for how to specify secondary axes

Other position scales: [scale\\_x\\_date](#), [scale\\_x\\_discrete](#)

### Examples

```
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))

# * add what labels they have
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:
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::percent)
p2 + scale_y_continuous(labels = scales::dollar)
p2 + scale_x_continuous(labels = scales::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(trans = scales::reciprocal_trans())

# You can also create your own. See ?scales::trans_new

```

---

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

```

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(),
  position = "bottom")

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(),
  position = "left")

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(), position = "bottom")

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(), position = "left")

```

```
scale_x_time(name = waiver(), breaks = waiver(), minor_breaks = waiver(),
  labels = waiver(), limits = NULL, expand = waiver(), oob = censor,
  na.value = NA_real_, position = "bottom")
```

```
scale_y_time(name = waiver(), breaks = waiver(), minor_breaks = waiver(),
  labels = waiver(), limits = NULL, expand = waiver(), oob = censor,
  na.value = NA_real_, position = "left")
```

## Arguments

name	The name of the scale. Used as axis or legend title. If NULL, the default, the name of the scale is taken from the first mapping used for that aesthetic.
breaks	One of: <ul style="list-style-type: none"> <li>• NULL for no breaks</li> <li>• waiver() for the default breaks computed by the transformation object</li> <li>• A numeric vector of positions</li> <li>• A function that takes the limits as input and returns breaks as output</li> </ul>
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.
labels	One of: <ul style="list-style-type: none"> <li>• NULL for no labels</li> <li>• waiver() for the default labels computed by the transformation object</li> <li>• A character vector giving labels (must be same length as breaks)</li> <li>• A function that takes the breaks as input and returns labels as output</li> </ul>
date_labels	A string giving the formatting specification for the labels. Codes are defined in <a href="#">strftime</a> . If both labels and date_labels are specified, date_labels wins.
minor_breaks	One of: <ul style="list-style-type: none"> <li>• NULL for no minor breaks</li> <li>• waiver() for the default breaks (one minor break between each major break)</li> <li>• A numeric vector of positions</li> <li>• A function that given the limits returns a vector of minor breaks.</li> </ul>
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.
limits	A numeric vector of length two providing limits of the scale. Use NA to refer to the existing minimum or maximum.
expand	A numeric vector of length two giving multiplicative and additive expansion constants. These constants ensure that the data is placed some distance away from the axes. The defaults are c(0.05, 0) for continuous variables, and c(0, 0.6) for discrete variables.
position	The position of the axis. "left" or "right" for vertical scales, "top" or "bottom" for horizontal scales

timezone	The timezone to use for display on the axes. The default (NULL) uses the timezone encoded in the data.
oob	Function that handles limits outside of the scale limits (out of bounds). The default replaces out of bounds values with NA.
na.value	Missing values will be replaced with this value.

### See Also

Other position scales: [scale\\_x\\_continuous](#), [scale\\_x\\_discrete](#)

### Examples

```
last_month <- Sys.Date() - 0:29
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	<i>Use values without scaling</i>
----------------	-----------------------------------

---

### 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. This will not produce a legend unless you also supply the breaks and labels.

### Usage

```
scale_colour_identity(..., guide = "none")

scale_fill_identity(..., guide = "none")

scale_shape_identity(..., guide = "none")

scale_linetype_identity(..., guide = "none")
```

```
scale_alpha_identity(..., guide = "none")
```

```
scale_size_identity(..., guide = "none")
```

### Arguments

... Other arguments passed on to [discrete\\_scale](#) or [continuous\\_scale](#)

guide Guide to use for this scale. Defaults to "none".

### Examples

```
ggplot(luv_colours, aes(u, v)) +
  geom_point(aes(colour = col), size = 3) +
  scale_color_identity() +
  coord_equal()

df <- data.frame(
  x = 1:4,
  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()
```

**Description**

Default line types based on a set supplied by Richard Pearson, University of Manchester. Continuous values can not be mapped to line types.

**Usage**

```
scale_linetype(..., na.value = "blank")

scale_linetype_continuous(...)

scale_linetype_discrete(..., na.value = "blank")
```

**Arguments**

...	common discrete scale parameters: name, breaks, labels, na.value, limits and guide. See <a href="#">discrete_scale</a> for more details
na.value	The linetype to use for NA values.

**Examples**

```
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), size = 2) +
  scale_linetype_identity() +
  facet_grid(linetype ~ .) +
  theme_void(20)
```

**Description**

This allows you to specify you own set of mappings from levels in the data to aesthetic values.

**Usage**

```
scale_colour_manual(..., values)

scale_fill_manual(..., values)

scale_size_manual(..., values)

scale_shape_manual(..., values)

scale_linetype_manual(..., values)

scale_alpha_manual(..., values)
```

**Arguments**

<code>...</code>	common discrete scale parameters: name, breaks, labels, na.value, limits and guide. See <a href="#">discrete_scale</a> for more details
<code>values</code>	a set of aesthetic values to map data values to. If this is a named vector, then the values will be matched based on the names. If unnamed, values will be matched in order (usually alphabetical) with the limits of the scale. Any data values that don't match will be given na.value.

**Examples**

```
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)

# 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.

## Usage

```
scale_shape(..., solid = TRUE)
```

## Arguments

...	common discrete scale parameters: name, breaks, labels, na.value, limits and guide. See <a href="#">discrete_scale</a> for more details
solid	Should the shapes be solid, TRUE, or hollow, FALSE?

## Examples

```
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)) +
  geom_point(aes(shape = shape), size = 5, fill = 'red') +
  scale_shape_identity() +
  facet_wrap(~shape) +
  theme_void()
```

---

scale_size	<i>Scales for area or radius</i>
------------	----------------------------------

---

### 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.

### Usage

```
scale_radius(name = waiver(), breaks = waiver(), labels = waiver(),
  limits = NULL, range = c(1, 6), trans = "identity", guide = "legend")

scale_size(name = waiver(), breaks = waiver(), labels = waiver(),
  limits = NULL, range = c(1, 6), trans = "identity", guide = "legend")

scale_size_area(..., max_size = 6)
```

### Arguments

name	The name of the scale. Used as axis or legend title. If NULL, the default, the name of the scale is taken from the first mapping used for that aesthetic.
breaks	One of: <ul style="list-style-type: none"> <li>• NULL for no breaks</li> <li>• waiver() for the default breaks computed by the transformation object</li> <li>• A numeric vector of positions</li> <li>• A function that takes the limits as input and returns breaks as output</li> </ul>
labels	One of: <ul style="list-style-type: none"> <li>• NULL for no labels</li> <li>• waiver() for the default labels computed by the transformation object</li> <li>• A character vector giving labels (must be same length as breaks)</li> <li>• A function that takes the breaks as input and returns labels as output</li> </ul>
limits	A numeric vector of length two providing limits of the scale. Use NA to refer to the existing minimum or maximum.
range	a numeric vector of length 2 that specifies the minimum and maximum size of the plotting symbol after transformation.
trans	Either the name of a transformation object, or the object itself. Built-in transformations include "asn", "atanh", "boxcox", "exp", "identity", "log", "log10", "log1p", "log2", "logit", "probability", "probit", "reciprocal", "reverse" and "sqrt". A transformation object bundles together a transform, it's inverse, and methods for generating breaks and labels. Transformation objects are defined in the scales package, and are called name_trans, e.g. <a href="#">boxcox_trans</a> . You can create your own transformation with <a href="#">trans_new</a> .



guide	Name of guide object, or object itself.
...	Other arguments passed on to <a href="#">continuous_scale</a> to control name, limits, breaks, labels and so forth.
max_size	Size of largest points.

**See Also**

[scale\\_size\\_area](#) if you want 0 values to be mapped to points with size 0.

**Examples**

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

# 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	<i>Position scales for discrete data</i>
------------------	--

---

**Description**

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.

**Usage**

```
scale_x_discrete(..., expand = waiver(), position = "bottom")

scale_y_discrete(..., expand = waiver(), position = "left")
```

**Arguments**

...	common discrete scale parameters: name, breaks, labels, na.value, limits and guide. See <a href="#">discrete_scale</a> for more details
expand	a numeric vector of length two giving multiplicative and additive expansion constants. These constants ensure that the data is placed some distance away from the axes.
position	The position of the axis. left or right for y axes, top or bottom for x axes

**See Also**

Other position scales: [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("I1", "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
ggplot(mpg, aes(reorder(manufacturer, displ), cty)) +
  geom_point() +
  scale_x_discrete(labels = abbreviate)
```

---

seals

---

*Vector field of seal movements*


---

### Description

This vector field was produced from the data described in Brillinger, D.R., Preisler, H.K., Ager, A.A. and Kie, J.G. "An exploratory data analysis (EDA) of the paths of moving animals". J. Statistical Planning and Inference 122 (2004), 43-63, using the methods of Brillinger, D.R., "Learning a potential function from a trajectory", Signal Processing Letters. December (2007).

### Usage

```
seals
```

### Format

A data frame with 1155 rows and 4 variables

### References

<http://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

```
sec_axis(trans = NULL, name = waiver(), breaks = waiver(),
  labels = waiver())
```

```
dup_axis(trans = ~., name = derive(), breaks = derive(),
  labels = derive())
```

```
derive()
```

**Arguments**

trans	A transformation formula
name	The name of the secondary axis
breaks	One of: <ul style="list-style-type: none"> <li>• NULL for no breaks</li> <li>• waiver() for the default breaks computed by the transformation object</li> <li>• A numeric vector of positions</li> <li>• A function that takes the limits as input and returns breaks as output</li> </ul>
labels	One of: <ul style="list-style-type: none"> <li>• NULL for no labels</li> <li>• waiver() for the default labels computed by the transformation object</li> <li>• A character vector giving labels (must be same length as breaks)</li> <li>• A function that takes the breaks as input and returns labels as output</li> </ul>

**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.

**Examples**

```
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("Miles/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)
```

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

```
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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
n	if <code>NULL</code> , do not interpolate. If not <code>NULL</code> , this is the number of points to interpolate with.
pad	If <code>TRUE</code> , pad the ecdf with additional points $(-\infty, 0)$ and $(\infty, 1)$
na.rm	If <code>FALSE</code> (the default), removes missing values with a warning. If <code>TRUE</code> silently removes missing values.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

**Computed variables**

**x** x in data  
**y** cumulative density corresponding x

**Examples**

```
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	<i>Compute normal confidence ellipses</i>
--------------	---

---

**Description**

The method for calculating the ellipses has been modified from `car::ellipse` (Fox and Weisberg, 2011)

**Usage**

```
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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
geom	The geometric object to use display the data

position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <code>layer</code> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . 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 <code>level</code> , representing the euclidean distance from the center. This ellipse probably won't appear circular unless <code>coord_fixed()</code> is applied.
level	The confidence level at which to draw an ellipse (default is 0.95), or, if <code>type="euclid"</code> , the radius of the circle to be drawn.
segments	The number of segments to be used in drawing the ellipse.
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.
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. <code>borders</code> .

## References

John Fox and Sanford Weisberg (2011). An R Companion to Applied Regression, Second Edition. Thousand Oaks CA: Sage. URL: <http://socserv.socsci.mcmaster.ca/jfox/Books/Companion>

## Examples

```
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")
```

stat\_function

*Compute function for each x value*

## Description

This stat 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

```
stat_function(mapping = NULL, data = NULL, geom = "path",
  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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
fun	function to use. Must be vectorised.
xlim	Optionally, restrict the range of the function to this range.
n	number of points to interpolate along
args	list of additional arguments to pass to fun
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , 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.
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. <a href="#">borders</a> .

## Aesthetics

stat\_function understands the following aesthetics (required aesthetics are in bold):

- group
- y

## Computed variables

**x** x's along a grid

**y** value of function evaluated at corresponding x

## Examples

```
set.seed(1492)
df <- data.frame(
  x = rnorm(100)
)
x <- df$x
base <- ggplot(df, aes(x)) + geom_density()
base + stat_function(fun = dnorm, colour = "red")
base + stat_function(fun = dnorm, colour = "red", args = list(mean = 3))

# Plot functions without data
# Examples adapted from Kohnske Takahashi

# Specify range of x-axis
ggplot(data.frame(x = c(0, 2)), aes(x)) +
  stat_function(fun = exp, geom = "line")

# Plot a normal curve
ggplot(data.frame(x = c(-5, 5)), aes(x)) + stat_function(fun = dnorm)

# To specify a different mean or sd, use the args parameter to supply new values
ggplot(data.frame(x = c(-5, 5)), aes(x)) +
  stat_function(fun = dnorm, args = list(mean = 2, sd = .5))

# Two functions on the same plot
f <- ggplot(data.frame(x = c(0, 10)), aes(x))
f + stat_function(fun = sin, colour = "red") +
  stat_function(fun = cos, colour = "blue")

# Using a custom function
test <- function(x) {x ^ 2 + x + 20}
f + stat_function(fun = test)
```

---

stat\_identity

Leave data as is

---

## Description

The identity statistic leaves the data unchanged.

## Usage

```
stat_identity(mapping = NULL, data = NULL, geom = "point",
  position = "identity", ..., show.legend = NA, inherit.aes = TRUE)
```

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> ., and will be used as the layer data.
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

## Examples

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

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 <a href="#">aes</a> or <a href="#">aes_</a> . 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	<p>The data to be displayed in this layer. There are three options:</p> <p>If NULL, the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a>.</p> <p>A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created.</p> <p>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.</p>
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like color = "red" or size = 3. They may also be parameters to the paired geom/stat.
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.

<code>drop</code>	drop if the output of fun is NA.
<code>fun</code>	function for summary.
<code>fun.args</code>	A list of extra arguments to pass to fun
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .

### Aesthetics

- `x`: horizontal position
- `y`: vertical position
- `z`: value passed to the summary function

### Computed variables

**x,y** Location

**value** Value of summary statistic.

### See Also

[stat\\_summary\\_hex](#) for hexagonal summarization. [stat\\_bin2d](#) for the binning options.

### Examples

```
d <- ggplot(diamonds, aes(carat, depth, z = price))
d + stat_summary_2d()

# Specifying function
d + stat_summary_2d(fun = function(x) sum(x^2))
d + stat_summary_2d(fun = var)
d + stat_summary_2d(fun = "quantile", fun.args = list(probs = 0.1))

if (requireNamespace("hexbin")) {
  d + stat_summary_hex()
}
```

---

stat_summary_bin	<i>Summarise y values at unique/binned x</i>
------------------	--

---

## Description

stat\_summary operates on unique x; stat\_summary\_bin operators on binned x. They are more flexible versions of [stat\\_bin](#): instead of just counting, they can compute any aggregate.

## Usage

```
stat_summary_bin(mapping = NULL, data = NULL, geom = "pointrange",
  position = "identity", ..., fun.data = NULL, fun.y = NULL,
  fun.ymax = NULL, fun.ymin = NULL, fun.args = list(), na.rm = FALSE,
  show.legend = NA, inherit.aes = TRUE)
```

```
stat_summary(mapping = NULL, data = NULL, geom = "pointrange",
  position = "identity", ..., fun.data = NULL, fun.y = NULL,
  fun.ymax = NULL, fun.ymin = NULL, fun.args = list(), na.rm = FALSE,
  show.legend = NA, inherit.aes = TRUE)
```

## Arguments

mapping	Set of aesthetic mappings created by <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> ., and will be used as the layer data.
geom	Use to override the default connection between <code>geom_histogram</code> / <code>geom_freqpoly</code> and <code>stat_bin</code> .
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
fun.data	A function that is given the complete data and should return a data frame with variables <code>ymin</code> , <code>y</code> , and <code>ymax</code> .
fun.ymin, fun.y, fun.ymax	Alternatively, supply three individual functions that are each passed a vector of <code>x</code> 's and should return a single number.

<code>fun.args</code>	Optional additional arguments passed on to the functions.
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
<code>show.legend</code>	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.
<code>inherit.aes</code>	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. <a href="#">borders</a> .

## Aesthetics

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

- **x**
- **y**
- group

## Summary functions

You can either supply summary functions individually (`fun.y`, `fun.ymax`, `fun.ymin`), 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.ymin** ymin summary function (should take numeric vector and return single number)

**fun.y** y summary function (should take numeric vector and return single number)

**fun.ymax** ymax 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. `ymin` and `ymax`), use `fun.data`.

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", size = 2)

# You can supply individual functions to summarise the value at
# each x:
d + stat_summary(fun.y = "median", colour = "red", size = 2, geom = "point")
d + stat_summary(fun.y = "mean", colour = "red", size = 2, geom = "point")
d + aes(colour = factor(vs)) + stat_summary(fun.y = mean, geom="line")
```

```

d + stat_summary(fun.y = mean, fun.ymin = min, fun.ymax = max,
  colour = "red")

d <- ggplot(diamonds, aes(cut))
d + geom_bar()
d + stat_summary_bin(aes(y = price), fun.y = "mean", geom = "bar")

# Don't use ylim to zoom into a summary plot - this throws the
# data away
p <- ggplot(mtcars, aes(cyl, mpg)) +
  stat_summary(fun.y = "mean", geom = "point")
p
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) + xlab("rating")
  m2
  # 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	<i>Remove duplicates</i>
-------------	--------------------------

---

## Description

Remove duplicates

## Usage

```
stat_unique(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 <a href="#">aes</a> or <a href="#">aes_</a> . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <a href="#">ggplot</a> . A <code>data.frame</code> , or other object, will override the plot data. All objects will be fortified to produce a data frame. See <a href="#">fortify</a> for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a <code>data.frame</code> , and will be used as the layer data.
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	other arguments passed on to <a href="#">layer</a> . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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. <a href="#">borders</a> .

## Aesthetics

stat\_unique understands the following aesthetics (required aesthetics are in bold):

- group



## Examples

```
ggplot(mtcars, aes(vs, am)) +
  geom_point(alpha = 0.1)
ggplot(mtcars, aes(vs, am)) +
  geom_point(alpha = 0.1, stat = "unique")
```

---

theme	<i>Modify components of a theme</i>
-------	-------------------------------------

---

## Description

Use `theme()` to modify individual components of a theme, allowing you to control the appearance of all non-data components of the plot. `theme()` only affects a single plot: see [theme\\_update](#) if you want modify the active theme, to affect all subsequent plots.

## Usage

```
theme(line, rect, text, title, aspect.ratio, axis.title, axis.title.x,
  axis.title.x.top, axis.title.y, axis.title.y.right, axis.text, axis.text.x,
  axis.text.x.top, axis.text.y, axis.text.y.right, axis.ticks, axis.ticks.x,
  axis.ticks.y, axis.ticks.length, axis.line, axis.line.x, axis.line.y,
  legend.background, legend.margin, legend.spacing, legend.spacing.x,
  legend.spacing.y, legend.key, legend.key.size, legend.key.height,
  legend.key.width, legend.text, legend.text.align, legend.title,
  legend.title.align, legend.position, legend.direction, legend.justification,
  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.subtitle,
  plot.caption, plot.margin, strip.background, strip.placement, strip.text,
  strip.text.x, strip.text.y, strip.switch.pad.grid, strip.switch.pad.wrap, ...,
  complete = FALSE, validate = TRUE)
```

## Arguments

line	all line elements ( <code>element_line</code> )
rect	all rectangular elements ( <code>element_rect</code> )
text	all text elements ( <code>element_text</code> )
title	all title elements: plot, axes, legends ( <code>element_text</code> ; inherits from <code>text</code> )
aspect.ratio	aspect ratio of the panel
axis.title	label of axes ( <code>element_text</code> ; inherits from <code>text</code> )
axis.title.x	x axis label ( <code>element_text</code> ; inherits from <code>axis.title</code> )
axis.title.x.top	x axis label on top axis ( <code>element_text</code> ; inherits from <code>axis.title.x</code> )

`axis.title.y` y axis label (element\_text; inherits from axis.title)  
`axis.title.y.right` y axis label on right axis (element\_text; inherits from axis.title.y)  
`axis.text` tick labels along axes (element\_text; inherits from text)  
`axis.text.x` x axis tick labels (element\_text; inherits from axis.text)  
`axis.text.x.top` x axis tick labels on top axis (element\_text; inherits from axis.text.x)  
`axis.text.y` y axis tick labels (element\_text; inherits from axis.text)  
`axis.text.y.right` y axis tick labels on right axis (element\_text; inherits from axis.text.y)  
`axis.ticks` tick marks along axes (element\_line; inherits from line)  
`axis.ticks.x` x axis tick marks (element\_line; inherits from axis.ticks)  
`axis.ticks.y` y axis tick marks (element\_line; inherits from axis.ticks)  
`axis.ticks.length` length of tick marks (unit)  
`axis.line` lines along axes (element\_line; inherits from line)  
`axis.line.x` line along x axis (element\_line; inherits from axis.line)  
`axis.line.y` line along y axis (element\_line; inherits from axis.line)  
`legend.background` background of legend (element\_rect; inherits from rect)  
`legend.margin` the margin around each legend (margin)  
`legend.spacing` the spacing between legends (unit)  
`legend.spacing.x` the horizontal spacing between legends (unit); inherits from legend.spacing  
`legend.spacing.y` the horizontal spacing between legends (unit); inherits from legend.spacing  
`legend.key` background underneath legend keys (element\_rect; inherits from rect)  
`legend.key.size` size of legend keys (unit)  
`legend.key.height` key background height (unit; inherits from legend.key.size)  
`legend.key.width` key background width (unit; inherits from legend.key.size)  
`legend.text` legend item labels (element\_text; inherits from text)  
`legend.text.align` alignment of legend labels (number from 0 (left) to 1 (right))  
`legend.title` title of legend (element\_text; inherits from title)  
`legend.title.align` alignment of legend title (number from 0 (left) to 1 (right))  
`legend.position` the position of legends ("none", "left", "right", "bottom", "top", or two-element numeric vector)

<code>legend.direction</code>	layout of items in legends ("horizontal" or "vertical")
<code>legend.justification</code>	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
<code>legend.box</code>	arrangement of multiple legends ("horizontal" or "vertical")
<code>legend.box.just</code>	justification of each legend within the overall bounding box, when there are multiple legends ("top", "bottom", "left", or "right")
<code>legend.box.margin</code>	margins around the full legend area, as specified using <code>margin</code>
<code>legend.box.background</code>	background of legend area ( <code>element_rect</code> ; inherits from <code>rect</code> )
<code>legend.box.spacing</code>	The spacing between the plotting area and the legend box (unit)
<code>panel.background</code>	background of plotting area, drawn underneath plot ( <code>element_rect</code> ; inherits from <code>rect</code> )
<code>panel.border</code>	border around plotting area, drawn on top of plot so that it covers tick marks and grid lines. This should be used with <code>fill=NA</code> ( <code>element_rect</code> ; inherits from <code>rect</code> )
<code>panel.spacing</code>	spacing between facet panels (unit)
<code>panel.spacing.x</code>	horizontal spacing between facet panels (unit; inherits from <code>panel.spacing</code> )
<code>panel.spacing.y</code>	vertical spacing between facet panels (unit; inherits from <code>panel.spacing</code> )
<code>panel.grid</code>	grid lines ( <code>element_line</code> ; inherits from <code>line</code> )
<code>panel.grid.major</code>	major grid lines ( <code>element_line</code> ; inherits from <code>panel.grid</code> )
<code>panel.grid.minor</code>	minor grid lines ( <code>element_line</code> ; inherits from <code>panel.grid</code> )
<code>panel.grid.major.x</code>	vertical major grid lines ( <code>element_line</code> ; inherits from <code>panel.grid.major</code> )
<code>panel.grid.major.y</code>	horizontal major grid lines ( <code>element_line</code> ; inherits from <code>panel.grid.major</code> )
<code>panel.grid.minor.x</code>	vertical minor grid lines ( <code>element_line</code> ; inherits from <code>panel.grid.minor</code> )
<code>panel.grid.minor.y</code>	horizontal minor grid lines ( <code>element_line</code> ; inherits from <code>panel.grid.minor</code> )
<code>panel.ontop</code>	option to place the panel (background, gridlines) over the data layers. Usually used with a transparent or blank <code>panel.background</code> . (logical)
<code>plot.background</code>	background of the entire plot ( <code>element_rect</code> ; inherits from <code>rect</code> )

<code>plot.title</code>	plot title (text appearance) ( <code>element_text</code> ; inherits from <code>title</code> ) left-aligned by default
<code>plot.subtitle</code>	plot subtitle (text appearance) ( <code>element_text</code> ; inherits from <code>title</code> ) left-aligned by default
<code>plot.caption</code>	caption below the plot (text appearance) ( <code>element_text</code> ; inherits from <code>title</code> ) right-aligned by default
<code>plot.margin</code>	margin around entire plot (unit with the sizes of the top, right, bottom, and left margins)
<code>strip.background</code>	background of facet labels ( <code>element_rect</code> ; inherits from <code>rect</code> )
<code>strip.placement</code>	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.
<code>strip.text</code>	facet labels ( <code>element_text</code> ; inherits from <code>text</code> )
<code>strip.text.x</code>	facet labels along horizontal direction ( <code>element_text</code> ; inherits from <code>strip.text</code> )
<code>strip.text.y</code>	facet labels along vertical direction ( <code>element_text</code> ; inherits from <code>strip.text</code> )
<code>strip.switch.pad.grid</code>	space between strips and axes when strips are switched (unit)
<code>strip.switch.pad.wrap</code>	space between strips and axes when strips are switched (unit)
<code>...</code>	additional element specifications not part of base <code>ggplot2</code> . If supplied <code>validate</code> needs to be set to <code>FALSE</code> .
<code>complete</code>	set this to <code>TRUE</code> if this is a complete theme, such as the one returned by <code>theme_grey()</code> . Complete themes behave differently when added to a <code>ggplot</code> object. Also, when setting <code>complete = TRUE</code> all elements will be set to inherit from blank elements.
<code>validate</code>	<code>TRUE</code> to run <code>validate_element</code> , <code>FALSE</code> to bypass checks.

### Theme inheritance

Theme elements inherit properties from other theme elements. For example, `axis.title.x` 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.

### See Also

`+.gg` and `%+replace%`, `element_blank`, `element_line`, `element_rect`, and `element_text` for details of the specific theme elements.

### Examples

```
p1 <- ggplot(mtcars, aes(wt, mpg)) +
  geom_point() +
  labs(title = "Fuel economy declines as weight increases")
p1
```

```

# 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 -----
p1 + theme(axis.line = element_line(size = 3, colour = "grey80"))
p1 + theme(axis.text = element_text(colour = "blue"))
p1 + theme(axis.ticks = element_line(size = 2))
p1 + theme(axis.ticks.length = unit(.25, "cm"))
p1 + theme(axis.title.y = element_text(size = rel(1.5), angle = 90))

# Legend -----
p2 <- ggplot(mtcars, aes(wt, mpg)) +
  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 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"))
p3 + theme(panel.spacing = unit(1, "lines"))

```

---

theme\_get

*Get, set, and modify the active theme*


---

## Description

The current/active 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

```

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 NULLs.

**See Also**

[+.gg](#)

**Examples**

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

# Use theme_set() to completely override 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)
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_e1 <- 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

# theme_update() and theme_replace() are similar except they
# apply directly to the current/active theme.

```

---

txhousing

*Housing sales in TX*


---

## Description

Information about the housing market in Texas provided by the TAMU real estate center, <http://recenter.tamu.edu/>.

## Usage

```
txhousing
```

## Format

A data frame with 8602 observations and 9 variables:

**city** Name of MLS area

**year,month,date** 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.



# Index

## \*Topic **datasets**

- diamonds, [29](#)
- economics, [30](#)
- faithfuld, [36](#)
- luv\_colours, [126](#)
- midwest, [129](#)
- mpg, [130](#)
- msleep, [131](#)
- presidential, [138](#)
- seals, [163](#)
- txhousing, [184](#)

## \*Topic **hplot**

- print.ggplot, [139](#)

`+.gg`, [5](#), [180](#), [183](#)

`%%(+.gg)`, [5](#)

`%+replace%(theme_get)`, [182](#)

`%+replace%`, [180](#)

`aes`, [5](#), [6](#), [7](#), [8](#), [37](#), [39](#), [42](#), [44](#), [45](#), [48](#), [50](#), [53](#),  
[55](#), [58](#), [60](#), [63](#), [65](#), [68](#), [69](#), [71](#), [75](#), [77](#),  
[80](#), [83](#), [85](#), [87](#), [89](#), [91](#), [93](#), [95](#), [97](#),  
[101](#), [102](#), [165](#), [166](#), [168](#), [170](#), [171](#),  
[173](#), [176](#)

`aes_`, [6](#), [7](#), [37](#), [39](#), [42](#), [44](#), [45](#), [48](#), [50](#), [53](#), [55](#),  
[58](#), [60](#), [63](#), [65](#), [68](#), [69](#), [71](#), [75](#), [77](#), [80](#),  
[83](#), [85](#), [87](#), [89](#), [91](#), [93](#), [95](#), [97](#), [101](#),  
[102](#), [165](#), [166](#), [168](#), [170](#), [171](#), [173](#),  
[176](#)

`aes_colour_fill_alpha`, [8](#)

`aes_group_order`, [9](#)

`aes_linetype_size_shape`, [11](#)

`aes_position`, [12](#)

`aes_q(aes_)`, [7](#)

`aes_string(aes_)`, [7](#)

`annotate`, [13](#)

`annotation_custom`, [14](#)

`annotation_logticks`, [15](#)

`annotation_map`, [17](#)

`annotation_raster`, [18](#)

`arrow`, [78](#), [127](#)

`as_labeller`, [119](#), [120](#), [122](#)

`autoplot`, [19](#)

`bandwidth.nrd`, [58](#)

`borders`, [19](#), [40](#), [43](#), [44](#), [46](#), [49](#), [51](#), [53](#), [55](#), [58](#),  
[60](#), [63](#), [65](#), [68](#), [70](#), [72](#), [75](#), [78](#), [81](#), [83](#),  
[86](#), [88](#), [90](#), [92](#), [94](#), [96](#), [98](#), [101](#), [103](#),  
[165](#), [167](#), [169](#), [170](#), [172](#), [174](#), [176](#)

`boxcox_trans`, [151](#), [160](#)

`boxplot.stats`, [46](#)

`bquote`, [122](#)

`brewer.pal`, [144](#)

`bw.nrd`, [56](#), [103](#)

`capitalize`, [119](#)

`color(aes_colour_fill_alpha)`, [8](#)

`colors`, [126](#)

`colour(aes_colour_fill_alpha)`, [8](#)

`continuous_scale`, [143](#), [146](#), [156](#), [161](#)

`coord_cartesian`, [20](#), [125](#)

`coord_equal(coord_fixed)`, [21](#)

`coord_fixed`, [21](#)

`coord_flip`, [22](#)

`coord_map`, [23](#)

`coord_polar`, [25](#)

`coord_quickmap(coord_map)`, [23](#)

`coord_trans`, [16](#), [26](#)

`curveGrob`, [95](#)

`cut`, [29](#)

`cut_interval`, [28](#)

`cut_number`, [29](#)

`cut_number(cut_interval)`, [28](#)

`cut_width(cut_interval)`, [28](#)

`density`, [56](#), [103](#)

`derive(sec_axis)`, [163](#)

`diamonds`, [29](#)

`discrete_scale`, [143](#), [144](#), [148](#), [149](#),  
[156–159](#), [162](#)

`dup_axis(sec_axis)`, [163](#)

- economics, [30](#)
- economics\_long (economics), [30](#)
- element\_blank, [180](#)
- element\_blank (margin), [126](#)
- element\_line, [180](#)
- element\_line (margin), [126](#)
- element\_rect, [180](#)
- element\_rect (margin), [126](#)
- element\_text, [113](#), [115](#), [180](#)
- element\_text (margin), [126](#)
- eqscplot, [21](#)
- expand\_limits, [31](#), [43](#), [125](#)
- facet\_grid, [31](#), [34](#), [119](#), [141](#)
- facet\_wrap, [34](#), [122](#), [141](#)
- faithful, [36](#)
- faithfuld, [36](#)
- fill (aes\_colour\_fill\_alpha), [8](#)
- format.ggproto (print.ggproto), [140](#)
- fortify, [17](#), [19](#), [36](#), [37](#), [40](#), [42](#), [44](#), [45](#), [48](#), [51](#),  
[53](#), [55](#), [58](#), [60](#), [63](#), [65](#), [68](#), [69](#), [71](#), [75](#),  
[77](#), [80](#), [83](#), [85](#), [87](#), [89](#), [92](#), [93](#), [95](#), [98](#),  
[101](#), [102](#), [105](#), [165](#), [166](#), [168](#), [170](#),  
[171](#), [173](#), [176](#)
- fortify.lm, [37](#)
- gam, [98](#)
- geom\_abline, [37](#)
- geom\_area, [137](#)
- geom\_area (geom\_ribbon), [91](#)
- geom\_bar, [39](#), [66](#), [92](#), [137](#)
- geom\_bin2d, [42](#), [51](#), [59](#), [67](#), [80](#)
- geom\_blank, [31](#), [43](#)
- geom\_boxplot, [44](#), [70](#), [81](#), [87](#), [102](#)
- geom\_col, [39](#)
- geom\_col (geom\_bar), [39](#)
- geom\_contour, [48](#), [59](#)
- geom\_count, [50](#), [80](#), [81](#)
- geom\_crossbar, [52](#), [174](#)
- geom\_curve (geom\_segment), [95](#)
- geom\_density, [55](#), [57](#), [102](#)
- geom\_density2d, [81](#)
- geom\_density2d (geom\_density\_2d), [57](#)
- geom\_density\_2d, [49](#), [57](#), [81](#)
- geom\_dotplot, [59](#)
- geom\_errorbar, [62](#), [174](#)
- geom\_errorbar (geom\_crossbar), [52](#)
- geom\_errorbarh, [54](#), [62](#)
- geom\_freqpoly, [56](#), [64](#)
- geom\_hex, [67](#), [81](#)
- geom\_histogram, [40](#), [41](#), [56](#), [165](#)
- geom\_histogram (geom\_freqpoly), [64](#)
- geom\_hline (geom\_abline), [37](#)
- geom\_jitter, [47](#), [69](#), [80](#)
- geom\_label, [71](#)
- geom\_line, [38](#), [66](#), [96](#)
- geom\_line (geom\_path), [77](#)
- geom\_linerange, [92](#), [174](#)
- geom\_linerange (geom\_crossbar), [52](#)
- geom\_map, [75](#)
- geom\_path, [77](#), [83](#), [84](#), [96](#)
- geom\_point, [42](#), [50](#), [70](#), [80](#)
- geom\_pointrange, [174](#)
- geom\_pointrange (geom\_crossbar), [52](#)
- geom\_polygon, [19](#), [78](#), [83](#), [92](#)
- geom\_qq, [85](#)
- geom\_quantile, [47](#), [81](#), [87](#)
- geom\_raster, [18](#), [89](#)
- geom\_rect (geom\_raster), [89](#)
- geom\_ribbon, [84](#), [91](#)
- geom\_rug, [93](#)
- geom\_segment, [38](#), [78](#), [95](#), [100](#)
- geom\_smooth, [54](#), [81](#), [97](#)
- geom\_spoke, [96](#), [100](#)
- geom\_step (geom\_path), [77](#)
- geom\_text, [135](#)
- geom\_text (geom\_label), [71](#)
- geom\_tile, [24](#), [48](#)
- geom\_tile (geom\_raster), [89](#)
- geom\_violin, [47](#), [56](#), [102](#), [104](#)
- geom\_vline (geom\_abline), [37](#)
- ggplot, [5](#), [19](#), [37](#), [39](#), [42](#), [44](#), [45](#), [48](#), [51](#), [53](#),  
[55](#), [58](#), [60](#), [63](#), [65](#), [68](#), [69](#), [71](#), [75](#), [77](#),  
[80](#), [83](#), [85](#), [87](#), [89](#), [91](#), [93](#), [95](#), [98](#),  
[101](#), [102](#), [105](#), [141](#), [165](#), [166](#), [168](#),  
[170](#), [171](#), [173](#), [176](#)
- ggplot2, [6](#)
- ggplot\_build, [139](#)
- ggproto, [107](#)
- ggproto\_parent (ggproto), [107](#)
- ggsave, [108](#)
- ggtheme, [109](#)
- ggtitle (labs), [124](#)
- glm, [99](#)
- gray.colors, [148](#)
- group (aes\_group\_order), [9](#)
- guide\_colorbar (guide\_colourbar), [112](#)

- guide\_colourbar, [111](#), [112](#), [116](#)
- guide\_legend, [111](#), [114](#), [115](#)
- guides, [111](#), [114](#), [116](#)
- hmisc, [118](#)
- is.ggproto (ggproto), [107](#)
- kde2d, [57](#)
- label\_both (labellers), [121](#)
- label\_bquote, [122](#), [123](#)
- label\_context (labellers), [121](#)
- label\_parsed (labellers), [121](#)
- label\_value, [32](#), [34](#)
- label\_value (labellers), [121](#)
- label\_wrap\_gen (labellers), [121](#)
- labeller, [32](#), [34](#), [119](#), [122](#), [123](#)
- labellers, [120](#), [121](#), [123](#)
- labs, [113](#), [115](#), [124](#), [152](#)
- layer, [13](#), [37](#), [40](#), [42](#), [44](#), [45](#), [49](#), [51](#), [53](#), [55](#),  
[58](#), [60](#), [63](#), [65](#), [68](#), [70](#), [72](#), [75](#), [78](#), [81](#),  
[83](#), [85](#), [87](#), [89](#), [92](#), [93](#), [95](#), [98](#), [101](#),  
[103](#), [165](#), [167](#), [168](#), [170](#), [171](#), [173](#),  
[176](#)
- lims, [125](#), [152](#)
- linetype (aes\_linetype\_size\_shape), [11](#)
- lm, [99](#)
- loess, [98](#), [99](#)
- luv\_colours, [126](#)
- map, [19](#)
- mapproject, [23](#)
- margin, [126](#), [127](#), [179](#)
- mean\_cl\_boot (hmisc), [118](#)
- mean\_cl\_normal (hmisc), [118](#)
- mean\_sdl (hmisc), [118](#)
- mean\_se, [128](#), [174](#)
- median\_hilow (hmisc), [118](#)
- midwest, [129](#)
- mpg, [130](#)
- msleep, [131](#)
- plot, [141](#)
- plot.ggplot (print.ggplot), [139](#)
- png, [108](#)
- position\_dodge, [40](#), [41](#), [132](#), [133–135](#), [137](#)
- position\_fill, [40](#)
- position\_fill (position\_stack), [136](#)
- position\_identity, [132](#), [133](#), [134](#), [135](#), [137](#)
- position\_jitter, [132](#), [133](#), [133](#), [135](#), [137](#)
- position\_jitterdodge, [132–134](#), [134](#), [135](#),  
[137](#)
- position\_nudge, [132–135](#), [135](#), [137](#)
- position\_stack, [40](#), [92](#), [132–135](#), [136](#)
- predict, [98](#)
- presidential, [138](#)
- print.ggplot, [139](#)
- print.ggproto, [140](#)
- qplot, [141](#)
- quickplot (qplot), [141](#)
- rel (margin), [126](#)
- rescale, [144](#), [147](#)
- resolution, [142](#)
- rq, [88](#)
- scale\_alpha, [143](#), [145](#), [147–149](#)
- scale\_alpha\_continuous (scale\_alpha),  
[143](#)
- scale\_alpha\_discrete (scale\_alpha), [143](#)
- scale\_alpha\_identity (scale\_identity),  
[155](#)
- scale\_alpha\_manual (scale\_manual), [157](#)
- scale\_color\_brewer  
(scale\_colour\_brewer), [144](#)
- scale\_color\_continuous  
(scale\_colour\_gradient), [146](#)
- scale\_color\_discrete  
(scale\_colour\_hue), [149](#)
- scale\_color\_distiller  
(scale\_colour\_brewer), [144](#)
- scale\_color\_gradient  
(scale\_colour\_gradient), [146](#)
- scale\_color\_gradient2  
(scale\_colour\_gradient), [146](#)
- scale\_color\_gradientn  
(scale\_colour\_gradient), [146](#)
- scale\_color\_grey (scale\_colour\_grey),  
[148](#)
- scale\_color\_hue (scale\_colour\_hue), [149](#)
- scale\_color\_identity (scale\_identity),  
[155](#)
- scale\_color\_manual (scale\_manual), [157](#)
- scale\_colour\_brewer, [143](#), [144](#), [147–149](#)
- scale\_colour\_continuous  
(scale\_colour\_gradient), [146](#)

- scale\_colour\_date  
    (scale\_colour\_gradient), 146
- scale\_colour\_datetime  
    (scale\_colour\_gradient), 146
- scale\_colour\_discrete  
    (scale\_colour\_hue), 149
- scale\_colour\_distiller  
    (scale\_colour\_brewer), 144
- scale\_colour\_gradient, 143, 145, 146, 148, 149
- scale\_colour\_gradient2  
    (scale\_colour\_gradient), 146
- scale\_colour\_gradientn  
    (scale\_colour\_gradient), 146
- scale\_colour\_grey, 143, 145, 147, 148, 149
- scale\_colour\_hue, 143, 145, 147, 148, 149
- scale\_colour\_identity (scale\_identity), 155
- scale\_colour\_manual (scale\_manual), 157
- scale\_continuous, 150
- scale\_date, 153
- scale\_fill\_brewer  
    (scale\_colour\_brewer), 144
- scale\_fill\_continuous  
    (scale\_colour\_gradient), 146
- scale\_fill\_date  
    (scale\_colour\_gradient), 146
- scale\_fill\_datetime  
    (scale\_colour\_gradient), 146
- scale\_fill\_discrete (scale\_colour\_hue), 149
- scale\_fill\_distiller  
    (scale\_colour\_brewer), 144
- scale\_fill\_gradient  
    (scale\_colour\_gradient), 146
- scale\_fill\_gradient2  
    (scale\_colour\_gradient), 146
- scale\_fill\_gradientn  
    (scale\_colour\_gradient), 146
- scale\_fill\_grey (scale\_colour\_grey), 148
- scale\_fill\_hue (scale\_colour\_hue), 149
- scale\_fill\_identity (scale\_identity), 155
- scale\_fill\_manual (scale\_manual), 157
- scale\_identity, 155
- scale\_linetype, 156
- scale\_linetype\_continuous  
    (scale\_linetype), 156
- scale\_linetype\_discrete  
    (scale\_linetype), 156
- scale\_linetype\_identity  
    (scale\_identity), 155
- scale\_linetype\_manual (scale\_manual), 157
- scale\_manual, 157
- scale\_radius (scale\_size), 160
- scale\_shape, 159
- scale\_shape\_continuous (scale\_shape), 159
- scale\_shape\_discrete (scale\_shape), 159
- scale\_shape\_identity (scale\_identity), 155
- scale\_shape\_manual, 159
- scale\_shape\_manual (scale\_manual), 157
- scale\_size, 160
- scale\_size\_area, 161
- scale\_size\_area (scale\_size), 160
- scale\_size\_continuous (scale\_size), 160
- scale\_size\_date (scale\_size), 160
- scale\_size\_datetime (scale\_size), 160
- scale\_size\_discrete (scale\_size), 160
- scale\_size\_identity (scale\_identity), 155
- scale\_size\_manual (scale\_manual), 157
- scale\_x\_continuous, 155, 162
- scale\_x\_continuous (scale\_continuous), 150
- scale\_x\_date, 152, 162
- scale\_x\_date (scale\_date), 153
- scale\_x\_datetime (scale\_date), 153
- scale\_x\_discrete, 152, 155, 161
- scale\_x\_log10 (scale\_continuous), 150
- scale\_x\_reverse (scale\_continuous), 150
- scale\_x\_sqrt (scale\_continuous), 150
- scale\_x\_time (scale\_date), 153
- scale\_y\_continuous, 16
- scale\_y\_continuous (scale\_continuous), 150
- scale\_y\_date (scale\_date), 153
- scale\_y\_datetime (scale\_date), 153
- scale\_y\_discrete (scale\_x\_discrete), 161
- scale\_y\_log10, 16
- scale\_y\_log10 (scale\_continuous), 150
- scale\_y\_reverse (scale\_continuous), 150
- scale\_y\_sqrt (scale\_continuous), 150
- scale\_y\_time (scale\_date), 153

seals, 163  
 sec\_axis, 152, 163  
 seq\_gradient\_pal, 147  
 shape(aes\_linetype\_size\_shape), 11  
 size(aes\_linetype\_size\_shape), 11  
 smean.cl.boot, 118  
 smean.cl.normal, 118  
 smean.sdl, 118  
 smedian.hilow, 118  
 stat\_bin, 41, 66, 173  
 stat\_bin(geom\_freqpoly), 64  
 stat\_bin2d, 69, 172  
 stat\_bin2d(geom\_bin2d), 42  
 stat\_bin\_2d(geom\_bin2d), 42  
 stat\_bin\_hex(geom\_hex), 67  
 stat\_binhex, 43  
 stat\_binhex(geom\_hex), 67  
 stat\_boxplot(geom\_boxplot), 44  
 stat\_contour, 59  
 stat\_contour(geom\_contour), 48  
 stat\_count, 64, 66  
 stat\_count(geom\_bar), 39  
 stat\_density, 104  
 stat\_density(geom\_density), 55  
 stat\_density2d(geom\_density\_2d), 57  
 stat\_density\_2d(geom\_density\_2d), 57  
 stat\_ecdf, 165  
 stat\_ellipse, 166  
 stat\_function, 168  
 stat\_identity, 170  
 stat\_qq(geom\_qq), 85  
 stat\_quantile(geom\_quantile), 87  
 stat\_smooth(geom\_smooth), 97  
 stat\_spoke(geom\_spoke), 100  
 stat\_sum(geom\_count), 50  
 stat\_summary, 54, 118, 128, 171  
 stat\_summary(stat\_summary\_bin), 173  
 stat\_summary2d(stat\_summary\_2d), 171  
 stat\_summary\_2d, 171, 171  
 stat\_summary\_bin, 173  
 stat\_summary\_hex, 172  
 stat\_summary\_hex(stat\_summary\_2d), 171  
 stat\_unique, 176  
 stat\_ydensity(geom\_violin), 102  
 strftime, 154  
 strwrap, 122  
 substitute, 7  
 theme, 5, 6, 109, 113, 115, 116, 126, 177  
 theme\_bw(ggtheme), 109  
 theme\_classic(ggtheme), 109  
 theme\_dark(ggtheme), 109  
 theme\_get, 182  
 theme\_gray(ggtheme), 109  
 theme\_grey(ggtheme), 109  
 theme\_light(ggtheme), 109  
 theme\_linedraw(ggtheme), 109  
 theme\_minimal(ggtheme), 109  
 theme\_replace(theme\_get), 182  
 theme\_set(theme\_get), 182  
 theme\_update, 177  
 theme\_update(theme\_get), 182  
 theme\_void(ggtheme), 109  
 trans\_new, 27, 151, 160  
 txhousing, 184  
 unit, 16, 113, 116  
 waiver, 113, 115  
 x(aes\_position), 12  
 xend(aes\_position), 12  
 xlab(labs), 124  
 xlim(lims), 125  
 xmax(aes\_position), 12  
 xmin(aes\_position), 12  
 y(aes\_position), 12  
 yend(aes\_position), 12  
 ylab(labs), 124  
 ylim(lims), 125  
 ymax(aes\_position), 12  
 ymin(aes\_position), 12