

# Package ‘ggdist’

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**Title** Visualizations of Distributions and Uncertainty

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## Description

Provides primitives for visualizing distributions using 'ggplot2' that are particularly tuned for visualizing uncertainty in either a frequentist or Bayesian mode. Both analytical distributions (such as frequentist confidence distributions or Bayesian priors) and distributions represented as samples (such as bootstrap distributions or Bayesian posterior samples) are easily visualized. Visualization primitives include but are not limited to: points with multiple uncertainty intervals, eye plots (Spiegelhalter D., 1999) <doi:10.1111/1467-985X.00120>, density plots, gradient plots, dot plots (Wilkinson L., 1999) <doi:10.1080/00031305.1999.10474474>, quantile dot plots (Kay M., Kola T., Hullman J., Munson S., 2016) <doi:10.1145/2858036.2858558>, complementary cumulative distribution function barplots (Fernandes M., Walls L., Munson S., Hullman J., Kay M., 2018) <doi:10.1145/3173574.3173718>, and fit curves with multiple uncertainty ribbons.

**Depends** R (>= 3.5.0)

**Imports** tidyselect, dplyr (>= 1.0.0), tidyr (>= 1.0.0), ggplot2 (>= 3.3.0), purrr (>= 0.2.3), rlang (>= 0.3.0), scales, grid, forcats, HDInterval, tibble, vctrs, fda, distributional (>= 0.2.0)

**Suggests** knitr, testthat, vdiff (>= 0.3.0), svglite, broom (>= 0.5.6), modelr, cowplot, covr, gdttools, rmarkdown, png, pkgdown

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 ``geom\_dotsinterval.R``geom\_interval.R``geom\_lineribbon.R"  
 ``geom\_pointinterval.R``lkjcorr\_marginal.R``parse\_dist.R"  
 ``point\_interval.R``scale\_colour\_ramp.R``scales.R``stat.R"  
 ``stat\_slabinterval.R``stat\_dist\_slabinterval.R"  
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ggdist-package	<i>Visualizations of Distributions and Uncertainty</i>
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## Description

ggdist is an R package that aims to make it easy to integrate popular Bayesian modeling methods into a tidy data + ggplot workflow.

## Details

ggdist is an R package that provides a flexible set of ggplot2 geoms and stats designed especially for visualizing distributions and uncertainty. It is designed for both frequentist and Bayesian uncertainty visualization, taking the view that uncertainty visualization can be unified through the perspective of distribution visualization: for frequentist models, one visualizes confidence distributions or bootstrap distributions (see `vignette("freq-uncertainty-vis")`); for Bayesian models, one visualizes probability distributions (see `vignette("tidybayes", package = "tidybayes")`).

The `geom_slabinterval()` / `stat_slabinterval()` / `stat_dist_slabinterval()` family (see `vignette("slabinterval")`) includes point summaries and intervals, eye plots, half-eye plots, CCDF bar plots, gradient plots, dotplots, and histograms.

The `geom_lineribbon()` / `stat_lineribbon()` / `stat_dist_lineribbon()` family (see `vignette("lineribbon")`) makes it easy to visualize fit lines with an arbitrary number of uncertainty bands.

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curve_interval	<i>Curvewise point and interval summaries for tidy data frames of draws from distributions</i>
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## Description

Translates draws from distributions in a grouped data frame into a set of point and interval summaries using a curve boxplot-inspired approach.

## Usage

```
curve_interval(
  .data,
  ...,
  .along = NULL,
  .width = 0.5,
  .interval = c("mhd", "mbd", "bd", "bd-mbd"),
  .simple_names = TRUE,
  na.rm = FALSE,
  .exclude = c(".chain", ".iteration", ".draw", ".row")
)
```

**Arguments**

<code>.data</code>	Data frame (or grouped data frame as returned by <code>group_by()</code> ) that contains draws to summarize.
<code>...</code>	Bare column names or expressions that, when evaluated in the context of <code>.data</code> , represent draws to summarize. If this is empty, then by default all columns that are not group columns and which are not in <code>.exclude</code> (by default <code>".chain"</code> , <code>".iteration"</code> , <code>".draw"</code> , and <code>".row"</code> ) will be summarized. This can be list columns.
<code>.along</code>	Which columns are the input values to the function describing the curve (e.g., the "x" values). Supports tidyselect syntax, as in <code>dplyr::select()</code> . Intervals are calculated jointly with respect to these variables, conditional on all other grouping variables in the data frame. The default (NULL) causes <code>curve_interval()</code> to use all grouping variables in the input data frame, which will generate the most conservative intervals. However, if you want to calculate intervals for some function $y = f(x)$ conditional on some other variable(s) (say, conditional on a factor <code>g</code> ), you would group by <code>g</code> , then use <code>.along = x</code> to calculate intervals jointly over <code>x</code> conditional on <code>g</code> .
<code>.width</code>	vector of probabilities to use that determine the widths of the resulting intervals. If multiple probabilities are provided, multiple rows per group are generated, each with a different probability interval (and value of the corresponding <code>.width</code> column).
<code>.interval</code>	The method used to calculate the intervals. Currently, all methods rank the curves using some measure of <i>data depth</i> , then create envelopes containing the <code>.width%</code> "deepest" curves. Available methods are: <ul style="list-style-type: none"> <li>• "mhd": mean halfspace depth (Fraiman and Muniz 2001).</li> <li>• "mbd": modified band depth (Sun and Genton 2011): calls <code>fda::fbplot()</code> with <code>method = "MBD"</code>.</li> <li>• "bd": band depth (Sun and Genton 2011): calls <code>fda::fbplot()</code> with <code>method = "BD2"</code>.</li> <li>• "bd-mbd": band depth, breaking ties with modified band depth (Sun and Genton 2011): calls <code>fda::fbplot()</code> with <code>method = "Both"</code>.</li> </ul>
<code>.simple_names</code>	When TRUE and only a single column / vector is to be summarized, use the name <code>.lower</code> for the lower end of the interval and <code>.upper</code> for the upper end. If <code>.data</code> is a vector and this is TRUE, this will also set the column name of the point summary to <code>.value</code> . When FALSE and <code>.data</code> is a data frame, names the lower and upper intervals for each column <code>x</code> <code>x.lower</code> and <code>x.upper</code> . When FALSE and <code>.data</code> is a vector, uses the naming scheme <code>y</code> , <code>ymin</code> and <code>ymax</code> (for use with <code>ggplot</code> ).
<code>na.rm</code>	logical value indicating whether NA values should be stripped before the computation proceeds. If FALSE (the default), the presence of NA values in the columns to be summarized will generally result in an error. If TRUE, NA values will be removed in the calculation of intervals so long as <code>.interval</code> is "mhd"; other methods do not currently support <code>na.rm</code> . Be cautious in applying this parameter: in general, it is unclear what a joint interval should be when any of the values are missing!

`.exclude` A character vector of names of columns to be excluded from summarization if no column names are specified to be summarized. Default ignores several meta-data column names used in tidybayes.

### Details

Intervals are calculated by ranking the curves using some measure of *data depth*, then creating envelopes containing the `.width%` "deepest" curves (for each value of `.width`). Thus, the intervals are guaranteed to contain *at least* `.width%` of the full curves, but may be conservative (i.e. they may contain more than `.width%` of the curves). See Mirzargar *et al.* (2014) or Juul *et al.* (2020) for an accessible introduction to the idea.

### Value

A data frame containing point summaries and intervals, with at least one column corresponding to the point summary, one to the lower end of the interval, one to the upper end of the interval, the width of the interval (`.width`), the type of point summary (`.point`), and the type of interval (`.interval`).

### Author(s)

Matthew Kay

### References

- Fraiman, Ricardo and Graciela Muniz. (2001). "Trimmed means for functional data". *Test* 10: 419–440. doi: [10.1007/BF02595706](https://doi.org/10.1007/BF02595706).
- Sun, Ying and Marc G. Genton. (2011). "Functional Boxplots". *Journal of Computational and Graphical Statistics*, 20(2): 316-334. doi: [10.1198/jcgs.2011.09224](https://doi.org/10.1198/jcgs.2011.09224)
- Mirzargar, Mahsa, Ross T Whitaker, and Robert M Kirby. (2014). "Curve Boxplot: Generalization of Boxplot for Ensembles of Curves". *IEEE Transactions on Visualization and Computer Graphics*. 20(12): 2654-2663. doi: [10.1109/TVCG.2014.2346455](https://doi.org/10.1109/TVCG.2014.2346455)
- Juul Jonas, Kaare Græsbøll, Lasse Engbo Christiansen, and Sune Lehmann. (2020). "Fixed-time descriptive statistics underestimate extremes of epidemic curve ensembles". *arXiv e-print*. [arXiv:2007.05035](https://arxiv.org/abs/2007.05035)

### See Also

`point_interval()` for pointwise intervals. See `vignette("lineribbon")` for more examples and discussion of the differences between pointwise and curvewise intervals.

### Examples

```
library(dplyr)
library(tidyr)
library(ggplot2)

# generate a set of curves
```

```

k = 11 # number of curves
n = 201
df = tibble(
  .draw = 1:k,
  mean = seq(-5,5, length.out = k),
  x = list(seq(-15,15,length.out = n))
) %>%
unnest(x) %>%
mutate(y = dnorm(x, mean, 3))

# see pointwise intervals...
df %>%
  group_by(x) %>%
  median_qi(y, .width = c(.5)) %>%
  ggplot(aes(x = x, y = y)) +
  geom_lineribbon(aes(ymin = .lower, ymax = .upper)) +
  geom_line(aes(group = .draw), alpha=0.15, data = df) +
  scale_fill_brewer() +
  ggtitle("50% pointwise intervals with point_interval()") +
  theme_ggdist()

# ... compare them to curvewise intervals
df %>%
  group_by(x) %>%
  curve_interval(y, .width = c(.5)) %>%
  ggplot(aes(x = x, y = y)) +
  geom_lineribbon(aes(ymin = .lower, ymax = .upper)) +
  geom_line(aes(group = .draw), alpha=0.15, data = df) +
  scale_fill_brewer() +
  ggtitle("50% curvewise intervals with curve_interval()") +
  theme_ggdist()

```

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cut\_cdf\_qi

*Categorize values from a CDF into quantile intervals*


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## Description

Given a vector of probabilities from a cumulative distribution function (CDF) and a list of desired quantile intervals, return a vector categorizing each element of the input vector according to which quantile interval it falls into. Useful for drawing slabs with intervals overlaid on the density, e.g. using [stat\\_halfeye\(\)](#) or [stat\\_dist\\_halfeye\(\)](#)

## Usage

```
cut_cdf_qi(p, .width = c(0.66, 0.95, 1), labels = NULL)
```

**Arguments**

p	A numeric vector of values from a cumulative distribution function, such as values returned by p-prefixed distribution functions in base R (e.g. <code>pnorm()</code> ), the <code>cdf()</code> function, or values of the cdf computed aesthetic from the <code>stat_sample_slabinterval()</code> or <code>stat_dist_slabinterval()</code> stats.
.width	vector of probabilities to use that determine the widths of the resulting intervals.
labels	One of: <ul style="list-style-type: none"> <li>• NULL to use the default labels (<code>.width</code> converted to a character vector).</li> <li>• A character vector giving labels (must be same length as <code>.width</code>)</li> <li>• A function that takes numeric probabilities as input and returns labels as output (a good candidate might be <code>scales::percent_format()</code>).</li> </ul>

**Value**

An `ordered` factor of the same length as `p` giving the quantile interval to which each value of `p` belongs.

**See Also**

See `stat_sample_slabinterval()` or `stat_dist_slabinterval()` and their shortcut stats, which generate cdf aesthetics that can be used with `cut_cdf_qi()` to draw slabs colored by their intervals.

**Examples**

```
library(ggplot2)
library(dplyr)
library(scales)
library(distributional)

theme_set(theme_ggdist())

# with a slab
tibble(x = dist_normal(0, 1)) %>%
  ggplot(aes(dist = x, y = "a")) +
  stat_dist_slab(aes(
    fill = stat(cut_cdf_qi(cdf))
  )) +
  scale_fill_brewer(direction = -1, na.value = "gray90")

# With a halfeye (or other geom with slab and interval), NA values will
# show up in the fill scale from the CDF function applied to the internal
# interval geometry data and can be ignored, hence na.translate = FALSE
tibble(x = dist_normal(0, 1)) %>%
  ggplot(aes(dist = x, y = "a")) +
  stat_dist_halfeye(aes(
    fill = stat(cut_cdf_qi(cdf, .width = c(.5, .8, .95, 1)))
  )) +
  scale_fill_brewer(direction = -1, na.translate = FALSE)
```

```
# we could also use the labels parameter to apply nicer formatting
# and provide a better name for the legend, and omit the 100% interval
# if desired
tibble(x = dist_normal(0, 1)) %>%
  ggplot(aes(dist = x, y = "a")) +
  stat_dist_halfeye(aes(
    fill = stat(cut_cdf_qi(cdf, .width = c(.5, .8, .95), labels = percent_format(accuracy = 1)))
  )) +
  labs(fill = "Interval") +
  scale_fill_brewer(direction = -1, na.translate = FALSE)
```

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geom_dotsinterval	<i>Automatic dotplots, dots + intervals, and quantile dotplots (ggplot geom)</i>
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## Description

Geoms and stats for creating dotplots that automatically determines a bin width that ensures the plot fits within the available space. Also ensures dots do not overlap, and allows generation of quantile dotplots using the quantiles argument to `stat_dotsinterval/stat_dots` and `stat_dist_dotsinterval/stat_dist_dots`. Generally follows the naming scheme and arguments of the `geom_slabinterval()` and `stat_slabinterval()` family of geoms and stats.

## Usage

```
geom_dotsinterval(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  dotsize = 1,
  stackratio = 1,
  binwidth = NA,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

```
geom_dots(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  na.rm = FALSE,
  show.legend = NA,
```

```
    inherit.aes = TRUE
  )

stat_dotsinterval(
  mapping = NULL,
  data = NULL,
  geom = "dotsinterval",
  position = "identity",
  ...,
  quantiles = NA,
  point_interval = median_qi,
  na.rm = FALSE,
  show.legend = c(size = FALSE),
  inherit.aes = TRUE
)

stat_dots(
  mapping = NULL,
  data = NULL,
  geom = "dots",
  position = "identity",
  ...,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_dist_dotsinterval(
  mapping = NULL,
  data = NULL,
  geom = "dotsinterval",
  position = "identity",
  ...,
  quantiles = 100,
  na.rm = FALSE,
  show.legend = c(size = FALSE),
  inherit.aes = TRUE
)

stat_dist_dots(
  mapping = NULL,
  data = NULL,
  geom = "dots",
  position = "identity",
  ...,
  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	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 <code>ggplot()</code> . 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. 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. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code> ).
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.
...	Arguments passed on to <code>geom_slabinterval</code>
side	Which side to draw the slab on. "topright", "top", and "right" are synonyms which cause the slab to be drawn on the top or the right depending on if orientation is "horizontal" or "vertical". "bottomleft", "bottom", and "left" are synonyms which cause the slab to be drawn on the bottom or the left depending on if orientation is "horizontal" or "vertical". "topleft" causes the slab to be drawn on the top or the left, and "bottomright" causes the slab to be drawn on the bottom or the right. "both" draws the slab mirrored on both sides (as in a violin plot).
scale	What proportion of the region allocated to this geom to use to draw the slab. If <code>scale = 1</code> , slabs that use the maximum range will just touch each other. Default is <code>0.9</code> to leave some space.
orientation	Whether this geom is drawn horizontally ("horizontal") or vertically ("vertical"). The default, <code>NA</code> , automatically detects the orientation based on how the aesthetics are assigned, and should generally do an okay job at this. When horizontal (resp. vertical), the geom uses the <code>y</code> (resp. <code>x</code> ) aesthetic to identify different groups, then for each group uses the <code>x</code> (resp. <code>y</code> ) aesthetic and the <code>thickness</code> aesthetic to draw a function as an slab, and draws points and intervals horizontally (resp. vertically) using the <code>xmin</code> , <code>x</code> , and <code>xmax</code> (resp. <code>ymin</code> , <code>y</code> , and <code>ymax</code> ) aesthetics. For compatibility with the base <code>ggplot</code> naming scheme for orientation, "x" can be used as an alias for "vertical" and "y" as an alias for "horizontal" (tidybayes had an orientation parameter before <code>ggplot</code> did, and I think the tidybayes naming scheme is more intuitive: "x" and "y" are not orientations and their mapping to orientations is, in my opinion, backwards; but the base <code>ggplot</code> naming scheme is allowed for compatibility).
justification	Justification of the interval relative to the slab, where <code>0</code> indicates bottom/left justification and <code>1</code> indicates top/right justification (depending on orientation). If <code>justification</code> is <code>NULL</code> (the default), then it is set automatically based on the value of <code>side</code> : when <code>side</code> is "top"/"right"

justification is set to 0, when side is "bottom"/"left" justification is set to 1, and when side is "both" justification is set to 0.5.

**normalize** How to normalize heights of functions input to the thickness aesthetic. If "all" (the default), normalize so that the maximum height across all data is 1; if "panels", normalize within panels so that the maximum height in each panel is 1; if "xy", normalize within the x/y axis opposite the orientation of this geom so that the maximum height at each value of the opposite axis is 1; if "groups", normalize within values of the opposite axis and within groups so that the maximum height in each group is 1; if "none", values are taken as is with no normalization (this should probably only be used with functions whose values are in [0,1], such as CDFs).

**interval\_size\_domain** The minimum and maximum of the values of the size aesthetic that will be translated into actual sizes for intervals drawn according to `interval_size_range` (see the documentation for that argument.)

**interval\_size\_range** (Deprecated). This geom scales the raw size aesthetic values when drawing interval and point sizes, as they tend to be too thick when using the default settings of `scale_size_continuous()`, which give sizes with a range of `c(1, 6)`. The `interval_size_domain` value indicates the input domain of raw size values (typically this should be equal to the value of the range argument of the `scale_size_continuous()` function), and `interval_size_range` indicates the desired output range of the size values (the min and max of the actual sizes used to draw intervals). Most of the time it is not recommended to change the value of this argument, as it may result in strange scaling of legends; this argument is a holdover from earlier versions that did not have size aesthetics targeting the point and interval separately. If you want to adjust the size of the interval or points separately, you can instead use the `interval_size` or `point_size` aesthetics; see [scales](#).

**fatten\_point** A multiplicative factor used to adjust the size of the point relative to the size of the thickest interval line. If you wish to specify point sizes directly, you can also use the `point_size` aesthetic and `scale_point_size_continuous()` or `scale_point_size_discrete()`; sizes specified with that aesthetic will not be adjusted using `fatten_point`.

**show\_slab** Should the slab portion of the geom be drawn? Default TRUE.

**show\_point** Should the point portion of the geom be drawn? Default TRUE.

**show\_interval** Should the interval portion of the geom be drawn? Default TRUE.

<code>dotsize</code>	The size of the dots relative to the bin width. The default, 1, makes dots be just about as wide as the bin width.
<code>stackratio</code>	The distance between the center of the dots in the same stack relative to the bin height. The default, 1, makes dots in the same stack just touch each other.
<code>binwidth</code>	The bin width to use for drawing the dotplots. The default value, NA, will dynamically select a bin width based on the size of the plot when drawn.
<code>na.rm</code>	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders()</code> .
geom	Use to override the default connection between <code>stat_slabinterval</code> and <code>geom_slabinterval()</code>
quantiles	For the <code>stat_</code> and <code>stat_dist_</code> stats, setting this to a value other than NA will produce a quantile dotplot: that is, a dotplot of quantiles from the sample (for <code>stat_</code> ) or a dotplot of quantiles from the distribution (for <code>stat_dist_</code> ). The value of <code>quantiles</code> determines the number of quantiles to plot. See Kay et al. (2016) and Fernandes et al. (2018) for more information on quantile dotplots.
point_interval	A function from the <code>point_interval()</code> family (e.g., <code>median_qi</code> , <code>mean_qi</code> , etc). This function should take in a vector of value, and should obey the <code>.width</code> and <code>.simple_names</code> parameters of <code>point_interval()</code> functions, such that when given a vector with <code>.simple_names = TRUE</code> should return a data frame with variables <code>.value</code> , <code>.lower</code> , <code>.upper</code> , and <code>.width</code> . Output will be converted to the appropriate x- or y-based aesthetics depending on the value of <code>orientation</code> . See the <code>point_interval()</code> family of functions for more information.

## Details

The dots geoms are similar to `geom_dotplot()` but with a number of differences:

- Dots geoms act like slabs in `geom_slabinterval()` and can be given x positions (or y positions when in a horizontal orientation).
- Given the available space to lay out dots, the dots geoms will automatically determine how many bins to use to fit the available space.
- Dots geoms use a dynamic layout algorithm that lays out dots from the center out if the input data are symmetrical, guaranteeing that symmetrical data results in a symmetrical plot. The layout algorithm also prevents dots from overlapping each other.
- The shape of the dots in a in these geoms can be changed using the `slab_shape` aesthetic (when using the `dotsinterval` family) or the `shape` or `slab_shape` aesthetic (when using the `dots` family)

The `stat_...` and `stat_dist_...` versions of the stats when used with the `quantiles` argument are particularly useful for constructing quantile dotplots, which can be an effective way to communicate uncertainty using a frequency framing that may be easier for laypeople to understand (Kay et al. 2016, Fernandes et al. 2018).

## Value

A `ggplot2::Geom` or `ggplot2::Stat` representing a dotplot or combined dotplot+interval geometry which can be added to a `ggplot()` object.

**Aesthetics**

These stats support the following aesthetics:

- x
- y
- datatype
- thickness
- size
- group

In addition, in their default configuration (paired with `geom_dotsinterval()`) the following aesthetics are supported by the underlying geom:

- x
- y
- slab\_shape
- datatype
- alpha
- colour
- colour\_ramp
- linetype
- fill
- shape
- stroke
- point\_colour
- point\_fill
- point\_alpha
- point\_size
- size
- interval\_colour
- interval\_alpha
- interval\_size
- interval\_linetype
- slab\_size
- slab\_colour
- slab\_fill
- slab\_alpha
- slab\_linetype
- fill\_ramp

- ymin
- ymax
- xmin
- xmax
- width
- height
- thickness
- group

See examples of some of these aesthetics in action in `vignette("slabinterval")`. Learn more about the sub-geom aesthetics (like `interval_color`) in the [scales](#) documentation. Learn more about basic ggplot aesthetics in `vignette("ggplot2-specs")`.

### Author(s)

Matthew Kay

### References

Kay, M., Kola, T., Hullman, J. R., & Munson, S. A. (2016). When (ish) is My Bus? User-centered Visualizations of Uncertainty in Everyday, Mobile Predictive Systems. *Conference on Human Factors in Computing Systems - CHI '16*, 5092–5103. doi: [10.1145/2858036.2858558](https://doi.org/10.1145/2858036.2858558).

Fernandes, M., Walls, L., Munson, S., Hullman, J., & Kay, M. (2018). Uncertainty Displays Using Quantile Dotplots or CDFs Improve Transit Decision-Making. *Conference on Human Factors in Computing Systems - CHI '18*. doi: [10.1145/3173574.3173718](https://doi.org/10.1145/3173574.3173718).

### See Also

See `stat_sample_slabinterval()` and `stat_dist_slabinterval()` for families of other stats built on top of `geom_slabinterval()`. See `vignette("slabinterval")` for a variety of examples of use.

### Examples

```
library(dplyr)
library(ggplot2)

data(RankCorr_u_tau, package = "ggdist")

# orientation is detected automatically based on
# which axis is discrete

RankCorr_u_tau %>%
  ggplot(aes(x = u_tau)) +
  geom_dots()

RankCorr_u_tau %>%
```

```

ggplot(aes(y = u_tau)) +
  geom_dots()

# stat_dots can summarize quantiles, creating quantile dotplots

RankCorr_u_tau %>%
  ggplot(aes(x = u_tau, y = factor(i))) +
  stat_dots(quantiles = 100)

# color and fill aesthetics can be mapped within the geom
# dotsinterval adds an interval

RankCorr_u_tau %>%
  ggplot(aes(x = u_tau, y = factor(i), fill = stat(x > 6))) +
  stat_dotsinterval(quantiles = 100)

```

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geom_interval	<i>Multiple uncertainty interval plots (ggplot geom)</i>
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## Description

Multiple interval geoms with default aesthetics designed for use with output from [point\\_interval\(\)](#). Wrapper around [geom\\_slabinterval\(\)](#).

## Usage

```

geom_interval(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  side = "both",
  orientation = NA,
  interval_size_range = c(1, 6),
  show_slab = FALSE,
  show_point = FALSE
)

```

## 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 <code>fortify()</code> 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. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code> ).
<code>stat</code>	The statistical transformation to use on the data for this layer, as a string.
<code>position</code>	The position adjustment to use for overlapping points on this layer. Setting this equal to "dodge" can be useful if you have overlapping intervals.
<code>...</code>	Arguments passed on to <code>geom_slabinterval</code>
<code>scale</code>	What proportion of the region allocated to this geom to use to draw the slab. If <code>scale = 1</code> , slabs that use the maximum range will just touch each other. Default is <code>0.9</code> to leave some space.
<code>justification</code>	Justification of the interval relative to the slab, where <code>0</code> indicates bottom/left justification and <code>1</code> indicates top/right justification (depending on orientation). If justification is <code>NULL</code> (the default), then it is set automatically based on the value of <code>side</code> : when <code>side</code> is "top"/"right" justification is set to <code>0</code> , when <code>side</code> is "bottom"/"left" justification is set to <code>1</code> , and when <code>side</code> is "both" justification is set to <code>0.5</code> .
<code>normalize</code>	How to normalize heights of functions input to the thickness aesthetic. If "all" (the default), normalize so that the maximum height across all data is 1; if "panels", normalize within panels so that the maximum height in each panel is 1; if "xy", normalize within the x/y axis opposite the orientation of this geom so that the maximum height at each value of the opposite axis is 1; if "groups", normalize within values of the opposite axis and within groups so that the maximum height in each group is 1; if "none", values are taken as is with no normalization (this should probably only be used with functions whose values are in <code>[0,1]</code> , such as CDFs).
<code>interval_size_domain</code>	The minimum and maximum of the values of the size aesthetic that will be translated into actual sizes for intervals drawn according to <code>interval_size_range</code> (see the documentation for that argument.)
<code>fatten_point</code>	A multiplicative factor used to adjust the size of the point relative to the size of the thickest interval line. If you wish to specify point sizes directly, you can also use the <code>point_size</code> aesthetic and <code>scale_point_size_continuous()</code> or <code>scale_point_size_discrete()</code> ; sizes specified with that aesthetic will not be adjusted using <code>fatten_point</code> .
<code>show_interval</code>	Should the interval portion of the geom be drawn? Default <code>TRUE</code> .
<code>na.rm</code>	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? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes. It can also be a named logical vector to finely select the aesthetics to display.
<code>inherit.aes</code>	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. `borders()`.

side	Which side to draw the slab on. "topright", "top", and "right" are synonyms which cause the slab to be drawn on the top or the right depending on if orientation is "horizontal" or "vertical". "bottomleft", "bottom", and "left" are synonyms which cause the slab to be drawn on the bottom or the left depending on if orientation is "horizontal" or "vertical". "topleft" causes the slab to be drawn on the top or the left, and "bottomright" causes the slab to be drawn on the bottom or the right. "both" draws the slab mirrored on both sides (as in a violin plot).
orientation	Whether this geom is drawn horizontally ("horizontal") or vertically ("vertical"). The default, NA, automatically detects the orientation based on how the aesthetics are assigned, and should generally do an okay job at this. When horizontal (resp. vertical), the geom uses the y (resp. x) aesthetic to identify different groups, then for each group uses the x (resp. y) aesthetic and the thickness aesthetic to draw a function as an slab, and draws points and intervals horizontally (resp. vertically) using the xmin, x, and xmax (resp. ymin, y, and ymax) aesthetics. For compatibility with the base ggplot naming scheme for orientation, "x" can be used as an alias for "vertical" and "y" as an alias for "horizontal" (tidybayes had an orientation parameter before ggplot did, and I think the tidybayes naming scheme is more intuitive: "x" and "y" are not orientations and their mapping to orientations is, in my opinion, backwards; but the base ggplot naming scheme is allowed for compatibility).
interval_size_range	(Deprecated). This geom scales the raw size aesthetic values when drawing interval and point sizes, as they tend to be too thick when using the default settings of <code>scale_size_continuous()</code> , which give sizes with a range of <code>c(1, 6)</code> . The <code>interval_size_domain</code> value indicates the input domain of raw size values (typically this should be equal to the value of the range argument of the <code>scale_size_continuous()</code> function), and <code>interval_size_range</code> indicates the desired output range of the size values (the min and max of the actual sizes used to draw intervals). Most of the time it is not recommended to change the value of this argument, as it may result in strange scaling of legends; this argument is a holdover from earlier versions that did not have size aesthetics targeting the point and interval separately. If you want to adjust the size of the interval or points separately, you can instead use the <code>interval_size</code> or <code>point_size</code> aesthetics; see <a href="#">scales</a> .
show_slab	Should the slab portion of the geom be drawn? Default TRUE.
show_point	Should the point portion of the geom be drawn? Default TRUE.

## Details

These geoms are wrappers around `geom_slabinterval()` with defaults designed to produce multiple interval plots. These geoms set some default aesthetics equal to the `.lower`, `.upper`, and `.width` columns generated by the `point_interval` family of functions, making them often more convenient than vanilla `geom_linerange()` when used with functions like `median_qi()`, `mean_qi()`, `mode_hdi()`, etc.

Specifically, `geom_interval` acts as if its default aesthetics are `aes(color = fct_rev(ordered(.width)))`.

**Value**

A `ggplot2::Geom` representing a multiple interval geometry which can be added to a `ggplot()` object.

**Aesthetics**

These geoms support the following aesthetics:

- x
- y
- datatype
- alpha
- colour
- colour\_ramp
- linetype
- fill
- shape
- stroke
- point\_colour
- point\_fill
- point\_alpha
- point\_size
- size
- interval\_colour
- interval\_alpha
- interval\_size
- interval\_linetype
- slab\_size
- slab\_colour
- slab\_fill
- slab\_alpha
- slab\_linetype
- fill\_ramp
- ymin
- ymax
- xmin
- xmax
- width
- height

- thickness
- group

See examples of some of these aesthetics in action in `vignette("slabinterval")`. Learn more about the sub-geom aesthetics (like `interval_color`) in the [scales](#) documentation. Learn more about basic ggplot aesthetics in `vignette("ggplot2-specs")`.

### Author(s)

Matthew Kay

### See Also

See `stat_interval()` for the stat version, intended for use on samples from a distribution. See `geom_interval()` for a similar geom intended for intervals without point summaries. See `stat_sample_slabinterval()` for a variety of other stats that combine intervals with densities and CDFs. See `geom_slabinterval()` for the geom that these geoms wrap. All parameters of that geom are available to these geoms.

### Examples

```
library(dplyr)
library(ggplot2)

theme_set(theme_ggdist())

data(RankCorr_u_tau, package = "ggdist")

# orientation is detected automatically based on
# use of xmin/xmax or ymin/ymax

RankCorr_u_tau %>%
  group_by(i) %>%
  median_qi(.width = c(.5, .8, .95, .99)) %>%
  ggplot(aes(y = i, x = u_tau, xmin = .lower, xmax = .upper)) +
  geom_interval() +
  scale_color_brewer()

RankCorr_u_tau %>%
  group_by(i) %>%
  median_qi(.width = c(.5, .8, .95, .99)) %>%
  ggplot(aes(x = i, y = u_tau, ymin = .lower, ymax = .upper)) +
  geom_interval() +
  scale_color_brewer()
```

---

geom\_lineribbon      *Line + multiple uncertainty ribbon plots (ggplot geom)*

---

### Description

A combination of `geom_line()` and `geom_ribbon()` with default aesthetics designed for use with output from `point_interval()`.

### Usage

```
geom_lineribbon(  
  mapping = NULL,  
  data = NULL,  
  stat = "identity",  
  position = "identity",  
  ...,  
  step = FALSE,  
  orientation = NA,  
  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	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 <code>ggplot()</code> . 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. 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. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code> ).
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 to <code>layer()</code> .
step	Should the line/ribbon be drawn as a step function? One of: <code>FALSE</code> (do not draw as a step function, the default), <code>TRUE</code> (draw a step function using the "mid" approach), "mid" (draw steps midway between adjacent x values), "hv" (draw horizontal-then-vertical steps), "vh" (draw as vertical-then-horizontal steps).

	TRUE is an alias for "mid" because for a step function with ribbons, "mid" is probably what you want (for the other two step approaches the ribbons at either the vert first or vert last x value will not be visible).
orientation	Whether this geom is drawn horizontally ("horizontal") or vertically ("vertical"). The default, NA, automatically detects the orientation based on how the aesthetics are assigned, and should generally do an okay job at this. When horizontal (resp. vertical), the geom uses the y (resp. x) aesthetic to identify different groups, then for each group uses the x (resp. y) aesthetic and the thickness aesthetic to draw a function as an slab, and draws points and intervals horizontally (resp. vertically) using the xmin, x, and xmax (resp. ymin, y, and ymax) aesthetics. For compatibility with the base ggplot naming scheme for orientation, "x" can be used as an alias for "vertical" and "y" as an alias for "horizontal" (tidybayes had an orientation parameter before ggplot did, and I think the tidybayes naming scheme is more intuitive: "x" and "y" are not orientations and their mapping to orientations is, in my opinion, backwards; but the base ggplot naming scheme is allowed for compatibility).
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders()</code> .

### Details

`geom_lineribbon` is a combination version of a `geom_line()`, and `geom_ribbon` designed for use with output from `point_interval()`. This geom sets some default aesthetics equal to the `.width` column generated by the `point_interval` family of functions, making them often more convenient than a vanilla `geom_ribbon()` + `geom_line()`.

Specifically, `geom_lineribbon` acts as if its default aesthetics are `aes(fill = forcats::fct_rev(ordered(.width)))`.

### Value

A `ggplot2::Geom` representing a combined line+uncertainty ribbon geometry which can be added to a `ggplot()` object.

### Author(s)

Matthew Kay

### See Also

See `stat_lineribbon()` for a version that does summarizing of samples into points and intervals within `ggplot`. See `geom_pointinterval()` for a similar geom intended for point summaries and intervals. See `geom_ribbon()` and `geom_line()` for the geoms this is based on.

## Examples

```
library(dplyr)
library(ggplot2)

theme_set(theme_ggdist())

tibble(x = 1:10) %>%
  group_by_all() %>%
  do(tibble(y = rnorm(100, .$x))) %>%
  median_qi(.width = c(.5, .8, .95)) %>%
  ggplot(aes(x = x, y = y, ymin = .lower, ymax = .upper)) +
  # automatically uses aes(fill = fct_rev(ordered(.width)))
  geom_lineribbon() +
  scale_fill_brewer()
```

---

geom\_pointinterval      *Point + multiple uncertainty interval plots (ggplot geom)*

---

## Description

Combined point + multiple interval geoms with default aesthetics designed for use with output from [point\\_interval\(\)](#). Wrapper around [geom\\_slabinterval\(\)](#).

## Usage

```
geom_pointinterval(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  side = "both",
  orientation = NA,
  show_slab = FALSE,
  show.legend = c(size = FALSE)
)
```

## 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 data.frame, 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.
	A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code> ).
stat	The statistical transformation to use on the data for this layer, as a string.
position	The position adjustment to use for overlapping points on this layer. Setting this equal to "dodge" can be useful if you have overlapping intervals.
...	Arguments passed on to <code>geom_slabinterval</code>
scale	What proportion of the region allocated to this geom to use to draw the slab. If <code>scale = 1</code> , slabs that use the maximum range will just touch each other. Default is <code>0.9</code> to leave some space.
justification	Justification of the interval relative to the slab, where <code>0</code> indicates bottom/left justification and <code>1</code> indicates top/right justification (depending on orientation). If justification is NULL (the default), then it is set automatically based on the value of side: when side is "top"/"right" justification is set to <code>0</code> , when side is "bottom"/"left" justification is set to <code>1</code> , and when side is "both" justification is set to <code>0.5</code> .
normalize	How to normalize heights of functions input to the thickness aesthetic. If "all" (the default), normalize so that the maximum height across all data is 1; if "panels", normalize within panels so that the maximum height in each panel is 1; if "xy", normalize within the x/y axis opposite the orientation of this geom so that the maximum height at each value of the opposite axis is 1; if "groups", normalize within values of the opposite axis and within groups so that the maximum height in each group is 1; if "none", values are taken as is with no normalization (this should probably only be used with functions whose values are in <code>[0,1]</code> , such as CDFs).
interval_size_domain	The minimum and maximum of the values of the size aesthetic that will be translated into actual sizes for intervals drawn according to <code>interval_size_range</code> (see the documentation for that argument.)
interval_size_range	(Deprecated). This geom scales the raw size aesthetic values when drawing interval and point sizes, as they tend to be too thick when using the default settings of <code>scale_size_continuous()</code> , which give sizes with a range of <code>c(1, 6)</code> . The <code>interval_size_domain</code> value indicates the input domain of raw size values (typically this should be equal to the value of the range argument of the <code>scale_size_continuous()</code> function), and <code>interval_size_range</code> indicates the desired output range of the size values (the min and max of the actual sizes used to draw intervals). Most of the time it is not recommended to change the value of this argument, as it may result in strange scaling of legends; this argument is a holdover from earlier versions that did not have size aesthetics targeting the point and interval separately. If you want to adjust the size of the interval or points separately, you can instead use the <code>interval_size</code> or <code>point_size</code> aesthetics; see <a href="#">scales</a> .
fatten_point	A multiplicative factor used to adjust the size of the point relative to the size of the thickest interval line. If you wish to specify point sizes

directly, you can also use the `point_size` aesthetic and `scale_point_size_continuous()` or `scale_point_size_discrete()`; sizes specified with that aesthetic will not be adjusted using `fatten_point`.

`show_point` Should the point portion of the geom be drawn? Default TRUE.

`show_interval` Should the interval portion of the geom be drawn? Default TRUE.

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

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

`side` Which side to draw the slab on. "topright", "top", and "right" are synonyms which cause the slab to be drawn on the top or the right depending on if orientation is "horizontal" or "vertical". "bottomleft", "bottom", and "left" are synonyms which cause the slab to be drawn on the bottom or the left depending on if orientation is "horizontal" or "vertical". "topleft" causes the slab to be drawn on the top or the left, and "bottomright" causes the slab to be drawn on the bottom or the right. "both" draws the slab mirrored on both sides (as in a violin plot).

`orientation` Whether this geom is drawn horizontally ("horizontal") or vertically ("vertical"). The default, NA, automatically detects the orientation based on how the aesthetics are assigned, and should generally do an okay job at this. When horizontal (resp. vertical), the geom uses the y (resp. x) aesthetic to identify different groups, then for each group uses the x (resp. y) aesthetic and the thickness aesthetic to draw a function as an slab, and draws points and intervals horizontally (resp. vertically) using the `xmin`, `x`, and `xmax` (resp. `ymin`, `y`, and `ymax`) aesthetics. For compatibility with the base ggplot naming scheme for orientation, "x" can be used as an alias for "vertical" and "y" as an alias for "horizontal" (tidybayes had an orientation parameter before ggplot did, and I think the tidybayes naming scheme is more intuitive: "x" and "y" are not orientations and their mapping to orientations is, in my opinion, backwards; but the base ggplot naming scheme is allowed for compatibility).

`show_slab` Should the slab portion of the geom be drawn? Default TRUE.

`show.legend` Should this layer be included in the legends? Default is `c(size = FALSE)`, unlike most geoms, to match its common use cases. FALSE hides all legends, TRUE shows all legends, and NA shows only those that are mapped (the default for most geoms).

## Details

These geoms are wrappers around `geom_slabinterval()` with defaults designed to produce points+interval plots. These geoms set some default aesthetics equal to the `.lower`, `.upper`, and `.width` columns generated by the `point_interval` family of functions, making them often more convenient than vanilla `geom_pointrange()` when used with functions like `median_qi()`, `mean_qi()`, `mode_hdi()`, etc.

Specifically, `geom_pointinterval` acts as if its default aesthetics are `aes(size = -.width)`.

**Value**

A `ggplot2::Geom` representing a point+multiple uncertainty interval geometry which can be added to a `ggplot()` object.

**Aesthetics**

These geoms support the following aesthetics:

- x
- y
- datatype
- alpha
- colour
- colour\_ramp
- linetype
- fill
- shape
- stroke
- point\_colour
- point\_fill
- point\_alpha
- point\_size
- size
- interval\_colour
- interval\_alpha
- interval\_size
- interval\_linetype
- slab\_size
- slab\_colour
- slab\_fill
- slab\_alpha
- slab\_linetype
- fill\_ramp
- ymin
- ymax
- xmin
- xmax
- width
- height

- thickness
- group

See examples of some of these aesthetics in action in `vignette("slabinterval")`. Learn more about the sub-geom aesthetics (like `interval_color`) in the [scales](#) documentation. Learn more about basic ggplot aesthetics in `vignette("ggplot2-specs")`.

### Author(s)

Matthew Kay

### See Also

See `geom_slabinterval()` for the geom that these geoms wrap. All parameters of that geom are available to these geoms.

See `stat_pointinterval()` for the stat version, intended for use on samples from a distribution. See `geom_interval()` for a similar stat intended for intervals without point summaries. See `stat_sample_slabinterval()` for a variety of other stats that combine intervals with densities and CDFs. See `geom_slabinterval()` for the geom that these geoms wrap. All parameters of that geom are available to these geoms.

### Examples

```
library(dplyr)
library(ggplot2)

data(RankCorr_u_tau, package = "ggdist")

# orientation is detected automatically based on
# use of xmin/xmax or ymin/ymax

RankCorr_u_tau %>%
  group_by(i) %>%
  median_qi(.width = c(.8, .95)) %>%
  ggplot(aes(y = i, x = u_tau, xmin = .lower, xmax = .upper)) +
  geom_pointinterval()

RankCorr_u_tau %>%
  group_by(i) %>%
  median_qi(.width = c(.8, .95)) %>%
  ggplot(aes(x = i, y = u_tau, ymin = .lower, ymax = .upper)) +
  geom_pointinterval()
```

---

geom\_slabinterval      *Slab + point + interval meta-geom*

---

### Description

This meta-geom supports drawing combinations of functions (as slabs, aka ridge plots or joy plots), points, and intervals. It acts as a meta-geom for many other tidybayes geoms that are wrappers around this geom, including eye plots, half-eye plots, CCDF barplots, and point+multiple interval plots, and supports both horizontal and vertical orientations, dodging (via the `position` argument), and relative justification of slabs with their corresponding intervals.

### Usage

```
geom_slabinterval(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,
  side = c("topright", "top", "right", "bottomleft", "bottom", "left", "topleft",
           "bottomright", "both"),
  scale = 0.9,
  orientation = NA,
  justification = NULL,
  normalize = c("all", "panels", "xy", "groups", "none"),
  interval_size_domain = c(1, 6),
  interval_size_range = c(0.6, 1.4),
  fatten_point = 1.8,
  show_slab = TRUE,
  show_point = TRUE,
  show_interval = TRUE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

geom_slab(
  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 <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	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 <code>ggplot()</code> . 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. 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. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code> ).
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 to <code>layer()</code> .
side	Which side to draw the slab on. "topright", "top", and "right" are synonyms which cause the slab to be drawn on the top or the right depending on if orientation is "horizontal" or "vertical". "bottomleft", "bottom", and "left" are synonyms which cause the slab to be drawn on the bottom or the left depending on if orientation is "horizontal" or "vertical". "topleft" causes the slab to be drawn on the top or the left, and "bottomright" causes the slab to be drawn on the bottom or the right. "both" draws the slab mirrored on both sides (as in a violin plot).
scale	What proportion of the region allocated to this geom to use to draw the slab. If <code>scale = 1</code> , slabs that use the maximum range will just touch each other. Default is <code>0.9</code> to leave some space.
orientation	Whether this geom is drawn horizontally ("horizontal") or vertically ("vertical"). The default, <code>NA</code> , automatically detects the orientation based on how the aesthetics are assigned, and should generally do an okay job at this. When horizontal (resp. vertical), the geom uses the <code>y</code> (resp. <code>x</code> ) aesthetic to identify different groups, then for each group uses the <code>x</code> (resp. <code>y</code> ) aesthetic and the thickness aesthetic to draw a function as an slab, and draws points and intervals horizontally (resp. vertically) using the <code>xmin</code> , <code>x</code> , and <code>xmax</code> (resp. <code>ymin</code> , <code>y</code> , and <code>ymax</code> ) aesthetics. For compatibility with the base <code>ggplot</code> naming scheme for orientation, "x" can be used as an alias for "vertical" and "y" as an alias for "horizontal" (tidybayes had an <code>orientation</code> parameter before <code>ggplot</code> did, and I think the tidybayes naming scheme is more intuitive: "x" and "y" are not orientations and their mapping to orientations is, in my opinion, backwards; but the base <code>ggplot</code> naming scheme is allowed for compatibility).
justification	Justification of the interval relative to the slab, where <code>0</code> indicates bottom/left justification and <code>1</code> indicates top/right justification (depending on orientation). If <code>justification</code> is <code>NULL</code> (the default), then it is set automatically based on the value of <code>side</code> : when <code>side</code> is "top"/"right" justification is set to <code>0</code> , when

	side is "bottom"/"left" justification is set to 1, and when side is "both" justification is set to 0.5.
normalize	How to normalize heights of functions input to the thickness aesthetic. If "all" (the default), normalize so that the maximum height across all data is 1; if "panels", normalize within panels so that the maximum height in each panel is 1; if "xy", normalize within the x/y axis opposite the orientation of this geom so that the maximum height at each value of the opposite axis is 1; if "groups", normalize within values of the opposite axis and within groups so that the maximum height in each group is 1; if "none", values are taken as is with no normalization (this should probably only be used with functions whose values are in [0,1], such as CDFs).
interval_size_domain	The minimum and maximum of the values of the size aesthetic that will be translated into actual sizes for intervals drawn according to interval_size_range (see the documentation for that argument.)
interval_size_range	(Deprecated). This geom scales the raw size aesthetic values when drawing interval and point sizes, as they tend to be too thick when using the default settings of <code>scale_size_continuous()</code> , which give sizes with a range of <code>c(1, 6)</code> . The <code>interval_size_domain</code> value indicates the input domain of raw size values (typically this should be equal to the value of the range argument of the <code>scale_size_continuous()</code> function), and <code>interval_size_range</code> indicates the desired output range of the size values (the min and max of the actual sizes used to draw intervals). Most of the time it is not recommended to change the value of this argument, as it may result in strange scaling of legends; this argument is a holdover from earlier versions that did not have size aesthetics targeting the point and interval separately. If you want to adjust the size of the interval or points separately, you can instead use the <code>interval_size</code> or <code>point_size</code> aesthetics; see <a href="#">scales</a> .
fatten_point	A multiplicative factor used to adjust the size of the point relative to the size of the thickest interval line. If you wish to specify point sizes directly, you can also use the <code>point_size</code> aesthetic and <code>scale_point_size_continuous()</code> or <code>scale_point_size_discrete()</code> ; sizes specified with that aesthetic will not be adjusted using <code>fatten_point</code> .
show_slab	Should the slab portion of the geom be drawn? Default TRUE.
show_point	Should the point portion of the geom be drawn? Default TRUE.
show_interval	Should the interval portion of the geom be drawn? Default TRUE.
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. <code>borders()</code> .

## Details

geom\_slabinterval is a flexible meta-geom that you can use directly or through a variety of "short-cut" geoms that represent useful combinations of the various parameters of this geom. In many cases you will want to use the shortcut geoms instead as they create more useful mnemonic primitives, such as eye plots, half-eye plots, point+interval plots, or CCDF barplots.

The *slab* portion of the geom is much like a ridge or "joy" plot: it represents the value of a function scaled to fit between values on the x or y axis (depending on the value of orientation). Values of the functions are specified using the thickness aesthetic and are scaled to fit into scale times the distance between points on the relevant axis. E.g., if orientation is "horizontal", scale is 0.9, and y is a discrete variable, then the thickness aesthetic specifies the value of some function of x that is drawn for every y value and scaled to fit into 0.9 times the distance between points on the y axis.

For the *interval* portion of the geom, x and y aesthetics specify the location of the point and ymin/ymax or xmin/xmax (depending on the value of orientation specifying the endpoints of the interval). A scaling factor for interval line width and point size is applied through the interval\_size\_domain, interval\_size\_range, and fatten\_point parameters. These scaling factors are designed to give multiple uncertainty intervals reasonable scaling at the default settings for [scale\\_size\\_continuous\(\)](#).

As a combination geom, this geom expects a datatype aesthetic specifying which part of the geom a given row in the input data corresponds to: "slab" or "interval". However, specifying this aesthetic manually is typically only necessary if you use this geom directly; the numerous wrapper geoms will usually set this aesthetic for you as needed, and their use is recommended unless you have a very custom use case.

Wrapper geoms and stats include:

- [stat\\_sample\\_slabinterval\(\)](#) and associated stats
- [stat\\_dist\\_slabinterval\(\)](#) and associated stats
- [geom\\_pointinterval\(\)](#) / [stat\\_pointinterval\(\)](#)
- [geom\\_interval\(\)](#) / [stat\\_interval\(\)](#)
- [geom\\_dots\(\)](#) / [stat\\_dots\(\)](#)

Typically, the geom\_\* versions are meant for use with already-summarized data (such as intervals) and the stat\_\* versions are summarize the data themselves (usually draws from a distribution) to produce the geom.

## Value

A [ggplot2::Geom](#) representing a slab or combined slab+interval geometry which can be added to a [ggplot\(\)](#) object.

## Aesthetics

These geoms support the following aesthetics:

- x
- y
- datatype

- alpha
- colour
- colour\_ramp
- linetype
- fill
- shape
- stroke
- point\_colour
- point\_fill
- point\_alpha
- point\_size
- size
- interval\_colour
- interval\_alpha
- interval\_size
- interval\_linetype
- slab\_size
- slab\_colour
- slab\_fill
- slab\_alpha
- slab\_linetype
- fill\_ramp
- ymin
- ymax
- xmin
- xmax
- width
- height
- thickness
- group

See examples of some of these aesthetics in action in `vignette("slabinterval")`. Learn more about the sub-geom aesthetics (like `interval_color`) in the [scales](#) documentation. Learn more about basic ggplot aesthetics in `vignette("ggplot2-specs")`.

**Author(s)**

Matthew Kay

**See Also**

See [geom\\_lineribbon\(\)](#) for a combination geom designed for fit curves plus probability bands. See [stat\\_sample\\_slabininterval\(\)](#) and [stat\\_dist\\_slabininterval\(\)](#) for families of stats built on top of this geom for common use cases (like [stat\\_halfeye\(\)](#)). See [vignette\("slabininterval"\)](#) for a variety of examples of use.

**Examples**

```
# geom_slabininterval() is typically not that useful on its own.
# See vignette("slabininterval") for a variety of examples of the use of its
# shortcut geoms and stats, which are more useful than using
# geom_slabininterval() directly.
```

---

lkjcorr_marginal	<i>Marginal distribution of a single correlation from an LKJ distribution</i>
------------------	---

---

**Description**

Marginal distribution for the correlation in a single cell from a correlation matrix distributed according to an LKJ distribution.

**Usage**

```
dlkjcorr_marginal(x, K, eta, log = FALSE)

plkjcorr_marginal(q, K, eta, lower.tail = TRUE, log.p = FALSE)

qlkjcorr_marginal(p, K, eta, lower.tail = TRUE, log.p = FALSE)

rlkjcorr_marginal(n, K, eta)
```

**Arguments**

x	vector of quantiles.
K	Dimension of the correlation matrix. Must be greater than or equal to 2.
eta	Parameter controlling the shape of the distribution
log	logical; if TRUE, probabilities p are given as log(p).
q	vector of quantiles.
lower.tail	logical; if TRUE (default), probabilities are $P[X \leq x]$ otherwise, $P[X > x]$ .
log.p	logical; if TRUE, probabilities p are given as log(p).
p	vector of probabilities.
n	number of observations. If $\text{length}(n) > 1$ , the length is taken to be the number required.

## Details

The LKJ distribution is a distribution over correlation matrices with a single parameter,  $\eta$ . For a given  $\eta$  and a  $K \times K$  correlation matrix  $R$ :

$$R \sim \text{LKJ}(\eta)$$

Each off-diagonal entry of  $R$ ,  $r_{ij} : i \neq j$ , has the following marginal distribution (Lewandowski, Kurowicka, and Joe 2009):

$$\frac{r_{ij} + 1}{2} \sim \text{Beta} \left( \eta - 1 + \frac{K}{2}, \eta - 1 + \frac{K}{2} \right)$$

In other words,  $r_{ij}$  is marginally distributed according to the above Beta distribution scaled into  $(-1, 1)$ .

## Value

- `dlkcorr_marginal` gives the density
- `plkcorr_marginal` gives the cumulative distribution function (CDF)
- `qlkcorr_marginal` gives the quantile function (inverse CDF)
- `rlkcorr_marginal` generates random draws.

The length of the result is determined by `n` for `rlkcorr_marginal`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

## References

Lewandowski, D., Kurowicka, D., & Joe, H. (2009). Generating random correlation matrices based on vines and extended onion method. *Journal of Multivariate Analysis*, 100(9), 1989–2001. doi: [10.1016/j.jmva.2009.04.008](https://doi.org/10.1016/j.jmva.2009.04.008).

## See Also

`parse_dist()` and `marginalize_lkjcorr()` for parsing specs that use the LKJ correlation distribution and the `stat_dist_slabinterval()` family of stats for visualizing them.

## Examples

```
library(dplyr)
library(ggplot2)
library(forcats)

theme_set(theme_ggdist())

expand.grid(
  eta = 1:6,
```

```

K = 2:6
) %>%
ggplot(aes(y = fct_rev(ordered(eta)), dist = "lkjcorr_marginal", arg1 = K, arg2 = eta)) +
  stat_dist_slab() +
  facet_grid(~ paste0(K, "x", K)) +
  labs(
    title = paste0(
      "Marginal correlation for LKJ(eta) prior on different matrix sizes:\n",
      "dlkjcorr_marginal(K, eta)"
    ),
    subtitle = "Correlation matrix size (KxK)",
    y = "eta",
    x = "Marginal correlation"
  ) +
  theme(axis.title = element_text(hjust = 0))

```

---

marginalize\_lkjcorr    *Turn spec for LKJ distribution into spec for marginal LKJ distribution*

---

## Description

Turns specs for an LKJ correlation matrix distribution as returned by `parse_dist()` into specs for the marginal distribution of a single cell in an LKJ-distributed correlation matrix (i.e., `lkjcorr_marginal()`). Useful for visualizing prior correlations from LKJ distributions.

## Usage

```
marginalize_lkjcorr(data, K, predicate = NULL, dist = ".dist", args = ".args")
```

## Arguments

<code>data</code>	A data frame containing a column with distribution names (" <code>.dist</code> " by default) and a list column of distribution arguments (" <code>.args</code> " by default), such as output by <code>parse_dist()</code> .
<code>K</code>	Dimension of the correlation matrix. Must be greater than or equal to 2.
<code>predicate</code>	a bare expression for selecting the rows of data to modify. This is useful if data contains more than one row with an LKJ prior in it and you only want to modify some of the distributions; if this is the case, give row a predicate expression (such as you might supply to <code>dplyr::filter()</code> ) that evaluates to TRUE on the rows you want to modify. If NULL (the default), all <code>lkjcorr</code> distributions in data are modified.
<code>dist</code>	The name of the column containing distribution names. See <code>parse_dist()</code> .
<code>args</code>	The name of the column containing distribution arguments. See <code>parse_dist()</code> .

## Details

The LKJ( $\eta$ ) prior on a correlation matrix induces a marginal prior on each correlation in the matrix that depends on both the value of  $\eta$  *and*  $K$ , the dimension of the  $K \times K$  correlation matrix. Thus to visualize the marginal prior on the correlations, it is necessary to specify the value of  $K$ , which depends on what your model specification looks like.

Given a data frame representing parsed distribution specifications (such as returned by `parse_dist()`), this function updates any rows with `.dist == "lkjcorr"` so that the first argument to the distribution is equal to the specified dimension of the correlation matrix ( $K$ ) and changes the distribution name to "lkjcorr\_marginal", allowing the distribution to be easily visualized using the `stat_dist_slabinterval()` family of `ggplot2` stats.

## Value

A data frame of the same size and column names as the input, with the `dist` and `args` columns modified on rows where `dist == "lkjcorr"` such that they represent a marginal LKJ correlation distribution with name `lkjcorr_marginal` and `args` having  $K$  equal to the input value of  $K$ .

## See Also

`parse_dist()`, `lkjcorr_marginal()`

## Examples

```
library(dplyr)
library(ggplot2)

# Say we have an LKJ(3) prior on a 2x2 correlation matrix. We can visualize
# its marginal distribution as follows...
data.frame(prior = "lkjcorr(3)") %>%
  parse_dist(prior) %>%
  marginalize_lkcorr(K = 2) %>%
  ggplot(aes(y = prior, dist = .dist, args = .args)) +
  stat_dist_halfeye() +
  xlim(-1, 1) +
  xlab("Marginal correlation for LKJ(3) prior on 2x2 correlation matrix")

# Say our prior list has multiple LKJ priors on correlation matrices
# of different sizes, we can supply a predicate expression to select
# only those rows we want to modify
data.frame(coef = c("a", "b"), prior = "lkjcorr(3)") %>%
  parse_dist(prior) %>%
  marginalize_lkcorr(K = 2, coef == "a") %>%
  marginalize_lkcorr(K = 4, coef == "b")
```

---

 parse\_dist

*Parse distribution specifications into columns of a data frame*


---

## Description

Parses simple string distribution specifications, like "normal(0,1)", into two columns of a data frame, suitable for use with `stat_dist_slabinterval()` and its shortcut stats (like `stat_dist_halfeye`). This format is output by `brms::get_prior`, making it particularly useful for visualizing priors from brms models.

## Usage

```
parse_dist(object, ..., dist = ".dist", args = ".args", to_r_names = TRUE)
```

```
## Default S3 method:
parse_dist(object, ...)
```

```
## S3 method for class 'data.frame'
```

```
parse_dist(
  object,
  dist_col,
  ...,
  dist = ".dist",
  args = ".args",
  to_r_names = TRUE
)
```

```
## S3 method for class 'character'
```

```
parse_dist(object, ..., dist = ".dist", args = ".args", to_r_names = TRUE)
```

```
## S3 method for class 'factor'
```

```
parse_dist(object, ..., dist = ".dist", args = ".args", to_r_names = TRUE)
```

```
## S3 method for class 'brmsprior'
```

```
parse_dist(
  object,
  dist_col = prior,
  ...,
  dist = ".dist",
  args = ".args",
  to_r_names = TRUE
)
```

```
r_dist_name(dist_name)
```

**Arguments**

object	A character vector containing distribution specifications or a data frame with a column containing distribution specifications.
...	Arguments passed to other implementations of parse_dist.
dist	The name of the output column to contain the distribution name
args	The name of the output column to contain the arguments to the distribution
to_r_names	If TRUE (the default), certain common aliases for distribution names are automatically translated into names that R can recognize (i.e., names which have functions starting with r, p, q, and d representing random number generators, distribution functions, etc. for that distribution), using the r_dist_name function. For example, "normal" is translated into "norm" and "lognormal" is translated into "lnorm".
dist_col	A bare (unquoted) column or column expression that resolves to a character vector of distribution specifications.
dist_name	For r_dist_name, a character vector of distribution names to be translated into distribution names R recognizes. Unrecognized names are left as-is.

**Details**

parse\_dist() can be applied to character vectors or to a data frame + bare column name of the column to parse, and returns a data frame with ".dist" and ".args" columns added. parse\_dist() uses r\_dist\_name() to translate distribution names into names recognized by R.

r\_dist\_name() takes a character vector of names and translates common names into R distribution names. Names are first made into valid R names using make.names(), then translated (ignoring character case, ".", and "\_"). Thus, "lognormal", "LogNormal", "log\_normal", "log-Normal", and any number of other variants all get translated into "lnorm".

**Value**

- parse\_dist returns a data frame containing at least two columns named after the dist and args parameters. If the input is a data frame, the output is a data frame of the same length with those two columns added. If the input is a character vector or factor, the output is a two-column data frame with the same number of rows as the length of the input.
- r\_dist\_name returns a character vector the same length as the input containing translations of the input names into distribution names R can recognize.

**See Also**

See [stat\\_dist\\_slabinterval\(\)](#) and its shortcut stats, which can easily make use of the output of this function using the dist and args aesthetics.

**Examples**

```
library(dplyr)

# parse dist can operate on strings directly...
```

```

parse_dist(c("normal(0,1)", "student_t(3,0,1)"))

# ... or on columns of a data frame, where it adds the
# parsed specs back on as columns
data.frame(prior = c("normal(0,1)", "student_t(3,0,1)")) %>%
  parse_dist(prior)

# parse_dist is particularly useful with the output of brms::prior(),
# which follow the same format as above

```

---

point_interval	<i>Point and interval summaries for tidy data frames of draws from distributions</i>
----------------	--

---

### Description

Translates draws from distributions in a (possibly grouped) data frame into point and interval summaries (or set of point and interval summaries, if there are multiple groups in a grouped data frame).

### Usage

```

point_interval(
  .data,
  ...,
  .width = 0.95,
  .point = median,
  .interval = qi,
  .simple_names = TRUE,
  na.rm = FALSE,
  .exclude = c(".chain", ".iteration", ".draw", ".row"),
  .prob
)

## Default S3 method:
point_interval(
  .data,
  ...,
  .width = 0.95,
  .point = median,
  .interval = qi,
  .simple_names = TRUE,
  na.rm = FALSE,
  .exclude = c(".chain", ".iteration", ".draw", ".row"),
  .prob
)

## S3 method for class 'numeric'

```

```

point_interval(
  .data,
  ...,
  .width = 0.95,
  .point = median,
  .interval = qi,
  .simple_names = FALSE,
  na.rm = FALSE,
  .exclude = c(".chain", ".iteration", ".draw", ".row"),
  .prob
)

qi(x, .width = 0.95, .prob, na.rm = FALSE)

hdi(x, .width = 0.95, .prob, na.rm = FALSE)

Mode(x, na.rm = FALSE)

hdci(x, .width = 0.95, na.rm = FALSE)

mean_qi(.data, ..., .width = 0.95)

median_qi(.data, ..., .width = 0.95)

mode_qi(.data, ..., .width = 0.95)

mean_hdi(.data, ..., .width = 0.95)

median_hdi(.data, ..., .width = 0.95)

mode_hdi(.data, ..., .width = 0.95)

mean_hdci(.data, ..., .width = 0.95)

median_hdci(.data, ..., .width = 0.95)

mode_hdci(.data, ..., .width = 0.95)

```

### Arguments

<code>.data</code>	Data frame (or grouped data frame as returned by <code>group_by()</code> ) that contains draws to summarize.
<code>...</code>	Bare column names or expressions that, when evaluated in the context of <code>.data</code> , represent draws to summarize. If this is empty, then by default all columns that are not group columns and which are not in <code>.exclude</code> (by default <code>".chain"</code> , <code>".iteration"</code> , <code>".draw"</code> , and <code>".row"</code> ) will be summarized. This can be list columns.
<code>.width</code>	vector of probabilities to use that determine the widths of the resulting intervals.

	If multiple probabilities are provided, multiple rows per group are generated, each with a different probability interval (and value of the corresponding <code>.width</code> column).
<code>.point</code>	Point summary function, which takes a vector and returns a single value, e.g. <code>mean()</code> , <code>median()</code> , or <code>Mode()</code> .
<code>.interval</code>	Interval function, which takes a vector and a probability ( <code>.width</code> ) and returns a two-element vector representing the lower and upper bound of an interval; e.g. <code>qi()</code> , <code>hdi()</code>
<code>.simple_names</code>	When TRUE and only a single column / vector is to be summarized, use the name <code>.lower</code> for the lower end of the interval and <code>.upper</code> for the upper end. If <code>.data</code> is a vector and this is TRUE, this will also set the column name of the point summary to <code>.value</code> . When FALSE and <code>.data</code> is a data frame, names the lower and upper intervals for each column <code>x.lower</code> and <code>x.upper</code> . When FALSE and <code>.data</code> is a vector, uses the naming scheme <code>y</code> , <code>ymin</code> and <code>ymax</code> (for use with <code>ggplot</code> ).
<code>na.rm</code>	logical value indicating whether NA values should be stripped before the computation proceeds. If FALSE (the default), any vectors to be summarized that contain NA will result in point and interval summaries equal to NA.
<code>.exclude</code>	A character vector of names of columns to be excluded from summarization if no column names are specified to be summarized. Default ignores several meta-data column names used in <code>tidybayes</code> .
<code>.prob</code>	Deprecated. Use <code>.width</code> instead.
<code>x</code>	vector to summarize (for interval functions: <code>qi</code> and <code>hdi</code> )

## Details

If `.data` is a data frame, then `...` is a list of bare names of columns (or expressions derived from columns) of `.data`, on which the point and interval summaries are derived. Column expressions are processed using the tidy evaluation framework (see `rlang::eval_tidy()`).

For a column named `x`, the resulting data frame will have a column named `x` containing its point summary. If there is a single column to be summarized and `.simple_names` is TRUE, the output will also contain columns `.lower` (the lower end of the interval), `.upper` (the upper end of the interval). Otherwise, for every summarized column `x`, the output will contain `x.lower` (the lower end of the interval) and `x.upper` (the upper end of the interval). Finally, the output will have a `.width` column containing the probability for the interval on each output row.

If `.data` includes groups (see e.g. `dplyr::group_by()`), the points and intervals are calculated within the groups.

If `.data` is a vector, `...` is ignored and the result is a data frame with one row per value of `.width` and three columns: `y` (the point summary), `ymin` (the lower end of the interval), `ymax` (the upper end of the interval), and `.width`, the probability corresponding to the interval. This behavior allows `point_interval` and its derived functions (like `median_qi`, `mean_qi`, `mode_hdi`, etc) to be easily used to plot intervals in `ggplot` stats using methods like `stat_eye()`, `stat_halfeye()`, or `stat_summary()`.

`median_qi`, `mode_hdi`, etc are short forms for `point_interval(..., .point = median, .interval = qi)`, etc.

qi yields the quantile interval (also known as the percentile interval or equi-tailed interval) as a 1x2 matrix.

hdi yields the highest-density interval(s) (also known as the highest posterior density interval). **Note:** If the distribution is multimodal, hdi may return multiple intervals for each probability level (these will be spread over rows). You may wish to use hdi (below) instead if you want a single highest-density interval, with the caveat that when the distribution is multimodal hdi is not a highest-density interval. Internally hdi uses `HDInterval::hdi()` with `allowSplit = TRUE` (when multimodal) and with `allowSplit = FALSE` (when not multimodal).

hdi yields the highest-density *continuous* interval. **Note:** If the distribution is multimodal, this may not actually be the highest-density interval (there may be a higher-density discontinuous interval). Internally hdi uses `HDInterval::hdi()` with `allowSplit = FALSE`; see that function for more information on multimodality and continuous versus discontinuous intervals.

## Value

A data frame containing point summaries and intervals, with at least one column corresponding to the point summary, one to the lower end of the interval, one to the upper end of the interval, the width of the interval (`.width`), the type of point summary (`.point`), and the type of interval (`.interval`).

## Author(s)

Matthew Kay

## Examples

```
library(dplyr)
library(ggplot2)

set.seed(123)

rnorm(1000) %>%
  median_qi()

data.frame(x = rnorm(1000)) %>%
  median_qi(x, .width = c(.50, .80, .95))

data.frame(
  x = rnorm(1000),
  y = rnorm(1000, mean = 2, sd = 2)
) %>%
  median_qi(x, y)

data.frame(
  x = rnorm(1000),
  group = "a"
) %>%
  rbind(data.frame(
    x = rnorm(1000, mean = 2, sd = 2),
    group = "b")
```

```

) %>%
  group_by(group) %>%
  median_qi(.width = c(.50, .80, .95))

multimodal_draws = data.frame(
  x = c(rnorm(5000, 0, 1), rnorm(2500, 4, 1))
)

multimodal_draws %>%
  mode_hdi(.width = c(.66, .95))

multimodal_draws %>%
  ggplot(aes(x = x, y = 0)) +
  stat_halfeye(point_interval = mode_hdi, .width = c(.66, .95))

```

---

scales

*Custom ggplot scales for geom\_slabinterval (and derivatives)*


---

### Description

These scales allow more specific aesthetic mappings to be made when using `geom_slabinterval()` and stats/geoms based on it (like eye plots).

### Usage

```

scale_point_colour_discrete(..., aesthetics = "point_colour")

scale_point_color_discrete(..., aesthetics = "point_colour")

scale_point_colour_continuous(
  ...,
  aesthetics = "point_colour",
  guide = "colourbar2"
)

scale_point_color_continuous(
  ...,
  aesthetics = "point_colour",
  guide = "colourbar2"
)

scale_point_fill_discrete(..., aesthetics = "point_fill")

scale_point_fill_continuous(
  ...,
  aesthetics = "point_fill",
  guide = "colourbar2"
)

```

```
)  
scale_point_alpha_continuous(..., range = c(0.1, 1))  
scale_point_alpha_discrete(..., range = c(0.1, 1))  
scale_point_size_continuous(..., range = c(1, 6))  
scale_point_size_discrete(..., range = c(1, 6), na.translate = FALSE)  
scale_interval_colour_discrete(..., aesthetics = "interval_colour")  
scale_interval_color_discrete(..., aesthetics = "interval_colour")  
scale_interval_colour_continuous(  
  ...,  
  aesthetics = "interval_colour",  
  guide = "colourbar2"  
)  
scale_interval_color_continuous(  
  ...,  
  aesthetics = "interval_colour",  
  guide = "colourbar2"  
)  
scale_interval_alpha_continuous(..., range = c(0.1, 1))  
scale_interval_alpha_discrete(..., range = c(0.1, 1))  
scale_interval_size_continuous(..., range = c(1, 6))  
scale_interval_size_discrete(..., range = c(1, 6), na.translate = FALSE)  
scale_interval_linetype_discrete(..., na.value = "blank")  
scale_interval_linetype_continuous(...)  
scale_slab_colour_discrete(..., aesthetics = "slab_colour")  
scale_slab_color_discrete(..., aesthetics = "slab_colour")  
scale_slab_colour_continuous(  
  ...,  
  aesthetics = "slab_colour",  
  guide = "colourbar2"  
)
```

```

scale_slab_color_continuous(
  ...,
  aesthetics = "slab_colour",
  guide = "colourbar2"
)

scale_slab_fill_discrete(..., aesthetics = "slab_fill")

scale_slab_fill_continuous(..., aesthetics = "slab_fill", guide = "colourbar2")

scale_slab_alpha_continuous(
  ...,
  limits = function(l) c(min(0, l[[1]]), l[[2]]),
  range = c(0, 1)
)

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

scale_slab_size_continuous(..., range = c(1, 6))

scale_slab_size_discrete(..., range = c(1, 6), na.translate = FALSE)

scale_slab_linetype_discrete(..., na.value = "blank")

scale_slab_linetype_continuous(...)

scale_slab_shape_discrete(..., solid = TRUE)

scale_slab_shape_continuous(...)

guide_colourbar2(...)

guide_colorbar2(...)

```

### Arguments

...	Arguments passed to underlying scale or guide functions. E.g. <code>scale_point_color_discrete</code> passes arguments to <code>scale_color_discrete()</code> . See those functions for more details.
aesthetics	Names of aesthetics to set scales for.
guide	Guide to use for legends for an aesthetic.
range	a numeric vector of length 2 that specifies the minimum and maximum size of the plotting symbol after transformation.
na.translate	In discrete scales, should we show missing values?
na.value	When <code>na.translate</code> is true, what value should be shown?
limits	One of: <ul style="list-style-type: none"> <li>• NULL to use the default scale range</li> </ul>

- A numeric vector of length two providing limits of the scale. Use NA to refer to the existing minimum or maximum
- A function that accepts the existing (automatic) limits and returns new limits. Note that setting limits on positional scales will **remove** data outside of the limits. If the purpose is to zoom, use the `limit` argument in the coordinate system (see [coord\\_cartesian\(\)](#)).

`solid` Should the shapes be solid, TRUE, or hollow, FALSE?

## Details

The following additional scales / aesthetics are defined for use with [geom\\_slabinterval\(\)](#) and related geoms:

1. `scale_point_color_*` Point color
2. `scale_point_fill_*` Point fill color
3. `scale_point_alpha_*` Point alpha level / opacity
4. `scale_point_size_*` Point size
5. `scale_interval_color_*` Interval line color
6. `scale_interval_alpha_*` Interval alpha level / opacity
7. `scale_interval_size_*` Interval line width
8. `scale_interval_linetype_*` Interval line type
9. `scale_slab_color_*` Slab outline color
10. `scale_slab_fill_*` Slab fill color
11. `scale_slab_alpha_*` Slab alpha level / opacity. The default settings of `scale_slab_alpha_continuous` differ from [scale\\_alpha\\_continuous\(\)](#) and are designed for gradient plots (e.g. [stat\\_gradientinterval\(\)](#)) by ensuring that densities of 0 get mapped to 0 in the output.
12. `scale_slab_size_*` Slab outline line width
13. `scale_slab_linetype_*` Slab outline line type
14. `scale_slab_shape_*` Slab dot shape (for [geom\\_dotsinterval\(\)](#))

See the corresponding scale documentation in ggplot for more information; e.g. [scale\\_color\\_discrete\(\)](#), [scale\\_color\\_continuous\(\)](#), etc.

Other scale functions can be used with the aesthetics/scales defined here by using the `aesthetics` argument to that scale function. For example, to use color brewer scales with the `point_color` aesthetic:

```
scale_color_brewer(..., aesthetics = "point_color")
```

With continuous color scales, you may also need to provide a guide as the default guide does not work properly; this is what `guide_colorbar2` is for:

```
scale_color_distiller(..., guide = "colorbar2", aesthetics = "point_color")
```

## Value

A `ggplot2::Scale` representing one of the aesthetics used to target the appearance of specific parts of composite ggdist geoms. Can be added to a [ggplot\(\)](#) object.

**Author(s)**

Matthew Kay

**See Also**Other ggplot2 scales: [scale\\_color\\_discrete\(\)](#), [scale\\_color\\_continuous\(\)](#), etc.Other ggdist scales: [scale\\_colour\\_ramp](#)**Examples**

```

library(dplyr)
library(ggplot2)

# This plot shows how to set multiple specific aesthetics
# NB it is very ugly and is only for demo purposes.
data.frame(distribution = "Normal(1,2)") %>%
  parse_dist(distribution) %>%
  ggplot(aes(y = distribution, dist = .dist, args = .args)) +
  stat_dist_halfeye(
    shape = 21, # this point shape has a fill and outline
    point_color = "red",
    point_fill = "black",
    point_alpha = .1,
    point_size = 6,
    stroke = 2,
    interval_color = "blue",
    # interval sizes are scaled from [1, 6] onto [0.6, 1.4] by default
    # see the interval_size_range parameter in help("geom_slabinterval")
    interval_size = 8,
    interval_linetype = "dashed",
    interval_alpha = .25,
    # fill sets the fill color of the slab (here the density)
    slab_color = "green",
    slab_fill = "purple",
    slab_size = 3,
    slab_linetype = "dotted",
    slab_alpha = .5
  )

```

---

scale\_colour\_ramp

*Secondary ggplot color scale that ramps from another color*


---

**Description**

This scale creates a secondary scale that modifies the fill or color scale of geoms that support it ([geom\\_lineribbon\(\)](#) and [geom\\_slabinterval\(\)](#)) to "ramp" from a secondary color (by default white) to the primary fill color (determined by the standard color or fill aesthetics).

**Usage**

```

scale_colour_ramp_continuous(
  from = "white",
  ...,
  limits = function(l) c(min(0, l[[1]]), l[[2]]),
  range = c(0, 1),
  aesthetics = "colour_ramp"
)

scale_color_ramp_continuous(
  from = "white",
  ...,
  limits = function(l) c(min(0, l[[1]]), l[[2]]),
  range = c(0, 1),
  aesthetics = "colour_ramp"
)

scale_colour_ramp_discrete(
  from = "white",
  ...,
  range = c(0.2, 1),
  aesthetics = "colour_ramp"
)

scale_color_ramp_discrete(
  from = "white",
  ...,
  range = c(0.2, 1),
  aesthetics = "colour_ramp"
)

scale_fill_ramp_continuous(..., aesthetics = "fill_ramp")

scale_fill_ramp_discrete(..., aesthetics = "fill_ramp")

```

**Arguments**

from	The color to ramp from. Corresponds to 0 on the scale.
...	Arguments passed to underlying scale or guide functions. E.g. <code>scale_colour_ramp_discrete()</code> , passes arguments to <code>discrete_scale()</code> , <code>scale_colour_ramp_continuous()</code> passes arguments to <code>continuous_scale()</code> . See those functions for more details.
limits	One of: <ul style="list-style-type: none"> <li>• NULL to use the default scale range</li> <li>• A numeric vector of length two providing limits of the scale. Use NA to refer to the existing minimum or maximum</li> </ul>

- A function that accepts the existing (automatic) limits and returns new limits. Note that setting limits on positional scales will **remove** data outside of the limits. If the purpose is to zoom, use the `limit` argument in the coordinate system (see `coord_cartesian()`).
- `range` a numeric vector of length 2 that specifies the minimum and maximum values after the scale transformation. These values should be between 0 (the from color) and 1 (the color determined by the fill aesthetic).
- `aesthetics` Names of aesthetics to set scales for.

### Value

A `ggplot2::Scale` representing a scale for the `colour_ramp` and/or `fill_ramp` aesthetics for `ggdist` geoms. Can be added to a `ggplot()` object.

### Author(s)

Matthew Kay

### See Also

Other `ggdist` scales: [scales](#)

### Examples

```
library(dplyr)
library(ggplot2)
library(distributional)

tibble(d = dist_uniform(0, 1)) %>%
  ggplot(aes(y = 0, dist = d)) +
  stat_dist_slab(aes(fill_ramp = stat(x)))

tibble(d = dist_uniform(0, 1)) %>%
  ggplot(aes(y = 0, dist = d)) +
  stat_dist_slab(aes(fill_ramp = stat(x)), fill = "blue") +
  scale_fill_ramp_continuous(from = "red")

# you can invert the order of `range` to change the order of the blend
tibble(d = dist_normal(0, 1)) %>%
  ggplot(aes(y = 0, dist = d)) +
  stat_dist_slab(aes(fill_ramp = stat(cut_cdf_qi(cdf))), fill = "blue") +
  scale_fill_ramp_discrete(from = "red", range = c(1, 0))
```

---

`stat_dist_slabinterval`

*Distribution + interval plots (eye plots, half-eye plots, CCDF barplots, etc) for analytical distributions (ggplot stat)*

---

## Description

Stats for computing distribution functions (densities or CDFs) + intervals for use with `geom_slabinterval()`. Uses the `dist` aesthetic to specify a distribution using objects from the **distributional** package, or using distribution names and `arg1, ... arg9` aesthetics (or `args` as a list column) to specify distribution arguments. See *Details*.

## Usage

```
stat_dist_slabinterval(  
  mapping = NULL,  
  data = NULL,  
  geom = "slabinterval",  
  position = "identity",  
  ...,  
  slab_type = c("pdf", "cdf", "ccdf"),  
  p_limits = c(NA, NA),  
  orientation = NA,  
  limits = NULL,  
  n = 501,  
  .width = c(0.66, 0.95),  
  show_slab = TRUE,  
  show_interval = TRUE,  
  na.rm = FALSE,  
  show.legend = c(size = FALSE),  
  inherit.aes = TRUE  
)
```

```
stat_dist_halfeye(...)
```

```
stat_dist_eye(..., side = "both")
```

```
stat_dist_ccdfinterval(  
  ...,  
  slab_type = "ccdf",  
  justification = 0.5,  
  side = "topleft",  
  normalize = "none"  
)
```

```
stat_dist_cdfinterval(  
  ...,
```

```

    slab_type = "cdf",
    justification = 0.5,
    side = "topleft",
    normalize = "none"
  )

stat_dist_gradientinterval(
  mapping = NULL,
  data = NULL,
  geom = "slabinterval",
  position = "identity",
  ...,
  justification = 0.5,
  thickness = 1,
  show.legend = c(size = FALSE, slab_alpha = FALSE),
  inherit.aes = TRUE
)

stat_dist_pointinterval(..., show_slab = FALSE)

stat_dist_interval(
  mapping = NULL,
  data = NULL,
  geom = "interval",
  position = "identity",
  ...,
  show_slab = FALSE,
  show_point = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)

stat_dist_slab(
  mapping = NULL,
  data = NULL,
  geom = "slab",
  position = "identity",
  ...,
  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	The data to be displayed in this layer. There are three options:

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

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

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

<code>geom</code>	Use to override the default connection between <code>stat_slabinterval</code> and <code>geom_slabinterval()</code>
<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 to <code>layer()</code> . They may also be arguments to the paired geom (e.g., <code>geom_pointinterval()</code> )
<code>slab_type</code>	The type of slab function to calculate: probability density (or mass) function ("pdf"), cumulative distribution function ("cdf"), or complementary CDF ("ccdf").
<code>p_limits</code>	Probability limits (as a vector of size 2) used to determine the lower and upper limits of the slab. E.g., if this is <code>c(.001, .999)</code> , then a slab is drawn for the distribution from the quantile at $p = .001$ to the quantile at $p = .999$ . If the lower (respectively upper) limit is NA, then the lower (upper) limit will be the minimum (maximum) of the distribution's support if it is finite, and <code>0.001</code> ( <code>0.999</code> ) if it is not finite. E.g., if <code>p_limits</code> is <code>c(NA, NA)</code> on a gamma distribution the effective value of <code>p_limits</code> would be <code>c(0, .999)</code> since the gamma distribution is defined on $(0, \text{Inf})$ ; whereas on a normal distribution it would be equivalent to <code>c(.001, .999)</code> since the normal distribution is defined on $(-\text{Inf}, \text{Inf})$ .
<code>orientation</code>	Whether this geom is drawn horizontally ("horizontal") or vertically ("vertical"). The default, NA, automatically detects the orientation based on how the aesthetics are assigned, and should generally do an okay job at this. When horizontal (resp. vertical), the geom uses the y (resp. x) aesthetic to identify different groups, then for each group uses the x (resp. y) aesthetic and the thickness aesthetic to draw a function as an slab, and draws points and intervals horizontally (resp. vertically) using the <code>xmin</code> , <code>x</code> , and <code>xmax</code> (resp. <code>ymin</code> , <code>y</code> , and <code>ymax</code> ) aesthetics. For compatibility with the base ggplot naming scheme for orientation, "x" can be used as an alias for "vertical" and "y" as an alias for "horizontal" (tidybayes had an <code>orientation</code> parameter before ggplot did, and I think the tidybayes naming scheme is more intuitive: "x" and "y" are not orientations and their mapping to orientations is, in my opinion, backwards; but the base ggplot naming scheme is allowed for compatibility).
<code>limits</code>	Manually-specified limits for the slab, as a vector of length two. These limits are combined with those computed based on <code>p_limits</code> as well as the limits defined by the scales of the plot to determine the limits used to draw the slab functions: these limits specify the maximal limits; i.e., if specified, the limits will not be wider than these (but may be narrower). Use NA to leave a limit alone; e.g. <code>limits = c(0, NA)</code> will ensure that the lower limit does not go below 0, but let the upper limit be determined by either <code>p_limits</code> or the scale settings.
<code>n</code>	Number of points at which to evaluate <code>slab_function</code>
<code>.width</code>	The <code>.width</code> argument passed to <code>interval_function</code> or <code>point_interval</code> .

show_slab	Should the slab portion of the geom be drawn? Default TRUE.
show_interval	Should the interval portion of the geom be drawn? Default TRUE.
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend	Should this layer be included in the legends? Default is <code>c(size = FALSE)</code> , unlike most geoms, to match its common use cases. FALSE hides all legends, TRUE shows all legends, and NA shows only those that are mapped (the default for most geoms).
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> .
side	Which side to draw the slab on. "topright", "top", and "right" are synonyms which cause the slab to be drawn on the top or the right depending on if orientation is "horizontal" or "vertical". "bottomleft", "bottom", and "left" are synonyms which cause the slab to be drawn on the bottom or the left depending on if orientation is "horizontal" or "vertical". "topleft" causes the slab to be drawn on the top or the left, and "bottomright" causes the slab to be drawn on the bottom or the right. "both" draws the slab mirrored on both sides (as in a violin plot).
justification	Justification of the interval relative to the slab, where 0 indicates bottom/left justification and 1 indicates top/right justification (depending on orientation). If justification is NULL (the default), then it is set automatically based on the value of side: when side is "top"/"right" justification is set to 0, when side is "bottom"/"left" justification is set to 1, and when side is "both" justification is set to 0.5.
normalize	How to normalize heights of functions input to the thickness aesthetic. If "all" (the default), normalize so that the maximum height across all data is 1; if "panels", normalize within panels so that the maximum height in each panel is 1; if "xy", normalize within the x/y axis opposite the orientation of this geom so that the maximum height at each value of the opposite axis is 1; if "groups", normalize within values of the opposite axis and within groups so that the maximum height in each group is 1; if "none", values are taken as is with no normalization (this should probably only be used with functions whose values are in [0,1], such as CDFs).
thickness	Override for the thickness aesthetic in <code>geom_slabinterval()</code> : the thickness of the slab at each x / y value of the slab (depending on orientation).
show_point	Should the point portion of the geom be drawn? Default TRUE.

## Details

A highly configurable stat for generating a variety of plots that combine a "slab" that describes a distribution plus an interval. Several "shortcut" stats are provided which combine multiple options to create useful geoms, particularly *eye plots* (a combination of a violin plot and interval), *half-eye plots* (a density plus interval), and *CCDF bar plots* (a complementary CDF plus interval).

The shortcut stat names follow the pattern `stat_dist_[name]`.

Stats include:

- `stat_dist_eye`: Eye plots (violin + interval)
- `stat_dist_halfeye`: Half-eye plots (density + interval)
- `stat_dist_ccdfinterval`: CCDF bar plots (CCDF + interval)
- `stat_dist_cdfinterval`: CDF bar plots (CDF + interval)
- `stat_dist_gradientinterval`: Density gradient + interval plots
- `stat_dist_pointinterval`: Point + interval plots
- `stat_dist_interval`: Interval plots

These stats expect a `dist` aesthetic to specify a distribution. This aesthetic can be used in one of two ways:

- `dist` can be any distribution object from the **distributional** package, such as `dist_normal()`, `dist_beta()`, etc. Since these functions are vectorized, other columns can be passed directly to them in an `aes()` specification; e.g. `aes(dist = dist_normal(mu, sigma))` will work if `mu` and `sigma` are columns in the input data frame.
- `dist` can be a character vector giving the distribution name. Then the `arg1`, ... `arg9` aesthetics (or `args` as a list column) specify distribution arguments. Distribution names should correspond to R functions that have "p", "q", and "d" functions; e.g. "norm" is a valid distribution name because R defines the `pnorm()`, `qnorm()`, and `dnorm()` functions for Normal distributions.

See the `parse_dist()` function for a useful way to generate `dist` and `args` values from human-readable distribution specs (like "normal(0,1)"). Such specs are also produced by other packages (like the `brms::get_prior` function in `brms`); thus, `parse_dist()` combined with the stats described here can help you visualize the output of those functions.

## Value

A `ggplot2::Stat` representing a slab or combined slab+interval geometry which can be added to a `ggplot()` object.

## Aesthetics

These stats support the following aesthetics:

- `dist`
- `args`
- `arg1`
- `arg2`
- `arg3`
- `arg4`
- `arg5`
- `arg6`
- `arg7`
- `arg8`

- `arg9`
- `x`
- `y`
- `datatype`
- `thickness`
- `size`
- `group`

In addition, in their default configuration (paired with `geom_slabinterval()`) the following aesthetics are supported by the underlying geom:

- `x`
- `y`
- `datatype`
- `alpha`
- `colour`
- `colour_ramp`
- `linetype`
- `fill`
- `shape`
- `stroke`
- `point_colour`
- `point_fill`
- `point_alpha`
- `point_size`
- `size`
- `interval_colour`
- `interval_alpha`
- `interval_size`
- `interval_linetype`
- `slab_size`
- `slab_colour`
- `slab_fill`
- `slab_alpha`
- `slab_linetype`
- `fill_ramp`
- `ymin`
- `ymax`
- `xmin`

- xmax
- width
- height
- thickness
- group

See examples of some of these aesthetics in action in `vignette("slabinterval")`. Learn more about the sub-geom aesthetics (like `interval_color`) in the [scales](#) documentation. Learn more about basic `ggplot` aesthetics in `vignette("ggplot2-specs")`.

### Computed Variables

- x or y: For slabs, the input values to the slab function. For intervals, the point summary from the interval function. Whether it is x or y depends on orientation
- xmin or ymin: For intervals, the lower end of the interval from the interval function.
- xmax or ymax: For intervals, the upper end of the interval from the interval function.
- f: For slabs, the output values from the slab function (such as the PDF, CDF, or CCDF), determined by `slab_type`.
- pdf: For slabs, the probability density function.
- cdf: For slabs, the cumulative distribution function.

### See Also

See `geom_slabinterval()` for more information on the geom these stats use by default and some of the options they have. See `stat_sample_slabinterval()` for the versions of these stats that can be used on samples. See `vignette("slabinterval")` for a variety of examples of use.

### Examples

```
library(dplyr)
library(ggplot2)
library(distributional)

theme_set(theme_ggdist())

dist_df = tribble(
  ~group, ~subgroup, ~mean, ~sd,
  "a",     "h",       5,    1,
  "b",     "h",       7,    1.5,
  "c",     "h",       8,    1,
  "c",     "i",       9,    1,
  "c",     "j",       7,    1
)

dist_df %>%
  ggplot(aes(x = group, dist = "norm", arg1 = mean, arg2 = sd, fill = subgroup)) +
  stat_dist_eye(position = "dodge")
```

```

# Using functions from the distributional package (like dist_normal()) with the
# dist aesthetic can lead to more compact/expressive specifications

dist_df %>%
  ggplot(aes(x = group, dist = dist_normal(mean, sd), fill = subgroup)) +
  stat_dist_eye(position = "dodge")

# the stat_dist_... family applies a Jacobian adjustment to densities
# when plotting on transformed scales in order to plot them correctly.
# For example, here is a log-Normal distribution plotted on the log
# scale, where it will appear Normal:
data.frame(dist = "lnorm") %>%
  ggplot(aes(y = 1, dist = dist, arg1 = log(10), arg2 = 2*log(10))) +
  stat_dist_halfeye() +
  scale_x_log10(breaks = 10^seq(-5,7, by = 2))

# see vignette("slabinterval") for many more examples.

```

---

stat\_interval

*Multiple uncertainty interval plots (ggplot stat)*


---

## Description

A combination of [stat\\_sample\\_slabinterval\(\)](#) and [geom\\_slabinterval\(\)](#) with sensible defaults. While the corresponding geoms are intended for use on data frames that have already been summarized using a [point\\_interval\(\)](#) function, these stats are intended for use directly on data frames of draws, and will perform the summarization using a [point\\_interval\(\)](#) function.

## Usage

```

stat_interval(
  mapping = NULL,
  data = NULL,
  geom = "interval",
  position = "identity",
  ...,
  orientation = NA,
  interval_function = NULL,
  interval_args = list(),
  point_interval = median_qi,
  .width = c(0.5, 0.8, 0.95),
  show_point = FALSE,
  show_slab = FALSE,
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,

```

```

    .prob,
    fun.data,
    fun.args
  )

```

## 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. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).</p>
geom	Use to override the default connection between <code>stat_slabinterval</code> and <a href="#">geom_slabinterval()</a>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	Other arguments passed to <a href="#">layer()</a> . They may also be arguments to the paired geom (e.g., <a href="#">geom_pointinterval()</a> )
orientation	Whether this geom is drawn horizontally ("horizontal") or vertically ("vertical"). The default, <code>NA</code> , automatically detects the orientation based on how the aesthetics are assigned, and should generally do an okay job at this. When horizontal (resp. vertical), the geom uses the <code>y</code> (resp. <code>x</code> ) aesthetic to identify different groups, then for each group uses the <code>x</code> (resp. <code>y</code> ) aesthetic and the <code>thickness</code> aesthetic to draw a function as an slab, and draws points and intervals horizontally (resp. vertically) using the <code>xmin</code> , <code>x</code> , and <code>xmax</code> (resp. <code>ymin</code> , <code>y</code> , and <code>ymax</code> ) aesthetics. For compatibility with the base <code>ggplot</code> naming scheme for orientation, "x" can be used as an alias for "vertical" and "y" as an alias for "horizontal" (tidybayes had an <code>orientation</code> parameter before <code>ggplot</code> did, and I think the tidybayes naming scheme is more intuitive: "x" and "y" are not orientations and their mapping to orientations is, in my opinion, backwards; but the base <code>ggplot</code> naming scheme is allowed for compatibility).
interval_function	Custom function for generating intervals (for most common use cases the <code>point_interval</code> argument will be easier to use). This function takes a data frame of aesthetics and a <code>.width</code> parameter (a vector of interval widths), and returns a data frame with columns <code>.width</code> (from the <code>.width</code> vector), <code>.value</code> (point summary) and <code>.lower</code> and <code>.upper</code> (endpoints of the intervals, given the <code>.width</code> ). Output will be converted to the appropriate x- or y-based aesthetics depending on the value of orientation. If <code>interval_function</code> is <code>NULL</code> , <code>point_interval</code> is used instead.

interval_args	Additional arguments passed to interval_function or point_interval.
point_interval	A function from the <code>point_interval()</code> family (e.g., <code>median_qi</code> , <code>mean_qi</code> , etc). This function should take in a vector of value, and should obey the <code>.width</code> and <code>.simple_names</code> parameters of <code>point_interval()</code> functions, such that when given a vector with <code>.simple_names = TRUE</code> should return a data frame with variables <code>.value</code> , <code>.lower</code> , <code>.upper</code> , and <code>.width</code> . Output will be converted to the appropriate x- or y-based aesthetics depending on the value of orientation. See the <code>point_interval()</code> family of functions for more information.
<code>.width</code>	The <code>.width</code> argument passed to interval_function or point_interval.
show_point	Should the point portion of the geom be drawn? Default TRUE.
show_slab	Should the slab portion of the geom be drawn? Default TRUE.
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend	Should this layer be included in the legends? Default is <code>c(size = FALSE)</code> , unlike most geoms, to match its common use cases. FALSE hides all legends, TRUE shows all legends, and NA shows only those that are mapped (the default for most geoms).
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> .
<code>.prob</code>	Deprecated. Use <code>.width</code> instead.
fun.data	Deprecated. Use <code>point_interval</code> or <code>interval_function</code> instead.
fun.args	Deprecated. Use <code>interval_args</code> instead.

### Value

A `ggplot2::Stat` representing a multiple interval geometry which can be added to a `ggplot()` object.

### Aesthetics

These stats support the following aesthetics:

- colour
- datatype
- x
- y
- thickness
- group

In addition, in their default configuration (paired with `geom_interval()`) the following aesthetics are supported by the underlying geom:

- x
- y
- datatype

- alpha
- colour
- colour\_ramp
- linetype
- fill
- shape
- stroke
- point\_colour
- point\_fill
- point\_alpha
- point\_size
- size
- interval\_colour
- interval\_alpha
- interval\_size
- interval\_linetype
- slab\_size
- slab\_colour
- slab\_fill
- slab\_alpha
- slab\_linetype
- fill\_ramp
- ymin
- ymax
- xmin
- xmax
- width
- height
- thickness
- group

See examples of some of these aesthetics in action in `vignette("slabinterval")`. Learn more about the sub-geom aesthetics (like `interval_color`) in the [scales](#) documentation. Learn more about basic ggplot aesthetics in `vignette("ggplot2-specs")`.

### See Also

See [geom\\_interval\(\)](#) for the geom versions, intended for use on points and intervals that have already been summarized using a [point\\_interval\(\)](#) function. See [stat\\_pointinterval\(\)](#) for a similar stat intended for point summaries and intervals. See [stat\\_sample\\_slabinterval\(\)](#) for a variety of other stats that combine intervals with densities and CDFs. See [geom\\_slabinterval\(\)](#) for the geom that these geoms wrap. All parameters of that geom are available to these geoms.

**Examples**

```

library(dplyr)
library(ggplot2)

theme_set(theme_ggdist())

data(RankCorr_u_tau, package = "ggdist")

RankCorr_u_tau %>%
  group_by(i) %>%
  ggplot(aes(y = factor(i), x = u_tau)) +
  stat_interval() +
  scale_color_brewer()

RankCorr_u_tau %>%
  group_by(i) %>%
  ggplot(aes(x = factor(i), y = u_tau)) +
  stat_interval() +
  scale_color_brewer()

```

---

stat\_lineribbon

---

*Line + multiple probability ribbon plots (ggplot stat)*


---

**Description**

A combination of [stat\\_slabinterval\(\)](#) and [geom\\_lineribbon\(\)](#) with sensible defaults. While [geom\\_lineribbon](#) is intended for use on data frames that have already been summarized using a [point\\_interval\(\)](#) function, [stat\\_lineribbon](#) is intended for use directly on data frames of draws, and will perform the summarization using a [point\\_interval\(\)](#) function; [stat\\_dist\\_lineribbon](#) is intended for use on analytical distributions through the `dist`, `arg1`, ... `arg9`, and `args` aesthetics.

**Usage**

```

stat_lineribbon(
  mapping = NULL,
  data = NULL,
  geom = "lineribbon",
  position = "identity",
  ...,
  interval_function = NULL,
  interval_args = list(),
  point_interval = median_qi,
  .width = c(0.5, 0.8, 0.95),
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,

```

```

    .prob,
    fun.data,
    fun.args
  )

stat_dist_lineribbon(
  mapping = NULL,
  data = NULL,
  geom = "lineribbon",
  position = "identity",
  ...,
  n = 501,
  .width = c(0.5, 0.8, 0.95),
  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	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 <code>ggplot()</code> . 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. 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. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code> ).
geom	Use to override the default connection between <code>geom_lineribbon</code> and <code>stat_lineribbon</code> .
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	Other arguments passed to <code>layer()</code> . They may also be arguments to the paired geom (e.g., <code>geom_pointinterval()</code> )
interval_function	Custom function for generating intervals (for most common use cases the <code>point_interval</code> argument will be easier to use). This function takes a data frame of aesthetics and a <code>.width</code> parameter (a vector of interval widths), and returns a data frame with columns <code>.width</code> (from the <code>.width</code> vector), <code>.value</code> (point summary) and <code>.lower</code> and <code>.upper</code> (endpoints of the intervals, given the <code>.width</code> ). Output will be converted to the appropriate x- or y-based aesthetics depending on the value of <code>orientation</code> . If <code>interval_function</code> is <code>NULL</code> , <code>point_interval</code> is used instead.
interval_args	Additional arguments passed to <code>interval_function</code> or <code>point_interval</code> .

point_interval	A function from the <code>point_interval()</code> family (e.g., <code>median_qi</code> , <code>mean_qi</code> , etc). This function should take in a vector of value, and should obey the <code>.width</code> and <code>.simple_names</code> parameters of <code>point_interval()</code> functions, such that when given a vector with <code>.simple_names = TRUE</code> should return a data frame with variables <code>.value</code> , <code>.lower</code> , <code>.upper</code> , and <code>.width</code> . Output will be converted to the appropriate x- or y-based aesthetics depending on the value of orientation. See the <code>point_interval()</code> family of functions for more information.
<code>.width</code>	The <code>.width</code> argument passed to <code>interval_function</code> or <code>point_interval</code> .
<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>	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>.prob</code>	Deprecated. Use <code>.width</code> instead.
<code>fun.data</code>	Deprecated. Use <code>point_interval</code> or <code>interval_function</code> instead.
<code>fun.args</code>	Deprecated. Use <code>interval_args</code> instead.
<code>n</code>	Number of points at which to evaluate <code>slab_function</code>

### Value

A `ggplot2::Stat` representing a combined line+uncertainty ribbon geometry which can be added to a `ggplot()` object.

### See Also

See `geom_lineribbon()` for the geom version, intended for use on points and intervals that have already been summarized using a `point_interval()` function. See `stat_pointinterval()` for a similar stat intended for point summaries and intervals.

### Examples

```
library(dplyr)
library(ggplot2)
library(distributional)

tibble(x = 1:10) %>%
  group_by_all() %>%
  do(tibble(y = rnorm(100, .$x))) %>%
  ggplot(aes(x = x, y = y)) +
  stat_lineribbon() +
  scale_fill_brewer()

tibble(
  x = 1:10,
  sd = seq(1, 3, length.out = 10)
```

```

) %>%
  ggplot(aes(x = x, dist = dist_normal(x, sd))) +
  stat_dist_lineribbon() +
  scale_fill_brewer()

```

---

stat\_pointinterval      *Point summary + multiple uncertainty interval plots (ggplot stat)*

---

### Description

A combination of `stat_sample_slabinterval()` and `geom_slabinterval()` with sensible defaults. While the corresponding geoms are intended for use on data frames that have already been summarized using a `point_interval()` function, these stats are intended for use directly on data frames of draws, and will perform the summarization using a `point_interval()` function.

### Usage

```

stat_pointinterval(
  mapping = NULL,
  data = NULL,
  geom = "pointinterval",
  position = "identity",
  ...,
  orientation = NA,
  interval_function = NULL,
  interval_args = list(),
  point_interval = median_qi,
  .width = c(0.66, 0.95),
  show_slab = FALSE,
  na.rm = FALSE,
  show.legend = c(size = FALSE),
  inherit.aes = TRUE,
  .prob,
  fun.data,
  fun.args
)

```

### 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	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 <code>ggplot()</code> .

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

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

geom	Use to override the default connection between <code>stat_slabinterval</code> and <code>geom_slabinterval()</code>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	Other arguments passed to <code>layer()</code> . They may also be arguments to the paired geom (e.g., <code>geom_pointinterval()</code> )
orientation	Whether this geom is drawn horizontally ("horizontal") or vertically ("vertical"). The default, NA, automatically detects the orientation based on how the aesthetics are assigned, and should generally do an okay job at this. When horizontal (resp. vertical), the geom uses the y (resp. x) aesthetic to identify different groups, then for each group uses the x (resp. y) aesthetic and the thickness aesthetic to draw a function as an slab, and draws points and intervals horizontally (resp. vertically) using the <code>xmin</code> , <code>x</code> , and <code>xmax</code> (resp. <code>ymin</code> , <code>y</code> , and <code>ymax</code> ) aesthetics. For compatibility with the base <code>ggplot</code> naming scheme for orientation, "x" can be used as an alias for "vertical" and "y" as an alias for "horizontal" (tidybayes had an orientation parameter before <code>ggplot</code> did, and I think the tidybayes naming scheme is more intuitive: "x" and "y" are not orientations and their mapping to orientations is, in my opinion, backwards; but the base <code>ggplot</code> naming scheme is allowed for compatibility).
interval_function	Custom function for generating intervals (for most common use cases the <code>point_interval</code> argument will be easier to use). This function takes a data frame of aesthetics and a <code>.width</code> parameter (a vector of interval widths), and returns a data frame with columns <code>.width</code> (from the <code>.width</code> vector), <code>.value</code> (point summary) and <code>.lower</code> and <code>.upper</code> (endpoints of the intervals, given the <code>.width</code> ). Output will be converted to the appropriate x- or y-based aesthetics depending on the value of orientation. If <code>interval_function</code> is NULL, <code>point_interval</code> is used instead.
interval_args	Additional arguments passed to <code>interval_function</code> or <code>point_interval</code> .
point_interval	A function from the <code>point_interval()</code> family (e.g., <code>median_qi</code> , <code>mean_qi</code> , etc). This function should take in a vector of value, and should obey the <code>.width</code> and <code>.simple_names</code> parameters of <code>point_interval()</code> functions, such that when given a vector with <code>.simple_names = TRUE</code> should return a data frame with variables <code>.value</code> , <code>.lower</code> , <code>.upper</code> , and <code>.width</code> . Output will be converted to the appropriate x- or y-based aesthetics depending on the value of orientation. See the <code>point_interval()</code> family of functions for more information.
.width	The <code>.width</code> argument passed to <code>interval_function</code> or <code>point_interval</code> .
show_slab	Should the slab portion of the geom be drawn? Default TRUE.
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.

show.legend	Should this layer be included in the legends? Default is <code>c(size = FALSE)</code> , unlike most geoms, to match its common use cases. <code>FALSE</code> hides all legends, <code>TRUE</code> shows all legends, and <code>NA</code> shows only those that are mapped (the default for most geoms).
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> .
.prob	Deprecated. Use <code>.width</code> instead.
fun.data	Deprecated. Use <code>point_interval</code> or <code>interval_function</code> instead.
fun.args	Deprecated. Use <code>interval_args</code> instead.

### Value

A `ggplot2::Stat` representing a point+multiple uncertainty interval geometry which can be added to a `ggplot()` object.

### Aesthetics

These stats support the following aesthetics:

- `datatype`
- `x`
- `y`
- `thickness`
- `size`
- `group`

In addition, in their default configuration (paired with `geom_pointinterval()`) the following aesthetics are supported by the underlying geom:

- `x`
- `y`
- `datatype`
- `alpha`
- `colour`
- `colour_ramp`
- `linetype`
- `fill`
- `shape`
- `stroke`
- `point_colour`
- `point_fill`
- `point_alpha`

- point\_size
- size
- interval\_colour
- interval\_alpha
- interval\_size
- interval\_linetype
- slab\_size
- slab\_colour
- slab\_fill
- slab\_alpha
- slab\_linetype
- fill\_ramp
- ymin
- ymax
- xmin
- xmax
- width
- height
- thickness
- group

See examples of some of these aesthetics in action in `vignette("slabinterval")`. Learn more about the sub-geom aesthetics (like `interval_color`) in the [scales](#) documentation. Learn more about basic `ggplot` aesthetics in `vignette("ggplot2-specs")`.

### See Also

See `geom_pointinterval()` for the geom versions, intended for use on points and intervals that have already been summarized using a `point_interval()` function. See `stat_interval()` for a similar stat intended for intervals without point summaries. See `stat_sample_slabinterval()` for a variety of other stats that combine intervals with densities and CDFs.

See `geom_pointinterval()` for the geom versions, intended for use on points and intervals that have already been summarized using a `point_interval()` function. See `stat_interval()` for a similar stat intended for intervals without point summaries. See `stat_sample_slabinterval()` for a variety of other stats that combine intervals with densities and CDFs. See `geom_slabinterval()` for the geom that these geoms wrap. All parameters of that geom are available to these geoms.

### Examples

```
library(dplyr)
library(ggplot2)
```

```

data(RankCorr_u_tau, package = "ggdist")

RankCorr_u_tau %>%
  ggplot(aes(y = factor(i), x = u_tau)) +
  stat_pointinterval(.width = c(.66, .95))

RankCorr_u_tau %>%
  ggplot(aes(x = factor(i), y = u_tau)) +
  stat_pointinterval(.width = c(.66, .95))

```

---

```
stat_sample_slabinterval
```

*Distribution + interval plots (eye plots, half-eye plots, CCDF barplots, etc) for samples (ggplot stat)*

---

## Description

Stats for computing densities and CDFs + intervals from samples for use with [geom\\_slabinterval\(\)](#). Useful for creating eye plots, half-eye plots, CCDF bar plots etc.

## Usage

```

stat_sample_slabinterval(
  mapping = NULL,
  data = NULL,
  geom = "slabinterval",
  position = "identity",
  ...,
  slab_type = c("pdf", "cdf", "ccdf", "histogram"),
  adjust = 1,
  trim = TRUE,
  breaks = "Sturges",
  outline_bars = FALSE,
  orientation = NA,
  limits = NULL,
  n = 501,
  interval_function = NULL,
  interval_args = list(),
  point_interval = median_qi,
  .width = c(0.66, 0.95),
  na.rm = FALSE,
  show.legend = c(size = FALSE),
  inherit.aes = TRUE
)

stat_halfeye(...)

```

```

stat_eye(..., side = "both")

stat_ccdfinterval(
  ...,
  slab_type = "ccdf",
  justification = 0.5,
  side = "topleft",
  normalize = "none"
)

stat_cdfinterval(
  ...,
  slab_type = "cdf",
  justification = 0.5,
  side = "topleft",
  normalize = "none"
)

stat_gradientinterval(
  mapping = NULL,
  data = NULL,
  geom = "slabinterval",
  position = "identity",
  ...,
  justification = 0.5,
  thickness = 1,
  show.legend = c(size = FALSE, slab_alpha = FALSE),
  inherit.aes = TRUE
)

stat_histinterval(..., slab_type = "histogram")

stat_slab(
  mapping = NULL,
  data = NULL,
  geom = "slab",
  position = "identity",
  ...,
  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	The data to be displayed in this layer. There are three options:

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

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

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

geom	Use to override the default connection between <code>stat_slabinterval</code> and <code>geom_slabinterval()</code>
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
...	Other arguments passed to <code>layer()</code> . They may also be arguments to the paired geom (e.g., <code>geom_pointinterval()</code> )
slab_type	The type of slab function to calculate: probability density (or mass) function ("pdf"), cumulative distribution function ("cdf"), complementary CDF ("ccdf"), or histogram ("histogram").
adjust	If <code>slab_type</code> is "pdf", bandwidth for the density estimator is adjusted by multiplying it by this value. See <code>density()</code> for more information.
trim	If <code>slab_type</code> is "pdf", should the density estimate be trimmed to the range of the input data? Default TRUE.
breaks	If <code>slab_type</code> is "histogram", the breaks parameter that is passed to <code>hist()</code> to determine where to put breaks in the histogram.
outline_bars	If <code>slab_type</code> is "histogram", <code>outline_bars</code> determines if outlines in between the bars are drawn when the <code>slab_color</code> aesthetic is used. If FALSE (the default), the outline is drawn only along the tops of the bars; if TRUE, outlines in between bars are also drawn.
orientation	Whether this geom is drawn horizontally ("horizontal") or vertically ("vertical"). The default, NA, automatically detects the orientation based on how the aesthetics are assigned, and should generally do an okay job at this. When horizontal (resp. vertical), the geom uses the y (resp. x) aesthetic to identify different groups, then for each group uses the x (resp. y) aesthetic and the thickness aesthetic to draw a function as an slab, and draws points and intervals horizontally (resp. vertically) using the <code>xmin</code> , <code>x</code> , and <code>xmax</code> (resp. <code>ymin</code> , <code>y</code> , and <code>ymax</code> ) aesthetics. For compatibility with the base <code>ggplot</code> naming scheme for orientation, "x" can be used as an alias for "vertical" and "y" as an alias for "horizontal" (tidybayes had an <code>orientation</code> parameter before <code>ggplot</code> did, and I think the tidybayes naming scheme is more intuitive: "x" and "y" are not orientations and their mapping to orientations is, in my opinion, backwards; but the base <code>ggplot</code> naming scheme is allowed for compatibility).
limits	Limits for <code>slab_function</code> , as a vector of length two. These limits are combined with those computed by the <code>limits_function</code> as well as the limits defined by the scales of the plot to determine the limits used to draw the slab functions: these limits specify the maximal limits; i.e., if specified, the limits will not be wider than these (but may be narrower). Use NA to leave a limit alone; e.g. <code>limits = c(0, NA)</code> will ensure that the lower limit does not go below 0.

n	Number of points at which to evaluate slab_function
interval_function	Custom function for generating intervals (for most common use cases the point_interval argument will be easier to use). This function takes a data frame of aesthetics and a .width parameter (a vector of interval widths), and returns a data frame with columns .width (from the .width vector), .value (point summary) and .lower and .upper (endpoints of the intervals, given the .width). Output will be converted to the appropriate x- or y-based aesthetics depending on the value of orientation. If interval_function is NULL, point_interval is used instead.
interval_args	Additional arguments passed to interval_function or point_interval.
point_interval	A function from the <a href="#">point_interval()</a> family (e.g., median_qi, mean_qi, etc). This function should take in a vector of value, and should obey the .width and .simple_names parameters of <a href="#">point_interval()</a> functions, such that when given a vector with .simple_names = TRUE should return a data frame with variables .value, .lower, .upper, and .width. Output will be converted to the appropriate x- or y-based aesthetics depending on the value of orientation. See the <a href="#">point_interval()</a> family of functions for more information.
.width	The .width argument passed to interval_function or point_interval.
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend	Should this layer be included in the legends? Default is c(size = FALSE), unlike most geoms, to match its common use cases. FALSE hides all legends, TRUE shows all legends, and NA shows only those that are mapped (the default for most geoms).
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> .
side	Which side to draw the slab on. "topright", "top", and "right" are synonyms which cause the slab to be drawn on the top or the right depending on if orientation is "horizontal" or "vertical". "bottomleft", "bottom", and "left" are synonyms which cause the slab to be drawn on the bottom or the left depending on if orientation is "horizontal" or "vertical". "topleft" causes the slab to be drawn on the top or the left, and "bottomright" causes the slab to be drawn on the bottom or the right. "both" draws the slab mirrored on both sides (as in a violin plot).
justification	Justification of the interval relative to the slab, where 0 indicates bottom/left justification and 1 indicates top/right justification (depending on orientation). If justification is NULL (the default), then it is set automatically based on the value of side: when side is "top"/"right" justification is set to 0, when side is "bottom"/"left" justification is set to 1, and when side is "both" justification is set to 0.5.
normalize	How to normalize heights of functions input to the thickness aesthetic. If "all" (the default), normalize so that the maximum height across all data is 1; if "panels", normalize within panels so that the maximum height in each panel is 1; if "xy", normalize within the x/y axis opposite the orientation of

this geom so that the maximum height at each value of the opposite axis is 1; if "groups", normalize within values of the opposite axis and within groups so that the maximum height in each group is 1; if "none", values are taken as is with no normalization (this should probably only be used with functions whose values are in [0,1], such as CDFs).

**thickness** Override for the thickness aesthetic in `geom_slabinterval()`: the thickness of the slab at each x / y value of the slab (depending on orientation).

## Details

A highly configurable stat for generating a variety of plots that combine a "slab" that summarizes a sample plus an interval. Several "shortcut" stats are provided which combine multiple options to create useful geoms, particularly *eye* plots (a combination of a violin plot and interval), *half-eye* plots (a density plus interval), and *CCDF bar plots* (a complementary CDF plus interval). These can be handy for visualizing posterior distributions in Bayesian inference, amongst other things.

The shortcut stat names follow the pattern `stat_[name]`.

Stats include:

- `stat_eye`: Eye plots (violin + interval)
- `stat_halfeye`: Half-eye plots (density + interval)
- `stat_ccdfinterval`: CCDF bar plots (CCDF + interval)
- `stat_cdfinterval`: CDF bar plots (CDF + interval)
- `stat_gradientinterval`: Density gradient + interval plots
- `stat_histinterval`: Histogram + interval plots
- `stat_pointinterval`: Point + interval plots
- `stat_interval`: Interval plots

## Value

A `ggplot2::Stat` representing a slab or combined slab+interval geometry which can be added to a `ggplot()` object.

## Aesthetics

These stats support the following aesthetics:

- `x`
- `y`
- `datatype`
- `thickness`
- `size`
- `group`

In addition, in their default configuration (paired with `geom_slabinterval()`) the following aesthetics are supported by the underlying geom:

- x
- y
- datatype
- alpha
- colour
- colour\_ramp
- linetype
- fill
- shape
- stroke
- point\_colour
- point\_fill
- point\_alpha
- point\_size
- size
- interval\_colour
- interval\_alpha
- interval\_size
- interval\_linetype
- slab\_size
- slab\_colour
- slab\_fill
- slab\_alpha
- slab\_linetype
- fill\_ramp
- ymin
- ymax
- xmin
- xmax
- width
- height
- thickness
- group

See examples of some of these aesthetics in action in `vignette("slabinterval")`. Learn more about the sub-geom aesthetics (like `interval_color`) in the [scales](#) documentation. Learn more about basic ggplot aesthetics in `vignette("ggplot2-specs")`.

### Computed Variables

- x or y: For slabs, the input values to the slab function. For intervals, the point summary from the interval function. Whether it is x or y depends on orientation
- xmin or ymin: For intervals, the lower end of the interval from the interval function.
- xmax or ymax: For intervals, the upper end of the interval from the interval function.
- f: For slabs, the output values from the slab function (such as the PDF, CDF, or CCDF), determined by slab\_type.
- pdf: For slabs, the probability density function.
- cdf: For slabs, the cumulative distribution function.
- n: For slabs, the number of data points summarized into that slab.

### See Also

See [geom\\_slabinterval\(\)](#) for more information on the geom these stats use by default and some of the options they have. See [stat\\_dist\\_slabinterval\(\)](#) for the versions of these stats that can be used on analytical distributions. See [vignette\("slabinterval"\)](#) for a variety of examples of use.

### Examples

```
library(dplyr)
library(tidyr)
library(ggplot2)

# consider the following example data:
set.seed(1234)
df = tribble(
  ~group, ~subgroup, ~value,
  "a",      "h", rnorm(500, mean = 5),
  "b",      "h", rnorm(500, mean = 7, sd = 1.5),
  "c",      "h", rnorm(500, mean = 8),
  "c",      "i", rnorm(500, mean = 9),
  "c",      "j", rnorm(500, mean = 7)
) %>%
  unnest(value)

# here are vertical eyes:
df %>%
  ggplot(aes(x = group, y = value)) +
  stat_eye()

# note the sample size is not automatically incorporated into the
# area of the densities in case one wishes to plot densities against
# a reference (e.g. a prior generated by a stat_dist_... function).
# But you may wish to account for sample size if using these geoms
# for something other than visualizing posteriors; in which case
# you can use stat(f*n):
df %>%
```

```
ggplot(aes(x = group, y = value)) +
  stat_eye(aes(thickness = stat(f*n)))

# see vignette("slabinterval") for many more examples.
```

---

student\_t

*Scaled and shifted Student's t distribution*


---

### Description

Density, distribution function, quantile function and random generation for the scaled and shifted Student's t distribution, parameterized by degrees of freedom (df), location (mu), and scale (sigma).

### Usage

```
dstudent_t(x, df, mu = 0, sigma = 1, log = FALSE)

pstudent_t(q, df, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)

qstudent_t(p, df, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)

rstudent_t(n, df, mu = 0, sigma = 1)
```

### Arguments

x	vector of quantiles.
df	degrees of freedom (> 0, maybe non-integer). df = Inf is allowed.
mu	Location parameter (median)
sigma	Scale parameter
log	logical; if TRUE, probabilities p are given as log(p).
q	vector of quantiles.
lower.tail	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .
log.p	logical; if TRUE, probabilities p are given as log(p).
p	vector of probabilities.
n	number of observations. If length(n) > 1, the length is taken to be the number required.

### Value

- dstudent\_t gives the density
- pstudent\_t gives the cumulative distribution function (CDF)
- qstudent\_t gives the quantile function (inverse CDF)

- `rstudent_t` generates random draws.

The length of the result is determined by `n` for `rstudent_t`, and is the maximum of the lengths of the numerical arguments for the other functions.

The numerical arguments other than `n` are recycled to the length of the result. Only the first elements of the logical arguments are used.

### See Also

[parse\\_dist\(\)](#) and parsing distribution specs and the [stat\\_dist\\_slabinterval\(\)](#) family of stats for visualizing them.

### Examples

```
library(dplyr)
library(ggplot2)
library(forcats)

expand.grid(
  df = c(3,5,10,30),
  scale = c(1,1.5)
) %>%
  ggplot(aes(y = 0, dist = "student_t", arg1 = df, arg2 = 0, arg3 = scale, color = ordered(df))) +
  stat_dist_slab(p_limits = c(.01, .99), fill = NA) +
  scale_y_continuous(breaks = NULL) +
  facet_grid( ~ scale) +
  labs(
    title = "dstudent_t(x, df, 0, sigma)",
    subtitle = "Scale (sigma)",
    y = NULL,
    x = NULL
  ) +
  theme_ggdist() +
  theme(axis.title = element_text(hjust = 0))
```

---

theme\_ggdist

*Simple, light ggplot2 theme for ggdist and tidybayes*

---

### Description

A simple, relatively minimalist ggplot2 theme, and some helper functions to go with it.

### Usage

```
theme_ggdist()
```

```
theme_tidybayes()
```

```
facet_title_left_horizontal()
facet_title_right_horizontal()
axis_titles_bottom_left()
```

### Details

This is a relatively minimalist ggplot2 theme, intended to be used for making publication-ready plots. It is currently based on `ggplot2::theme_light()`.

A word of warning: this theme may (and very likely will) change in the future as I tweak it to my taste.

`theme_ggdist()` and `theme_tidybayes()` are aliases.

### Value

A named list in the format of `ggplot2::theme()`

### Author(s)

Matthew Kay

### See Also

`ggplot2::theme()`, `ggplot2::theme_set()`

### Examples

```
library(ggplot2)
theme_set(theme_ggdist())
```

---

tidy-format-translators

*Translate between different tidy data frame formats for draws from distributions*

---

### Description

These functions translate ggdist/tidybayes-style data frames to/from different data frame formats (each format using a different naming scheme for its columns).

**Usage**

```
to_broom_names(data)

from_broom_names(data)

to_ggmcmc_names(data)

from_ggmcmc_names(data)
```

**Arguments**

`data`            A data frame to translate.

**Details**

Function prefixed with `to_` translate from the `ggdist/tidybayes` format to another format, functions prefixed with `from_` translate from that format back to the `ggdist/tidybayes` format. Formats include:

`to_broom_names()` / `from_broom_names()`:

- `.variable` <-> `term`
- `.value` <-> `estimate`
- `.prediction` <-> `.fitted`
- `.lower` <-> `conf.low`
- `.upper` <-> `conf.high`

`to_ggmcmc_names()` / `from_ggmcmc_names()`:

- `.chain` <-> `Chain`
- `.iteration` <-> `Iteration`
- `.variable` <-> `Parameter`
- `.value` <-> `value`

**Value**

A data frame with (possibly) new names in some columns, according to the translation scheme described in *Details*.

**Author(s)**

Matthew Kay

**Examples**

```
library(dplyr)

data(RankCorr_u_tau, package = "ggdist")

df = RankCorr_u_tau %>%
  dplyr::rename(.variable = i, .value = u_tau) %>%
  group_by(.variable) %>%
  median_qi(.value)

df

df %>%
  to_broom_names()
```

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