Package 'ggbeeswarm'

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Type Package

Title Categorical Scatter (Violin Point) Plots

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Description Provides two methods of plotting categorical scatter plots such that the arrangement of points within a category reflects the density of data at that region, and avoids over-plotting.

URL https://github.com/eclarke/ggbeeswarm

BugReports https://github.com/eclarke/ggbeeswarm/issues

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License GPL (>= 3)

Depends R (>= 3.5.0), ggplot2 (>= 3.3.0)

Imports beeswarm, lifecycle, vipor, cli

Suggests gridExtra

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NeedsCompilation no

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geom_beeswarm   *Points, jittered to reduce overplotting using the beeswarm package*

Description

The beeswarm geom is a convenient means to offset points within categories to reduce overplotting.
Uses the beeswarm package.

Usage

```
geom_beeswarm(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  ...,
  method = "swarm",
  cex = 1,
  side = 0L,
  priority = "ascending",
  fast = TRUE,
  dodge.width = NULL,
  corral = "none",
  corral.width = 0.9,
  preserve.data.axis = FALSE,
  groupOnX = NULL,
  orientation = NULL,
  beeswarmArgs = list(),
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

Arguments

mapping	Set of aesthetic mappings created by [aes](#) or [aes_](#). If specified and inherit.aes = TRUE (the default), is combined with the default mapping at the top level of the plot. You only need to supply mapping if there isn't a mapping defined for the plot.
data	A data frame. If specified, overrides the default data frame defined at the top level of the plot.
stat	The statistical transformation to use on the data for this layer, as a string.
...	other arguments passed to [ggplot2::layer](#) params argument.
method	Method for arranging points. Options are "swarm" (default), "compactswarm", "square", "hex", and "center". See Details below.

cex	Scaling for adjusting point spacing (see `beeswarm::swarmx()`). Values between 1 (default) and 3 tend to work best.
side	Direction to perform jittering: 0: both directions; 1: to the right or upwards; -1: to the left or downwards.
priority	Method used to perform point layout. Options are `"ascending"` (default), `"descending"`, `"density"`, `"random"`, or `"none"`. See Details below.
fast	If `TRUE` (default), use compiled version of swarm algorithm. This option is ignored for all methods except `"swarm"` and `"compactswarm"`.
dodge.width	Amount by which points from different aesthetic groups will be dodged. This requires that one of the aesthetics is a factor.
corral	Method used to adjust points that would be placed too wide horizontally. Options are `"none"` (default), `"gutter"`, `"wrap"`, `"random"`, and `"omit"`. See Details below.
corral.width	Width of the corral, if not `"none"`. Default is `0.9`.
preserve.data.axis	
	If `TRUE`, prevent `method` from modifying the data axis (default FALSE). See Details for more info.
groupOnX	**[Superseded]** See `orientation`.
orientation	The orientation (i.e., which axis to group on) is inferred from the data. This can be overridden by setting `orientation` to either `"x"` or `"y"`.
beeswarmArgs	**[Deprecated]** No longer used.
na.rm	If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. `borders`.

Details

method: specifies the algorithm used to avoid overlapping points. The default `"swarm"` method places points in increasing order. If a point would overlap with an existing point, it is shifted sideways (along the group axis) by a minimal amount sufficient to avoid overlap.

While the `"swarm"` method places points in a predetermined order, the `"compactswarm"` method uses a greedy strategy to determine which point will be placed next. This often leads to a more tightly-packed layout. The strategy is very simple: on each iteration, a point that can be placed as close as possible to the non-data axis is chosen and placed. If there are two or more equally good points, `priority` is used to break ties.

The other 3 methods first discretise the values along the data axis, in order to create more efficient packing. The `"square"` method places points on a square grid, whereas `"hex"` uses a hexagonal grid. `"centre"`/`"center"` uses a square grid to produce a symmetric swarm. The number of break points for discretisation is determined by a combination of the available plotting area and the `cex` argument.

priority: controls the order in which points are placed, which generally has a noticeable effect on the plot appearance. ″ascending″ gives the 'traditional' beeswarm plot. ″descending″ is the opposite. ″density″ prioritizes points with higher local density. ″random″ places points in a random order. ″none″ places points in the order provided.

corral: By default, swarms from different groups are not prevented from overlapping, i.e. ″corral = ″none″. Thus, datasets that are very large or unevenly distributed may produce ugly overlapping beeswarms. To control runaway points one can use the following methods. ″gutter″ collects runaway points along the boundary between groups. ″wrap″ implement periodic boundaries. ″random″ places runaway points randomly in the region. ″omit″ omits runaway points.

#' **preserve.data.axis:** In some cases, the underlying method may attempt to change the position of points along the ungrouped, or data, axis, in order to keep them from overlapping. To prevent this, set this option to TRUE.

See Also

[geom_quasirandom()](#) an alternative method, [beeswarm::swarmx()](#) how spacing is determined, [ggplot2::geom_point()](#) for regular, unjittered points, [ggplot2::geom_jitter()](#) for jittered points, [ggplot2::geom_boxplot()](#) for another way of looking at the conditional distribution of a variable

Examples

```
# Generate fake data
distro <- data.frame(
  'variable'=rep(c('runif','rnorm'),each=100),
  'value'=c(runif(100, min=-3, max=3), rnorm(100))
)
ggplot2::ggplot(distro,ggplot2::aes(variable, value)) +
  geom_beeswarm(priority='density',size=2.5)
```

---

geom_quasirandom   *Points, jittered to reduce overplotting using the vipor package*

Description

The quasirandom geom is a convenient means to offset points within categories to reduce overplotting. Uses the vipor package.

Usage

```
geom_quasirandom(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  ...,
  method = "quasirandom",
  width = NULL,
  varwidth = FALSE,
```

```
    bandwidth = 0.5,
    nbins = NULL,
    dodge.width = NULL,
    groupOnX = NULL,
    orientation = NULL,
    na.rm = FALSE,
    show.legend = NA,
    inherit.aes = TRUE
)
```

Arguments

mapping	Set of aesthetic mappings created by [aes](#) or [aes_](#). If specified and inherit.aes = TRUE (the default), is combined with the default mapping at the top level of the plot. You only need to supply mapping if there isn't a mapping defined for the plot.
data	A data frame. If specified, overrides the default data frame defined at the top level of the plot.
stat	The statistical transformation to use on the data for this layer, as a string.
...	other arguments passed to [ggplot2::layer](#) params argument.
method	Method used for distributing points. Options are "quasirandom" (default), "pseudorandom", "smiley", "maxout", "frowney", "minout", "tukey", "tukeyDense". See [vipor::offsetSingleGroup()](#) for the details of each method.
width	Maximum amount of spread (default: 0.4)
varwidth	Vary the width by the relative size of each group. (default: FALSE)
bandwidth	the bandwidth adjustment to use when calculating density Smaller numbers (< 1) produce a tighter "fit". (default: 0.5)
nbins	the number of bins used when calculating density (has little effect with quasirandom/random distribution)
dodge.width	Amount by which points from different aesthetic groups will be dodged. This requires that one of the aesthetics is a factor. To disable dodging between groups, set this to NULL. (default: 0)
groupOnX	**[Superseded]** See orientation.
orientation	The orientation (i.e., which axis to group on) is inferred from the data. This can be overridden by setting orientation to either "x" or "y".
na.rm	if FALSE (default), missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. [borders](#).

See Also

vipor::offsetSingleGroup() how spacing is determined, ggplot2::geom_point() for regular, unjittered points, ggplot2::geom_jitter() for jittered points, ggplot2::geom_boxplot() for another way of looking at the conditional distribution of a variable

Examples

```
# Generate fake data
distro <- data.frame(
  'variable'=rep(c('runif','rnorm'),each=100),
  'value'=c(runif(100, min=-3, max=3), rnorm(100))
)
ggplot2::ggplot(distro, ggplot2::aes(variable, value)) +
geom_quasirandom(width=0.1)
```

---

ggbeeswarm   *ggbeeswarm extends ggplot2 with violin point/beeswarm plots*

Description

This package allows plotting of several groups of one dimensional data as a violin point/beeswarm plot in ggplot2 by arranging data points to resemble the underlying distribution. The development version of this package is on https://github.com/eclarke/ggbeeswarm.

Author(s)

Erik Clarke, <erikclarke@gmail.com>

See Also

position_quasirandom(), position_beeswarm()

Examples

```
ggplot2::ggplot(ggplot2::mpg,aes(class, hwy)) + geom_quasirandom()
# Generate fake data
distro <- data.frame(
  'variable'=rep(c('runif','rnorm'),each=100),
  'value'=c(runif(100, min=-3, max=3), rnorm(100))
)
ggplot2::ggplot(distro,aes(variable, value)) + geom_quasirandom()
ggplot2::ggplot(distro,aes(variable, value)) + geom_quasirandom(width=.1)
```

---

position_beeswarm   *Arrange points using the* \link[beeswarm] *package.*

Description

Arrange points using the \link[beeswarm] package.

Usage

```
position_beeswarm(
  method = "swarm",
  cex = 1,
  side = 0L,
  priority = "ascending",
  fast = TRUE,
  orientation = NULL,
  groupOnX = NULL,
  dodge.width = 0,
  corral = "none",
  corral.width = 0.2,
  preserve.data.axis = FALSE
)
```

Arguments

method	Method for arranging points. Options are `"swarm"` (default), `"compactswarm"`, `"square"`, `"hex"`, and `"center"`. See Details below.
cex	Scaling for adjusting point spacing (see `beeswarm::swarmx()`). Values between 1 (default) and 3 tend to work best.
side	Direction to perform jittering: 0: both directions; 1: to the right or upwards; -1: to the left or downwards.
priority	Method used to perform point layout. Options are `"ascending"` (default), `"descending"`, `"density"`, `"random"`, or `"none"`. See Details below.
fast	If TRUE (default), use compiled version of swarm algorithm. This option is ignored for all methods except `"swarm"` and `"compactswarm"`.
orientation	The orientation (i.e., which axis to group on) is inferred from the data. This can be overridden by setting `orientation` to either `"x"` or `"y"`.
groupOnX	**[Superseded]** See `orientation`.
dodge.width	Amount by which points from different aesthetic groups will be dodged. This requires that one of the aesthetics is a factor.
corral	Method used to adjust points that would be placed too wide horizontally. Options are `"none"` (default), `"gutter"`, `"wrap"`, `"random"`, and `"omit"`. See Details below.
corral.width	Width of the corral, if not `"none"`. Default is `0.9`.

preserve.data.axis

> If TRUE, prevent method from modifying the data axis (default FALSE). See Details for more info.

Details

method: specifies the algorithm used to avoid overlapping points. The default "swarm" method places points in increasing order. If a point would overlap with an existing point, it is shifted sideways (along the group axis) by a minimal amount sufficient to avoid overlap.

While the "swarm" method places points in a predetermined order, the "compactswarm" method uses a greedy strategy to determine which point will be placed next. This often leads to a more tightly-packed layout. The strategy is very simple: on each iteration, a point that can be placed as close as possible to the non-data axis is chosen and placed. If there are two or more equally good points, priority is used to break ties.

The other 3 methods first discretise the values along the data axis, in order to create more efficient packing. The "square" method places points on a square grid, whereas "hex" uses a hexagonal grid. "centre"/"center" uses a square grid to produce a symmetric swarm. The number of break points for discretisation is determined by a combination of the available plotting area and the cex argument.

priority: controls the order in which points are placed, which generally has a noticeable effect on the plot appearance. "ascending" gives the 'traditional' beeswarm plot. "descending" is the opposite. "density" prioritizes points with higher local density. "random" places points in a random order. "none" places points in the order provided.

corral: By default, swarms from different groups are not prevented from overlapping, i.e. "corral = "none". Thus, datasets that are very large or unevenly distributed may produce ugly overlapping beeswarms. To control runaway points one can use the following methods. "gutter" collects runaway points along the boundary between groups. "wrap" implement periodic boundaries. "random" places runaway points randomly in the region. "omit" omits runaway points.

#' **preserve.data.axis:** In some cases, the underlying method may attempt to change the position of points along the ungrouped, or data, axis, in order to keep them from overlapping. To prevent this, set this option to TRUE.

See Also

[geom_beeswarm()](), [position_quasirandom()](), [beeswarm::swarmx()]()

Other position adjustments: [offset_beeswarm()](), [position_quasirandom()]()

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position_quasirandom   *Arrange points using quasirandom noise to avoid overplotting*

Description

Arrange points using quasirandom noise to avoid overplotting

Usage

```
position_quasirandom(
  method = "quasirandom",
  width = NULL,
  varwidth = FALSE,
  bandwidth = 0.5,
  nbins = NULL,
  dodge.width = 0,
  orientation = NULL,
  groupOnX = NULL,
  na.rm = FALSE
)
```

Arguments

method	Method used for distributing points. Options are `"quasirandom"` (default), `"pseudorandom"`, `"smiley"`, `"maxout"`, `"frowney"`, `"minout"`, `"tukey"`, `"tukeyDense"`. See `vipor::offsetSingleGroup()` for the details of each method.
width	Maximum amount of spread (default: 0.4)
varwidth	Vary the width by the relative size of each group. (default: FALSE)
bandwidth	the bandwidth adjustment to use when calculating density Smaller numbers (< 1) produce a tighter "fit". (default: 0.5)
nbins	the number of bins used when calculating density (has little effect with quasirandom/random distribution)
dodge.width	Amount by which points from different aesthetic groups will be dodged. This requires that one of the aesthetics is a factor. To disable dodging between groups, set this to NULL. (default: 0)
orientation	The orientation (i.e., which axis to group on) is inferred from the data. This can be overridden by setting `orientation` to either `"x"` or `"y"`.
groupOnX	**[Superseded]** See `orientation`.
na.rm	if FALSE (default), missing values are removed with a warning. If TRUE, missing values are silently removed.

See Also

`vipor::offsetSingleGroup()`, `geom_quasirandom()`

Other position adjustments: `offset_beeswarm()`, `position_beeswarm()`

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