

Package ‘ggbeeswarm’

October 13, 2022

Type Package

Title Categorical Scatter (Violin Point) Plots

Version 0.6.0

Date 2017-08-03

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>

License GPL (>= 2)

Depends R (>= 3.0.0), ggplot2 (>= 2.0)

Imports beeswarm, vipor

Suggests gridExtra

RoxygenNote 6.0.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2017-08-07 13:45:36 UTC

R topics documented:

geom_beeswarm	2
geom_quasirandom	4
ggbeeswarm	6
position_beeswarm	6
position_quasirandom	7

Index	9
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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, priority = c("ascending",
  "descending", "density", "random", "none"), cex = 1, groupOnX = NULL,
  dodge.width = 0, stat = "identity", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE, ...)
```

Arguments

mapping	Set of aesthetic mappings created by aes or aes_ . 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 ggplot . A <code>data.frame</code> , 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 <code>data.frame</code> , and will be used as the layer data.
priority	Method used to perform point layout (see swarmx)
cex	Scaling for adjusting point spacing (see swarmx)
groupOnX	if <code>TRUE</code> then jitter is added to the x axis and if <code>FALSE</code> jitter is added to the y axis. Prior to v0.6.0, the default <code>NULL</code> causes the function to guess which axis is the categorical one based on the number of unique entries in each. This could result in unexpected results when the x variable has few unique values and so in v0.6.0 the default was changed to always jitter on the x axis unless <code>groupOnX=FALSE</code> . Also consider coord_flip .
dodge.width	Amount by which points from different aesthetic groups will be dodged. This requires that one of the aesthetics is a factor.
stat	The statistical transformation to use on the data for this layer, as a string.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.

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

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

Aesthetics

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

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

See Also

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

Examples

```
ggplot2::qplot(class, hwy, data = ggplot2::mpg, geom='beeswarm')
# Generate fake data
distro <- data.frame(
  'variable'=rep(c('runif', 'rnorm'), each=100),
  'value'=c(runif(100, min=-3, max=3), rnorm(100))
)
ggplot2::qplot(variable, value, data = distro, geom='beeswarm')
ggplot2::ggplot(distro, aes(variable, value)) +
  geom_beeswarm(priority='density', cex=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, width = NULL,
  varwidth = FALSE, bandwidth = 0.5, nbins = NULL,
  method = "quasirandom", groupOnX = NULL, dodge.width = 0,
  stat = "identity", position = "quasirandom", na.rm = FALSE,
  show.legend = NA, inherit.aes = TRUE, ...)
```

Arguments

mapping	Set of aesthetic mappings created by aes or aes_ . 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 ggplot . A <code>data.frame</code> , 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 <code>data.frame.</code> , and will be used as the layer data.
width	the maximum amount of spread (default: 0.4)
varwidth	vary the width by the relative size of each group
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)
method	the method used for distributing points (quasirandom, pseudorandom, smiley or frowney)
groupOnX	if <code>TRUE</code> then jitter is added to the x axis and if <code>FALSE</code> jitter is added to the y axis. Prior to v0.6.0, the default <code>NULL</code> causes the function to guess which axis is the categorical one based on the number of unique entries in each. This could result in unexpected results when the x variable has few unique values and so in v0.6.0 the default was changed to always jitter on the x axis unless <code>groupOnX=FALSE</code> . Also consider coord_flip .

dodge.width	Amount by which points from different aesthetic groups will be dodged. This requires that one of the aesthetics is a factor.
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.
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 .
...	other arguments passed on to layer . These are often aesthetics, used to set an aesthetic to a fixed value, like <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.

Aesthetics

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

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

See Also

[offsetX](#) how spacing is determined, [geom_point](#) for regular, unjittered points, [geom_jitter](#) for jittered points, [geom_boxplot](#) for another way of looking at the conditional distribution of a variable

Examples

```
ggplot2::qplot(class, hwy, data = ggplot2::mpg, 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::qplot(variable, value, data = distro, geom = 'quasirandom')
ggplot2::ggplot(distro, 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 by arranging data points to resemble the underlying distribution. The development version of this package is on <http://github.com/eclarke/ggbeeswarm>.

Author(s)

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See Also

[position_quasirandom](#)

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*Violin point-style plots to show overlapping points. x must be discrete.*

Description

Violin point-style plots to show overlapping points. x must be discrete.

Usage

```
position_beeswarm(priority = c("ascending", "descending", "density", "random",
  "none"), cex = 1, groupOnX = NULL, dodge.width = 0)
```

Arguments

priority	Method used to perform point layout (see swarmx)
cex	Scaling for adjusting point spacing (see swarmx)
groupOnX	if TRUE then jitter is added to the x axis and if FALSE jitter is added to the y axis. Prior to v0.6.0, the default NULL causes the function to guess which axis is the categorical one based on the number of unique entries in each. This could result in unexpected results when the x variable has few unique values and so in v0.6.0 the default was changed to always jitter on the x axis unless groupOnX=FALSE. Also consider coord_flip .
dodge.width	Amount by which points from different aesthetic groups will be dodged. This requires that one of the aesthetics is a factor.

See Also

[position_quasirandom](#), [swarmx](#)

Other position adjustments: [position_quasirandom](#)

Examples

```
ggplot2::qplot(class, hwy, data = ggplot2::mpg, position=position_beeswarm())
```

position_quasirandom *Violin point-style plots to show overlapping points. x must be discrete.*

Description

Violin point-style plots to show overlapping points. x must be discrete.

Usage

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

Arguments

width	the maximum amount of spread (default: 0.4)
varwidth	vary the width by the relative size of each group
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)

method	the method used for distributing points (quasirandom, pseudorandom, smiley or frowney)
groupOnX	if TRUE then jitter is added to the x axis and if FALSE jitter is added to the y axis. Prior to v0.6.0, the default NULL causes the function to guess which axis is the categorical one based on the number of unique entries in each. This could result in unexpected results when the x variable has few unique values and so in v0.6.0 the default was changed to always jitter on the x axis unless groupOnX=FALSE. Also consider coord_flip .
dodge.width	Amount by which points from different aesthetic groups will be dodged. This requires that one of the aesthetics is a factor.

See Also[offsetX](#)Other position adjustments: [position_beeswarm](#)**Examples**

```
ggplot2::qplot(class, hwy, data = ggplot2::mpg, position=position_quasirandom())
```

Index

[aes](#), [2](#), [4](#)

[aes_](#), [2](#), [4](#)

[borders](#), [3](#), [5](#)

[coord_flip](#), [2](#), [4](#), [7](#), [8](#)

[fortify](#), [2](#), [4](#)

[geom_beeswarm](#), [2](#)

[geom_boxplot](#), [3](#), [5](#)

[geom_jitter](#), [3](#), [5](#)

[geom_point](#), [3](#), [5](#)

[geom_quasirandom](#), [3](#), [4](#)

[ggbeeswarm](#), [6](#)

[ggbeeswarm-package \(ggbeeswarm\)](#), [6](#)

[ggplot](#), [2](#), [4](#)

[layer](#), [3](#), [5](#)

[offsetX](#), [5](#), [8](#)

[position_beeswarm](#), [6](#), [8](#)

[position_quasirandom](#), [6](#), [7](#), [7](#)

[swarmx](#), [2](#), [3](#), [7](#)