Package 'gghighlight'

June 5, 2022

Type Package

Title Highlight Lines and Points in 'ggplot2'

Version 0.3.3

Description Make it easier to explore data with highlights.

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URL https://github.com/yutannihilation/gghighlight/

BugReports https://github.com/yutannihilation/gghighlight/issues

Depends ggplot2 (>= 3.0.0),
   R (>= 3.4.0)

Imports dplyr (>= 1.0.4),
   ggrepel,
   lifecycle,
   purrr,
   rlang,
   tibble

Suggests knitr,
   rmarkdown,
   sf,
   testthat,
   vdiffr (>= 0.3.0)

VignetteBuilder knitr

RdMacros lifecycle

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.0

Config/testthat/edition 3

R topics documented:

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gghighlight-package   *Highlight Lines and Points in 'ggplot2'*

Description

Make it easier to explore data with highlights.

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gghighlight   *Highlight Data With Predicate*

Description

[Maturing]

gghiglight() highlights (almost) any geoms according to the given predicates.

Usage

```
gghighlight(
  ...,
  n = NULL,
  max_highlight = 5L,
  unhighlighted_params = list(),
  use_group_by = NULL,
  use_direct_label = NULL,
  label_key = NULL,
  label_params = list(fill = "white"),
  keep_scales = FALSE,
  calculate_per_facet = FALSE,
  unhighlighted_colour = NULL
)
```

Arguments

...	Expressions to filter data, which is passed to `dplyr::filter()`.
n	Number of layers to clone.
max_highlight	Max number of series to highlight.
unhighlighted_params	
	Aesthetics (e.g. colour, fill, and size) for unhighlighted geoms. Specifying `colour = NULL` or `fill = NULL` will preserve the original colour.
use_group_by	If TRUE, use `dplyr::group_by()` to evaluate `predicate`.
use_direct_label	
	If TRUE, add labels directly on the plot instead of using a legend.
label_key	Column name for `label` aesthetics.
label_params	A list of parameters, which is passed to `ggrepel::geom_label_repel()`.
keep_scales	If TRUE, keep the original data with `ggplot2::geom_blank()` so that the highlighted plot has the same scale with the data.

calculate_per_facet

> (Experimental) If TRUE, include the facet variables to calculate the grouping; in other words, highlighting is done on each facet individually.

unhighlighted_colour

> (Deprecated) Colour for unhighlighted geoms.

Examples

```
d <- data.frame(
  idx = c(1, 1, 1, 2, 2, 2, 3, 3, 3),
  value = c(1, 2, 3, 10, 11, 12, 9, 10, 11),
  category = rep(c("a", "b", "c"), 3),
  stringsAsFactors = FALSE
)

# Highlight the lines whose max values are larger than 10
ggplot(d, aes(idx, value, colour = category)) +
  geom_line() + gghighlight(max(value) > 10)

# Highlight the points whose values are larger than 10
ggplot(d, aes(idx, value)) +
  geom_point() +
  gghighlight(value > 10, label_key = category)

# Specify the styles for unhighlighted layer
ggplot(d, aes(idx, value, colour = category)) +
  geom_line(size = 5) +
  gghighlight(max(value) > 10,
    unhighlighted_params = list(size = 1)
  )
```

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