

Package ‘ggquickeda’

February 1, 2026

Title Quickly Explore Your Data Using 'ggplot2' and 'table1' Summary Tables

Version 0.3.3

Description Quickly and easily perform exploratory data analysis by uploading your data as a 'csv' file. Start generating insights using 'ggplot2' plots and 'table1' tables with descriptive stats, all using an easy-to-use point and click 'Shiny' interface.

URL <https://github.com/smouksassi/ggquickeda>,
<https://smouksassi.github.io/ggquickeda/>

BugReports <https://github.com/smouksassi/ggquickeda/issues>

Depends R (>= 4.1.0)

Imports colourpicker, dplyr, data.table, DT, Formula, forcats, GGally (>= 2.1.0), ggbeeswarm, ggh4x, ggplot2 (>= 3.4.0), ggpmisc, ggrepel (>= 0.7.0), ggridges, ggpubr, ggstance, glue, gridExtra, Hmisc, markdown, methods, patchwork (>= 1.2.0), plotly, quantreg, rlang, rms, RPostgres, scales, shiny (>= 1.0.4), shinyFiles, shinyjs (>= 1.1), shinyjqui, stringr, survival, survminer, tibble, tidyr, table1 (>= 1.4.2), zoo

Suggests knitr, rmarkdown

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SystemRequirements pandoc with https support

LazyData true

VignetteBuilder knitr

RoxygenNote 7.3.3

Encoding UTF-8

NeedsCompilation no

Author Samer Mouksassi [aut, cre] (ORCID:

<<https://orcid.org/0000-0002-7152-6654>>),

Dean Attali [aut],

James Craig [aut] (implemented bookmarking and created pkgdown website),

Benjamin Rich [aut] (provided summary stats tables table1 tab code),

Michael Sachs [aut] (provided ggkm initial code)

Maintainer Samer Mouksassi <samerbouksassi@gmail.com>
Repository CRAN
Date/Publication 2026-02-01 20:40:02 UTC

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geom_km	<i>Add a Kaplan-Meier survival curve</i>
---------	--

Description

Add a Kaplan-Meier survival curve

Usage

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

Arguments

mapping	Set of aesthetic mappings created by 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. 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. When using a <code>geom_*()</code> function to construct a layer, the <code>stat</code> argument can be used to override the default coupling between geoms and stats. The <code>stat</code> argument accepts the following: • A Stat ggproto subclass, for example <code>StatCount</code>. • A string naming the stat. To give the stat as a string, strip the function name of the <code>stat_</code> prefix. For example, to use <code>stat_count()</code>, give the stat as <code>"count"</code>. • For more information and other ways to specify the stat, see the layer stat documentation.
position	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The <code>position</code> argument accepts the following: • The result of calling a position function, such as <code>position_jitter()</code>. This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the <code>position_</code> prefix. For example, to use <code>position_jitter()</code>, give the position as <code>"jitter"</code>. • For more information and other ways to specify the position, see the layer position documentation.
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. It can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use <code>TRUE</code> . If <code>NA</code> , all levels are shown in legend, but unobserved levels are omitted.
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. annotation_borders() .
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.

... Other arguments passed on to `layer()`'s `params` argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the `position` argument, or aesthetics that are required can *not* be passed through ... Unknown arguments that are not part of the 4 categories below are ignored.

- Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, `colour = "red"` or `linewidth = 3`. The geom's documentation has an **Aesthetics** section that lists the available options. The 'required' aesthetics cannot be passed on to the `params`. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data.
- When constructing a layer using a `stat_*()` function, the ... argument can be used to pass on parameters to the geom part of the layer. An example of this is `stat_density(geom = "area", outline.type = "both")`. The geom's documentation lists which parameters it can accept.
- Inversely, when constructing a layer using a `geom_*()` function, the ... argument can be used to pass on parameters to the stat part of the layer. An example of this is `geom_area(stat = "density", adjust = 0.5)`. The stat's documentation lists which parameters it can accept.
- The `key_glyph` argument of `layer()` may also be passed on through ... This can be one of the functions described as **key glyphs**, to change the display of the layer in the legend.

Aesthetics

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

- **x** The survival/censoring times. This is automatically mapped by `stat_km()`
- **y** The survival probability estimates. This is automatically mapped by `stat_km()` smallest level in sort order is assumed to be 0, with a warning.
- `alpha`
- `color`
- `linetype`
- `size`

See Also

The default stat for this geom is `stat_km()` see that documentation for more options to control the underlying statistical transformation.

Examples

```
library(ggplot2)
set.seed(123)
sex <- rbinom(250, 1, .5)
df <- data.frame(time = exp(rnorm(250, mean = sex)), status = rbinom(250, 1, .75), sex = sex)
ggplot(df, aes(time = time, status = status, color = factor(sex))) + geom_km()
```

geom_kmband

*Add confidence bands to a Kaplan-Meier survival curve***Description**

Add confidence bands to a Kaplan-Meier survival curve

Usage

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

Arguments

- | | |
|---------|---|
| mapping | Set of aesthetic mappings created by 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 | <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 ggplot().</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 fortify() 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> |
| stat | <p>The statistical transformation to use on the data for this layer. When using a <code>geom_*()</code> function to construct a layer, the <code>stat</code> argument can be used to override the default coupling between geoms and stats. The <code>stat</code> argument accepts the following:</p> <ul style="list-style-type: none"> • A Stat ggproto subclass, for example <code>StatCount</code>. • A string naming the stat. To give the stat as a string, strip the function name of the <code>stat_</code> prefix. For example, to use <code>stat_count()</code>, give the stat as <code>"count"</code>. • For more information and other ways to specify the stat, see the layer stat documentation. |

position	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The position argument accepts the following: • The result of calling a position function, such as <code>position_jitter()</code>. This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the <code>position_</code> prefix. For example, to use <code>position_jitter()</code>, give the position as "jitter". • For more information and other ways to specify the position, see the layer position documentation.
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. To include legend keys for all levels, even when no data exists, use TRUE. If NA, all levels are shown in legend, but unobserved levels are omitted.
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>annotation_borders()</code>.
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
...	Other arguments passed on to <code>layer()</code>'s <code>params</code> argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the position argument, or aesthetics that are required can <i>not</i> be passed through ... Unknown arguments that are not part of the 4 categories below are ignored. • Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, <code>colour = "red"</code> or <code>linewidth = 3</code>. The geom's documentation has an Aesthetics section that lists the available options. The 'required' aesthetics cannot be passed on to the params. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data. • When constructing a layer using a <code>stat_*()</code> function, the ... argument can be used to pass on parameters to the geom part of the layer. An example of this is <code>stat_density(geom = "area", outline.type = "both")</code>. The geom's documentation lists which parameters it can accept. • Inversely, when constructing a layer using a <code>geom_*()</code> function, the ... argument can be used to pass on parameters to the stat part of the layer. An example of this is <code>geom_area(stat = "density", adjust = 0.5)</code>. The stat's documentation lists which parameters it can accept. • The <code>key_glyph</code> argument of <code>layer()</code> may also be passed on through ... This can be one of the functions described as key glyphs, to change the display of the layer in the legend.

Aesthetics

geom_kmband understands the following aesthetics (required aesthetics are in bold):

- x The survival/censoring times. This is automatically mapped by `stat_kmband()`
- y The survival probability estimates. This is automatically mapped by `stat_kmband()` smallest level in sort order is assumed to be 0, with a warning
- alpha
- color
- linetype
- linewidth

See Also

The default stat for this geom is `stat_kmband()`. See that documentation for more options to control the underlying statistical transformation.

Examples

```
library(ggplot2)
sex <- rbinom(250, 1, .5)
df <- data.frame(time = exp(rnorm(250, mean = sex)), status = rbinom(250, 1, .75), sex = sex)
ggplot(df, aes(time = time, status = status, color = factor(sex), fill = factor(sex))) +
  geom_km() + geom_kmband()
```

geom_kmticks

Add tick marks to a Kaplan-Meier survival curve

Description

Adds tickmarks at the times when there are censored observations but no events

Usage

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

Arguments

mapping	Set of aesthetic mappings created by 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. 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. When using a <code>geom_*()</code> function to construct a layer, the <code>stat</code> argument can be used to override the default coupling between geoms and stats. The <code>stat</code> argument accepts the following: • A Stat ggproto subclass, for example <code>StatCount</code>. • A string naming the stat. To give the stat as a string, strip the function name of the <code>stat_</code> prefix. For example, to use <code>stat_count()</code>, give the stat as <code>"count"</code>. • For more information and other ways to specify the stat, see the layer stat documentation.
position	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The <code>position</code> argument accepts the following: • The result of calling a position function, such as <code>position_jitter()</code>. This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the <code>position_</code> prefix. For example, to use <code>position_jitter()</code>, give the position as <code>"jitter"</code>. • For more information and other ways to specify the position, see the layer position documentation.
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. It can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use <code>TRUE</code> . If <code>NA</code> , all levels are shown in legend, but unobserved levels are omitted.
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. annotation_borders() .
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.

... Other arguments passed on to `layer()`'s `params` argument. These arguments broadly fall into one of 4 categories below. Notably, further arguments to the `position` argument, or aesthetics that are required can *not* be passed through ... Unknown arguments that are not part of the 4 categories below are ignored.

- Static aesthetics that are not mapped to a scale, but are at a fixed value and apply to the layer as a whole. For example, `colour = "red"` or `linewidth = 3`. The geom's documentation has an **Aesthetics** section that lists the available options. The 'required' aesthetics cannot be passed on to the `params`. Please note that while passing unmapped aesthetics as vectors is technically possible, the order and required length is not guaranteed to be parallel to the input data.
- When constructing a layer using a `stat_*()` function, the ... argument can be used to pass on parameters to the geom part of the layer. An example of this is `stat_density(geom = "area", outline.type = "both")`. The geom's documentation lists which parameters it can accept.
- Inversely, when constructing a layer using a `geom_*()` function, the ... argument can be used to pass on parameters to the stat part of the layer. An example of this is `geom_area(stat = "density", adjust = 0.5)`. The stat's documentation lists which parameters it can accept.
- The `key_glyph` argument of `layer()` may also be passed on through ... This can be one of the functions described as [key glyphs](#), to change the display of the layer in the legend.

Aesthetics

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

- `x` The survival/censoring times. This is automatically mapped by `stat_kmticks()`
- `y` The survival probability estimates. This is automatically mapped by `stat_kmticks()` smallest level in sort order is assumed to be 0, with a warning
- `alpha`
- `color`
- `linetype`
- `size`

See Also

The default stat for this geom is `stat_kmticks` see that documentation for more options to control the underlying statistical transformation.

Examples

```
library(ggplot2)
sex <- rbinom(250, 1, .5)
df <- data.frame(time = exp(rnorm(250, mean = sex)), status = rbinom(250, 1, .75), sex = sex)
ggplot(df, aes(time = time, status = status, color = factor(sex), group = factor(sex))) +
  geom_km() + geom_kmticks(col="black")
```

ggcontinuousexpdist	<i>Create a continuous fit vs exposure(s) plot replaced by ggresponseexpdist</i>
---------------------	--

Description

Produces a logistic fit plot with a facetable exposures/quantiles/distributions in ggplot2

Usage

```
ggcontinuousexpdist(
  data = effICGI,
  response = "response",
  endpoint = "Endpoint",
  model_type = c("linear", "loess", "none"),
  DOSE = "DOSE",
  color_fill = "DOSE",
  fit_by_color_fill = FALSE,
  exposure_metrics = c("AUC", "CMAx"),
  exposure_metric_split = c("median", "tertile", "quartile", "none"),
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  exposure_distribution = c("distributions", "linerranges", "boxplots", "none"),
  exposure_distribution_percent = TRUE,
  exposure_distribution_percent_text_size = 5,
  dose_plac_value = "Placebo",
  xlab = "Exposure Values",
  ylab = "Response",
  points_alpha = 0.2,
  points_show = TRUE,
  mean_obs_byexptile = TRUE,
  mean_obs_byexptile_plac = TRUE,
  mean_obs_byexptile_group = "none",
  mean_text_size = 5,
  mean_obs_bydose = TRUE,
  mean_obs_bydose_plac = FALSE,
  N_text_show = TRUE,
  N_text_size = 5,
  N_text_ypos = c("with means", "top"),
  N_text_sep = "\n",
  binlimits_show = TRUE,
  binlimits_text_size = 5,
  binlimits_ypos = -Inf,
  binlimits_color = "#B3B3B80",
  dist_position_scaler = 0.2,
  dist_offset = 0,
  dist_scale = 0.9,
```

```

    lineranges_ypos = -1,
    lineranges_dodge = 1,
    lineranges_doselabel = FALSE,
    proj_bydose = TRUE,
    yproj = TRUE,
    yproj_xpos = 0,
    yproj_dodge = 0.2,
    yaxis_position = c("left", "right"),
    facet_formula = NULL,
    theme_certara = TRUE,
    return_list = FALSE
  )

```

Arguments

<code>data</code>	Data to use with multiple endpoints stacked into response (values), Endpoint(endpoint name)
<code>response</code>	name of the column holding the response values
<code>endpoint</code>	name of the column holding the name/key of the endpoint default to Endpoint
<code>model_type</code>	type of the trend fit one of "linear", "loess", "none"
<code>DOSE</code>	name of the column holding the DOSE values default to DOSE
<code>color_fill</code>	name of the column to be used for color/fill default to DOSE column
<code>fit_by_color_fill</code>	fit split by color? default FALSE
<code>exposure_metrics</code>	name(s) of the column(s) to be stacked into expname exptile and split into exposure_metric_split
<code>exposure_metric_split</code>	one of "median", "tertile", "quartile", "none"
<code>exposure_metric_soc_value</code>	special exposure code for standard of care default -99
<code>exposure_metric_plac_value</code>	special exposure code for placebo default 0
<code>exposure_distribution</code>	one of distributions, lineranges, boxplots or none
<code>exposure_distribution_percent</code>	show percent of distribution between binlimits TRUE/FALSE
<code>exposure_distribution_percent_text_size</code>	distribution percentages text size default to 5
<code>dose_plac_value</code>	string identifying placebo in DOSE column
<code>xlab</code>	text to be used as x axis label
<code>ylab</code>	text to be used as y axis label
<code>points_alpha</code>	alpha transparency for points

points_show show the observations TRUE/FALSE
 mean_obs_byexptile observed mean by exptile TRUE/FALSE
 mean_obs_byexptile_plac observed mean by exptile placebo TRUE/FALSE
 mean_obs_byexptile_group additional grouping for exptile means default none
 mean_text_size mean text size default to 5
 mean_obs_bydose observed mean by dose TRUE/FALSE
 mean_obs_bydose_plac observed mean by placebo dose TRUE/FALSE
 N_text_show show the N by exptile TRUE/FALSE
 N_text_size N by exposure text size default to 5
 N_text_ypos y position for N two text elements the first for by exptile and the second for by dose/color options include with means top bottom
 N_text_sep character string to separate N from mean default \n
 binlimits_show show the binlimits vertical lines TRUE/FALSE
 binlimits_text_size binlimits text size default to 5
 binlimits_ypos binlimits y position default to -Inf
 binlimits_color binlimits text color default to alpha("gray70",0.5)
 dist_position_scaler space occupied by the distribution default to 0.2
 dist_offset offset where the distribution position starts default to 0
 dist_scale scaling parameter for ggridges default to 0.9
 lineranges_ypos where to put the lineranges -1
 lineranges_dodge lineranges vertical dodge value 1
 lineranges_doselabel TRUE/FALSE
 proj_bydose project the predictions on logistic curve TRUE/FALSE
 yproj project the predictions on y axis TRUE/FALSE
 yproj_xpos y projection x position 0
 yproj_dodge y projection dodge value 0.2
 yaxis_position where to put y axis "left" or "right"
 facet_formula facet formula to be use otherwise endpoint ~ expname
 theme_certara apply certara colors and format for strips and default colour/fill
 return_list What to return if True a list of the datasets and plot is returned instead of only the plot

Examples

```
## Not run:
# Example 1
library(ggplot2)
library(patchwork)
effICGI <- logistic_data |>
dplyr::filter(!is.na(ICGI7))|>
dplyr::filter(!is.na(AUC))
effICGI$DOSE <- factor(effICGI$DOSE,
                      levels=c("0", "600", "1200", "1800", "2400"),
                      labels=c("Placebo", "600 mg", "1200 mg", "1800 mg", "2400 mg"))
effICGI$STUDY <- factor(effICGI$STUDY)
effICGI <- tidyr::gather(effICGI, Endpoint, response, ICGI7, BRLS)
a <- ggcontinuousexpdist(data = effICGI |> dplyr::filter(Endpoint == "ICGI7"),
                        response = "response",
                        endpoint = "Endpoint",
                        exposure_metrics = c("AUC"),
                        exposure_metric_split = c("quartile"),
                        exposure_metric_soc_value = -99,
                        exposure_metric_plac_value = 0,
                        dist_position_scaler = 1, dist_offset = -1 ,
                        yproj_xpos = -20 ,
                        yproj_dodge = 20 ,
                        exposure_distribution = "distributions",
                        mean_obs_bydose_plac = TRUE,
                        mean_obs_byexptile_plac=FALSE,
                        return_list = FALSE
                        )

b <- ggcontinuousexpdist(data = effICGI |> dplyr::filter(Endpoint == "BRLS"),
                        response = "response",
                        endpoint = "Endpoint",
                        exposure_metrics = c("AUC"),
                        exposure_metric_split = c("quartile"),
                        exposure_metric_soc_value = -99,
                        exposure_metric_plac_value = 0,
                        dist_position_scaler = 4.2, dist_offset = 5 ,
                        yproj_xpos = -20 ,
                        yproj_dodge = 20 ,
                        exposure_distribution = "distributions",
                        mean_obs_bydose_plac = TRUE,
                        mean_obs_byexptile_plac=FALSE,
                        return_list = FALSE)

(a / b) +
plot_layout(guides = "collect") &
theme(legend.position = "top")

#Example 2 loess fit
effICGI$SEX <- as.factor(effICGI$SEX)
ggcontinuousexpdist(data = effICGI |>
  dplyr::filter(Endpoint == "ICGI7"),
  model_type = "loess",
```

```

    response = "response",
    endpoint = "Endpoint",
    color_fill = "SEX",
    exposure_metrics = c("AUC"),
    exposure_metric_split = c("quartile"),
    exposure_metric_soc_value = -99,
    exposure_metric_plac_value = 0,
    dist_position_scaler = 1, dist_offset = -1 ,
    yproj_xpos = -20 ,
    yproj_dodge = 20 ,
    exposure_distribution = "linerranges",
    linerranges_ypos = -0.2,
    linerranges_dodge = 0.2,
    linerranges_doselabel = TRUE)

#Example 3
library(ggplot2)
library(patchwork)
effICGI <- logistic_data |>
  dplyr::filter(!is.na(ICGI7))|>
  dplyr::filter(!is.na(AUC))
effICGI$DOSE <- factor(effICGI$DOSE,
  levels=c("0", "600", "1200","1800","2400"),
  labels=c("Placebo", "600 mg", "1200 mg","1800 mg","2400 mg"))
effICGI$STUDY <- factor(effICGI$STUDY)
effICGI <- tidyr::gather(effICGI,Endpoint,response,PRLS,BRLS)
effICGI$Endpoint2 <- effICGI$Endpoint
ggcontinuousexpdist(data = effICGI ,
  model_type = "loess",
  response = "response",
  endpoint = "Endpoint",
  color_fill = "Endpoint2",
  fit_by_color_fill = TRUE,
  exposure_metrics = c("AUC"),
  exposure_metric_split = c("quartile"),
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  yproj = FALSE, points_show = FALSE,
  exposure_distribution = "none",
  N_text_sep = " | N = ",
  N_text_ypos = c("bottom","with means"),
  binlimits_color = "red",
  binlimits_ypos = 10,
  facet_formula = ~expname)

## End(Not run)

```

ggkmrisktable

Create a Kaplan-Meier plot with risk table

Description

Produces a km plot with a facettable risk table in ggplot2

Usage

```

ggkmrisktable(
  data = lung_long,
  time = "time",
  status = "DV",
  endpoint = "Endpoint",
  groupvar1 = "Endpoint",
  groupvar2 = "expname",
  groupvar3 = "none",
  exposure_metrics = c("age", "ph.karno"),
  exposure_metric_split = c("median", "tertile", "quartile", "none"),
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  exposure_metric_soc_name = "SOC",
  exposure_metric_plac_name = "Placebo",
  show_exptile_values = FALSE,
  show_exptile_values_pos = c("left", "right"),
  show_exptile_values_textsize = 5,
  show_exptile_values_order = c("default", "reverse"),
  color_fill = "exptile",
  linetype = "exptile",
  xlab = "Time of follow_up",
  ylab = "Overall survival probability",
  nrisk_table_plot = TRUE,
  nrisk_table_variables = c("n.risk", "pct.risk", "n.event", "cum.n.event", "n.censor"),
  nrisk_table_breaktimeby = NULL,
  nrisk_table_textsize = 4,
  nrisk_position_scaler = 0.2,
  nrisk_position_dodge = 0.2,
  nrisk_offset = 0,
  nrisk_filterout0 = FALSE,
  km_logrank_pvalue = FALSE,
  km_logrank_pvalue_pos = c("left", "right"),
  km_logrank_pvalue_textsize = 5,
  km_logrank_pvalue_cutoff = 0.001,
  km_logrank_pvalue_digits = 3,
  km_trans = c("identity", "event", "cumhaz", "cloglog"),
  km_linewidth = 1,
  km_ticks = TRUE,
  km_band = TRUE,
  km_conf_int = 0.95,
  km_conf_type = c("log", "plain", "log", "log-log", "logit", "none"),
  km_conf_lower = c("usual", "peto", "modified"),
  km_median = c("none", "median", "medianci", "table"),
  km_median_table_pos = c("left", "right"),
  km_median_table_order = c("default", "reverse"),
  km_median_table_y_multiplier = 0.09,
  km_yaxis_position = c("left", "right"),

```

```

facet_formula = NULL,
facet_ncol = NULL,
facet_strip_position = c("top", "top", "top", "top"),
theme_certara = TRUE,
return_list = FALSE
)

```

Arguments

<code>data</code>	Data to use with multiple endpoints stacked into time, status, endpoint name
<code>time</code>	name of the column holding the time to event information default to <code>time</code>
<code>status</code>	name of the column holding the event information default to <code>DV</code>
<code>endpoint</code>	name of the column holding the name/key of the endpoint default to <code>Endpoint</code>
<code>groupvar1</code>	name of the column to group by, default <code>Endpoint</code>
<code>groupvar2</code>	name of the column to group by in addition to <code>groupvar1</code> , default <code>expname</code>
<code>groupvar3</code>	name of the column to group by in addition to <code>groupvar1</code> and <code>groupvar2</code> , default <code>"none"</code>
<code>exposure_metrics</code>	name(s) of the column(s) to be stacked into <code>expname</code> <code>exptile</code> and split into <code>exposure_metric_split</code>
<code>exposure_metric_split</code>	one of <code>"median"</code> , <code>"tertile"</code> , <code>"quartile"</code> , <code>"none"</code>
<code>exposure_metric_soc_value</code>	special exposure code for standard of care default <code>-99</code>
<code>exposure_metric_plac_value</code>	special exposure code for placebo default <code>0</code>
<code>exposure_metric_soc_name</code>	soc name default to <code>"soc"</code>
<code>exposure_metric_plac_name</code>	placebo name default to <code>"placebo"</code>
<code>show_exptile_values</code>	<code>FALSE</code>
<code>show_exptile_values_pos</code>	<code>"left"</code> or <code>"right"</code>
<code>show_exptile_values_textsize</code>	default to <code>5</code>
<code>show_exptile_values_order</code>	the order of the entries <code>"default"</code> or <code>"reverse"</code>
<code>color_fill</code>	name of the column to be used for color/fill default to <code>exptile</code>
<code>linetype</code>	name of the column to be used for linetype default to <code>exptile</code>
<code>xlab</code>	text to be used as x axis label
<code>ylab</code>	text to be used as y axis label
<code>nrisk_table_plot</code>	<code>TRUE</code>

```

nrisk_table_variables
    one or more from: "n.risk", "pct.risk", "n.event", "cum.n.event", "n.censor"
nrisk_table_breaktimeby
    NULL
nrisk_table_textsize
    4
nrisk_position_scaler
    0.2
nrisk_position_dodge
    0.2, negative values will reverse the order
nrisk_offset    0
nrisk_filterout0
    filter out data when number at risk becomes zero default to FALSE
km_logrank_pvalue
    FALSE
km_logrank_pvalue_pos
    "left" or "right"
km_logrank_pvalue_textsize
    pvalue text size default to 5
km_logrank_pvalue_cutoff
    pvalue below which to print as p < cutoff
km_logrank_pvalue_digits
    pvalue ndigits for round function
km_trans
    one of "identity", "event", "cumhaz", "cloglog"
km_linewidth
    linewidth for the km curves default to 1
km_ticks
    TRUE
km_band
    TRUE
km_conf_int
    0.95
km_conf_type
    default one of "log", "plain", "log-log", "logit", "none"
km_conf_lower
    one of "usual", "peto", "modified"
km_median
    add median survival information one of "none", "median", "medianci", "table"
km_median_table_pos
    when table is chosen where to put it "left" or "right"
km_median_table_order
    when table is chosen the order of the entries "default" or "reverse"
km_median_table_y_multiplier
    enable to control where the median table start default to 0.09
km_yaxis_position
    where to put y axis on "left" or "right"
facet_formula
    facet formula to be used otherwise ~ groupvar1 + groupvar2 + groupvar3
facet_ncol
    NULL if not specified the automatic waiver will be used
facet_strip_position
    position in sequence for the variable used in faceting default to c("top", "top", "top", "top")
theme_certara
    apply certara colors and format for strips and default colour/fill
return_list
    What to return if True a list of the datasets and plot is returned instead of only
    the plot

```

Examples

```
library(tidyr)
# Example 1
lung_long <- survival::lung |>
  dplyr::mutate(status = ifelse(status==1,0,1)) |>
  tidyr::gather(Endpoint,DV,status) |>
  dplyr::filter(!is.na(ph.karno))|>
  dplyr::filter(!is.na(pat.karno))|>
  dplyr::filter(!is.na(ph.ecog))
lung_long$ph.ecog <- ifelse(lung_long$ph.ecog>1,2,lung_long$ph.ecog)
lung_long$ph.ecog <- as.factor(lung_long$ph.ecog )
lung_long$ph.ecog <- as.factor(lung_long$ph.ecog )
lung_long$facetdum <- "(all)"

ggkmrisktable(data = lung_long, time= "time", status = "DV",
  exposure_metrics =c("age","ph.karno"),
  exposure_metric_split = "tertile",
  color_fill = "exptile",
  linetype = "expname",
  groupvar1 = "Endpoint",
  groupvar2 = "exptile",
  xlab = "Time of follow_up",
  ylab ="Overall survival probability",
  nrisk_table_variables = c("n.risk","n.event"),
  km_median = "medianci",
  km_band = FALSE,
  nrisk_table_breaktimeby = 200,
  facet_ncol = 3)

#Example 2
ggkmrisktable(data = lung_long, time= "time", status = "DV",
  exposure_metrics =c("age","ph.karno"),
  exposure_metric_split = "quartile",
  color_fill = "exptile",
  linetype = "none",
  groupvar1 = "Endpoint",
  groupvar2 = "exptile",
  xlab = "Time of follow_up",
  ylab ="Overall survival probability",
  nrisk_table_variables = c("cum.n.event","pct.risk","n.censor"),
  km_median = "medianci",
  km_band = TRUE,
  km_trans = "event",
  show_exptile_values = TRUE,
  show_exptile_values_pos = "right",
  nrisk_table_breaktimeby = 200,
  facet_ncol = 3,
  facet_formula = ~expname)

## Not run:
#Example 3
ggkmrisktable(data = lung_long, time = "time", status = "DV",
  exposure_metrics =c("ph.karno","pat.karno"),
  exposure_metric_split = "median",
```

```

        color_fill = "exptile",
        linetype = "exptile",
        groupvar1 = "Endpoint",
        groupvar2 = "expname",
        xlab = "Time of follow_up",
        ylab = "Overall survival probability",
        nrisk_table_variables = c("n.event"),
        km_trans = "event",
        km_median = "table",
        km_median_table_pos = "right",
        km_logrank_pvalue = TRUE,
        km_logrank_pvalue_cutoff = 0.0001,
        km_logrank_pvalue_digits = 3,
        km_band = TRUE,
        nrisk_table_breaktimeby = 200,
        facet_ncol = 3,
        facet_formula = ~expname)

#Example 4
ggkmrisktable(data=lung_long,
              exposure_metrics = c("ph.karno","age"),
              exposure_metric_split = "median",
              time = "time",
              status = "DV",
              color_fill = "ph.ecog",
              linetype = "ph.ecog",
              groupvar1 = "Endpoint",
              groupvar2 = "expname",
              groupvar3 = "exptile",
              nrisk_filterout0 = FALSE,
              nrisk_table_breaktimeby = 200,
              km_logrank_pvalue = TRUE,
              km_median = "table",
              km_median_table_pos = "left",
              facet_formula = ~expname+exptile)

#Example 5

ggkmrisktable(data=lung_long,
              exposure_metrics = c("ph.karno","age"),
              exposure_metric_split = "none",
              color_fill = "none",
              linetype = "none",
              nrisk_table_variables = c("n.risk", "pct.risk", "n.event", "cum.n.event", "n.censor"),
              km_median = "table",
              nrisk_position_scaler = 0.1
              )

## End(Not run)

```

Description

Produces a logistic fit plot with a facetable exposures/quantiles/distributions in ggplot2

Usage

```
gglogisticexpdist(
  data = effICGI,
  response = "response",
  endpoint = "Endpoint",
  model_type = c("logistic"),
  DOSE = "DOSE",
  color_fill = "DOSE",
  logistic_by_color_fill = FALSE,
  exposure_metrics = c("AUC", "CMAx"),
  exposure_metric_split = c("median", "tertile", "quartile", "none"),
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  exposure_distribution = c("distributions", "linerranges", "boxplots", "none"),
  exposure_distribution_percent = TRUE,
  exposure_distribution_percent_text_size = 5,
  dose_plac_value = "Placebo",
  xlab = "Exposure Values",
  ylab = "Probability of Response",
  points_alpha = 0.2,
  points_show = TRUE,
  prob_obs_byexptile = TRUE,
  prob_obs_byexptile_plac = TRUE,
  prob_obs_byexptile_group = "none",
  prob_text_size = 5,
  prob_obs_bydose = TRUE,
  prob_obs_bydose_plac = FALSE,
  Nresp_Ntot_show = TRUE,
  Nresp_Ntot_size = 5,
  Nresp_Ntot_ypos = c("with percentages", "top"),
  Nresp_Ntot_sep = "/",
  binlimits_show = TRUE,
  binlimits_text_size = 5,
  binlimits_ypos = 0,
  binlimits_color = "#B3B3B380",
  dist_position_scaler = 0.2,
  dist_offset = 0,
  dist_scale = 0.9,
  linerranges_ypos = 0.2,
  linerranges_dodge = 0.15,
  linerranges_doselabel = FALSE,
  proj_bydose = TRUE,
  yproj = TRUE,
  yproj_xpos = 0,
```

```

    yproj_dodge = 0.2,
    yaxis_position = c("left", "right"),
    facet_formula = NULL,
    theme_certara = TRUE,
    return_list = FALSE
  )

```

Arguments

<code>data</code>	Data to use with multiple endpoints stacked into response (values), Endpoint(endpoint name)
<code>response</code>	name of the column holding the response values
<code>endpoint</code>	name of the column holding the name/key of the endpoint default to Endpoint
<code>model_type</code>	type of the trend fit one of "logistic", "none"
<code>DOSE</code>	name of the column holding the DOSE values default to DOSE
<code>color_fill</code>	name of the column to be used for color/fill default to DOSE column
<code>logistic_by_color_fill</code>	fit split by color? default FALSE
<code>exposure_metrics</code>	name(s) of the column(s) to be stacked into expname exptile and split into exposure_metric_split
<code>exposure_metric_split</code>	one of "median", "tertile", "quartile", "none"
<code>exposure_metric_soc_value</code>	special exposure code for standard of care default -99
<code>exposure_metric_plac_value</code>	special exposure code for placebo default 0
<code>exposure_distribution</code>	one of distributions, lineranges, boxplots or none
<code>exposure_distribution_percent</code>	show percent of distribution between binlimits TRUE/FALSE
<code>exposure_distribution_percent_text_size</code>	distribution percentages text size default to 5
<code>dose_plac_value</code>	string identifying placebo in DOSE column
<code>xlab</code>	text to be used as x axis label
<code>ylab</code>	text to be used as y axis label
<code>points_alpha</code>	alpha transparency for points
<code>points_show</code>	show the observations TRUE/FALSE
<code>prob_obs_byexptile</code>	observed probability by exptile TRUE/FALSE
<code>prob_obs_byexptile_plac</code>	observed probability by exptile placebo TRUE/FALSE

prob_obs_byexptile_group additional grouping for exptile probabilities default none
 prob_text_size probability text size default to 5
 prob_obs_bydose observed probability by dose TRUE/FALSE
 prob_obs_bydose_plac observed probability by placebo dose TRUE/FALSE
 Nresp_Ntot_show show N responders/Ntotal ? TRUE/FALSE
 Nresp_Ntot_size N responders/Ntotal text size default to 5
 Nresp_Ntot_ypos y position for N responders/Ntotal two text elements the first for by exptile and the second for by dose/color options include with percentages top bottom
 Nresp_Ntot_sep character string to separate N responders/ Ntotal default /
 binlimits_show show the binlimits vertical lines TRUE/FALSE
 binlimits_text_size binlimits text size default to 5
 binlimits_ypos binlimits y position default to 0
 binlimits_color binlimits text color default to alpha("gray70",0.5)
 dist_position_scaler space occupied by the distribution default to 0.2
 dist_offset offset where the distribution position starts default to 0
 dist_scale scaling parameter for ggridges default to 0.9
 lineranges_ypos where to put the lineranges -1
 lineranges_dodge lineranges vertical dodge value 1
 lineranges_doselabel TRUE/FALSE
 proj_bydose project the probabilities on logistic curve TRUE/FALSE
 yproj project the probabilities on y axis TRUE/FALSE
 yproj_xpos y projection x position 0
 yproj_dodge y projection dodge value 0.2
 yaxis_position where to put y axis "left" or "right"
 facet_formula facet formula to be use otherwise endpoint ~ expname
 theme_certara apply certara colors and format for strips and default colour/fill
 return_list What to return if True a list of the datasets and plot is returned instead of only the plot

Examples

```
## Not run:
# Example 1
library(ggplot2)
effICGI <- logistic_data |>
dplyr::filter(!is.na(ICGI))|>
dplyr::filter(!is.na(AUC))
effICGI$DOSE <- factor(effICGI$DOSE,
  levels=c("0", "600", "1200","1800","2400"),
  labels=c("Placebo", "600 mg", "1200 mg","1800 mg","2400 mg"))
effICGI$STUDY <- factor(effICGI$STUDY)
effICGI$ICGI2 <- effICGI$ICGI
effICGI <- tidyr::gather(effICGI,Endpoint,response,ICGI,ICGI2)
gglogisticexpdist(data = effICGI |>
  dplyr::filter(Endpoint=="ICGI"),
  response = "response",
  endpoint = "Endpoint",
  exposure_metrics = c("AUC"),
  exposure_metric_split = c("quartile"),
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  exposure_distribution ="distributions",
  yproj_xpos = -15,
  yproj_dodge = 10,
  dist_position_scaler = 0.1,
  dist_offset = -0.1,
  Nresp_Ntot_ypos = c("with percentages","bottom"),
  prob_obs_bydose_plac = TRUE,
  prob_obs_byexptile_plac = FALSE,
  prob_obs_byexptile_group = "none",
  binlimits_ypos = 0.3,
  binlimits_color = "#475c6b",
  points_alpha= 0.8)

# Example 2
gglogisticexpdist(data = effICGI |>
  dplyr::filter(Endpoint=="ICGI"),
  response = "response",
  endpoint = "Endpoint",
  exposure_metrics = c("CMAX"),
  exposure_metric_split = c("tertile"),
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  exposure_distribution ="linranges",
  linranges_ypos = -0.2,
  linranges_dodge = 0.2,
  linranges_doselabel = TRUE,
  Nresp_Ntot_ypos = c("with percentages","bottom"),
  prob_obs_bydose_plac = TRUE,
  prob_obs_byexptile_plac = FALSE,
  prob_obs_byexptile_group = "none",yproj_xpos = -1,
  yproj_dodge = 2,
```

```

    binlimits_color = "#475c6b",
    dist_position_scaler = 0.1)

#' # Example 3
library(ggh4x)
gglogisticexpdist(data = effICGI |>
  dplyr::filter(Endpoint=="ICGI"),
  response = "response",
  endpoint = "Endpoint",
  DOSE = "DOSE",
  exposure_metrics = c("AUC"),
  exposure_metric_split = c("quartile"),
  exposure_distribution = "distributions",
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  dist_position_scaler = 0.15)+
  facet_grid2(Endpoint~expname+DOSE2,scales="free",
  margins = "DOSE2",strip = strip_nested())

# Example 4
effICGI$SEX <- as.factor(effICGI$SEX)
gglogisticexpdist(data = effICGI |>
  dplyr::filter(Endpoint=="ICGI"),
  response = "response",
  endpoint = "Endpoint",
  DOSE = "DOSE",
  color_fill = "SEX",
  exposure_metrics = c("AUC"),
  exposure_metric_split = c("quartile"),
  exposure_distribution = "distributions",
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  lineranges_ypos = -0.2,
  yproj_xpos = -10,
  yproj_dodge = 20,
  prob_text_size = 6,
  binlimits_text_size = 6,
  Nresp_Ntot_show = TRUE,
  dist_position_scaler = 0.15)+
  ggplot2::scale_x_continuous(breaks = seq(0,350,50),
  expand = ggplot2::expansion(add= c(0,0),mult=c(0,0)))+
  ggplot2::coord_cartesian(xlim = c(-30,355))+
  ggplot2::facet_grid(Endpoint~expname+color_fill2, margins = "color_fill2" )

#Example 4b
effICGI$SEX <- as.factor(effICGI$SEX)
gglogisticexpdist(data = effICGI |>
  dplyr::filter(Endpoint == "ICGI"),
  response = "response",
  endpoint = "Endpoint",
  color_fill = "SEX",
  exposure_metrics = c("AUC"),
  exposure_metric_split = c("quartile"),
  exposure_metric_soc_value = -99,

```

```

exposure_metric_plac_value = 0,
dist_position_scaler = 1, dist_offset = -1 ,
yproj_xpos = -20 ,
yproj_dodge = 20 ,
exposure_distribution = "linerranges",
linerranges_doselabel = TRUE)

```

#Example 5

```

gglogisticexpdist(data = effICGI |> dplyr::filter(Endpoint=="ICGI"),
  response = "response",
  endpoint = "Endpoint",
  DOSE = "DOSE",
  exposure_metrics = c("AUC"),
  exposure_metric_split = c("quartile"),
  exposure_distribution = "distributions",
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  dist_position_scaler = 0.15)+
  facet_grid(Endpoint~expname+exptile,scales="free",
  margins = "exptile")

```

#Example 6

```

a <- gglogisticexpdist(data = effICGI, #
  response = "response",
  endpoint = "Endpoint",
  DOSE = "DOSE",yproj_dodge = 36,
  exposure_metrics = c("AUC"),
  exposure_metric_split = c("quartile"),
  exposure_distribution = "linerranges",
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0) +
  facet_grid(Endpoint~expname,switch = "both")
b <- gglogisticexpdist(data = effICGI, #
  response = "response",
  endpoint = "Endpoint",
  DOSE = "DOSE",yproj_dodge = 2,
  exposure_metrics = c("CMAx"),
  exposure_metric_split = c("quartile"),
  exposure_distribution = "linerranges",
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  yaxis_position = "right")+
  facet_grid(Endpoint~expname,switch = "x")+
  theme(strip.text.y.right = element_blank(),
  strip.background.y = element_blank())
library(patchwork)
(a | b ) +
  plot_layout(guides = "collect", axes = "collect_x")&
  theme(legend.position = "top")

```

#Example 7

```

effICGI <- logistic_data |>
dplyr::filter(!is.na(ICGI))|>
dplyr::filter(!is.na(AUC))

```

```

effICGI$DOSE <- factor(effICGI$DOSE,
                      levels=c("0", "600", "1200", "1800", "2400"),
                      labels=c("Placebo", "600 mg", "1200 mg", "1800 mg", "2400 mg"))
effICGI$STUDY <- factor(effICGI$STUDY)
effICGI$ICGI2 <- ifelse(effICGI$ICGI7 < 4, 1, 0)
effICGI$ICGI3 <- ifelse(effICGI$ICGI7 < 5, 1, 0)

effICGI <- tidyr::gather(effICGI, Endpoint, response, ICGI, ICGI2, ICGI3)
effICGI$endpointcol2 <- effICGI$Endpoint
effICGI$endpointcol3 <- effICGI$Endpoint
gglogisticexpdist(data = effICGI,
                  response = "response",
                  endpoint = "Endpoint",
                  exposure_metrics = c("AUC"),
                  exposure_metric_split = c("tertile"),
                  exposure_metric_soc_value = -99,
                  exposure_metric_plac_value = 0,
                  color_fill = "endpointcol2",
                  logistic_by_color_fill = TRUE,
                  Nresp_Ntot_show = TRUE,
                  Nresp_Ntot_ypos = c("with percentages", "bottom"),
                  prob_obs_byexptile = FALSE,
                  prob_obs_byexptile_group = "endpointcol3",
                  prob_obs_byexptile_plac = FALSE,
                  prob_obs_bydose_plac = TRUE,
                  binlimits_color = "#475c6b",
                  exposure_distribution = "distributions",
                  prob_obs_bydose = TRUE,
                  proj_bydose = FALSE,
                  yproj = FALSE,
                  dist_position_scaler = 0.1,
                  dist_offset = -0.1) +
  facet_grid(expname~Endpoint, scales="free_x")
#Example 8
gglogisticexpdist(data = effICGI,
                  response = "response",
                  endpoint = "endpointcol2",
                  exposure_metrics = c("AUC"),
                  exposure_metric_split = c("quartile"),
                  exposure_metric_soc_value = -99,
                  exposure_metric_plac_value = 0,
                  color_fill = "Endpoint",
                  logistic_by_color_fill = TRUE,
                  Nresp_Ntot_show = FALSE, points_show = FALSE,
                  prob_obs_byexptile = TRUE,
                  prob_obs_byexptile_group = "endpointcol3",
                  prob_obs_byexptile_plac = TRUE,
                  prob_obs_bydose = FALSE,
                  prob_obs_bydose_plac = FALSE,
                  binlimits_color = "#475c6b",
                  exposure_distribution = "distributions",
                  proj_bydose = FALSE,
                  yproj = FALSE,

```

```

        dist_position_scaler = 0.1,
        dist_offset = -0.1)+
  facet_grid(expname~., scales="free_x")

## End(Not run)

```

ggresponseexpdist	<i>Create a general fit vs exposure(s) plot</i>
-------------------	---

Description

Produces a fit as per model_type plot with a facettable exposures/quantiles/distributions in ggplot2

Usage

```

ggresponseexpdist(
  data = dplyr::filter(logistic_data, !is.na(ICGI)),
  response = "response",
  endpoint = "Endpoint",
  model_type = c("loess", "linear", "logistic", "none"),
  DOSE = "DOSE",
  color_fill = "DOSE",
  fit_by_color_fill = FALSE,
  exposure_metrics = c("AUC", "CMAx"),
  exposure_metric_split = c("median", "tertile", "quartile", "none"),
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  exposure_metric_soc_name = "SOC",
  exposure_metric_plac_name = "Placebo",
  exposure_distribution = c("distributions", "linerranges", "boxplots", "none"),
  exposure_distribution_percent = c("none", "%", "N (%)", "N"),
  exposure_distribution_Ntotal = c("none", "left", "right"),
  exposure_distribution_percent_text_size = 5,
  dose_plac_value = "Placebo",
  xlab = "Exposure Values",
  ylab = "Response",
  points_alpha = 0.2,
  points_show = TRUE,
  mean_obs_byexptile = TRUE,
  mean_obs_byexptile_plac = TRUE,
  mean_obs_byexptile_text_size = 5,
  mean_obs_byexptile_group = "none",
  mean_obs_bydose = FALSE,
  mean_obs_bydose_plac = FALSE,
  mean_obs_bydose_text_size = 5,
  N_byexptile_ypos = c("with means", "top", "bottom", "none"),
  N_bydose_ypos = c("with means", "top", "bottom", "none"),

```

```

N_text_size = 5,
N_text_sep = NULL,
binlimits_show = TRUE,
binlimits_text_size = 5,
binlimits_ypos = 0,
binlimits_color = "#B3B3B380",
dist_position_scaler = 0.2,
dist_offset = 0,
dist_scale = 0.9,
linerranges_ypos = NULL,
linerranges_dodge = NULL,
linerranges_doselabel = FALSE,
linerranges_Ntotal = c("none", "left", "right"),
proj_bydose = FALSE,
yproj = FALSE,
yproj_xpos = 0,
yproj_dodge = 0.2,
yaxis_position = c("left", "right"),
facet_formula = NULL,
theme_certara = TRUE,
color_legend_title = "",
fill_legend_title = "",
linetype_legend_title = "",
shape_legend_title = "",
combine_fill_linetype_legend = TRUE,
legend_order = c("model", "color", "linetype", "shape"),
return_list = FALSE
)

```

Arguments

data	Data to use with multiple endpoints stacked into response (values), Endpoint(endpoint name)
response	name of the column holding the response values
endpoint	name of the column holding the name/key of the endpoint default to Endpoint
model_type	type of the trend fit one of "loess", "linear", "logistic", "none"
DOSE	name of the column holding the DOSE/regimen values default to DOSE should be a factor
color_fill	name of the column to be used for color/fill default to DOSE column should be a factor
fit_by_color_fill	split fit by color/fill? default FALSE
exposure_metrics	name(s) of the column(s) to be stacked into expname exptile and split into exposure_metric_split
exposure_metric_split	one of "median", "tertile", "quartile", "none"

exposure_metric_soc_value
 special exposure code for standard of care default -99
 exposure_metric_plac_value
 special exposure code for placebo default 0
 exposure_metric_soc_name
 soc name default to "soc"
 exposure_metric_plac_name
 placebo name default to "placebo"
 exposure_distribution
 one of distributions, lineranges, boxplots or none
 exposure_distribution_percent
 show N/percent of distribution between binlimits one of "%", "N (%)", "N", "none"
 exposure_distribution_Ntotal
 show Ntotal by dose level next to the distribution one of "left", "right", "none"
 exposure_distribution_percent_text_size
 distribution percentages text size default to 5
 dose_plac_value
 string identifying placebo in DOSE column
 xlab
 text to be used as x axis label
 ylab
 text to be used as y axis label
 points_alpha
 alpha transparency for points
 points_show
 show the observations TRUE/FALSE
 mean_obs_byexptile
 observed mean by exptile TRUE/FALSE
 mean_obs_byexptile_plac
 observed mean by exptile placebo TRUE/FALSE
 mean_obs_byexptile_text_size
 by exptile mean text size default to 5
 mean_obs_byexptile_group
 additional grouping for exptile means default none
 mean_obs_bydose
 observed mean by dose TRUE/FALSE
 mean_obs_bydose_plac
 observed mean by placebo dose TRUE/FALSE
 mean_obs_bydose_text_size
 by dose mean text size default to 5
 N_byexptile_ypos
 N responders/Ntotal y position by exptile one of with means top bottom none
 N_bydose_ypos
 N responders/Ntotal y position by dose/color one of with means top bottom none
 N_text_size
 N responders/Ntotal text size default to 5
 N_text_sep
 character string to separate N responders/Ntotal or N/mean defaults to / otherwise \n

binlimits_show show the binlimits vertical lines TRUE/FALSE
 binlimits_text_size
 binlimits text size default to 5
 binlimits_ypos binlimits y position default to -Inf
 binlimits_color
 binlimits text color default to alpha("gray70",0.5)
 dist_position_scaler
 space occupied by the distribution default to 0.2
 dist_offset offset where the distribution position starts default to 0
 dist_scale scaling parameter for ggridges default to 0.9
 lineranges_ypos
 where to put the lineranges -1
 lineranges_dodge
 lineranges vertical dodge value 1
 lineranges_doselabel
 TRUE/FALSE
 lineranges_Ntotal
 show Ntotal by dose level next to the lineranges one of "left", "right", "none"
 proj_bydose project the predictions on the fit curve TRUE/FALSE
 yproj project the predictions on y axis TRUE/FALSE
 yproj_xpos y projection x position 0
 yproj_dodge y projection dodge value 0.2
 yaxis_position where to put y axis "left" or "right"
 facet_formula facet formula to be use otherwise endpoint ~ expname
 theme_certara apply certara colors and format for strips and default colour/fill
 color_legend_title
 text for colour legend title
 fill_legend_title
 text for fill legend title
 linetype_legend_title
 text for linetype legend title
 shape_legend_title
 text for shape legend title
 combine_fill_linetype_legend
 defaults to true
 legend_order Legend order. A four-element vector with the following items ordered in your desired order: "model", "color", "linetype", "shape". if an item is absent the legend will be omitted.
 return_list What to return if True a list of the datasets and plot is returned instead of only the plot

Examples

```
# Example 1
library(ggplot2)
effICGI <- logistic_data |>
dplyr::filter(!is.na(ICGI))|>
dplyr::filter(!is.na(AUC))
effICGI$DOSE <- factor(effICGI$DOSE,
                      levels=c("0", "600", "1200", "1800", "2400"),
                      labels=c("Placebo", "600 mg", "1200 mg", "1800 mg", "2400 mg"))
effICGI$STUDY <- factor(effICGI$STUDY)
effICGI$ICGI2 <- effICGI$ICGI
effICGI <- tidyr::gather(effICGI, Endpoint, response, ICGI, ICGI2)

ggresponseexpdist(data = effICGI |>
dplyr::filter(Endpoint=="ICGI"),
model_type = "loess",
exposure_metrics = c("AUC", "CMAx"),
legend_order = c("color", "shape", "model"),
color_legend_title = "Dose\nLevels")

## Not run:
# Example 2
ggresponseexpdist(data = effICGI |>
dplyr::filter(Endpoint=="ICGI"),
model_type = "logistic",
exposure_metrics = c("AUC", "CMAx"),
exposure_distribution = "boxplots")

# Example 3
ggresponseexpdist(data = effICGI|>
dplyr::filter(Endpoint=="ICGI"),
model_type = "linear",
exposure_metrics = c("AUC", "WT"),
exposure_distribution = "linerranges")

# Example 4
ggresponseexpdist(data = effICGI |>
  dplyr::filter(Endpoint=="ICGI"),
  response = "response",
  endpoint = "Endpoint",
  model_type = "loess",
  DOSE = "DOSE",
  color_fill = "DOSE",
  exposure_metrics = c("AUC", "CMAx"),
  exposure_metric_split = c("tertile"),
  exposure_metric_soc_value = -99,
  exposure_metric_plac_value = 0,
  exposure_distribution = "distributions",
  exposure_distribution_Ntotal="right",
  N_byexptile_ypos = "top",
  mean_obs_bydose = TRUE,
  mean_obs_bydose_text_size = 0,
```

```

      mean_obs_byexptile_text_size = 5,
      N_bydose_ypos = "none",
      N_text_sep = "/",
      binlimits_color = "#475c6b",
      binlimits_ypos = 0.2,
      points_alpha= 0.1)

# Example 5
effICGI <- logistic_data |>
dplyr::filter(!is.na(ICGI))|>
dplyr::filter(!is.na(AUC))
effICGI$DOSE <- factor(effICGI$DOSE,
                      levels=c("0", "600", "1200", "1800", "2400"),
                      labels=c("Placebo", "600 mg", "1200 mg", "1800 mg", "2400 mg"))
effICGI$STUDY <- factor(effICGI$STUDY)
effICGI$ICGI2 <- ifelse(effICGI$ICGI7 < 4,1,0)
effICGI$ICGI3 <- ifelse(effICGI$ICGI7 < 5,1,0)

effICGI <- tidyr::gather(effICGI,Endpoint,response,ICGI,ICGI2,ICGI3)
effICGI$endpointcol2 <- effICGI$Endpoint
effICGI$endpointcol3 <- effICGI$Endpoint

ggresponseexpdist(data = effICGI,
                  points_show = FALSE,
                  exposure_metrics = c("AUC"),
                  exposure_distribution = "linerranges",
                  color_fill = "endpointcol2",
                  model_type = "logistic",
                  fit_by_color_fill = TRUE,
                  mean_obs_byexptile_text_size = 0,
                  mean_obs_byexptile_group="endpointcol3",
                  facet_formula = Endpoint~expname,
                  N_byexptile_ypos = "none",
                  binlimits_text_size = 0
                )+
  ggplot2::facet_grid(expname~Endpoint,margin="Endpoint")

# Example 6 retrun a list and customize
plist <- ggresponseexpdist(data = effICGI |>
dplyr::filter(Endpoint=="ICGI"),
model_type = "logistic",
mean_obs_byexptile = TRUE,
N_byexptile_ypos = "none",
mean_obs_byexptile_text_size = 4,
binlimits_ypos = -Inf,
exposure_metric_split = "tertile",
exposure_metrics = c("AUC"),
return_list = TRUE)
byexptileinformation <- plist[[7]]
plotwithoutlabels <- plist[[9]]

#construct text label
byexptileinformation <- byexptileinformation %>%

```

```

dplyr::group_by(exptile,expname)%>%
dplyr::mutate(meanbin = mean(c(minexp,maxexp))) %>%
dplyr::mutate(label = ifelse(exptile!="Placebo",
                             paste0(exptile,"\n","[",round(minexp,0),"-",round(maxexp,0),"]",
                                      "\n",N,"\n",Ntot),
                             paste0(exptile,"\n","",
                                      "\n",N,"\n",Ntot)),
              x_pos = ifelse(exptile=="Placebo",-25,meanbin )
)

plotwihoutlabels +
  geom_text(data=byexptileinformation,size = 3,
            aes(x=x_pos ,label=label,y = 0.5),
            inherit.aes = FALSE,
            vjust= 1, hjust = 0.5)+
  geom_text(data=data.frame(
    label="exposure ntile\n[min-max]\nN responders\nN Total"),size = 3,
    x=Inf,y = 0.5,
    aes(label=label),inherit.aes = FALSE,
    vjust= 1, hjust = 1)+
  facet_wrap(~expname,ncol=2,scales = "free_x")

## End(Not run)

```

logistic_data

*Simulated Exposure Response Data***Description**

A dataset containing data suitable for logistic regression

Usage

```
logistic_data
```

Format

A data frame with 600 rows and 10 variables

STUDY Study identifier

ID Subject Identifier

DOSE Dose, in mg

GBDS Dose, in alternative salt

SEX Sex of the subject

AGE age of the subject, in years

WT weight of the subject, in kg

RACE Race of the subject

CRCL Creatinine clearance
BRLS RLS score
PRLS RLS score
AUC Area under the curve exposure
CMAx Maximun concentration exposure
ICGI response 0/1
ICGI7 response 1 to 7

Source

inspired from a real data submission

Examples

```
logistic_data
```

run_ggquicked	<i>Run the ggquicked application</i>
---------------	--------------------------------------

Description

Run the ggquicked application.

Usage

```
run_ggquicked(data = NULL, ...)
```

Arguments

<code>data</code>	The initial data.frame to load into the application.
<code>...</code>	Additional arguments for bookmarking

Examples

```
if (interactive()) {
  run_ggquicked()
}
```

sample_data*Simulated Pharmacokinetic Concentration Data*

Description

A dataset containing concentration-time data with the given dose and some subject characteristics to help in the app exploration.

Usage

```
sample_data
```

Format

A data frame with 600 rows and 10 variables

ID Subject Identifier, an integer from 1 to 150

Time Time of dose given or drug sample measured, in hours

Amt dose given at the corresponding Time, in milligrams

Conc drug concentrations in the plasma sample, in mg/L

Age age of the subject, in years

Weight weight of the subject, in kg

Gender Sex of the subject, a factor with Female and Male levels

Race Race of the subject, a factor with Asian, Black, Caucasian, Hispanic and Other levels

Dose dose group of the subject, in milligrams

AGECAT age category of the subject, a variable cutting Age into two values 0/1

Source

"sd_oral_richpk" from 'PKPDmisc' R package with an additional AGECAT variable

Examples

```
sample_data
```

stat_km	<i>Adds a Kaplan Meier Estimate of Survival</i>
---------	---

Description

Adds a Kaplan Meier Estimate of Survival

Usage

```
stat_km(
  mapping = NULL,
  data = NULL,
  geom = "km",
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
  trans = scales::identity_trans(),
  firstx = 0,
  firsty = 1,
  type = "kaplan-meier",
  start.time = 0,
  ...
)
```

Arguments

- | | |
|---------|---|
| mapping | Set of aesthetic mappings created by 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 | <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 ggplot().</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 fortify() 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 | <p>The geometric object to use to display the data for this layer. When using a <code>stat_*()</code> function to construct a layer, the <code>geom</code> argument can be used to override the default coupling between stats and geoms. The <code>geom</code> argument accepts the following:</p> <ul style="list-style-type: none"> • A <code>Geom</code> ggproto subclass, for example <code>GeomPoint</code>. • A string naming the geom. To give the geom as a string, strip the function name of the <code>geom_</code> prefix. For example, to use <code>geom_point()</code>, give the <code>geom</code> as <code>"point"</code>. |

	• For more information and other ways to specify the geom, see the layer geom documentation.
position	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The position argument accepts the following: • The result of calling a position function, such as <code>position_jitter()</code>. This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the <code>position_</code> prefix. For example, to use <code>position_jitter()</code>, give the position as "jitter". • For more information and other ways to specify the position, see the layer position documentation.
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. To include legend keys for all levels, even when no data exists, use TRUE. If NA, all levels are shown in legend, but unobserved levels are omitted.
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. annotation_borders() .
trans	Transformation to apply to the survival probabilities. Defaults to "identity". Other options include "event", "cumhaz", "cloglog", or define your own using trans_new .
firstx, firsty	the starting point for the survival curves. By default, the plot program obeys tradition by having the plot start at (0, 1).
type	an older argument that combined stype and ctype, now deprecated. Legal values were "kaplan-meier" which is equivalent to stype=1, ctype=1, "fleming-harrington" which is equivalent to stype=2, ctype=1, and "fh2" which is equivalent to stype=2, ctype=2.
start.time	numeric value specifying a time to start calculating survival information. The resulting curve is the survival conditional on surviving to start.time.
...	Other arguments passed to survfit.formula

Details

This stat is for computing the confidence intervals for the Kaplan-Meier survival estimate for right-censored data. It requires the aesthetic mapping `x` for the observation times and `status` which indicates the event status, 0=alive, 1=dead or 1/2 (2=death). Logical status is not supported.

Value

a data.frame with additional columns:

x	x in data
y	Kaplan-Meier Survival Estimate at x

Aesthetics

stat_km understands the following aesthetics (required aesthetics are in bold):

- **time** The survival times
- **status** The censoring indicator, see [Surv](#) for more information.
- **alpha**
- **color**
- **linetype**
- **size**

Examples

```
library(ggplot2)
sex <- rbinom(250, 1, .5)
df <- data.frame(time = exp(rnorm(250, mean = sex)), status = rbinom(250, 1, .75), sex = sex)
ggplot(df, aes(time = time, status = status, color = factor(sex))) +
  stat_km()

## Examples illustrating the options passed to survfit.formula

p1 <- ggplot(df, aes(time = time, status = status))
p1 + stat_km()
p1 + stat_km(trans = "cumhaz")
# for cloglog plots also log transform the time axis
p1 + stat_km(trans = "cloglog") + scale_x_log10()
p1 + stat_km(type = "fleming-harrington")
p1 + stat_km(start.time = 5)
```

stat_kmband

Adds confidence bands to a Kaplan Meier Estimate of Survival

Description

Adds confidence bands to a Kaplan Meier Estimate of Survival

Usage

```
stat_kmband(
  mapping = NULL,
  data = NULL,
  geom = "kmband",
  position = "identity",
  show.legend = NA,
  inherit.aes = TRUE,
  trans = "identity",
  firstx = 0,
```

```

    firsty = 1,
    type = "kaplan-meier",
    error = "greenwood",
    conf.type = "log",
    conf.lower = "usual",
    start.time = 0,
    conf.int = 0.95,
    ...
  )

```

Arguments

mapping	Set of aesthetic mappings created by 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. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).
geom	The geometric object to use to display the data for this layer. When using a <code>stat_*()</code> function to construct a layer, the <code>geom</code> argument can be used to override the default coupling between stats and geoms. The <code>geom</code> argument accepts the following: • A <code>Geom</code> ggproto subclass, for example <code>GeomPoint</code>. • A string naming the geom. To give the geom as a string, strip the function name of the <code>geom_</code> prefix. For example, to use <code>geom_point()</code>, give the geom as "point". • For more information and other ways to specify the geom, see the layer geom documentation.
position	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The <code>position</code> argument accepts the following: • The result of calling a position function, such as <code>position_jitter()</code>. This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the <code>position_</code> prefix. For example, to use <code>position_jitter()</code>, give the position as "jitter". • For more information and other ways to specify the position, see the layer position documentation.
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. It

	can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use TRUE. If NA, all levels are shown in legend, but unobserved levels are omitted.
<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. annotation_borders() .
<code>trans</code>	Transformation to apply to the survival probabilities. Defaults to "identity". Other options include "event", "cumhaz", "cloglog", or define your own using scales::trans_new() .
<code>firstx, firsty</code>	the starting point for the survival curves. By default, the plot program obeys tradition by having the plot start at (0,1).
<code>type</code>	an older argument that combined <code>stype</code> and <code>ctype</code> , now deprecated. Legal values were "kaplan-meier" which is equivalent to <code>stype=1</code> , <code>ctype=1</code> , "fleming-harrington" which is equivalent to <code>stype=2</code> , <code>ctype=1</code> , and "fh2" which is equivalent to <code>stype=2</code> , <code>ctype=2</code> .
<code>error</code>	either the string "greenwood" for the Greenwood formula or "tsiatis" for the Tsiatis formula, (only the first character is necessary). The default is "greenwood".
<code>conf.type</code>	One of "none", "plain", "log" (the default), "log-log" or "logit".
<code>conf.lower</code>	a character string to specify modified lower limits to the curve, the upper limit remains unchanged. Possible values are "usual" (unmodified), "peto", and "modified". The modified lower limit is based on an "effective n" argument. The confidence bands will agree with the usual calculation at each death time, but unlike the usual bands the confidence interval becomes wider at each censored observation. The extra width is obtained by multiplying the usual variance by a factor m/n , where n is the number currently at risk and m is the number at risk at the last death time. (The bands thus agree with the un-modified bands at each death time.) This is especially useful for survival curves with a long flat tail. The Peto lower limit is based on the same "effective n" argument as the modified limit, but also replaces the usual Greenwood variance term with a simple approximation. It is known to be conservative.
<code>start.time</code>	numeric value specifying a time to start calculating survival information. The resulting curve is the survival conditional on surviving to <code>start.time</code> .
<code>conf.int</code>	the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.
<code>...</code>	Other arguments passed to survfit.formula

Details

This stat is for computing the confidence intervals for the Kaplan-Meier survival estimate for right-censored data. It requires the aesthetic mapping `x` for the observation times and `status` which indicates the event status, 0=alive, 1=dead or 1/2 (2=death). Logical status is not supported.

Value

a data.frame with additional columns:

x	x in data
ymin	Lower confidence limit of KM curve
ymax	Upper confidence limit of KM curve

Aesthetics

stat_kmband understands the following aesthetics (required aesthetics are in bold):

- time The survival times
- status The censoring indicator, see [Surv](#) for more information.
- alpha
- color
- linetype
- linewidth

Examples

```
library(ggplot2)
sex <- rbinom(250, 1, .5)
df <- data.frame(time = exp(rnorm(250, mean = sex)), status = rbinom(250, 1, .75), sex = sex)
ggplot(df, aes(time = time, status = status, color = factor(sex))) +
  stat_km()

## Examples illustrating the options passed to survfit.formula

p1 <- ggplot(df, aes(time = time, status = status))
p1 + stat_km() + stat_kmband(conf.int = .99)
p1 + stat_kmband(error = "greenwood", fill="red", alpha=0.2) +
  stat_kmband(error = "tsiatis", fill="blue", alpha=0.2)+ stat_km()
p1 + stat_km() + stat_kmband(conf.type = "log-log")+ stat_kmband(conf.type = "log")
```

stat_kmticks

Adds tick marks to a Kaplan Meier Estimate of Survival

Description

Adds tick marks to a Kaplan Meier Estimate of Survival

Usage

```
stat_kmticks(
  mapping = NULL,
  data = NULL,
  geom = "kmticks",
  position = "identity",
  show.legend = NA,
```

```

    inherit.aes = TRUE,
    trans,
    ...
  )

```

Arguments

mapping	Set of aesthetic mappings created by 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. A function can be created from a formula (e.g. <code>~ head(.x, 10)</code>).
geom	The geometric object to use to display the data for this layer. When using a <code>stat_*()</code> function to construct a layer, the <code>geom</code> argument can be used to override the default coupling between stats and geoms. The <code>geom</code> argument accepts the following: • A <code>Geom</code> ggproto subclass, for example <code>GeomPoint</code>. • A string naming the geom. To give the geom as a string, strip the function name of the <code>geom_</code> prefix. For example, to use <code>geom_point()</code>, give the geom as "point". • For more information and other ways to specify the geom, see the layer geom documentation.
position	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The <code>position</code> argument accepts the following: • The result of calling a position function, such as <code>position_jitter()</code>. This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the <code>position_</code> prefix. For example, to use <code>position_jitter()</code>, give the position as "jitter". • For more information and other ways to specify the position, see the layer position documentation.
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. It can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use <code>TRUE</code> . If <code>NA</code> , all levels are shown in legend, but unobserved levels are omitted.
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. annotation_borders() .

trans	Transformation to apply to the survival probabilities. Defaults to "identity". Other options include "event", "cumhaz", "cloglog", or define your own using trans_new
...	Other arguments passed to survfit.formula

Details

This stat is for computing the tick marks for a Kaplan-Meier survival estimate for right-censored data. The tick marks will appear at each censoring time which is also not a death time, which is the default for [plot.survfit](#). It requires the aesthetic mapping `x` for the observation times and `status` which indicates the event status, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death).

Value

a data.frame with additional columns:

x	x in data
y	Kaplan-Meier Survival Estimate at x

Aesthetics

stat_kmticks understands the following aesthetics (required aesthetics are in bold):

- time The survival times
- status The censoring indicator, see [Surv](#) for more information.
- alpha
- color
- linetype
- size

See Also

[stat_km](#); [stat_kmband](#)

Examples

```
library(ggplot2)
sex <- rbinom(250, 1, .5)
df <- data.frame(time = exp(rnorm(250, mean = sex)), status = rbinom(250, 1, .75), sex = sex)
ggplot(df, aes(time = time, status = status, color = factor(sex))) +
  stat_km() + stat_kmticks()
```

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