# Package 'ggupset'

June 24, 2024

valle 2 1, 202 1
Type Package
Title Combination Matrix Axis for 'ggplot2' to Create 'UpSet' Plots
Version 0.4.0
<pre>URL https://github.com/const-ae/ggupset</pre>
<pre>BugReports https://github.com/const-ae/ggupset/issues</pre>
<b>Description</b> Replace the standard x-axis in 'ggplots' with a combination matrix to visualize complex set overlaps. 'UpSet' has introduced a new way to visualize the overlap of sets as an alternative to Venn diagrams.  This package provides a simple way to produce such plots using 'ggplot2'.  In addition it can convert any categorical axis into a combination matrix axis.
License GPL-3
Encoding UTF-8
LazyData true
RoxygenNote 7.3.1
<b>Depends</b> R (>= $2.10$ )
Suggests testthat
<b>Imports</b> ggplot2 (>= 3.3.0), gtable, grid, tibble, rlang, scales
NeedsCompilation no
Author Constantin Ahlmann-Eltze [aut, cre] ( <a href="https://orcid.org/0000-0002-3762-068X">https://orcid.org/0000-0002-3762-068X</a> )
Maintainer Constantin Ahlmann-Eltze <artjom31415@googlemail.com></artjom31415@googlemail.com>
Repository CRAN
<b>Date/Publication</b> 2024-06-24 10:10:04 UTC
Contents
axis_combmatrix

2 axis\_combmatrix

Index		11
	tidy_movies	9
	theme_combmatrix	7
	scale_x_upset	
	scale_x_mergelist	5
	gene_pathway_membership	

 $axis\_combmatrix$ 

Convert delimited text labels into a combination matrix axis

# Description

The function splits the text based on the sep argument and views each occurring element as potential set.

# Usage

```
axis_combmatrix(
  sep = "[^[:alnum:]]+",
  levels = NULL,
  override_plotting_function = NULL,
  xlim = NULL,
  ylim = NULL,
  expand = TRUE,
  clip = "on",
  ytrans = "identity"
)
```

# Arguments

sep	The separator that is used to split the string labels. Can be a regex. Default: $"[^{[:alnum:]}+"]$		
levels	The selection of string elements that are displayed in the combination matrix axis. Default: NULL, which means simply all elements in the text labels are used		
override_plotting_function			
	to achieve maximum flexibility, you can provide a custom plotting function. For more information, see details. Default: NULL		
xlim, ylim	The limits fort the x and y axes		
expand	Boolean with the same effect as in ggplot2::coord_cartesian(). Default: TRUE		
clip	String with the same effect as in ggplot2::coord_cartesian(). Default: "on"		
ytrans	transformers for y axis. For more information see ggplot2::coord_trans(). Default: "identity"		

axis\_combmatrix 3

#### **Details**

Technically the function appends a coord system to the ggplot object. To maintain compatibility additional arguments like ytrans, ylim, and clip are forwarded to coord\_trans().

*Note:* make sure that the argument to the 'x' aesthetic is character vector that contains the sep sequence. The only exception is if axis\_combmatrix() is combined with a scale\_x\_mergelist(). This pattern works because in the first step scale\_x\_mergelist() turns a list argument to 'x' into a character vector that axis\_combmatrix() can work with.

For maximum flexibility, you can use the 'override\_plotting\_function' parameter which returns a ggplot and is called with a tibble with one entry per point of the combination matrix. Specifically, it contains

labels the collapsed label string

single label an ordered factor with the labels on the left of the plot

id consecutive numbering of the points

labels\_split a list column that contains the splitted labels

at the x-position of the point

**observed** boolean to indicate if this element is active in the intersection

index the row of the point

See the examples how the override\_plotting\_function looks that recreates the default combination matrix

# Examples

```
library(ggplot2)
 mtcars$combined <- paste0("Cyl: ", mtcars$cyl, "_Gears: ", mtcars$gear)</pre>
 head(mtcars)
 ggplot(mtcars, aes(x=combined)) +
   geom_bar() +
    axis_combmatrix(sep = "_")
# Example of 'override_plotting_function'
ggplot(mtcars, aes(x=combined)) +
 geom_bar() +
   axis_combmatrix(sep = "_", override_plotting_function = function(df){
      ggplot(df, aes(x= at, y= single_label)) +
        geom_rect(aes(fill= index %% 2 == 0), ymin=df$index-0.5,
                  ymax=df$index+0.5, xmin=0, xmax=1) +
        geom_point(aes(color= observed), size = 3) +
        geom_line(data= function(dat) dat[dat$observed, ,drop=FALSE],
                 aes(group = labels), size= 1.2) +
        ylab("") + xlab("") +
        scale_x_continuous(limits = c(0, 1), expand = c(0, 0)) +
        scale_fill_manual(values= c(`TRUE` = "white", `FALSE` = "#F7F7F7")) +
        scale_color_manual(values= c(`TRUE` = "black", `FALSE` = "#E0E0E0")) +
        guides(color="none", fill="none") +
        theme(
```

```
panel.background = element_blank(),
    axis.text.x = element_blank(),
    axis.ticks.y = element_blank(),
    axis.ticks.length = unit(0, "pt"),
    axis.title.y = element_blank(),
    axis.title.x = element_blank(),
    axis.line = element_blank(),
    panel.border = element_blank()
)
})
```

df\_complex\_conditions A fictional biological dataset with a complex experimental design

#### Description

A fictional biological dataset with a complex experimental design

#### Usage

```
df_complex_conditions
```

#### Format

a data frame with 360 rows and 4 variables

- KO. Boolean value if the sample had a knock out.
- DrugA. character vector with "Yes" and "No" elements indicating if the sample was treated with drug A.
- Timepoint. Numeric vector with elements 8, 24, and 48 indicating the time of measurement since the beginning of the experiment.
- response. Numeric vector with the response of the sample to the treatment conditions. Could for example be the concentration of a metabolite.

#### **Examples**

```
dim(df_complex_conditions)
head(df_complex_conditions)
```

```
gene_pathway_membership
```

A fictional dataset describing which genes belong to certain pathways

#### **Description**

A fictional dataset describing which genes belong to certain pathways

#### Usage

```
gene_pathway_membership
```

#### **Format**

a matrix with 6 rows and 37 columns. Each row is one pathway, with its name given as 'rownames' and each column is a gene. The values in the matrix are Boolean indicators if the gene is a member of the pathway.

#### **Examples**

```
dim(gene_pathway_membership)
gene_pathway_membership[, 1:15]
```

scale\_x\_mergelist

Merge list columns into character vectors

# Description

The function handles list columns by collapsing them into delimited strings using the sep argument. This is useful to show sets and in combination with the axis\_combmatrix() function.

#### Usage

```
scale_x_mergelist(sep = "-", ..., position = "bottom")
```

#### **Arguments**

sep	String the is used to delimit the elements in each list entry. Default: "-".
	additional arguments that are passed on to ggplot2::scale_x_discrete
position	either "top" or "bottom" to specify where the x axis drawn. Default: "bottom"

#### See Also

```
discrete_scale
```

6 scale\_x\_upset

#### **Examples**

```
library(ggplot2)
ggplot(tidy_movies[1:100, ], aes(x=Genres)) +
  geom_bar() +
  scale_x_mergelist() +
  theme(axis.text.x = element_text(angle = 90, hjust=1, vjust = 0.5))

ggplot(tidy_movies[1:100, ], aes(x=Genres)) +
  geom_bar() +
  scale_x_mergelist(sep = " & ", name = "Merged Movie Genres", position = "top") +
  theme(axis.text.x = element_text(angle = 90, hjust=0, vjust = 0.5))
```

scale\_x\_upset

Scale to make UpSet plots

### Description

This function takes a list column and turns it into a combination matrix axis. It internally wraps the call to scale\_x\_mergelist() and axis\_combmatrix() and makes sure that the elements are sorted by size.

#### Usage

```
scale_x_upset(
  order_by = c("freq", "degree"),
  n_sets = Inf,
  n_intersections = Inf,
  sets = NULL,
  intersections = NULL,
  reverse = FALSE,
  ytrans = "identity",
  ...,
  position = "bottom"
)
```

#### Arguments

```
order_by either "freq" or "degree". Default: "freq"

n_sets maximum number of sets that are displayed. Default: Inf

n_intersections

maximum number of intersections that are displayed. Default: Inf

sets character vector that specifies which sets are displayed

intersections a list of character vectors that specifies which intersections are displayed

reverse boolean if the order of the intersections is reversed. Default: FALSE
```

theme\_combmatrix 7

```
ytrans transformers for y axis. For more information see axis_combmatrix(). Default: "identity"
... additional parameters for ggplot2::discrete_scale()
position either "top" or "bottom" to specify where the combination matrix is drawn. Default: "bottom"
```

#### **Examples**

theme\_combmatrix

Theme for the combination matrix

#### Description

This theme sets the default styling for the combination matrix axis by extending the default ggplot2 theme().

#### Usage

```
theme_combmatrix(
  combmatrix.label.make_space = TRUE,
  combmatrix.label.width = NULL,
  combmatrix.label.height = NULL,
  combmatrix.label.extra_spacing = 3,
  combmatrix.label.total_extra_spacing = unit(10, "pt"),
  combmatrix.label.text = NULL,
  combmatrix.panel.margin = unit(c(1.5, 1.5), "pt"),
  combmatrix.panel.striped_background = TRUE,
 combmatrix.panel.striped_background.color.one = "white",
  combmatrix.panel.striped_background.color.two = "#F7F7F7",
  combmatrix.panel.point.size = 3,
  combmatrix.panel.line.size = 1.2,
  combmatrix.panel.line.color = "black",
  combmatrix.panel.point.color.fill = "black",
  combmatrix.panel.point.color.empty = "#E0E0E0",
```

8 theme\_combmatrix

```
) ...
```

#### **Arguments**

combmatrix.label.make\_space

Boolean indicator if the y-axis label is moved so far to the left to make enough space for the combination matrix labels. Default: TRUE

combmatrix.label.width

A unit that specifies how much space to make for the labels of the combination matrix. Default: NULL, which means the width of the label text is used

combmatrix.label.height

A unit that specifies how high the combination matrix should be. Default: NULL, which means that the height of the label text + combmatrix.label.total\_extra\_spacing + #rows \* combmatrix.label.extra\_spacing is used. Default: 3

combmatrix.label.extra\_spacing

A single number for the additional height per row. Default: unit(10, "pt")

combmatrix.label.total\_extra\_spacing

A unit that specifies the total offset for the height of the combination matrix

combmatrix.label.text

A element\_text() to style the label text of the combination matrix. Default NULL, which means the style of axis.text.y is used.

combmatrix.panel.margin

A two element unit vector to specify top and bottom margin around the combination matrix. Default: unit(c(1.5, 1.5), "pt")

combmatrix.panel.striped\_background

Boolean to indicate if the background of the plot is striped. Default: TRUE

combmatrix.panel.striped\_background.color.one

Color of the first kind of stripes. Default: "white"

 $\verb|combmatrix.panel.striped_background.color.two|\\$ 

Color of the second kind of stripes. Default: "#F7F7F7"

combmatrix.panel.point.size

Number to specify the size of the points in the combination matrix. Default: 3

combmatrix.panel.line.size

Number to specify the size of the lines connecting the points. Default: 1.2

combmatrix.panel.line.color

Color of the lines connecting the points. Default: "black"

combmatrix.panel.point.color.fill

Color of the filled points. Default: "black"

combmatrix.panel.point.color.empty

Color of the empty points. Default: "#E0E0E0"

.. additional arguments that are passed to theme()

tidy\_movies 9

#### **Examples**

tidy\_movies

Tidy version of the movies dataset from the ggplot2 package

#### **Description**

The original ggplot2movies::movies dataset has 7 columns that contain indicators if a movies belongs to a certain genre. In this version the 7 columns are collapsed to a single list column to create a tidy dataset. It also has information on only 5,000 movies to reduce the size of the dataset. Furthermore each star rating is in its on row.

#### Usage

tidy\_movies

#### **Format**

a data frame with 50,000 rows and 10 columns

- title. The title of the movie.
- year. Year of release.
- budget. Total budget (if known) in US dollars.
- length. Length in minutes.
- rating. Average IMDB user rating.
- votes. Number of IMDB user who rated this movie.
- mpaa. MPAA rating
- Genres. List column with all genres the movie belongs to
- stars, percent\_rating. The number of stars and the corresponding percentage of people rating the movie with this many stars.

10 tidy\_movies

# Examples

dim(tidy\_movies)
head(tidy\_movies)

# **Index**

```
* datasets
    df_complex_conditions, 4
    gene_pathway_membership, 5
    tidy_movies, 9

axis_combmatrix, 2

df_complex_conditions, 4
discrete_scale, 5
gene_pathway_membership, 5

scale_x_mergelist, 5
scale_x_upset, 6

theme_combmatrix, 7
tidy_movies, 9
```