Package ‘ggparallel’

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Type Package

Title Variations of Parallel Coordinate Plots for Categorical Data

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Description R package for creating hammock plots, parallel sets, and common angle plots using the ggplot2 framework.

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Depends R (>= 2.10.0), ggplot2 (>= 0.9.2), reshape2, plyr

Suggests RColorBrewer

Collate 'help.R' 'genes.R' 'parallel.R'

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NeedsCompilation no

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genes

Data linking genes and pathways.

Description

Table knownGene from track UCSC Genes was downloaded from the UCSC table browser for the human genome assembly (hg18, May 2006) and filtered for a selection of pathways associated with human metabolism was obtained from KEGG PATHWAY database. Bioconductor package KEGG.db was used to provide mappings between gene and pathway identifiers.

Author(s)

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References


Marc Carlson, Seth Falcon, Herve Pages and Nianhua Li (). KEGG.db: A set of annotation maps for KEGG. R package version 2.6.1.


Examples

data(genes)
require(RColorBrewer)
genesis$chrom <- factor(genes$chrom, levels=c(paste("chr", 1:22, sep=""), "chrX", "chrY"))
ggparallel(list("path", "chrom"), text.offset=c(0.03, 0,-0.03), data = genes, width=0.1, order=c(1,0), angle=0, factorlevels = c(sapply(unique(genes$chrom), as.character),
unique(genes$path)))) +
scale_fill_manual(values = c( brewer.pal("YlOrRd", n = 9), rep("grey80", 24)), guide="none") +
scale_color_manual(values = c( brewer.pal("YlOrRd", n = 9), rep("grey80", 24)), guide="none") +
coord_flip()
Description

`ggparallel` implements and combines different types of parallel coordinate plots for categorical data: hammock plots, parallel sets plots, common angle plots, and common angle plots with a hammock-like adjustment for line widths.

Usage

```r
ggparallel(vars = list(), data, weight = NULL,
  method = "angle", alpha = 0.5, width = 0.25, order = 1,
  ratio = 0.2, asp = NULL, label = TRUE, text.angle = 90,
  text.offset = NULL, color = "white", ...)
```

Arguments

- **vars**: list of variable names to be included in the plotting. order of the variables is preserved in the display.
- **data**: data frame
- **weight**: weighting variable - use character string
- **method**: plotting method to use - one of angle, adj.angle, parset, or hammock, for a hammock plot the aspect ratio needs to be fixed.
- **alpha**: level of alpha blending for the fill color in ribbons, value has to be between 0 and 1, defaults to 0.5.
- **width**: width of variables
- **order**: flag variable with three levels -1, 0, 1 for levels in decreasing order, levels in increasing order and levels unchanged. This variable can be either a scalar or a vector
- **ratio**: used for methods with angle adjustments (method = 'hammock', 'adj.angle'): specifies the height (width for horizontal displays) of the widest line as ratio of the overall display height (width for horizontal displays).
- **label**: binary variable (vector), whether labels should be shown.
- **text.angle**: numeric value in degrees, by which text for labelling is rotated. Ignored if label = FALSE
- **text.offset**: (vector) of values for offset the labels
- **asp**: aspect ratio of the plot - it will be set to a default of 1 in the case of hammock plots.
- **color**: value used for color of the boxes.
- **...**: passed on directly to all of the ggplot2 commands
Details

Parallel sets have been suggested by Kosara et al (2006) as a visualization technique to incorporate categorical variables into a parallel coordinate plot (Wegman, Inselberg reference). However, perceptual problems with interpreting line widths, make this chart type a victim of wrong conclusions. The hammock display (Schonlau 2003) and the common angle plots are two approaches at fixing this problem: in Hammock plots the linewidth is adjusted by a factor countering the strength of the illusion, in the common angle plot all lines are adjusted to show the same angle - making line widths again comparable across ribbons. Additionally, we can also adjust ribbons in the common angle display for the angle, to make them appear having the same width (or height) across the display. We refer to this method as adj.angle.

Value

returns a ggplot2 object that can be plotted directly or used as base layer for additional modifications.

References


Examples

data(mtcars)
ggparallel(list("gear", "cyl"), data=mtcars)
ggparallel(list("gear", "cyl"), data=mtcars, method="hammock")

## combination of common angle plot and hammock adjustment:
ggparallel(list("gear", "cyl"), data=mtcars, method="adj.angle")

## compare with method='parset'
ggparallel(list("gear", "cyl"), data=mtcars, method='parset')

## flip plot and rotate text
ggparallel(list("gear", "cyl"), data=mtcars, text.angle=0) + coord_flip()

## change colour scheme
ggparallel(list("gear", "cyl"), data=mtcars, text.angle=0) + coord_flip() +
  scale_fill_brewer(palette="Set1") +
  scale_colour_brewer(palette="Set1")

## example with more than two variables:
titanic <- as.data.frame(Titanic)
ggparallel(names(titanic)[c(1,4,2,1)], order=0, titanic, weight="Freq") +
  scale_fill_brewer(palette="Paired", guide="none") +
  scale_colour_brewer(palette="Paired", guide="none")
### hammock plot with same width lines

```r
ggparallel(names(titanic)[c(1,2,3)], titanic, weight=1, asp=0.5, method="hammock", ratio=0.2, order=c(0,0)) + theme(legend.position="none") + scale_fill_brewer(palette="Paired") + scale_colour_brewer(palette="Paired")
```

### hammock plot with line widths adjusted by frequency

```r
ggparallel(names(titanic)[c(1,2,3)], titanic, weight="Freq", asp=0.5, method="hammock", order=c(0,0)) + theme(legend.position="none")
```

## Not run:

### biological examples: genes and pathways

```r
data(genes)
genesc$chrom <- factor(genes$chrom, levels = c(paste("chr", 1:22, sep=""), "chrX", "chrY"))
ggparallel(list("path", "chrom"), text.offset = c(0.03, 0,-0.03), data = genes, width = 0.1, order = c(1,0), text.angle = 45, factorlevels = c(sapply(unique(genes$chrom), as.character), unique(genes$path))) +
  scale_fill_manual(values = c(brewer.pal("YlOrRd", n = 9), rep("grey80", 24)), guide="none") +
  scale_colour_manual(values = c(brewer.pal("YlOrRd", n = 9), rep("grey80", 24)), guide="none") +
  coord_flip()
```

## End(Not run)

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**package-ggparallel**  
*A package for creating parallel coordinates for categorical data*

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### Description

The main function `ggparallel` implements three types of parallel coordinate plots for categorical data: hammock plots, parallel sets plots, and common angle plots.
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