

Package ‘PantaRhei’

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Title Plots Sankey Diagrams

Version 0.1.2

Description Sankey diagrams are a powerfull and visually attractive way to visualize the flow of conservative substances through a system. They typically consists of a network of nodes, and fluxes between them, where the total balance in each internal node is 0, i.e. input equals output. Sankey diagrams are typically used to display energy systems, material flow accounts etc. Unlike so-called alluvial plots, Sankey diagrams also allow for cyclic flows: flows originating from a single node can, either direct or indirect, contribute to the input of that same node. This package, named after the Greek aphorism Panta Rhei (everything flows), provides functions to create publication-quality diagrams, using data in tables (or spread sheets) and a simple syntax.

Depends R (>= 3.5.0)

License EUPL

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Imports grid, grDevices, utils

Suggests knitr, rmarkdown, tibble

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

check_balance	2
check_consistency	3

MFA	3
PantaRhei	4
parse_flows	4
parse_nodes	5
parse_palette	5
sankey	6
strformat	8
Index	9

check_balance	<i>Checks the mass balance of the flows involved</i>
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Description

For each substance involved, the balance per (internal) node is inspected. If outflow exceed inflow, or vice versa, a message is printed, and the function returns FALSE.

Usage

```
check_balance(nodes, flows, tolerance = 0.01)
```

Arguments

nodes	data.frame containing the nodes definition
flows	data.frame containing the flows definition
tolerance	numeric specifying a tolerance. Default is 0.01 (1%)

Value

TRUE if balanced, FALSE if not.

Examples

```
nodes <- data.frame(ID=c("A","B","C"), x=1:3, y=1:3, dir=c("right","right","stock"))
flows <- data.frame(from=c("A","B"), to=c("B","C"), quantity=c(10,10))
check_balance(nodes,flows)
```

check_consistency	<i>Check the consistence of the nodes, flows and palette data.frames</i>
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Description

Check the consistence of the nodes, flows and palette data.frames

Usage

```
check_consistency(nodes, flows, palette = NULL)
```

Arguments

nodes	data.frame containing the nodes definition
flows	data.frame containing the flows definition
palette	data.frame containing the palette definition

Value

TRUE if all checks are passed; FALSE otherwise.

Examples

```
nodes <- data.frame(ID=c("A","B"), x=1:2, y=0)
flows <- data.frame(from="A", to="B", quantity=10)
check_consistency(nodes, flows)
```

MFA	<i>Material Flow Account sample data</i>
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Description

Dataset containing sample material flow account data, formatted for use within 'PantaRhei'

Usage

```
MFA
```

Format

A list with three data frames:

- nodes
- flows
- colors

PantaRhei	<i>PantaRhei: Publication-quality Sankey diagrams</i>
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Description

Please read the [user manual](#) for more information.

parse_flows	<i>Parse the information from a 'flows' definition table.</i>
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Description

This function checks the content of a flows definition, and appends some missing columns. It is mainly used internally, but can be invoked by the users to see what it does.

Usage

```
parse_flows(flows, verbose = FALSE)
```

Arguments

flows	data.frame containing the nodes definition
verbose	logical: print some information?

Value

modified flows data.frame

Examples

```
Q0 <- data.frame(from="A", to="B", qty=10) # Note 'qty' as alias for quantity
str(Q0)
Q1 <- parse_flows(Q0)
str(Q1)
```

parse_nodes	<i>Parse the information from a 'nodes' definition table.</i>
-------------	---

Description

This function checks the content of a nodes definition, and appends some missing columns. It is mainly used internally, but can be invoked by the uses to see what it does.

Usage

```
parse_nodes(nodes, verbose = FALSE)
```

Arguments

nodes	data.frame containing the nodes definition
verbose	logical: print some information?

Value

modified nodes data.frame

Examples

```
n0 <- data.frame(ID=c("A","B"), x=1:2, y=0)
str(n0)
n1 <- parse_nodes(n0)
str(n1)
```

parse_palette	<i>Parse the information from a 'palette' definition table.</i>
---------------	---

Description

This function checks the content of a palette definition, and appends some missing columns. It is mainly used internally, but can be invoked by the uses to see what it does.

Usage

```
parse_palette(palette, verbose = TRUE)
```

Arguments

palette	data.frame containing the palette definition
verbose	logical: print some information?

Value

modified palette data.frame

Examples

```
p0 <- data.frame(substance="any", color="red")
str(p0)
p1 <- parse_palette(p0)
str(p1) # Should be the same!
```

sankey

Plots a Sankey diagram

Description

Plots a Sankey diagram

Usage

```
sankey(
  nodes,
  flows,
  palette,
  node_style = list(),
  title = NULL,
  legend = FALSE,
  page_margin = 0.1,
  max_width = 0.2,
  rmin = 0.2,
  copyright = NULL,
  grill = NULL,
  verbose = FALSE
)
```

Arguments

nodes	data.frame, containing the nodes definition
flows	data.frame, containing the nodes definition
palette	data.frame, containing the nodes definition
node_style	list: containing node style specifiers: type Character: Node type; possible values are "box", "bar" and "arrow". length numeric: node length, as fraction plot size (default: 0.1). gp an object of class gpar, typically the output from a call to the function gpar(). This is basically a list of graphical parameter settings, describing the colors etc of the node.

	label_pos character: label position. values: auto, above, below, left, right, none.
	label_anchor character: label position (overrides label_pos). Values are NW, N, NE, W, E, SW, S, SE.
	label_align character: label alignment with respect to label_anchor. Values are NW, N, etc.
	label_gp an object of class gpar, describing the font and color of the label text.
	mag_pos similar to label_pos, but controls location of the node magnitude. Value inside plots the node magnitude inside the node. Value label plots the node magnitude beneath the node label.
	mag_anchor similar to label_anchor.
	mag_align similar to label_align.
	mag_gp similar to label_gp.
	mag_fmt character: format string for the node magnitude. default: "%.1f". see ?sprintf for more information.
title	character: plot title. use sprintf() to specify formatting.
legend	logical or gpar: Specifies the plotting of a legend. valid values are NULL (default; no legend), TRUE (plot a legend using standard text size and color), or the output of a call to gpar(), to control legend text size and color.
page_margin	numeric: Page margin. Either a scalar, an (x,y) vector or an (left,bot,rt,top) vector
max_width	numeric: Maximum width of the flow bundles, in fraction of the plot size
rmin	numeric: Minimum radius for flow path bends (as fraction of the diagram's units)
copyright	character: optional copyright statement?
grill	logical: Plot a coordinate grill?
verbose	logical: print some diagnostic messages?

Value

The modified nodes data.frame

Examples

```

nodes <- data.frame(ID=c("A","B"), x=1:2, y=0)
flows <- data.frame(from="A", to="B", quantity=10, substance="stuff")
sankey(nodes, flows)

colors <- data.frame(substance="stuff", color="blue")
sankey(nodes, flows, colors)

sankey(nodes, flows, legend=TRUE) # Plots default legend
sankey(nodes, flows, legend=grid::gpar(fontsize=18, ncols=2)) # Large fonts; 2 columns

```

`strformat`*Format a string*

Description

This function adds formatting information to a character string by storing this information as the character string's attributes. Run the example to see how it works.

Usage

```
strformat(s, ...)
```

Arguments

<code>s</code>	character string to be formatted
<code>...</code>	formatting specifiers to be forwarded to <code>gpar()</code>

Details

All formatting specifiers work as if `gpar()` would be called. (It is, behind the screen.)

Value

formatted string

Examples

```
s <- strformat("Hello, World", fontsize=18, col="red")
str(s) # show object structure
```


Index

* datasets

MFA, [3](#)

check_balance, [2](#)

check_consistency, [3](#)

MFA, [3](#)

PantaRhei, [4](#)

parse_flows, [4](#)

parse_nodes, [5](#)

parse_palette, [5](#)

sankey, [6](#)

strformat, [8](#)